PRECISION HEALTH

PRECISYA

HEALTH

PANEL

ULTIMATE SPORTS PANEL

ENGLISH VERSION

Patient data

Name	Sample
Age	
Gender	F
Test date	
Report date	12/09/2025
Prescriber	
Health insurance	

What does testing make possible?

Based on personalized and comparative gene studies, Precysia looks for genetic alterations among the billions of information a patient's DNA carries, and in-depth information on each individual's predispositions to developing disease, as well as recommendations and specific information for their correction and prevention, whenever such information is available.

Technical Manager: Dr. Eyal Cohen, MD

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WARNING

The values of the results of genetic tests are not diagnostic, but show trends that are influenced by physiological, pathological conditions, use of medications and other personal conditions of the examinee.
Only your clinician is able to correctly interpret these results and to prescribe the most appropriate treatment for you, and the company is not responsible for any treatment based on the results.
If necessary, our science team is available to discuss the results with the attending clinician upon request.

The genetic test

The genetic examination is the most current and advanced technological leap in the health area, mainly for the clinical area because DNA is the true **Instruction Manual** of the individual.

In DNA, all individual needs, susceptibilities and psycho-behavioral, structural, functional and reaction characteristics that an individual has and will have throughout his life are determined with high precision.

The genetic examination is within the modern disruptive concept of Genetic Identity where the individual is able to have all the precise and personalized information necessary to, from them, know what to do to achieve more Health, Vitality, Beauty and Longevity.

The current level of our technology, allows the high level of precision and reliability of our tests in the fundamental aspects for a genetic test.

In the WGS (total genome sequencing) extraction that provides 80 million SNPs (polymorphisms) - in the market in general we have up to 800 SNPs - and in the reading and analysis of the extraction done by our own AI system (Artificial Intelligence) , through a complex algorithm, which considers, among other factors, the number, presence and magnitude of the SNPs related to the analyzed condition.

How to interpret the exam:

We adopted a color bar divided into 5 levels of magnitude.

Each genetic condition (whether characteristic, need, benefit or susceptibility) ranges from a low to a very high magnitude resulting from the exam.

These result levels are calculated using a complex algorithm, developed internally, which considers, among other factors, the quantity, presence and magnitude of the SNPs related to the condition.

The result will then appear as follows:

FIRST PART

The first part interprets the magnitudes of each condition, using an algorithm that considers the following aspects:

- Presence or Absence of Polymorphism
- Amount of Polymorphisms present for the condition
- Magnitude of each Polymorphism
- Validation of the Scientific Base

Due to the decimal places of the magnitudes of the results that must be strictly taken into account in the results, we present 5 divisions, which should be interpreted as follows:

🔵 indicates that the result shown is LOW

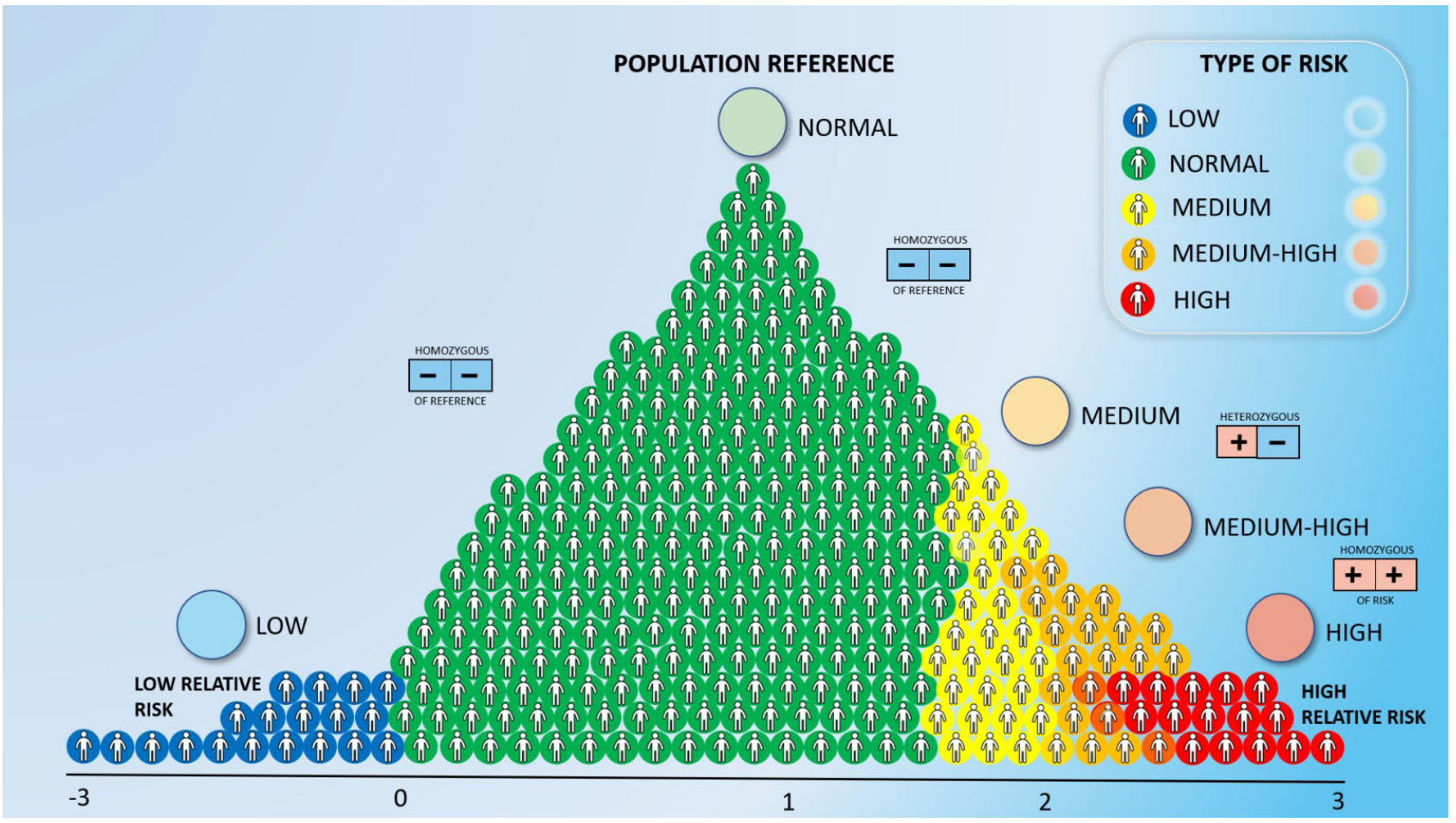
🟢 indicates that the result shown is NORMAL

🟡 indicates that the result shown is MEDIUM-NORMAL

🟠 indicates that the result shown is MEDIUM-HIGH

🔴 indicates that the result shown is HIGH

⚪ indicates that it was not possible to calculate a result

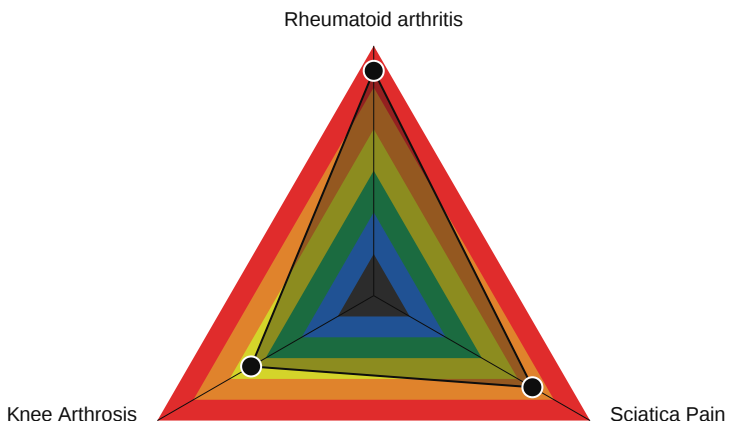


Important notes about the results:

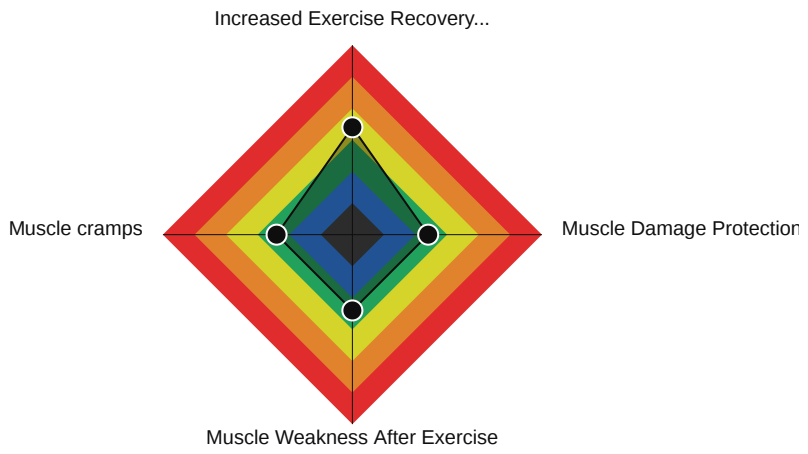
- LOW refers to a predisposition to lack or low susceptibility.
- NORMAL often refers to the majority of the population, in which the incidence of Needs or Susceptibilities is considered normal.
- MEDIUM-NORMAL refers to medium susceptibility. Usually heterozygous at-risk individuals.
- MEDIUM-HIGH refers to high susceptibility. Usually individuals with homozygous or heterozygous alleles at risk.
- HIGH refers to high susceptibility. Usually individuals with homozygous risk alleles.
- If there is no filled sphere in the result, it indicates that the polymorphism (or polymorphisms) related to the specific condition were not detected, or that, as of the date of the report, there are no solid scientific evidences that justify a result.

MOST RELEVANT CONDITIONS BY CATEGORY

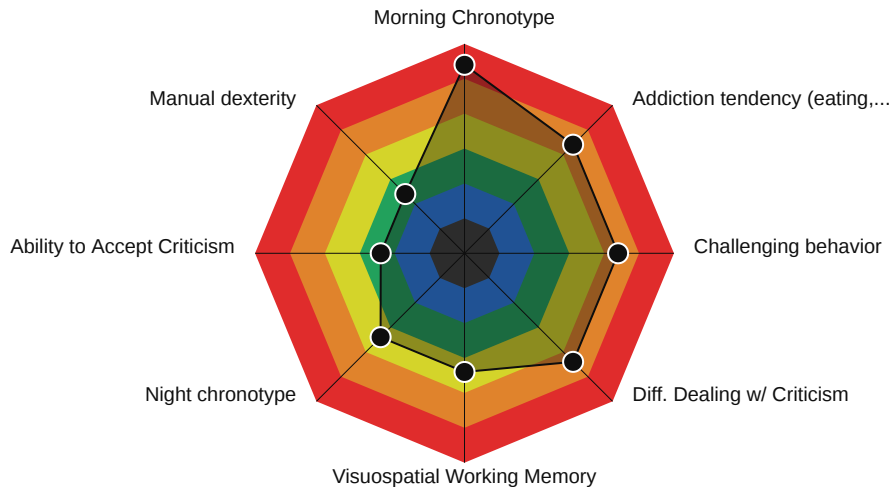
INFLAMMATION



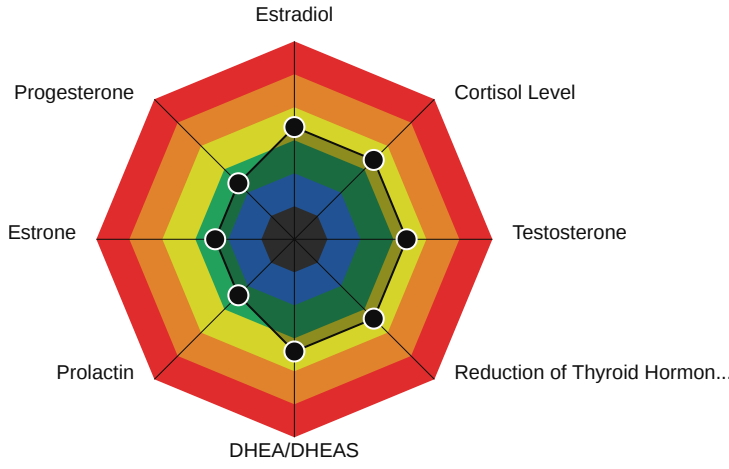
MUSCLE RECOVERY & PROTECTION



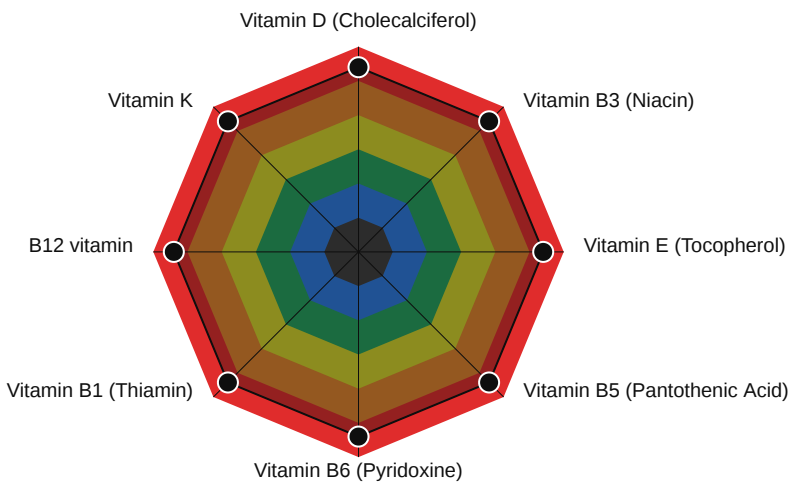
PSYCHOLOGICAL, COGNITIVE & BEHAVIORAL



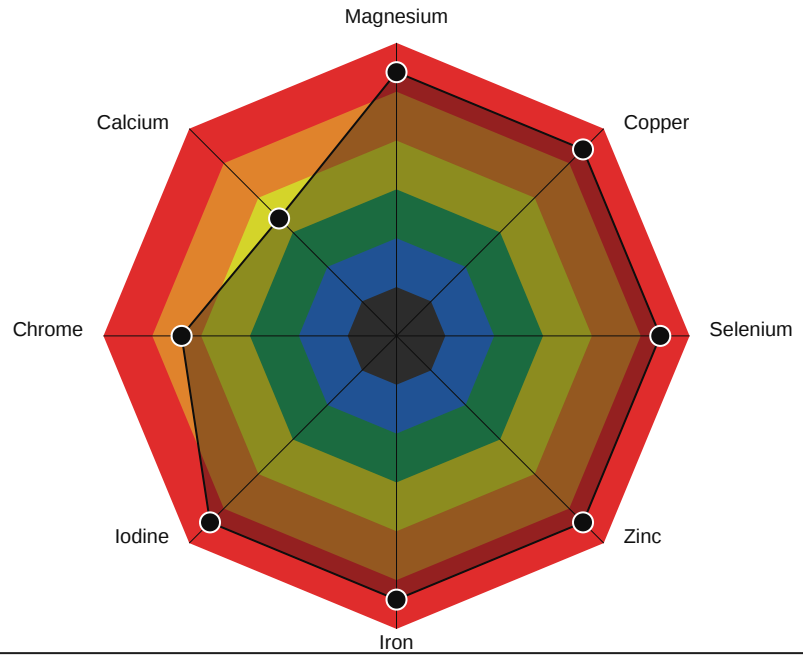
HORMONAL PROFILE



VITAMINS

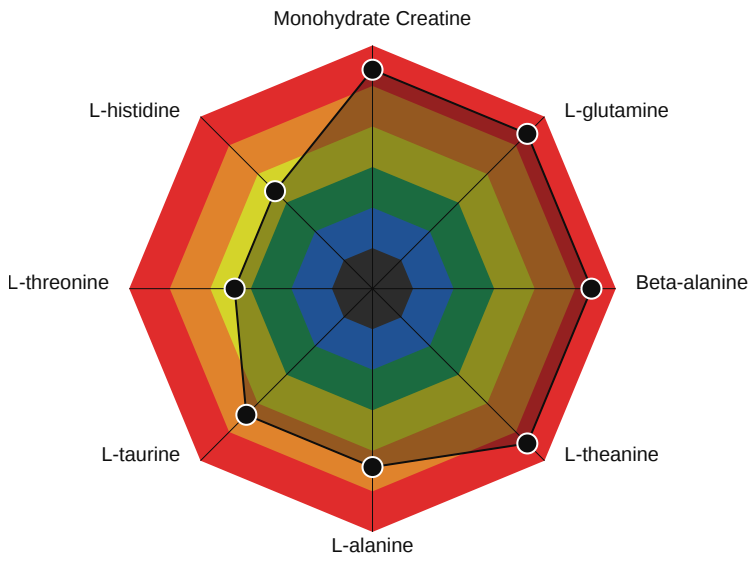


MINERALS

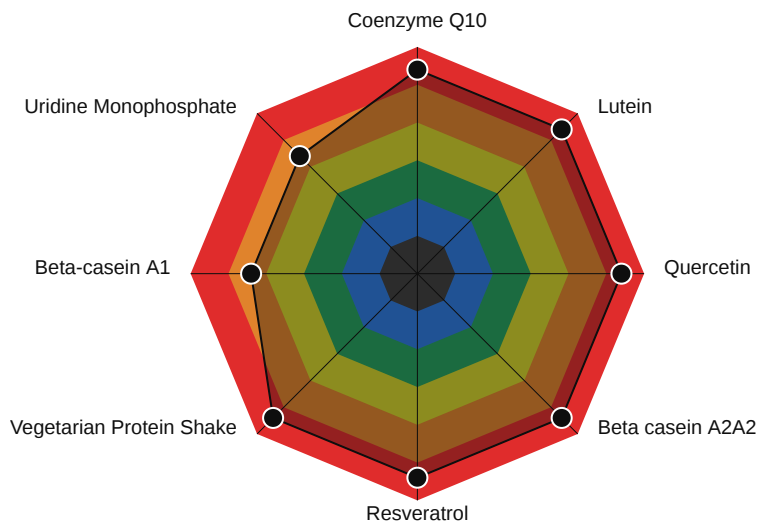


MOST RELEVANT CONDITIONS BY CATEGORY

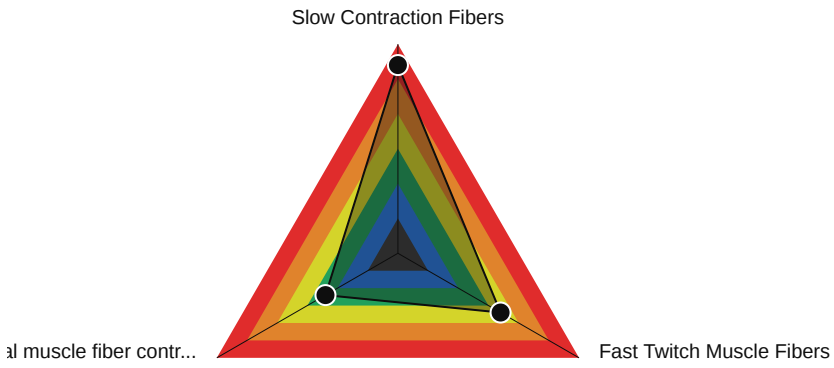
AMINO ACIDS



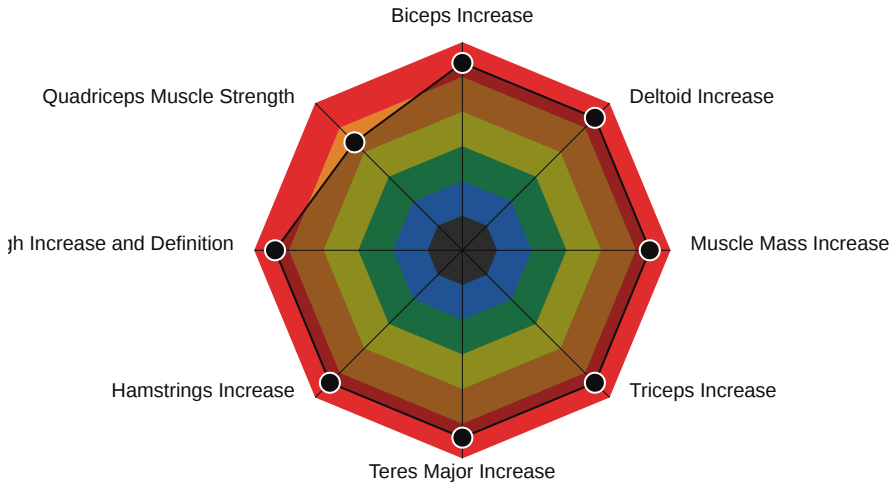
SUPPLEMENTS AND ANTIOXIDANTS



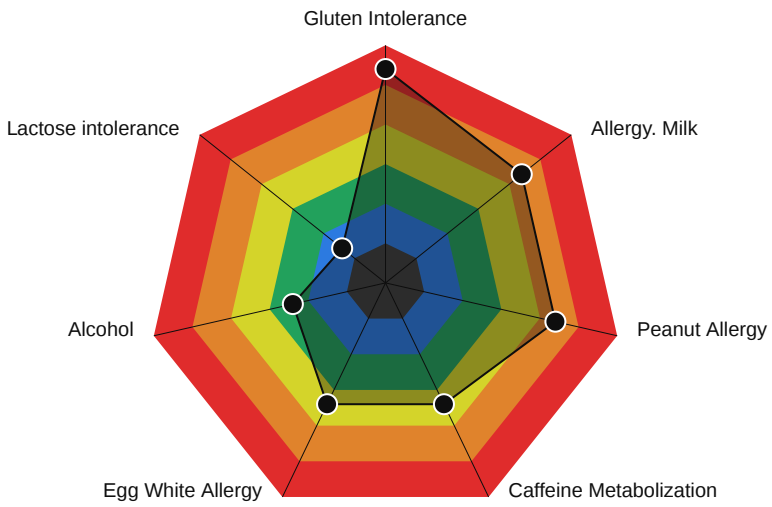
MUSCLE FIBER TYPE & CONTRACTION



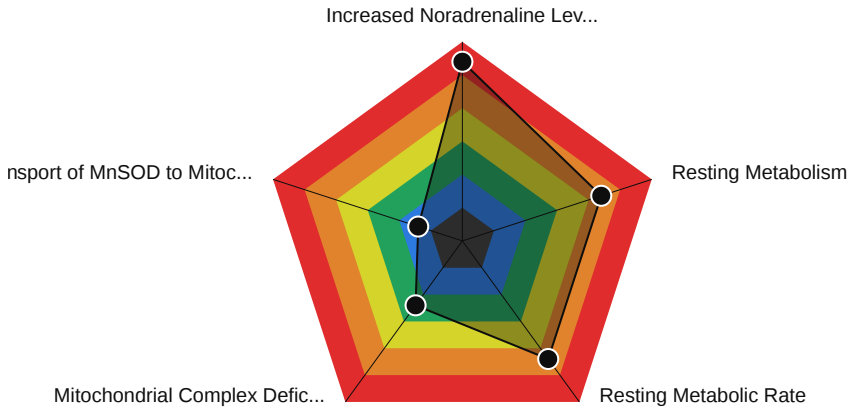
MUSCLE MASS & HYPERTROPHY



FOOD INTOLERANCES

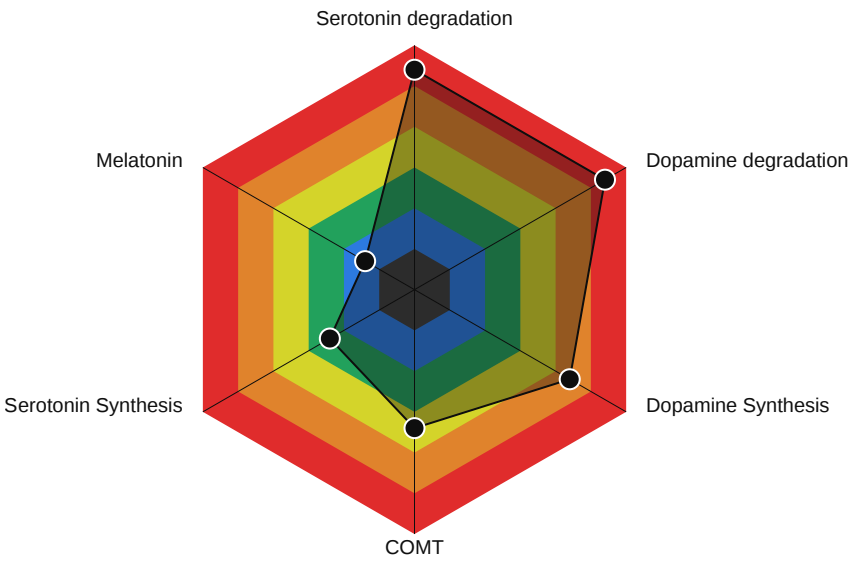


ENERGY METABOLISM

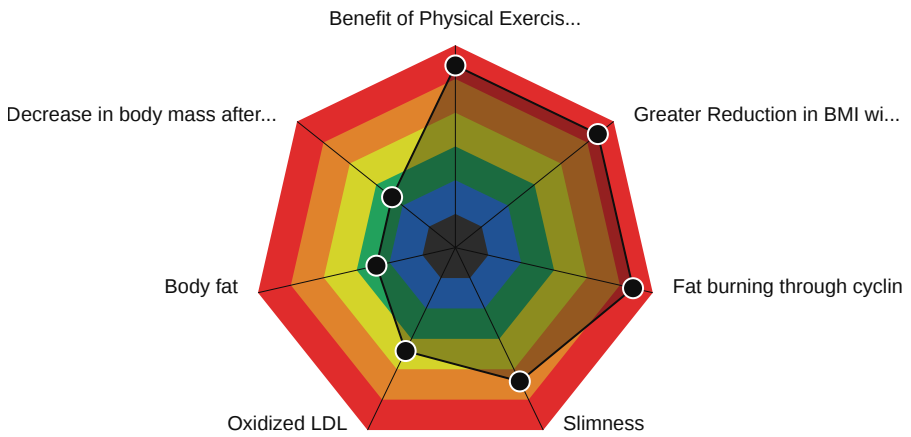


MOST RELEVANT CONDITIONS BY CATEGORY

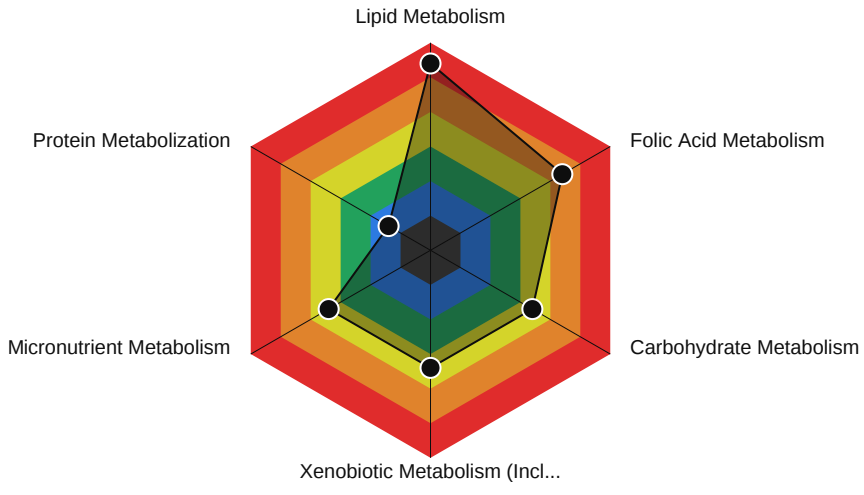
NEUROTRANSMITTER METABOLISM



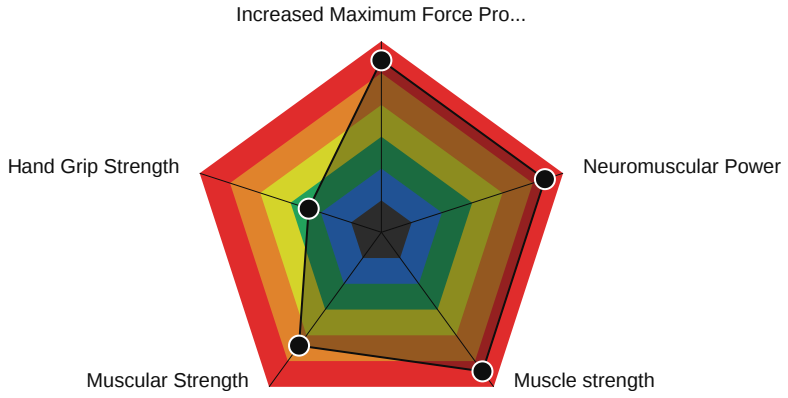
WEIGHT REGULATION & FAT METABOLISM



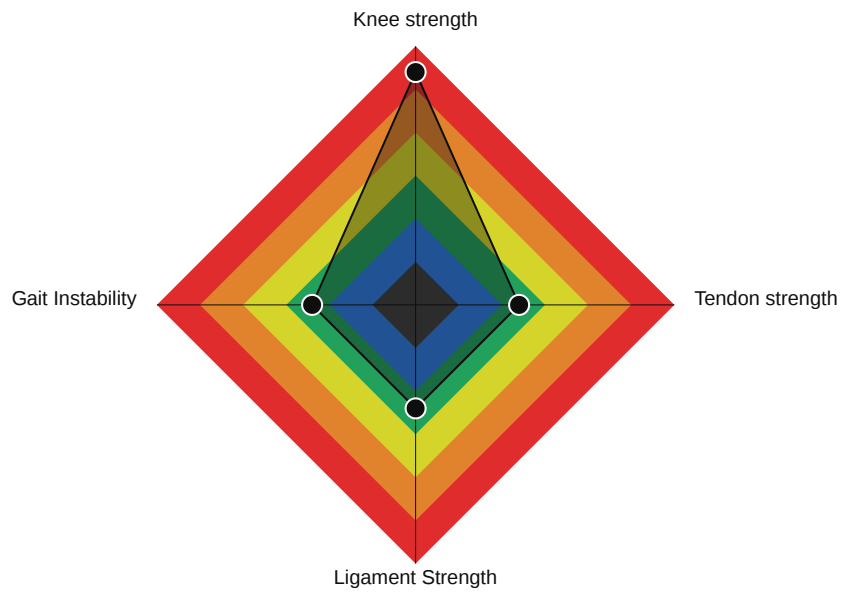
MACRONUTRIENT METABOLISM



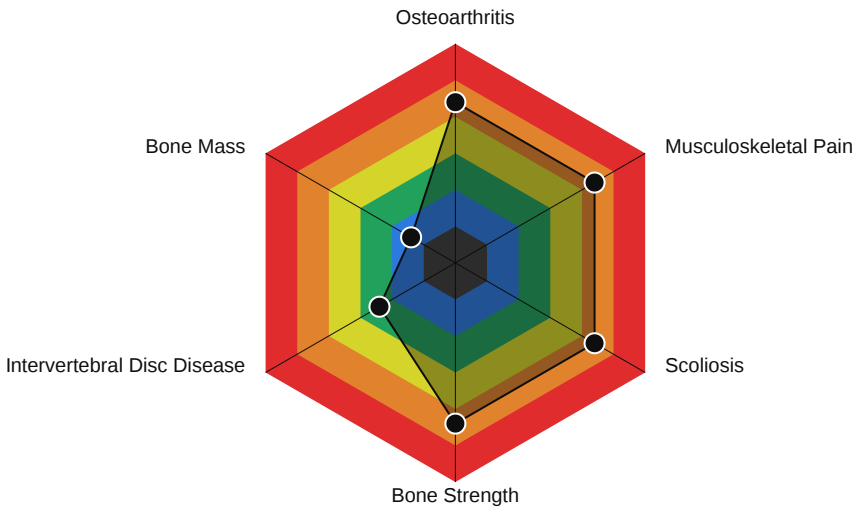
MUSCLE STRENGTH & POWER



TENDON & JOINT SUPPORT

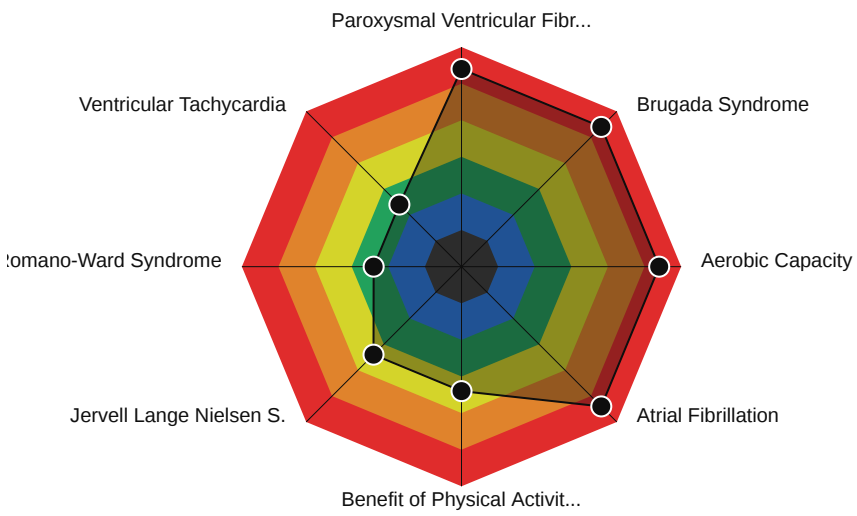


SKELETAL SYSTEM (BONES)

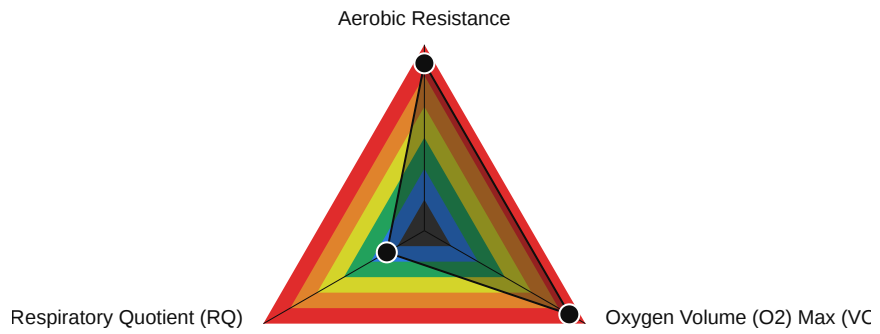


MOST RELEVANT CONDITIONS BY CATEGORY

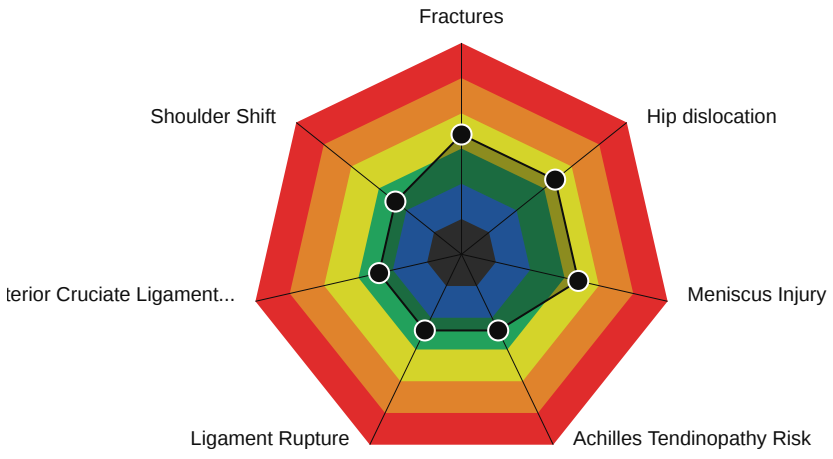
CARDIOVASCULAR SYSTEM



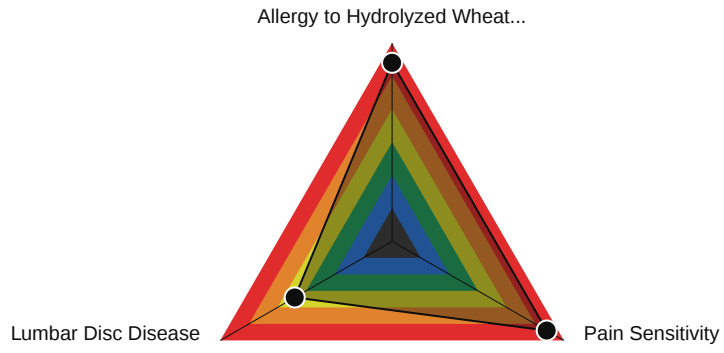
RESPIRATORY SYSTEM



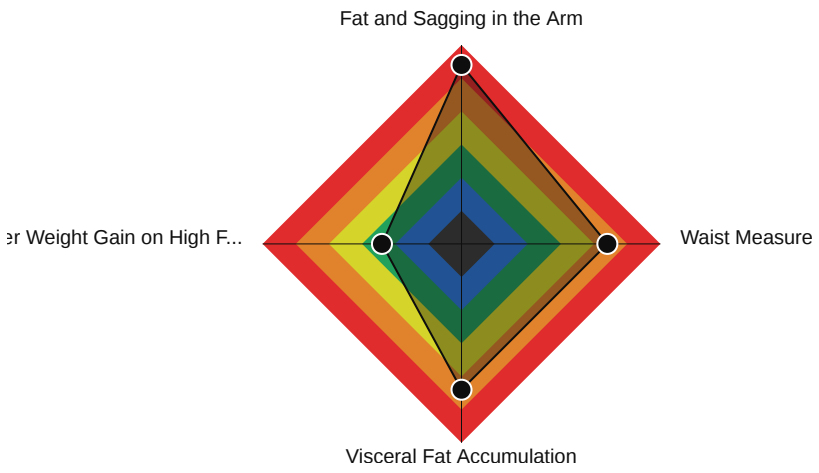
TENDON & LIGAMENT INJURIES



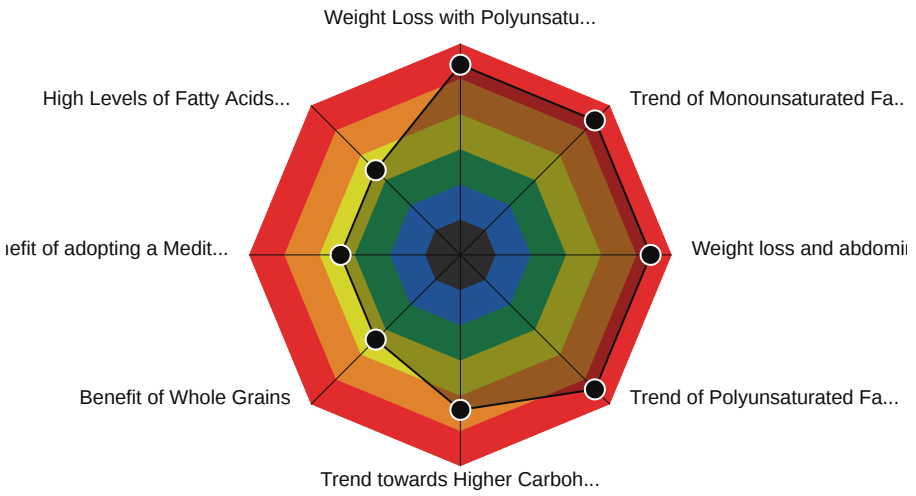
PAINS



BODY FAT & WEIGHT DISTRIBUTION

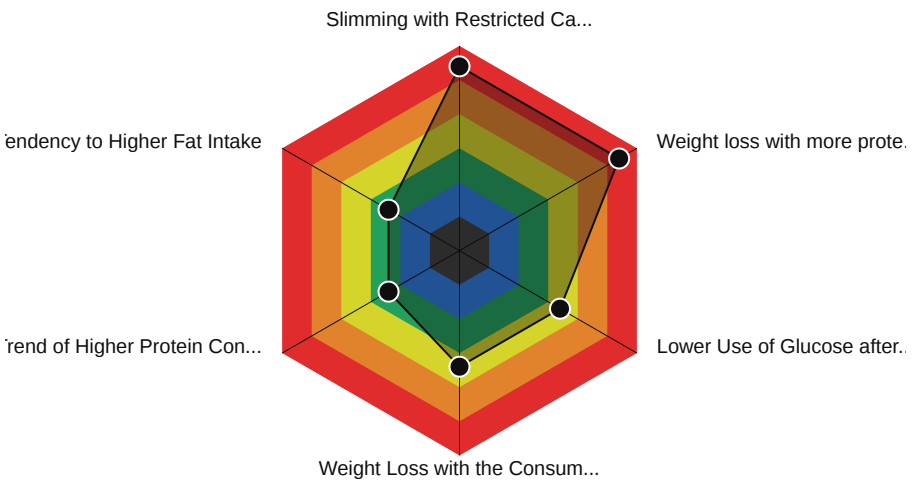


DIET TYPE & FAT RESPONSE

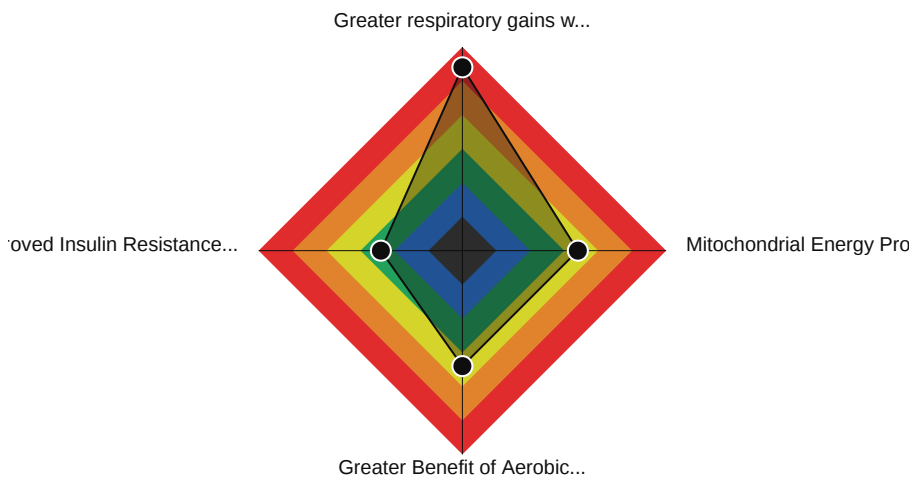


MOST RELEVANT CONDITIONS BY CATEGORY

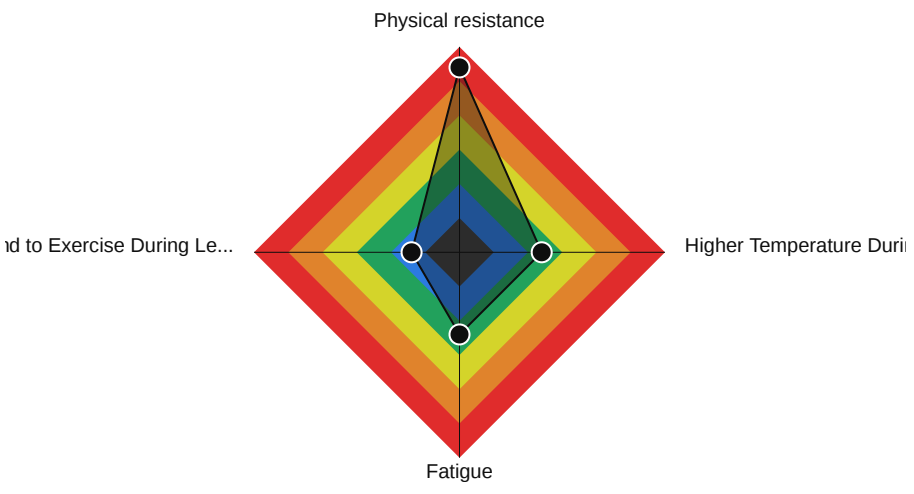
CARBOHYDRATE & PROTEIN METABOLISM



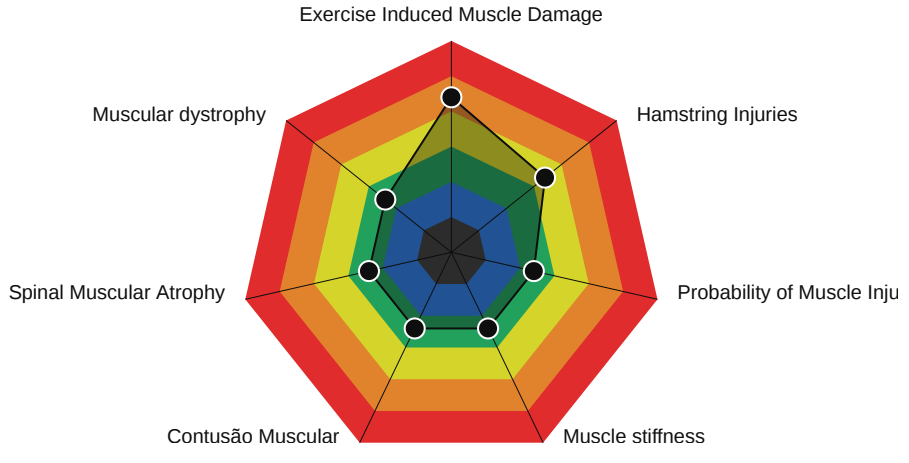
CARDIORESPIRATORY FITNESS



PHYSICAL PERFORMANCE & RECOVERY



MUSCLE INJURIES & DAMAGE



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SUMMARY OF RESULTS

1. Oxidative stress

Oxidative stress	29	- -	11	+ -	5	+ +	🔴	HIGH
Regulation of Oxidative Phosphorylation in Skeletal Muscle	1	- -	0	+ -	0	+ +	⚪	UNDEFINED
Worst oxidative stress with selenium	2	- -	0	+ -	0	+ +	🟢	NORMAL

2. Inflammation

Rheumatoid arthritis	41	- -	15	+ -	5	+ +	🔴	HIGH
Arthrosis of the Knee	5	- -	1	+ -	2	+ +	🟡	MEDIUM
Hip Osteoarthritis	1	- -	0	+ -	0	+ +	⚪	UNDEFINED
Sciatica Pain	6	- -	2	+ -	1	+ +	🟠	MEDIUM-HIGH

3. Muscle Recovery & Protection

Increased Exercise Recovery Time	4	- -	1	+ -	0	+ +	🟡	MEDIUM
Muscle Weakness After Exercise	4	- -	0	+ -	0	+ +	🟢	NORMAL
Muscle Damage Protection	1	- -	0	+ -	0	+ +	🟢	NORMAL
Muscle cramps	7	- -	0	+ -	0	+ +	🟢	NORMAL

4. Psychological, Cognitive & Behavioral

Morning Chronotype	3	- -	0	+ -	1	+ +	🔴	HIGH
Night chronotype	3	- -	1	+ -	0	+ +	🟡	MEDIUM
Ability to Accept Criticism	1	- -	1	+ -	0	+ +	🟢	NORMAL
Difficulties in Dealing with Criticism	23	- -	5	+ -	3	+ +	🟠	MEDIUM-HIGH
Visuospatial Working Memory	3	- -	1	+ -	1	+ +	🟡	MEDIUM
Manual dexterity	8	- -	0	+ -	0	+ +	🟢	NORMAL
Challenging behavior	5	- -	0	+ -	1	+ +	🟠	MEDIUM-HIGH
Addiction tendency (eating, gambling, alcohol, smoking)	5	- -	1	+ -	0	+ +	🟠	MEDIUM-HIGH

5. Hormonal Profile

Cortisol Level	8	- -	2	+ -	1	+ +	🟡	MEDIUM
Testosterone	6	- -	3	+ -	1	+ +	🟡	MEDIUM
Prolactin Promoter Polymorphism	0	- -	1	+ -	0	+ +	🟢	NORMAL

Estradiol	1	-	-	0	+	-	1	+	+	MEDIUM
Estrone	4	-	-	2	+	-	0	+	+	NORMAL
DHEA/DHEAS	7	-	-	1	+	-	1	+	+	MEDIUM
Progesterone	4	-	-	0	+	-	0	+	+	NORMAL
Reduction of Thyroid Hormonal Metabolism	2	-	-	1	+	-	0	+	+	MEDIUM
Thyroid Hormone Metabolism (T3: T4 Reduced Ratio)	0	-	-	0	+	-	0	+	+	UNDEFINED

6. Vitamins

Vitamin B1 (Thiamin)	11	-	-	0	+	-	1	+	+	HIGH
Vitamin B3 (Niacin)	3	-	-	0	+	-	4	+	+	HIGH
Vitamin B5 (Pantothenic Acid)	75	-	-	19	+	-	6	+	+	HIGH
Vitamin B6 (Pyridoxine)	114	-	-	18	+	-	11	+	+	HIGH
Vitamin B7 (Biotin)	94	-	-	11	+	-	3	+	+	MEDIUM-HIGH
Folate (Vitamin B9)	10	-	-	3	+	-	1	+	+	MEDIUM
B12 vitamin	15	-	-	4	+	-	3	+	+	HIGH
Choline	13	-	-	3	+	-	1	+	+	MEDIUM-HIGH
Vitamin C (Ascorbic acid)	123	-	-	18	+	-	4	+	+	MEDIUM
Vitamin A (Retinol)	4	-	-	0	+	-	0	+	+	NORMAL
Vitamin D (Cholecalciferol)	420	-	-	41	+	-	22	+	+	HIGH
Vitamin E (Tocopherol)	324	-	-	31	+	-	16	+	+	HIGH
Vitamin K	125	-	-	22	+	-	4	+	+	HIGH
Vitamin K2	1	-	-	0	+	-	0	+	+	NORMAL
Inositol (Vitamin B8)	2	-	-	0	+	-	0	+	+	NORMAL

7. Minerals

Zinc	205	-	-	25	+	-	14	+	+	HIGH
Copper	104	-	-	12	+	-	11	+	+	HIGH
Manganese	4	-	-	1	+	-	0	+	+	NORMAL
Selenium	406	-	-	37	+	-	15	+	+	HIGH
Iron	9	-	-	2	+	-	4	+	+	HIGH
Calcium	23	-	-	8	+	-	0	+	+	MEDIUM
Magnesium	328	-	-	29	+	-	26	+	+	HIGH
Potassium	4	-	-	0	+	-	0	+	+	NORMAL
Phosphor	6	-	-	0	+	-	0	+	+	NORMAL

Iodine	124	-	-	20	+	-	3	+	+	HIGH
Molybdenum	11	-	-	0	+	-	0	+	+	NORMAL
Chrome	23	-	-	7	+	-	1	+	+	MEDIUM-HIGH

8. Amino Acids

L-theanine	117	-	-	11	+	-	10	+	+	HIGH
L-tyrosine	1	-	-	0	+	-	0	+	+	NORMAL
L-methionine	24	-	-	0	+	-	0	+	+	NORMAL
L-arginine	11	-	-	0	+	-	0	+	+	NORMAL
L-lysine	31	-	-	0	+	-	0	+	+	LOW
L-alanine	2	-	-	1	+	-	2	+	+	MEDIUM-HIGH
L-asparagine	1	-	-	0	+	-	0	+	+	UNDEFINED
L-cysteine	2	-	-	2	+	-	0	+	+	NORMAL
L-phenylalanine	2	-	-	0	+	-	0	+	+	NORMAL
L-glycine	3	-	-	1	+	-	0	+	+	NORMAL
L-glutamine	2	-	-	4	+	-	2	+	+	HIGH
L-histidine	5	-	-	0	+	-	1	+	+	MEDIUM
L-homoarginine	3	-	-	0	+	-	0	+	+	NORMAL
L-isoleucine	0	-	-	1	+	-	0	+	+	NORMAL
L-leucine	0	-	-	1	+	-	0	+	+	NORMAL
L-ornithine	1	-	-	0	+	-	0	+	+	NORMAL
L-proline	1	-	-	0	+	-	0	+	+	NORMAL
L-serine	5	-	-	1	+	-	0	+	+	NORMAL
L-taurine	8	-	-	1	+	-	1	+	+	MEDIUM-HIGH
L-threonine	2	-	-	2	+	-	0	+	+	MEDIUM
L-valine	0	-	-	1	+	-	0	+	+	NORMAL
Beta-alanine	6	-	-	0	+	-	1	+	+	HIGH
L-carnitine Deficiency	1	-	-	0	+	-	0	+	+	NORMAL
Monohydrate Creatine	0	-	-	2	+	-	0	+	+	HIGH

9. Supplements and Antioxidants

Betaine	6	-	-	2	+	-	0	+	+	MEDIUM
Tetrahydropiobterine (BH4)	3	-	-	0	+	-	0	+	+	NORMAL
Coenzyme Q10	151	-	-	12	+	-	11	+	+	HIGH

Resveratrol	73	-	-	13	+	-	3	+	+	HIGH
Quercetin	121	-	-	13	+	-	10	+	+	HIGH
Zeaxanthin	56	-	-	10	+	-	1	+	+	MEDIUM
Lutein	153	-	-	20	+	-	12	+	+	HIGH
Uridine Monophosphate	32	-	-	3	+	-	2	+	+	MEDIUM-HIGH
Lycopene	4	-	-	1	+	-	0	+	+	MEDIUM
CLA	3	-	-	0	+	-	0	+	+	NORMAL
Turmeric (Turmeric)	1	-	-	1	+	-	0	+	+	MEDIUM
Beta-casein A1	10	-	-	0	+	-	3	+	+	MEDIUM-HIGH
Beta casein A2A2	6	-	-	0	+	-	2	+	+	HIGH
Whey Protein	11	-	-	0	+	-	0	+	+	LOW
Benefit of Green Tea	0	-	-	2	+	-	0	+	+	MEDIUM
BCAA levels	5	-	-	0	+	-	0	+	+	NORMAL
Green Tea	0	-	-	1	+	-	0	+	+	MEDIUM
Vegetarian Protein Shake	9	-	-	1	+	-	0	+	+	HIGH

10. Muscle Fiber type & Contraction

Slow Contraction Fibers	0	-	-	1	+	-	1	+	+	HIGH
Fast Twitch Muscle Fibers	0	-	-	1	+	-	0	+	+	MEDIUM
Skeletal muscle fiber contraction	0	-	-	2	+	-	0	+	+	NORMAL

11. Muscle Mass & Hypertrophy

Biceps Increase	3	-	-	1	+	-	1	+	+	HIGH
Muscle Mass Increase	11	-	-	0	+	-	2	+	+	HIGH
Triceps Increase	1	-	-	1	+	-	2	+	+	HIGH
Pectoralis Major Increase	3	-	-	2	+	-	0	+	+	MEDIUM
Pectoralis Minor Augmentation	2	-	-	1	+	-	0	+	+	NORMAL
Teres Major Increase	2	-	-	0	+	-	1	+	+	HIGH
Teres Minor Increase	0	-	-	1	+	-	0	+	+	MEDIUM
Serratus Anterior Increase	1	-	-	1	+	-	0	+	+	MEDIUM
Trapezius Increase	0	-	-	1	+	-	0	+	+	MEDIUM
Forearms Increase	3	-	-	1	+	-	0	+	+	NORMAL
Deltoid Increase	4	-	-	0	+	-	2	+	+	HIGH
Hamstrings Increase	1	-	-	3	+	-	1	+	+	HIGH

Calves Muscles Hyperthrophy	2	-	-	1	+	-	0	+	+	LOW
Thigh Increase and Definition	2	-	-	2	+	-	2	+	+	HIGH
Quadriceps Muscle Strength	1	-	-	1	+	-	1	+	+	MEDIUM-HIGH
Vastus Lateral Muscle	1	-	-	1	+	-	0	+	+	NORMAL
Platelet Aggregation with Clopidogrel	1	-	-	2	+	-	0	+	+	LOW

12. Vitamin Metabolism

MTHFR 677 mutation (rs1801133)	1	-	-	0	+	-	0	+	+	NORMAL
MTHFR 1298 mutation (rs1801131)	0	-	-	1	+	-	0	+	+	MEDIUM-HIGH

13. Food Intolerances

Lactose intolerance	19	-	-	1	+	-	0	+	+	LOW
Gluten Intolerance	3	-	-	2	+	-	1	+	+	HIGH
Milk Allergy	8	-	-	1	+	-	1	+	+	MEDIUM-HIGH
Peanut Allergy	5	-	-	2	+	-	1	+	+	MEDIUM-HIGH
Caffeine Metabolization	6	-	-	2	+	-	0	+	+	MEDIUM
Egg White Allergy	4	-	-	3	+	-	0	+	+	MEDIUM
Alcohol	2	-	-	0	+	-	0	+	+	NORMAL

14. Energy Metabolism

Resting Metabolism	0	-	-	2	+	-	1	+	+	MEDIUM-HIGH
Resting Metabolic Rate	0	-	-	2	+	-	0	+	+	MEDIUM-HIGH
Mitochondrial Complex Deficiency 1	4	-	-	0	+	-	0	+	+	NORMAL
Transport of MnSOD to Mitochondria	0	-	-	1	+	-	0	+	+	LOW
Increased Noradrenaline Level During Exercise	0	-	-	0	+	-	1	+	+	HIGH

15. Neurotransmitter Metabolism

Dopamine Synthesis	52	-	-	6	+	-	1	+	+	MEDIUM-HIGH
Dopamine degradation	38	-	-	12	+	-	3	+	+	HIGH
Serotonin Synthesis	76	-	-	7	+	-	0	+	+	NORMAL
Serotonin degradation	18	-	-	0	+	-	2	+	+	HIGH
COMT	0	-	-	1	+	-	0	+	+	MEDIUM

Melatonin	3	-	-	2	+	-	0	+	+	LOW

16. carbohydrate Metabolism

Greater Insulin Sensitivity with Physical Exercise	0	-	-	0	+	-	1	+	+	MEDIUM-HIGH
Improving Insulin Sensitivity with Physical Exercise	3	-	-	1	+	-	0	+	+	MEDIUM

17. Hematologic System

Benefit of Physical Exercise for HDL	1	-	-	0	+	-	0	+	+	NORMAL

18. Fatty Acids

Arachidonic Acid Deficiency	2	-	-	0	+	-	0	+	+	NORMAL

19. Weight Regulation & Fat Metabolism

Body fat	2	-	-	0	+	-	0	+	+	NORMAL
Oxidized LDL	0	-	-	1	+	-	0	+	+	MEDIUM
Slimness	2	-	-	0	+	-	1	+	+	MEDIUM-HIGH
Greater Reduction in BMI with Exercise	1	-	-	0	+	-	1	+	+	HIGH
Benefit of Physical Exercise for Weight Loss	5	-	-	1	+	-	1	+	+	HIGH
Fat burning through cycling	2	-	-	2	+	-	0	+	+	HIGH
Decrease in body mass after training	3	-	-	0	+	-	0	+	+	NORMAL

20. Macronutrient Metabolism

Carbohydrate Metabolism	6	-	-	1	+	-	0	+	+	MEDIUM
Lipid Metabolism	191	-	-	12	+	-	0	+	+	HIGH
Micronutrient Metabolism	5	-	-	3	+	-	0	+	+	MEDIUM
Xenobiotic Metabolism (Including Caffeine and P-450)	1	-	-	1	+	-	0	+	+	MEDIUM
Folic Acid Metabolism	6	-	-	2	+	-	2	+	+	MEDIUM-HIGH
Protein Metabolization	1	-	-	0	+	-	0	+	+	LOW

21. Muscle Strength & Power

Muscle strength	7	-	-	2	+	-	2	+	+	HIGH
Hand Grip Strength	15	-	-	1	+	-	0	+	+	NORMAL
Muscular Strength	0	-	-	1	+	-	0	+	+	MEDIUM-HIGH

Neuromuscular Power	4	-	-	4	+	-	3	+	+	🔴	HIGH
Increased Maximum Force Production	0	-	-	0	+	-	1	+	+	🔴	HIGH

22. Tendon & Joint Support

Tendon strength	3	-	-	0	+	-	0	+	+	🟢	NORMAL
Knee strength	2	-	-	2	+	-	2	+	+	🔴	HIGH
Ligament Strength	5	-	-	0	+	-	0	+	+	🟢	NORMAL
Gait Instability	2	-	-	0	+	-	0	+	+	🟢	NORMAL

23. Skeletal System (bones)

Osteoarthritis	18	-	-	3	+	-	2	+	+	🟠	MEDIUM-HIGH
Musculoskeletal Pain	3	-	-	1	+	-	1	+	+	🟠	MEDIUM-HIGH
Scoliosis	1	-	-	1	+	-	0	+	+	🟠	MEDIUM-HIGH
Intervertebral Disc Disease	2	-	-	1	+	-	0	+	+	🟢	NORMAL
Bone Mass	1	-	-	0	+	-	0	+	+	🔵	LOW
Bone Strength	0	-	-	1	+	-	0	+	+	🟠	MEDIUM-HIGH

24. Cardiovascular System

Paroxysmal Ventricular Fibrillation	1	-	-	0	+	-	1	+	+	🔴	HIGH
Increased blood pressure during exercise	1	-	-	0	+	-	0	+	+	🟢	NORMAL
Jervell and Lange-Nielsen Syndrome	1	-	-	1	+	-	0	+	+	🟡	MEDIUM
Brugada Syndrome	5	-	-	1	+	-	1	+	+	🔴	HIGH
Romano-Ward Syndrome	8	-	-	1	+	-	0	+	+	🟢	NORMAL
Ventricular Tachycardia	8	-	-	1	+	-	0	+	+	🟢	NORMAL
Aerobic Capacity	8	-	-	0	+	-	1	+	+	🔴	HIGH
Wolff-Parkinson-White Syndrome	3	-	-	0	+	-	0	+	+	🟢	NORMAL
Familial Hypertrophic Cardiomyopathy	15	-	-	0	+	-	0	+	+	🟢	NORMAL
Cardiac Capacity	5	-	-	0	+	-	0	+	+	🔵	LOW
Benefit of Physical Activity to Reduce Cardiovascular Risk	3	-	-	0	+	-	1	+	+	🟡	MEDIUM
Benefit of Potassium in Blood Pressure Control	2	-	-	0	+	-	0	+	+	⚪	UNDEFINED
Atrial Fibrillation	20	-	-	2	+	-	0	+	+	🔴	HIGH
Sudden Cardiac Death	2	-	-	1	+	-	0	+	+	🟢	NORMAL

25. Respiratory System

Aerobic Resistance	19	-	-	1	+	-	5	+	+	HIGH
Oxygen Volume (O2) Max (VO2 Max)	2	-	-	1	+	-	2	+	+	HIGH
Respiratory Quotient (RQ)	1	-	-	1	+	-	0	+	+	LOW

26. Tendon & Ligament Injuries

Achilles Tendinopathy Risk	1	-	-	1	+	-	0	+	+	NORMAL
Ligament Rupture	0	-	-	1	+	-	0	+	+	NORMAL
Anterior Cruciate Ligament Injury (ACL)	0	-	-	1	+	-	0	+	+	NORMAL
Shoulder Shift	0	-	-	1	+	-	0	+	+	NORMAL
Hip dislocation	1	-	-	2	+	-	0	+	+	MEDIUM
Fractures	1	-	-	3	+	-	1	+	+	MEDIUM
Meniscus Injury	0	-	-	1	+	-	0	+	+	MEDIUM

27. Pains

Pain Sensitivity	1	-	-	1	+	-	2	+	+	HIGH
Lumbar Disc Disease	3	-	-	0	+	-	0	+	+	MEDIUM
Allergy to Hydrolyzed Wheat Protein	0	-	-	1	+	-	1	+	+	HIGH

28. Body Fat & weight Distribution

Waist Measure	34	-	-	14	+	-	2	+	+	MEDIUM-HIGH
Visceral Fat Accumulation	3	-	-	3	+	-	0	+	+	MEDIUM-HIGH
Fat and Sagging in the Arm	693	-	-	9	+	-	13	+	+	HIGH
Lower Weight Gain on High Fat Diets	1	-	-	0	+	-	0	+	+	NORMAL

29. Diet Type & Fat Response

Weight loss and abdominal fat loss in caloric restriction	6	-	-	0	+	-	1	+	+	HIGH
Weight Loss on Fat Reduction Diets	4	-	-	1	+	-	0	+	+	NORMAL
Trend of Monounsaturated Fat Intake and Weight Gain	185	-	-	10	+	-	2	+	+	HIGH
Reduction of body fat with intervention of polyphenols	0	-	-	1	+	-	0	+	+	NORMAL
Weight Loss with the Intake of Monounsaturated Fats	2	-	-	1	+	-	0	+	+	NORMAL
Weight Loss with Polyunsaturated Fat Intake	3	-	-	2	+	-	2	+	+	HIGH
Trend of Polyunsaturated Fat Intake and Weight Gain	170	-	-	8	+	-	0	+	+	HIGH

Weight Loss in Diets with Olive Oil	0	-	-	1	+	-	0	+	+	NORMAL
Benefit of adopting a Mediterranean diet	3	-	-	1	+	-	0	+	+	MEDIUM
Benefit of Whole Grains	1	-	-	0	+	-	1	+	+	MEDIUM
Trend towards Higher Carbohydrate Consumption	5	-	-	0	+	-	1	+	+	MEDIUM-HIGH
High Levels of Fatty Acids after Fat Ingestion	0	-	-	1	+	-	0	+	+	MEDIUM

30. Carbohydrate & protein Metabolism

Weight Loss with the Consumption of Complex Carbohydrates	1	-	-	2	+	-	0	+	+	MEDIUM
Slimming with Restricted Carbohydrates Intake	6	-	-	0	+	-	1	+	+	HIGH
Lower Use of Glucose after Carbohydrate Ingestion	0	-	-	1	+	-	0	+	+	MEDIUM
Trend of Higher Protein Consumption	2	-	-	0	+	-	0	+	+	NORMAL
Tendency to Higher Fat Intake	1	-	-	0	+	-	0	+	+	NORMAL
Weight loss with more protein than carbohydrate intake	186	-	-	10	+	-	0	+	+	HIGH

31. Cardiorespiratory Fitness

Greater Benefit of Aerobic Exercise for Vascular Function	0	-	-	1	+	-	0	+	+	MEDIUM
Improved Insulin Resistance in High-Protein Weight-Loss Diets	1	-	-	0	+	-	0	+	+	NORMAL
Greater respiratory gains with exercise	0	-	-	1	+	-	0	+	+	HIGH
Mitochondrial Energy Production	62	-	-	4	+	-	1	+	+	MEDIUM

32. Physical Performance & Recovery

Trend to Exercise During Leisure	1	-	-	1	+	-	0	+	+	LOW
Higher Temperature During Exercise	2	-	-	0	+	-	0	+	+	NORMAL
Physical resistance	55	-	-	6	+	-	2	+	+	HIGH
Increased Probability of Fatigue	10	-	-	1	+	-	0	+	+	NORMAL

33. Muscle Injuries & Damage

Exercise Induced Muscle Damage	2	-	-	2	+	-	1	+	+	MEDIUM-HIGH
Hamstring Injuries	0	-	-	2	+	-	1	+	+	MEDIUM
Muscle Damage in Low Choline Diets	6	-	-	0	+	-	0	+	+	UNDEFINED
Contusão Muscular	1	-	-	1	+	-	0	+	+	NORMAL
Muscle stiffness	1	-	-	1	+	-	0	+	+	NORMAL
Probability of Muscle Injuries	1	-	-	1	+	-	0	+	+	NORMAL
Progressive Muscle Atrophy	1	-	-	0	+	-	0	+	+	UNDEFINED

Spinal Muscular Atrophy	21	-	-	0	+	-	0	+	+	NORMAL
Muscular dystrophy	4	-	-	0	+	-	0	+	+	NORMAL

1. Oxidative stress

Oxidative stress

HIGH

Evaluation of a set of genes associated with the functioning of the reduction and oxidation (redox) system as a whole. Orange or red indicates poorer functioning, that is, greater risk of oxidative stress.

Genes

ADA, ALDH2, AOC1, ATF1, CAT, CBS, EPHX1, G6PD, GCLC, GPX1, GPX3, GPX4, GSR, GSTM1, GSTP1, HFE, IL-6, LCT, LTA, NFE2L2, NQO1, SELENOF, SIRT6, SLC2A14, SOD1, SOD2, SOD3, TLR4, TNF, ZNF648

Regulation of Oxidative Phosphorylation in Skeletal Muscle

UNDEFINED

Insulin resistance and type 2 diabetes are associated with decreased expression of genes that regulate oxidative phosphorylation in skeletal muscle. A polymorphism in the NDUFB6 promoter region that creates a possible DNA methylation site (rs629566, A/G) was associated with a decline in muscle NDUFB6 expression with age. Although young people with the rs629566 G / G genotype exhibit greater expression of muscle NDUFB6, this genotype was associated with reduced expression in the elderly. This was subsequently explained by the discovery of increased DNA methylation in the promoter of elderly, but not young, individuals carrying the rs629566 G/G genotype. Furthermore, the degree of DNA methylation was negatively correlated with the expression of muscle NDUFB6, which in turn it was associated with insulin sensitivity. Larger result in red indicates susceptibility to dysregulation

Genes

NDUFB6

1. Oxidative stress

Worst oxidative stress with selenium

NORMAL

Individuals with certain polymorphisms of the glutathione peroxidase enzyme gene, indicated by an orange or red result, worsen oxidative stress when supplemented with selenium.

Recommendations

If indicated in orange or red, assess plasma / serum selenium, and maintain levels around 110 to 120 ng/ml (or mcg/L), never above that.

Complement

Use Brazil nuts, chelated selenium or yeast selenium to achieve and maintain optimal levels.

Genes

GPX1, GPX4

2. Inflammation

Rheumatoid arthritis

HIGH

A chronic inflammatory disease that affects many joints, including those in the hands and feet.

Genes

AHCY, AIRE, ANAPC4, ANXA3, C5, CDK6, CTLA4, EOMES, FCRL3, GUCY1B2, HLA-DRB1, HTR2A, HYKK, ICAM3, IL-2RA, IL-2RB, INTERGENIC, IRF5, ITGAV, KIAA1109, MMEL1, NFKBIE, NOD2, PADI4, PER2, PHF19, PHTF1, PLD4, PRL, PSMA4, PTPN2, PTPN22, SLC6A11, STAT4, TNFAIP3, TRAF1, TRAF1/C5, UBASH3A, VARS2, WDFY4, ZNF175

Arthrosis of the Knee

MEDIUM

Arthrosis is an inflammatory and degenerative disease of the body's joints (joints), marked by the wear of the cartilage that line the bone ends, causing pain and possibly leading to deformities. The joints most affected by arthrosis are those that support weight, such as the spine, hips and knees. Knee pain is usually the first symptom of osteoarthritis. This pain is progressive in nature. It is accentuated with physical activity (steps, going up and down stairs, contact sports and repetitive movements) and is directly proportional to excess weight.

Genes

COL6A4P1, GDF5, IL-1RN, INTERGENIC, LRCH1, MCF2L

Hip Osteoarthritis

UNDEFINED

Sometimes called "wear and tear" arthritis, osteoarthritis is a common condition that many people develop during middle age or later. It can occur in any joint in the body, but most often develops in weight-bearing joints such as the hip and knee. Hip osteoarthritis causes pain and stiffness. It can make it difficult to perform daily activities such as bending over to tie a shoe, getting up from a chair, or taking a short walk.

Genes

FRZB

2. Inflammation

Sciatica Pain

MEDIUM-HIGH

The main causes of radiculopathy are herniated discs and spondyloarthrosis, which is occurring in the joints between vertebrae; other causes are spinal instability (spondylolisthesis), trauma to the spine and, more rarely, tumor, stroke, etc. Spondyloarthrosis is one of the main components of spine aging, which can lead to root and / or spinal compression due to the proliferation of bone and ligament tissue; the result of this process is a progressive narrowing (stenosis) of the space (s) between the spine and / or of the root foramina (foraminopathy) in the spine.

Genes

COMT, IL-1A, IL-1RN, IL-6, MMP1, OPRM1

3. Muscle Recovery & Protection

Increased Exercise Recovery Time

MEDIUM

This damage can be transient, lasting minutes, hours or even several days after training or competition (BARNETT, 2006), and is the result of post-exercise metabolic disorders, in which recovery depends on the restoration of muscle glycogen stores, the which usually occurs within 24 hours of exercise.

Genes

AMPD1, SLC17A7, SOD2, TNF

Muscle Weakness After Exercise

NORMAL

Muscle weakness, also known as adynamia or asthenia, is common after heavy physical exertion. For example, after participating in a marathon or exercising excessively in the gym, or after repeating the same task/action for a long time, among other causes.

Genes

ADRB3, MT-ND4, NOS3, PPARGC1A

Muscle Damage Protection

NORMAL

Studies show that the C allele of the ESR1 rs2234693 polymorphism has a greater protective effect against muscle damage than the T allele, since it reduces muscle stiffness.

Genes

ESR1

3. Muscle Recovery & Protection

Muscle cramps

NORMAL

Cramps are involuntary and painful contractions of a muscle or muscle group. They affect only the striated musculature and mainly affect the posterior muscles of the leg. A cramp can start during physical activity, at rest and even during sleep.

Genes

AMPD1, CYP24A1, DMD, MYF6, PGAM2, PYGM

4. Psychological, Cognitive & Behavioral

Morning Chronotype

HIGH

Morning Chronotype: Peak melatonin production occurs before midnight. These are individuals who need to go to bed early and are most active in the early hours of the day. In general, they sleep between 10 pm and 6 am. According to the International Melatonin Institute 25% of the population is morning. Result in orange or red indicates a greater tendency to the morning chronotype.

Genes
AANAT, CRY2, PER2, PER3

Night chronotype

MEDIUM

Nocturnal or afternoon chronotype: the peak occurs much later, at 6 am. They are those people who do better at night, but need to prolong their rest until early morning. Sleep time is usually between 3:00 and 11:00. It corresponds to 25% of individuals. Result in orange or red indicates a tendency to have the night chronotype.

Genes
CRY1, NR1D1, PER3

Ability to Accept Criticism

NORMAL

Often the main reason for criticism to affect negatively is a problem of insecurity. Lack of self-esteem by itself would be a problem and not an effect of other issues. But genetics has a strong impact on this topic.

Genes
CRHR1, DBH

4. Psychological, Cognitive & Behavioral

Difficulties in Dealing with Criticism

MEDIUM-HIGH

Being sensitive to criticism is a common trait for many people and requires skills. Some people use criticism in a positive way to improve or in a negative way that can lower their self-esteem and cause stress, anger or even aggression.

Genes

ADH4, CHADL, CLOCK, CRHR1, CTNNA2, DBH, ELP1, EP300, FAM86B3P, FBXL17, FYN, GAD1, GRIK3, INTERGENIC, MAGI1, MTMR9, OPCML, PLEKHM1, PTPRF, SNAP25, SNCA, TMEM16D, VRK2, XKR6

Visuospatial Working Memory

MEDIUM

The visuospatial storage area stores visual and spatial information. It can be used, for example, to construct and manipulate visual images and to represent mind maps. It is also beneficial for strategic organization and sports such as football and basketball.

Genes

CACNA1C, CAMTA1, NRG1, SLC6A3

Manual dexterity

NORMAL

Manual dexterity is the ability of the hands and fingers to make coordinated movements. It indicates people with better motor skills and aptitude for manual work, such as sewing, painting, crafts, technical assembly and surgeries. It also relates to sports that require the use of hands.

Genes

CTNNA2, NRG1, PCSK6

4. Psychological, Cognitive & Behavioral

Challenging behavior

MEDIUM-HIGH

Defiant Behavior (unrelated to Oppositional Defiant Disorder) is characterized by antisocial behaviors such as disobedience, defiant posture, and hostility. The individual has difficulties to follow rules and recognize his mistakes, resenting more than usual when he is contradicted.

Genes

ADH4, CLOCK, CTNNA2, ELP1, OPCML

Addiction tendency (eating, gambling, alcohol, smoking)

MEDIUM-HIGH

Genetics might influence the tendency to addictions.

Genes

ANKK1, DRD2, OPRM1

5. Hormonal Profile

Cortisol Level

MEDIUM

Research shows a clear relationship between obesity, increased cortisol (stress hormone) and depression. The incidence of depression is quite high, but it often manifests itself in an unconventional way, making diagnosis difficult, especially in women. It can appear in the form of binge eating or obesity and not through the common, which is loss of appetite and weight loss. Or through insomnia and fibromyalgia (with pain throughout the body), or migraine, among other examples. You still don't know which came first. Whether depression elevates cortisol or cortisol is elevated in depression. The hypothalamus, the pituitary gland (the body's mother gland), both located "in the brain", are responsible for the production of cortisol through the adrenal gland. In the face of everyday stress situations, these glands constitute the hypothalamic-pituitary-adrenal axis, responsible for a healthy response to stress or for the formation of the unhealthy "cascade" of stress-depression-obesity. Although cortisol is a beneficial hormone, it can be produced beyond conventional needs causing us to get sick. Thus, excess cortisol would routinely be able to produce negative effects similar to the side effects of corticosteroid medications, those routinely used for arthritis and asthma, causing what we call Cushing's Syndrome, in which full moon faces predominate " (chubby and rounded, associated with abdominal fat). For the treatment of this hormonal change, specific antidepressants (related to the neurotransmitter serotonin) seem to positively increase the expression (action) of cortisol in the brain, which would then be beneficial, as it would reduce the excitation of this axis and also the production of cortisol by the supra gland -renal relieving cardiac risk.

Genes

CRHR1, DGKH, FKBP5, HSD11B1, HTR2C, NR3C1, OXTR

Testosterone

MEDIUM

Testosterone is the main male sex hormone and an anabolic steroid. In humans and male animals, testosterone plays a key role in the development of male reproductive tissues such as the testes and prostate, as well as the promotion of secondary sexual characteristics such as increased muscle mass, bone growth and maturation, and growth of body hair. In addition, testosterone is involved in health, well-being and the prevention of osteoporosis. Insufficient testosterone levels in men can lead to abnormalities, including frailty and bone loss. Its decrease can lead to fatigue, memory loss, hair loss, muscular dystrophy, irritability, depression and obesity, in addition to increasing the susceptibility to diabetes, osteoporosis and cardiovascular disease.

Genes

CYP17A1, CYP19A1, FAM9B, FSHR, HSD17B2, HSD17B3, PDE7B, SHBG

5. Hormonal Profile

Prolactin Promoter Polymorphism

NORMAL

Prolactin (PRL) is a protein hormone that is primarily synthesized by the anterior pituitary gland. However, PRL can also be synthesized and secreted by extrapituitary tissues, particularly immune cells. A biallelic polymorphism (-1149G/T) in the prolactin promoter proved to be functionally important, as the modulation of prolactin expression was associated with lupus in some populations. Systemic lupus erythematosus (SLE) was associated with high levels of prolactin, low levels of dehydroepiandrosterone (DHEA) and induction of inflammatory cytokines in the serum of patients with the disease. One study suggests that the ?1149TT genotype may be a risk factor for lupus and may predict who could benefit from DHEA therapy.

Genes

PRL

Estradiol

MEDIUM

Estradiol is the most important estrogen for a woman. It is a hormone produced by the ovaries that acts on reproductive function, skin, blood vessels, bones and brain. According to studies, estradiol plays more than 300 functions in the female body. In reproduction, estradiol stimulates the release of eggs from the ovarian follicles. It also acts on the fallopian tubes, stimulating muscle contractions that take the fertilized egg to the uterus. Also in the reproductive function, estradiol promotes the reaction of the uterus to the hormone progesterone, whose function is to prepare the organ for the arrival of the fertilized egg, producing a thicker endometrium. Another important function of estradiol is to drive the development of secondary sexual characteristics, such as breast growth and body changes, affecting bones, joints and fat distribution. Estradiol is also responsible for maintaining skin elasticity, blood vessel dilation and bone health. In the brain, estradiol plays a significant role in protecting brain functions such as memory, mood and mental well-being. Estradiol levels change during a woman's menstrual cycle. It starts to increase in the middle of the follicular phase (when some ovarian follicles are stimulated) and peaks in the middle of the cycle. Until it starts to fall, reaching a second peak in the luteal phase (a phase in which the corpus luteum, the structure that remains in the ovary after the egg is released, produces progesterone). Orange or red result indicates higher estradiol.

Genes

ESR2, SHBG

5. Hormonal Profile

Estrone

NORMAL

Estrone is an estrogenic hormone secreted by the ovary. It is produced from androstenedione. Estrone which is the second predominant estrogen in circulation in women and predominant after menopause. After menopause, estrone continues to be synthesized through the conversion of the adrenal steroid, mainly in fat tissues and muscle cells. The more fat, the more estrone is produced. For example, in women after menopause, if the levels of estrone are higher than those of estradiol or estriol, there may be an increased risk of cardiovascular disease and even of developing some types of cancer.

Genes

CYP19A1

DHEA/DHEAS

MEDIUM

Popularly known as the "youth hormone", dehydroepiandrosterone (DHEA) and its sulfated form, dehydroepiandrosterone sulfate (DHEA-S), are the most abundant steroids in our circulation. However, its natural production declines from the age of 20 onwards, after reaching the maximum level of concentration. This fact has been increasing the number of supporters of antiaging hormone therapy, motivating studies on the importance of this hormone and the risks of its excess in our body. Both DHEA-S and DHEA are produced mainly in the adrenal glands from cholesterol and very important hormonal precursors, especially estrogens and testosterone. In addition to acting as a substrate for other hormones, some scientific evidence indicates that DHEA also plays more roles in our bodies. Recent studies show that higher physiological levels of DHEA have been associated with greater well-being, better fitness, and greater muscle strength. There is also evidence of the effects of DHEA on bone density, as well as its anti-inflammatory and immune system effects. DHEA is the main precursor of human sex steroid synthesis and is inactivated by sulfonation into DHEAS. A previous genome-wide association study linked the single nucleotide polymorphism (SNP) rs2637125, located near the coding region of DHEA sulfotransferase, SULT2A1, to serum DHEAS concentrations.

Genes

ARPC1A, BCL2L11, HHEX, INTERGENIC, SHBG, SULT2A1, TRIM4

5. Hormonal Profile

Progesterone

NORMAL

In men, high levels of progesterone increase estrogen levels, which can result in symptoms such as depression, fatigue, and the development of heart disease. For women, high progesterone is associated with symptoms such as anxiety, bloating, depression, reduced sex drive, and/or weight fluctuations. In women, progesterone is produced by the corpus luteum, under the stimulus of HGC (chorionic gonadotropin) 15 days after the start of menstruation, after ovulation and is released in the second phase of the menstrual cycle, preparing the uterus and the woman's body for a possible pregnancy, as it is a hormone directly related to reproduction. Progesterone, unlike estrogen, has no activity on the determination of female sexual characteristics. The activity of progesterone is to prepare the uterus for a possible pregnancy, receiving the fertilized egg and stimulating the production of milk. Progesterone was the basis for the development of oral contraceptives, and, combined with estrogens, promotes the inhibition of ovulation, preventing follicular maturity, as it inhibits the secretion of gonadotropins by the pituitary. It is fundamental in the processes of menstruation, fertilization, transport and implantation of the fertilized egg, maintenance of pregnancy and lactation. Higher levels of circulating progesterone were associated with a modestly increased risk of breast cancer. The inclusion of progesterone during hormone therapy intervention leads to a persistently increased risk of breast cancer after the intervention and leads to the development of hormone receptor negative tumors in addition to those that are hormone receptor positive. Result in blue indicates lower levels. Result in green indicates normal levels. Yellow result indicates average levels. Result in orange or red indicates high levels.

Genes

INTERGENIC, PGR, SLC22A10, ZKSCAN5

Reduction of Thyroid Hormonal Metabolism

MEDIUM

Thyroid hormones stimulate nearly every aspect of carbohydrate metabolism, including rapid glucose uptake by cells, greater absorption by the gastrointestinal system, and increased insulin secretion (thus influencing whether or not diabetes occurs). The increase in thyroid hormone decreases the amount of cholesterol and triglycerides in the blood. Conversely, decreased thyroid secretion greatly increases blood cholesterol and triglyceride concentrations, often causing an excessive deposition of fat in the liver. The large increase in blood cholesterol in prolonged (ie, untreated) hypothyroidism is often associated with the onset of artherosclerosis.

Genes

DIO1

5. Hormonal Profile

Thyroid Hormone Metabolism (T3: T4 Reduced Ratio)

UNDEFINED

Reduced proportion T3: T4. The thyroid produces two hormones, triiodothyronine (T3) and thyroxine (T4), which regulate your metabolism, which is the way your body uses and stores energy. Thyroid function is controlled by the pituitary gland, located in your brain. The thyroid is still responsible for the production of calcitonin, a hormone related to calcium metabolism. Higher results indicate a risk of reduced thyroid hormone metabolism.

Genes

6. Vitamins

Vitamin B1 (Thiamin)

HIGH

Indication in orange or red indicates an increased need for vitamin B1 (thiamine).

Genes

PNPLA3, SLC19A2, SLC19A3, SLC25A19, SLC35F3, TPK1

Vitamin B3 (Niacin)

HIGH

Result in orange or red indicates greater need for the vitamin.

Complement

If indicated in orange or red, consider the use of niacinamide, the preferred form of general use, in food supplementation. Nicotinamide and nicotinic acid can also be used.

Genes

BST1, CD38, GAD1, NAMPT, SIRT1, SIRT3, SIRT6

Vitamin B5 (Pantothenic Acid)

HIGH

Indication in orange or red, indicates an increased need for vitamin B5 (pantothenic acid).

Complement

Calcium pantothenate is the most used form of nutritional supplementation

Genes

ABCA1, ABCG8, AHCY, AIRE, ANAPC4, ANXA3, AOC1, APOA5, APOC1, APOE, AR, BRCA2, C5, CDK6, CPS1, CR1L, CTLA4, DNAH11, DOCK7, EOMES, FABP2, FADS1, FADS2, FCRL3, GAD1, GCKR, GPX1, GUCY1B2, HLA-DQA1, HLA-DRB1, HTR2A, HYKK, ICAM3, IL-2RA, IL-2RB, INTERGENIC, IRF5, ITGAV, JMJD1C, KIAA1109, LDLR, LPL, MAT1A, MCT1, MLXIPL, MMEL1, MTHFR, NAF1, NFKBIE, NOD2, OR4A46P, PADI4, PCIF1, PHF19, PHTF1, PHYHIP, PLD4, PSMA4, PTPN2, PTPN22, RAB11B, SLC6A11, STAT4, TMEM241, TNF, TRAF1, TRAF1/C5, UBASH3A, VARS2, WDFY4, ZNF175, ZPR1

6. Vitamins

Vitamin B6 (Pyridoxine)

HIGH

Result in orange or red indicates greater need.

Recommendations

If indicated in orange or red, consider evaluating plasma pyridoxine, but, as with other plasma markers, may not reflect increased need for pyridoxine.

Complement

Consider, if indicated, increasing the dietary intake or via food complementation, of pyridoxine, also of other nutrients involved in its metabolism, according to their specific genetic evaluation, such as B12, B2 and magnesium.

Genes

ABCA1, ABCB1, ADA, ADORA2A, AHCY, ALPL, ARMS2, BCR, BDNF, C2, C3, CBS, CETP, CFB, CFH, CHRM2, CLOCK, COL8A1, COMT, CRYBB2, CRYBB3, CRYGD, CX3CR1, DAT, DCDC2, DTNBP1, EPHA2, FGD6, FGF20, FKBP5, GAD1, GJA8, GPHN, GPX4, GRIA3, GSR, HTR2A, HTR2C, HTRA1, IL-1B, INTERGENIC, KIAA0319, MAF, MAOA, MTHFR, MTRR, NBPF3, NOTCH4, NPAS2, NR3C1, OXTR, PDE11A, PDE9A, PITX2, REST, SERPINF1, SKIV2L, SLC64A, SOD2, TDP2, TLR3, TPH1, TTRAP, VEGFA

Vitamin B7 (Biotin)

MEDIUM-HIGH

Orange or red result indicates increased need for biotin.

Complement

Biotin

Informations

Involved in the synthesis of heme, mitochondrial complex IV, its deficit increases the formation of reactive oxygen species. Biotin is one of the B-complex vitamins involved in energy production, production of keratin (nails and hair) and good skin health.

Genes

ABCA1, ACHE, ACP7, ADRA2A, AR, ARL15, ARMS2, C2, C3, CAPN10, CDKAL1, CDKN2A, CDKN2A/B, CDKN2B-AS1, CETP, CFH, COL8A1, CRYBB2, CRYGD, CX3CR1, DNER, EPHA2, FGD6, FGFR3, FTO, GAD1, GCKR, GJA8, GRK5, GSR, HHEX, HTRA1, IL-6, INTERGENIC, IRS1, JAZF1, KCNJ11, KCNQ1, MAF, MTTP, NOS3, NOTCH2, NOTCH4, PAX4, PITX2, PPARG, RBMS1, REST, RHOU, RPSAP52, SKIV2L, SLC2A14, SLC30A8, SOD2, TCF7L2, TGFBR3, TLR3, TRIB3, TRPS1, VEGFA, VPS26A, VPS33B

6. Vitamins

Folate (Vitamin B9)

MEDIUM

Orange or red result indicates increased need for folate.

Recommendations

Check serum folate (folic acid) level. Polymorphisms that reduce MTHFR activity lead to an increased need for riboflavin, which can accelerate this enzyme, restoring at least partially its speed.

Complement

Methyltetrahydrofolate (MTHF), riboflavin. Vitamin B6 and B12 must be evaluated and optimized whenever necessary, as they work in synergism.

Avoid

The use of folic acid should be avoided by individuals with a high need for folate, as, with MTHFR polymorphisms, the tendency to accumulate unmetabolized metabolites will be greater, always preferring methyltetrahydrofolate (MTHF) and riboflavin, as well as other accessory nutrients .

Where to find

Liver, brewer's yeast, lentils, okra, black beans, spinach, soy, broccoli, orange juice, leafy in general.

Genes

BHMT, FOLR1, FOLR2, MTHFD1, MTHFR, SHMT1

B12 vitamin

HIGH

In orange or red, it indicates a higher requirement for vitamin B12.

Complement

Assess serum vitamin B12 and, if reduced, take appropriate action. If indicated in green or yellow, check the possibility of using pre and probiotics. These individuals have less fixation of probiotics in the gastrointestinal mucosa.

Where to find

Beef from cattle, sheep (lamb), pigs and other animals that do not use antibiotics in the feed.

Genes

ABCD4, APTX, CD320, CLYBL, CUBN, FUT2, FUT6, INTERGENIC, MMAA, MS4A3, MTHFR, PRELID2, TCN1, TCN2

6. Vitamins

Choline

MEDIUM-HIGH

Individuals in orange or red have a lower biosynthetic capacity and therefore a greater need for dietary supplementation.

Recommendations

Evaluate plasma homocysteine. Present in all cell membranes, in individuals in orange or red it can be useful in improving memory, hepatic steatosis and placental health, in maintaining optimal homocysteine levels, among other functions.

Complement

Ingest phosphatidylcholine, egg yolk, soy lecithin, egg lecithin. Individuals in orange or red need to ingest more, or supplement, for optimal levels of it.

Where to find

Egg yolk, liver and viscera in general.

Genes

CHAT, CHDH, CHKA, CHKB, FMO3, MTHFD1, MTHFD1L, PEMT, SLC44A1

6. Vitamins

Vitamin C (Ascorbic acid)

MEDIUM

Result in orange or red indicates greater need.

Recommendations

If indicated in orange or red, consider that vitamin C intake should be kept above the usual average desired for the general population. Also consider evaluating the serum ascorbic acid level. As with other serum markers, finding a result within the reference does not mean that the need is being met if the above indication is in orange or red.

Complement

Some studies reveal that vitamin C supplementation combined with other nutrients and antioxidant substances, such as lutein, zeaxanthin, vitamin E, zinc, copper and beta-carotene, can reduce disease progression.

Where to find

Camu-camu (Amazonian fruit), acerola, guava, kiwi, strawberry, orange, pepper, broccoli, Brussels sprouts, goji berry, cranberry and cashew.

Effect

Example: Vitamin C is one of the three cofactors required by DAO to function properly, resulting in histamine breakdown. Therefore, carriers of the 'T' allele of C995T risk, which is associated with histamine intolerance, may benefit from supplementation of vitamin C, to ensure DAO Activity limiting the effect of histamine.

Genes

ABCA1, ABCB1, ABI3BP, ALDH2, AOC1, APOB, ATM, AURKA, B3GALT1, BCO1, CCHCR1, CDKN1A, CDKN2A, CETP, CFH, CLPTM1L, CYP1A1, CYP1B1, CYP2E1, CYP3A4, CYP3A5, DEF8, DHFR, DIRC3, DPYD, E2F3, EPHX1, ERI1, FASLG, FOXE1, G6PD, GPX1, GSTP1, HDAC4, HLA-DRA, HLA-DRB1, HNF1A, HTRA1, IGF1R, IL4R, INTERGENIC, IRF4, KL, LMNA, MC1R, MDM2, MTHFR, MTRR, PIK3CA, PPARG, PPARGC1A, PTEN, RNASEL, SIRT1, SLC23A1, SLC2A14, SLC39A6, SLC45A2, SOD2, SOD3, SPIRE2, STAT4, TERT, TYR, XPC, XRCC1

6. Vitamins

Vitamin A (Retinol)

NORMAL

Indication in orange or red indicates increased need for retinol, including the possibility of poor conversion of beta-carotene to retinol.

Recommendations

If indicated in orange or red, the assessment of the serum level of beta-carotene and retinol may be interesting. As with other serum markers, finding a result within the reference does not mean that the need is being met if the above indication is in orange or red.

Complement

According to plasma evaluation, there may be a need for retinol supplementation, as there may be BCO1 polymorphism and thus, low conversion of beta-carotene into retinol. Consider increasing the dietary intake of both nutrients, if indicated in orange or red.

Effect

Example: In carriers of the "T" risk allele of C599T, associated with reduced antioxidant capacity, vitamin A supplementation may be beneficial.

Genes

BCO1

6. Vitamins

Vitamin D (Cholecalciferol)

HIGH

Result in orange or red, indicates increased need for vitamin D. There may be genetic problems in intestinal absorption, skin conversion, conversion to active forms, transport, binding to receptors or detoxification of the same.

Recommendations

For a complete evaluation, we suggest evaluating 25-hydroxy and 1,25 dihydroxy-vitamin D3, as one of these polymorphisms can lead to a reduction in this conversion. Assess intact PTH, ionic calcium, urinary calcium (1st morning sample or 24h urine) and serum magnesium, all involved in vitamin D metabolism.

Complement

Only by increasing sun exposure or using vitamin D supplements can we achieve its adequacy.

Effect

Example: Individuals following a vegan or non-dairy diet should consider supplementation, especially if they carry the "G" allele of T-1127C.

Genes

ABCA1, ABCB1, ABI3BP, ACE, ACHE, ACP7, ADCY5, ADD1, ADD2, ADIPOQ, ADRA2A, ADRB2, AGAP2, AGT, AGTR1, AHI1, ALDH2, ALK, ANKRD1, AOC1, APOB, APOE, APOE4, ARL15, ASIC2, ATM, ATP2B1, ATP6V1B1, AURKA, B3GALT1, BAG3, BAG6, BATF, BCAT1, BCO1, BDNF, BMPR1B, BMPR2, BRAP, BRCA2, BTD, C1ORF106, CACNB2, CALCA, CAPN10, CASZ1, CAV3, CBLB, CBS, CCHCR1, CCL2, CD58, CD86, CDH13, CDKAL1, CDKN1A, CDKN2A, CDKN2A/B, CDKN2B-AS1, CETP, CFH, CHRDL1, CHST12, CLCN6, CLEC16A, CLPTM1L, CLSTN2, CRP, CYP1A1, CYP1B1, CYP24A1, CYP27B1, CYP2E1, CYP2R1, CYP3A4, CYP3A5, CYP4A11, DAPK1, DBC1, DEF8, DHFR, DIRC3, DKKL1, DLEU1, DMD, DNAJC5B, DNER, DPYD, DSG2, E2F3, ENPP1, EPHX1, ERG, ERI1, ESR1, EVI5, F12, F7, FAM58A, FAM69A, FASLG, FGF20, FLJ25967, FMN2, FOXE1, FTO, G6PD, GAD1, GATA2, GATA4, GC, GCK, GCKR, GPX1, GPX4, GRK5, GSTP1, GUCY1A3, HDAC4, HHEX, HIVEP2, HLA-DRA, HLA-DRB1, HNF1A, HSPD1, HSPE1, IFNL4, IGF1R, IGF2BP2, IL-2RA, IL-4, IL-6, IL-7R, IL4R, INSIG2, INTERGENIC, IRF4, IRF5, IRS1, ITGA11, ITGB3, JAG1, JAZF1, KCNE1, KCNE2, KCNE3, KCNJ11, KCNQ1, KL, KLC1, KLRB1, LAG3, LEPR, LIPA, LMNA, LRP8, M6PR, MACROD2, MALT1, MAOA, MC1R, MDM2, MERTK, MMP3, MMP9, MOV10, MPV17L2, MRAS, MTHFD1, MTHFD1L, MTHFR, MTNR1B, MTRR, MTTP, MYBPC1, MYBPC3, MYO16, NADSYN1, NAF1, NCKAP5, NEDD4L, NFE2L2, NGF, NLRP1, NOS3, NOTCH2, NOV, NPPA, NR2F2-AS1, NR3C1, OLR1, OPRM1, PAX4, PCK1, PDE4B, PECAM1, PEX5L, PHACTR1, PIK3CA, PLCL2, PLPP3, PPARG, PPARGC1A, PSMA6, PSRC1, PTEN, PTH, PTPRD, PTPRS, RASGRP1, RBMS1, RHOU, RNASEL, RPL5, RPS6KB1, RPSAP52, RYR2, SAMD12, SCN5A, SDHAF4, SEZ6L, SH2B3, SHMT1, SIRT1, SLC2A14, SLC30A7, SLC30A8, SLC39A6, SLC45A2, SMAD3, SOD2, SPIRE2, STAT4, STK39, SYK, TAP2, TCF7L2, TERT, TGFBR3, THADA, THBS2, TLR4, TMPO, TNF, TNFSF14, TNFSF4, TRIB3, TRPM6, TTN, TTR, TXNRD2, TYR, UBE2E2, VDR, VPS26A, VPS33B, WFS1, WSCD2, XPC, XRCC1, ZNF767P

6. Vitamins

Vitamin E (Tocopherol)

HIGH

Orange or red result indicates increased need for vitamin E.

Recommendations

If indicated in orange or red, it is suggested to assess the plasma level of vitamin E. As with other serum markers, finding a result within the reference does not mean that the need is being met, if the indication above is in orange or red.

Complement

Increase your intake of foods rich in tocopherols and tocotrienols, such as oil seeds and fruits, avocados and palm oil. Supplement to tocopherols and tocotrienols. The consumption of vitamin E together with carotenes, such as beta-carotene, lycopene, astaxanthin, lutein and others, which come preferably from food, is also interesting, as they act synergistically, regenerating the oxidized forms.

Effect

Example: For those carriers of the "A" allele of G66 + 1594A, who are at risk of developing Age-Associated Macular Degeneration, vitamin E may prevent or limit disease onset.

Genes

A2M, ABCA2, ABCA7, ACE, ADD1, ADRB2, AGAP2, AHI1, ALK, ANKRD1, AOC1, APH1B, APOA5, APOC1, APOE, APOE4, APP, ARHGAP20, ARVCF, ASIC2, ATP2B1, ATP8B4, BACE1, BAG3, BATF, BDNF, BIN1, BRAP, BRCA2, BTD, C1ORF106, CACNB2, CALHM1, CASC17, CASC21, CASC8, CAV3, CBLB, CCL2, CD2AP, CD58, CD86, CDH1, CDH13, CDKN1B, CDKN2B-AS1, CETP, CFH, CHAT, CHEK2, CHRDL1, CHST12, CLEC16A, CLSTN2, CLU, CNTNAP2, COMT, CPS1, CR1, CRP, CTNNA3, CYP17A1, CYP24A1, CYP2R1, CYP3A4, CYP4F2, DAB2IP, DAPK1, DBC1, DKK1, DKKL1, DLEU1, DMD, DNAJC5B, DPP6, DSG2, EHBP1, EIF2AK2, ELAC2, ENTPD7, ERG, ESR2, EVI5, F12, F7, FAM124A, FAM171A2, FAM69A, FCHSD1, FGF20, FGFR4, FLJ10986, FLJ25967, FMN2, FRMD4A, FYCO1, GAB2, GATA2, GATA4, GCKR, GOLM1, GPX1, GRN, GSTP1, HLA-DRA, HLA-DRB1, HNF1B, HSPD1, HSPE1, HTRA1, IDE, IL-10, IL-18RAP, IL-2RA, IL-4, IL-6, IL-7R, INTERGENIC, IRF5, ITGA2, ITGA6, ITGB3, JAG1, JAZF1, KCNE1, KCNE2, KCNE3, KCNQ1, KIAA1211, KL, KLC1, KLF6, KLRB1, LAG3, LDLR, LIPA, LIPC, LOXHD1, LRP6, LRP8, LTA, MAGEC3, MAGI2, MALT1, MAOA, MERTK, MME, MMP3, MMP9, MPO, MPV17L2, MRAS, MS4A6A, MSMB, MTHFD1, MTHFD1L, MYBPC3, NAF1, NCKAP5, NKAIN3, NLRP1, NOS3, NPPA, OLR1, PCAT19, PCDH11X, PCK1, PDE4B, PECAM1, PEX6, PHACTR1, PICALM, PLAU, PLCL2, PLD3, PLPP3, POLN, PON2, PPP1R3B, PRRC2C, PSEN1, PSEN2, PSMA6, PSRC1, RNASEL, RPL5, RPS6KB1, RYR2, SAMD12, SCN5A, SELENOP, SEZ6L, SH2B3, SLC30A7, SMAD3, SOD1, SOD3, SORL1, SYK, TAP2, TCF2, TCF7L2, TET1, THBS2, TLR4, TM2D3, TMPO, TMPRSS2, TNF, TNFSF14, TNFSF4, TREM2, TRPM7, TTN, TTPA, TTR, TXNRD2, VDR, XRCC1, ZNF767P, ZNF827, ZPR1

Vitamin K

HIGH

Orange or red result indicates greater need for Vitamin K.

Genes

ABCA1, ACE, ADD1, ADD2, AGT, AGTR1, ARHGEF3, ARMS2, ATP2B1, ATP6V1B1, BAG6, BCAT1, BDNF, BMP2, BMPR1B, BMPR2, C2, C3, CALCA, CASZ1, CBS, CETP, CFB, CFH, CLCN6, COL8A1, CX3CR1, CYP19A1, CYP4A11, CYP4F2, DAPK1, F12, FDPS, FGD6, FTCDNL1, GAD1, GGCX, GPX1, GUCY1A3, HIVEP2, HTRA1, IL-1B, INTERGENIC, ITGA11, LRP4, LRP5, M6PR, MACROD2, MAOA, MOV10, MTHFR, MTRR, MYBPC1, MYO16, NEDD4L, NFE2L2, NGF, NOS3, NOTCH4, NOV, NPPA, NR2F2-AS1, NR3C1, OPRM1, PPARG, PPARGC1A, QPCT, REST, SERPINF1, SHMT1, SKIV2L, STK39, TAP2, TLR3, TRPM6, VDR, VEGFA, VKORC1, WNT16, WSCD2

6. Vitamins

Vitamin K2

NORMAL

Vitamin K is well known for its activity in blood clotting, but in studies carried out in recent years it has also been associated with the treatment of osteoporosis, in which Vitamin K2 is responsible for the use of calcium for bone mineralization.

Genes
VKORC1

Inositol (Vitamin B8)

NORMAL

Indicated to reduce bad cholesterol (LDL) levels and help control diabetes, inositol is a natural compound (mostly found in dark green fruits and vegetables) that helps in the action of neurotransmitters, such as serotonin. Therefore, this substance is very useful for the treatment of anxiety, depression and panic attacks. In addition, inositol contributes to calcium absorption and is important for healthy bones, teeth and muscles. Also known as vitamin B8, inositol is actually considered a pseudovitamin and is naturally produced by our bodies. Like the B-complex vitamins, it is used to digest and extract energy from the food we eat - it is critical to the overall digestion process.

Genes
BDNF, NGF

7. Minerals

Zinc

HIGH

Orange or red result indicates greater need for zinc.

Recommendations

If necessary, the evaluation of serum and/or erythrocyte zinc is suggested. As with other serum markers, finding a result within the reference does not mean that the need is being met if the above indication is in orange or red.

Complement

Chelated zinc, zinc citrate, zinc acetate, zinc sulfate and zinc carnosine are the main forms used in nutritional supplementation.

Where to find

The main sources of zinc are oysters, shrimp, beef, chicken and fish, liver, nuts and oil seeds such as sunflower and pumpkin nuggets.

Informations

Among the various functions: strengthen the immune system, stimulate child growth, combat physical and mental fatigue, increase energy levels, delay aging, improve memory, balance blood sugar levels, regulate the production of various hormones , improve skin appearance and strengthen hair. Zinc enables several biochemical functions, as it is a component of numerous enzymes, including alcohol dehydrogenase, superoxide dismutase, carbonic anhydrase, alkaline phosphatase and central nervous system enzymes.

Genes

ABCA1, ABCB1, ACHE, ACP7, ADA, ADCY5, ADIPOQ, ADORA2A, ADRA2A, AHCY, ALDH2, ARL15, ATM, AURKA, BCO1, BCR, BDNF, CA1, CAPN10, CCHCR1, CDKAL1, CDKN1A, CDKN2A, CDKN2A/B, CDKN2B-AS1, CFH, CHRM2, CLOCK, CLPTM1L, CTLA4, CYP1A1, CYP1B1, CYP2E1, CYP3A4, CYP3A5, DAT, DHFR, DIRC3, DNER, DPYD, E2F3, ENPP1, EPHX1, ESR1, FAM58A, FASLG, FGF20, FKBP5, FOXE1, FTO, G6PD, GAD1, GCK, GCKR, GPHN, GPX1, GPX4, GRK5, GSTP1, HHEX, HLA-DRA, HLA-DRB1, HNF1A, HTR2A, HTR2C, HTRA1, IGF2BP2, IL-1B, IL4R, INSIG2, INTERGENIC, IRS1, JAZF1, KCNJ11, KCNQ1, LEPR, MAOA, MDM2, MT1A, MTHFR, MTNR1B, MTRR, MTTP, NAF1, NBDY, NOS3, NOTCH2, NPAS2, NR3C1, OXTR, PAX4, PDE11A, PDE9A, PEX5L, PIK3CA, PPARG, PPCDC, PTEN, PTPRD, PTPRS, RASGRP1, RBMS1, RHOU, RNASEL, RPSAP52, SDHAF4, SLC2A14, SLC30A3, SLC30A8, SLC39A6, SLC64A, SOD2, SOD3, STAT4, TCF7L2, TERT, TG, TGFBR3, THADA, TPH1, TRIB3, TYR, UBE2E2, VPS26A, VPS33B, WFS1, XPC, XRCC1

7. Minerals

Copper

HIGH

If indicated in orange or red, it means that your copper requirement is above average or greatly increased.

Recommendations

Assess blood copper level before using any nutritional supplements.

Complement

Chelated copper. If in orange or red, consider increasing your intake of dietary sources of copper.

Avoid

Individuals with high serum copper levels should avoid foods rich in copper, such as veal or cooked beef liver, mussels, oysters, cashews, peanuts, almonds, walnuts, cocoa.

Where to find

Boiled beef or veal liver, mussels, oysters, cashews, peanuts, almonds, walnuts, cocoa.

Effect

Example: To ensure maximum DAO activity while limiting the effect of histamine, carriers of the C47T "T" risk allele may consider copper supplementation.

Genes

ABCB1, ACE, ADD1, ADRB2, AOC1, APOE, APOE4, ASIC2, ATP2B1, ATP7B, BAG3, BRAP, BTD, CACNB2, CAV3, CCL2, CDH13, CDKN2B-AS1, CETP, CFH, CHRDL1, CRP, CYP2R1, DHFR, DMD, DNAJC5B, DPYD, DSG2, F12, F7, FGF20, FLJ25967, FMN2, FOXE1, GATA2, GATA4, HLA-DRA, HLA-DRB1, HSPD1, HSPE1, HTRA1, IL-4, IL4R, INTERGENIC, ITGB3, JAG1, KCNE1, KCNE2, KCNE3, KCNQ1, KL, LIPA, LRP8, MAOA, MMP3, MMP9, MRAS, MTHFD1, MTHFD1L, MYBPC3, NAF1, NOS3, NPPA, OLR1, PECAM1, PHACTR1, PLCL2, PLPP3, PSMA6, PSRC1, RYR2, SCN5A, SELENBP1, SEZ6L, SH2B3, SMAD3, SMIM1, SOD3, STAT4, THBS2, TLR4, TMPO, TNF, TNFSF4, TTN, TTR, TXNRD2, TYR

7. Minerals

Manganese

NORMAL

Indication in orange or red indicates greater need.

Recommendations

If indicated in orange or red, we suggest evaluating manganese in whole blood or erythrocytes. As with other serum markers, finding a result within the reference does not mean that the need is being met if the above indication is in orange or red.

Complement

Chelated manganese

Genes

ARG1, SLC30A10, SLC39A8, SOD2

7. Minerals

Selenium

HIGH

Orange or red result indicates increased need for selenium.

Recommendations

Assess for selenium in plasma, serum or whole blood. Despite the three forms being well studied, the evaluation in whole blood seems to be the most indicated. Maintain optimal selenium levels.

Complement

All individuals must maintain a regular intake of Brazil nuts to optimize serum selenium levels. However, in those indicated in orange or red, a higher intake of nuts, or addition of chelated selenium, yeast selenium, may be necessary, depending on the results of blood tests.

Where to find

Brazil nuts are the only appreciable source of selenium in the usual diet. Its concentration in food varies according to its presence in the region's soil. European and South American soils are generally poor, and North American soil has higher concentrations of it.

Effect

Example: In carriers of the "C" allele of C599T, selenium supplementation provided a beneficial effect by decreasing DNA damage. However, in those carrying the "T" allele at risk, DNA damage was increased in those with higher selenium intake.

Genes

A2M, ABCA1, ABCA2, ABCA7, ABCB1, ACE, ADD1, ADH1C, ADRB2, AGAP2, AHI1, ALDH2, ALK, ANKRD1, AOC1, APH1B, APOC1, APOE, APOE4, APP, ARHGAP20, ASIC2, ATM, ATP2B1, ATP8B4, AURKA, BACE1, BAG3, BATF, BCKDK, BCO1, BDNF, BIN1, BRAP, BRCA2, BTD, C1ORF106, CACNB2, CALHM1, CAPZB, CAV3, CBLB, CCDC62, CCHCR1, CCL2, CD2AP, CD58, CD86, CDH13, CDKN1A, CDKN2B-AS1, CETP, CHAT, CHRDL1, CHST12, CLEC16A, CLPTM1L, CLSTN2, CLU, CNKSR3, CNTNAP2, CPS1, CR1, CRP, CTC1, CTLA4, CTNNA3, CYP1A1, CYP1B1, CYP24A1, CYP2E1, CYP2R1, CYP3A4, CYP3A5, DAPK1, DBC1, DHFR, DIO1, DIRC3, DKK1, DKKL1, DLEU1, DLG2, DMD, DMGDH, DNAJC5B, DPYD, DSG2, E2F3, EIF2AK2, ENTPD7, EPHX1, ERG, EVI5, F12, F7, FAM171A2, FAM47E, FAM69A, FASLG, FGF20, FGF7, FLJ25967, FMN2, FOXE1, FRMD4A, G6PD, GAB2, GALNT3, GATA2, GATA4, GBF1, GCKR, GLUD2, GNAI3, GOLM1, GPX1, GPX4, GSTP1, HLA, HLA-DRA, HLA-DRB1, HNF1A, HSPD1, HSPE1, IDE, IL-2RA, IL-4, IL-6, IL-7R, IL4R, INTERGENIC, IRF5, ITGB3, IYD, JAG1, KCNE1, KCNE2, KCNE3, KCNQ1, KL, KLC1, KLRB1, LAG3, LDLR, LIPA, LRP6, LRP8, LRRK2, LTA, MALT1, MAOA, MAOB, MAPT, MC1R, MCCC1, MDM2, MERTK, MME, MMP3, MMP9, MPO, MPV17L2, MRAS, MS4A6A, MTF1, MTHFD1, MTHFD1L, MTHFR, MTRR, MYBPC3, NAF1, NCKAP5, NFE2L2, NLRP1, NOS3, NPPA, OLR1, PCDH11X, PCK1, PDE4B, PDE8B, PECAM1, PEX6, PHACTR1, PHTF1, PICALM, PIK3CA, PLAU, PLCL2, PLD3, PLPP3, POLN, PPP1R3B, PRDM2, PRRC2C, PSEN1, PSEN2, PSMA6, PSRC1, PTCSC2, PTEN, RAB25, RNASEL, RPL5, RPS6KB1, RYR2, SAMD12, SCN5A, SELENOF, SELENOP, SEMA5A, SEZ6L, SH2B3, SH3GL2, SLC30A7, SLC39A11, SLC39A6, SMAD3, SNCA, SOD2, SORL1, STAT4, SYK, TAP2, TERT, TET1, TG, THBS2, TLR4, TM2D3, TMPO, TNF, TNFSF14, TNFSF4, TPO, TREM2, TSHR, TTN, TTR, TXNRD2, TYR, USP24, USP40, VAV3, XPC, XRCC1, ZNF767P

7. Minerals

Iron

HIGH

Orange or red result indicates increased iron requirement.

Recommendations

To assess iron nutritional status, monitor ferritin levels and transferrin saturation, and if necessary, total and latent iron binding capacity. Hemoglobin is a late marker of iron deficiency.

Complement

Chelated iron is a great way to complement it. Always encourage increased intake of heme and non-heme iron, accompanied by sources of vitamin C. Therefore, include foods that source this nutrient, such as oranges, cashews, guavas, mangoes, strawberries, peppers and tomatoes, in the same meal. Vitamin B2 also helps in the absorption of this mineral. Have this behavior if the need for iron is indicated in orange or red.

Avoid

Foods rich in calcium, coffee and teas, in the same meal with iron, as they impair iron absorption.

Where to find

Red meat from all animals, dark green vegetables (broccoli, kale and other brassicas), pulses (chickpeas, lentils, peas, beans), tofu, seaweed, oats, quinoa, cashew nuts, sesame seeds and pumpkin, cane molasses, brown sugar.

Effect

Example: iron is a cofactor of CYP2R1. For those with the 'G' allele of A226-2810C, which is associated with reduced levels of circulating vitamin D, iron supplementation can ensure that CYP2R1 is working at peak, despite the importance of this SNP in bone health and other cellular functions is probably smaller.

Genes

HFE, NOS3, TF, TFR2, TMPRSS6

7. Minerals

Calcium

MEDIUM

Indication in orange or red, indicates increased need for calcium.

Recommendations

Assess ionic calcium, total serum calcium, 24-hour urine calcium, intact PTH, and vitamin D.

Complement

Chelated calcium, calcium citrate, calcium citrate malate are some of the main forms used in nutritional supplements

Where to find

Calcium: Animal origin: Milk, Yogurt, Cheese. Vegetable origin: Broccoli, Okra, Plums, Brazil Nut, Baked Beans, Tofu.

Genes

CARS, CASR, CYP24A1, CYP2R1, DGKH, F13A1, F13B, F2, F5, F9, GATA3, GC, LPL, MCM6, NR3C1, SELE, TNFRSF11B, VDR

Magnesium

HIGH

Orange or red result indicates increased magnesium requirement.

Complement

Magnesium, in the form of citrate, glycinate / bisglycinate, aspartate, ascorbate, chloride, among others.

Where to find

Among the foods that contain magnesium are seeds and nuts such as sesame, peanuts, sunflowers, almonds, chestnuts, hazelnuts, baru; pulses such as soybeans, chickpeas, beans and lentils and peas; in addition to dark green leaves, such as several Non-Conventional Food Plants (PANCs), kale and spinach.

Genes

ABCB1, ACE, ACHE, ACP7, ADCY5, ADD1, ADD2, ADIPOQ, ADRA2A, ADRB2, AGT, AGTR1, AOC1, APOE, APOE4, ARHGAP30, ARHGEF3, ARL15, AS3MT, ASIC2, ATP2B1, ATP6V1B1, AVPR1A, BAG3, BAG6, BCAT1, BCR, BDNF, BMP2, BMPR1B, BMPR2, BRAP, BTD, CACNB2, CALCA, CAPN10, CASR, CASZ1, CAV3, CBLB, CCL2, CDH13, CDKAL1, CDKN2A, CDKN2A/B, CDKN2B-AS1, CELSR2, CETP, CHRDL1, CHRM2, CLCN6, CLEC16A, CLOCK, CNNM1, COMT, CRP, CTLA4, CYP19A1, CYP2R1, CYP4A11, DAPK1, DAT, DCDC5, DMD, DNAJC5B, DNER, DSG2, ENPP1, ERBB3, ESR1, F12, F7, FAM58A, FDPS, FGF20, FKBP5, FLJ25967, FMN2, FTCDNL1, FTO, GAD1, GATA2, GATA4, GCK, GCKR, GPHN, GPX1, GPX4, GRIA3, GRK5, GUCY1A3, HCG17, HHEX, HIVEP2, HLA-DQA1, HLA-DQB1, HNF1A, HSPD1, HSPE1, HTR2A, HTR2C, IFIH1, IGF2, IGF2BP2, IL-1B, IL-2RA, IL-4, IL-6, IL-7R, INSIG2, INTERGENIC, IRS1, ITGA11, ITGB3, JAG1, JAZF1, KCNE1, KCNE2, KCNE3, KCNJ11, KCNQ1, KL, LEPR, LIPA, LIPC, LPL, LRP4, LRP5, LRP8, LUZP2, M6PR, MACROD2, MAGT1, MAOA, MC4R, MDS1, MMP3, MMP9, MOV10, MRAS, MTHFD1, MTHFD1L, MTHFR, MTNR1B, MTRR, MTTP, MUC1, MYBPC1, MYBPC3, MYO16, NAA25, NAF1, NEDD4L, NFE2L2, NGF, NOS3, NOTCH2, NOV, NPAS2, NPPA, NR2F2-AS1, NR3C1, OLR1, OPRM1, PAX4, PDE11A, PDE9A, PECAM1, PEX5L, PHACTR1, PHTF1, PLCL2, PLPP3, PLTP, PPARG, PPARGC1A, PRMT7, PSMA6, PSRC1, PTPN2, PTPN22, PTPRD, PTPRS, QPCT, RASGRP1, RBMS1, RHOU, RPSAP52, RYR2, SCN5A, SDHAF4, SEZ6L, SH2B3, SHROOM3, SLC2A14, SLC30A8, SLC64A, SMAD3, SOD2, STK39, TAP2, TAS2R16, TCF7L2, TGFBR3, THADA, THBS2, TLR2, TLR4, TMPO, TNF, TNFSF4, TPH1, TPH2, TRIB3, TRPM6, TRPM7, TTN, TTR, TXNRD2, UBE2E2, UBQLN1P, VDR, VPS26A, VPS33B, WFS1, WNT16, WSCD2

7. Minerals

Potassium

NORMAL

Orange or red result indicates increased potassium requirement.

Recommendations

If indicated in orange or red, as well as in any individual, evaluating serum potassium levels will not help to verify the sufficiency of this mineral. The 24-hour urine potassium assessment is the most accurate way to estimate the intake that occurred throughout that day.

Complement

Chelated potassium, potassium citrate, potassium rich foods.

Avoid

If indicated in orange or red, avoid L-methionine supplementation

Where to find

Banana, Beetroot (it has 350 mg of potassium in 100 grams, practically the same amount as a banana), Sweet Potato (337 mg of potassium in every 100 grams), Tomato sauce, Spinach, Oatmeal, Avocado, Raisin, Almond.

Effect

Example: Potassium is one of two cofactors for MAT1A needed for it to work properly. In those carriers of a single 'A' risk allele, G791A supplementation can ensure that MAT1A is working optimally, potentially limiting methionine accumulation and generating more SAMe.

Genes

MAT1A, SCNN1B

Phosphor

NORMAL

Result in orange or red indicates greater need for phosphorus.

Genes

ALPL, C12ORF4, CSTA, PDE7B, TKT

7. Minerals

Iodine

HIGH

Results in orange and red indicate increased iodine requirement.

Recommendations

For people indicated in orange or red, adequate iodine intake is especially important to minimize the risk of thyroid dysfunction and its consequences.

Complement

Chelated iodine, kelp iodine, IPlus are the main forms of iodine on the market.

Where to find

Seaweed, fish and seafood.

Genes

ABCC4, ARVCF, ATM, AURKA, BARD1, BMPR1B, BRCA1, BRCA2, CAPZB, CASC16, CASC17, CASC21, CASC8, CASP8, CCNE1, CDH1, CDKN1A, CDKN1B, CDKN2A, CDKN2B-AS1, CHEK2, COMT, CTLA4, CYP17A1, CYP24A1, CYP3A4, DAB2IP, DIO2, EHBP1, ELAC2, EPCAM, ESR2, FAM124A, FANCA, FCHSD1, FGF7, FGFR2, FGFR4, FTO, FYCO1, GAD1, GPX4, GSTP1, HER2, HLA, HMMR, HNF1B, IL-10, INTERGENIC, ITGA2, ITGA6, JAZF1, KIAA1211, KLF6, LPAR6, LSP1, MAGEC3, MAP3K1, MRPS30, MSMB, NCOA3, NOS3, NQO1, PCAT19, PDE8B, PHTF1, PTCSC2, RNASEL, SELENOP, SH2B3, SLCO1B3, STAT5B, TCF2, TCF7L2, TG, TMPRSS2, TNF, TP53, TPD52, VAV3, VDR, VTCN1, WRN, XRCC1, XRCC2, ZNF827

Molybdenum

NORMAL

Orange or red result indicates increased need for molybdenum.

Recommendations

Molybdenum aids in liver detoxification, acting as a cofactor for three essential enzymes. Furthermore, molybdenum can regulate the metabolism of calcium, magnesium, copper and facilitate the utilization of iron.

Complement

Chelated molybdenum, if indicated in orange or red. The IDR is 45mcg.

Genes

GPHN, MOCS1, MOCS2

7. Minerals

Chrome

MEDIUM-HIGH

Result in orange or red, indicates increased need for chrome

Recommendations

Intestinal absorption of chromium is increased by the concomitant intake of foods rich in vitamin C, such as oranges and pineapples.

Complement

GFTF chromium, DNG chromium, chromium picolinate

Informations

Chromium Picolinate acts by potentiating the action of insulin and can increase the fluidity of the cell membrane, facilitating the binding of insulin with its receptor and its internalization. Its role in lipid metabolism is related to an increase in high density lipoproteins (HDL) and a reduction in total cholesterol and low density lipoproteins (LDL, VLDL) in individuals with initially high values.

Genes

ABCA1, ABCG8, APOA5, APOC1, APOE, AR, BRCA2, CPS1, CR1L, DNAH11, DOCK7, FABP2, FADS1, FADS2, GCKR, GPX1, JMJD1C, LDLR, LPL, MLXIPL, MTHFR, NAF1, OR4A46P, PHYHIP, RAB11B, TMEM241

8. Amino Acids

L-theanine

HIGH

Result in green or blue indicates greater benefit from food supplementation with L-theanine.

Recommendations

L-theanine is a natural amino acid with several benefits in the modulation of sleep and anxiety, cognition, elevation of serotonin and dopamine levels and the cardiovascular system.

Complement

L-theanine, orally or sublingually.

Genes

ACE, ADD1, ADRB2, AOC1, APOE, APOE4, ASIC2, ATP2B1, AVPR1A, BAG3, BDNF, BRAP, BTD, CACNB2, CAV3, CCL2, CDH13, CDKN2B-AS1, CETP, CHRDL1, CRP, CYP2R1, DCDC2, DCLK1, DMD, DNAJC5B, DSG2, DTNBP1, F12, F7, FGF20, FLJ25967, FMN2, GATA2, GATA4, GCLC, GTF2I, HSPD1, HSPE1, IL-17A, IL-17F, IL-4, IL-6, INTERGENIC, ITGB3, JAG1, KCNE1, KCNE2, KCNE3, KCNQ1, KIAA0319, KL, KLF6, LIPA, LRP8, MAOA, MMP3, MMP9, MRAS, MTHFD1, MTHFD1L, MYBPC3, NAF1, NGF, NOS3, NPPA, OLR1, PECAM1, PHACTR1, PLCL2, PLPP3, PNPLA3, PPARGC1A, PSMA6, PSRC1, RGS2, RYR2, SCN5A, SEZ6L, SH2B3, SLC38A8, SLC64A, SMAD3, TDP2, THBS2, TLR4, TMPO, TNF, TNFSF4, TPH2, TTN, TTR, TTRAP, TXNRD2

8. Amino Acids

L-tyrosine

NORMAL

Result in green or blue indicates greater benefit from food supplementation with L-tyrosine.

Recommendations

The need for tyrosine increases especially when the individual is overworked or has to face unforeseen problems. In individuals in green or blue, the use of L-tyrosine can increase dopamine levels, aiding in mood and cognitive function, since in these individuals this polymorphism reduces the number of dopamine receptors in the brain, and may partially compensate for this deficit

Complement

L-tyrosine (500 to 1500mg/day)

Where to find

Chicken, turkey, fish, peanuts, almonds, avocado, milk, cheese, yogurt, bananas and soy products.

Effect

Example: For carriers of the 'T' risk allele of C957T in the DRD2 gene, who demonstrate reduced levels of dopamine in the brain, supplementation may be beneficial. A 2016 study demonstrated that a 2g dose of tyrosine 1 hour before testing improved performance for those carrying two copies of the 'T' risk allele. Practical experience shows that 1g doses can already have a noticeable clinical effect in about 30 to 60 minutes.

Informations

Increasing the level of dopamine, in deficient individuals, indicated in orange or red, can help to reduce the feeling of stress, the feeling of cold, fatigue, tiredness and insomnia. There is also some evidence that there may be improvement in mental performance, depression, and improved sexual desire.

Genes

DRD2

8. Amino Acids

L-methionine

NORMAL

Resultado em verde ou azul indica maior benefício de uma maior ingestão ou complementação com L-metionina.

Recommendations

Check serum levels of vitamin B12 and zinc, and ensure optimal levels, since, in individuals indicated in green or blue, these nutrients help to improve the endogenous resynthesis of L-methionine.

Complement

L-methionine (500 to 1500mg/day), vitamin B12 (methylcobalamin) and zinc.

Where to find

Animal proteins are very rich in methionine: beef, pork, chicken, fish (tuna, cod, mahi mahi, salmon, tilapia, sole and others), eggs (especially the white), chicken, turkey, buffalo, crustaceans, rabbit, cheeses. Plant sources: Brazil nuts, sesame, sunflower and oats. Exposure to boiling and soaking generates significant reductions in methionine levels, since it is very soluble in water.

Effect

Example: The "T" risk allele of C1080T has been associated with an increased risk of cancer when dietary methionine intake is low. It is unclear how low methionine interacts with the "T" allele of C1080T.

Informations

Methionine is an essential sulfur amino acid that is a precursor to cysteine (which in turn is a precursor to glutathione) and taurine (the most abundant amino acid in our bodies). In addition, methionine is necessary for the production of creatine, which is found in muscle.

Genes

DCLK1, GAD1, GCLC, KLF6, MAT1A, MTRR, PNPLA3, PPARGC1A, SLC38A8

8. Amino Acids

L-arginine

NORMAL

Result in green or blue indicates greater benefit from an increased intake of L-arginine or its supplementation.

Recommendations

Arginine is an amino acid that stimulates the production of lymphocytes, essential in the body's defense, helps to inhibit the growth of various types of tumors, and is a precursor of nitric oxide, a molecule with important immunological, neurological and vascular action.

Complement

L-arginine (500 to 1000mg/day)

Avoid

Individuals with herpes should avoid supplementing with L-arginine as there may be an increased frequency of infections.

Genes

ASL, GATM, HBA1, HBB, INTERGENIC, KLKB1, SLC7A2

L-lysine

LOW

Result in green or blue indicates the benefit of L-Lysine consumption or its complementation.

Recommendations

Lysine is an essential amino acid, which means the human body cannot make it. Collagen is mostly composed of three main amino acids: proline, glycine and lysine (which forms hydroxyproline).

Genes

ASS-1, INTERGENIC, PARK2, SCCPDH, SLC7A9

8. Amino Acids

L-alanine

MEDIUM-HIGH

L-alanine

Genes
AGXT2, CCSER1, DLGAP1, GCKR, PRODH

L-asparagine

UNDEFINED

L-asparagine

Genes
ASPG

L-cysteine

NORMAL

L-cysteine

Genes
CD2AP, CTH, GCLM, PCK1

L-phenylalanine

NORMAL

L-phenylalanine

Genes
PAH

8. Amino Acids

L-glycine

NORMAL

L-glycine

Genes
ACADM, CPS1, INTERGENIC, PHGDH

L-glutamine

HIGH

L-glutamine

Genes
COL1A1, COL3A1, EPHX1, MCT1, MMP3, OPRM1, SOD3, SPRYD4

L-histidine

MEDIUM

L-histidine

Genes
HAL, HDC, HNMT

L-homoarginine

NORMAL

L-homoarginine

Genes
AGXT2, MED23

8. Amino Acids

L-isoleucine

NORMAL

L-isoleucine

Genes
GCKR

L-leucine

NORMAL

L-leucine

Genes
PPM1K

L-ornithine

NORMAL

L-ornithine

Genes
SLC7A2

L-proline

NORMAL

Proline is considered a non-essential amino acid because it is produced by the body from glutamic acid. Therefore, consuming this nutrient through diet helps in the synthesis of collagen and influences the support of tissues. In this article, we will explain in more detail its importance and how it can play a role in the healing process.

Genes
PRODH

8. Amino Acids

L-serine

NORMAL

Serine is an amino acid that is a constituent of proteins (chains of amino acids), which is not essential in the human diet, since it can be synthesized from other compounds. Its deficiency includes a group of inborn errors of metabolism in which there is a defect in this amino acid due to alteration in its synthesis, preferentially affecting the nervous system. Serine also helps in the production of antibodies and immunoglobulin, molecules essential for maintaining a healthy immune system. Although in small quantities, to synthesize tryptophan, serine is required together with vitamins such as folic acid, vitamin B3 and vitamin B6. Tryptophan is in turn a precursor of serotonin, which regulates mood and spirit. It performs other functions related to maintaining skin hydration, synthesis of compounds such as creatine and purines. It is necessary for the metabolism of fats, correct functioning of cell replication, muscle development and is essential for the correct functioning of the immune system.

Genes

PHGDH

L-taurine

MEDIUM-HIGH

Taurine is found in large amounts in the brain, retina, heart, and blood cells called platelets. The best dietary sources are meat, fish, and eggs. The body usually produces taurine on its own. However, some people cannot survive and need to get taurine from their diet or supplements.

Genes

ADRB2, APOE4, BCAT1, C5ORF67, CYP1A1, ENPP1, GRK4, IL-6, IRS1, PLIN1

8. Amino Acids

L-threonine

MEDIUM

Threonine is classified as an essential amino acid, meaning the only way to get it is through diet or supplementation. Meat, dairy, soy products, legumes, and seeds are the best natural sources of threonine. Threonine is a key component of structural proteins such as collagen and elastin, which are important components of skin and connective tissue. It also plays a role in fat metabolism and immune function.

Genes

PEMT, PNPLA3, PPARGC1A, SH2B1

L-valine

NORMAL

Valine is one of the three branched-chain amino acids. It helps stimulate muscle growth and regeneration and is involved in energy production.

Genes

PPM1K

Beta-alanine

HIGH

Beta-alanine is a non-essential amino acid that is produced naturally in the body. Beta-alanine aids in the production of carnosine. That's a compound that plays a role in muscle endurance in high-intensity exercise.

Genes

ADRB2, AMPD1, GABPB1, PPARD, SLC17A7, TNF

8. Amino Acids

L-carnitine Deficiency

NORMAL

L-carnitine deficiency can cause muscle necrosis, myoglobinuria, lipid storage myopathy, hypoglycemia, liver fat and hyperammonemia with muscle pain, fatigue, confusion and cardiomyopathy.

Genes
SLC22A5

Monohydrate Creatine

HIGH

Creatine improves overall performance, increases muscle mass, strength, and endurance performance. When it comes time to train, if your muscles have been saturated with creatine, they will use the stored creatine to provide fuel for your body - giving you the ability to maximize your output during training.

Genes
ACTN3, CNTF

9. Supplements and Antioxidants

Betaine

MEDIUM

Result in orange or red indicates greater need for it (since there is less endogenous production).

Recommendations

Betaine acts as a methyl donor in the conversion of homocysteine to methionine by BHMT. However, it is not clear whether the "G" or "A" allele of G716A increases the need for betaine, a fact that can be evaluated if there are other changes in homocysteine metabolism.

Complement

Trimethylglycine (Betaine) and betaine hydrochloride (Betaine HCl). Both work.

Where to find

Beetroot, Fish, Spinach, Broccoli, Legumes.

Genes

BHMT, MTHFR, SLC19A1

Tetrahydropiobterine (BH4)

NORMAL

Orange or red indicates increased need for tetrahydrobiopterin supplementation, with the aim of optimizing nitric oxide synthesis.

Recommendations

Tetrahydrobiopterin is a cofactor in the synthesis of nitric oxide and several neurotransmitters, together with vitamin B2 and iron. Individual analysis of polymorphisms: rs1800779 - presence of the G allele rs1799983 - presence of the T allele rs1800783 - presence of the A allele If any of the alleles indicated above are present, in their respective rs numbers, consider: Optimizing the intake of vitamin B2 and iron. Supplement with tetrahydrobiopterin. Use the enzyme nattokinase, and coenzyme Q10, to reduce cardiovascular risk. Restrict sodium intake. Furthermore, in individuals with rs1799983 - presence of the T allele, optimize intake/supplement with omega 3 fatty acids to reduce cardiovascular risk. In individuals with rs1800779, bergamot oil, rich in melitidine and brutieridine, should be considered for having statin-like and antihypertensive properties.

Complement

In addition to the above, note in this panel the need and/or benefit of supplements such as Natto (nattokinase), Coenzyme Q10, bergamot oil, omega 3, as they may be complementary to this assessment.

Genes

NOS3

9. Supplements and Antioxidants

Coenzyme Q10

HIGH

Orange or red result indicates increased need for Coenzyme Q10.

Recommendations

Assess serum ubiquinol levels, and keep them optimal. It evaluates a set of genes associated with the metabolism of ubiquinone and ubiquinol, implying their nutritional needs.

Complement

Coenzyme Q10 (ubiquinone) or ubiquinol, its reduced form, both can be found as dietary supplements. Always prefer those with a lipid base, which increases its bioavailability.

Effect

Example: Supplementation may be beneficial for those carrying the "G" allele of G2328A.

Genes

ABCB1, ACE, ADD1, ADRB2, AOC1, APOE, APOE4, ARHGAP30, ASIC2, ATP2B1, BAG3, BRAP, BTD, CACNB2, CAT, CAV3, CCL2, CDH13, CDKN2B-AS1, CELSR2, CETP, CHRDL1, COLEC12, COQ2, COQ4, COQ6, COQ7, COQ8A, COQ9, CRP, CYP2R1, DHFR, DMD, DNAJC5B, DPYD, DSG2, F12, F7, FGF20, FLJ25967, FMN2, FOXE1, GAD1, GATA2, GATA4, HLA-DRA, HLA-DRB1, HSPD1, HSPE1, IL-4, IL4R, INTERGENIC, ITGB3, JAG1, KCNE1, KCNE2, KCNE3, KCNQ1, KL, LIPA, LIPC, LPL, LRP8, MAOA, MAT1A, MC1R, MC4R, MCT1, MMP3, MMP9, MRAS, MTHFD1, MTHFD1L, MYBPC3, NAF1, NOS3, NPPA, NQO1, NQO2, OLR1, PACERR, PDSS1, PDSS2, PECAM1, PHACTR1, PLCL2, PLPP3, PLTP, PSMA6, PSRC1, RYR2, SCN5A, SEZ6L, SH2B3, SIRT1, SMAD3, STAT4, THBS2, TLR4, TMPO, TNF, TNFSF4, TTN, TTR, TXNRD2, TYR

9. Supplements and Antioxidants

Resveratrol

HIGH

Green or blue results indicate increased benefit from the use of resveratrol.

Complement

Food supplements based on resveratrol.

Where to find

Grapes, strawberry, cranberry, lingonberry and other foods.

Informations

Studies seem to indicate that resveratrol can help lower LDL levels and raise HDL cholesterol levels. LDL, particularly in its oxidized state, can accumulate in blood vessel walls, leading to the formation of atheromatous plaques, and resveratrol reduces LDL oxidation. Thus, it plays an important role in reducing the risk of developing cardiovascular disease.

Genes

ABCA1, ABCG8, ABI3BP, APOC1, APOE, AR, ARVCF, B3GALT1, BRCA2, CASC17, CASC21, CASC8, CDH1, CDKN1B, CHEK2, CPS1, CR1L, CYP17A1, CYP1A1, CYP24A1, CYP3A4, DAB2IP, DEF8, DNAH11, EHBP1, ELAC2, ERI1, ESR2, FABP2, FADS2, FAM124A, FCHSD1, FGFR4, FYCO1, GPX1, HDAC4, HNF1A, HNF1B, IL-10, INTERGENIC, IRF4, ITGA2, ITGA6, JAZF1, KIAA1211, KLF6, LDLR, MAGEC3, MC1R, MGMT, MSMB, MTHFR, NAF1, OR4A46P, PCAT19, PCIF1, RNASEL, SELENON, SELENOP, SIRT1, SLC45A2, TCF2, TCF7L2, TGFBR1, TMPRSS2, VDR, XRCC1, ZNF827

9. Supplements and Antioxidants

Quercetin

HIGH

Result in green or blue indicate greater benefit from dietary supplementation with quercetin.

Recommendations

Quercetin has benefits in modulating allergies, oxidative stress, thrombosis risk, immune and cardiovascular health. If indicated in green or blue, it is especially interesting to increase the consumption of foods source of quercetin.

Complement

If indicated in green or blue, it is suggested to increase the intake of quercetin, via food supplements, and via food, in particular, through foods such as red onion, red lettuce, black tea, apple, pepper, broccoli, among others.

Where to find

Unpeeled apples, red grapes, red onions, yellow peppers, capers, broccoli, cranberry, black olives, green beans, black tea, romaine lettuce, kiwi are sources of quercitin.

Informations

Quercetin is a flavonoid with anti-inflammatory, antioxidant, hepatoprotective, antihistamine properties and alleviates some symptoms of allergic problems such as runny nose, hives and swelling of the lips.

Genes

ABCB1, ACE, ADD1, ADRB2, AOC1, APOE, APOE4, ASIC2, ATP2B1, BAG3, BRAP, BTD, CACNB2, CAV3, CCL2, CDH13, CDKN2B-AS1, CETP, CHRDL1, CLEC16A, CRP, CRTH2, CYP2R1, DHFR, DMD, DNAJC5B, DPYD, DSG2, F12, F13A1, F13B, F2, F5, F7, F9, FGF20, FLJ25967, FMN2, FOXE1, GATA2, GATA4, HLA-DQB1, HLA-DRA, HLA-DRB1, HSPD1, HSPE1, IL-10, IL-13, IL-1RL1, IL-4, IL-6, IL4R, INTERGENIC, ITGB3, JAG1, KCNE1, KCNE2, KCNE3, KCNQ1, KL, LIPA, LPL, LRP8, MAOA, MMP3, MMP9, MRAS, MTHFD1, MTHFD1L, MYBPC3, NAF1, NOS3, NPPA, OLR1, PECAM1, PHACTR1, PLCL2, PLPP3, PSMA6, PSRC1, RYR2, SCN5A, SELE, SEZ6L, SH2B3, SMAD3, STAT4, TBX21, TGFB1, THBS2, TLR2, TLR4, TMPO, TNF, TNFSF4, TSLP, TTN, TTR, TXNRD2, TYR, WDR36, ZBTB10

9. Supplements and Antioxidants

Zeaxanthin

MEDIUM

Green or blue result indicates greater benefit from increased zeaxanthin consumption.

Recommendations

Zeaxanthin is a carotenoid with antioxidant action. Low plasma concentrations increase the risk of developing age-related macular degeneration. In Brazil there are more than 3 million people with this condition.

Complement

Zeaxanthin

Where to find

Cabbage, Swiss chard, spinach and watercress, plus corn, red peppers, boiled peppers, orange and tangerine.

Effect

Example: In carriers of the 'A' allele of G66 + 1594A who are at risk of free radical production in the macula, leading to the development of AMD and vision loss, zeaxanthin can serve two purposes. Protect against oxidative damage from free radicals and protect against additional damage resulting from exposure to light.

Genes

ABCA1, ARMS2, BCO1, C2, C3, CETP, CFB, CFH, COL8A1, CRYBB2, CRYBB3, CRYGD, CX3CR1, EPHA2, FGD6, GJA8, GSR, HTRA1, INTERGENIC, KL, MAF, MC1R, NOTCH4, PITX2, REST, SERPINF1, SIRT1, SKIV2L, SOD2, SOD3, TLR3, VEGFA

9. Supplements and Antioxidants

Lutein

HIGH

Result in green or blue, indicates increased benefit of lutein consumption.

Recommendations

In individuals indicated in green or blue, in particular, there will be a great benefit from increased consumption of lutein which can protect against oxidative stress and against damage resulting from exposure to light, preventing Macular Degeneration. In addition, lutein can protect against premature skin aging, it helps to strengthen the immune system, protect against tumor cell replication and cardiovascular protection, by reducing LDL oxidation.

Complement

Lutein

Where to find

Kale, Spinach, Watercress, Corn, Egg, Celery, Green lettuce, edible petals of the nasturtium flower. The presence of lipids increases the absorption of lutein, whereby the naturally emulsification of lutein with egg yolk fats gives it a high bioavailability and incorporation into the body in this food.

Effect

Example: Carriers of the 'A' allele of G66 + 1594A are at increased risk of oxidative stress in the retinal macula, leading to the development of Age Related Macular Degeneration.

Genes

ABCA1, ABCB1, ACE, ADD1, ADRB2, AOC1, APOE, APOE4, ARMS2, ASIC2, ATP2B1, BAG3, BCO1, BRAP, BTD, C2, C3, CACNB2, CAV3, CCL2, CD36, CDH13, CDKN2B-AS1, CETP, CFB, CFH, CFI, CHRDL1, COL8A1, CRP, CRYBB2, CRYBB3, CRYGD, CX3CR1, CYP2R1, DHFR, DMD, DNAJC5B, DPYD, DSG2, EPHA2, F12, F7, FGD6, FGF20, FLJ25967, FMN2, FOXE1, GATA2, GATA4, GJA8, GSR, HLA-DRA, HLA-DRB1, HSPD1, HSPE1, HTRA1, IL-4, IL4R, INTERGENIC, ITGB3, JAG1, KCNE1, KCNE2, KCNE3, KCNQ1, KL, LIPA, LRP8, MAF, MAOA, MC1R, MMP3, MMP9, MRAS, MTHFD1, MTHFD1L, MYBPC3, NAF1, NOS3, NOTCH4, NPPA, OLR1, PECAM1, PHACTR1, PITX2, PLCL2, PLPP3, PSMA6, PSRC1, REST, RYR2, SCN5A, SERPINF1, SEZ6L, SH2B3, SIRT1, SKIV2L, SMAD3, STAT4, THBS2, TLR3, TLR4, TMPO, TNF, TNFSF4, TTN, TTR, TXNRD2, TYR, VEGFA

9. Supplements and Antioxidants

Uridine Monophosphate

MEDIUM-HIGH

Result in green or blue indicates greater benefit from complementing with this element.

Recommendations

It stimulates the growth of axons, stabilizes cell membranes in nerve cells and increases acetylcholine synthesis. It is used in the prevention and treatment of neurological disorders including Alzheimer's.

Complement

Uridine can be supplemented orally or sublingually with good results in humans, especially if supplemented with phosphatidylcholine and DHA (omega 3), to improve cognition, and may be useful in individuals indicated in green or blue.

Genes

ARRB2, BDNF, CLOCK, CLSTN2, DBH, DDC, DRD4, DTNBP1, FADS2, GRK3, HES1, HTR1B, HTR2A, NT5C3A, NTF3, PNMT, SIRT1, SLC1A3, SLC64A, SLC6A2, SLC6A3, SLC9A9, SNAP25, TPH2, WWC1

9. Supplements and Antioxidants

Lycopene

MEDIUM

Lycopene is a carotenoid substance that gives tomatoes, watermelons, guavas, and other foods their reddish color. It is an antioxidant that, when absorbed by the body, helps prevent and repair cell damage caused by free radicals. Free radicals are produced during normal bodily functions, such as breathing and physical activity. They are also formed as a result of smoking, overexposure to the sun, air pollution, and stress. They are highly reactive and, if left unchecked, can damage important molecules in healthy cells in the human body. This can contribute to the development of various diseases, such as cancer and cardiovascular disease.

Genes

BCO1, SCARB1, SETD7, SOD2

CLA

NORMAL

CLA is a fatty acid from the same family as omega-6, and it has health benefits such as weight control, reducing body fat and strengthening the immune system.

Genes

LEP, PPARG, TNF

Turmeric (Turmeric)

MEDIUM

Benefit from regular turmeric intake, by stimulating the endogenous antioxidant system, and stimulating DNA repair.

Genes

BIN1, SOD3

9. Supplements and Antioxidants

Beta-casein A1

MEDIUM-HIGH

Casein is often referred to as an “anti-catabolic” protein. What exactly does that mean? Your body catabolizes, or basically breaks down, muscle tissue to obtain the amino acids that are stored within muscle protein. It uses these stored amino acids for energy and helps with various functions, such as growth and development. The more you exercise, the more your body will seek out available protein to keep you going. Anti-catabolic supplements provide amino acids that help minimize this breakdown process, sparing you the hard-earned muscle mass. It lasts longer than other protein sources. Although it is absorbed quickly, casein is still considered a relatively “slow-digesting” protein due to the length of time its amino acids remain within the bloodstream. Just as slower-release carbohydrates are beneficial, as opposed to the fast-acting types that can spike blood sugar quickly, protein foods can sometimes work in the same way.The body can digest casein protein slowly, which means that muscle tissue has a greater opportunity to use the amino acids for repair and growth work. As you’ll learn below, casein timing definitely has its advantages, however, depending on your goals, there are certain times when you want to skip casein and use a faster-acting protein. A1 is the “newer type of casein,” which evolved sometime in the last few thousand years after animal domestication. It happened after certain genes caused the protein to change, resulting in the amino acid proline changing to histidine. Today, A1 beta-casein is most abundant in dairy cows, which are used to produce the vast majority of milk in the West. Each cow has a certain genotype of A1/A1, A1/A2, or A2/A2 that affects the milk she produces. It is preferable to consume dairy products, including all dairy products and whey/casein protein supplements, made from cows (or goats) that contain predominantly A2 casein.Why? When A1 beta-casein caused a shift from proline to histidine amino acids, it resulted in problems with humans properly digesting and metabolizing milk. In fact, most people who are intolerant to cow's milk are actually sensitive to one of the proteins found in it, A1 casein. They essentially lack the ability to digest A1. This intolerance is now linked to a wide range of diseases, including autoimmune reactions, food allergies, digestive problems, type 1 diabetes, heart disease, and more. A1 is also believed to promote inflammation, however, milk that contains mostly or exclusively A2 casein produces much less (or no) inflammatory effects. An orange or red result indicates a better response, but one should always look at the inflammatory aspects of A1 casein.

Genes

CBLB, ERAP1, FOXO3, HCG17, IL-6R, INTERGENIC, MCM6, NFE2L2, NOD2, STAT6, TLR6, UBQLN1P

9. Supplements and Antioxidants

Beta casein A2A2

HIGH

Casein is one of the main nutrients in milk and is important for the growth and maintenance of muscle tissue. β-casein makes up 30% of the total protein in cow's milk, with types A1 and A2A2 being the most common. According to studies carried out on dairy herds of the Guzerá (97%) and GIR (96%) breeds, they have a higher occurrence of A2A2 alleles, which determines the presence of the A2A2 beta-casein protein in the milk produced by animals of these breeds. These results demonstrate the potential for A2A2 production by zebu breeds. This type of casein comes from milk produced by cows of the A2A2 genotype that produce milk with only A2A2 β-casein. Some studies indicate that people who are allergic to milk may actually be allergic to type A1 casein protein. If this is the restriction for some, type A2A2 milk may be the solution. Casein is generally known as an “anti-catabolic” protein.What exactly does this mean? Your body catabolizes, or basically breaks down, muscle tissue to get the amino acids that are stored inside muscle protein. It uses these stored amino acids for energy and to help with various functions, such as growth and development. The more you exercise, the more your body will seek out available protein to keep you going. Anti-catabolic supplements provide amino acids that help minimize this breakdown process, sparing you the hard-earned muscle mass. It lasts longer than other protein sources. Although it is absorbed quickly, casein is still considered a relatively “slow-digesting” protein due to the length of time its amino acids remain within the bloodstream. Just as slower-release carbohydrates are beneficial, as opposed to the fast-acting types that can spike blood sugar quickly, protein foods can sometimes work in the same way. The body can digest casein protein slowly, which means that muscle tissues have a greater opportunity to use the amino acids for repair and growth work. Casein timing definitely has its advantages, however, depending on your goals, there are certain times when you may want to skip casein and use a faster-acting protein. Red or orange results indicate a better response to Casein A2A2.

Genes

DLK1, DMD, INTERGENIC, MTRR, PPARD, STAT6

Whey Protein

LOW

Whey Protein is a protein supplement made from protein extracted from whey, composed mainly of alpha-globulin and beta-globulin. The product contains essential amino acids that are quickly absorbed by the body, substances that actively participate in the construction of muscles and tissues.

Genes

ANOS1, GEMIN8, INTERGENIC, MCM6, PPARD, STAT6, TLR6, TRIM63

9. Supplements and Antioxidants

BCAA levels

NORMAL

A branched-chain amino acid (BCAA) is an amino acid having an aliphatic side-chain with a branch (a central carbon atom bound to three or more carbon atoms). Among the proteinogenic amino acids, there are three BCAAs: leucine, isoleucine, and valine. Non-proteinogenic BCAAs include 2-aminoisobutyric acid, Leucine, Isoleucine, Valine. The three proteinogenic BCAAs are among the nine essential amino acids for humans, accounting for 35% of the essential amino acids in muscle proteins and 40% of the preformed amino acids required by mammals. Synthesis for BCAAs occurs in all locations of plants, within the plastids of the cell, as determined by presence of mRNAs which encode for enzymes in the metabolic pathway. BCAAs fill several metabolic and physiologic roles. Metabolically, BCAAs promote protein synthesis and turnover, signaling pathways, and metabolism of glucose. Oxidation of BCAAs may increase fatty acid oxidation and play a role in obesity. Physiologically, BCAAs take on roles in the immune system and in brain function. BCAAs are broken down effectively by dehydrogenase and decarboxylase enzymes expressed by immune cells, and are required for lymphocyte growth and proliferation and cytotoxic T lymphocyte activity. Lastly, BCAAs share the same transport protein into the brain with aromatic amino acids (Trp, Tyr, and Phe). Once in the brain BCAAs may have a role in protein synthesis, synthesis of neurotransmitters, and production of energy.

Genes

AMPD1, BCKDHA, GAD1, SLC17A7

Green Tea

MEDIUM

Slow metabolism of caffeine in green tea, leading to increased anxiety or sleep disturbances.

Genes

CYP1A2

9. Supplements and Antioxidants

Vegetarian Protein Shake

HIGH

Plant-based protein powders and shakes can fit into an overall healthy diet; however, the ideal goal is to first consume a variety of plant-based proteins from whole foods to meet the primary needs and then to supplement with plant-based protein powders when needed

Genes

ACVR2B, CAPN3, DLK1, FTO, GCH1, MCM6, PPARG, TRIM63

9. Supplements and Antioxidants

Benefit of Green Tea

MEDIUM

Result in green or blue indicates greater benefit of green tea in protecting against hepatic steatosis.

Recommendations

For individuals in the green or blue range, drinking green tea regularly, or using dry extract standardized in EGCG 50% or 95%, can be beneficial, as it accelerates PEMT, increasing the endogenous synthesis of phosphatidylcholine from phosphatidylserine, protecting the steatosis liver

Complement

Green tea. It significantly reduces the occurrence of alcoholic hepatic steatosis and its progression, especially in individuals carrying the "A" allele of G523A.

Informations

Green tea, as well as white, oolong and black tea, comes from Camellia sinensis. The main difference between these lies in the method of transformation. While oolong and black teas are made from fermented tea leaves, green tea is practically unfermented, thus keeping most of its active ingredients intact. Green tea leaf extract is rich in polyphenols that have strong antioxidant, hypolipidemic and anti-inflammatory effects. Several studies have been carried out, and it has been suggested that this tea is rich in polyphenols, beneficial for the prevention of heart disease, cancer, neurodegenerative diseases, skin health and many others.

Genes

COMT, PEMT

10. Muscle Fiber type & Contraction

Slow Contraction Fibers

HIGH

They are called slow oxidative fibers or slow contraction fibers, they contain many oxidative enzymes and are involved by more capillaries than any other type of fiber, in addition to having higher myoglobin concentrations than fast fibers, the high myoglobin concentration, the large number of capillaries and the high mitochondrial enzymatic activity make these fibers have a great capacity for aerobic metabolism and high resistance to fatigue. The main difference between a slow-twitch muscle fiber and a fast-twitch muscle fiber is that the fast-twitch muscle fiber is larger and can thus produce more force. The body recruits the lower threshold motor units first (slow twitch), followed by the higher threshold motor units (fast twitch) and continues to recruit and fire motor units until you've applied enough force to do anything, trying to do in relation to the movement.

Genes

AGTR2, PPARA

Fast Twitch Muscle Fibers

MEDIUM

Fast-twitch fibers have a low amount of myoglobin – and therefore also low oxygen content – and for this reason they are not red or reddish, but rather clear. They are also described as white muscle fibers.

Genes

AGTR2

Skeletal muscle fiber contraction

NORMAL

Skeletal muscle fibers contain several hundred to several thousand myofibrils. Each myofibril in turn contains, arranged side by side, about 3000 myosin filaments and about 3000 actin filaments, both responsible for muscle contraction. Results on the right correspond to slower contractions and on the left to faster contractions.

Genes

ACTN3, CNTF

11. Muscle Mass & Hypertrophy

Biceps Increase

HIGH

The biceps is an important muscle that is present in two parts of the body: biceps brachii muscle (located in the arm) and biceps femoris muscle (located in the leg, thigh). However, it is noteworthy that the use of the term biceps is more common to refer to the important muscle of the arm. It is usually the most worked muscle in gyms.

Genes

ACTN3, AGT, ANOS1, IGF2, TRIM63

Muscle Mass Increase

HIGH

Muscle mass is also known as lean mass. Our body is made up of water, lean mass and fat mass. These are the components that give us a weight when we step on the scale, but each of them indicates different aspects. When a person steps on the scale, they may have gained weight. This does not mean that they have gained weight, that is, that they have accumulated fat. On the contrary, they may have burned fat and gained muscle mass, which also weighs, but is healthy for the body.

Genes

ACVR2B, ANOS1, BDNF, CAPN3, DLK1, DMD, GEMIN8, IGFBP3, MTHFR, MTRR, TRIM63

Triceps Increase

HIGH

The triceps is a muscle located in the posterior region of the arm and is divided into three portions: the lateral head, the medial head and the long head. It is responsible for important movements in the region, such as the strength to push. 1) Triceps on the forehead. 2) Triceps rope on the pulley. 3) Support on the ground with closed hands (military flexion). 4) Closed bench press. 5) Dip on parallel bars. 6) Dip on the machine. 7) Dip on the bench. 8) French triceps with dumbbells.

Genes

AGT, COL5A1, MSTN, TRIM63

11. Muscle Mass & Hypertrophy

Pectoralis Major Increase

MEDIUM

The pectoralis major is a muscle group that is divided into two main muscles: the pectoralis major and the pectoralis minor. Generally, the group that is worked in the gym and for aesthetic purposes is the pectoralis major, which is on top and therefore more visible. However, this muscle is also divided into 3 smaller parts: upper, middle and lower, which need to be worked. 1) Incline dumbbell bench press (Exercise focused on working: upper chest), 2) Flat barbell bench press (Exercise focused on working: middle chest), 3) Push-ups and 5) High grip crossover.

Genes

ACTN3, AGT, MSTN, NOS3, VDR

Pectoralis Minor Augmentation

NORMAL

The chest is a muscle group that is divided into two main muscles: the pectoralis major and the pectoralis minor. Generally, the group that is worked in the gym and for aesthetic purposes is the pectoralis major, which is on top and therefore more visible. However, this muscle is also divided into 3 smaller parts: upper, middle and lower, which need to be worked. 1) Lunges on the parallel bars (Exercise focused on working: lower chest), 2) Push-ups and 3) Crossover with high grip.

Genes

AGT, MSTN, NOS3

Teres Major Increase

HIGH

The teres major originates on the posterior surface, lower 1/3 of the lateral border and lower angle of the scapula. It inserts into the medial lip of the intertubercular groove and has the function of adducting and medially rotating the arm.

Genes

COL5A1, NOS3, VDR

11. Muscle Mass & Hypertrophy

Teres Minor Increase

MEDIUM

Barbell row. The rotator cuff muscles that are most worked are the supraspinatus, infraspinatus, and teres minor. Standing, the individual will hold the bar so that the back of the hand is facing upwards, with the arms extended, shoulder-width apart.

Genes
AGT

Serratus Anterior Increase

MEDIUM

Contraction of the entire serratus anterior leads to a ventral and lateral movement of the scapula along the ribs. ... In contrast, the superior portion of the muscle depresses the scapula and thus acts in an antagonistic manner. Another function of the serratus anterior is the active stabilization of the scapula at the shoulder.

Genes
PPARA, VDR

Trapezius Increase

MEDIUM

The trapezius is responsible for supporting the arms, shoulders and even the spine, in addition to being essential for their stability and alignment. Located in the back, the trapezius is much more than the upper and visible part that connects the shoulders and the neck. 1) Dumbbell shrug. 2) Barbell shrug from behind. 3) Barbell shrug from the front. 4) High row. 5) Inverted crucifix on the pulley. 6) Lying inverted crucifix with dumbbells. 7) Alternating lateral raise with low pulley.

Genes
VDR

11. Muscle Mass & Hypertrophy

Forearms Increase

NORMAL

In addition to bodybuilding and training modalities, such as cross-training, strong forearms are the basis for sports such as judo, boxing, climbing and MMA. To obtain a more efficient result in the growth of the forearms: 1) Flexion of the wrists with a bar (wrist curl). 2) Extension of the wrists with a bar. 3) Farmer walk. 4) Wrist roller. 5) Hammer curl.

Genes

LRPPRC, MSTN, NOS3, VDR

Deltoid Increase

HIGH

The deltoids are the muscles of the shoulder, divided into Anterior Head, Lateral Head and Posterior Head. Flexion with feet elevated. 1) The flexion with feet elevated is an exercise that helps to work the strength and endurance of the deltoids, triceps and biceps. 2) Lateral raise. 3) Front raise. 4) Plank with arm elevation. 5) Development. 6) High row.

Genes

ANOS1, COL5A1, MSTN, NOS3, TRIM63, VDR

Hamstrings Increase

HIGH

The hamstrings are a muscle group composed of the semitendinosus, semimembranosus and biceps femoris muscles, which are located in the posterior region of the thigh and hip, and are responsible for performing knee flexion (bending the knee backwards).

Genes

ACVR1B, MMP3, NOS3, TNC, VDR

11. Muscle Mass & Hypertrophy

Calves Muscles Hyperthrophy

LOW

The calf is also known as the potato or the calf and is a muscular prominence called the triceps surae, located on the posterosuperior side of each leg, formed mainly by the gastrocnemius and soleus muscles. Step up on a step or a step; Leave only the tip of one foot supported, keeping the heel unsupported; Leave the other leg bent or straight, but without supporting it on the step, step or the floor; Stretch the calf, pushing the body upwards until the muscle is completely contracted;

Genes

ACTN3, CAPN3, DMD

Thigh Increase and Definition

HIGH

Exercises for strengthening or hypertrophy of the lower limbs must be performed respecting the limits of the body itself and, preferably, under the guidance of a physical education professional to avoid the occurrence of injuries. To achieve hypertrophy it is necessary that the exercises are done intensely, with a progressive increase in the load and following an adequate diet for the objective. In addition to strengthening and hypertrophy, exercises for the lower limbs guarantee good results in terms of reducing sagging and cellulite, in addition to improving body balance due to better stabilization of the knee and ankle. 1) Squats (quadriceps and glutes). 2) 4 sets of 12 to 15 repetitions. 3) Lunge (quadriceps and glutes). 4) 3 sets of 15 reps on each side. 5) Modified Stiff (posterior thigh and glutes). 6) 3 sets of 12 to 15 reps on each side. 7) Leg abduction (side of thigh and glutes)

Genes

ACTN3, ANOS1, DNMT3L, MTRR, TRIM63, VDR

11. Muscle Mass & Hypertrophy

Quadriceps Muscle Strength

MEDIUM-HIGH

The quadriceps (quadriceps) femoral muscle is a four-headed thigh muscle that covers the femur almost completely. It is one of the strongest muscles in the human body (physiological cross-sectional area> 150 cm2). The quadriceps, the large muscles in front of the thighs, are responsible for extending the leg (kicking and passing the ball). The quadriceps of an ordinary person are already slightly stronger than the hamstrings, but in a soccer player, the difference in muscle strength is greater because the quadriceps are more used. If there is a major imbalance, it can result in injury and pain for the player. The best way to avoid this is to make sure that you are training your entire leg. This means doing similar amounts of exercises that focus on each muscle group. An example of this would be: Squats for the glutes and quadriceps, Hip Raises for the hind legs and Calf Raises for the calves. By following your training plan with the Freeletics Training Coach, you ensure that each muscle group in the leg is being worked on effectively and specifically at the same time.

Genes

AGT, COL5A1, MSTN

Vastus Lateral Muscle

NORMAL

The quadriceps muscle performs the knee extension movement and the rectus femoris muscle performs the hip flexion movement. The vastus medial performs medial rotation and the vastus lateralis, lateral rotation.

Genes

AGT, PPARA

Platelet Aggregation with Clopidogrel

LOW

Platelet Aggregation with Clopidogrel

Genes

CES1P1, CYP1A2, PEAR1

12. Vitamin Metabolism

MTHFR 677 mutation (rs1801133)

NORMAL

MTHFR is a key enzyme for certain biological processes, including the conversion of homocysteine into methionine. Mutations in genes that encode this enzyme cause a significant reduction in its activity, causing hyperhomocysteinemia. This condition is related to increased risk for cardiovascular disease and poor pregnancy outcomes. The homozygous genotype for the C677T polymorphism is associated with a 25% increase in the plasma concentration of homocysteine, which can generate genetic alterations in the fetus of pregnant women and thromboembolism.

Genes
MTHFR

MTHFR 1298 mutation (rs1801131)

MEDIUM-HIGH

Another known point mutation for the gene encoding the MTHFR enzyme is the nitrogenous base substitution at nucleotide 1298 (A1298C polymorphism). This mutation, like the C677T polymorphism, results in elevated levels of homocysteine. The homozygous genotype for the A1298C polymorphism is also considered pathogenic, as it considerably increases the risks for thrombotic events and recurrent miscarriages. Individuals heterozygous for the two polymorphisms (C677T and A1298C) are also at high risk for vascular events.

Genes
MTHFR

13. Food Intolerances

Lactose intolerance

LOW

Lactose intolerance is an impaired ability to digest lactose, a sugar found in milk and other dairy products. Lactose is normally broken down by an enzyme called lactase, which is produced by the cells lining the small intestine. Congenital lactase deficiency, also called congenital alactasia, is a condition in which babies are unable to break down lactose in breast milk or formula. This form of lactose intolerance results in severe diarrhea. If affected babies are not given lactose-free infant formula, they can develop severe dehydration and weight loss. Lactose intolerance in adulthood is caused by reduced lactase production after childhood (non-persistence of lactase). If lactose-intolerant individuals consume lactose-containing dairy products, they may experience abdominal pain, bloating, flatulence, nausea, and diarrhea beginning 30 minutes to 2 hours later. Most people with lactase non-persistence retain some lactase activity and may include variable amounts of lactose in their diets without experiencing symptoms. Affected individuals often have difficulty digesting fresh milk, but they can eat certain dairy products, such as cheese or yogurt, without discomfort. These foods are made through fermentation processes that break down much of the lactose in milk.

Genes
LCT, MCM6

Gluten Intolerance

HIGH

Non-celiac gluten intolerance is the inability or difficulty in digesting gluten, which is a protein found in wheat, rye and barley. In these people, gluten damages the walls of the small intestine, causing diarrhea, pain and abdominal swelling, in addition to making nutrient absorption difficult. In celiac disease, gluten intolerance also occurs, but there is a reaction of the immune system causing a more serious condition, with inflammation, intense pain and frequent diarrhea.

Genes
HLA, HLA-DQB1, IL-18RAP, KIAA1109

13. Food Intolerances

Milk Allergy

MEDIUM-HIGH

Tendency to hypersensitivity to cow's milk proteins.

Genes

FAM117A, IL-10, IMPAD1, INTERGENIC, STAT6, TLR6, TMEM26

Peanut Allergy

MEDIUM-HIGH

Tendency to peanut allergy.

Genes

HLA-DQB1, HLA-DRA, HMGA2, INTERGENIC, STAT6, STXBP6

Caffeine Metabolization

MEDIUM

Analysis of a set of genes involved in caffeine metabolism. Indicates whether this metabolism is more or less efficient. Indication in orange or red indicates faster metabolism, and thus, less effect, with smaller doses of it. Results in red is beneficial.

Genes

ADORA2A, AHR, CYP1A1, CYP1A2, RYR1, UBL7

Egg White Allergy

MEDIUM

Egg allergy happens when the immune system identifies the egg white proteins as a foreign body, triggering an allergic reaction.

Genes

ABCB11, COG7, ERCC4, INTERGENIC, ITIH6

13. Food Intolerances

Alcohol

NORMAL

Reduced ability to metabolize acetaldehyde, causing alcohol flushing syndrome and increased cancer risk.

Genes

ADH1B, ALDH2

14. Energy Metabolism

Resting Metabolism

MEDIUM-HIGH

Resting metabolism corresponds to burning up to 75% of what you consume daily. The remaining 25% is spent on food digestion and daily activities, including exercise. In other words, the organs (liver, heart, kidney, brain, lung, etc) and muscles that burn most of the energy in the food we eat are the ones who burn. So if the resting metabolism slows down for some reason, and the calorie intake doesn't change, it's almost certain that we're going to get fat, that is, we're going to store the unused energy in fat cells ("fat" cells).

Genes
CRY2, LEPR

Resting Metabolic Rate

MEDIUM-HIGH

Resting metabolic rate (often referred to as basal metabolism) represents about 70% of total energy expenditure and refers to the calories expended by the body to maintain basic resting functions such as heart rate, breathing, body temperature control, etc. Orange or red result indicates lower resting metabolism.

Genes
CRY2, LEPR

14. Energy Metabolism

Mitochondrial Complex Deficiency 1

NORMAL

Mitochondrial complex I deficiency is a deficiency (deficiency) of a protein complex called complex I or a loss of its function. Complex I is found in cell structures called mitochondria, which convert food energy into a form that cells can use. Complex I is the first of five mitochondrial complexes that carry out a multistep process called oxidative phosphorylation, through which cells obtain much of their energy. Deficiency of mitochondrial complex I can cause a wide variety of signs and symptoms that affect many organs and systems in the body, particularly the nervous system, heart, and muscles used for movement (skeletal muscles). These signs and symptoms can appear at any time from birth to adulthood.

Genes
MTFMT, NDUFS4

Transport of MnSOD to Mitochondria

LOW

Manganese superoxide dismutase (MnSOD), encoded by the SOD2 gene, is an antioxidant enzyme that catalyzes the dismutation of reactive superoxide radicals into hydrogen peroxide. The SOD2 c.47T> C (rs4880) polymorphism within exon 2 results in an amino acid substitution Val16Ala, which causes less efficient transport of MnSOD to the mitochondria, which leads to the neutralization of impaired intramitochondrial ROS.

Genes
SOD2

Increased Noradrenaline Level During Exercise

HIGH

Carriers of the G allele of the rs1799971 polymorphism showed an increase in the level of norepinephrine (norepinephrine) during physical exercise.

Genes
OPRM1

15. Neurotransmitter Metabolism

Dopamine Synthesis

MEDIUM-HIGH

This neurotransmitter plays important roles in the body. The first one is the feeling of pleasure. During pleasant circumstances, dopamine is released, triggering nerve impulses, which lead to a feeling of pleasure and well-being. Tasty foods, sex, games and drugs are some examples of situations that stimulate the action of dopamine. The substance also acts in the motor function of the human body, being responsible for the execution of voluntary movements, which are those that occur according to our will, such as muscle activity. Recent studies also show that the neurotransmitter is related to the memory capacity. According to scientists, this feeling of satisfaction and pleasure generated by the action of dopamine is associated, in the brain, with moments that are also pleasurable, which causes the information to be stored for a longer period in our memory. The concentration of dopamine in the body is also related to the emergence of diseases. Parkinson's disease, for example, has its origins linked to a lack of dopamine. This is because, with aging, there is a natural death of neurons, which reduces the production of the neurotransmitter. This lack of dopamine ends up altering body movements, making them uncoordinated, the main symptom of the disease. Addiction is another disorder associated with dopamine values in the body. Drugs act on neurotransmitter receptors, so when the individual uses these substances, the brain produces a large amount of dopamine, increasing the state of pleasure. Hence the need to consume the drug constantly in order to always have that feeling of pleasure. To stimulate the healthy production and release of dopamine, the consumption of foods rich in tyrosine such as dairy products, avocado, pumpkin, almond, beans, nuts, meat, eggs and others is recommended; avoid caffeine consumption and exercise regularly. Result in red or orange indicates less dopamine synthesis.

Genes

DDC, IGF2, TH

15. Neurotransmitter Metabolism

Dopamine degradation

HIGH

This neurotransmitter plays important roles in the body. The first one is the feeling of pleasure. During pleasant circumstances, dopamine is released, triggering nerve impulses, which lead to a feeling of pleasure and well-being. Tasty foods, sex, games and drugs are some examples of situations that stimulate the action of dopamine. The substance also acts in the motor function of the human body, being responsible for the execution of voluntary movements, which are those that occur according to our will, such as muscle activity. Recent studies also show that the neurotransmitter is related to the memory capacity. According to scientists, this feeling of satisfaction and pleasure generated by the action of dopamine is associated, in the brain, with moments that are also pleasurable, which causes the information to be stored for a longer period in our memory. The concentration of dopamine in the body is also related to the emergence of diseases. Parkinson's disease, for example, has its origins linked to a lack of dopamine. This is because, with aging, there is a natural death of neurons, which reduces the production of the neurotransmitter. This lack of dopamine ends up altering body movements, making them uncoordinated, the main symptom of the disease. Addiction is another disorder associated with dopamine values in the body. Drugs act on neurotransmitter receptors, so when the individual uses these substances, the brain produces a large amount of dopamine, increasing the state of pleasure. Hence the need to consume the drug constantly in order to always have that feeling of pleasure. To stimulate the healthy production and release of dopamine, the consumption of foods rich in tyrosine such as dairy products, avocado, pumpkin, almond, beans, nuts, meat, eggs and others is recommended; avoid caffeine consumption and exercise regularly. Result in red or orange indicates greater Dopamine degradation.

Genes

ARVCF, COMT, MAOA, MAOB

15. Neurotransmitter Metabolism

Serotonin Synthesis

NORMAL

In different behavioral states, extracellular changes in Serotonin levels occur. Decreased serotonin levels increase pain sensitivity, exploratory behavior, locomotor activity, and aggressive and sexual behaviors. In both men and animals, psychic disturbances have been correlated with alterations in serotonin functions, such as aggressive and obsessive behavior, in addition to attention deficit. Serotonin is the main inhibitor of the ventromedial hypothalamic nucleus, a site in the CNS where the satiety center is located. This hypothalamic effect is highly specific for carbohydrates, requiring other cofactors to act on proteins and lipids. Thus, when serotonin decreases, weight gain occurs. Conversely, when it is elevated, it causes loss of appetite. Orange or red result indicates reduced serotonin.

Genes

DDC, PLEKHA7, PTPRR, TPH1, TPH2

Serotonin degradation

HIGH

In different behavioral states, extracellular changes in Serotonin levels occur. Decreased serotonin levels increase pain sensitivity, exploratory behavior, locomotor activity, and aggressive and sexual behaviors. In both men and animals, psychic disturbances have been correlated with alterations in serotonin functions, such as aggressive and obsessive behavior, in addition to attention deficit. Serotonin is the main inhibitor of the ventromedial hypothalamic nucleus, a site in the CNS where the satiety center is located. This hypothalamic effect is highly specific for carbohydrates, requiring other cofactors to act on proteins and lipids. Thus, when serotonin decreases, weight gain occurs. Conversely, when it is elevated, it causes loss of appetite. Red result indicates reduced serotonin.

Genes

MAOA

15. Neurotransmitter Metabolism

COMT

MEDIUM

Rs4680 - COMT V158M (risk allele: A), rs4633 - COMT H62H (risk allele: T), rs769224 - COMT P199P (risk allele: A). This gene helps break down dopamine and norepinephrine. A defect causes higher dopamine due to slower breakdown. More susceptible to dopamine fluctuations, hence mood swings. People without COMT mutations are generally more temperate.

Genes
COMT

Melatonin

LOW

Melatonin is a hormone linked to the circadian cycle, that is, the way the body organizes its functions when we are awake and during sleep. The substance begins to be produced in the pineal gland when the day gets dark, to help the body prepare for sleep. It reaches its maximum level when we are sleeping. With the rising of the sun and the return of light, the gland reduces the production of melatonin, which signals that it is time to wake up.

Genes
ASMT, MTNR1A, MTNR1B, TPH2

16. carbohydrate Metabolism

Greater Insulin Sensitivity with Physical Exercise

MEDIUM-HIGH

Result in orange or red indicates having greater insulin sensitivity when playing physical sports.

Genes

LIPC

Improving Insulin Sensitivity with Physical Exercise

MEDIUM

Result in orange or red indicates benefit of physical exercise to improve insulin resistance.

Genes

LIPC, PPM1K

17. Hematologic System

Benefit of Physical Exercise for HDL

NORMAL

Exercise positively modifies the level of HDL, the good cholesterol, and the increase is proportional to the amount spent during the practice. As an example, 12 weeks of moderate exercise can increase HDL levels. Overall, the combination of exercise and diet has benefits for body composition and greater effects on HDL. Physical training alone can increase HDL, but to a lesser extent than when there is associated body fat loss. It is important to emphasize that the decrease in the risk of developing heart disease is more related to the increase in HDL, either by increasing the energy spent during exercise, by increasing the intensity or by the execution time, in addition to the reduction in body fat.

Genes

PPARD

18. Fatty Acids

Arachidonic Acid Deficiency

NORMAL

Arachidonic acid (AA) is an essential fatty acid of the omega-6 family. It plays an important role in muscle building and helps manage body fat thermogenesis. It serves as a regulator of core protein synthesis (muscle growth).

Genes

FADS2, MYRF

19. Weight Regulation & Fat Metabolism

Body fat

NORMAL

The ideal amount of body fat in men can vary between 16 and 20% and in women between 20 and 24%, but these values usually increase with age and, in most cases, it is higher in women.

Genes
IL-1RN

Oxidized LDL

MEDIUM

Oxidized low-density lipoprotein (LDL) is a potentially harmful type of cholesterol that is produced in the body when normal LDL cholesterol is damaged by chemical interactions with free radicals. Together with inflammatory responses, free radicals can result in hardening of the arteries (atherosclerosis).

Genes
APOB

Slimness

MEDIUM-HIGH

Genetic susceptibility to being a thinner person.

Genes
AHSG

19. Weight Regulation & Fat Metabolism

Greater Reduction in BMI with Exercise

HIGH

Bearers of the TT allele of the rs3751812 polymorphism show decreased BMI with physical exercise, despite being susceptible to a higher BMI.

Genes

FTO

Benefit of Physical Exercise for Weight Loss

HIGH

Physical activity helps anyone to lose weight and maintain body weight more easily, but for individuals with more right results, this benefit is even greater.

Genes

ADRB2, FTO, IL-6, INSIG2, LEP

Fat burning through cycling

HIGH

Cycling habitually, especially at a high intensity, helps lower body fat levels, which promotes healthy weight management. Plus, you'll increase your metabolism and build muscle, which allows you to burn more calories, even while at rest.

Genes

COLEC12, INTERGENIC, RASEF

19. Weight Regulation & Fat Metabolism

Decrease in body mass after training

NORMAL

Polymorphisms rs2267668 / rs2016520 / rs1053049 (G / C / T haplotypes) exhibited less post-training body mass decrease, suggesting that these specific G / C / T haplotypes are unfavorable for achieving the desired training-induced body mass changes (exercise). Result in red or orange indicates worse decrease in body mass after exercise.

Genes

PPARD

20. Macronutrient Metabolism

Carbohydrate Metabolism

MEDIUM

Carbohydrates have a centralizing monomer which is glucose. From glucose, carbohydrates can be stored in the form of glycogen. When the body needs energy, the glycolytic pathway is activated, where glucose is converted to pyruvate.

Genes

ABCC9, AGER, CEBPA, LRP1, PPARGC1B, TCF7L2

Lipid Metabolism

HIGH

Speed that the body carries out the metabolism of fats. In orange or red indicates slower metabolism, negative characteristic.

Genes

AATK, ACE, ACMSD, ADCYAP1, ADIPOQ, ADRA2A, ADRB3, ADSS, AK8, ALLC, ANKAR, ANKK1, APOA5, APOE, ARHGAP11A, ARHGAP24, ARMC4, ASIC2, ASTN2, AUTS2, BICC1, BICD1, C2CD4C, C8ORF34, CA8, CADM1, CAMK2A, CCDC33, CCDC77, CD46, CDCA3, CDHR3, CELF2, COL4A1, COLEC12, CSMD1, CTNNBL1, CYP2E1, DAPL1, DDX60L, DLC1, DLG2, DMRT1, DOCK8, ECT2, EEPD1, EHF, EVA1A, FAM129A, FAM19A2, FAM209B, FAM71F1, FARP1, FLJ33534, FSIP1, FTO, GCH1, GHRL, GMDS, GPC5, GSG1L, HDAC9, IFI16, IFNGR2, IL-1A, IL-1B, INSIG2, INTERGENIC, JDP2, KCNB1, KIF6, KIRREL, LEPR, LGALS17A, LHPP, LINC00704, LINC01299, LINC01500, LIPC, LPP, MC4R, MDFIC, NAT2, NDUFA8, NIPSNAP3B, NLRP8, NMNAT2, NPM2, NXPH1, PCDH9, PCSK1, PFKP, PIP4K2A, PKNOX2, PLEKHG1, PLIN1, POC5, PON1, PPARG, PPARGC1A, PPM1H, PTPRD, PTPRN2, PVALB, RAB17, RASEF, RBBP6, RBFOX1, RIC3, RLN3, RPTOR, RSU1, RYR2, S100P, SCG3, SDC3, SERPINA12, SLC22A2, SLC22A23, SLC29A3, SMYD3, SNRPN, SORBS1, SPAG16, SPOCK3, STON2, SYT1, TBC1D1, TCF4, TM9SF2, TMEM18, TMEM229B, TMEM45B, TMOD1, TNFRSF1B, TPTE2P1, TRABD2B, TRAPPC9, TRIM66, TUB, UGT2B7, UNC13A, UNC5C, VSIG10, WDPCP, WDR11-AS1, ZBTB46, ZNF536

Micronutrient Metabolism

MEDIUM

Speed that the body carries out the metabolism of multiple micronutrients. Note that results indicate that the individual has a better micronutrient metabolism.

Genes

DLAT, ENO3, MTNR1B, PCK1, SLC2A9, SLC5A1

20. Macronutrient Metabolism

Xenobiotic Metabolism (Including Caffeine and P-450)

MEDIUM

The metabolism of xenobiotics is carried out by liver enzymes in several steps: the xenobiotic is initially activated by oxidation, reduction, hydrolysis or hydration; it is then conjugated to molecules such as sulfate, glucuronate or glutathione, and is subsequently excreted in bile or urine.

Genes

CYP1A2

Folic Acid Metabolism

MEDIUM-HIGH

Like every amino acid, methionine is metabolized by the liver, and one of the results of its metabolism is the production of homocysteine. The level of homocysteine in the body, in turn, is regulated by the process of remethylation, which converts the substance back to methionine, in a reaction that requires folic acid and vitamin B12, or through transsulfurization, which transforms it into cysteine. Some factors, however, can cause the body to concentrate high amounts of methionine or homocysteine, and in excess, both substances can be very harmful. The high concentration of homocysteine, configured by hyperhomocysteinemia, is considered a risk factor for cardiovascular and brain pathologies, atherosclerosis, stroke, thrombosis and for neurodegenerative diseases such as Alzheimer's and Parkinson's. The excess of methionine, characterized by hypermethioninemia, can cause neurological disorders, cognitive deficit and cerebral edema. Among the main causes of the accumulation of methionine and homocysteine are diets low in folic acid and vitamin B12 or with an exaggerated intake of protein, sedentary lifestyle and genetic alterations in the enzymes involved in the metabolism of the two amino acids, as is the case of homocystinuria, a disease caused by deficiency of the enzyme cystathionine beta-synthetase (CBS). Result in red or orange indicates greater homocysteine and less efficiency in processing Vitamin B12 and Folic Acid.

Genes

BHMT, CBS, COMT, FOLH1, MTHFR, MTR, MTRR, SLC19A1

20. Macronutrient Metabolism

Protein Metabolization

LOW

Proteins degraded in the digestive process result in amino acids, which are absorbed by the epithelial cells of the small intestine, transported to the bloodstream and distributed to different tissues. Amino acids are fundamental in protein synthesis and are precursors of all non-protein nitrogenous compounds, such as the nitrogenous bases of nucleotides, and amines and their derivatives, such as histamine and adrenaline. It is estimated that in a healthy adult human being there is a turnover of approximately 400g of protein per day. About 300g can be reused, while the remaining 100g are discarded. Living beings are not able to store stores of amino acids or proteins and, therefore, daily protein intake is necessary. The rise in the plasma level of amino acids, as well as glucose, stimulates the β cells of the endocrine pancreas to secrete insulin. This hormone stimulates the uptake of amino acids by muscle and liver, in addition to activating the enzymatic apparatus responsible for protein synthesis.

Genes

FTO

21. Muscle Strength & Power

Muscle strength

HIGH

It can be defined as the amount of tension that a muscle or muscle group can generate within a specific movement pattern and with a given movement speed. Result in orange or red indicates greater muscle strength.

Genes

ACTN3, ACVR1B, AGT, HIF1A, IL-6, MSTN, NOS3, PPARA, TRHR, VDR

Hand Grip Strength

NORMAL

Strength of hands. Grip strength tests are commonly used to assess patients with upper extremity disorders, before and after therapeutic procedures. These tests are simple to administer and, when properly performed, can provide objective information that contributes to the analysis of hand function.

Genes

GBF1, GLIS1, HOXB3, KANSL1, LRPPRC, MGMT, MSTN, SLC8A1, SYT1, TGFA, VDR

Muscular Strength

MEDIUM-HIGH

Muscular Strength

Genes

ACTN3

21. Muscle Strength & Power

Neuromuscular Power

HIGH

Neuromuscular Potency is the ability of the muscle to respond to a stimulus coming from the brain (neuro-brain-muscle communication). The ability of the neuromuscular system to generate maximum power is affected by a variety of interrelated factors. Maximal muscle strength is defined and limited by the force-velocity relationship and affected by the length-tension relationship.

Genes

ACTN3, AGT, AMPD1, FAAH, GABPB1, HIF1A, IL-6, NOS3, PPARA, TFAM

Increased Maximum Force Production

HIGH

It is the greatest muscle strength a student/athlete can develop. Generally, to quantitatively assess this type of strength, maximum repetition protocols such as 1RM are used. This assessment format makes the maximum force represent the greatest available strength that the neuromuscular system can mobilize through a maximum voluntary contraction.

Genes

IGF1

22. Tendon & Joint Support

Tendon strength

NORMAL

Strength in the tendon, formed by connective tissue, thanks to which the muscles are inserted into the Skeletal System (bones) or other organs

Genes
GDF5, MMP3

Knee strength

HIGH

Indicates the susceptibility to greater or lesser strength of the knee.

Genes
ACVR1B, COL1A1, DNMT3L, MTRR, VDR

Ligament Strength

NORMAL

Ligament strength, greater thrust and advantage in some movements.

Genes
CILP, COL5A1, MSTN

22. Tendon & Joint Support

Gait Instability

NORMAL

Also known as Gait Apraxia, it is a neurological disorder that is characterized by loss of the ability to perform precise movements and gestures, despite the patient having the will and physical ability to perform them. Apraxia leads to reduced conditions to perform some types of movements – although the individual maintains the motor capacity, sensory function and understanding of the required task intact. This disease leads to problems with the use of objects (for example, brushing the hair) and in performing known motor acts (eg, waving goodbye).

Genes

DHX30, VPS13B

23. Skeletal System (bones)

Osteoarthritis

MEDIUM-HIGH

A type of arthritis that occurs when the flexible tissue at the ends of the Skeletal System (bones) wears down.

Genes

ALDH1A2, COG5, COL6A4P1, CRTC1, CSMD1, DIO2, FRZB, FTO, GDF5, HLA-DQB1, IL-1B, IL-1RN, IL-6, INTERGENIC, LPAR1, MCF2L, PON1

Musculoskeletal Pain

MEDIUM-HIGH

Musculoskeletal pain arises from repetitive strain, overuse, and work-related disorders, which lead to pain in adjacent bones, joints, muscles, or structures. Pain can be focal or diffuse, acute or chronic, with low back pain being the most common example of the latter. Diagnoses include peripheral neuropathies, medial or lateral epicondylitis/tendinitis, rotator cuff tendinitis, biceps or wrist tendinitis, myositis, myalgia, osteoarthritis, cervical distension, and low back pain.

Genes

ADRB2, INTERGENIC, POMC, SERPINA6

Scoliosis

MEDIUM-HIGH

Lateral curvature of the spine.

Genes

LBX1, MAGI1

23. Skeletal System (bones)

Intervertebral Disc Disease

NORMAL

When subjected to stress or trauma, the discs can swell, compressing the surrounding structures and causing various symptoms. This condition corresponds to a herniated disc. Disc diseases are a common cause of pain in the adult population but are relatively rare in the younger sporting population. This type of illness may or may not be associated with sciatica (pain that radiates along the leg). The most common disc diseases are degenerative diseases, ruptured discs and sciatica.

Genes
COL1A1, COL9A2, COL9A3

Bone Mass

LOW

Bone Mass

Genes
WNT16

Bone Strength

MEDIUM-HIGH

The variant C allele of SNP rs3751143 was associated with less bone strength (SSI), periosteal circumference, total and cortical area. The known cellular function of rs3751143 makes the present findings unsurprising. Homozygosity for the C allele has been shown to cause a complete loss of receptor function, whereas heterozygotes have half of the receptor functionality. Our data are in line with studies conducted in vitro, showing the C allele of rs3751143 to be associated with osteoclast apoptosis, reduced pore formation and a reduction in pro-inflammatory cytokine secretion. In vivo, the C allele has been associated with lower hip BMD and a greater risk of fracture in elderly participants, and stress fracture prevalence in military personal and elite athletes.

Genes
P2RX7

24. Cardiovascular System

Paroxysmal Ventricular Fibrillation

HIGH

Uniform and fast heart rate (from 160 to 220 beats per minute), which starts and ends suddenly and originates in cardiac tissues outside the ventricles

Genes
SCN5A

Increased blood pressure during exercise

NORMAL

Increased blood pressure during exercise

Genes
FTO

Jervell and Lange-Nielsen Syndrome

MEDIUM

It is a type of long QT syndrome that causes the heart muscle to repolarize more slowly than usual. The disorder also usually occurs with hearing loss. It is known that mutations in genes KCNE1 and KCNQ1 are responsible for this disorder. These genes are responsible for the production of proteins that act in the formation of cell channels found in the plasma membrane of cells, through which potassium ions are transported out of the cell, an essential factor for the maintenance of normal ear and cardiac muscle functions . Clinical manifestations include: Ventricular tachycardia; Ventricular fibrillation; Iron deficiency anemia; Elevated gastrin levels; Hearing loss; Syncopal episodes, especially during periods of stress, fear and exercise. Only symptomatic treatment is done. Cochlear implant can be used to treat hearing loss, beta-blockers treat long QT interval, implantable cardioverter defibrillator is recommended for patients with a history of cardiac arrest and/or lack of response to other forms of treatment. Standard treatment for iron deficiency anemia is also provided.

Genes
KCNE1, KCNQ1

24. Cardiovascular System

Brugada Syndrome

HIGH

It is an inherited arrhythmia (autosomal dominant) that predisposes to ventricular arrhythmias that can be fatal.

Genes

CACNB2, GPD1L, KCNE3, SCN5A, TRPM4

Romano-Ward Syndrome

NORMAL

Romano-Ward syndrome (RWS) is an autosomal dominant variant of long QT syndrome, characterized by episodes of syncope and electrocardiographic anomalies (QT interval prolongation, and T-wave anomalies and torsade de pointes (TdP) ventricular tachycardia). Most patients develop symptoms during exercise or in response to stress or emotional disturbances; symptoms rarely occur at rest or during sleep. Syncopal episodes are caused by TdP, a polymorphic ventricular tachycardia. TdP often degenerates into ventricular fibrillation and can lead to cardiac arrest or sudden death. Diagnosis is based on typical electrocardiographic findings, clinical manifestations, and family history. Molecular diagnosis should always be performed in patients with a clinically suspected diagnosis. It should also be performed on affected family members with normal/limit QT intervals to identify people at risk of sudden death. Disease control and treatment: The following pathologies should be considered: catecholaminergic polymorphic ventricular tachycardia (PBVt), orthostatic hypotension, hypertrophic cardiomyopathy, Jervell and Lange-Nielsen syndrome and other forms of LQTS, Brugada syndrome, as well as vasovagal syncope, tachycardia ventricular, drug-induced LQTS and epilepsy. Beta-adrenergic blockers represent the therapy of first choice in symptomatic patients. Whenever syncope episodes occur despite full-dose beta-blocker therapy, left-sided cardiac sympathetic denervation (LCSD) should be considered and implemented whenever possible.

Genes

CAV3, KCNE1, KCNH2, KCNQ1, SCN5A

24. Cardiovascular System

Ventricular Tachycardia

NORMAL

Ventricular tachycardia (VT) is a rapid heart rhythm that occurs in one of your heart's ventricles. It looks like a small electrical circuit that runs in a circle. In a ventricular tachycardia, the heart beats each turn in the circuit at frequencies of 150 to 250 bpm. A special type of ventricular tachycardia is called right ventricular outflow tract tachycardia or RVOT tachycardia. This rhythm occurs in the part of the heart where blood flows from the right ventricle to the lungs. As the heart beats faster, it pumps less blood, and there is not enough time for it to fill with blood between beats. If this rapid heartbeat continues, the brain and body may not receive enough blood and oxygen.

Genes

CASQ2, INTERGENIC, RYR2

Aerobic Capacity

HIGH

Potential that the individual has to produce body energy through oxygen. Orange or red result indicates greater aerobic capacity. Results in red means beneficial.

Genes

ADRB2, GABPB1, PPARA, PPARGC1A, VEGFA

Wolff-Parkinson-White Syndrome

NORMAL

Wolff-Parkinson-White (WPW) syndrome is a relatively common heart condition that causes the heart to beat abnormally fast for periods of time. The cause is an extra electrical connection in the heart. This problem with the heart is present at birth (congenital), although symptoms may not develop until later in life.

Genes

NODAL, PRKAG2

24. Cardiovascular System

Familial Hypertrophic Cardiomyopathy

NORMAL

Hypertrophic cardiomyopathy (HCM) is the most common type of genetic heart disease. It is characterized by thickening of the heart muscle (myocardium), making it more difficult for the heart to pump blood.

Genes

GLA, MYBPC3, MYH7, MYL2, PLN, PRKAG2, TNNT2, TPM1, TTN

Cardiac Capacity

LOW

Heart rate is the speed of the heart cycle as measured by the number of heart contractions per minute.

Genes

CREB1, KIF5B, NOS3, NPY

Benefit of Physical Activity to Reduce Cardiovascular Risk

MEDIUM

Studies demonstrate evidence that the effects of common polymorphisms in the LPL, LIPC and CETP genes on HDL-C levels are modified by physical activity.

Genes

CETP, FTO, LIPC, LPL

24. Cardiovascular System

Benefit of Potassium in Blood Pressure Control

UNDEFINED

Relationship between potassium and sodium: The relationship between these two substances is essential to balance the amount of water in the body. While sodium retains fluids, potassium causes excretion, so that cells are left with the right amount of water. In addition, the double sodium and potassium participates in muscle contractions and the supply of energy to the body.

Genes

ACE2, APLN

Atrial Fibrillation

HIGH

Irregular and often accelerated heart rate that often causes poor blood circulation.

Genes

ABCC9, ACE2, AF, AGT, ASAH1, CUX2, EDN2, GJA5, HCN4, KCNH2, KCNQ1, LY96, NEBL, NPPA, PITX2, WNT8A

Sudden Cardiac Death

NORMAL

Sudden cardiac death corresponds to 20% of all deaths, with an incidence of about 1 per 1000 inhabitants / year. In 2/3 of the situations it is caused by coronary disease, and contributes to the mortality of coronary patients in more than 50% of the cases. In this situation, one of the main problems comes from the fact that in the vast majority of patients, Sudden Death is the first manifestation of Cardiovascular Disease. The main mechanism that leads to it is a fatal arrhythmia, called Ventricular Fibrillation, which occurs in 75 to 80% of cases and is also often the first manifestation of heart disease. This arrhythmia leads to death within minutes if it is not treated immediately. It is responsible for 95% of prehospital mortality from heart disease, and the only way we have to reverse it is through the immediate application of an electric shock, called Electric Defibrillation.

Genes

CASQ2, GJA5, IL-18

25. Respiratory System

Aerobic Resistance

HIGH

It is the ability of a person to develop an effort of low or medium intensity for a long time. A person with good aerobic endurance can tolerate the fatigue that exercise causes, therefore maintaining the pace and intensity for a considerable amount of time.

Genes

ADRB2, ADRB3, AMPD1, AQP1, CDCA3, GABPB1, HFE, KCNJ11, NOS3, PPARA, PPARD, PPARGC1A, PPARGC1B, PPP3CA, PPP3CB, VEGFA

Oxygen Volume (O2) Max (VO2 Max)

HIGH

VO2 Max is the expression defined as the maximum volume of oxygen that our body captures, transports and uses for energy production. Through its measurement it is possible to predict the level of cardiorespiratory fitness of each person, the oxidative metabolic capacity during exercise, capacity to work in occupational activities and also to prescribe physical exercise. It is a complete physiological measure, as it allows the analysis of the cardiovascular, respiratory and muscular systems, thus, the more each system is trained together, the better the body will respond to situations of effort.

Genes

ACSL1, CREB1, CRP, INTERGENIC, MYBPC3

Respiratory Quotient (RQ)

LOW

Respiratory quotient, also known as the respiratory ratio (RQ), is defined as the volume of carbon dioxide released over the volume of oxygen absorbed during respiration. It is a dimensionless number used in a calculation for basal metabolic rate when estimated from carbon dioxide production to oxygen absorption. Results in orange or red indicate higher Respiratory Quotient.

Genes

CRY2, MTNR1B

26. Tendon & Ligament Injuries

Achilles Tendinopathy Risk

NORMAL

It is the condition in which there is inflammation or degeneration of the Achilles tendon, with swelling and pain.

Genes
MMP3

Ligament Rupture

NORMAL

Ligaments have the function of joining two or more bones and protecting the body's joints. They are formed by a very resistant fibrous tissue, but with little elasticity. These two characteristics make it, in the first place, it resists your needs very well, but in cases of greater demand — like a sprain — it breaks down. A very common injury in sports practice is the rupture of the cruciate ligaments, precisely due to a sprain. It happens when our foot is firmly on the floor and the leg is rotated sharply. The ligament, responsible precisely for containing this movement, cannot bear the weight of the body and breaks.

Genes
COL1A1

26. Tendon & Ligament Injuries

Anterior Cruciate Ligament Injury (ACL)

NORMAL

An anterior cruciate ligament injury occurs when the anterior cruciate ligament (ACL) is either stretched, partially torn, or completely torn. The most common injury is a complete tear. Symptoms include pain, a popping sound during injury, instability of the knee, and joint swelling.

Genes

COL1A1

Shoulder Shift

NORMAL

Shoulder dislocations account for about half of major joint dislocations. The shoulder dislocation can be anterior, posterior or inferior.

Genes

COL1A1

26. Tendon & Ligament Injuries

Hip dislocation

MEDIUM

Hip dislocation is a displacement of the bones of the hip joint, where the acetabulum and femur meet.

Genes

GDF5

Fractures

MEDIUM

Greater or lesser ease in having fractures.

Genes

CALCR, ESR1, ITGB3, P2RX7

26. Tendon & Ligament Injuries

Meniscus Injury

MEDIUM

The meniscus is a cartilage structure present in the knee that serves to protect the knees when there is an impact or a blow directly to the knee or leg, for example. This cartilage is very prone to injury in athletes, overweight people, people with arthritis, osteoarthritis, or any other condition that affects the knee joint.

Genes

GDF5

27. Pains

Pain Sensitivity

HIGH

Pain sensitivity

Genes
COMT, OPRM1

Lumbar Disc Disease

MEDIUM

It occurs when part of an intervertebral disc leaves its normal position and compresses the nerve roots that branch from the spinal cord and emerge from the spinal column.

Genes
CHST3, CILP, COL11A1

Allergy to Hydrolyzed Wheat Protein

HIGH

Hydrolyzed wheat protein consists of wheat amino acids and oligosaccharides. Some kinds of hydrolyzed wheat proteins induce contact urticaria, some induce generalized urticaria or anaphylaxis, some induce immediate allergic reactions through air passage and some induce contact dermatitis.

Genes
INTERGENIC, RBFOX1

28. Body Fat & weight Distribution

Waist Measure

MEDIUM-HIGH

Extremely important measure to check the risk that a person has of suffering from cardiovascular disease and stroke. Result in orange or red indicates a tendency to a larger waist measurement.

Genes

ADIPOQ, APOA1, APOE, C5ORF67, CCDC40, CDH12, CLOCK, ELP4, ESR1, FTO, GCH1, GCKR, GDAP1, HMGCR, IL-15, IL-1A, IL-1B, INTERGENIC, KLF7, MC4R, MYO1B, OVCH2, PCSK1, PER2, PLIN1, PPM1L, SH2B1, SLC6A2, SSTR2, TXN, UCP2, UCP3

Visceral Fat Accumulation

MEDIUM-HIGH

Analysis of allele variants (carriers of the high-risk CC genotype and carriers of the low-risk T allele) of the SNP rs340874 demonstrated that the carriers of the PROX1 CC genotype showed greater accumulation of visceral fat despite the reduction in daily food consumption.

Genes

FTO, MSRA, PROX1, TFAP2B, UCP1

Fat and Sagging in the Arm

HIGH

The famous "bye muscle" is the nightmare of many women who dream of having their arms dry. As much as a person goes to the gym and controls himself with food, he often cannot stiffen the triceps region and dodge the genetic factor.

Genes

AGRP, APOA1, APOA2, APOA5, B4GALT7, CBS, COL11A1, COL11A2, COL17A1, COL1A1, COL1A2, COL27A1, COL2A1, COL3A1, COL4A3, COL4A4, COL4A5, COL4A6, COL5A1, COL5A2, CTNNBL1, FTO, FUT2, HIF1A, INTERGENIC, MC4R, MMP1, MMP3, PCSK1, QPCTL, RIC3, STXBP5L, TCF7L2, TNF, UCP1

28. Body Fat & weight Distribution

Lower Weight Gain on High Fat Diets

NORMAL

Less weight gain on high fat diets. Variation of the APOA5 gene modulates the effects of dietary fat intake on body mass index and obesity risk. In individuals homozygous for the major -1131T allele, BMI increased as total fat intake increased. On the other hand, this increase was not present in carriers of the minor allele -1131C. Consequently, we found significant interactions in determining the risks of obesity and overweight. Carriers of minor APOA5-1131C alleles had lower risk of obesity (OR, 0.61, 95%; CI, 0.39-0.98; P = 0.032) and risk of overweight (OR, 0.63, 95% ; CI, 0.41-0.96; P = 0.031) compared with TT subjects in the high fat intake group (> or = 30% energy), but not when the fat intake was low (OR, 1, 16, 95%; CI, 0.77-1.74; P = 0.47 and OR = 1.15, 95%; CI, 0.77-1.71; P = 0.48) for obesity and overweight , respectively). When specific groups of fatty acids were analyzed, monounsaturated fatty acids had the greatest statistical significance for these interactions. In conclusion, the SNP APOA5-1131T>C, present in approximately 13% of this population, modulates the effect of fat intake on BMI and on the risk of obesity in men and women.

Genes

APOA5

29. Diet Type & Fat Response

Weight loss and abdominal fat loss in caloric restriction

HIGH

Result in Orange or Red indicates greater ease of weight loss and loss of abdominal fat in calorie-restricted diets.

Genes

AMY1A, BDNF, FTO, LEPR, PLIN1, TCF7L2

Weight Loss on Fat Reduction Diets

NORMAL

Some people lose more weight on reduced-fat diets, depending on their genetic characteristics.

Genes

ADIPOQ, CLOCK, IRS1, MTNR1B, PPM1K

Trend of Monounsaturated Fat Intake and Weight Gain

HIGH

Usually associated with genetic problems. Indication in orange or red indicate greater trend.

Genes

AATK, ACMSD, ADCYAP1, ADIPOQ, ADRA2A, ADRB3, ADSS, AK8, ALLC, ANKAR, ANKK1, APOA5, ARHGAP11A, ARHGAP24, ARMC4, ASIC2, ASTN2, AUTS2, BICC1, BICD1, C2CD4C, C8ORF34, CA8, CADM1, CAMK2A, CCDC33, CCDC77, CD46, CDCA3, CDHR3, CEBPB-AS1, CELF2, COL4A1, COLEC12, CSMD1, CYP2E1, DAPL1, DDX60L, DLC1, DLG2, DMRT1, DOCK8, ECT2, EEPD1, EHF, EVA1A, FAM129A, FAM19A2, FAM209B, FAM71F1, FARP1, FLJ33534, FSIP1, FTO, GCH1, GHRL, GMDS, GPC5, GSG1L, HDAC9, IFI16, IFNGR2, IL-1A, IL-1B, INSIG2, INTERGENIC, JDP2, KCNB1, KIF6, KIRREL, LEPR, LGALS17A, LHPP, LINC00704, LINC01299, LINC01500, LIPC, LPP, MC4R, MDFIC, NAT2, NDUFA8, NIPSNAP3B, NLRP8, NMNAT2, NPM2, NR1D1, NXPH1, PCDH9, PCSK1, PIP4K2A, PKNOX2, PLEKHG1, POC5, PPARG, PPM1H, PTPRD, PTPRN2, PVALB, RAB17, RASEF, RBBP6, RBFOX1, RIC3, RLN3, RPTOR, RSU1, RYR2, S100P, SCG3, SDC3, SERPINA12, SLC22A2, SLC22A23, SLC29A3, SMYD3, SNRPN, SORBS1, SPAG16, SPOCK3, STON2, SYT1, TBC1D1, TCF4, TM9SF2, TMEM18, TMEM229B, TMEM45B, TMOD1, TNF, TNFRSF1B, TPTE2P1, TRABD2B, TRAPPC9, TRIM66, TUB, UGT2B7, UNC13A, UNC5C, VSIG10, WDPCP, WDR11-AS1, ZBTB46, ZNF536

29. Diet Type & Fat Response

Reduction of body fat with intervention of polyphenols

NORMAL

Polyphenols are organic compounds found mainly in plants and fruits, which have the function of protecting them against insects, ultraviolet radiation and microbial infections. These substances can be ingested by humans through food, and can be found in foods such as red wine, green tea, chocolate or saffron, for example. Due to their properties, mainly antioxidant and anti-inflammatory, polyphenols bring several health benefits, from regulating metabolism and helping with weight control, to preventing chronic diseases and preventing the emergence of cancer. Result in red or orange indicates greater reduction in body fat with the intervention of polyphenols.

Genes
IL-6

Weight Loss with the Intake of Monounsaturated Fats

NORMAL

Researches associate the −11391G> A polymorphism with the BMI and the risk of obesity, due to the ingestion of monounsaturated fats. In researches carried out, individuals with above average intake of monounsaturated fats, carriers of the A allele, had lower BMI and reduced risk of obesity.

Genes
ADIPOQ, ADRB2, PPARG

Weight Loss with Polyunsaturated Fat Intake

HIGH

Polyunsaturated fats: These fats have a different chemical structure than monounsaturated fats, and can also help lower bad cholesterol, as well as being beneficial to the brain and promoting healthy cell growth. Omega-3s and Omega-6s fall into this category. In addition to heart benefits, they have been shown to reduce inflammatory responses, which has wider implications for our well-being. Polyunsaturated Fats should be limited to 5-10% of total calories, or 11-22g for a 2000kcal diet.

Genes
ADAM17, BDNF, CEBPB-AS1, FADS1, FTO, LPL, MYRF

29. Diet Type & Fat Response

Trend of Polyunsaturated Fat Intake and Weight Gain

HIGH

Gaining weight on excess calories from polyunsaturated fat appears to cause more gain in muscle mass, and less body fat than overeating a similar amount of saturated fat. New research from Uppsala University shows that saturated fat builds more fat and less muscle than polyunsaturated fat.

Genes

AATK, ACMSD, ADCYAP1, ADIPOQ, ADRA2A, ADRB3, ADSS, AK8, ALLC, ANKAR, ANKK1, ARHGAP11A, ARHGAP24, ARMC4, ASIC2, ASTN2, AUTS2, BDNF, BICC1, BICD1, C2CD4C, C8ORF34, CA8, CADM1, CAMK2A, CCDC33, CCDC77, CD46, CDCA3, CDHR3, CELF2, COL4A1, COLEC12, CSMD1, CYP2E1, DAPL1, DDX60L, DLC1, DLG2, DMRT1, DOCK8, ECT2, EEPD1, EHF, EVA1A, FAM129A, FAM19A2, FAM209B, FAM71F1, FARP1, FLJ33534, FSIP1, FTO, GCH1, GHRL, GMDS, GPC5, GSG1L, HDAC9, IFI16, IFNGR2, IL-1A, IL-1B, INSIG2, INTERGENIC, JDP2, KCNB1, KIF6, KIRREL, LEPR, LGALS17A, LHPP, LINC00704, LINC01299, LINC01500, LIPC, LPP, MC4R, MDFIC, NDUFA8, NIPSNAP3B, NLRP8, NMNAT2, NPM2, NXPH1, PCDH9, PCSK1, PIP4K2A, PKNOX2, PLEKHG1, POC5, PPARG, PPM1H, PTPRD, PTPRN2, PVALB, RAB17, RASEF, RBBP6, RBFOX1, RIC3, RLN3, RPTOR, RSU1, RYR2, S100P, SCG3, SDC3, SERPINA12, SLC22A23, SLC29A3, SMYD3, SNRPN, SORBS1, SPAG16, SPOCK3, STON2, SYT1, TBC1D1, TCF4, TM9SF2, TMEM18, TMEM229B, TMEM45B, TMOD1, TNFRSF1B, TPTE2P1, TRABD2B, TRAPPC9, TRIM66, TUB, UGT2B7, UNC13A, UNC5C, VSIG10, WDPCP, WDR11-AS1, ZBTB46, ZNF536

Weight Loss in Diets with Olive Oil

NORMAL

One study detected an interaction between diet and the IL-6 gene (Genotype -174G / C) and SNP rs1800795, in which carriers of smaller homozygous (CC) alleles lost more weight compared to main homozygous (GG) and heterozygous individuals (GC) only in the diet supplemented with virgin olive oil. The authors note that, despite the higher total fat content of the diet supplemented with olive oil compared to the low fat diet, the low fat diet contained a high proportion of Saturated Fatty Acids. Differences in the content of Saturated Fatty Acids, unlike the specific components of olive oil, may therefore be contributing to the differences observed based on the genotype.

Genes

IL-6

Benefit of adopting a Mediterranean diet

MEDIUM

The Mediterranean diet, also called the Mediterranean diet, is based on the consumption of fresh and natural foods such as olive oil, fruits, vegetables, cereals, milk and cheese, and it is necessary to avoid industrialized products such as sausage, frozen food and powdered cakes. Orange or red result indicates greater benefit.

Genes

APOA1, CLOCK, TCF7L2

29. Diet Type & Fat Response

Benefit of Whole Grains

MEDIUM

Benefits of Whole Grains in the Diet

Genes
TCF7L2

Trend towards Higher Carbohydrate Consumption

MEDIUM-HIGH

Carbohydrates are macronutrients, which are part of the group of three main sources of energy for the human body, since they complement fat and protein. They are called that because, at the chemical level, they contain carbon, hydrogen and oxygen. Carbohydrates are organic molecules typically classified according to their structure. Structurally speaking, there are two types of carbohydrates: simple and complex. Simple ones are smaller, more easily digested molecules known as monosaccharides and disaccharides, as they contain one or two sugar molecules linked together. The simplest of all sugars is the famous glucose, but there are also fructose and galactose among the monosaccharides. Disaccharides are named as sucrose, maltose, lactose. Complexes, on the other hand, are called polysaccharides, since they have more than two sugar groups linked together. Result in red or orange indicates a greater tendency to consume carbohydrates.

Genes
FGF21, FTO, GCK, RARB, SLC2A2

High Levels of Fatty Acids after Fat Ingestion

MEDIUM

Analysis of allele variants (carriers of the high-risk CC genotype and carriers of the low-risk T allele) of the SNP rs340874 demonstrated that the carriers of the PROX1 CC genotype had high levels of free fatty acids after eating a high-fat meal and less use of glucose after high carbohydrate intake at mealtime, compared to individuals with other PROX1 genotypes. Likewise, carriers of the PROX1 CC genotype showed greater accumulation of visceral fat despite the reduction in daily food consumption.

Genes
PROX1

30. Carbohydrate & protein Metabolism

Weight Loss with the Consumption of Complex Carbohydrates

MEDIUM

Some people lose weight more easily when consuming complex carbohydrates because of their genetic susceptibility. Result indicates greater ease in losing weight with this consumption. Results in red is beneficial.

Genes

IRS1, PPM1K, QPCTL

Slimming with Restricted Carbohydrates Intake

HIGH

Diets that restrict carbohydrates have proven to be a successful dietary treatment for obesity for many people, but the degree of weight loss varies among individuals. If indicated in orange or red, it is likely that this individual has a greater benefit from carbohydrate restriction in inducing weight loss.

Genes

AMY1A, CETP, FABP2, GAL, GYS2, LIPF, PPM1K

Lower Use of Glucose after Carbohydrate Ingestion

MEDIUM

Analysis of allele variants (carriers of the high-risk CC genotype and carriers of the low-risk T allele) of the SNP rs340874 demonstrated that the carriers of the PROX1 CC genotype had less glucose utilization after high carbohydrate intake in the meal compared to individuals with other PROX1 genotypes.

Genes

PROX1

30. Carbohydrate & protein Metabolism

Trend of Higher Protein Consumption

NORMAL

The richest foods in protein are those of animal origin such as meat, fish, eggs, milk, cheese and yogurt. In addition to being present in large quantities, the proteins in these foods are also of better quality, being more easily used by the body. Approved Dietary Recommendations (RDA): Intake of adequate amounts of protein in the diet is essential for the maintenance of cell function and integrity, as well as for general health and reproduction. The RDAs for nutrients are determined at a level that should meet the needs of the majority (97-98%) of individuals at a certain stage of life, with specifications according to sex. The following RDAs are goals for healthy individuals. Adult men and women: The RDA for men and women is a daily intake of 0.80 grams of good quality protein per kilogram of body weight. Although this amount is less than what most Americans typically consume, the Dietary Reference Intake (Canada) report suggests that increased protein intakes can help people meet recommendations for essential micronutrients associated with high-protein foods , such as iron and zinc. Pregnancy and lactation: The RDA for women during pregnancy and lactation is 1.1 grams of protein per kilogram of body weight, which represents an increased need of about 25 grams of protein per day. Results in orange or red indicate a greater tendency for protein intake.

Genes

DRAM1, FTO

Tendency to Higher Fat Intake

NORMAL

Tendency to Higher Fat Intake

Genes

FTO

30. Carbohydrate & protein Metabolism

Weight loss with more protein than carbohydrate intake

HIGH

Some people tend to lose weight more than others, by eating a diet with a higher proportion of proteins than usual and less than usual carbohydrates. Indication more to the right indicates a greater tendency for this type of diet to be the most adequate.

Genes

AATK, ACMSD, ADCYAP1, ADIPOQ, ADRA2A, ADRB3, ADSS, AK8, ALLC, ANKAR, ANKK1, APOA5, ARHGAP11A, ARHGAP24, ARMC4, ASIC2, ASTN2, AUTS2, BICC1, BICD1, C2CD4C, C8ORF34, CA8, CADM1, CAMK2A, CCDC33, CCDC77, CD46, CDCA3, CDHR3, CELF2, COL4A1, COLEC12, CSMD1, CTNNBL1, CYP2E1, DAPL1, DDX60L, DLC1, DLG2, DMRT1, DOCK8, ECT2, EEPD1, EHF, EVA1A, FAM129A, FAM19A2, FAM209B, FAM71F1, FARP1, FLJ33534, FSIP1, FTO, GCH1, GHRL, GMDS, GPC5, GSG1L, HDAC9, IFI16, IFNGR2, IL-1A, IL-1B, INSIG2, INTERGENIC, JDP2, KCNB1, KIF6, KIRREL, LEPR, LGALS17A, LHPP, LINC00704, LINC01299, LINC01500, LIPC, LPP, MC4R, MDFIC, NAT2, NDUFA8, NIPSNAP3B, NLRP8, NMNAT2, NPM2, NXPH1, PCDH9, PCSK1, PFKP, PIP4K2A, PKNOX2, PLEKHG1, POC5, PPARG, PPM1H, PTPRD, PTPRN2, PVALB, RAB17, RASEF, RBBP6, RBFOX1, RIC3, RLN3, RPTOR, RSU1, RYR2, S100P, SCG3, SDC3, SERPINA12, SLC22A2, SLC22A23, SLC29A3, SMYD3, SNRPN, SORBS1, SPAG16, SPOCK3, STON2, SYT1, TBC1D1, TCF4, TM9SF2, TMEM18, TMEM229B, TMEM45B, TMOD1, TNFRSF1B, TPTE2P1, TRABD2B, TRAPPC9, TRIM66, TUB, UGT2B7, UNC13A, UNC5C, VSIG10, WDPCP, WDR11-AS1, ZBTB46, ZNF536

31. Cardiorespiratory Fitness

Greater Benefit of Aerobic Exercise for Vascular Function

MEDIUM

Genetics are associated with greater benefits of aerobic exercise for improving vascular function. Results in orange or red indicate greater benefit from aerobic exercise. But always talk to your doctor first.

Genes
EDN1

Improved Insulin Resistance in High-Protein Weight-Loss Diets

NORMAL

Research indicates that individuals with the T allele of the rs12785878 polymorphism benefit from weight-loss diets with higher amounts of protein to improve insulin resistance.

Genes
NADSYN1

Greater respiratory gains with exercise

HIGH

After 8 weeks of training, individuals with the CG and GG genotype of the rs1800795 polymorph, showed greater gains in their VO2max.

Genes
IL-6

31. Cardiorespiratory Fitness

Mitochondrial Energy Production

MEDIUM

It refers to the general efficiency of mitochondrial energy production processes, considering multiple interacting genes.

Genes

ACTN3, ADRB2, ADRB3, AGTR2, AMPD1, ARHGEF28, ATP5G3, CALCR, CKM, CLOCK, CLSTN2, CREM, CRP, DMD, EPAS1, FOCAD, GABRR1, GALNT13, GPC5, HIF1A, IGF1, IL-6, IP6K3, MCT1, MMP3, MPRIP, MSTN, MT-ND4, MTHFR, MTR, MTRR, NDUFS3, NDUFS7, NDUFS8, NOS3, NRG1, PPARA, PPARD, PPARG, PPARGC1A, PPARGC1B, SLC16A1, SUCLA2, TPK1, TRHR, UCP2, UQCRC2, VDR, ZNF423

32. Physical Performance & Recovery

Trend to Exercise During Leisure

LOW

The individual with this mutation is more likely to exercise during leisure time. They are usually practitioners of exercise and sports.

Genes

GABRG3, MC4R

Higher Temperature During Exercise

NORMAL

Individuals with the AG and AA alleles of the 2253206 polymorphism have a higher temperature during physical exercise.

Genes

CREB1, INTERGENIC

Physical resistance

HIGH

It is one of the fundamental skills in everyday life and is closely related to lifestyle habits. Related to time to reach fatigue.

Genes

ACE, ACOXL, ACTN3, ADRB1, ADRB2, ADRB3, AGTR2, APOE, CAMK1D, CDCA3, CLSTN2, CPQ, CRP, EPAS1, FMNL2, GABPB1, GALM, GNB3, GRM3, HFE, HIF1A, IL-15RA, ITPR1, KCNJ11, L3MBTL4, MCT1, NALCN-AS1, NFATC4, NFIA-AS2, NRF2, PPARA, PPARD, PPARGC1B, RBFOX1, SGMS1, SLC2A4, SOD2, SPOCK1, TPK1, TSHR, UCP2, UCP3, VEGFA, VEGFR2

32. Physical Performance & Recovery

Increased Probability of Fatigue

NORMAL

Fatigue is the name given to a symptom that is characterized by a feeling of weariness, tiredness and lack of energy.

Genes

AMPD1, AOC1, COL1A1, GAD1, MAT1A, MCT1, TNF

33. Muscle Injuries & Damage

Exercise Induced Muscle Damage

MEDIUM-HIGH

Exercise-induced muscle damage (EIDM) in humans occurs when the individual performs unusual, very intense, or long-lasting exercises. Orange or red result indicates slower DMIE recovery.

Genes

COL2A1, COL5A1, ESR1, HIF1A, TNC

Hamstring Injuries

MEDIUM

Hamstrings are a group of muscles located in the posterior thigh area, at the back of the lower limbs. This musculature is mainly responsible for the movements of hip extension and knee flexion, and crosses both joints.

Genes

MMP3, NOS3, TNC

Muscle Damage in Low Choline Diets

UNDEFINED

Individuals who can develop muscle damage when fed a low-choline diet. Research indicates several polymorphisms of the SLC44A1 gene associated with muscle damage related to low choline.

Genes

CPT1B, SLC44A1

33. Muscle Injuries & Damage

Contusão Muscular

NORMAL

Contusão muscular é considerada uma lesão traumática aguda, sem corte, decorrente de trauma direto aos tecidos moles, e que provoca dor e edema. A contusão vai de leve até uma grande infiltração de sangue nos tecidos circundantes, levando a equimose e, em casos graves, a síndrome compartimental.

Genes
APOE, COMT

Muscle stiffness

NORMAL

Muscle stiffness is a symptom that occurs when muscles cannot move quickly without being accompanied by pain and/or spasm. If the person moves too quickly, they may experience sharp pain and possibly spasm. It most often occurs in the muscles behind the neck, near the shoulder and hips.

Genes
DMD, ESR1

Probability of Muscle Injuries

NORMAL

Some people are more likely to be injured.

Genes
COL1A1, MMP3

33. Muscle Injuries & Damage

Progressive Muscle Atrophy

UNDEFINED

Progressive muscle atrophy (MPA) is a rare type of motor neuron disease (DNM) with exclusive involvement of the lower motor neuron (NMI) and with well-defined clinical features. It causes loss of muscle control, muscle weakness and wasting (atrophy).

Genes

GJB1

Spinal Muscular Atrophy

NORMAL

Spinal muscular atrophy (SMA), also called spinal muscular atrophy, is a degenerative genetic pathology that affects the cells of the anterior horn of the spinal cord, resulting in weakness and muscle atrophy characterized by problems in voluntary movement. It is estimated that childhood-onset EBF affects 1 individual for every 10,000 live births and, starting in adulthood, 1 for every 100,000 live births.

Genes

CHCHD10, IGHMBP2, SMN1

Muscular dystrophy

NORMAL

It is a term that refers to various genetic diseases that cause progressive loss of strength and degeneration of skeletal muscles.

Genes

DMD, SELENON

Visceral Fat Accumulation

Gene	SNP	Genotype	Rare Allele	Result
FTO	rs1421085	TT+	C	🟢
FTO	rs1558902	TT+	A	🟢
MSRA	rs545854	CG-	G	🟠
PROX1	rs340874	AG-	C	🟡
TFAP2B	rs987237	AA+	G	🟢
UCP1	rs1800592	AG-	C	🟠

Platelet Aggregation with Clopidogrel

Gene	SNP	Genotype	Rare Allele	Result
CES1P1	rs3785161	AA+	C	🔵
CYP1A2	rs762551	AC+	C	🔵
PEAR1	rs12041331	AG+	A	🔵

Peanut Allergy

Gene	SNP	Genotype	Rare Allele	Result
HLA-DQB1	rs1049225	Variant not found	G	⚪
HLA-DRA	rs7192	GG+	G	🟢
HMGA2	rs1042725	CT+	T	🟡
HMGA2	rs10784502	TT+	T	🟡
INTERGENIC	rs9275596	TT+	T	🟢
INTERGENIC	rs57265082	GT+	T	🔴
STAT6	rs1059513	AA-	T	🟠
STXBP6	rs11850957	CC+	A,T	🟢

Milk Allergy

Gene	SNP	Genotype	Rare Allele	Result
FAM117A	rs9898058	CC+	T	🟢
IL-10	rs1518111	AG-	C	🟢
IL-10	rs1800871	CT-	G	🟢
IMPAD1	rs387907101	Variant not found	T	⚪
IMPAD1	rs387907103	Variant not found	A	⚪
INTERGENIC	rs17616434	CC+	C	🔴
STAT6	rs1059513	AA-	T	🟢
STAT6	rs324015	Variant not found	C	⚪
TLR6	rs35220466	Variant not found	T	⚪
TMEM26	rs7088627	Variant not found	A	⚪

Egg White Allergy

Gene	SNP	Genotype	Rare Allele	Result
ABCB11	rs2287622	GT-	C,G,T	🟢
ABCB11	rs497692	AG-	C	🟢
ABCB11	rs16823014	AG+	A	🟡
COG7	rs797044712	---		🟢
ERCC4	rs1800067	AG+	A	🟠
INTERGENIC	rs6498482	TT+	C	🟢
ITIH6	rs5961136	TT+	G	🟢

Allergy to Hydrolyzed Wheat Protein

Gene	SNP	Genotype	Rare Allele	Result
INTERGENIC	rs9271588	CC+	C	🔴
RBFOX1	rs74575857	AC+	C	🔴

Rheumatoid arthritis

Gene	SNP	Genotype	Rare Allele	Result
AHCY	rs13043752	Variant not found	A	⚪
AHCY	rs41301825	Variant not found	T	⚪
AIRE	rs1055311	Variant not found	G,T	⚪
AIRE	rs1800520	Variant not found	A,G,T	⚪
ANAPC4	rs3816587	Variant not found	T	⚪
ANXA3	rs2867461	AG+	G,T	🟢
C5	rs10985112	GG+	A	🟢
CDK6	rs42041	Variant not found		⚪
CDK6	rs606231255	Variant not found	T	⚪
CTLA4	rs3087243	AG+	G	🟡
EOMES	rs3806624	CT-	G	🟢
FCRL3	rs7528684	AG+	G	🟢

Gene	SNP	Genotype	Rare Allele	Result
GUCY1B2	rs3790022	CC-	A	🟢
HLA-DRB1	rs6457617	TT+	A,T	🟠
HLA-DRB1	rs660895	GG+	G	🔴
HTR2A	rs1328674	AG-	C,G	🔴
HTR2A	rs6313	CT-	A	🟡
HTR2A	rs6314	CC-	A	🟡
HYKK	rs8034191	TT+	C	🟢
ICAM3	rs2304240	AG+	G	🟢
IL-2RA	rs2104286	AG-	C	🟡
IL-2RB	rs743777	AG+	G	🟢
INTERGENIC	rs11162922	Variant not found	G	⚪
INTERGENIC	rs11761231	CT+	C	🟢
INTERGENIC	rs13192841	GG+	A	🟢
INTERGENIC	rs2327832	AG+	G	🟡
INTERGENIC	rs2837960	GT+	A,G	🟢
INTERGENIC	rs2872507	AG+	A	🟢
INTERGENIC	rs6920220	AG+	A	🔴
INTERGENIC	rs9550642	Variant not found	A	⚪
IRF5	rs2004640	Variant not found	G	⚪
ITGAV	rs3738919	AA+	A	🔵
KIAA1109	rs13119723	GG+	G	🔴
KIAA1109	rs6822844	GT+	T	🟢
MMEL1	rs3890745	Variant not found	C	⚪
MMEL1	rs6684865	Variant not found	A	⚪
NFKBIE	rs2233434	TT-	G	🟢
NFKBIE	rs2233437	Variant not found	A	⚪
NOD2	rs2066845	GG+	C,T	🟢
PADI4	rs11203366	AG+	A	🟢
PADI4	rs2240340	AG-	C	🟡
PER2	rs2304674	CT-	G	🔵
PHF19	rs1953126	Variant not found	C	⚪
PHTF1	rs6679677	CC+	A	🟢
PLD4	rs2841277	CT+	T	🟢
PRL	rs1341239	GT-	A	🟢
PSMA4	rs12901682	CC+	C,T	🟢
PTPN2	rs1893217	CC-	G	🟠
PTPN2	rs2542151	GG+	T	🟠
PTPN22	rs2476601	GG+	G	🟢
PTPN22	rs2488457	Variant not found	A,C	⚪
SLC6A11	rs1809529	CT+	T	🟢
STAT4	rs10181656	CG+	C	🟡
STAT4	rs7574865	GT+	G	🔴
TNFAIP3	rs2230926	TT+	C,G	🟢
TRAF1	rs10818488	Variant not found	G	⚪
TRAF1/C5	rs3761847	AA+	A	🟢
UBASH3A	rs11203203	AG+	A	🟠
VARS2	rs4678	CC-	A	🟢
WDFY4	rs877819	AG+	G	🟢
ZNF175	rs1543922	CC+	T	🟢

Arthrosis of the Knee

Gene	SNP	Genotype	Rare Allele	Result
COL6A4P1	rs7639618	TT+	T	🟠
GDF5	rs143383	CT-	A	🟡
IL-1RN	rs315952	Variant not found	A,C	⚪
IL-1RN	rs419598	TT+	C	🟢
IL-1RN	rs9005	GG+	A	🟢
INTERGENIC	rs4140564	AA+	A	🟢
LRCH1	rs912428	Variant not found	G	⚪
MCF2L	rs11842874	AA+	G	🟠

Spinal Muscular Atrophy

Gene	SNP	Genotype	Rare Allele	Result
CHCHD10	rs730880031	Variant not found	A,T	⚪
IGHMBP2	rs10896380	AA+	G	🟢
SMN1	rs104893922	Variant not found	G	⚪
SMN1	rs104893930	Variant not found	A	⚪
SMN1	rs104893931	Variant not found	T	⚪

Gene	SNP	Genotype	Rare Allele	Result
SMN1	rs104893932	Variant not found	G	○
SMN1	rs104893933	Variant not found	T	○
SMN1	rs104893935	Variant not found	G	○
SMN1	rs75660264	Variant not found	T	○
SMN1	rs77804083	Variant not found	A	○
SMN1	rs104893927	Variant not found	C	○
SMN1	rs104893934	Variant not found	G	○
SMN1	rs397514517	Variant not found	G	○
SMN1	rs397514518	Variant not found	C	○
SMN1	rs75030631	Variant not found	G	○
SMN1	rs76163360	Variant not found	A	○
SMN1	rs76871093	Variant not found	T	○
SMN1	rs77301881	Variant not found	A	○
SMN1	rs77969175	Variant not found	A	○
SMN1	rs796541855	Variant not found		○
SMN1	rs79784540	Variant not found	A	○

Progressive Muscle Atrophy

Gene	SNP	Genotype	Rare Allele	Result
GJB1	rs1057518946	Variant not found	T	○

Increased blood pressure during exercise

Gene	SNP	Genotype	Rare Allele	Result
FTO	rs9941349	CC+	T	●

Increased Maximum Force Production

Gene	SNP	Genotype	Rare Allele	Result
IGF1	rs7136446	CC+	C	●

Triceps Increase

Gene	SNP	Genotype	Rare Allele	Result
AGT	rs699	CT-	G	●
COL5A1	rs12722	CC+	T	●
MSTN	rs1805086	AA-	C	●
TRIM63	rs2275950	AA-	C,G	●

Biceps Increase

Gene	SNP	Genotype	Rare Allele	Result
ACTN3	rs1815739	CT+	T	●
AGT	rs699	CT-	G	●
ANOS1	rs5978942	Variant not found	C	○
IGF2	rs680	Variant not found	C,G	○
TRIM63	rs2275950	AA-	C,G	●

Increased Noradrenaline Level During Exercise

Gene	SNP	Genotype	Rare Allele	Result
OPRM1	rs1799971	GG+	G	●

Pectoralis Major Increase

Gene	SNP	Genotype	Rare Allele	Result
ACTN3	rs1815739	CT+	T	●
AGT	rs699	CT-	G	●
MSTN	rs1805086	AA-	C	●
NOS3	rs1799983	GG+	T	●
VDR	rs1544410	AG-	C,T	●

Pectoralis Minor Augmentation

Gene	SNP	Genotype	Rare Allele	Result
AGT	rs699	CT-	G	●
MSTN	rs1805086	AA-	C	●
NOS3	rs1799983	GG+	T	●

Teres Major Increase

Gene	SNP	Genotype	Rare Allele	Result
COL5A1	rs12722	CC+	T	●
NOS3	rs1799983	GG+	T	●
VDR	rs1544410	AG-	C,T	●

Teres Minor Increase

Gene	SNP	Genotype	Rare Allele	Result
AGT	rs699	CT-	G	🟡

Serratus Anterior Increase

Gene	SNP	Genotype	Rare Allele	Result
PPARA	rs4253778	GG+	C,T	🟢
VDR	rs1544410	AG-	C,T	🟡

Trapezius Increase

Gene	SNP	Genotype	Rare Allele	Result
VDR	rs1544410	AG-	C,T	🟡

Forearms Increase

Gene	SNP	Genotype	Rare Allele	Result
LRPPRC	rs119466000	CC-	A	🟢
MSTN	rs1805086	AA-	C	🟢
NOS3	rs1799983	GG+	T	🟢
VDR	rs7975232	AC+	A	🟢

Deltoid Increase

Gene	SNP	Genotype	Rare Allele	Result
ANOS1	rs5978942	Variant not found	C	⚪
COL5A1	rs12722	CC+	T	🔴
MSTN	rs1805086	AA-	C	🟢
NOS3	rs1799983	GG+	T	🟢
TRIM63	rs2275950	AA-	C,G	🔴
VDR	rs1544410	AG-	C,T	🟢

Hamstrings Increase

Gene	SNP	Genotype	Rare Allele	Result
ACVR1B	rs2854464	AA+	C,G	🔴
MMP3	rs679620	AG-	C	🟡
NOS3	rs2070744	TT+	T	🟢
TNC	rs2104772	AT+	A	🔵
VDR	rs7975232	AC+	A	🟠

Thigh Increase and Definition

Gene	SNP	Genotype	Rare Allele	Result
ACTN3	rs1815739	CT+	T	🟡
ANOS1	rs5978942	Variant not found	C	⚪
DNMT3L	rs7354779	TT+	C	🟢
MTRR	rs7703033	GG+	A	🔴
TRIM63	rs2275950	AA-	C,G	🔴
VDR	rs7975232	AC+	A	🟠

Benefit of Physical Activity to Reduce Cardiovascular Risk

Gene	SNP	Genotype	Rare Allele	Result
CETP	rs1532624	TT-	A	🟠
FTO	rs9939609	TT+	A	🟢
LIPC	rs1800588	CC+	T	🟢
LPL	rs10096633	CC+	T	🟢

BCAA levels

Gene	SNP	Genotype	Rare Allele	Result
AMPD1	rs17602729	CC-	A	🟢
BCKDHA	rs45500792	TT+	G	🟢
GAD1	rs3791878	Variant not found	T	⚪
GAD1	rs3762555	Variant not found	A,G	⚪
SLC17A7	rs74174284	Variant not found	G	⚪

Benefit of Whole Grains

Gene	SNP	Genotype	Rare Allele	Result
TCF7L2	rs7903146	CC+	G,T	🟠
TCF7L2	rs12255372	GG+	T	🟢

Benefit of adopting a Mediterranean diet

Gene	SNP	Genotype	Rare Allele	Result
APOA1	rs670	AG-	T	🟠

Gene	SNP	Genotype	Rare Allele	Result
CLOCK	rs1801260	AA+	C,G,T	🟢
TCF7L2	rs7903146	CC+	G,T	🟢
TCF7L2	rs12255372	GG+	T	🟢

Weight Loss in Diets with Olive Oil

Gene	SNP	Genotype	Rare Allele	Result
IL-6	rs1800795	CG+	G	🟢

Benefit of Green Tea

Gene	SNP	Genotype	Rare Allele	Result
COMT	rs4680	AG+	A	🟢
PEMT	rs7946	CT+	T	🟡

Benefit of Physical Exercise for Weight Loss

Gene	SNP	Genotype	Rare Allele	Result
ADRB2	rs1042713	GG+	A	🟢
FTO	rs10852521	Variant not found	A,C	⚪
FTO	rs9939609	TT+	A	🟢
FTO	rs8050136	CC+	A	🔴
IL-6	rs1800795	CG+	G	🔴
INSIG2	rs9308762	TT+	A,G,T	🟢
LEP	rs7799039	Variant not found	A	⚪

Benefit of Physical Exercise for HDL

Gene	SNP	Genotype	Rare Allele	Result
PPARD	rs2016520	AA-	T	🟢

Benefit of Potassium in Blood Pressure Control

Gene	SNP	Genotype	Rare Allele	Result
ACE2	rs4646174	Variant not found	C	⚪
APLN	rs2235306	Variant not found	C	⚪

CLA

Gene	SNP	Genotype	Rare Allele	Result
LEP	rs7799039	Variant not found	A	⚪
PPARG	rs3856806	CC+	T	🟢
TNF	rs1800629	GG+	A	🟢

Beta-casein A1

Gene	SNP	Genotype	Rare Allele	Result
CBLB	rs3772534	Variant not found	T	⚪
ERAP1	rs1363907	GG+	A	🟢
FOXO3	rs12212067	Variant not found	T	⚪
HCG17	rs3130380	GG+	A	🟢
IL-6R	rs2228145	AA+	C,T	🟠
INTERGENIC	rs17616434	CC+	C	🔵
MCM6	rs4988235	AG+	A	🟢
MCM6	rs182549	TT+	T	🔴
NFE2L2	rs6721961	GG+	C,G	🟠
NOD2	rs2066844	CC+	T	🟢
STAT6	rs324015	Variant not found	C	⚪
TLR6	rs35220466	Variant not found	T	⚪
UBQLN1P	rs3130352	CC+	T	🟢

Beta casein A2A2

Gene	SNP	Genotype	Rare Allele	Result
DLK1	rs2273608	Variant not found	T	⚪
DMD	rs7066036	Variant not found	G	⚪
INTERGENIC	rs17616434	CC+	C	🔴
MTRR	rs162031	Variant not found	T	⚪
PPARD	rs1053049	Variant not found	C	⚪
PPARD	rs2267668	AA+	A,C	🟢
STAT6	rs324015	Variant not found	C	⚪
STAT6	rs1059513	AA-	T	🔴

Beta-alanine

Gene	SNP	Genotype	Rare Allele	Result
ADRB2	rs1800888	CC+	T	🔴

Gene	SNP	Genotype	Rare Allele	Result
AMPD1	rs17602729	CC-	A	
GABPB1	rs12594956	Variant not found	A	
PPARD	rs2267668	AA+	A,C	
PPARD	rs1053049	Variant not found	C	
SLC17A7	rs74174284	Variant not found	G	
TNF	rs673	Variant not found	A	

Betaine

Gene	SNP	Genotype	Rare Allele	Result
BHMT	rs3733890	GG+	A	
MTHFR	rs1476413	AG-	G,T	
MTHFR	rs17037390	Variant not found	A	
MTHFR	rs1801131	AC-	G	
MTHFR	rs1801133	CC-	A	
MTHFR	rs2066470	Variant not found	A,C	
MTHFR	rs4846049	Variant not found	A,G	
SLC19A1	rs1051266	GG-	C,G	

Bone Mass

Gene	SNP	Genotype	Rare Allele	Result
WNT16	rs2707466	GG-	G,T	

COMT

Gene	SNP	Genotype	Rare Allele	Result
COMT	rs4680	AG+	A	

Aerobic Capacity

Gene	SNP	Genotype	Rare Allele	Result
ADRB2	rs1042713	GG+	A	
ADRB2	rs1800888	CC+	T	
GABPB1	rs7181866	AA+	G	
GABPB1	rs8031031	Variant not found	T	
PPARA	rs4253778	GG+	C,T	
PPARGC1A	rs13117172	Variant not found	T	
PPARGC1A	rs8192678	GG-	T	
VEGFA	rs3024994	CC+	T	
VEGFA	rs3025039	CC+	T	

Cardiac Capacity

Gene	SNP	Genotype	Rare Allele	Result
CREB1	rs10932201	Variant not found	A	
KIF5B	rs1775715	Variant not found	G	
NOS3	rs2070744	TT+	T	
NOS3	rs4496877	Variant not found	G	
NPY	rs1468271	Variant not found	T	

Ability to Accept Criticism

Gene	SNP	Genotype	Rare Allele	Result
CRHR1	rs111433752	Variant not found	G	
DBH	rs1611115	CT+	A,C,G	

Familial Hypertrophic Cardiomyopathy

Gene	SNP	Genotype	Rare Allele	Result
GLA	rs104894845	GG-		
GLA	rs28935197	AA-		
MYBPC3	rs375882485	GG+	A	
MYBPC3	rs397515963	---	C	
MYH7	rs3218713	GG-	T	
MYH7	rs3218714	CC-	A,C	
MYL2	rs28932774	Variant not found	G	
MYL2	rs28933099	Variant not found	A,T	
PLN	rs111033560	TT+	G	
PRKAG2	rs28938173	CC-	T	
PRKAG2	rs121908987	GG-	T	
TNNT2	rs4523540	TT+	A,C	
TPM1	rs28934269	Variant not found	G,T	
TPM1	rs28934270	Variant not found	A	
TTN	rs28933405	Variant not found	A,T	

Green Tea

Gene	SNP	Genotype	Rare Allele	Result
CYP1A2	rs762551	AC+	C	🟡

Copper

Gene	SNP	Genotype	Rare Allele	Result
ABCB1	rs1128503	CT-	G	🟢
ABCB1	rs3213619	TT-	G	🟢
ACE	rs1799752	Variant not found		⚪
ACE	rs4343	AG+	A	🟠
ADD1	rs4961	GT+	A,T	🟠
ADRB2	rs1800888	CC+	T	🟢
AOC1	rs10156191	Variant not found	T	⚪
APOE	rs7412	TT+	T	🔴
APOE4	rs429358	TT+	C	🟢
ASIC2	rs9901756	Variant not found	C	⚪
ATP2B1	rs2681472	CT-	G	🟢
ATP7B	rs60986317	GG+	A	🟢
BAG3	rs2234962	CT+	C	🟢
BRAP	rs3782886	AA-	C	🟢
BTD	rs104893686	TT+	G	🟢
BTD	rs104893687	CC+	T	🟢
CACNB2	rs2228645	Variant not found	A,T	⚪
CAV3	rs1008642	Variant not found	A,G,T	⚪
CCL2	rs1024611	CT-	G	🟠
CDH13	rs8055236	GG+	A,C,T	🟠
CDKN2B-AS1	rs10116277	TT+	T	🔵
CDKN2B-AS1	rs1011970	GT+	T	🟢
CDKN2B-AS1	rs1063192	TT-	A,T	🔵
CDKN2B-AS1	rs10757272	TT+	T	🟠
CDKN2B-AS1	rs10757274	GG+	G	🟠
CDKN2B-AS1	rs1537375	Variant not found	C,G	⚪
CDKN2B-AS1	rs2383206	Variant not found	G	⚪
CETP	rs2303790	AA+	G	🟢
CFH	rs1061170	TT+	T	🔵
CHRDL1	rs387906713	Variant not found	A	⚪
CHRDL1	rs387906714	Variant not found	A	⚪
CRP	rs3091244	Variant not found	A,T	⚪
CYP2R1	rs117913124	Variant not found	A	⚪
DHFR	rs1643649	Variant not found	C	⚪
DMD	rs1800278	AA-	C	🟢
DMD	rs1801187	GG-	T	🟢
DNAJC5B	rs13279522	TT+	C	🟢
DPYD	rs1801266	CC-	A	🟢
DPYD	rs1801267	GG-	T	🟢
DPYD	rs1801268	GG-	A	🟢
DSG2	rs2230234	AA+	G,T	🟢
F12	rs1801020	CT-	G	🟡
F7	rs6046	CT-	A	🟢
FGF20	rs1721100	Variant not found	G,T	⚪
FLJ25967	rs2331291	Variant not found	T	⚪
FMN2	rs17672135	TT+	C	🟠
FOXE1	rs10984009	Variant not found	A	⚪
GATA2	rs3803	Variant not found	A	⚪
GATA4	rs104894073	Variant not found	A,G,T	⚪
GATA4	rs104894074	Variant not found	A	⚪
HLA-DRA	rs3135391	CC-	A	🟢
HLA-DRB1	rs660895	GG+	G	🔴
HSPD1	rs2340690	Variant not found	G	⚪
HSPD1	rs2565163	Variant not found	A,C	⚪
HSPD1	rs788016	Variant not found	A	⚪
HSPE1	rs2305560	Variant not found	T	⚪
HTRA1	rs11200638	AG+	A	🟠
IL-4	rs2243250	CC+	T	🟢
IL4R	rs1801275	Variant not found	G	⚪
INTERGENIC	rs10757278	GG+	G	🔴
INTERGENIC	rs1333049	CC+	C	🔴
INTERGENIC	rs2383207	GG+	G	🟠

Gene	SNP	Genotype	Rare Allele	Result
INTERGENIC	rs383830	Variant not found	T	⚪
INTERGENIC	rs501120	AG-	C	🟡
INTERGENIC	rs7250581	Variant not found	G	⚪
ITGB3	rs5918	TT+	C	🟢
JAG1	rs28939668	Variant not found	T	⚪
KCNE1	rs1805127	AG-	A,C,G	🟡
KCNE2	rs2234916	AA+	G	🟢
KCNE3	rs2270676	CT-	G	🟢
KCNQ1	rs1057128	Variant not found	A	⚪
KL	rs9527025	Variant not found	C,T	⚪
KL	rs9536314	TT+	A,G	🟢
LIPA	rs1051338	Variant not found	G	⚪
LIPA	rs1131706	Variant not found	T	⚪
LIPA	rs3802656	Variant not found	A	⚪
LRP8	rs5174	GG-	T	🔵
MAOA	rs1137070	TT+	C	🟢
MAOA	rs3027399	GG+	C	🟢
MAOA	rs909525	GG-	T	🟠
MMP3	rs3025058	DI+	G	🔴
MMP9	rs17576	Variant not found	G	⚪
MMP9	rs3918242	Variant not found	T	⚪
MRAS	rs2306374	TT+	C	🟢
MTHFD1	rs1076991	AG-	C,G	🟢
MTHFD1L	rs11754661	GG+	A,T	🟢
MTHFD1L	rs17349743	TT+	C	🟢
MTHFD1L	rs6922269	AG+	A	🟡
MTHFD1L	rs803422	Variant not found	C,G	⚪
MYBPC3	rs11570112	CC-	A,C	🟢
NAF1	rs7675998	GG+	G,T	🟢
NOS3	rs1800779	AA+	G	🟢
NOS3	rs1800783	Variant not found	C,G,T	⚪
NOS3	rs207044	Variant not found	T	⚪
NOS3	rs3918188	Variant not found	A,T	⚪
NPPA	rs5065	AA+	G	🟢
OLR1	rs11053646	Variant not found	G	⚪
PECAM1	rs281865545	Variant not found	G,T	⚪
PHACTR1	rs9349379	AA+	A	🟢
PLCL2	rs10510468	Variant not found	A,T	⚪
PLPP3	rs17114036	AA+	G	🟢
PSMA6	rs1048990	CG+	G,T	🟢
PSRC1	rs599839	AA+	A,C	🟡
RYR2	rs34967813	AA+	G	🟢
SCN5A	rs1805124	GG-	T	🟢
SELENBP1	rs2769264	AC-	G	🔴
SEZ6L	rs688034	Variant not found	T	⚪
SH2B3	rs3184504	CC+	A,C,G	🟢
SMAD3	rs17228212	TT+	C	🟢
SMIM1	rs1175550	TT-	G	🔴
SOD3	rs1799895	CC+	G	🟢
SOD3	rs2855262	TT+	C	🟢
STAT4	rs10181656	CG+	C	🟡
THBS2	rs8089	Variant not found	C	⚪
TLR4	rs4986790	AA+	G,T	🟢
TLR4	rs4986791	CC+	T	🟢
TMPO	rs17028450	CC+	T	🟢
TNF	rs1800629	GG+	A	🟢
TNFSF4	rs1234313	AG+	G	🟢
TNFSF4	rs1234315	Variant not found	T	⚪
TNFSF4	rs3850641	Variant not found	G	⚪
TNFSF4	rs3861950	TT+	C	🟢
TTN	rs16866412	Variant not found	A	⚪
TTN	rs2244492	GG-	T	🟢
TTR	rs1800458	Variant not found	A	⚪
TXNRD2	rs5748469	AA+	A	🟢
TYR	rs28940879	Variant not found	A,C	⚪

Coenzyme Q10

Gene	SNP	Genotype	Rare Allele	Result

Gene	SNP	Genotype	Rare Allele	Result
ABCB1	rs1128503	CT-	G	
ABCB1	rs3213619	TT-	G	
ACE	rs1799752	Variant not found		
ACE	rs4343	AG+	A	
ADD1	rs4961	GT+	A,T	
ADRB2	rs1800888	CC+	T	
AOC1	rs10156191	Variant not found	T	
APOE	rs7412	TT+	T	
APOE4	rs429358	TT+	C	
ARHGAP30	rs2774279	Variant not found	T	
ASIC2	rs9901756	Variant not found	C	
ATP2B1	rs2681472	CT-	G	
BAG3	rs2234962	CT+	C	
BRAP	rs3782886	AA-	C	
BTD	rs104893686	TT+	G	
BTD	rs104893687	CC+	T	
CACNB2	rs2228645	Variant not found	A,T	
CAT	rs1001179	AA-	T	
CAV3	rs1008642	Variant not found	A,G,T	
CCL2	rs1024611	CT-	G	
CDH13	rs8055236	GG+	A,C,T	
CDKN2B-AS1	rs10116277	TT+	T	
CDKN2B-AS1	rs1011970	GT+	T	
CDKN2B-AS1	rs1063192	TT-	A,T	
CDKN2B-AS1	rs10757272	TT+	T	
CDKN2B-AS1	rs10757274	GG+	G	
CDKN2B-AS1	rs1537375	Variant not found	C,G	
CDKN2B-AS1	rs2383206	Variant not found	G	
CELSR2	rs4970834	CC+	T	
CETP	rs2303790	AA+	G	
CETP	rs5882	AG+	A	
CHRDL1	rs387906713	Variant not found	A	
CHRDL1	rs387906714	Variant not found	A	
COLEC12	rs9952641	Variant not found	A	
COQ2	rs121918230	AA-	C	
COQ2	rs121918231	GG-	T	
COQ2	rs121918232	AA-	C	
COQ2	rs121918233	GG-	T	
COQ4	rs143441644	CC+	T	
COQ4	rs766317663	Variant not found	T	
COQ4	rs774395996	Variant not found	G,T	
COQ4	rs775607037	Variant not found	A,T	
COQ4	rs786204770	Variant not found	C	
COQ6	rs189840848	CC+	G,T	
COQ6	rs397514479	Variant not found	A	
COQ7	rs864321686	Variant not found	A	
COQ8A	rs119468004	GG+	A,C	
COQ8A	rs119468005	CC+	T	
COQ8A	rs145034527	CC+	T	
COQ8A	rs387906298	DD+	G	
COQ8A	rs387906299	II+		
COQ8A	rs578189699	CC+	T	
COQ8A	rs606231138	Variant not found	C	
COQ8A	rs771578775	CC+	T	
COQ8A	rs886043382	Variant not found	A,T	
COQ9	rs267606751	CC+	T	
COQ9	rs786205897	II+		
CRP	rs3091244	Variant not found	A,T	
CYP2R1	rs117913124	Variant not found	A	
DHFR	rs1643649	Variant not found	C	
DMD	rs1800278	AA-	C	
DMD	rs1801187	GG-	T	
DNAJC5B	rs13279522	TT+	C	
DPYD	rs1801266	CC-	A	
DPYD	rs1801267	GG-	T	
DPYD	rs1801268	GG-	A	
DSG2	rs2230234	AA+	G,T	
F12	rs1801020	CT-	G	

Gene	SNP	Genotype	Rare Allele	Result
F7	rs6046	CT-	A	
FGF20	rs1721100	Variant not found	G,T	
FLJ25967	rs2331291	Variant not found	T	
FMN2	rs17672135	TT+	C	
FOXE1	rs10984009	Variant not found	A	
GAD1	rs1978340	Variant not found	A	
GAD1	rs3762555	Variant not found	A,G	
GAD1	rs3791878	Variant not found	T	
GATA2	rs2713604	Variant not found	C	
GATA2	rs3803	Variant not found	A	
GATA4	rs104894073	Variant not found	A,G,T	
GATA4	rs104894074	Variant not found	A	
HLA-DRA	rs3135391	CC-	A	
HLA-DRB1	rs660895	GG+	G	
HSPD1	rs2340690	Variant not found	G	
HSPD1	rs2565163	Variant not found	A,C	
HSPD1	rs788016	Variant not found	A	
HSPE1	rs2305560	Variant not found	T	
IL-4	rs2243250	CC+	T	
IL4R	rs1801275	Variant not found	G	
INTERGENIC	rs10757278	GG+	G	
INTERGENIC	rs1333049	CC+	C	
INTERGENIC	rs2383207	GG+	G	
INTERGENIC	rs2943634	AC+	C,G	
INTERGENIC	rs383830	Variant not found	T	
INTERGENIC	rs501120	AG-	C	
INTERGENIC	rs7250581	Variant not found	G	
ITGB3	rs5918	TT+	C	
JAG1	rs28939668	Variant not found	T	
KCNE1	rs1805127	AG-	A,C,G	
KCNE2	rs2234916	AA+	G	
KCNE3	rs2270676	CT-	G	
KCNQ1	rs1057128	Variant not found	A	
KL	rs9527025	Variant not found	C,T	
KL	rs9536314	TT+	A,G	
LIPA	rs1051338	Variant not found	G	
LIPA	rs1131706	Variant not found	T	
LIPA	rs3802656	Variant not found	A	
LIPC	rs1800588	CC+	T	
LPL	rs326	AG+	G	
LRP8	rs5174	GG-	T	
MAOA	rs1137070	TT+	C	
MAOA	rs3027399	GG+	C	
MAOA	rs909525	GG-	T	
MAT1A	rs118204001	TT-	C	
MAT1A	rs2993763	Variant not found	A	
MAT1A	rs72558181	Variant not found	T	
MC1R	rs1805005	GG+	T	
MC1R	rs1805007	CC+	T	
MC1R	rs1805008	CC+	T	
MC1R	rs1805009	GG+	A,C	
MC4R	rs2229616	GG-	C	
MCT1	rs1049434	Variant not found	T	
MMP3	rs3025058	DI+	G	
MMP9	rs17576	Variant not found	G	
MMP9	rs3918242	Variant not found	T	
MRAS	rs2306374	TT+	C	
MTHFD1	rs1076991	AG-	C,G	
MTHFD1L	rs11754661	GG+	A,T	
MTHFD1L	rs17349743	TT+	C	
MTHFD1L	rs6922269	AG+	A	
MTHFD1L	rs803422	Variant not found	C,G	
MYBPC3	rs11570112	CC-	A,C	
NAF1	rs7675998	GG+	G,T	
NOS3	rs1800779	AA+	G	
NOS3	rs1800783	Variant not found	C,G,T	
NOS3	rs207044	Variant not found	T	
NOS3	rs3918188	Variant not found	A,T	

Gene	SNP	Genotype	Rare Allele	Result
NPPA	rs5065	AA+	G	🟢
NQO1	rs1800566	CC-	A	🟢
NQO2	rs1143684	TT+	C	🟢
OLR1	rs11053646	Variant not found	G	⚪
PACERR	rs689466	AG-	C	🟡
PDSS1	rs119463988	Variant not found	A,G	⚪
PDSS2	rs118203955	Variant not found	A,C	⚪
PDSS2	rs118203956	CC-	A	🟢
PDSS2	rs35555197	Variant not found	T	⚪
PECAM1	rs281865545	Variant not found	G,T	⚪
PHACTR1	rs9349379	AA+	A	🟢
PLCL2	rs10510468	Variant not found	A,T	⚪
PLPP3	rs17114036	AA+	G	🟢
PLTP	rs3843763	Variant not found	T	⚪
PSMA6	rs1048990	CG+	G,T	🟢
PSRC1	rs599839	AA+	A,C	🟡
RYR2	rs34967813	AA+	G	🟢
SCN5A	rs1805124	GG-	T	🟢
SEZ6L	rs688034	Variant not found	T	⚪
SH2B3	rs3184504	CC+	A,C,G	🟢
SIRT1	rs3758391	Variant not found	C	⚪
SMAD3	rs17228212	TT+	C	🟢
STAT4	rs10181656	CG+	C	🟡
THBS2	rs8089	Variant not found	C	⚪
TLR4	rs4986790	AA+	G,T	🟢
TLR4	rs4986791	CC+	T	🟢
TMPO	rs17028450	CC+	T	🟢
TNF	rs1800610	CT-	A	🟢
TNF	rs1800629	GG+	A	🟢
TNFSF4	rs1234313	AG+	G	🟢
TNFSF4	rs1234315	Variant not found	T	⚪
TNFSF4	rs3850641	Variant not found	G	⚪
TNFSF4	rs3861950	TT+	C	🟢
TTN	rs16866412	Variant not found	A	⚪
TTN	rs2244492	GG-	T	🟢
TTR	rs1800458	Variant not found	A	⚪
TXNRD2	rs5748469	AA+	A	🟢
TYR	rs28940879	Variant not found	A,C	⚪

Choline

Gene	SNP	Genotype	Rare Allele	Result
CHAT	rs2177369	CC-	G	🟢
CHAT	rs3810950	GG+	A	🟢
CHDH	rs12676	Variant not found	C,T	⚪
CHDH	rs9001	Variant not found	G	⚪
CHKA	rs7928739	Variant not found	C	⚪
CHKB	rs10791957	AA+	C	🟢
FMO3	rs2266782	AG+	A	🟡
MTHFD1	rs2236225	CC-	A	🟢
MTHFD1L	rs17349743	TT+	C	🟢
MTHFD1L	rs6922269	AG+	A	🟡
MTHFD1L	rs803422	Variant not found	C,G	⚪
PEMT	rs4244593	AA-	A,G	🟠
PEMT	rs4646406	AA-	A	🟢
PEMT	rs7946	CT+	T	🔴
PEMT	rs12325817	Variant not found	A,G,T	⚪
PEMT	rs2278952	Variant not found	A	⚪
SLC44A1	rs3199966	Variant not found	G	⚪

Challenging behavior

Gene	SNP	Genotype	Rare Allele	Result
ADH4	rs1800759	Variant not found	T	⚪
CLOCK	rs1801260	AA+	C,G,T	🟢
CLOCK	rs6832769	GG+	G	🟠
CTNNA2	rs2861913	Variant not found	G	⚪
ELP1	rs10118853	Variant not found	A	⚪
OPCML	rs11223249	Variant not found	A	⚪

Skeletal muscle fiber contraction

Gene	SNP	Genotype	Rare Allele	Result
ACTN3	rs1815739	CT+	T	🔵
CNTF	rs1800169	AG+	A	🟡

Contusão Muscular

Gene	SNP	Genotype	Rare Allele	Result
APOE	rs405509	CC-	G	🔵
COMT	rs4680	AG+	A	🟡

Monohydrate Creatine

Gene	SNP	Genotype	Rare Allele	Result
ACTN3	rs1815739	CT+	T	🔴
CNTF	rs1800169	AG+	A	🔴

Chrome

Gene	SNP	Genotype	Rare Allele	Result
ABCA1	rs1883025	AG-	T	🟢
ABCG8	rs6544713	CC+	C	🟢
APOA5	rs2075291	Variant not found	A,T	⚪
APOA5	rs2266788	TT-	A	🟢
APOA5	rs3135506	GG+	C	🟢
APOC1	rs4420638	AA+	G	🟢
APOE	rs7412	TT+	T	🔴
AR	rs5031002	GG+	A	🟢
BRCA2	rs4942486	CT+	C	🟢
CPS1	rs1047891	CC+	A	🟢
CR1L	rs4844614	GT+	T	🟡
DNAH11	rs12670798	TT+	C	🟢
DOCK7	rs10889353	AC+	C,T	🟢
FABP2	rs1799883	GG-	A,C,G	🟢
FADS1	rs174547	TT+	C	🟢
FADS2	rs174570	CC+	T	🟢
GCKR	rs1260326	CT+	C	🟡
GPX1	rs1050450	CC-	A	🟢
JMJD1C	rs10761731	Variant not found	T	⚪
LDLR	rs6511720	GG+	T	🟢
LPL	rs13702	AG-	A,C	🟢
LPL	rs285	CT+	T	🟢
LPL	rs320	GT+	G	🟢
LPL	rs328	Variant not found	G	⚪
MLXIPL	rs1051921	Variant not found	A	⚪
MTHFR	rs2066470	Variant not found	A,C	⚪
NAF1	rs7675998	GG+	G,T	🟢
OR4A46P	rs7395662	GG+	A	🟢
PHYHIP	rs4871976	Variant not found	A	⚪
RAB11B	rs2967605	GG-	T	🟢
TMEM241	rs9949617	CC+	T	🟢

Morning Chronotype

Gene	SNP	Genotype	Rare Allele	Result
AANAT	rs11077821	Variant not found	C	⚪
CRY2	rs7123390	Variant not found	A	⚪
PER2	rs934945	Variant not found	T	⚪
PER3	rs228697	CC+	G	🔴

Night chronotype

Gene	SNP	Genotype	Rare Allele	Result
CRY1	rs184039278	Variant not found	C,G	⚪
CRY1	rs8192440	AG+	A,G	🟢
NR1D1	rs12941497	AG+	A	🟡
PER3	rs228697	CC+	G	🟢

Calcium

Gene	SNP	Genotype	Rare Allele	Result
CARS	rs739401	Variant not found	T	⚪
CASR	rs13068893	CC+	G	🟢
CYP24A1	rs1570669	AG+	G	🟢

Gene	SNP	Genotype	Rare Allele	Result
CYP24A1	rs2296241	GG+	A	🟢
CYP24A1	rs4809957	AG+	G	🟢
CYP24A1	rs6068816	CT+	T	🟢
CYP2R1	rs10741657	GG+	G	🟡
DGKH	rs1012053	AC+	A	🔵
DGKH	rs994856	Variant not found	G	⚪
F13A1	rs121913066	Variant not found	A,T	⚪
F13B	rs121913075	Variant not found	A	⚪
F13B	rs6003	AA-	T	🟢
F2	rs1799963	GG+	A	🟢
F5	rs4524	AG-	C	🟢
F5	rs6025	GG-	T	🟢
F9	rs6048	Variant not found	G	⚪
GATA3	rs104894162	Variant not found	T	⚪
GATA3	rs104894163	Variant not found	A	⚪
GATA3	rs4143094	GG+	G	🟢
GC	rs7041	GT-	G	🟡
GC	rs4588	CC-	A,T	🟢
LPL	rs268	AA+	G	🟢
MCM6	rs4988235	AG+	A	🟢
NR3C1	rs2918419	Variant not found	C	⚪
SELE	rs5361	AC-	G	🟢
TNFRSF11B	rs3134069	AA+	C	🟢
VDR	rs1544410	AG-	C,T	🟢
VDR	rs2228570	CC-	C,T	🟢
VDR	rs4516035	CT+	C	🟠
VDR	rs731236	CT-	G	🟢
VDR	rs7975232	AC+	A	🟢

Muscle cramps

Gene	SNP	Genotype	Rare Allele	Result
AMPD1	rs17602729	CC-	A	🟢
CYP24A1	rs114368325	GG+	A,C	🟢
DMD	rs1057518834	Variant not found	C	⚪
DMD	rs1057518962	Variant not found	A,G,T	⚪
MYF6	rs28928909	GG+	T	🟢
PGAM2	rs10250779	GG-	A,G,T	🟢
PYGM	rs764313717	TT+	C	🟢

Turmeric (Turmeric)

Gene	SNP	Genotype	Rare Allele	Result
BIN1	rs744373	CT-	G	🟠
SOD3	rs1799895	CC+	G	🟢

DHEA/DHEAS

Gene	SNP	Genotype	Rare Allele	Result
ARPC1A	rs740160	CC+	T	🟢
BCL2L11	rs6738028	CG+	G	🟢
HHEX	rs1111875	Variant not found	T	⚪
HHEX	rs5015480	TT+	T	🟢
INTERGENIC	rs2497306	TT-	C,T	🟠
SHBG	rs1799941	GG+	A	🟢
SULT2A1	rs2637125	GG+	A	🟢
SULT2A1	rs182420	AA-	C	🟢
TRIM4	rs17277546	GG+	A	🟢

Exercise Induced Muscle Damage

Gene	SNP	Genotype	Rare Allele	Result
COL2A1	rs2070739	Variant not found	T	⚪
COL5A1	rs12722	CC+	T	🟢
ESR1	rs2234693	CT+	A,T	🟢
HIF1A	rs11549465	CC+	T	🔴
TNC	rs2104772	AT+	A	🟡

Muscle Damage in Low Choline Diets

Gene	SNP	Genotype	Rare Allele	Result
CPT1B	rs1557502	Variant not found	A	⚪
SLC44A1	rs7873937	Variant not found	C	⚪

Gene	SNP	Genotype	Rare Allele	Result
SLC44A1	rs2771040	Variant not found	G	○
SLC44A1	rs6479313	Variant not found	G	○
SLC44A1	rs16924529	Variant not found	A	○
SLC44A1	rs3199966	Variant not found	G	○

Mitochondrial Complex Deficiency 1

Gene	SNP	Genotype	Rare Allele	Result
MTFMT	rs201431517	GG+		●
NDUFS4	rs104893898	Variant not found		○
NDUFS4	rs104893899	Variant not found		○
NDUFS4	rs587776949	II+		●

Arachidonic Acid Deficiency

Gene	SNP	Genotype	Rare Allele	Result
FADS2	rs174570	CC+	T	●
MYRF	rs174537	GG+	T	●

Dopamine degradation

Gene	SNP	Genotype	Rare Allele	Result
ARVCF	rs165599	AG+	A	●
COMT	rs13306278	CC+	T	●
COMT	rs165631	CC+	T	●
COMT	rs165656	Variant not found	A,C,T	○
COMT	rs165688	Variant not found	A	○
COMT	rs165722	Variant not found	T	○
COMT	rs165774	GG+	A	●
COMT	rs17849308	Variant not found		○
COMT	rs2020917	CT+	T	●
COMT	rs2075507	Variant not found	A,T	○
COMT	rs2097603	Variant not found	A,T	○
COMT	rs2239393	AG+	G	●
COMT	rs3087869	Variant not found	G	○
COMT	rs4633	CT+	T	◐
COMT	rs4646312	CT+	C	●
COMT	rs4646316	CT+	G,T	●
COMT	rs4680	AG+	A	◐
COMT	rs4818	CC+	G,T	●
COMT	rs5993882	Variant not found	C,G	○
COMT	rs6267	GG+	A,T	●
COMT	rs6269	AG+	G	●
COMT	rs737865	CT-	G	●
COMT	rs737866	AG-	A,C	●
COMT	rs740602	Variant not found	A	○
COMT	rs740603	AG+	G	●
COMT	rs769224	GG+	A	●
COMT	rs8192488	CC+	T	●
COMT	rs933271	TT+	A,C	●
MAOA	rs1137070	TT+	C	●
MAOA	rs1465107	Variant not found	G	○
MAOA	rs2072743	AA-	C	●
MAOA	rs2235186	TT-	G	●
MAOA	rs2283725	Variant not found	G,T	○
MAOA	rs3027400	Variant not found	G	○
MAOA	rs3027407	AA+	G	●
MAOA	rs3027409	TT+	G	●
MAOA	rs3788862	Variant not found	G	○
MAOA	rs587777457	Variant not found	T	○
MAOA	rs5906883	AA+	C	◑
MAOA	rs5906957	Variant not found	C,G	○
MAOA	rs5953210	GG+	A	●
MAOA	rs6323	GG+	T	●
MAOA	rs6609257	GG+	A	●
MAOA	rs72554632	Variant not found	T	○
MAOA	rs796065311	DD+	T	●
MAOA	rs796065312	CC+	T	●
MAOA	rs909525	GG-	T	◐
MAOA	rs979606	Variant not found	T	○
MAOB	rs10521432	AG+	A	●

Gene	SNP	Genotype	Rare Allele	Result
MAOB	rs1799836	AA-	A,C	🟢
MAOB	rs2283729	AG+	A	🟠
MAOB	rs3027415	Variant not found	C	⚪
MAOB	rs6651806	Variant not found	C	⚪

Serotonin degradation

Gene	SNP	Genotype	Rare Allele	Result
MAOA	rs1137070	TT+	C	🟢
MAOA	rs1465107	Variant not found	G	⚪
MAOA	rs2072743	AA-	C	🟢
MAOA	rs2235186	TT-	G	🟢
MAOA	rs2283725	Variant not found	G,T	⚪
MAOA	rs3027400	Variant not found	G	⚪
MAOA	rs3027407	AA+	G	🟢
MAOA	rs3027409	TT+	G	🟢
MAOA	rs3788862	Variant not found	G	⚪
MAOA	rs587777457	Variant not found	T	⚪
MAOA	rs5906883	AA+	C	🟢
MAOA	rs5906957	Variant not found	C,G	⚪
MAOA	rs5953210	GG+	A	🟢
MAOA	rs6323	GG+	T	🔴
MAOA	rs6609257	GG+	A	🟢
MAOA	rs72554632	Variant not found	T	⚪
MAOA	rs796065311	DD+	T	🔴
MAOA	rs796065312	CC+	T	🟢
MAOA	rs909525	GG-	T	🔴
MAOA	rs979606	Variant not found	T	⚪

Shoulder Shift

Gene	SNP	Genotype	Rare Allele	Result
COL1A1	rs1800012	GT-	A	🟢

Manual dexterity

Gene	SNP	Genotype	Rare Allele	Result
CTNNA2	rs1007371	Variant not found	A	⚪
CTNNA2	rs1446109	Variant not found	G	⚪
CTNNA2	rs723524	Variant not found	T	⚪
NRG1	rs10503929	Variant not found	C	⚪
PCSK6	rs11855415	Variant not found	T	⚪
PCSK6	rs7182874	CC+	C	🟢
PCSK6	rs8029797	Variant not found	A,G	⚪
PCSK6	rs9806256	Variant not found	C	⚪

Difficulties in Dealing with Criticism

Gene	SNP	Genotype	Rare Allele	Result
ADH4	rs1800759	Variant not found	T	⚪
CHADL	rs9611519	CT+	T	🟡
CLOCK	rs1801260	AA+	C,G,T	🟢
CLOCK	rs6832769	GG+	G	🟠
CRHR1	rs111433752	Variant not found	G	⚪
CTNNA2	rs2861913	Variant not found	G	⚪
DBH	rs1611115	CT+	A,C,G	🟡
ELP1	rs10118853	Variant not found	A	⚪
EP300	rs11090039	Variant not found	A	⚪
FAM86B3P	rs2945232	CC+	C	🟠
FBXL17	rs10463586	Variant not found	C,G,T	⚪
FYN	rs706897	Variant not found	G	⚪
GAD1	rs12185692	Variant not found	A	⚪
GRIK3	rs490647	Variant not found	A	⚪
INTERGENIC	rs10186791	Variant not found	A	⚪
INTERGENIC	rs10456089	GG+	A	🟢
INTERGENIC	rs10460051	Variant not found	T	⚪
INTERGENIC	rs2048656	Variant not found	A	⚪
INTERGENIC	rs2572431	Variant not found	T	⚪
INTERGENIC	rs35753505	Variant not found	A,C	⚪
INTERGENIC	rs6047641	GG+	A,G	🟠
MAGI1	rs35855737	Variant not found	C	⚪
MTMR9	rs2164273	Variant not found	G	⚪

Gene	SNP	Genotype	Rare Allele	Result
OPCML	rs11223249	Variant not found	A	⚪
PLEKHM1	rs9899111	Variant not found	G	⚪
PTPRF	rs2039528	GG+	G	🟢
SNAP25	rs362584	AG+	A	🟡
SNCA	rs10005233	Variant not found	T	⚪
TMEM16D	rs1849710	CG+	C	🟠
VRK2	rs10188070	Variant not found	A,G,T	⚪
XKR6	rs6981523	CT+	T	🟢

Decrease in body mass after training

Gene	SNP	Genotype	Rare Allele	Result
PPARD	rs2016520	AA-	T	🟢
PPARD	rs2267668	AA+	A,C	🟢
PPARD	rs1053049	Variant not found	C	⚪

Muscular dystrophy

Gene	SNP	Genotype	Rare Allele	Result
DMD	rs1800278	AA-	C	🟢
SELENON	rs121908182	Variant not found	A	⚪
SELENON	rs121908184	Variant not found	G	⚪
SELENON	rs121908185	GG+	A	🟢

Intervertebral Disc Disease

Gene	SNP	Genotype	Rare Allele	Result
COL1A1	rs1800012	GT-	A	🟢
COL9A2	rs137853213	Variant not found	A,C	⚪
COL9A3	rs61734651	Variant not found	T	⚪

Lumbar Disc Disease

Gene	SNP	Genotype	Rare Allele	Result
CHST3	rs4148941	CC+	A	🟡
CILP	rs2073711	GG+	G	🟢
COL11A1	rs1676486	Variant not found	G,T	⚪

Sciatica Pain

Gene	SNP	Genotype	Rare Allele	Result
COMT	rs4680	AG+	A	🟡
IL-1A	rs1800587	CT-	A,C	🟡
IL-1RN	rs2234677	Variant not found	A	⚪
IL-6	rs13306435	Variant not found	A,C	⚪
IL-6	rs1800795	CG+	G	🟢
IL-6	rs1800796	GG+	C	🟢
IL-6	rs1800797	AG+	G	🟢
MMP1	rs1799750	---	C	🟢
OPRM1	rs1799971	GG+	G	🔴

Musculoskeletal Pain

Gene	SNP	Genotype	Rare Allele	Result
ADRB2	rs1042717	AA+	A,C	🟠
ADRB2	rs2400707	GG+	G,T	🟢
INTERGENIC	rs1581492	Variant not found	A,T	⚪
POMC	rs3769671	Variant not found	C	⚪
SERPINA6	rs941601	AG-	T	🟠

Slimming with Restricted Carbohydrates Intake

Gene	SNP	Genotype	Rare Allele	Result
AMY1A	rs11185098	Variant not found	A	⚪
CETP	rs5883	CC+	T	🟢
FABP2	rs1799883	GG-	A,C,G	🔴
GAL	rs694066	Variant not found	A	⚪
GYS2	rs2306179	Variant not found	T	⚪
LIPF	rs814628	Variant not found	G	⚪
PPM1K	rs1440581	AG-	A,C	🟢

Weight Loss with the Intake of Monounsaturated Fats

Gene	SNP	Genotype	Rare Allele	Result
ADIPOQ	rs17300539	GG+	A	🟢
ADRB2	rs1042714	GT+	C,T	🟢

Gene	SNP	Genotype	Rare Allele	Result
PPARG	rs1801282	CG+	C	🟢

Weight Loss with Polyunsaturated Fat Intake

Gene	SNP	Genotype	Rare Allele	Result
ADAM17	rs10495563	AG+	G	🟢
BDNF	rs6265	GG-	T	🔴
CEBPB-AS1	rs4253449	GG+	A	🟢
FADS1	rs174547	TT+	C	🟢
FTO	rs9939609	TT+	A	🟢
LPL	rs320	GT+	G	🟢
MYRF	rs174537	GG+	T	🔴

Weight loss with more protein than carbohydrate intake

Gene	SNP	Genotype	Rare Allele	Result
AATK	rs7220048	TT+	C	🟢
ACMSD	rs387906598	Variant not found	T	⚪
ADCYAP1	rs1893154	CC-	G	🟢
ADIPOQ	rs6444175	Variant not found	A	⚪
ADRA2A	rs553668	Variant not found	G,T	⚪
ADRB3	rs4994	TT-	G	🟢
ADSS	rs3102460	CT+	T	🟢
AK8	rs12552369	Variant not found	A	⚪
ALLC	rs387907075	Variant not found	C	⚪
ANKAR	rs12053254	TT+	C	🟢
ANKK1	rs1800497	CT-	A	🟠
APOA5	rs662799	AA+	T	🟢
ARHGAP11A	rs555387669	Variant not found		⚪
ARHGAP24	rs11732231	Variant not found	C,T	⚪
ARMC4	rs587777047	AA+	C	🟢
ARMC4	rs587777049	GG+	T	🟢
ASIC2	rs28936	Variant not found	C	⚪
ASTN2	rs111033570	Variant not found	A	⚪
AUTS2	rs1057517708	Variant not found	T	⚪
AUTS2	rs1057518198	Variant not found		⚪
BICC1	rs11006263	AA+	G	🟢
BICD1	rs2630578	Variant not found	C	⚪
C2CD4C	rs12978500	AC+	A	🟢
C8ORF34	rs1517114	CC+	A,G,T	🟢
CA8	rs267606695	Variant not found	C,G	⚪
CADM1	rs6589488	Variant not found	T	⚪
CAMK2A	rs2053053	Variant not found	A,C	⚪
CCDC33	rs2930291	Variant not found	A,C	⚪
CCDC77	rs1048466	AG+	A,C	🟢
CD46	rs35366573	CC+	T	🟢
CD46	rs7144	Variant not found	C	⚪
CDCA3	rs5443	CT+	T	🟠
CDHR3	rs6967330	GG+	A	🟢
CELF2	rs3740194	Variant not found	C	⚪
COL4A1	rs113994104	Variant not found	A,T	⚪
COL4A1	rs3742207	AC-	A,G	🟢
COLEC12	rs16944558	Variant not found	T	⚪
CSMD1	rs995322	Variant not found	C,G	⚪
CTNNBL1	rs6013029	Variant not found	T	⚪
CYP2E1	rs2031920	CC+	T	🟢
CYP2E1	rs2070672	AA+	G	🟢
CYP2E1	rs72559710	GG+	A,C,T	🟢
DAPL1	rs16843372	TT+	C	🟢
DDX60L	rs17612333	Variant not found	A,G	⚪
DLC1	rs121908500	Variant not found	C	⚪
DLG2	rs10501570	Variant not found	C	⚪
DMRT1	rs1057519638	Variant not found	T	⚪
DOCK8	rs112321280	Variant not found	G	⚪
DOCK8	rs192864327	GG+	C,T	🟢
ECT2	rs7646507	AG+	A	🟢
EEPD1	rs4302748	AG+	A	🟢
EHF	rs286913	CC-	G,T	🟢
EVA1A	rs17011455	TT+	C	🟢
FAM129A	rs147815528	Variant not found	A,C	⚪

Gene	SNP	Genotype	Rare Allele	Result
FAM19A2	rs10784285	Variant not found	T	
FAM209B	rs6024938	CT+	T	
FAM71F1	rs6971091	GG+	A	
FARP1	rs688872	TT-	G	
FLJ33534	rs16857178	GG+	A	
FSIP1	rs10152640	AG+	G	
FTO	rs1121980	CC-	A	
FTO	rs121918214	GG+	A	
FTO	rs1421085	TT+	C	
FTO	rs17817449	TT+	A,G	
FTO	rs3751812	GG+	T	
FTO	rs9930506	AA+	G	
FTO	rs9939609	TT+	A	
FTO	rs1558902	TT+	A	
GCH1	rs10483639	Variant not found	C	
GCH1	rs104894433	Variant not found	A,C,T	
GCH1	rs104894434	Variant not found	G	
GHRL	rs696217	Variant not found	T	
GMDS	rs9378688	Variant not found	A	
GPC5	rs2352028	CT+	G,T	
GSG1L	rs205391	CT+	C,G	
HDAC9	rs11984041	CC+	T	
IFI16	rs6940	Variant not found	T	
IFNGR2	rs74315444	Variant not found	A	
IL-1A	rs1800587	CT-	A,C	
IL-1B	rs1143634	CT-	A	
INSIG2	rs7566605	GG+	C	
INTERGENIC	rs10207060	GT+	A,G	
INTERGENIC	rs11070098	TT+	C	
INTERGENIC	rs11845134	Variant not found	T	
INTERGENIC	rs12986207	Variant not found	A,C	
INTERGENIC	rs17054265	CC+	G,T	
INTERGENIC	rs17468244	AA+	G	
INTERGENIC	rs2153299	AA-	C	
INTERGENIC	rs2575029	CC+	C	
INTERGENIC	rs5767992	CC+	C	
INTERGENIC	rs6486986	GT+	T	
JDP2	rs741846	Variant not found	A,T	
KCNB1	rs1057518621	Variant not found	T	
KCNB1	rs1057521887	Variant not found	C	
KIF6	rs20455	Variant not found	G	
KIF6	rs9380880	GG+	A	
KIRREL	rs6427419	Variant not found	A	
LEPR	rs1137101	AA+	G	
LGALS17A	rs8103033	AG+	A	
LHPP	rs12773846	GG+	A,C	
LINC00704	rs1391511	Variant not found	G	
LINC01299	rs6981992	GT+	A,T	
LINC01500	rs405460	AC-	A,T	
LIPC	rs113298164	Variant not found	T	
LIPC	rs1800588	CC+	T	
LIPC	rs261332	GG+	G	
LPP	rs1152846	AG-	C	
LPP	rs4686484	Variant not found	A	
MC4R	rs1057517991	Variant not found	G	
MC4R	rs10871777	AG+	G	
MC4R	rs12970134	AG+	A	
MDFIC	rs7784447	GG+	A	
NAT2	rs1041983	CC+	T	
NAT2	rs1208	GG+	G	
NAT2	rs1799929	CT+	T	
NAT2	rs1801279	GG+	A	
NAT2	rs1801280	CC+	C	
NAT2	rs1805158	CC+	A,T	
NDUFA8	rs3818638	AG-	C	
NIPSNAP3B	rs2472476	AG-	T	
NLRP8	rs306450	Variant not found	G	
NMNAT2	rs4652795	CT+	T	

Gene	SNP	Genotype	Rare Allele	Result
NPM2	rs11776272	GG+	G	
NXPH1	rs765855	GG+	G	
PCDH9	rs17081231	AA+	G	
PCSK1	rs6232	AG-	C	
PFKP	rs6602024	GG+	A	
PIP4K2A	rs746203	Variant not found	T	
PKNOX2	rs10893366	CT+	T	
PLEKHG1	rs17427389	GG+	A,T	
POC5	rs2112347	GT+	G	
PPARG	rs13306747	Variant not found	A,G,T	
PPARG	rs1801282	CG+	C	
PPARG	rs3856806	CC+	T	
PPM1H	rs2029721	Variant not found	A	
PTPRD	rs10116682	Variant not found	A	
PTPRD	rs1975197	CC-	A	
PTPRN2	rs10274279	TT+	C	
PVALB	rs2022068	AA+	G	
RAB17	rs2292873	AG-	T	
RASEF	rs10867921	AG+	A	
RBBP6	rs11860248	Variant not found	G	
RBFOX1	rs1057521725	Variant not found	A	
RBFOX1	rs1064794750	Variant not found	G	
RIC3	rs1528133	Variant not found	C,G	
RLN3	rs123277666	Variant not found		
RPTOR	rs2289759	Variant not found	G	
RSU1	rs11254160	AG+	A	
RYR2	rs1057517873	AA+	G	
S100P	rs3822262	AA-	G	
SCG3	rs16964476	Variant not found	G	
SCG3	rs3764220	Variant not found	G,T	
SDC3	rs2282440	Variant not found	A,C	
SERPINA12	rs61757459	Variant not found	A	
SLC22A2	rs316019	GG-	C	
SLC22A2	rs8177504	CC-	A,T	
SLC22A2	rs8177507	GG-	G,T	
SLC22A2	rs8177516	CC-	A,T	
SLC22A2	rs8177517	AA-	C,G	
SLC22A23	rs4959235	Variant not found	C	
SLC29A3	rs1084004	CC+	C,G	
SLC29A3	rs121912583	GG+	A	
SLC29A3	rs869025176	Variant not found	C	
SMYD3	rs11800820	CC+	A,T	
SNRPN	rs220030	Variant not found	A,C	
SORBS1	rs11188352	Variant not found	G	
SPAG16	rs16851771	AA+	G	
SPOCK3	rs9312517	AA+	G	
STON2	rs6574644	AA+	A	
SYT1	rs17005598	Variant not found	A	
TBC1D1	rs35859249	CC+	A,T	
TCF4	rs613872	TT+	T	
TCF4	rs9960767	CC+	C,G	
TM9SF2	rs9513627	AA+	A	
TMEM18	rs6548238	CC+	C	
TMEM229B	rs1077989	AC+	C	
TMEM45B	rs10894147	CC+	T	
TMOD1	rs1475545	AG-	T	
TNFRSF1B	rs5746059	Variant not found	G	
TPTE2P1	rs2483374	AC+	C,T	
TRABD2B	rs946836	Variant not found	G,T	
TRAPPC9	rs267607137	CC-	A	
TRIM66	rs4929923	CC+	C	
TUB	rs2272382	Variant not found	C	
UGT2B7	rs12233719	GG+	A,C,T	
UGT2B7	rs7439366	Variant not found	C	
UNC13A	rs12608932	AC+	C	
UNC5C	rs12643654	Variant not found	G	
VSIG10	rs7957470	GG+	G	
WDPCP	rs11683229	Variant not found	G,T	

Gene	SNP	Genotype	Rare Allele	Result
WDPCP	rs200322968	Variant not found	T	⚪
WDR11-AS1	rs10937273	Variant not found	A	⚪
WDR11-AS1	rs318240760	Variant not found	A,C	⚪
WDR11-AS1	rs4783244	GG+	T	🟢
ZBTB46	rs6062314	TT+	G,T	🟢
ZNF536	rs3786800	AA-	C	🟢

Weight loss and abdominal fat loss in caloric restriction

Gene	SNP	Genotype	Rare Allele	Result
AMY1A	rs11185098	Variant not found	A	⚪
BDNF	rs10767664	AA+	T	🔴
FTO	rs1558902	TT+	A	🟢
LEPR	rs1805134	TT+	C	🟢
PLIN1	rs894160	GG-	T	🟢
PLIN1	rs2289487	TT+	C	🟢
TCF7L2	rs7903146	CC+	G,T	🟢

Scoliosis

Gene	SNP	Genotype	Rare Allele	Result
LBX1	rs11190870	CT+	A,C	🟠
MAGI1	rs7649739	AA+	A	🟢

Estradiol

Gene	SNP	Genotype	Rare Allele	Result
ESR2	rs1256031	CC-	A,T	🟠
SHBG	rs1799941	GG+	A	🟢

Oxidative stress

Gene	SNP	Genotype	Rare Allele	Result
ADA	rs73598374	GG-	A,G,T	🟢
ALDH2	rs671	GG+	A	🟢
AOC1	rs10156191	Variant not found	T	⚪
ATF1	rs11169571	CC+	C	🟠
CAT	rs1001179	AA-	T	🔴
CAT	rs480575	Variant not found	G,T	⚪
CBS	rs234706	GG+	A	🟢
CBS	rs2851391	CT+	C	🟢
EPHX1	rs1051740	TT+	C	🟢
EPHX1	rs2234922	AG+	G,T	🟠
G6PD	rs1050829	AA-	C	🟢
G6PD	rs2230037	CC-	G	🟢
GCLC	rs17883901	CC-	A,T	🟢
GPX1	rs1050450	CC-	A	🟢
GPX1	rs3448	CT+	T	🟠
GPX3	rs8177412	Variant not found	C	⚪
GPX4	rs713041	Variant not found	A,C	⚪
GSR	rs1002149	TT+	T	🟡
GSR	rs2978663	TT+	T	🟠
GSR	rs3594	Variant not found	A	⚪
GSR	rs4628224	Variant not found	G,T	⚪
GSR	rs8190924	Variant not found	T	⚪
GSTM1	rs366631	CT-	G	🟠
GSTP1	rs1138272	CT+	T	🟠
GSTP1	rs1695	GG+	G	🟠
HFE	rs1799945	GG+	G	🔴
HFE	rs1800562	GG+	A	🟢
IL-6	rs1800795	CG+	G	🔵
LCT	rs2322659	CT+	C	🟢
LTA	rs909253	CT-	G,T	🟢
NFE2L2	rs6721961	GG+	C,G	🟢
NQO1	rs1800566	CC-	A	🟢
SELENOF	rs5845	Variant not found	A	⚪
SIRT6	rs107251	Variant not found	C	⚪
SLC2A14	rs10846086	Variant not found	G	⚪
SOD1	rs2070424	Variant not found	G	⚪
SOD1	rs1041740	CT+	T	🟡
SOD2	rs2758331	Variant not found	A	⚪
SOD2	rs4880	CT-	G	🟡

Gene	SNP	Genotype	Rare Allele	Result
SOD2	rs8031	Variant not found	T	○
SOD3	rs1799895	CC+	G	●
SOD3	rs2855262	TT+	C	●
TLR4	rs4986790	AA+	G,T	●
TNF	rs1800629	GG+	A	●
ZNF648	rs10911021	CT+	C	●

Worst oxidative stress with selenium

Gene	SNP	Genotype	Rare Allele	Result
GPX1	rs1050450	CC-	A	●
GPX4	rs713041	Variant not found	A,C	○

Estrone

Gene	SNP	Genotype	Rare Allele	Result
CYP19A1	rs749292	GG+	A	●
CYP19A1	rs727479	TT-	C	●
CYP19A1	rs28566535	Variant not found	C	○
CYP19A1	rs730154	CT+	C	●
CYP19A1	rs936306	CT+	T	●
CYP19A1	rs10046	CC-	A	●

Iron

Gene	SNP	Genotype	Rare Allele	Result
HFE	rs1799945	GG+	G	●
HFE	rs1800562	GG+	A	●
NOS3	rs1800779	AA+	G	●
NOS3	rs1800783	Variant not found	C,G,T	○
NOS3	rs3918188	Variant not found	A,T	○
TF	rs1049296	CT+	T	●
TF	rs1130459	Variant not found	G	○
TF	rs121918680	GG+	A	●
TF	rs1799852	CC+	T	●
TF	rs3811647	AG+	G	●
TFR2	rs2075674	Variant not found	A	○
TFR2	rs41303501	Variant not found	T	○
TFR2	rs7385804	CC+	C	●
TMPRSS6	rs855791	TT-	G,T	●
TMPRSS6	rs4820268	GG+	A	●

Slow Contraction Fibers

Gene	SNP	Genotype	Rare Allele	Result
AGTR2	rs11091046	AC+	C	●
PPARA	rs4253778	GG+	C,T	●

Fast Twitch Muscle Fibers

Gene	SNP	Genotype	Rare Allele	Result
AGTR2	rs11091046	AC+	C	●

Atrial Fibrillation

Gene	SNP	Genotype	Rare Allele	Result
ABCC9	rs1001916923	Variant not found	G,T	○
ABCC9	rs1057516044	Variant not found	G	○
ABCC9	rs11046205	AG+	A	●
ACE2	rs2285666	Variant not found	T	○
AF	rs10033464	GG+	T	●
AGT	rs699	CT-	G	●
ASAH1	rs137853596	Variant not found	C	○
ASAH1	rs137853597	Variant not found	A,C	○
CUX2	rs3847953	Variant not found	T	○
EDN2	rs5800	Variant not found	G,T	○
GJA5	rs35594137	Variant not found	T	○
HCN4	rs104894485	Variant not found	T	○
HCN4	rs104894488	Variant not found	A,T	○
KCNH2	rs104894021	CC-	C,T	●
KCNH2	rs1057517742	CC-	C,T	●
KCNH2	rs1057517743	Variant not found	C	○
KCNQ1	rs1057128	Variant not found	A	○
LY96	rs11465996	Variant not found	G	○

Gene	SNP	Genotype	Rare Allele	Result
NEBL	rs12243039	Variant not found	A,G	⚪
NPPA	rs5065	AA+	G	🟢
PITX2	rs2200733	CT+	T	🔴
WNT8A	rs2040862	CC+	T	🟢

Paroxysmal Ventricular Fibrillation

Gene	SNP	Genotype	Rare Allele	Result
SCN5A	rs1805124	GG-	T	🔴
SCN5A	rs7626962	GG+	A,T	🟢

Folate (Vitamin B9)

Gene	SNP	Genotype	Rare Allele	Result
BHMT	rs492842	Variant not found	T	⚪
BHMT	rs651852	Variant not found	T	⚪
BHMT	rs6875201	Variant not found	G	⚪
FOLR1	rs2071010	Variant not found	A,T	⚪
FOLR2	rs651933	AA+	A	🟠
MTHFD1	rs1076991	AG-	C,G	🟢
MTHFD1	rs2236225	CC-	A	🟢
MTHFR	rs1476413	AG-	G,T	🟢
MTHFR	rs17037390	Variant not found	A	⚪
MTHFR	rs1801131	AC-	G	🟠
MTHFR	rs1801133	CC-	A	🟢
MTHFR	rs2066470	Variant not found	A,C	⚪
MTHFR	rs4846049	Variant not found	A,G	⚪
SHMT1	rs1979277	AG+	A	🟢

Muscle strength

Gene	SNP	Genotype	Rare Allele	Result
ACTN3	rs1815739	CT+	T	🟠
ACVR1B	rs2854464	AA+	C,G	🔴
AGT	rs699	CT-	G	🟡
HIF1A	rs11549465	CC+	T	🟢
IL-6	rs1800795	CG+	G	🟢
MSTN	rs1805086	AA-	C	🟢
NOS3	rs2070744	TT+	T	🔴
NOS3	rs1799983	GG+	T	🟢
PPARA	rs4253778	GG+	C,T	🟢
TRHR	rs16892496	AC+	C,G	🟢
VDR	rs1544410	AG-	C,T	🟢

Hand Grip Strength

Gene	SNP	Genotype	Rare Allele	Result
GBF1	rs3758549	Variant not found	A	⚪
GLIS1	rs797906	Variant not found	A,T	⚪
HOXB3	rs2229304	Variant not found	T	⚪
KANSL1	rs281865469	Variant not found	A,C	⚪
KANSL1	rs281865471	Variant not found	C,T	⚪
LRPPRC	rs1060499785	Variant not found	T	⚪
LRPPRC	rs119466000	CC-	A	🟢
MGMT	rs12917	CC+	T	🟢
MGMT	rs16906252	Variant not found	T	⚪
MSTN	rs1805086	AA-	C	🟢
SLC8A1	rs11274804	Variant not found		⚪
SYT1	rs2251214	Variant not found	G,T	⚪
TGFA	rs3771494	TT-	G	🟢
VDR	rs7975232	AC+	A	🟢
VDR	rs1544410	AG-	C,T	🟢
VDR	rs2228570	CC-	C,T	🟢

Knee strength

Gene	SNP	Genotype	Rare Allele	Result
ACVR1B	rs2854464	AA+	C,G	🔴
COL1A1	rs1800012	GT-	A	🔵
COL1A1	rs2249492	Variant not found	G,T	⚪
DNMT3L	rs7354779	TT+	C	🟢
MTRR	rs7703033	GG+	A	🟠
VDR	rs7975232	AC+	A	🟠

Ligament Strength

Gene	SNP	Genotype	Rare Allele	Result
CILP	rs2679117	Variant not found	A,C	⚪
COL5A1	rs1057518004	Variant not found	T	⚪
COL5A1	rs1057518653	Variant not found		⚪
COL5A1	rs61735045	GG+	A	🟢
MSTN	rs1805086	AA-	C	🟢

Quadriceps Muscle Strength

Gene	SNP	Genotype	Rare Allele	Result
AGT	rs699	CT-	G	🟠
COL5A1	rs12722	CC+	T	🟠
MSTN	rs1805086	AA-	C	🟢

Tendon strength

Gene	SNP	Genotype	Rare Allele	Result
GDF5	rs121909347	Variant not found	T	⚪
MMP3	rs563096	Variant not found	T	⚪
MMP3	rs591058	CT+	C	🟢

Muscle Weakness After Exercise

Gene	SNP	Genotype	Rare Allele	Result
ADRB3	rs4994	TT-	G	🟢
MT-ND4	rs869096886	Variant not found	G	⚪
NOS3	rs3918188	Variant not found	A,T	⚪
PPARGC1A	rs8192678	GG-	T	🟢

Fractures

Gene	SNP	Genotype	Rare Allele	Result
CALCR	rs1801197	TT-	G	🟠
ESR1	rs2234693	CT+	A,T	🟠
ESR1	rs9340799	AG+	G	🟠
ITGB3	rs5918	TT+	C	🟢
P2RX7	rs3751143	AC+	C	🟡

Phosphor

Gene	SNP	Genotype	Rare Allele	Result
ALPL	rs1697421	GG-	T	🟢
C12ORF4	rs2970818	TT+	A,C	🟢
CSTA	rs17265703	AA+	G	🟢
PDE7B	rs947583	TT+	C	🟢
TKT	rs782092363	GG+	A	🟢
TKT	rs868953318	Variant not found	T	⚪

Body fat

Gene	SNP	Genotype	Rare Allele	Result
IL-1RN	rs4252041	CC+	T	🟢
IL-1RN	rs419598	TT+	C	🟢

Fat and Sagging in the Arm

Gene	SNP	Genotype	Rare Allele	Result
AGRP	rs5030980	GG-	T	🟢
APOA1	rs670	AG-	T	🟢
APOA2	rs5082	TT-	A	🟢
APOA5	rs3135506	GG+	C	🟢
B4GALT7	rs28937869	CC+	T	🟢
CBS	rs2298758	GG+	A,C	🟢
CBS	rs234706	GG+	A	🟢
COL11A1	rs398122828	CC+	T	🟢
COL11A1	rs587782990	Variant not found	C,G	⚪
COL11A1	rs1057524237	Variant not found	T	⚪
COL11A1	rs730882190	Variant not found	C	⚪
COL11A1	rs1057518666	Variant not found	T	⚪
COL11A1	rs11809524	Variant not found	T	⚪
COL11A1	rs727503881	CC+	T	🟢
COL11A1	rs1676486	Variant not found	G,T	⚪
COL11A1	rs121912944	Variant not found	A	⚪
COL11A1	rs886044242	Variant not found	T	⚪

Gene	SNP	Genotype	Rare Allele	Result
COL11A1	rs886039743	Variant not found	T	⚪
COL11A1	rs12138977	Variant not found	T	⚪
COL11A1	rs1337185	Variant not found	G,T	⚪
COL11A1	rs1057517989	Variant not found		⚪
COL11A1	rs2615977	Variant not found	C	⚪
COL11A1	rs397514455	Variant not found	G	⚪
COL11A1	rs1064797115	Variant not found	G	⚪
COL11A1	rs886042653	Variant not found	A	⚪
COL11A1	rs387906611	Variant not found	G	⚪
COL11A1	rs2126642	Variant not found	A	⚪
COL11A1	rs121912943	Variant not found	A	⚪
COL11A1	rs886044244	Variant not found	G	⚪
COL11A1	rs3753841	AG+	A	🟡
COL11A1	rs2622848	TT+	C	🟢
COL11A2	rs121912949	GG+	A,T	🟢
COL11A2	rs121912947	Variant not found	A	⚪
COL11A2	rs786205578	AA+	G,T	🟢
COL11A2	rs121912946	Variant not found	T	⚪
COL11A2	rs745434198	Variant not found	A,T	⚪
COL11A2	rs121912951	Variant not found	A	⚪
COL11A2	rs374156844	Variant not found	A	⚪
COL11A2	rs2076311	AA+	A	🔴
COL11A2	rs911722283	Variant not found	A	⚪
COL11A2	rs606231410	Variant not found	A,T	⚪
COL11A2	rs121912948	Variant not found	T	⚪
COL11A2	rs121912952	GG+	T	🟢
COL11A2	rs768569721	Variant not found	A,T	⚪
COL11A2	rs750995470	Variant not found	T	⚪
COL11A2	rs2855429	CC+	C	🔴
COL11A2	rs2254287	Variant not found	A,G,T	⚪
COL11A2	rs797044915	CC+	A	🟢
COL11A2	rs121912945	CC+	G,T	🟢
COL11A2	rs121912950	Variant not found	A	⚪
COL11A2	rs864309523	Variant not found	T	⚪
COL11A2	rs387906556	Variant not found	T	⚪
COL11A2	rs770888294	CC+	A,T	🟢
COL17A1	rs805722	Variant not found	A,C	⚪
COL17A1	rs121912771	Variant not found	T	⚪
COL17A1	rs752317971	Variant not found	A,G	⚪
COL17A1	rs1320448	GG+	G	🔴
COL17A1	rs1064793760	Variant not found		⚪
COL17A1	rs886041555	Variant not found		⚪
COL17A1	rs754289857	Variant not found	T	⚪
COL17A1	rs17116350	Variant not found	C,G	⚪
COL17A1	rs201940939	Variant not found	T	⚪
COL17A1	rs121912770	Variant not found	A	⚪
COL17A1	rs760714959	Variant not found	A	⚪
COL17A1	rs121912769	Variant not found	A	⚪
COL17A1	rs767083273	Variant not found	G,T	⚪
COL17A1	rs797045142	Variant not found	A	⚪
COL17A1	rs121912773	Variant not found	T	⚪
COL17A1	rs805708	Variant not found	A	⚪
COL17A1	rs121912772	Variant not found	C	⚪
COL17A1	rs805698	TT+	G,T	🔴
COL17A1	rs121912774	Variant not found	A	⚪
COL17A1	rs775196743	Variant not found	A	⚪
COL17A1	rs775251483	Variant not found		⚪
COL1A1	rs1061237	Variant not found	C,G,T	⚪
COL1A1	rs17639446	Variant not found	C	⚪
COL1A1	rs1064796499	Variant not found	T	⚪
COL1A1	rs72645365	Variant not found	A	⚪
COL1A1	rs72651646	Variant not found	T	⚪
COL1A1	rs193922150	CC+	T	🟢
COL1A1	rs1085307454	Variant not found	T	⚪
COL1A1	rs193922155	TT+	C	🟢
COL1A1	rs193922144	GG+	A	🟢
COL1A1	rs2412298	Variant not found	A	⚪
COL1A1	rs72648320	CC+	T	🟢

Gene	SNP	Genotype	Rare Allele	Result
COL1A1	rs72645357	GG-	T	
COL1A1	rs67394386	Variant not found	A,T	
COL1A1	rs72645333	Variant not found	T	
COL1A1	rs113647555	Variant not found	A	
COL1A1	rs67682641	Variant not found	A,T	
COL1A1	rs193922137	Variant not found	A	
COL1A1	rs1107946	Variant not found	C	
COL1A1	rs72645353	CC+	A,T	
COL1A1	rs72648326	Variant not found	A	
COL1A1	rs72645321	Variant not found	T	
COL1A1	rs397514672	Variant not found	A	
COL1A1	rs72645347	GG+	A	
COL1A1	rs193922151	II+		
COL1A1	rs2586488	GG+	G	
COL1A1	rs193922145	GG+	A	
COL1A1	rs2141279	Variant not found	C	
COL1A1	rs193922148	II+		
COL1A1	rs1007086	Variant not found	G	
COL1A1	rs72645323	Variant not found	T	
COL1A1	rs1800215	Variant not found	T	
COL1A1	rs72645366	Variant not found	A,C	
COL1A1	rs72645318	Variant not found	A	
COL1A1	rs193922147	CC+	A,G	
COL1A1	rs72648363	Variant not found	G	
COL1A1	rs2075554	Variant not found	A,C	
COL1A1	rs139955975	CC+	T	
COL1A1	rs67507747	CC+	A,G,T	
COL1A1	rs72645334	Variant not found	T	
COL1A1	rs193922140	CC+	G	
COL1A1	rs193922138	Variant not found	C	
COL1A1	rs1064796415	Variant not found		
COL1A1	rs193922141	Variant not found		
COL1A1	rs67815019	Variant not found	A,T	
COL1A1	rs72651653	Variant not found	A	
COL1A1	rs1057518221	Variant not found	T	
COL1A1	rs193922158	TT+	C	
COL1A1	rs193922157	CC+	A,T	
COL1A1	rs72651622	Variant not found	G,T	
COL1A1	rs67693970	Variant not found	G,T	
COL1A1	rs144751329	CC+	A,T	
COL1A1	rs370865189	GG+	A,C,T	
COL1A1	rs72645331	Variant not found	A	
COL1A1	rs72651651	Variant not found	G,T	
COL1A1	rs72651645	Variant not found	T	
COL1A1	rs193922152	TT+	C	
COL1A1	rs72645320	Variant not found	T	
COL1A1	rs193922153	GG+	A	
COL1A1	rs1800012	GT-	A	
COL1A1	rs72645337	Variant not found	G	
COL1A1	rs66490707	Variant not found	G,T	
COL1A1	rs1061237	Variant not found	C,G,T	
COL1A1	rs72651657	Variant not found	A	
COL1A1	rs1057518930	Variant not found	G	
COL1A1	rs72648322	Variant not found	A,T	
COL1A1	rs34940368	Variant not found	A,C	
COL1A1	rs193922149	II+		
COL1A1	rs2075559	Variant not found	A,C,T	
COL1A1	rs1061970	Variant not found	G	
COL1A1	rs2075555	Variant not found	A,G	
COL1A1	rs72648337	Variant not found	T	
COL1A1	rs67771061	Variant not found	A,G,T	
COL1A1	rs72648356	Variant not found	T	
COL1A1	rs72648333	Variant not found	A	
COL1A1	rs2269336	CC-	A,C	
COL1A1	rs2249492	Variant not found	G,T	
COL1A1	rs193922143	II+		
COL1A1	rs66721653	Variant not found	A,T	
COL1A1	rs67828806	Variant not found	G,T	

Gene	SNP	Genotype	Rare Allele	Result
COL1A1	rs66929517	Variant not found	A,G	○
COL1A1	rs72651661	Variant not found	T	○
COL1A1	rs72653136	Variant not found	T	○
COL1A1	rs72645328	CC+	G,T	●
COL1A1	rs66523073	Variant not found	T	○
COL1A1	rs2586494	Variant not found	C	○
COL1A1	rs67368147	Variant not found	A,T	○
COL1A1	rs72651614	Variant not found	A,C	○
COL1A1	rs66527965	Variant not found	A,T	○
COL1A1	rs1057524547	Variant not found	T	○
COL1A1	rs72653131	Variant not found	T	○
COL1A1	rs72651642	Variant not found	A	○
COL1A1	rs398122835	Variant not found		○
COL1A1	rs67445413	Variant not found	A,T	○
COL1A1	rs72653137	Variant not found	T	○
COL1A1	rs66555264	Variant not found	A,T	○
COL1A1	rs72645356	Variant not found	T	○
COL1A2	rs1801182	TT+	C	●
COL1A2	rs1064794058	Variant not found	T	○
COL1A2	rs139446305	GG+	A	●
COL1A2	rs121912902	Variant not found	A	○
COL1A2	rs906553840	Variant not found	A,C	○
COL1A2	rs72658200	Variant not found	A	○
COL1A2	rs1057517953	Variant not found	T	○
COL1A2	rs68132885	Variant not found	A,C	○
COL1A2	rs121912910	Variant not found	A	○
COL1A2	rs193922167	Variant not found		○
COL1A2	rs1057524873	Variant not found	A,T	○
COL1A2	rs121912907	Variant not found	T	○
COL1A2	rs1057516036	Variant not found	A	○
COL1A2	rs72659343	Variant not found	A,T	○
COL1A2	rs267606742	Variant not found	A	○
COL1A2	rs72659319	GG+	A,C	●
COL1A2	rs72658152	Variant not found	A	○
COL1A2	rs72658137	Variant not found	A	○
COL1A2	rs1064793527	Variant not found		○
COL1A2	rs768171831	CC+	T	●
COL1A2	rs72656402	Variant not found	T	○
COL1A2	rs67162110	Variant not found	A,C	○
COL1A2	rs67865220	Variant not found	A,C,T	○
COL1A2	rs121912900	Variant not found	A	○
COL1A2	rs1057524847	Variant not found	A	○
COL1A2	rs72656386	Variant not found	A	○
COL1A2	rs1085307707	Variant not found	A	○
COL1A2	rs267606741	Variant not found	A	○
COL1A2	rs3736638	CC+	A	●
COL1A2	rs72658103	Variant not found	A,T	○
COL1A2	rs1800238	Variant not found	T	○
COL1A2	rs193922159	CC+	A,G	●
COL1A2	rs67609234	Variant not found	A,T	○
COL1A2	rs886041749	Variant not found	A	○
COL1A2	rs42524	CC+	G	●
COL1A2	rs797044949	GG+	T	●
COL1A2	rs72658176	GG+	A	●
COL1A2	rs121912904	Variant not found	A	○
COL1A2	rs72658185	Variant not found	A	○
COL1A2	rs72659325	Variant not found	C,T	○
COL1A2	rs1064796419	Variant not found	A	○
COL1A2	rs72656355	AA+	G	●
COL1A2	rs121912901	Variant not found	A	○
COL1A2	rs1057516053	Variant not found	A	○
COL1A2	rs72656357	Variant not found	C	○
COL1A2	rs1057518136	Variant not found		○
COL1A2	rs193922165	GG+	A	●
COL1A2	rs928361235	Variant not found	C	○
COL1A2	rs1801182	TT+	C	●
COL1A2	rs121912906	Variant not found	T	○
COL1A2	rs1057518967	Variant not found	A	○

Gene	SNP	Genotype	Rare Allele	Result
COL1A2	rs1064796593	Variant not found	A	○
COL1A2	rs72656396	Variant not found	A,T	○
COL1A2	rs1085307477	Variant not found	A	○
COL1A2	rs2621215	Variant not found	A,T	○
COL1A2	rs886039689	Variant not found	A	○
COL1A2	rs67768540	Variant not found	A,C,T	○
COL1A2	rs72658117	Variant not found	T	○
COL1A2	rs121912911	Variant not found	C	○
COL1A2	rs42517	Variant not found	G	○
COL1A2	rs66820119	Variant not found	A,C,T	○
COL1A2	rs72656354	Variant not found	G	○
COL1A2	rs121912903	Variant not found	T	○
COL1A2	rs72656370	Variant not found	A	○
COL1A2	rs441051	CT+	C	●
COL1A2	rs121912912	Variant not found	A,C	○
COL1A2	rs72658143	Variant not found	A	○
COL1A2	rs193922173	GG+	A	●
COL1A2	rs72658119	Variant not found	C	○
COL1A2	rs121912909	Variant not found	A	○
COL1A2	rs794727470	GG+	C	●
COL1A2	rs121912908	Variant not found	A,C	○
COL1A2	rs121912905	Variant not found	T	○
COL1A2	rs72659324	Variant not found	C	○
COL1A2	rs72658163	Variant not found	A,C	○
COL1A2	rs193922168	GG+	C	●
COL1A2	rs193922162	GG+	A	●
COL1A2	rs193922166	Variant not found		○
COL1A2	rs72659338	Variant not found	A	○
COL1A2	rs886041426	Variant not found		○
COL1A2	rs72656387	Variant not found	A	○
COL1A2	rs67729041	Variant not found	A,T	○
COL1A2	rs67707918	Variant not found	A,T	○
COL1A2	rs786205587	GG+	A	●
COL1A2	rs72658161	GG+	A	●
COL1A2	rs72658151	GG+	A	●
COL1A2	rs794727669	GG+	T	●
COL1A2	rs797044459	Variant not found	C	○
COL1A2	rs886042129	Variant not found	T	○
COL1A2	rs72658154	GG+	A	●
COL1A2	rs72658150	Variant not found	T	○
COL1A2	rs72659310	Variant not found	A	○
COL1A2	rs886043796	Variant not found	A	○
COL27A1	rs1249719	GG+	A	●
COL27A1	rs7868992	AA+	A	●
COL27A1	rs140950220	GG+	C	●
COL27A1	rs753085	Variant not found	A	○
COL27A1	rs946053	GG+	G	●
COL27A1	rs4143245	Variant not found	C	○
COL27A1	rs1249744	Variant not found	G	○
COL2A1	rs121912890	Variant not found	T	○
COL2A1	rs1057524114	Variant not found	A	○
COL2A1	rs794727438	CC+	A	●
COL2A1	rs794727261	GG+	T	●
COL2A1	rs121912878	Variant not found	T	○
COL2A1	rs1635531	Variant not found	C	○
COL2A1	rs121912876	Variant not found	A	○
COL2A1	rs1064793352	Variant not found	G	○
COL2A1	rs121912875	Variant not found	A	○
COL2A1	rs1064796660	Variant not found	T	○
COL2A1	rs886041843	Variant not found	A	○
COL2A1	rs794727462	CC+	T	●
COL2A1	rs765795867	Variant not found	A,T	○
COL2A1	rs1064797167	Variant not found	G	○
COL2A1	rs587776847	Variant not found		○
COL2A1	rs1064794264	Variant not found	T	○
COL2A1	rs794727026	Variant not found	T	○
COL2A1	rs794727472	CC+	A,T	●
COL2A1	rs2070739	Variant not found	T	○

Gene	SNP	Genotype	Rare Allele	Result
COL2A1	rs138498898	Variant not found	A	○
COL2A1	rs121912869	Variant not found	A	○
COL2A1	rs794727339	Variant not found	G,T	○
COL2A1	rs1057518908	Variant not found	T	○
COL2A1	rs1057524696	Variant not found	G	○
COL2A1	rs3803183	Variant not found	A	○
COL2A1	rs121912879	Variant not found	G	○
COL2A1	rs121912872	Variant not found	T	○
COL2A1	rs121912887	Variant not found	G,T	○
COL2A1	rs1057518911	Variant not found	G	○
COL2A1	rs121912897	Variant not found	A,T	○
COL2A1	rs121912898	Variant not found	T	○
COL2A1	rs121912865	Variant not found	A	○
COL2A1	rs121912867	Variant not found	T	○
COL2A1	rs1793953	Variant not found	A	○
COL2A1	rs121912888	Variant not found	T	○
COL2A1	rs121912884	GG+	A	●
COL2A1	rs794727202	CC+	T	●
COL2A1	rs121912877	CC+	T	●
COL2A1	rs1793933	AC-	T	●
COL2A1	rs886041429	Variant not found	A	○
COL2A1	rs886041713	Variant not found	A,T	○
COL2A1	rs121912881	Variant not found	A	○
COL2A1	rs121912874	GG+	A	●
COL2A1	rs121912882	GG+	A	●
COL2A1	rs121912893	CC-	A,T	●
COL2A1	rs794727596	CC+	A	●
COL2A1	rs1034762	Variant not found	C	○
COL2A1	rs121912892	Variant not found	T	○
COL2A1	rs1085307657	Variant not found	G	○
COL2A1	rs1085307608	Variant not found	A	○
COL2A1	rs121912871	Variant not found	T	○
COL2A1	rs121912885	GG+	A,T	●
COL2A1	rs121912866	GG+	A	●
COL2A1	rs1057524602	Variant not found	A	○
COL2A1	rs794727607	Variant not found	A	○
COL2A1	rs727503882	CC+	G,T	●
COL2A1	rs121912880	CC+	A,T	●
COL2A1	rs1057521852	Variant not found	C,G	○
COL2A1	rs121912868	Variant not found	T	○
COL2A1	rs794727684	CC+	T	●
COL2A1	rs1064794958	Variant not found	T	○
COL2A1	rs121912899	Variant not found	A	○
COL2A1	rs1057518157	Variant not found	A	○
COL2A1	rs121912896	Variant not found	T	○
COL2A1	rs121912889	Variant not found	C	○
COL2A1	rs121912894	Variant not found	T	○
COL2A1	rs864621973	Variant not found	A,T	○
COL2A1	rs60542319	Variant not found	A	○
COL2A1	rs121912895	Variant not found	C	○
COL2A1	rs786205477	CC+	A	●
COL2A1	rs886039543	Variant not found		○
COL2A1	rs121912886	GG+	A,T	●
COL2A1	rs794727185	Variant not found		○
COL2A1	rs121912873	II+		●
COL2A1	rs1635530	Variant not found	C	○
COL2A1	rs794727225	II+		●
COL2A1	rs121912883	Variant not found	G	○
COL2A1	rs1635529	Variant not found	G	○
COL2A1	rs886039542	Variant not found	T	○
COL2A1	rs121912870	CC+	T	●
COL2A1	rs1064796332	Variant not found	T	○
COL2A1	rs2276455	Variant not found	A	○
COL2A1	rs387906558	Variant not found	T	○
COL2A1	rs794727377	TT+	G	●
COL2A1	rs794727546	CC+	G	●
COL2A1	rs121912864	Variant not found	T	○
COL2A1	rs794727533	GG+	A,T	●

Gene	SNP	Genotype	Rare Allele	Result
COL2A1	rs121912891	Variant not found	T	○
COL2A1	rs869312907	CC+	T	●
COL2A1	rs672601354	Variant not found		○
COL2A1	rs748459670	GG+	A,C	●
COL2A1	rs760093841	Variant not found	A,G,T	○
COL2A1	rs672601355	Variant not found		○
COL2A1	rs3737548	Variant not found	A,T	○
COL2A1	rs398123628	II+		●
COL3A1	rs1516446	Variant not found	G	○
COL3A1	rs1800255	AG+	A	●
COL3A1	rs121912920	GG+	A	●
COL3A1	rs121912918	GG+	A,T	●
COL3A1	rs121912929	Variant not found	A,T	○
COL3A1	rs121912924	GG+	A	●
COL3A1	rs121912925	GG+	A,T	●
COL3A1	rs587779449	GG+	A,C	●
COL3A1	rs587779456	GG+	A	●
COL3A1	rs121912923	GG+	A,C,T	●
COL3A1	rs1060500187	Variant not found	A	○
COL3A1	rs111929073	GG+	A,C,T	●
COL3A1	rs267599120	GG+	A,C	●
COL3A1	rs1057521106	CC+	A,T	●
COL3A1	rs1057523593	AA+	C	●
COL3A1	rs113871730	GG+	A	●
COL3A1	rs397509373	GG+	A	●
COL3A1	rs3106796	Variant not found	G	○
COL3A1	rs1057521930	GG+	A,T	●
COL3A1	rs1085307964	GG+	T	●
COL3A1	rs1085307896	GG+	A	●
COL3A1	rs587779446	GG+	A	●
COL3A1	rs587779438	GG+	A	●
COL3A1	rs121912919	GG+	A	●
COL3A1	rs113485686	GG+	A	●
COL3A1	rs587779428	GG+	T	●
COL3A1	rs587779439	GG+	A	●
COL3A1	rs121912916	GG+	A	●
COL3A1	rs193922176	GG+	C	●
COL3A1	rs587779448	GG+	A	●
COL3A1	rs587779459	GG+	A,C	●
COL3A1	rs1516446	Variant not found	G	○
COL3A1	rs587779440	GG+	A,T	●
COL3A1	rs112371422	CC+	G,T	●
COL3A1	rs587779437	GG+	A	●
COL3A1	rs587779454	GG+	A,T	●
COL3A1	rs587779426	TT+	A,C	●
COL3A1	rs1060500204	Variant not found	C	○
COL3A1	rs587779417	GG+	A	●
COL3A1	rs121912915	GG+	T	●
COL3A1	rs121912913	GG+	A,T	●
COL3A1	rs587779457	GG+	A,T	●
COL3A1	rs1060500193	GG+	A	●
COL3A1	rs1057518075	CC+	T	●
COL3A1	rs587779444	GG+	A,C,T	●
COL3A1	rs587779434	GG+	A	●
COL3A1	rs587779447	GG+	A	●
COL3A1	rs121912926	GG+	A,C,T	●
COL3A1	rs587779422	GG+	A	●
COL3A1	rs587779418	GG+	A	●
COL3A1	rs553203474	GG+	A	●
COL3A1	rs397509372	GG+	A,T	●
COL3A1	rs587779443	GG+	A,T	●
COL3A1	rs1064796468	Variant not found	A	○
COL3A1	rs397509371	GG+	T	●
COL3A1	rs121912921	GG+	A	●
COL3A1	rs1060500194	Variant not found	C	○
COL3A1	rs397509377	DD+	T	●
COL3A1	rs587779436	GG+	C	●
COL3A1	rs1057518372	GG+	A	●

Gene	SNP	Genotype	Rare Allele	Result
COL3A1	rs121912928	GG+	A	
COL3A1	rs397509369	GG+	A	
COL3A1	rs587779460	GG+	A	
COL3A1	rs587779445	GG+	T	
COL3A1	rs1060500203	Variant not found	T	
COL3A1	rs121912917	GG+	A,T	
COL3A1	rs397509370	GG+	A,T	
COL3A1	rs1060500200	Variant not found		
COL3A1	rs387906557	GG+	C	
COL3A1	rs587779458	GG+	A,T	
COL3A1	rs1060500199	II+		
COL3A1	rs121912927	GG+	A,T	
COL3A1	rs1800255	AG+	A	
COL3A1	rs121912922	GG+	A,T	
COL3A1	rs112456072	GG+	A	
COL3A1	rs111505097	GG+	A,T	
COL3A1	rs587779453	AA+	C	
COL3A1	rs1064796733	Variant not found	C	
COL3A1	rs121912914	GG+	A,T	
COL3A1	rs587779429	TT+	C	
COL3A1	rs587779452	GG+	T	
COL3A1	rs397509375	TT+	A,C	
COL3A1	rs587779450	GG+	A,T	
COL3A1	rs587779432	GG+	A	
COL3A1	rs587779421	GG+	A	
COL3A1	rs587779427	GG+	T	
COL3A1	rs587779431	GG+	A,T	
COL3A1	rs587779433	GG+	A,C	
COL3A1	rs587779451	II+		
COL3A1	rs587779420	GG+	A,C	
COL3A1	rs587779423	TT+	A,C	
COL3A1	rs587779416	GG+	T	
COL3A1	rs587779441	GG+	A,C	
COL3A1	rs397509376	GG+	A,T	
COL3A1	rs587779424	GG+	A	
COL3A1	rs587779419	GG+	A	
COL3A1	rs587779455	II+		
COL3A1	rs587779435	GG+	A,C	
COL3A1	rs587779442	GG+	C	
COL4A3	rs869025324	Variant not found	A	
COL4A3	rs200672668	Variant not found	A	
COL4A3	rs200287952	Variant not found	A	
COL4A3	rs1085307955	Variant not found	A	
COL4A3	rs35212277	Variant not found	A	
COL4A3	rs1057519377	Variant not found	T	
COL4A3	rs759739044	GG+	A,T	
COL4A3	rs375040636	Variant not found	A	
COL4A3	rs10178458	CC+	A,C	
COL4A3	rs1060499654	Variant not found	T	
COL4A3	rs760462252	Variant not found	T	
COL4A3	rs6436669	Variant not found	G	
COL4A3	rs869025327	Variant not found	A	
COL4A3	rs34505188	GG+	A	
COL4A3	rs1057519376	Variant not found	C	
COL4A3	rs201697532	CC+	T	
COL4A3	rs121912827	GG+	A,T	
COL4A3	rs121912826	Variant not found	A	
COL4A3	rs869025328	Variant not found	A,T	
COL4A3	rs121912824	CC+	T	
COL4A3	rs7606754	AG+	G	
COL4A3	rs778034451	Variant not found	A	
COL4A3	rs267606745	Variant not found	A	
COL4A3	rs765661521	Variant not found	A,C	
COL4A3	rs1060499696	Variant not found	A	
COL4A3	rs11677877	AA+	G	
COL4A3	rs121912825	CC+	G,T	
COL4A3	rs869025326	Variant not found	C	
COL4A3	rs869025325	Variant not found	T	

Gene	SNP	Genotype	Rare Allele	Result
COL4A4	rs121912862	Variant not found	T	
COL4A4	rs869025329	Variant not found	G	
COL4A4	rs121912860	Variant not found	T	
COL4A4	rs121912859	Variant not found	T	
COL4A4	rs786205640	II+		
COL4A4	rs370474706	Variant not found	A,T	
COL4A4	rs569681869	Variant not found	G	
COL4A4	rs7558081	Variant not found	T	
COL4A4	rs2229813	CT+	G,T	
COL4A4	rs1064796549	Variant not found		
COL4A4	rs786205548	TT+	A	
COL4A4	rs2272205	TT+	C	
COL4A4	rs374815903	Variant not found	A,T	
COL4A4	rs121912861	Variant not found	A	
COL4A4	rs121912863	Variant not found	A	
COL4A4	rs121912858	Variant not found	T	
COL4A4	rs2228555	Variant not found	C	
COL4A5	rs104886044	Variant not found		
COL4A5	rs104886045	Variant not found		
COL4A5	rs104886055	Variant not found	C	
COL4A5	rs104886062	Variant not found	C,T	
COL4A5	rs104886079	Variant not found	A	
COL4A5	rs104886076	Variant not found	C	
COL4A5	rs104886065	Variant not found		
COL4A5	rs104886073	Variant not found	C	
COL4A5	rs104886112	Variant not found	A	
COL4A5	rs104886071	Variant not found	G,T	
COL4A5	rs104886110	Variant not found	A	
COL4A5	rs104886118	Variant not found	A	
COL4A5	rs104886120	Variant not found	T	
COL4A5	rs104886132	Variant not found	A	
COL4A5	rs104886133	Variant not found	T	
COL4A5	rs104886108	Variant not found	C	
COL4A5	rs104886092	Variant not found	T	
COL4A5	rs104886122	Variant not found	A	
COL4A5	rs104886123	Variant not found		
COL4A5	rs104886138	Variant not found	A	
COL4A5	rs104886143	Variant not found	C	
COL4A5	rs104886142	GG+	A	
COL4A5	rs104886137	Variant not found	C	
COL4A5	rs104886081	Variant not found	T	
COL4A5	rs104886060	Variant not found	A,T	
COL4A5	rs104886070	Variant not found	A	
COL4A5	rs104886047	Variant not found	C,G	
COL4A5	rs104886053	Variant not found		
COL4A5	rs104886114	Variant not found	A	
COL4A5	rs104886121	Variant not found	A,T	
COL4A5	rs104886094	Variant not found	T	
COL4A5	rs104886116	Variant not found	A	
COL4A5	rs104886080	Variant not found	A	
COL4A5	rs104886061	Variant not found	A,T	
COL4A5	rs104886119	Variant not found	A	
COL4A5	rs104886078	Variant not found	T	
COL4A5	rs104886058	Variant not found		
COL4A5	rs104886077	Variant not found		
COL4A5	rs104886124	Variant not found		
COL4A5	rs104886099	Variant not found	T	
COL4A5	rs104886085	Variant not found	C	
COL4A5	rs104886115	Variant not found	A	
COL4A5	rs104886063	Variant not found	A,T	
COL4A5	rs104886059	Variant not found	T	
COL4A5	rs104886066	Variant not found	A,T	
COL4A5	rs104886050	Variant not found	G	
COL4A5	rs104886046	Variant not found		
COL4A5	rs104886100	Variant not found	T	
COL4A5	rs104886083	Variant not found	A	
COL4A5	rs104886067	Variant not found	A	
COL4A5	rs104886084	Variant not found	A	

Gene	SNP	Genotype	Rare Allele	Result
COL4A5	rs104886088	Variant not found	A,T	
COL4A5	rs104886075	Variant not found	A	
COL4A5	rs104886103	Variant not found	A	
COL4A5	rs104886068	Variant not found	A	
COL4A5	rs104886054	Variant not found		
COL4A5	rs104886074	Variant not found	A,T	
COL4A5	rs104886093	Variant not found	T	
COL4A5	rs104886082	Variant not found	A	
COL4A5	rs104886117	Variant not found	A	
COL4A5	rs104886095	Variant not found		
COL4A5	rs104886141	Variant not found	A,T	
COL4A5	rs104886126	Variant not found	C	
COL4A5	rs104886042	Variant not found		
COL4A5	rs104886125	Variant not found	A	
COL4A5	rs104886091	Variant not found	A	
COL4A5	rs104886043	Variant not found	A	
COL4A5	rs104886102	Variant not found	T	
COL4A5	rs104886048	Variant not found	A	
COL4A5	rs104886072	Variant not found		
COL4A5	rs104886131	Variant not found	A	
COL4A5	rs104886408	Variant not found		
COL4A5	rs104886104	Variant not found		
COL4A5	rs104886135	Variant not found	C	
COL4A5	rs104886049	Variant not found	T	
COL4A5	rs104886056	Variant not found	C,T	
COL4A5	rs104886097	Variant not found	A	
COL4A5	rs104886051	Variant not found	T	
COL4A5	rs104886109	Variant not found		
COL4A5	rs104886144	Variant not found	A	
COL4A5	rs104886098	Variant not found	A	
COL4A5	rs104886111	Variant not found	A	
COL4A5	rs104886050	Variant not found	G	
COL4A5	rs104886086	Variant not found	A	
COL4A5	rs104886052	Variant not found	A,C	
COL4A5	rs104886134	Variant not found	A,C,T	
COL4A5	rs104886130	Variant not found	A	
COL4A5	rs104886101	Variant not found	A	
COL4A5	rs104886145	Variant not found	A	
COL4A5	rs104886127	Variant not found	T	
COL4A5	rs104886113	Variant not found		
COL4A5	rs104886128	Variant not found		
COL4A5	rs104886139	Variant not found	A	
COL4A5	rs281874765	Variant not found	C	
COL4A5	rs104886096	GG+	A	
COL4A5	rs104886069	Variant not found	C	
COL4A5	rs104886136	Variant not found	A	
COL4A5	rs104886049	Variant not found	T	
COL4A5	rs104886129	Variant not found	C	
COL4A5	rs104886057	Variant not found	A	
COL4A5	rs104886140	Variant not found	A,T	
COL4A5	rs104886105	Variant not found	A	
COL4A5	rs104886107	Variant not found	A	
COL4A5	rs104886146	Variant not found	A	
COL4A6	rs779748859	Variant not found	T	
COL4A6	rs769211787	AA+	C	
COL5A1	rs121912933	Variant not found	T	
COL5A1	rs10628678	Variant not found		
COL5A1	rs1060502255	Variant not found		
COL5A1	rs1060502256	Variant not found		
COL5A1	rs7044529	TT+	T	
COL5A1	rs786205100	Variant not found		
COL5A1	rs863223469	DD+	C	
COL5A1	rs12722	CC+	T	
COL5A1	rs764446683	CC+	A,G,T	
COL5A1	rs1057518653	Variant not found		
COL5A1	rs1060502248	Variant not found	A	
COL5A1	rs769752636	Variant not found	A,T	
COL5A1	rs863223453	GG+	A,C	

Gene	SNP	Genotype	Rare Allele	Result
COL5A1	rs765079080	TT+	G	
COL5A1	rs1064796684	Variant not found	T	
COL5A1	rs786205101	Variant not found	G	
COL5A1	rs863223444	TT+	A	
COL5A1	rs777625241	CC+	T	
COL5A1	rs863223445	GG+	A	
COL5A1	rs863223470	DD+	G	
COL5A1	rs1057518004	Variant not found	T	
COL5A1	rs863223454	CC+	T	
COL5A1	rs786205102	Variant not found		
COL5A1	rs886043641	Variant not found	T	
COL5A1	rs80338764	GG+	C	
COL5A1	rs786200922	Variant not found	T	
COL5A1	rs1060502259	Variant not found		
COL5A1	rs886042045	Variant not found	T	
COL5A1	rs374020067	CC+	T	
COL5A1	rs794727114	GG+	C	
COL5A1	rs863223471	Variant not found	T	
COL5A1	rs863223448	GG+	C	
COL5A1	rs863223473	DD+	C	
COL5A1	rs564375308	CC+	T	
COL5A1	rs863223475	DD+	T	
COL5A1	rs1057518871	Variant not found		
COL5A1	rs1057519596	Variant not found	C	
COL5A1	rs863223452	GG+	A	
COL5A1	rs121912932	Variant not found	A	
COL5A1	rs113452150	GG+	A	
COL5A1	rs7874142	AG+	A	
COL5A1	rs863223458	GG+	A	
COL5A1	rs1085307855	Variant not found		
COL5A1	rs794727760	II+		
COL5A1	rs1060502258	Variant not found	T	
COL5A1	rs863223472	Variant not found		
COL5A1	rs863223483	TT+	G	
COL5A1	rs863223478	CC+	T	
COL5A1	rs377138881	GG+	A	
COL5A1	rs926426117	Variant not found	A,C	
COL5A1	rs863223457	Variant not found	T	
COL5A1	rs61735045	GG+	A	
COL5A1	rs886042173	Variant not found	A	
COL5A1	rs183495554	TT+	A,C	
COL5A1	rs772445337	Variant not found	A	
COL5A1	rs863223466	GG+	A	
COL5A1	rs557361751	CC+	T	
COL5A1	rs863223474	II+		
COL5A1	rs387906606	CC+	T	
COL5A2	rs786205104	Variant not found	A	
COL5A2	rs762080305	GG+	A,C	
COL5A2	rs1057524163	Variant not found	A	
COL5A2	rs773726323	CC+	T	
COL5A2	rs863223501	CC+	T	
COL5A2	rs779153546	CC+	T	
COL5A2	rs771415085	Variant not found	A,C,T	
COL5A2	rs878853978	Variant not found	T	
COL5A2	rs886039694	Variant not found	T	
COL5A2	rs780495441	CC+	T	
COL5A2	rs1040238147	Variant not found	T	
COL5A2	rs770598613	CC+	G	
COL5A2	rs151187317	Variant not found	T	
COL5A2	rs863223491	CC+	T	
COL5A2	rs779614415	Variant not found	G	
COL5A2	rs747946828	CC+	A,T	
COL5A2	rs121912930	CC+	G	
CTNNBL1	rs6013029	Variant not found	T	
FTO	rs1121890	Variant not found	G,T	
FTO	rs1421085	TT+	C	
FTO	rs9939609	TT+	A	
FUT2	rs601338	AG+	A	

Gene	SNP	Genotype	Rare Allele	Result
HIF1A	rs1957757	Variant not found	C	⚪
INTERGENIC	rs9819506	Variant not found	C	⚪
MC4R	rs11152221	Variant not found	C	⚪
MC4R	rs17700633	AG+	A	🟢
MC4R	rs17782313	CT+	C	🟠
MC4R	rs2229616	GG-	C	🟢
MC4R	rs52820871	TT+	G	🟢
MMP1	rs1799750	---	C	🟢
MMP3	rs3025058	DI+	G	🔴
PCSK1	rs6232	AG-	C	🟠
PCSK1	rs6234	Variant not found	C	⚪
PCSK1	rs6235	Variant not found	G	⚪
QPCTL	rs2287019	CC+	T	🟠
RIC3	rs1528133	Variant not found	C,G	⚪
STXBP5L	rs11707293	Variant not found	T	⚪
TCF7L2	rs7903146	CC+	G,T	🟢
TNF	rs361525	GG+	A	🟠
UCP1	rs6536991	TT+	C	🟠

Calves Muscles Hyperthrophy

Gene	SNP	Genotype	Rare Allele	Result
ACTN3	rs1815739	CT+	T	🔵
CAPN3	rs80338800	II+	A	🔴
DMD	rs1057518962	Variant not found	A,G,T	⚪

Trend of Monounsaturated Fat Intake and Weight Gain

Gene	SNP	Genotype	Rare Allele	Result
AATK	rs7220048	TT+	C	🟢
ACMSD	rs387906598	Variant not found	T	⚪
ADCYAP1	rs1893154	CC-	G	🟢
ADIPOQ	rs17300539	GG+	A	🔴
ADIPOQ	rs6444175	Variant not found	A	⚪
ADRA2A	rs553668	Variant not found	G,T	⚪
ADRB3	rs4994	TT-	G	🟢
ADSS	rs3102460	CT+	T	🟢
AK8	rs12552369	Variant not found	A	⚪
ALLC	rs387907075	Variant not found	C	⚪
ANKAR	rs12053254	TT+	C	🟢
ANKK1	rs1800497	CT-	A	🔴
APOA5	rs662799	AA+	T	🟢
ARHGAP11A	rs555387669	Variant not found		⚪
ARHGAP24	rs11732231	Variant not found	C,T	⚪
ARMC4	rs587777047	AA+	C	🟢
ARMC4	rs587777049	GG+	T	🟢
ASIC2	rs28936	Variant not found	C	⚪
ASTN2	rs111033570	Variant not found	A	⚪
AUTS2	rs1057518198	Variant not found		⚪
BICC1	rs11006263	AA+	G	🟢
BICD1	rs2630578	Variant not found	C	⚪
C2CD4C	rs12978500	AC+	A	🟢
C8ORF34	rs1517114	CC+	A,G,T	🟢
CA8	rs267606695	Variant not found	C,G	⚪
CADM1	rs6589488	Variant not found	T	⚪
CAMK2A	rs2053053	Variant not found	A,C	⚪
CCDC33	rs2930291	Variant not found	A,C	⚪
CCDC77	rs1048466	AG+	A,C	🟢
CD46	rs35366573	CC+	T	🟢
CD46	rs7144	Variant not found	C	⚪
CDCA3	rs5443	CT+	T	🟠
CDHR3	rs6967330	GG+	A	🟢
CEBPB-AS1	rs4253449	GG+	A	🟢
CELF2	rs3740194	Variant not found	C	⚪
COL4A1	rs113994104	Variant not found	A,T	⚪
COL4A1	rs3742207	AC-	A,G	🟢
COLEC12	rs16944558	Variant not found	T	⚪
CSMD1	rs995322	Variant not found	C,G	⚪
CYP2E1	rs2031920	CC+	T	🟢

Gene	SNP	Genotype	Rare Allele	Result
CYP2E1	rs2070672	AA+	G	
CYP2E1	rs72559710	GG+	A,C,T	
DAPL1	rs16843372	TT+	C	
DDX60L	rs17612333	Variant not found	A,G	
DLC1	rs121908500	Variant not found	C	
DLG2	rs10501570	Variant not found	C	
DMRT1	rs1057519638	Variant not found	T	
DOCK8	rs112321280	Variant not found	G	
DOCK8	rs192864327	GG+	C,T	
ECT2	rs7646507	AG+	A	
EEPD1	rs4302748	AG+	A	
EHF	rs286913	CC-	G,T	
EVA1A	rs17011455	TT+	C	
FAM129A	rs147815528	Variant not found	A,C	
FAM19A2	rs10784285	Variant not found	T	
FAM209B	rs6024938	CT+	T	
FAM71F1	rs6971091	GG+	A	
FARP1	rs688872	TT-	G	
FLJ33534	rs16857178	GG+	A	
FSIP1	rs10152640	AG+	G	
FTO	rs1121980	CC-	A	
FTO	rs121918214	GG+	A	
FTO	rs1421085	TT+	C	
FTO	rs17817449	TT+	A,G	
FTO	rs3751812	GG+	T	
FTO	rs9930506	AA+	G	
FTO	rs9939609	TT+	A	
GCH1	rs10483639	Variant not found	C	
GCH1	rs104894433	Variant not found	A,C,T	
GCH1	rs104894434	Variant not found	G	
GHRL	rs696217	Variant not found	T	
GMDS	rs9378688	Variant not found	A	
GPC5	rs2352028	CT+	G,T	
GSG1L	rs205391	CT+	C,G	
HDAC9	rs11984041	CC+	T	
IFI16	rs6940	Variant not found	T	
IFNGR2	rs74315444	Variant not found	A	
IL-1A	rs1800587	CT-	A,C	
IL-1B	rs1143634	CT-	A	
INSIG2	rs7566605	GG+	C	
INTERGENIC	rs10207060	GT+	A,G	
INTERGENIC	rs11070098	TT+	C	
INTERGENIC	rs11845134	Variant not found	T	
INTERGENIC	rs12986207	Variant not found	A,C	
INTERGENIC	rs17054265	CC+	G,T	
INTERGENIC	rs17468244	AA+	G	
INTERGENIC	rs2153299	AA-	C	
INTERGENIC	rs2575029	CC+	C	
INTERGENIC	rs5767992	CC+	C	
INTERGENIC	rs6486986	GT+	T	
JDP2	rs741846	Variant not found	A,T	
KCNB1	rs1057518621	Variant not found	T	
KCNB1	rs1057521887	Variant not found	C	
KIF6	rs20455	Variant not found	G	
KIF6	rs9380880	GG+	A	
KIRREL	rs6427419	Variant not found	A	
LEPR	rs1137101	AA+	G	
LGALS17A	rs8103033	AG+	A	
LHPP	rs12773846	GG+	A,C	
LINC00704	rs1391511	Variant not found	G	
LINC01299	rs6981992	GT+	A,T	
LINC01500	rs405460	AC-	A,T	
LIPC	rs113298164	Variant not found	T	
LIPC	rs1800588	CC+	T	
LIPC	rs261332	GG+	G	
LPP	rs1152846	AG-	C	
LPP	rs4686484	Variant not found	A	
MC4R	rs1057517991	Variant not found	G	

Gene	SNP	Genotype	Rare Allele	Result
MC4R	rs10871777	AG+	G	🟠
MC4R	rs12970134	AG+	A	🟢
MDFIC	rs7784447	GG+	A	🟢
NAT2	rs1041983	CC+	T	🟢
NAT2	rs1208	GG+	G	🟡
NAT2	rs1799929	CT+	T	🟢
NAT2	rs1801279	GG+	A	🟢
NAT2	rs1801280	CC+	C	🟡
NAT2	rs1805158	CC+	A,T	🟢
NDUFA8	rs3818638	AG-	C	🟢
NIPSNAP3B	rs2472476	AG-	T	🟢
NLRP8	rs306450	Variant not found	G	⚪
NMNAT2	rs4652795	CT+	T	🟢
NPM2	rs11776272	GG+	G	🟢
NR1D1	rs2314339	CC+	T	🔴
NXPH1	rs765855	GG+	G	🟢
PCDH9	rs17081231	AA+	G	🟢
PCSK1	rs6232	AG-	C	🟠
PIP4K2A	rs746203	Variant not found	T	⚪
PKNOX2	rs10893366	CT+	T	🟢
PLEKHG1	rs17427389	GG+	A,T	🟢
POC5	rs2112347	GT+	G	🟢
PPARG	rs13306747	Variant not found	A,G,T	⚪
PPARG	rs3856806	CC+	T	🟢
PPARG	rs1801282	CG+	C	🟠
PPM1H	rs2029721	Variant not found	A	⚪
PTPRD	rs10116682	Variant not found	A	⚪
PTPRD	rs1975197	CC-	A	🔵
PTPRN2	rs10274279	TT+	C	🟢
PVALB	rs2022068	AA+	G	🟢
RAB17	rs2292873	AG-	T	🟢
RASEF	rs10867921	AG+	A	🟢
RBBP6	rs11860248	Variant not found	G	⚪
RBFOX1	rs1057521725	Variant not found	A	⚪
RBFOX1	rs1064794750	Variant not found	G	⚪
RIC3	rs1528133	Variant not found	C,G	⚪
RLN3	rs123277666	Variant not found		⚪
RPTOR	rs2289759	Variant not found	G	⚪
RSU1	rs11254160	AG+	A	🟢
RYR2	rs1057517873	AA+	G	🟢
S100P	rs3822262	AA-	G	🟢
SCG3	rs16964476	Variant not found	G	⚪
SCG3	rs3764220	Variant not found	G,T	⚪
SDC3	rs2282440	Variant not found	A,C	⚪
SERPINA12	rs61757459	Variant not found	A	⚪
SLC22A2	rs316019	GG-	C	🟢
SLC22A2	rs8177504	CC-	A,T	🟢
SLC22A2	rs8177507	GG-	G,T	🟢
SLC22A2	rs8177516	CC-	A,T	🟢
SLC22A2	rs8177517	AA-	C,G	🟢
SLC22A23	rs4959235	Variant not found	C	⚪
SLC29A3	rs1084004	CC+	C,G	🟢
SLC29A3	rs121912583	GG+	A	🟢
SLC29A3	rs869025176	Variant not found	C	⚪
SMYD3	rs11800820	CC+	A,T	🟢
SNRPN	rs220030	Variant not found	A,C	⚪
SORBS1	rs11188352	Variant not found	G	⚪
SPAG16	rs16851771	AA+	G	🟢
SPOCK3	rs9312517	AA+	G	🟢
STON2	rs6574644	AA+	A	🟢
SYT1	rs17005598	Variant not found	A	⚪
TBC1D1	rs35859249	CC+	A,T	🟢
TCF4	rs613872	TT+	T	🟢
TCF4	rs9960767	CC+	C,G	🟡
TM9SF2	rs9513627	AA+	A	🟢
TMEM18	rs6548238	CC+	C	🟢
TMEM229B	rs1077989	AC+	C	🟢
TMEM45B	rs10894147	CC+	T	🟢

Gene	SNP	Genotype	Rare Allele	Result
TMOD1	rs1475545	AG-	T	🟢
TNF	rs361525	GG+	A	🟢
TNFRSF1B	rs5746059	Variant not found	G	⚪
TPTE2P1	rs2483374	AC+	C,T	🟢
TRABD2B	rs946836	Variant not found	G,T	⚪
TRAPPC9	rs267607137	CC-	A	🟢
TRIM66	rs4929923	CC+	C	🟢
TUB	rs2272382	Variant not found	C	⚪
UGT2B7	rs12233719	GG+	A,C,T	🟢
UGT2B7	rs7439366	Variant not found	C	⚪
UNC13A	rs12608932	AC+	C	🟡
UNC5C	rs12643654	Variant not found	G	⚪
VSIG10	rs7957470	GG+	G	🟢
WDPCP	rs11683229	Variant not found	G,T	⚪
WDPCP	rs200322968	Variant not found	T	⚪
WDR11-AS1	rs10937273	Variant not found	A	⚪
WDR11-AS1	rs318240760	Variant not found	A,C	⚪
WDR11-AS1	rs4783244	GG+	T	🟢
ZBTB46	rs6062314	TT+	G,T	🟢
ZNF536	rs3786800	AA-	C	🟢

Inositol (Vitamin B8)

Gene	SNP	Genotype	Rare Allele	Result
BDNF	rs6265	GG-	T	🟢
NGF	rs6330	CC-	A	🟢

Gait Instability

Gene	SNP	Genotype	Rare Allele	Result
DHX30	rs1057519436	Variant not found	A	⚪
VPS13B	rs386834070	CC+	T	🟢

Gluten Intolerance

Gene	SNP	Genotype	Rare Allele	Result
HLA	rs4639334	Variant not found	A	⚪
HLA-DQB1	rs4988889	Variant not found	T	⚪
HLA-DQB1	rs7775228	TT+	C	🟢
IL-18RAP	rs917997	AG-	A,C	🟡
KIAA1109	rs13119723	GG+	G	🔴
KIAA1109	rs6822844	GT+	T	🟠

Lactose intolerance

Gene	SNP	Genotype	Rare Allele	Result
LCT	rs386833837	Variant not found	D	⚪
LCT	rs386833836	Variant not found	D	⚪
LCT	rs1312031160	Variant not found	A	⚪
LCT	rs1276818330	Variant not found	C	⚪
LCT	rs386833835	Variant not found	A	⚪
LCT	rs386833834	Variant not found	C	⚪
LCT	rs763006562	Variant not found	A	⚪
LCT	rs121908936	Variant not found	T	⚪
LCT	rs386833833	CC+	T	🟢
LCT	rs749118441	Variant not found	A	⚪
LCT	rs386833832	Variant not found	D	⚪
LCT	rs121908937	Variant not found	G	⚪
LCT	rs386833838	Variant not found	D	⚪
MCM6	rs145946881	CC+	G	🟢
MCM6	rs41380347	AA+	C	🟢
MCM6	rs4988235	AG+	A	🔵
MCM6	rs41525747	GG+	C	🟢
MCM6	rs182549	TT+	T	🔵
MCM6	rs4988233	Variant not found	A	⚪
MCM6	rs55660827	Variant not found	G	⚪

Iodine

Gene	SNP	Genotype	Rare Allele	Result
ABCC4	rs9561778	GT+	A,T	🟡
ARVCF	rs5993891	Variant not found	T	⚪
ATM	rs1800056	TT+	C	🟢

Gene	SNP	Genotype	Rare Allele	Result
ATM	rs1800057	Variant not found	A,G	⚪
ATM	rs1800058	CC+	T	🟢
ATM	rs1801673	AA+	T	🟢
ATM	rs3092856	CC+	T	🟢
ATM	rs3218695	CC+	A,T	🟢
ATM	rs3218707	GG+	C	🟢
ATM	rs4986761	TT+	C	🟢
ATM	rs4987945	Variant not found	G	⚪
AURKA	rs1047972	GG-	T	🟢
AURKA	rs2273535	Variant not found	T	⚪
BARD1	rs28997576	Variant not found	G,T	⚪
BMPR1B	rs1434536	Variant not found	T	⚪
BRCA1	rs16942	AG-	A,C	🟠
BRCA1	rs1799950	AA-	C	🟢
BRCA1	rs1799966	AG-	A,C	🟢
BRCA1	rs1800709	CC-	A	🟢
BRCA1	rs2227945	AA-	C,G	🟢
BRCA1	rs4986850	GG-	A,T	🟢
BRCA1	rs4986852	GG-	G,T	🟢
BRCA2	rs11571746	Variant not found	C	⚪
BRCA2	rs11571747	AA+	C	🟢
BRCA2	rs11571833	AA+	T	🟢
BRCA2	rs144848	GT-	C	🟡
BRCA2	rs1799944	AA+	G	🟢
BRCA2	rs1799954	CC+	A,T	🟢
BRCA2	rs1801406	Variant not found	C,G	⚪
BRCA2	rs1801426	AA+	G	🟢
BRCA2	rs28897743	GG+	A,C,T	🟢
BRCA2	rs4987047	AA+	T	🟢
BRCA2	rs4987117	CC+	T	🟢
BRCA2	rs766173	TT-	C,G	🟢
BRCA2	rs80358785	CC+	A,G	🟢
BRCA2	rs80359604	II+	T	🔴
CAPZB	rs1472565	Variant not found	A,C	⚪
CASC16	rs3803662	CT-	G	🟢
CASC17	rs1859962	GG+	T	🟠
CASC21	rs13281615	AG+	G	🟢
CASC21	rs16902104	CC+	G,T	🟢
CASC8	rs1447295	CC+	C,T	🟢
CASC8	rs6983267	GG+	T	🔴
CASP8	rs1045485	GG+	A,C,T	🟢
CASP8	rs17468277	Variant not found	A,T	⚪
CCNE1	rs997669	Variant not found	C	⚪
CDH1	rs16260	AC+	A	🟡
CDKN1A	rs1801270	CC+	A,T	🟢
CDKN1A	rs3176336	Variant not found	T	⚪
CDKN1B	rs34330	CT+	C	🟡
CDKN2A	rs3731239	Variant not found	G	⚪
CDKN2B-AS1	rs3218005	Variant not found	C	⚪
CHEK2	rs17879961	TT-	C,G	🟢
CHEK2	rs1805129	Variant not found	C	⚪
COMT	rs165631	CC+	T	🟢
COMT	rs4680	AG+	A	🟢
CTLA4	rs231775	AG+	G	🟡
CYP17A1	rs2486758	Variant not found	C	⚪
CYP24A1	rs480995	Variant not found	G	⚪
CYP24A1	rs8124792	Variant not found	A	⚪
CYP3A4	rs2740574	AA-	T	🟢
CYP3A4	rs4646438	---		🟢
CYP3A4	rs55785340	AA+	G	🟢
DAB2IP	rs1571801	AC-	T	🟢
DIO2	rs225012	Variant not found	A,G	⚪
EHBP1	rs2710646	Variant not found	A	⚪
ELAC2	rs4792311	GG+	A,C	🔵
EPCAM	rs1126497	Variant not found	C	⚪
ESR2	rs2987983	Variant not found	G	⚪
FAM124A	rs10492519	Variant not found	C,G	⚪
FANCA	rs1061646	Variant not found	A	⚪

Gene	SNP	Genotype	Rare Allele	Result
FCHSD1	rs251177	Variant not found	C	⚪
FGF7	rs4338740	CT+	C	🟡
FGFR2	rs1219648	AA+	G,T	🟢
FGFR2	rs2420946	Variant not found	C	⚪
FGFR2	rs2981582	CC-	G	🟢
FGFR4	rs2011077	Variant not found	T	⚪
FGFR4	rs351855	CC-	A	🟢
FTO	rs17817449	TT+	A,G	🟢
FYCO1	rs1545985	Variant not found	A	⚪
FYCO1	rs7652331	Variant not found	A,C	⚪
GAD1	rs1978340	Variant not found	A	⚪
GAD1	rs3791878	Variant not found	T	⚪
GPX4	rs713041	Variant not found	A,C	⚪
GSTP1	rs1695	GG+	G	🟠
HER2	rs1136201	AA+	G,T	🟢
HLA	rs2517532	CT-	G	🟢
HMMR	rs10515860	Variant not found	A	⚪
HMMR	rs299284	CC+	T	🟢
HNF1B	rs3760511	Variant not found	A,T	⚪
IL-10	rs1800896	AG-	C	🟠
INTERGENIC	rs10086908	Variant not found	C	⚪
INTERGENIC	rs10505483	AG-	T	🟠
INTERGENIC	rs10816625	AA+	G	🟢
INTERGENIC	rs10896449	AA+	G	🟢
INTERGENIC	rs13387042	AA+	G	🟡
INTERGENIC	rs16901979	AC+	A	🔴
INTERGENIC	rs2056116	AG+	G	🟡
INTERGENIC	rs4054823	Variant not found	C	⚪
INTERGENIC	rs4700485	Variant not found	G	⚪
INTERGENIC	rs5945572	AG+	G	🟡
INTERGENIC	rs672888	Variant not found	G	⚪
INTERGENIC	rs7965399	TT+	A,C	🟢
ITGA2	rs1126643	CC+	T	🟢
ITGA6	rs10207654	Variant not found	G	⚪
JAZF1	rs10486567	AG+	A	🟡
KIAA1211	rs629242	Variant not found	T	⚪
KLF6	rs3750861	CC+	T	🟢
LPAR6	rs2854344	Variant not found	A,T	⚪
LSP1	rs3817198	CT+	C	🟢
MAGEC3	rs176026	Variant not found	A	⚪
MAP3K1	rs889312	AA+	A	🟢
MRPS30	rs4415084	Variant not found	T	⚪
MSMB	rs10993994	AA-	G	🟢
NCOA3	rs2230782	GG+	A,C	🟢
NOS3	rs1800783	Variant not found	C,G,T	⚪
NQO1	rs1800566	CC-	A	🟢
PCAT19	rs11672691	AA+	T	🟢
PDE8B	rs4704397	AG+	A	🟡
PHTF1	rs6679677	CC+	A	🟢
PTCSC2	rs925489	CT+	C,T	🟢
RNASEL	rs3738579	CT-	G	🔵
RNASEL	rs486907	Variant not found	T	⚪
SELENOP	rs3877899	Variant not found		⚪
SH2B3	rs3184504	CC+	A,C,G	🟢
SLCO1B3	rs11045585	AA+	G	🔵
SLCO1B3	rs4149117	GG+	C,G	🟢
SLCO1B3	rs7311358	AA+	A	🟢
STAT5B	rs6503691	Variant not found	T	⚪
TCF2	rs4430796	AG+	G	🟢
TCF7L2	rs12255372	GG+	T	🟢
TG	rs180223	Variant not found	A,C,G	⚪
TMPRSS2	rs12329760	CT+	T	🟢
TNF	rs361525	GG+	A	🟢
TP53	rs1042522	CG-	C,T	🔵
TP53	rs2287499	Variant not found	G,T	⚪
TPD52	rs1042638	Variant not found	A,T	⚪
VAV3	rs4915077	TT+	C	🟢
VDR	rs2107301	Variant not found	A	⚪

Gene	SNP	Genotype	Rare Allele	Result
VDR	rs2238135	Variant not found	G	⚪
VDR	rs731236	CT-	G	🟢
VTCN1	rs10754339	AA+	A	🟢
WRN	rs1346044	CT+	C	🟢
WRN	rs3087425	CC+	T	🟢
XRCC1	rs25489	GG-	G,T	🟢
XRCC2	rs3218536	GG-	G,T	🟢
ZNF827	rs13149290	TT+	T	🟢

L-alanine

Gene	SNP	Genotype	Rare Allele	Result
AGXT2	rs37369	CC+	T	🟢
CCSER1	rs1544017	Variant not found	G	⚪
DLGAP1	rs588682	AA+	A	🟠
GCKR	rs1260326	CT+	C	🟡
PRODH	rs2238732	CC+	T	🔴

L-arginine

Gene	SNP	Genotype	Rare Allele	Result
ASL	rs28941472	AA+	G	🟢
GATM	rs397514708	Variant not found	A	⚪
GATM	rs397514709	Variant not found	G	⚪
GATM	rs80338737	Variant not found	A,T	⚪
GATM	rs80338738	Variant not found	A	⚪
HBA1	rs33991779	Variant not found	A,C,T	⚪
HBB	rs33935445	Variant not found	C,G	⚪
HBB	rs35849199	Variant not found	C,G	⚪
INTERGENIC	rs2545801	AG-	C	🟢
KLKB1	rs71640036	Variant not found	G	⚪
SLC7A2	rs56335308	GG+	A	🟢

L-asparagine

Gene	SNP	Genotype	Rare Allele	Result
ASPG	rs1744297	Variant not found	A	⚪

L-carnitine Deficiency

Gene	SNP	Genotype	Rare Allele	Result
SLC22A5	rs72552725	AA+	G	🟢

L-cysteine

Gene	SNP	Genotype	Rare Allele	Result
CD2AP	rs9349407	GG+	C	🟢
CTH	rs1021737	GT+	T	🟢
GCLM	rs41303970	Variant not found	A	⚪
PCK1	rs8192708	AG+	G	🟡

L-phenylalanine

Gene	SNP	Genotype	Rare Allele	Result
PAH	rs17450273	CC+	A	🟢
PAH	rs118092776	GG-	T	🟢

L-glycine

Gene	SNP	Genotype	Rare Allele	Result
ACADM	rs12126607	Variant not found	T	⚪
CPS1	rs1047891	CC+	A	🟢
INTERGENIC	rs10206976	Variant not found	T	⚪
PHGDH	rs478093	AG+	G	🟢

L-glutamine

Gene	SNP	Genotype	Rare Allele	Result
COL1A1	rs72645357	GG-	T	🔴
COL3A1	rs1800255	AG+	A	🟢
EPHX1	rs2234922	AG+	G,T	🔴
MCT1	rs1049434	Variant not found	T	⚪
MMP3	rs679620	AG-	C	🟠
OPRM1	rs1799971	GG+	G	🔴
SOD3	rs1799895	CC+	G	🟢
SPRYD4	rs7302925	AG+	A	🟢

L-histidine

Gene	SNP	Genotype	Rare Allele	Result
HAL	rs34457757	GG+	A	
HDC	rs2073440	AA-	G	
HDC	rs854158	Variant not found	G	
HDC	rs16963486	AA+	G	
HDC	rs17740607	Variant not found	A,C	
HNMT	rs11558538	CC+	T	

L-homoarginine

Gene	SNP	Genotype	Rare Allele	Result
AGXT2	rs37369	CC+	T	
AGXT2	rs16899974	Variant not found	A	
MED23	rs17060430	GG+	A	

L-isoleucine

Gene	SNP	Genotype	Rare Allele	Result
GCKR	rs1260326	CT+	C	

L-leucine

Gene	SNP	Genotype	Rare Allele	Result
PPM1K	rs1440581	AG-	A,C	

L-lysine

Gene	SNP	Genotype	Rare Allele	Result
ASS-1	rs4140745	TT+	T	
ASS-1	rs10488107	AA+	G	
ASS-1	rs2215359	CC+	T	
ASS-1	rs11771234	Variant not found	A	
ASS-1	rs1206361	Variant not found	T	
ASS-1	rs1206367	Variant not found	C	
ASS-1	rs12217	Variant not found	T	
ASS-1	rs17144099	Variant not found	G	
ASS-1	rs2268075	Variant not found	C	
ASS-1	rs2268076	Variant not found	A	
ASS-1	rs2270884	Variant not found	C	
ASS-1	rs3213699	Variant not found	G	
ASS-1	rs73224329	Variant not found	G	
INTERGENIC	rs9549153	GG+	A	
PARK2	rs992037	Variant not found	C	
PARK2	rs992037	Variant not found	C	
SCCPDH	rs10924820	AG+	T	
SCCPDH	rs6657743	CC+	T	
SCCPDH	rs7513496	GG+	T	
SCCPDH	rs10127783	Variant not found	T	
SCCPDH	rs1127149	Variant not found	A	
SCCPDH	rs12737081	Variant not found	T	
SCCPDH	rs10754532	Variant not found	G	
SCCPDH	rs147652217	Variant not found	C	
SCCPDH	rs3935011	Variant not found	C	
SCCPDH	rs4130317	Variant not found	T	
SCCPDH	rs4926440	Variant not found	C	
SCCPDH	rs4926448	Variant not found	G	
SCCPDH	rs6697063	Variant not found	C	
SCCPDH	rs7526237	Variant not found	T	
SLC7A9	rs12460876	CC+	C	

L-methionine

Gene	SNP	Genotype	Rare Allele	Result
DCLK1	rs7328278	AA+	C	
GAD1	rs10432420	Variant not found	A	
GAD1	rs12185692	Variant not found	A	
GAD1	rs2058725	Variant not found	C	
GAD1	rs2241165	AA-	T	
GAD1	rs3791850	Variant not found	A,C	
GAD1	rs3791851	Variant not found	C	
GAD1	rs3791878	Variant not found	T	
GAD1	rs3828275	Variant not found	T	

Gene	SNP	Genotype	Rare Allele	Result
GAD1	rs701492	TT+	T	
GAD1	rs769407	Variant not found	C	
GCLC	rs17883901	CC-	A,T	
KLF6	rs3750861	CC+	T	
MAT1A	rs72558181	Variant not found	T	
MAT1A	rs118204003	CC-	A	
MAT1A	rs118204006	GG-	T	
MAT1A	rs116659053	GG+	A	
MTRR	rs1801394	AA+	G	
PNPLA3	rs6006460	GG+	T	
PNPLA3	rs738409	GG-	G	
PPARGC1A	rs2290602	GG+	A,G	
SLC38A8	rs587777254	Variant not found	T	
SLC38A8	rs587777255	Variant not found	C	
SLC38A8	rs587777256	Variant not found	T	

L-ornithine

Gene	SNP	Genotype	Rare Allele	Result
SLC7A2	rs56335308	GG+	A	

L-proline

Gene	SNP	Genotype	Rare Allele	Result
PRODH	rs2238732	CC+	T	

L-serine

Gene	SNP	Genotype	Rare Allele	Result
PHGDH	rs121907987	GG+	A	
PHGDH	rs121907988	GG+	A	
PHGDH	rs267606947	Variant not found	A	
PHGDH	rs267606948	Variant not found	A	
PHGDH	rs267606949	CC+	A,G,T	
PHGDH	rs478093	AG+	G	

L-taurine

Gene	SNP	Genotype	Rare Allele	Result
ADRB2	rs1042713	GG+	A	
APOE4	rs429358	TT+	C	
BCAT1	rs7961152	Variant not found	C	
C5ORF67	rs459193	TT-	G	
CYP1A1	rs2470893	GG-	T	
ENPP1	rs1044498	AC+	C	
GRK4	rs2960306	GG+	T	
IL-6	rs1800795	CG+	G	
IRS1	rs1801278	Variant not found	G,T	
PLIN1	rs894160	GG-	T	

L-theanine

Gene	SNP	Genotype	Rare Allele	Result
ACE	rs1799752	Variant not found		
ACE	rs4343	AG+	A	
ADD1	rs4961	GT+	A,T	
ADRB2	rs1800888	CC+	T	
AOC1	rs10156191	Variant not found	T	
APOE	rs7412	TT+	T	
APOE4	rs429358	TT+	C	
ASIC2	rs9901756	Variant not found	C	
ATP2B1	rs2681472	CT-	G	
AVPR1A	rs10877969	Variant not found	C	
AVPR1A	rs11174811	Variant not found	A	
BAG3	rs2234962	CT+	C	
BDNF	rs6265	GG-	T	
BRAP	rs3782886	AA-	C	
BTD	rs104893686	TT+	G	
BTD	rs104893687	CC+	T	
CACNB2	rs2228645	Variant not found	A,T	
CAV3	rs1008642	Variant not found	A,G,T	
CCL2	rs1024611	CT-	G	
CDH13	rs8055236	GG+	A,C,T	

Gene	SNP	Genotype	Rare Allele	Result
CDKN2B-AS1	rs10116277	TT+	T	🔵
CDKN2B-AS1	rs1011970	GT+	T	🟢
CDKN2B-AS1	rs1063192	TT-	A,T	🔵
CDKN2B-AS1	rs10757272	TT+	T	🟠
CDKN2B-AS1	rs10757274	GG+	G	🟠
CDKN2B-AS1	rs1537375	Variant not found	C,G	⚪
CDKN2B-AS1	rs2383206	Variant not found	G	⚪
CETP	rs2303790	AA+	G	🟢
CHRDL1	rs387906713	Variant not found	A	⚪
CHRDL1	rs387906714	Variant not found	A	⚪
CRP	rs3091244	Variant not found	A,T	⚪
CYP2R1	rs117913124	Variant not found	A	⚪
DCDC2	rs7765678	Variant not found	C	⚪
DCDC2	rs793862	Variant not found	C,G,T	⚪
DCDC2	rs807701	Variant not found	A	⚪
DCLK1	rs7328278	AA+	C	🟢
DMD	rs1800278	AA-	C	🟢
DMD	rs1801187	GG-	T	🟢
DNAJC5B	rs13279522	TT+	C	🟢
DSG2	rs2230234	AA+	G,T	🟢
DTNBP1	rs2619522	GT-	C	🟢
F12	rs1801020	CT-	G	🟡
F7	rs6046	CT-	A	🟢
FGF20	rs1721100	Variant not found	G,T	⚪
FLJ25967	rs2331291	Variant not found	T	⚪
FMN2	rs17672135	TT+	C	🟠
GATA2	rs3803	Variant not found	A	⚪
GATA4	rs104894073	Variant not found	A,G,T	⚪
GATA4	rs104894074	Variant not found	A	⚪
GCLC	rs17883901	CC-	A,T	🟢
GTF2I	rs2527367	Variant not found	C	⚪
HSPD1	rs2340690	Variant not found	G	⚪
HSPD1	rs2565163	Variant not found	A,C	⚪
HSPD1	rs788016	Variant not found	A	⚪
HSPE1	rs2305560	Variant not found	T	⚪
IL-17A	rs2275913	AG+	A	🟠
IL-17A	rs3819025	Variant not found	A	⚪
IL-17F	rs763780	TT+	C	🟢
IL-4	rs2243250	CC+	T	🟢
IL-6	rs1800795	CG+	G	🟢
INTERGENIC	rs10757278	GG+	G	🔴
INTERGENIC	rs1333049	CC+	C	🔴
INTERGENIC	rs2383207	GG+	G	🟠
INTERGENIC	rs383830	Variant not found	T	⚪
INTERGENIC	rs501120	AG-	C	🟡
INTERGENIC	rs7250581	Variant not found	G	⚪
ITGB3	rs5918	TT+	C	🟢
JAG1	rs28939668	Variant not found	T	⚪
KCNE1	rs1805127	AG-	A,C,G	🟡
KCNE2	rs2234916	AA+	G	🟢
KCNE3	rs2270676	CT-	G	🟢
KCNQ1	rs1057128	Variant not found	A	⚪
KIAA0319	rs4504469	CC+	G,T	🟢
KIAA0319	rs761100	TT-	C	🟢
KL	rs9527025	Variant not found	C,T	⚪
KL	rs9536314	TT+	A,G	🟢
KLF6	rs3750861	CC+	T	🟢
LIPA	rs1051338	Variant not found	G	⚪
LIPA	rs1131706	Variant not found	T	⚪
LIPA	rs3802656	Variant not found	A	⚪
LRP8	rs5174	GG-	T	🔵
MAOA	rs1137070	TT+	C	🟢
MAOA	rs3027399	GG+	C	🟢
MAOA	rs909525	GG-	T	🟠
MMP3	rs3025058	DI+	G	🔴
MMP9	rs17576	Variant not found	G	⚪
MMP9	rs3918242	Variant not found	T	⚪
MRAS	rs2306374	TT+	C	🟢

Gene	SNP	Genotype	Rare Allele	Result
MTHFD1	rs1076991	AG-	C,G	
MTHFD1L	rs11754661	GG+	A,T	
MTHFD1L	rs17349743	TT+	C	
MTHFD1L	rs6922269	AG+	A	
MTHFD1L	rs803422	Variant not found	C,G	
MYBPC3	rs11570112	CC-	A,C	
NAF1	rs7675998	GG+	G,T	
NGF	rs6330	CC-	A	
NOS3	rs1800779	AA+	G	
NOS3	rs1800783	Variant not found	C,G,T	
NOS3	rs207044	Variant not found	T	
NOS3	rs3918188	Variant not found	A,T	
NPPA	rs5065	AA+	G	
OLR1	rs11053646	Variant not found	G	
PECAM1	rs281865545	Variant not found	G,T	
PHACTR1	rs9349379	AA+	A	
PLCL2	rs10510468	Variant not found	A,T	
PLPP3	rs17114036	AA+	G	
PNPLA3	rs6006460	GG+	T	
PNPLA3	rs738409	GG-	G	
PPARGC1A	rs2290602	GG+	A,G	
PSMA6	rs1048990	CG+	G,T	
PSRC1	rs599839	AA+	A,C	
RGS2	rs4606	CC+	G	
RYR2	rs34967813	AA+	G	
SCN5A	rs1805124	GG-	T	
SEZ6L	rs688034	Variant not found	T	
SH2B3	rs3184504	CC+	A,C,G	
SLC38A8	rs587777254	Variant not found	T	
SLC38A8	rs587777255	Variant not found	C	
SLC38A8	rs587777256	Variant not found	T	
SLC64A	rs140701	Variant not found	T	
SMAD3	rs17228212	TT+	C	
TDP2	rs2143340	TT-	G,T	
THBS2	rs8089	Variant not found	C	
TLR4	rs4986790	AA+	G,T	
TLR4	rs4986791	CC+	T	
TMPO	rs17028450	CC+	T	
TNF	rs1800629	GG+	A	
TNFSF4	rs1234313	AG+	G	
TNFSF4	rs1234315	Variant not found	T	
TNFSF4	rs3850641	Variant not found	G	
TNFSF4	rs3861950	TT+	C	
TPH2	rs4565946	CT+	A,G,T	
TPH2	rs4570625	GT+	G	
TTN	rs16866412	Variant not found	A	
TTN	rs2244492	GG-	T	
TTR	rs1800458	Variant not found	A	
TTRAP	rs3212236	Variant not found	C	
TXNRD2	rs5748469	AA+	A	

L-tyrosine

Gene	SNP	Genotype	Rare Allele	Result
DRD2	rs6277	CC-	A	

L-threonine

Gene	SNP	Genotype	Rare Allele	Result
PEMT	rs7946	CT+	T	
PNPLA3	rs738409	GG-	G	
PPARGC1A	rs2290602	GG+	A,G	
SH2B1	rs7359397	CT+	T	

L-valine

Gene	SNP	Genotype	Rare Allele	Result
PPM1K	rs1440581	AG-	A,C	

Anterior Cruciate Ligament Injury (ACL)

Gene	SNP	Genotype	Rare Allele	Result

Gene	SNP	Genotype	Rare Allele	Result
COL1A1	rs1800012	GT-	A	🟢

Meniscus Injury

Gene	SNP	Genotype	Rare Allele	Result
GDF5	rs143383	CT-	A	🟡

Hamstring Injuries

Gene	SNP	Genotype	Rare Allele	Result
MMP3	rs679620	AG-	C	🟢
NOS3	rs2070744	TT+	T	🟠
TNC	rs2104772	AT+	A	🟡

Lycopene

Gene	SNP	Genotype	Rare Allele	Result
BCO1	rs6564851	TT+	G	🟢
SCARB1	rs11057841	CC+	T	🟢
SCARB1	rs1672879	Variant not found	G	⚪
SETD7	rs7680948	TT-	T	🟢
SOD2	rs4880	CT-	G	🟠

Lutein

Gene	SNP	Genotype	Rare Allele	Result
ABCA1	rs1883025	AG-	T	🟢
ABCB1	rs1128503	CT-	G	🟢
ABCB1	rs3213619	TT-	G	🟢
ACE	rs1799752	Variant not found		⚪
ACE	rs4343	AG+	A	🟠
ADD1	rs4961	GT+	A,T	🟠
ADRB2	rs1800888	CC+	T	🟢
AOC1	rs10156191	Variant not found	T	⚪
APOE	rs7412	TT+	T	🔴
APOE4	rs429358	TT+	C	🟢
ARMS2	rs10490924	GT+	T	🔴
ARMS2	rs3750847	Variant not found	T	⚪
ASIC2	rs9901756	Variant not found	C	⚪
ATP2B1	rs2681472	CT-	G	🟢
BAG3	rs2234962	CT+	C	🟢
BCO1	rs6564851	TT+	G	🟢
BCO1	rs7501331	CC+	T	🟢
BRAP	rs3782886	AA-	C	🟢
BTD	rs104893686	TT+	G	🟢
BTD	rs104893687	CC+	T	🟢
C2	rs547154	CC-	T	🟢
C2	rs9332739	GG+	A,C	🟢
C3	rs2230199	CG-	C,T	🟠
C3	rs2230201	Variant not found	G,T	⚪
C3	rs2230205	AG-	T	🟢
C3	rs2287845	Variant not found	A	⚪
CACNB2	rs2228645	Variant not found	A,T	⚪
CAV3	rs1008642	Variant not found	A,G,T	⚪
CCL2	rs1024611	CT-	G	🟠
CD36	rs13230419	CC+	T	🟠
CDH13	rs8055236	GG+	A,C,T	🟠
CDKN2B-AS1	rs10116277	TT+	T	🔵
CDKN2B-AS1	rs1011970	GT+	T	🟢
CDKN2B-AS1	rs1063192	TT-	A,T	🔵
CDKN2B-AS1	rs10757272	TT+	T	🟠
CDKN2B-AS1	rs10757274	GG+	G	🟠
CDKN2B-AS1	rs1537375	Variant not found	C,G	⚪
CDKN2B-AS1	rs2383206	Variant not found	G	⚪
CETP	rs1532624	TT-	A	🟢
CETP	rs17231520	Variant not found	A	⚪
CETP	rs1864163	GG+	A	🔵
CETP	rs2303790	AA+	G	🟢
CETP	rs5880	GG+	C	🟢
CETP	rs5882	AG+	A	🔵
CETP	rs708272	CT-	A	🟠
CFB	rs4151667	TT+	A	🟢

Gene	SNP	Genotype	Rare Allele	Result
CFH	rs1061147	CC+	C	
CFH	rs1061170	TT+	T	
CFH	rs1065489	GT+	T	
CFH	rs1329428	AG-	T	
CFH	rs3753394	CT+	T	
CFH	rs800292	CT-	A	
CFI	rs10033900	Variant not found	C	
CHRDL1	rs387906713	Variant not found	A	
CHRDL1	rs387906714	Variant not found	A	
COL8A1	rs13081855	GG+	T	
COL8A1	rs13095226	Variant not found	C	
CRP	rs3091244	Variant not found	A,T	
CRYBB2	rs74315489	Variant not found		
CRYBB3	rs74315490	GG+		
CRYGD	rs28931605	Variant not found		
CX3CR1	rs3732378	AG+	A	
CX3CR1	rs3732379	CT+	T	
CYP2R1	rs117913124	Variant not found	A	
DHFR	rs1643649	Variant not found	C	
DMD	rs1800278	AA-	C	
DMD	rs1801187	GG-	T	
DNAJC5B	rs13279522	TT+	C	
DPYD	rs1801266	CC-	A	
DPYD	rs1801267	GG-	T	
DPYD	rs1801268	GG-	A	
DSG2	rs2230234	AA+	G,T	
EPHA2	rs116506614	CC+		
EPHA2	rs3754334	CC-	A	
F12	rs1801020	CT-	G	
F7	rs6046	CT-	A	
FGD6	rs12310399	Variant not found	C	
FGF20	rs1721100	Variant not found	G,T	
FLJ25967	rs2331291	Variant not found	T	
FMN2	rs17672135	TT+	C	
FOXE1	rs10984009	Variant not found	A	
GATA2	rs3803	Variant not found	A	
GATA4	rs104894073	Variant not found	A,G,T	
GATA4	rs104894074	Variant not found	A	
GJA8	rs2132397	Variant not found		
GJA8	rs6657114	Variant not found		
GJA8	rs6688578	Variant not found		
GJA8	rs7541950	Variant not found		
GJA8	rs864309684	Variant not found		
GSR	rs3594	Variant not found	A	
HLA-DRA	rs3135391	CC-	A	
HLA-DRB1	rs660895	GG+	G	
HSPD1	rs2340690	Variant not found	G	
HSPD1	rs2565163	Variant not found	A,C	
HSPD1	rs788016	Variant not found	A	
HSPE1	rs2305560	Variant not found	T	
HTRA1	rs11200638	AG+	A	
HTRA1	rs932275	Variant not found	A	
IL-4	rs2243250	CC+	T	
IL4R	rs1801275	Variant not found	G	
INTERGENIC	rs10468017	CC+	T	
INTERGENIC	rs10757278	GG+	G	
INTERGENIC	rs12678919	AA+	G	
INTERGENIC	rs1333049	CC+	C	
INTERGENIC	rs2383207	GG+	G	
INTERGENIC	rs383830	Variant not found	T	
INTERGENIC	rs493258	AG-	C	
INTERGENIC	rs501120	AG-	C	
INTERGENIC	rs7250581	Variant not found	G	
ITGB3	rs5918	TT+	C	
JAG1	rs28939668	Variant not found	T	
KCNE1	rs1805127	AG-	A,C,G	
KCNE2	rs2234916	AA+	G	
KCNE3	rs2270676	CT-	G	

Gene	SNP	Genotype	Rare Allele	Result
KCNQ1	rs1057128	Variant not found	A	⚪
KL	rs9527025	Variant not found	C,T	⚪
KL	rs9536314	TT+	A,G	🟢
LIPA	rs1051338	Variant not found	G	⚪
LIPA	rs1131706	Variant not found	T	⚪
LIPA	rs3802656	Variant not found	A	⚪
LRP8	rs5174	GG-	T	🔵
MAF	rs121917735	Variant not found	G,T	⚪
MAF	rs121917736	Variant not found	C	⚪
MAF	rs786205221	Variant not found	T	⚪
MAOA	rs1137070	TT+	C	🟢
MAOA	rs3027399	GG+	C	🟢
MAOA	rs909525	GG-	T	🟠
MC1R	rs1805005	GG+	T	🟢
MC1R	rs1805007	CC+	T	🟢
MC1R	rs1805008	CC+	T	🟢
MC1R	rs1805009	GG+	A,C	🟢
MMP3	rs3025058	DI+	G	🔴
MMP9	rs17576	Variant not found	G	⚪
MMP9	rs3918242	Variant not found	T	⚪
MRAS	rs2306374	TT+	C	🟢
MTHFD1	rs1076991	AG-	C,G	🟢
MTHFD1L	rs11754661	GG+	A,T	🟢
MTHFD1L	rs17349743	TT+	C	🟢
MTHFD1L	rs6922269	AG+	A	🟡
MTHFD1L	rs803422	Variant not found	C,G	⚪
MYBPC3	rs11570112	CC-	A,C	🟢
NAF1	rs7675998	GG+	G,T	🟢
NOS3	rs1800779	AA+	G	🟢
NOS3	rs1800783	Variant not found	C,G,T	⚪
NOS3	rs207044	Variant not found	T	⚪
NOS3	rs3918188	Variant not found	A,T	⚪
NOTCH4	rs422951	AG-	C	🟢
NPPA	rs5065	AA+	G	🟢
OLR1	rs11053646	Variant not found	G	⚪
PECAM1	rs281865545	Variant not found	G,T	⚪
PHACTR1	rs9349379	AA+	A	🟢
PITX2	rs6533526	GG+	A	🟢
PLCL2	rs10510468	Variant not found	A,T	⚪
PLPP3	rs17114036	AA+	G	🟢
PSMA6	rs1048990	CG+	G,T	🟢
PSRC1	rs599839	AA+	A,C	🟡
REST	rs1713985	AC-	T	🟢
REST	rs2227902	GG+	T	🟢
REST	rs3796530	Variant not found	A	⚪
RYR2	rs34967813	AA+	G	🟢
SCN5A	rs1805124	GG-	T	🟢
SERPINF1	rs1136287	CT+	T	🟡
SEZ6L	rs688034	Variant not found	T	⚪
SH2B3	rs3184504	CC+	A,C,G	🟢
SIRT1	rs3758391	Variant not found	C	⚪
SKIV2L	rs2734331	TT-	G	🟢
SKIV2L	rs429608	GG+	A	🟢
SMAD3	rs17228212	TT+	C	🟢
STAT4	rs10181656	CG+	C	🟡
THBS2	rs8089	Variant not found	C	⚪
TLR3	rs3775291	GG-	G,T	🟠
TLR4	rs4986790	AA+	G,T	🟢
TLR4	rs4986791	CC+	T	🟢
TMPO	rs17028450	CC+	T	🟢
TNF	rs1800629	GG+	A	🟢
TNFSF4	rs1234313	AG+	G	🟢
TNFSF4	rs1234315	Variant not found	T	⚪
TNFSF4	rs3850641	Variant not found	G	⚪
TNFSF4	rs3861950	TT+	C	🟢
TTN	rs16866412	Variant not found	A	⚪
TTN	rs2244492	GG-	T	🟢
TTR	rs1800458	Variant not found	A	⚪

Gene	SNP	Genotype	Rare Allele	Result
TXNRD2	rs5748469	AA+	A	
TYR	rs28940879	Variant not found	A,C	
VEGFA	rs3025039	CC+	T	

Hip dislocation

Gene	SNP	Genotype	Rare Allele	Result
GDF5	rs143383	CT-	A	
GDF5	rs143384	CT-	A	
GDF5	rs224334	Variant not found	G	

Magnesium

Gene	SNP	Genotype	Rare Allele	Result
ABCB1	rs10248420	AA+	G,T	
ABCB1	rs1128503	CT-	G	
ABCB1	rs11983225	TT+	C	
ABCB1	rs2032583	TT-	G	
ABCB1	rs2235015	GG-	A,T	
ABCB1	rs2235040	GG-	A,G,T	
ABCB1	rs2235067	GG-	T	
ABCB1	rs3213619	TT-	G	
ABCB1	rs4148739	AA-	C	
ACE	rs1799752	Variant not found		
ACE	rs4343	AG+	A	
ACHE	rs1799805	Variant not found	T	
ACHE	rs2571598	Variant not found	G,T	
ACP7	rs472265	AA+	G	
ADCY5	rs11708067	AA+	G	
ADD1	rs4961	GT+	A,T	
ADD1	rs4963	CG+	G,T	
ADD2	rs3755351	CC-	T	
ADIPOQ	rs17366743	TT+	C	
ADRA2A	rs553668	Variant not found	G,T	
ADRB2	rs1800888	CC+	T	
AGT	rs11568020	Variant not found	A,T	
AGT	rs121912702	Variant not found	A	
AGT	rs699	CT-	G	
AGTR1	rs104893677	Variant not found	T	
AGTR1	rs1492099	Variant not found	A,C	
AGTR1	rs5186	AA+	C	
AOC1	rs10156191	Variant not found	T	
APOE	rs7412	TT+	T	
APOE4	rs429358	TT+	C	
ARHGAP30	rs2774279	Variant not found	T	
ARHGEF3	rs7646054	Variant not found	G	
ARL15	rs1694089	Variant not found	C	
ARL15	rs788517	Variant not found	T	
AS3MT	rs3740393	Variant not found	C,T	
ASIC2	rs9901756	Variant not found	C	
ATP2B1	rs2681472	CT-	G	
ATP6V1B1	rs2266917	Variant not found	T	
AVPR1A	rs10877969	Variant not found	C	
AVPR1A	rs11174811	Variant not found	A	
BAG3	rs2234962	CT+	C	
BAG6	rs3117583	TT-	G	
BCAT1	rs7961152	Variant not found	C	
BCR	rs2156921	Variant not found	A	
BCR	rs2267012	Variant not found	A	
BCR	rs2267013	Variant not found	G	
BCR	rs2267015	Variant not found	G,T	
BCR	rs3313172	Variant not found		
BCR	rs3761418	Variant not found	G	
BDNF	rs13306221	Variant not found	T	
BDNF	rs6265	GG-	T	
BMP2	rs235754	Variant not found	A,G	
BMPR1B	rs11097457	Variant not found	G	
BMPR1B	rs121434417	Variant not found	A	
BMPR1B	rs1434536	Variant not found	T	
BMPR2	rs1006246556	Variant not found	A,T	

Gene	SNP	Genotype	Rare Allele	Result
BRAP	rs3782886	AA-	C	🟢
BTD	rs104893686	TT+	G	🟢
BTD	rs104893687	CC+	T	🟢
CACNB2	rs2228645	Variant not found	A,T	⚪
CALCA	rs3781719	Variant not found	G	⚪
CAPN10	rs3792267	GG+	A	🟢
CASR	rs17251221	AA+	G	🟢
CASZ1	rs880315	AA-	C	🟢
CAV3	rs1008642	Variant not found	A,G,T	⚪
CBLB	rs3772534	Variant not found	T	⚪
CCL2	rs1024611	CT-	G	🟠
CDH13	rs8055236	GG+	A,C,T	🟠
CDKAL1	rs4712523	AG+	G	🟢
CDKAL1	rs7756992	AG+	G,T	🟢
CDKN2A	rs10811661	TT+	T	🟠
CDKN2A/B	rs2383208	AA+	G,T	🟢
CDKN2B-AS1	rs10116277	TT+	T	🔵
CDKN2B-AS1	rs1011970	GT+	T	🟢
CDKN2B-AS1	rs1063192	TT-	A,T	🔵
CDKN2B-AS1	rs10757272	TT+	T	🟠
CDKN2B-AS1	rs10757274	GG+	G	🟠
CDKN2B-AS1	rs1537375	Variant not found	C,G	⚪
CDKN2B-AS1	rs2383206	Variant not found	G	⚪
CELSR2	rs4970834	CC+	T	🟢
CETP	rs2303790	AA+	G	🟢
CHRDL1	rs387906713	Variant not found	A	⚪
CHRDL1	rs387906714	Variant not found	A	⚪
CHRM2	rs1824024	GT-	A	🟢
CHRM2	rs2061174	CT-	A,C	🟢
CHRM2	rs324650	AT+	A	🟢
CLCN6	rs13306560	Variant not found	T	⚪
CLCN6	rs17376328	Variant not found	A	⚪
CLCN6	rs3737964	Variant not found	A,C,G	⚪
CLEC16A	rs725613	Variant not found	G	⚪
CLOCK	rs1801260	AA+	C,G,T	🟢
CNNM1	rs6584273	Variant not found	A	⚪
COMT	rs4680	AG+	A	🟢
CRP	rs3091244	Variant not found	A,T	⚪
CTLA4	rs11571316	CT-	A,C	🟢
CTLA4	rs231775	AG+	G	🟡
CTLA4	rs3087243	AG+	G	🟡
CYP19A1	rs12594287	Variant not found	A	⚪
CYP19A1	rs16964201	Variant not found	T	⚪
CYP19A1	rs17703883	Variant not found	C	⚪
CYP2R1	rs117913124	Variant not found	A	⚪
CYP4A11	rs1126742	Variant not found	G	⚪
DAPK1	rs11141915	AC+	C	🟢
DAT	rs1064795122	Variant not found	T	⚪
DCDC5	rs3925584	AG-	C	🟡
DMD	rs1800278	AA-	C	🟢
DMD	rs1801187	GG-	T	🟢
DNAJC5B	rs13279522	TT+	C	🟢
DNER	rs1861612	AG+	A,C	🟢
DSG2	rs2230234	AA+	G,T	🟢
ENPP1	rs997509	Variant not found	T	⚪
ERBB3	rs2292239	CC-	G	🟢
ESR1	rs11964281	Variant not found	T	⚪
F12	rs118204454	Variant not found	G,T	⚪
F12	rs118204455	Variant not found	C	⚪
F12	rs1801020	CT-	G	🟡
F7	rs6046	CT-	A	🟢
FAM58A	rs1057521251	Variant not found	A	⚪
FDPS	rs2297480	AC-	G	🟢
FGF20	rs1721100	Variant not found	G,T	⚪
FKBP5	rs1360780	CC+	A,C	🟢
FLJ25967	rs2331291	Variant not found	T	⚪
FMN2	rs17672135	TT+	C	🟠
FTCDNL1	rs12615435	Variant not found	G	⚪

Gene	SNP	Genotype	Rare Allele	Result
FTO	rs10163409	Variant not found	T	⚪
FTO	rs1121980	CC-	A	🟢
GAD1	rs10432420	Variant not found	A	⚪
GAD1	rs12185692	Variant not found	A	⚪
GAD1	rs1978340	Variant not found	A	⚪
GAD1	rs2058725	Variant not found	C	⚪
GAD1	rs2241165	AA-	T	🟢
GAD1	rs3762555	Variant not found	A,G	⚪
GAD1	rs3791850	Variant not found	A,C	⚪
GAD1	rs3791851	Variant not found	C	⚪
GAD1	rs3791878	Variant not found	T	⚪
GAD1	rs3828275	Variant not found	T	⚪
GAD1	rs701492	TT+	T	🟡
GAD1	rs769407	Variant not found	C	⚪
GATA2	rs3803	Variant not found	A	⚪
GATA4	rs104894073	Variant not found	A,G,T	⚪
GATA4	rs104894074	Variant not found	A	⚪
GCK	rs4607517	GG+	A,C	🟢
GCKR	rs780094	AG-	C	🟢
GPHN	rs104894470	CC+	T	🟢
GPX1	rs1050450	CC-	A	🟢
GPX4	rs713041	Variant not found	A,C	⚪
GRIA3	rs687577	CC+	C	🔴
GRK5	rs17098707	Variant not found	T	⚪
GUCY1A3	rs587777320	Variant not found	A,T	⚪
GUCY1A3	rs587777321	Variant not found	T	⚪
GUCY1A3	rs587777322	Variant not found		⚪
HCG17	rs3130380	GG+	A	🟢
HHEX	rs1111875	Variant not found	T	⚪
HHEX	rs5015480	TT+	T	🟢
HIVEP2	rs761993070	CC+	A,G,T	🟢
HIVEP2	rs878853251	Variant not found		⚪
HLA-DQA1	rs9272346	AA+	A,C,T	🔴
HLA-DQB1	rs7454108	CC+	C	🟠
HNF1A	rs2464196	Variant not found	A	⚪
HSPD1	rs2340690	Variant not found	G	⚪
HSPD1	rs2565163	Variant not found	A,C	⚪
HSPD1	rs788016	Variant not found	A	⚪
HSPE1	rs2305560	Variant not found	T	⚪
HTR2A	rs1328674	AG-	C,G	🟢
HTR2A	rs6314	CC-	A	🟠
HTR2C	rs3813929	CC+	G,T	🟢
IFIH1	rs1990760	CC+	T	🟢
IGF2	rs3741208	CC-	G,T	🟢
IGF2BP2	rs4402960	GG+	T	🟢
IL-1B	rs16944	AG+	G	🟠
IL-2RA	rs2104286	AG-	C	🟢
IL-4	rs2243250	CC+	T	🟢
IL-6	rs1800795	CG+	G	🟢
IL-7R	rs3194051	AA+	G	🟢
INSIG2	rs7566605	GG+	C	🟢
INTERGENIC	rs1031681	Variant not found	C	⚪
INTERGENIC	rs10757278	GG+	G	🔴
INTERGENIC	rs1333049	CC+	C	🔴
INTERGENIC	rs1545843	AG+	A	🟢
INTERGENIC	rs1937506	Variant not found	A	⚪
INTERGENIC	rs198358	Variant not found	C	⚪
INTERGENIC	rs2383207	GG+	G	🟠
INTERGENIC	rs2544677	Variant not found	A,C,T	⚪
INTERGENIC	rs2592394	CC-	G	🟢
INTERGENIC	rs2820037	AA+	T	🟢
INTERGENIC	rs2943634	AC+	C,G	🟢
INTERGENIC	rs383830	Variant not found	T	⚪
INTERGENIC	rs501120	AG-	C	🟡
INTERGENIC	rs632793	Variant not found	G	⚪
INTERGENIC	rs6746896	AA+	G	🟢
INTERGENIC	rs6997709	Variant not found	A,T	⚪
INTERGENIC	rs7250581	Variant not found	G	⚪

Gene	SNP	Genotype	Rare Allele	Result
INTERGENIC	rs751891	CC-	T	🟢
INTERGENIC	rs791595	AG+	G	🟡
INTERGENIC	rs7923837	AA+	A,T	🟢
IRS1	rs2943641	CT+	C	🟡
ITGA11	rs7174755	TT+	C,G	🟢
ITGB3	rs5918	TT+	C	🟢
JAG1	rs28939668	Variant not found	T	⚪
JAZF1	rs1635852	CT+	C	🟢
KCNE1	rs1805127	AG-	A,C,G	🟡
KCNE2	rs2234916	AA+	G	🟢
KCNE3	rs2270676	CT-	G	🟢
KCNJ11	rs1800467	Variant not found	C,T	⚪
KCNJ11	rs5215	TT+	T	🟢
KCNJ11	rs5219	CC+	T	🟢
KCNQ1	rs104894252	GG+	A,C	🟢
KCNQ1	rs1057128	Variant not found	A	⚪
KCNQ1	rs2283228	AA+	C	🟢
KL	rs9527025	Variant not found	C,T	⚪
KL	rs9536314	TT+	A,G	🟢
LEPR	rs1137101	AA+	G	🟢
LIPA	rs1051338	Variant not found	G	⚪
LIPA	rs1131706	Variant not found	T	⚪
LIPA	rs3802656	Variant not found	A	⚪
LIPC	rs1800588	CC+	T	🟡
LPL	rs326	AG+	G	🟢
LRP4	rs2306033	Variant not found	A	⚪
LRP5	rs3736228	CT+	T	🟠
LRP5	rs4988321	CT-	A,C	🟢
LRP8	rs5174	GG-	T	🔵
LUZP2	rs10500991	Variant not found	T	⚪
LUZP2	rs4561213	Variant not found	G	⚪
M6PR	rs1805762	Variant not found	G,T	⚪
MACROD2	rs398124654	Variant not found	C	⚪
MAGT1	rs137852222	Variant not found	C	⚪
MAGT1	rs200934080	Variant not found	G,T	⚪
MAGT1	rs387906724	Variant not found	A	⚪
MAOA	rs1137070	TT+	C	🟢
MAOA	rs3027399	GG+	C	🟢
MAOA	rs909525	GG-	T	🟠
MC4R	rs2229616	GG-	C	🟢
MDS1	rs6774494	GG+	A	🟢
MMP3	rs3025058	DI+	G	🔴
MMP9	rs17576	Variant not found	G	⚪
MMP9	rs3918242	Variant not found	T	⚪
MOV10	rs2932538	CC-	C,G	🟢
MRAS	rs2306374	TT+	C	🟢
MTHFD1	rs1076991	AG-	C,G	🟢
MTHFD1L	rs11754661	GG+	A,T	🟢
MTHFD1L	rs17349743	TT+	C	🟢
MTHFD1L	rs6922269	AG+	A	🟡
MTHFD1L	rs803422	Variant not found	C,G	⚪
MTHFR	rs1219515	Variant not found	A	⚪
MTHFR	rs1476413	AG-	G,T	🟢
MTHFR	rs17037390	Variant not found	A	⚪
MTHFR	rs1801131	AC-	G	🟠
MTHFR	rs1801133	CC-	A	🟢
MTHFR	rs2066470	Variant not found	A,C	⚪
MTHFR	rs4846049	Variant not found	A,G	⚪
MTNR1B	rs10830963	CC+	G	🟢
MTNR1B	rs10830964	CC+	T	🟢
MTRR	rs1801394	AA+	G	🟢
MTTP	rs3816873	Variant not found	C	⚪
MUC1	rs4072037	AA-	A,T	🟢
MYBPC1	rs11110912	Variant not found	G	⚪
MYBPC3	rs11570112	CC-	A,C	🟢
MYO16	rs17485138	Variant not found	T	⚪
NAA25	rs17696736	AA+	G	🟢
NAF1	rs7675998	GG+	G,T	🟢

Gene	SNP	Genotype	Rare Allele	Result
NEDD4L	rs2288774	CT+	A,C	🟢
NEDD4L	rs3865418	CC+	C	🟢
NEDD4L	rs4149601	AA+	A	🟢
NFE2L2	rs35652124	CT+	C	🟢
NFE2L2	rs6721961	GG+	C,G	🟢
NGF	rs11466112	CC-	A	🟢
NGF	rs6330	CC-	A	🟢
NOS3	rs1799983	GG+	T	🟢
NOS3	rs1800779	AA+	G	🟢
NOS3	rs1800783	Variant not found	C,G,T	⚪
NOS3	rs207044	Variant not found	T	⚪
NOS3	rs3918188	Variant not found	A,T	⚪
NOTCH2	rs10923931	Variant not found	T	⚪
NOTCH2	rs2793831	Variant not found	C	⚪
NOV	rs2071518	CC+	T	🟢
NPAS2	rs11123857	Variant not found	G	⚪
NPPA	rs5065	AA+	G	🟢
NPPA	rs5068	Variant not found	G,T	⚪
NR2F2-AS1	rs2398162	Variant not found	G	⚪
NR3C1	rs2918419	Variant not found	C	⚪
NR3C1	rs6198	Variant not found	C	⚪
OLR1	rs11053646	Variant not found	G	⚪
OPRM1	rs10485057	Variant not found	G	⚪
OPRM1	rs17174794	Variant not found	G,T	⚪
OPRM1	rs1799971	GG+	G	🔴
PAX4	rs2233578	Variant not found	A,T	⚪
PAX4	rs2233580	GG-	T	🟢
PDE11A	rs3770018	Variant not found	C	⚪
PDE9A	rs729861	Variant not found	G	⚪
PECAM1	rs281865545	Variant not found	G,T	⚪
PEX5L	rs7630877	GG+	A,C	🟢
PHACTR1	rs9349379	AA+	A	🟢
PHTF1	rs6679677	CC+	A	🟢
PLCL2	rs10510468	Variant not found	A,T	⚪
PLPP3	rs17114036	AA+	G	🟢
PLTP	rs3843763	Variant not found	T	⚪
PPARG	rs13306747	Variant not found	A,G,T	⚪
PPARG	rs1801282	CG+	C	🔴
PPARG	rs2197423	Variant not found	A	⚪
PPARG	rs4684847	Variant not found	T	⚪
PPARG	rs6802898	Variant not found	T	⚪
PPARGC1A	rs8192678	GG-	T	🟢
PRMT7	rs7197653	Variant not found	A,C	⚪
PSMA6	rs1048990	CG+	G,T	🟢
PSRC1	rs599839	AA+	A,C	🟡
PTPN2	rs1893217	CC-	G	🟠
PTPN2	rs2542151	GG+	T	🟠
PTPN2	rs478582	Variant not found	C	⚪
PTPN22	rs2476601	GG+	G	🟢
PTPRD	rs10116682	Variant not found	A	⚪
PTPRD	rs10481625	Variant not found	A,C,G	⚪
PTPRS	rs1143699	Variant not found	A	⚪
QPCT	rs3770748	Variant not found	G	⚪
RASGRP1	rs7403531	CC+	C,G	🟢
RBMS1	rs6718526	Variant not found	C	⚪
RHOU	rs6426514	GG+	A	🟢
RPSAP52	rs1531343	CC+	C,T	🟢
RYR2	rs34967813	AA+	G	🟢
SCN5A	rs1805124	GG-	T	🟢
SDHAF4	rs1048886	AA+	G	🟢
SEZ6L	rs688034	Variant not found	T	⚪
SH2B3	rs3184504	CC+	A,C,G	🟢
SHROOM3	rs13146355	GG+	A	🟢
SHROOM3	rs17319721	GG+	A	🟢
SLC2A14	rs12815313	Variant not found	G,T	⚪
SLC30A8	rs13266634	CC+	A,T	🔴
SLC64A	rs140701	Variant not found	T	⚪
SMAD3	rs17228212	TT+	C	🟢

Gene	SNP	Genotype	Rare Allele	Result
SOD2	rs2758331	Variant not found	A	⚪
STK39	rs3754777	Variant not found	T	⚪
STK39	rs6749447	GT+	G	🟢
TAP2	rs1800454	GG-	T	🟢
TAP2	rs241428	AA-	A,C,G	🟢
TAP2	rs241448	Variant not found	G	⚪
TAS2R16	rs846664	TT-	C	🟢
TCF7L2	rs12255372	GG+	T	🟢
TCF7L2	rs7901695	TT+	C	🟢
TCF7L2	rs7903146	CC+	G,T	🔵
TGFBR3	rs1805110	CC-	A	🟢
THADA	rs7578597	TT+	C	🟢
THBS2	rs8089	Variant not found	C	⚪
TLR2	rs3804100	Variant not found	C	⚪
TLR4	rs4986790	AA+	G,T	🟢
TLR4	rs4986791	CC+	T	🟢
TMPO	rs17028450	CC+	T	🟢
TNF	rs1800629	GG+	A	🟢
TNFSF4	rs1234313	AG+	G	🟢
TNFSF4	rs1234315	Variant not found	T	⚪
TNFSF4	rs3850641	Variant not found	G	⚪
TNFSF4	rs3861950	TT+	C	🟢
TPH1	rs1799913	AC-	A,T	🟢
TPH1	rs7933505	Variant not found	A	⚪
TPH2	rs4565946	CT+	A,G,T	🟢
TPH2	rs4570625	GT+	G	🟢
TRIB3	rs2295490	AG+	G,T	🟡
TRPM6	rs1060499646	Variant not found	A,C	⚪
TRPM6	rs11144134	CT+	C	🟠
TRPM6	rs121912622	Variant not found	C	⚪
TRPM6	rs121912623	Variant not found	A	⚪
TRPM6	rs121912624	Variant not found	A,C	⚪
TRPM6	rs121912625	CC-	A	🟢
TRPM6	rs2274924	AA-	C	🟢
TRPM6	rs3750425	CC+	A,T	🟢
TRPM6	rs797045204	Variant not found	C	⚪
TRPM6	rs869025214	GG-	T	🟢
TRPM7	rs17520099	Variant not found	A,T	⚪
TRPM7	rs55679040	TT+	C	🟢
TRPM7	rs8042919	Variant not found	A,T	⚪
TTN	rs16866412	Variant not found	A	⚪
TTN	rs2244492	GG-	T	🟢
TTR	rs1800458	Variant not found	A	⚪
TXNRD2	rs5748469	AA+	A	🟢
UBE2E2	rs7612463	AC+	A,G	🟢
UBQLN1P	rs3130352	CC+	T	🟢
VDR	rs1544410	AG-	C,T	🟢
VDR	rs7975232	AC+	A	🟢
VPS26A	rs4812829	AG+	A	🟢
VPS33B	rs121434383	Variant not found	A	⚪
WFS1	rs10010131	Variant not found	G	⚪
WFS1	rs10012946	Variant not found	C	⚪
WNT16	rs2707466	GG-	G,T	🟠
WSCD2	rs3794260	Variant not found	A	⚪
WSCD2	rs9739493	CC+	C,G	🟢

Slimness

Gene	SNP	Genotype	Rare Allele	Result
AHSG	rs2593813	Variant not found	G	⚪
AHSG	rs4917	CC+	C	🟠
AHSG	rs4918	Variant not found	G	⚪

Greater Benefit of Aerobic Exercise for Vascular Function

Gene	SNP	Genotype	Rare Allele	Result
EDN1	rs5370	GT+	T	🟡

Increased Probability of Fatigue

Gene	SNP	Genotype	Rare Allele	Result

Gene	SNP	Genotype	Rare Allele	Result
AMPD1	rs17602729	CC-	A	🟢
AOC1	rs10156191	Variant not found	T	⚪
COL1A1	rs1800012	GT-	A	🟢
GAD1	rs1978340	Variant not found	A	⚪
GAD1	rs3762555	Variant not found	A,G	⚪
GAD1	rs3791878	Variant not found	T	⚪
MAT1A	rs118204001	TT-	C	🟢
MAT1A	rs2993763	Variant not found	A	⚪
MAT1A	rs72558181	Variant not found	T	⚪
MCT1	rs1049434	Variant not found	T	⚪
TNF	rs1800610	CT-	A	🟢

Fat burning through cycling

Gene	SNP	Genotype	Rare Allele	Result
COLEC12	rs644435	AA+	G	🟢
INTERGENIC	rs2727405	CT-	A	🟢
INTERGENIC	rs13004938	Variant not found	G	⚪
RASEF	rs10867921	AG+	A	🔴

Greater Reduction in BMI with Exercise

Gene	SNP	Genotype	Rare Allele	Result
FTO	rs3751812	GG+	T	🟢
FTO	rs8044769	TT+	C	🔴

Higher Temperature During Exercise

Gene	SNP	Genotype	Rare Allele	Result
CREB1	rs2253206	GG+	G	🟢
INTERGENIC	rs2360969	Variant not found	T	⚪

Increased Exercise Recovery Time

Gene	SNP	Genotype	Rare Allele	Result
AMPD1	rs17602729	CC-	A	🟢
SLC17A7	rs74174284	Variant not found	G	⚪
SOD2	rs1141718	Variant not found	G	⚪
SOD2	rs4880	CT-	G	🟡
TNF	rs673	Variant not found	A	⚪

Greater Insulin Sensitivity with Physical Exercise

Gene	SNP	Genotype	Rare Allele	Result
LIPC	rs1800588	CC+	T	🟠

Greater respiratory gains with exercise

Gene	SNP	Genotype	Rare Allele	Result
IL-6	rs1800795	CG+	G	🔴

Manganese

Gene	SNP	Genotype	Rare Allele	Result
ARG1	rs28941474	Variant not found	C	⚪
SLC30A10	rs2275707	Variant not found	A	⚪
SLC39A8	rs13107325	CC+	T	🟢
SOD2	rs2758331	Variant not found	A	⚪
SOD2	rs4880	CT-	G	🟢

Muscle Mass Increase

Gene	SNP	Genotype	Rare Allele	Result
ACVR2B	rs2276541	Variant not found	A	⚪
ACVR2B	rs2284817	Variant not found	A	⚪
ANOS1	rs5978942	Variant not found	C	⚪
BDNF	rs6265	GG-	T	🔵
CAPN3	rs12439003	Variant not found	G	⚪
CAPN3	rs12441700	Variant not found	T	⚪
DLK1	rs2273608	Variant not found	T	⚪
DMD	rs7066036	Variant not found	G	⚪
GEMIN8	rs2158035	Variant not found	C	⚪
IGFBP3	rs3110697	GG+	A	🔴
MTHFR	rs2066470	Variant not found	A,C	⚪
MTRR	rs162031	Variant not found	T	⚪
TRIM63	rs2275950	AA-	C,G	🔴

Waist Measure

Gene	SNP	Genotype	Rare Allele	Result
ADIPOQ	rs266729	CC+	A,G,T	🔴
APOA1	rs670	AG-	T	🟢
APOE	rs7412	TT+	T	🔴
C5ORF67	rs6867983	CC+	T	🟢
CCDC40	rs2361701	Variant not found	A	⚪
CDH12	rs4701252	Variant not found	C	⚪
CLOCK	rs1801260	AA+	C,G,T	🟢
ELP4	rs986527	Variant not found	A,T	⚪
ESR1	rs851982	TT+	C	🟢
FTO	rs1558902	TT+	A	🟢
FTO	rs17817449	TT+	A,G	🟢
FTO	rs9939609	TT+	A	🟢
GCH1	rs7142517	Variant not found	A	⚪
GCKR	rs1260326	CT+	C	🟡
GDAP1	rs44711028	Variant not found		⚪
HMGCR	rs17238484	GT+	T	🟢
IL-15	rs10833	Variant not found	A,C	⚪
IL-1A	rs1800587	CT-	A,C	🟡
IL-1B	rs1143634	CT-	A	🟠
INTERGENIC	rs10487506	Variant not found	A	⚪
INTERGENIC	rs1547251	Variant not found	T	⚪
INTERGENIC	rs1555967	Variant not found	A	⚪
INTERGENIC	rs1875517	Variant not found	A	⚪
INTERGENIC	rs2083637	CT-	G	🟠
INTERGENIC	rs2286983	CC-	A	🟢
INTERGENIC	rs284495	Variant not found	C	⚪
INTERGENIC	rs3922812	Variant not found	A	⚪
INTERGENIC	rs4312989	Variant not found	T	⚪
INTERGENIC	rs489693	AC+	A,T	🟡
INTERGENIC	rs535043	CT-	A	🟢
INTERGENIC	rs539901	TT+	G	🟢
KLF7	rs7568369	Variant not found	T	⚪
MC4R	rs12970134	AG+	A	🟡
MC4R	rs2229616	GG-	C	🟢
MYO1B	rs1823913	Variant not found	C,G	⚪
OVCH2	rs7932813	AA+	G	🟢
PCSK1	rs6232	AG-	C	🟠
PCSK1	rs6234	Variant not found	C	⚪
PCSK1	rs6235	Variant not found	G	⚪
PER2	rs2304672	Variant not found	C	⚪
PER2	rs4663302	Variant not found	T	⚪
PLIN1	rs894160	GG-	T	🟢
PPM1L	rs9290065	CT+	T	🟢
SH2B1	rs7498665	AG+	G,T	🟡
SLC6A2	rs36017	CG-	A,C	🟢
SSTR2	rs1466113	Variant not found	G,T	⚪
TXN	rs2301241	CT-	C	🟢
UCP2	rs659366	CT+	T	🟡
UCP2	rs660339	CT-	T	🟡
UCP3	rs1800849	CT-	A,T	🟡

Improved Insulin Resistance in High-Protein Weight-Loss Diets

Gene	SNP	Genotype	Rare Allele	Result
NADSYN1	rs12785878	GG+	G	🟢

Improving Insulin Sensitivity with Physical Exercise

Gene	SNP	Genotype	Rare Allele	Result
LIPC	rs113298164	Variant not found	T	⚪
LIPC	rs1800588	CC+	T	🟡
LIPC	rs261332	GG+	G	🟢
PPM1K	rs1440581	AG-	A,C	🟠

Visuospatial Working Memory

Gene	SNP	Genotype	Rare Allele	Result
CACNA1C	rs1006737	GG+	A	🟢
CAMTA1	rs1476047	Variant not found	T	⚪

Gene	SNP	Genotype	Rare Allele	Result
NRG1	rs6994992	TT+	A,T	🟠
SLC6A3	rs2617605	AG-	C	🔵
SLC6A3	rs37020	Variant not found	C	⚪

Lower Weight Gain on High Fat Diets

Gene	SNP	Genotype	Rare Allele	Result
APOA5	rs662799	AA+	T	🟢

Lower Use of Glucose after Carbohydrate Ingestion

Gene	SNP	Genotype	Rare Allele	Result
PROX1	rs340874	AG-	C	🟡

Caffeine Metabolization

Gene	SNP	Genotype	Rare Allele	Result
ADORA2A	rs5751876	Variant not found	C	⚪
ADORA2A	rs2298383	CT+	C	🟢
AHR	rs6968865	AT+	T	🟠
CYP1A1	rs2472297	CC+	T	🟢
CYP1A1	rs2470893	GG-	T	🟢
CYP1A2	rs762551	AC+	C	🟠
RYR1	rs186983396	CC+	T	🟢
UBL7	rs2069514	Variant not found	A	⚪

Carbohydrate Metabolism

Gene	SNP	Genotype	Rare Allele	Result
ABCC9	rs7301876	Variant not found	T	⚪
AGER	rs184003	GG-	A	🟢
CEBPA	rs12691	Variant not found	A	⚪
LRP1	rs4759277	Variant not found	A	⚪
PPARGC1B	rs26125	Variant not found	T	⚪
TCF7L2	rs290481	CT+	T	🟠
TCF7L2	rs12255372	GG+	T	🟢

Lipid Metabolism

Gene	SNP	Genotype	Rare Allele	Result
AATK	rs7220048	TT+	C	🟢
ACE	rs4343	AG+	A	🟠
ACMSD	rs387906598	Variant not found	T	⚪
ADCYAP1	rs1893154	CC-	G	🟢
ADIPOQ	rs6444175	Variant not found	A	⚪
ADRA2A	rs553668	Variant not found	G,T	⚪
ADRB3	rs4994	TT-	G	🟢
ADSS	rs3102460	CT+	T	🟢
AK8	rs12552369	Variant not found	A	⚪
ALLC	rs387907075	Variant not found	C	⚪
ANKAR	rs12053254	TT+	C	🟢
ANKK1	rs1800497	CT-	A	🔴
APOA5	rs662799	AA+	T	🟢
APOA5	rs3135506	GG+	C	🟢
APOE	rs121918393	Variant not found	A	⚪
APOE	rs121918394	Variant not found	C,G	⚪
ARHGAP11A	rs555387669	Variant not found		⚪
ARHGAP24	rs11732231	Variant not found	C,T	⚪
ARMC4	rs587777047	AA+	C	🟢
ARMC4	rs587777049	GG+	T	🟢
ASIC2	rs28936	Variant not found	C	⚪
ASTN2	rs111033570	Variant not found	A	⚪
AUTS2	rs1057517708	Variant not found	T	⚪
AUTS2	rs1057518198	Variant not found		⚪
BICC1	rs11006263	AA+	G	🟢
BICD1	rs2630578	Variant not found	C	⚪
C2CD4C	rs12978500	AC+	A	🟢
C8ORF34	rs1517114	CC+	A,G,T	🟢
CA8	rs267606695	Variant not found	C,G	⚪
CADM1	rs6589488	Variant not found	T	⚪
CAMK2A	rs2053053	Variant not found	A,C	⚪
CCDC33	rs2930291	Variant not found	A,C	⚪
CCDC77	rs1048466	AG+	A,C	🟢

Gene	SNP	Genotype	Rare Allele	Result
CD46	rs35366573	CC+	T	
CD46	rs7144	Variant not found	C	
CDCA3	rs5443	CT+	T	
CDHR3	rs6967330	GG+	A	
CELF2	rs3740194	Variant not found	C	
COL4A1	rs113994104	Variant not found	A,T	
COL4A1	rs3742207	AC-	A,G	
COLEC12	rs16944558	Variant not found	T	
CSMD1	rs995322	Variant not found	C,G	
CTNNBL1	rs6013029	Variant not found	T	
CYP2E1	rs2031920	CC+	T	
CYP2E1	rs2070672	AA+	G	
CYP2E1	rs72559710	GG+	A,C,T	
DAPL1	rs16843372	TT+	C	
DDX60L	rs17612333	Variant not found	A,G	
DLC1	rs121908500	Variant not found	C	
DLG2	rs10501570	Variant not found	C	
DMRT1	rs1057519638	Variant not found	T	
DOCK8	rs112321280	Variant not found	G	
DOCK8	rs192864327	GG+	C,T	
ECT2	rs7646507	AG+	A	
EEPD1	rs4302748	AG+	A	
EHF	rs286913	CC-	G,T	
EVA1A	rs17011455	TT+	C	
FAM129A	rs147815528	Variant not found	A,C	
FAM19A2	rs10784285	Variant not found	T	
FAM209B	rs6024938	CT+	T	
FAM71F1	rs6971091	GG+	A	
FARP1	rs688872	TT-	G	
FLJ33534	rs16857178	GG+	A	
FSIP1	rs10152640	AG+	G	
FTO	rs1121980	CC-	A	
FTO	rs121918214	GG+	A	
FTO	rs1421085	TT+	C	
FTO	rs17817449	TT+	A,G	
FTO	rs3751812	GG+	T	
FTO	rs9930506	AA+	G	
FTO	rs9939609	TT+	A	
GCH1	rs10483639	Variant not found	C	
GCH1	rs104894433	Variant not found	A,C,T	
GCH1	rs104894434	Variant not found	G	
GHRL	rs696217	Variant not found	T	
GMDS	rs9378688	Variant not found	A	
GPC5	rs2352028	CT+	G,T	
GSG1L	rs205391	CT+	C,G	
HDAC9	rs11984041	CC+	T	
IFI16	rs6940	Variant not found	T	
IFNGR2	rs74315444	Variant not found	A	
IL-1A	rs1800587	CT-	A,C	
IL-1B	rs1143634	CT-	A	
INSIG2	rs7566605	GG+	C	
INTERGENIC	rs10207060	GT+	A,G	
INTERGENIC	rs11070098	TT+	C	
INTERGENIC	rs11845134	Variant not found	T	
INTERGENIC	rs12986207	Variant not found	A,C	
INTERGENIC	rs17054265	CC+	G,T	
INTERGENIC	rs17468244	AA+	G	
INTERGENIC	rs2153299	AA-	C	
INTERGENIC	rs2575029	CC+	C	
INTERGENIC	rs5767992	CC+	C	
INTERGENIC	rs6486986	GT+	T	
JDP2	rs741846	Variant not found	A,T	
KCNB1	rs1057518621	Variant not found	T	
KCNB1	rs1057521887	Variant not found	C	
KIF6	rs20455	Variant not found	G	
KIF6	rs9380880	GG+	A	
KIRREL	rs6427419	Variant not found	A	
LEPR	rs1137101	AA+	G	

Gene	SNP	Genotype	Rare Allele	Result
LGALS17A	rs8103033	AG+	A	
LHPP	rs12773846	GG+	A,C	
LINC00704	rs1391511	Variant not found	G	
LINC01299	rs6981992	GT+	A,T	
LINC01500	rs405460	AC-	A,T	
LIPC	rs113298164	Variant not found	T	
LIPC	rs1800588	CC+	T	
LIPC	rs261332	GG+	G	
LPP	rs1152846	AG-	C	
LPP	rs4686484	Variant not found	A	
MC4R	rs1057517991	Variant not found	G	
MC4R	rs10871777	AG+	G	
MC4R	rs12970134	AG+	A	
MDFIC	rs7784447	GG+	A	
NAT2	rs1041983	CC+	T	
NAT2	rs1208	GG+	G	
NAT2	rs1799929	CT+	T	
NAT2	rs1801279	GG+	A	
NAT2	rs1801280	CC+	C	
NAT2	rs1805158	CC+	A,T	
NDUFA8	rs3818638	AG-	C	
NIPSNAP3B	rs2472476	AG-	T	
NLRP8	rs306450	Variant not found	G	
NMNAT2	rs4652795	CT+	T	
NPM2	rs11776272	GG+	G	
NXPH1	rs765855	GG+	G	
PCDH9	rs17081231	AA+	G	
PCSK1	rs6232	AG-	C	
PFKP	rs6602024	GG+	A	
PIP4K2A	rs746203	Variant not found	T	
PKNOX2	rs10893366	CT+	T	
PLEKHG1	rs17427389	GG+	A,T	
PLIN1	rs894160	GG-	T	
POC5	rs2112347	GT+	G	
PON1	rs662	AG-	C	
PON1	rs854560	Variant not found	C,G,T	
PPARG	rs13306747	Variant not found	A,G,T	
PPARG	rs1801282	CG+	C	
PPARG	rs3856806	CC+	T	
PPARGC1A	rs8192678	GG-	T	
PPM1H	rs2029721	Variant not found	A	
PTPRD	rs10116682	Variant not found	A	
PTPRD	rs1975197	CC-	A	
PTPRN2	rs10274279	TT+	C	
PVALB	rs2022068	AA+	G	
RAB17	rs2292873	AG-	T	
RASEF	rs10867921	AG+	A	
RBBP6	rs11860248	Variant not found	G	
RBFOX1	rs1057521725	Variant not found	A	
RBFOX1	rs1064794750	Variant not found	G	
RIC3	rs1528133	Variant not found	C,G	
RLN3	rs123277666	Variant not found		
RPTOR	rs2289759	Variant not found	G	
RSU1	rs11254160	AG+	A	
RYR2	rs1057517873	AA+	G	
S100P	rs3822262	AA-	G	
SCG3	rs16964476	Variant not found	G	
SCG3	rs3764220	Variant not found	G,T	
SDC3	rs2282440	Variant not found	A,C	
SERPINA12	rs61757459	Variant not found	A	
SLC22A2	rs316019	GG-	C	
SLC22A2	rs8177504	CC-	A,T	
SLC22A2	rs8177507	GG-	G,T	
SLC22A2	rs8177516	CC-	A,T	
SLC22A2	rs8177517	AA-	C,G	
SLC22A23	rs4959235	Variant not found	C	
SLC29A3	rs1084004	CC+	C,G	
SLC29A3	rs121912583	GG+	A	

Gene	SNP	Genotype	Rare Allele	Result
SLC29A3	rs869025176	Variant not found	C	⚪
SMYD3	rs11800820	CC+	A,T	🟢
SNRPN	rs220030	Variant not found	A,C	⚪
SORBS1	rs11188352	Variant not found	G	⚪
SPAG16	rs16851771	AA+	G	🟢
SPOCK3	rs9312517	AA+	G	🟢
STON2	rs6574644	AA+	A	🟢
SYT1	rs17005598	Variant not found	A	⚪
TBC1D1	rs35859249	CC+	A,T	🟢
TCF4	rs613872	TT+	T	🟢
TCF4	rs9960767	CC+	C,G	🟡
TM9SF2	rs9513627	AA+	A	🟢
TMEM18	rs6548238	CC+	C	🟢
TMEM229B	rs1077989	AC+	C	🟢
TMEM45B	rs10894147	CC+	T	🟢
TMOD1	rs1475545	AG-	T	🟢
TNFRSF1B	rs5746059	Variant not found	G	⚪
TPTE2P1	rs2483374	AC+	C,T	🟢
TRABD2B	rs946836	Variant not found	G,T	⚪
TRAPPC9	rs267607137	CC-	A	🟢
TRIM66	rs4929923	CC+	C	🟢
TUB	rs2272382	Variant not found	C	⚪
UGT2B7	rs12233719	GG+	A,C,T	🟢
UGT2B7	rs7439366	Variant not found	C	⚪
UNC13A	rs12608932	AC+	C	🟡
UNC5C	rs12643654	Variant not found	G	⚪
VSIG10	rs7957470	GG+	G	🟢
WDPCP	rs11683229	Variant not found	G,T	⚪
WDPCP	rs200322968	Variant not found	T	⚪
WDR11-AS1	rs10937273	Variant not found	A	⚪
WDR11-AS1	rs318240760	Variant not found	A,C	⚪
WDR11-AS1	rs4783244	GG+	T	🟢
ZBTB46	rs6062314	TT+	G,T	🟢
ZNF536	rs3786800	AA-	C	🟢

Micronutrient Metabolism

Gene	SNP	Genotype	Rare Allele	Result
DLAT	rs2303436	AG-	T	🟢
DLAT	rs627441	Variant not found	C,G	⚪
ENO3	rs238238	AG+	G	🟢
MTNR1B	rs10830963	CC+	G	🟢
PCK1	rs8192708	AG+	G	🟡
SLC2A9	rs3733591	GG-	T	🟢
SLC5A1	rs17683011	Variant not found	G	⚪
SLC5A1	rs17683430	Variant not found	A	⚪

Xenobiotic Metabolism (Including Caffeine and P-450)

Gene	SNP	Genotype	Rare Allele	Result
CYP1A2	rs56107638	GG+	A,C	🟢
CYP1A2	rs762551	AC+	C	🟠

Folic Acid Metabolism

Gene	SNP	Genotype	Rare Allele	Result
BHMT	rs651852	Variant not found	T	⚪
CBS	rs234706	GG+	A	🟠
CBS	rs5742905	TT-	G	🟢
COMT	rs4680	AG+	A	🟢
FOLH1	rs61886492	Variant not found	T	⚪
MTHFR	rs1801131	AC-	G	🟠
MTHFR	rs1801133	CC-	A	🟢
MTR	rs1805087	GG+	G	🔴
MTRR	rs1801394	AA+	G	🟢
SLC19A1	rs1051266	GG-	C,G	🔵

Resting Metabolism

Gene	SNP	Genotype	Rare Allele	Result
CRY2	rs11605924	AC+	C	🟠
LEPR	rs1805094	CG+	C	🟠

Gene	SNP	Genotype	Rare Allele	Result
LEPR	rs2025804	AA+	A	🔴

Protein Metabolization

Gene	SNP	Genotype	Rare Allele	Result
FTO	rs9939609	TT+	A	🔵

Molybdenum

Gene	SNP	Genotype	Rare Allele	Result
GPHN	rs397518420	Variant not found	C	⚪
MOCS1	rs104893969	GG-	T	🟢
MOCS1	rs104893970	CC-	T	🟢
MOCS1	rs141982812	Variant not found	T	⚪
MOCS1	rs148579886	GG+	A	🟢
MOCS2	rs121908605	Variant not found	A	⚪
MOCS2	rs121908606	Variant not found	T	⚪
MOCS2	rs121908607	Variant not found	A	⚪
MOCS2	rs121908608	Variant not found	A	⚪
MOCS2	rs121908609	Variant not found	G	⚪
MOCS2	rs398122799	Variant not found	G	⚪

Uridine Monophosphate

Gene	SNP	Genotype	Rare Allele	Result
ARRB2	rs7208257	Variant not found	A,G,T	⚪
BDNF	rs6265	GG-	T	🟢
CLOCK	rs1801260	AA+	C,G,T	🟢
CLSTN2	rs17348572	TT+	C	🔴
CLSTN2	rs6439886	AA+	G	🟠
DBH	rs1611115	CT+	A,C,G	🟢
DDC	rs11575454	Variant not found	A,C,T	⚪
DRD4	rs1800955	CT+	C,G	🟠
DTNBP1	rs2619522	GT-	C	🟢
FADS2	rs518511	Variant not found	G	⚪
GRK3	rs3730315	AA+	G	🟢
HES1	rs4686673	CC+	T	🟢
HTR1B	rs6296	CC+	G	🟢
HTR2A	rs6314	CC-	A	🟢
NT5C3A	rs104894025	AA-	A	🟢
NT5C3A	rs104894026	Variant not found	A	⚪
NT5C3A	rs104894027	Variant not found	C	⚪
NT5C3A	rs104894028	Variant not found	C	⚪
NT5C3A	rs397518435	Variant not found	A,G	⚪
NTF3	rs6332	GG+	A,T	🟢
PNMT	rs200173	Variant not found	G,T	⚪
SIRT1	rs3758391	Variant not found	C	⚪
SLC1A3	rs2269272	Variant not found	T	⚪
SLC64A	rs25531	Variant not found	C,G	⚪
SLC6A2	rs3785143	CC+	T	🟢
SLC6A3	rs27072	CT+	A,T	🔵
SLC9A9	rs1242075	Variant not found	A,G,T	⚪
SNAP25	rs363026	Variant not found	A	⚪
SNAP25	rs3746544	AA-	T	🟢
SNAP25	rs3787283	Variant not found	C,G,T	⚪
TPH2	rs1386493	Variant not found	G,T	⚪
TPH2	rs17110747	Variant not found	A	⚪
TPH2	rs1843809	TT+	T	🟢
WWC1	rs10038727	Variant not found	A	⚪
WWC1	rs12514426	Variant not found	A	⚪
WWC1	rs17070145	CT+	T	🟢
WWC1	rs4576167	Variant not found	C	⚪

Sudden Cardiac Death

Gene	SNP	Genotype	Rare Allele	Result
CASQ2	rs6684209	CC+	T	🟢
GJA5	rs35594137	Variant not found	T	⚪
IL-18	rs187238	CG-	G	🟢

Muscular Strength

Gene	SNP	Genotype	Rare Allele	Result

Gene	SNP	Genotype	Rare Allele	Result
ACTN3	rs1815739	CT+	T	🟠

MTHFR 1298 mutation (rs1801131)

Gene	SNP	Genotype	Rare Allele	Result
MTHFR	rs1801131	AC-	G	🟠

MTHFR 677 mutation (rs1801133)

Gene	SNP	Genotype	Rare Allele	Result
MTHFR	rs1801133	CC-	A	🟢

Vastus Lateral Muscle

Gene	SNP	Genotype	Rare Allele	Result
AGT	rs699	CT-	G	🟢
PPARA	rs4253778	GG+	C,T	🟢

High Levels of Fatty Acids after Fat Ingestion

Gene	SNP	Genotype	Rare Allele	Result
PROX1	rs340874	AG-	C	🟡

Cortisol Level

Gene	SNP	Genotype	Rare Allele	Result
CRHR1	rs7209436	Variant not found	T	⚪
DGKH	rs1170109	GT+	T	🟡
FKBP5	rs4713902	Variant not found	C	⚪
FKBP5	rs9394309	Variant not found	A,G	⚪
FKBP5	rs9470080	Variant not found	T	⚪
FKBP5	rs7748266	Variant not found	T	⚪
FKBP5	rs1360780	CC+	A,C	🟢
HSD11B1	rs846910	AG+	A	🟠
HTR2C	rs6318	GG+	G,T	🟢
NR3C1	rs10052957	Variant not found	A	⚪
OXTR	rs53576	AA+	A	🟠

Osteoarthritis

Gene	SNP	Genotype	Rare Allele	Result
ALDH1A2	rs16939660	Variant not found	C	⚪
COG5	rs3815148	AA+	C	🟢
COL6A4P1	rs11718863	Variant not found	G,T	⚪
COL6A4P1	rs7639618	TT+	T	🟠
COL6A4P1	rs9864422	Variant not found	T	⚪
CRTC1	rs10419226	GT+	G	🟢
CSMD1	rs10503253	CC+	A	🟢
DIO2	rs225014	CC+	C	🔴
FRZB	rs7775	Variant not found	A,C,T	⚪
FTO	rs1121980	CC-	A	🟢
FTO	rs121918214	GG+	A	🟢
GDF5	rs143383	CT-	A	🟡
HLA-DQB1	rs7775228	TT+	C	🟡
IL-1B	rs16944	AG+	G	🟡
IL-1RN	rs315952	Variant not found	A,C	⚪
IL-1RN	rs419598	TT+	C	🟢
IL-1RN	rs9005	GG+	A	🟢
IL-6	rs1800796	GG+	C	🟢
IL-6	rs1800797	AG+	G	🟡
INTERGENIC	rs4140564	AA+	A	🟢
LPAR1	rs10980705	Variant not found	T	⚪
MCF2L	rs11842874	AA+	G	🟡
PON1	rs662	AG-	C	🟢

Hip Osteoarthritis

Gene	SNP	Genotype	Rare Allele	Result
FRZB	rs7775	Variant not found	A,C,T	⚪

Oxidized LDL

Gene	SNP	Genotype	Rare Allele	Result
APOB	rs676210	AG+	A,T	🟡

Weight Loss with the Consumption of Complex Carbohydrates

Gene	SNP	Genotype	Rare Allele	Result
IRS1	rs2943641	CT+	C	🟡
PPM1K	rs1440581	AG-	A,C	🟡
QPCTL	rs2287019	CC+	T	🟢

Weight Loss on Fat Reduction Diets

Gene	SNP	Genotype	Rare Allele	Result
ADIPOQ	rs17300539	GG+	A	🟢
CLOCK	rs1801260	AA+	C,G,T	🟢
IRS1	rs2943641	CT+	C	🟡
MTNR1B	rs10830963	CC+	G	🟢
PPM1K	rs1440581	AG-	A,C	🟢

Prolactin Promoter Polymorphism

Gene	SNP	Genotype	Rare Allele	Result
PRL	rs1341239	GT-	A	🟢

Potassium

Gene	SNP	Genotype	Rare Allele	Result
MAT1A	rs118204001	TT-	C	🟢
MAT1A	rs2993763	Variant not found	A	⚪
MAT1A	rs72558181	Variant not found	T	⚪
SCNN1B	rs889299	CC-	A	🟢

Neuromuscular Power

Gene	SNP	Genotype	Rare Allele	Result
ACTN3	rs1815739	CT+	T	🟠
AGT	rs699	CT-	G	🟠
AMPD1	rs17602729	CC-	A	🔴
FAAH	rs324420	AC+	A	🟢
GABPB1	rs12594956	Variant not found	A	⚪
HIF1A	rs11549465	CC+	T	🔴
IL-6	rs1800795	CG+	G	🔴
NOS3	rs1799983	GG+	T	🔵
NOS3	rs2070744	TT+	T	🟠
PPARA	rs4253778	GG+	C,T	🟢
TFAM	rs2306604	Variant not found	C,G,T	⚪

Probability of Muscle Injuries

Gene	SNP	Genotype	Rare Allele	Result
COL1A1	rs1800012	GT-	A	🟢
MMP3	rs650108	Variant not found	A	⚪

Mitochondrial Energy Production

Gene	SNP	Genotype	Rare Allele	Result
ACTN3	rs2228325	Variant not found	T	⚪
ADRB2	rs1042717	AA+	A,C	🟢
ADRB3	rs4994	TT-	G	🟢
AGTR2	rs121917813	Variant not found	T	⚪
AMPD1	rs121912682	GG-	G,T	🟢
AMPD1	rs17602729	CC-	A	🟢
AMPD1	rs35859650	GG+	A	🟢
ARHGEF28	rs16871023	AG+	A,C	🟢
ARHGEF28	rs7714670	TT+	C	🟢
ATP5G3	rs36089250	TT+	C	🟢
CALCR	rs1042138	CC-	A	🟢
CKM	rs8111989	Variant not found	C	⚪
CLOCK	rs1801260	AA+	C,G,T	🟢
CLSTN2	rs6439886	AA+	G	🟢
CREM	rs1531550	Variant not found	A,T	⚪
CRP	rs3093058	Variant not found	A,C,G	⚪
CRP	rs3093059	TT-	G	🟢
DMD	rs104894787	CC-	A	🟢
DMD	rs104894788	GG-	T	🟢
EPAS1	rs137853036	Variant not found	A,T	⚪
FOCAD	rs76495380	Variant not found	T	⚪
GABRR1	rs282129	CC-	A	🟢
GALNT13	rs707040	Variant not found	A,C	⚪
GPC5	rs2352028	CT+	G,T	🟠

Gene	SNP	Genotype	Rare Allele	Result
HIF1A	rs34005929	Variant not found	A	⚪
IGF1	rs121912430	Variant not found	T	⚪
IL-6	rs1524107	CC+	T	🟢
IP6K3	rs28607030	Variant not found	G	⚪
MCT1	rs1049434	Variant not found	T	⚪
MMP3	rs679620	AG-	C	🔵
MPRIP	rs6502557	GG+	A	🟢
MSTN	rs1805086	AA-	C	🟢
MT-ND4	rs869096886	Variant not found	G	⚪
MTHFR	rs1057519359	Variant not found	T	⚪
MTHFR	rs1476413	AG-	G,T	🟢
MTHFR	rs17037390	Variant not found	A	⚪
MTHFR	rs17367504	AA+	G	🟢
MTHFR	rs4846049	Variant not found	A,G	⚪
MTR	rs1050993	Variant not found	G,T	⚪
MTRR	rs10520873	Variant not found	C	⚪
NDUFS3	rs4147730	Variant not found	A	⚪
NDUFS7	rs1142530	Variant not found	T	⚪
NDUFS7	rs2332496	Variant not found	A	⚪
NDUFS7	rs7258846	Variant not found	A,T	⚪
NDUFS8	rs1051806	Variant not found	G,T	⚪
NDUFS8	rs2075626	Variant not found	C	⚪
NDUFS8	rs999571	CC-	A	🟠
NOS3	rs1799983	GG+	T	🟢
NOS3	rs2070744	TT+	T	🔵
NOS3	rs3918188	Variant not found	A,T	⚪
NRG1	rs10503887	GG+	A,T	🟢
NRG1	rs6994992	TT+	A,T	🟢
PPARA	rs135551	Variant not found	A	⚪
PPARD	rs2016520	AA-	T	🟢
PPARG	rs121909244	CC+	A,T	🟢
PPARGC1A	rs8192678	GG-	T	🟢
PPARGC1B	rs7732671	Variant not found	C	⚪
SLC16A1	rs387906403	Variant not found	T	⚪
SUCLA2	rs113994161	Variant not found	T	⚪
SUCLA2	rs121908538	CC-	A	🟢
TPK1	rs371271054	TT+	C	🟢
TRHR	rs121917847	Variant not found	T	⚪
UCP2	rs660339	CT-	T	🟡
UQCRC2	rs11648723	Variant not found	T	⚪
VDR	rs1057521095	Variant not found	A	⚪
VDR	rs1544410	AG-	C,T	🟢
ZNF423	rs200585917	Variant not found	A,T	⚪

Progesterone

Gene	SNP	Genotype	Rare Allele	Result
INTERGENIC	rs17724534	Variant not found	T	⚪
PGR	rs1042838	GG-	A,G	🟢
SLC22A10	rs112295236	CC+	A,G	🟢
ZKSCAN5	rs34670419	GG+	A,T	🟢

Muscle Damage Protection

Gene	SNP	Genotype	Rare Allele	Result
ESR1	rs2234693	CT+	A,T	🟢

Quercetin

Gene	SNP	Genotype	Rare Allele	Result
ABCB1	rs1128503	CT-	G	🟢
ABCB1	rs3213619	TT-	G	🟢
ACE	rs1799752	Variant not found		⚪
ACE	rs4343	AG+	A	🟠
ADD1	rs4961	GT+	A,T	🟠
ADRB2	rs1800888	CC+	T	🟢
AOC1	rs10156191	Variant not found	T	⚪
APOE	rs7412	TT+	T	🔴
APOE4	rs429358	TT+	C	🟢
ASIC2	rs9901756	Variant not found	C	⚪
ATP2B1	rs2681472	CT-	G	🟢

Gene	SNP	Genotype	Rare Allele	Result
BAG3	rs2234962	CT+	C	
BRAP	rs3782886	AA-	C	
BTD	rs104893686	TT+	G	
BTD	rs104893687	CC+	T	
CACNB2	rs2228645	Variant not found	A,T	
CAV3	rs1008642	Variant not found	A,G,T	
CCL2	rs1024611	CT-	G	
CDH13	rs8055236	GG+	A,C,T	
CDKN2B-AS1	rs10116277	TT+	T	
CDKN2B-AS1	rs1011970	GT+	T	
CDKN2B-AS1	rs1063192	TT-	A,T	
CDKN2B-AS1	rs10757272	TT+	T	
CDKN2B-AS1	rs10757274	GG+	G	
CDKN2B-AS1	rs1537375	Variant not found	C,G	
CDKN2B-AS1	rs2383206	Variant not found	G	
CETP	rs2303790	AA+	G	
CHRDL1	rs387906713	Variant not found	A	
CHRDL1	rs387906714	Variant not found	A	
CLEC16A	rs2854275	GG-	A,G,T	
CRP	rs3091244	Variant not found	A,T	
CRTH2	rs533116	Variant not found	T	
CYP2R1	rs117913124	Variant not found	A	
DHFR	rs1643649	Variant not found	C	
DMD	rs1800278	AA-	C	
DMD	rs1801187	GG-	T	
DNAJC5B	rs13279522	TT+	C	
DPYD	rs1801266	CC-	A	
DPYD	rs1801267	GG-	T	
DPYD	rs1801268	GG-	A	
DSG2	rs2230234	AA+	G,T	
F12	rs1801020	CT-	G	
F13A1	rs121913066	Variant not found	A,T	
F13B	rs121913075	Variant not found	A	
F13B	rs6003	AA-	T	
F2	rs1799963	GG+	A	
F5	rs4524	AG-	C	
F5	rs6025	GG-	T	
F7	rs6046	CT-	A	
F9	rs6048	Variant not found	G	
FGF20	rs1721100	Variant not found	G,T	
FLJ25967	rs2331291	Variant not found	T	
FMN2	rs17672135	TT+	C	
FOXE1	rs10984009	Variant not found	A	
GATA2	rs3803	Variant not found	A	
GATA4	rs104894073	Variant not found	A,G,T	
GATA4	rs104894074	Variant not found	A	
HLA-DQB1	rs1049225	Variant not found	G	
HLA-DQB1	rs7775228	TT+	C	
HLA-DRA	rs3135391	CC-	A	
HLA-DRB1	rs660895	GG+	G	
HSPD1	rs2340690	Variant not found	G	
HSPD1	rs2565163	Variant not found	A,C	
HSPD1	rs788016	Variant not found	A	
HSPE1	rs2305560	Variant not found	T	
IL-10	rs1800896	AG-	C	
IL-13	rs20541	CC-	G	
IL-1RL1	rs10197862	AA+	G	
IL-4	rs2243250	CC+	T	
IL-6	rs1800795	CG+	G	
IL4R	rs1801275	Variant not found	G	
INTERGENIC	rs10757278	GG+	G	
INTERGENIC	rs1333049	CC+	C	
INTERGENIC	rs2383207	GG+	G	
INTERGENIC	rs383830	Variant not found	T	
INTERGENIC	rs501120	AG-	C	
INTERGENIC	rs7250581	Variant not found	G	
ITGB3	rs5918	TT+	C	
JAG1	rs28939668	Variant not found	T	

Gene	SNP	Genotype	Rare Allele	Result
KCNE1	rs1805127	AG-	A,C,G	🟡
KCNE2	rs2234916	AA+	G	🟢
KCNE3	rs2270676	CT-	G	🟢
KCNQ1	rs1057128	Variant not found	A	⚪
KL	rs9527025	Variant not found	C,T	⚪
KL	rs9536314	TT+	A,G	🟢
LIPA	rs1051338	Variant not found	G	⚪
LIPA	rs1131706	Variant not found	T	⚪
LIPA	rs3802656	Variant not found	A	⚪
LPL	rs268	AA+	G	🟢
LRP8	rs5174	GG-	T	🔵
MAOA	rs1137070	TT+	C	🟢
MAOA	rs3027399	GG+	C	🟢
MAOA	rs909525	GG-	T	🟠
MMP3	rs3025058	DI+	G	🔴
MMP9	rs17576	Variant not found	G	⚪
MMP9	rs3918242	Variant not found	T	⚪
MRAS	rs2306374	TT+	C	🟢
MTHFD1	rs1076991	AG-	C,G	🟢
MTHFD1L	rs11754661	GG+	A,T	🟢
MTHFD1L	rs17349743	TT+	C	🟢
MTHFD1L	rs6922269	AG+	A	🟡
MTHFD1L	rs803422	Variant not found	C,G	⚪
MYBPC3	rs11570112	CC-	A,C	🟢
NAF1	rs7675998	GG+	G,T	🟢
NOS3	rs1800779	AA+	G	🟢
NOS3	rs1800783	Variant not found	C,G,T	⚪
NOS3	rs207044	Variant not found	T	⚪
NOS3	rs3918188	Variant not found	A,T	⚪
NPPA	rs5065	AA+	G	🟢
OLR1	rs11053646	Variant not found	G	⚪
PECAM1	rs281865545	Variant not found	G,T	⚪
PHACTR1	rs9349379	AA+	A	🟢
PLCL2	rs10510468	Variant not found	A,T	⚪
PLPP3	rs17114036	AA+	G	🟢
PSMA6	rs1048990	CG+	G,T	🟢
PSRC1	rs599839	AA+	A,C	🟡
RYR2	rs34967813	AA+	G	🟢
SCN5A	rs1805124	GG-	T	🟢
SELE	rs5361	AC-	G	🟢
SEZ6L	rs688034	Variant not found	T	⚪
SH2B3	rs3184504	CC+	A,C,G	🟢
SMAD3	rs17228212	TT+	C	🟢
STAT4	rs10181656	CG+	C	🟡
TBX21	rs11650354	Variant not found	A,T	⚪
TBX21	rs16947078	Variant not found	G,T	⚪
TGFB1	rs1800469	CT-	G	🟠
THBS2	rs8089	Variant not found	C	⚪
TLR2	rs3804100	Variant not found	C	⚪
TLR4	rs4986790	AA+	G,T	🟢
TLR4	rs4986791	CC+	T	🟢
TMPO	rs17028450	CC+	T	🟢
TNF	rs1800629	GG+	A	🟢
TNFSF4	rs1234313	AG+	G	🟢
TNFSF4	rs1234315	Variant not found	T	⚪
TNFSF4	rs3850641	Variant not found	G	⚪
TNFSF4	rs3861950	TT+	C	🟢
TSLP	rs1837253	CT+	C	🔵
TTN	rs16866412	Variant not found	A	⚪
TTN	rs2244492	GG-	T	🟢
TTR	rs1800458	Variant not found	A	⚪
TXNRD2	rs5748469	AA+	A	🟢
TYR	rs28940879	Variant not found	A,C	⚪
WDR36	rs11241095	Variant not found	C,G	⚪
ZBTB10	rs1051920	CT+	T	🟢

Respiratory Quotient (RQ)

Gene	SNP	Genotype	Rare Allele	Result

Gene	SNP	Genotype	Rare Allele	Result
CRY2	rs11605924	AC+	C	🔵
MTNR1B	rs10830963	CC+	G	🔵

Melatonin

Gene	SNP	Genotype	Rare Allele	Result
ASMT	rs4446909	Variant not found	G	⚪
ASMT	rs5989681	Variant not found	G	⚪
MTNR1A	rs12506228	GT-	A	🔵
MTNR1B	rs10830963	CC+	G	🔵
TPH2	rs4570625	GT+	G	🟢

Reduction of body fat with intervention of polyphenols

Gene	SNP	Genotype	Rare Allele	Result
IL-6	rs1800795	CG+	G	🟢

Reduction of Thyroid Hormonal Metabolism

Gene	SNP	Genotype	Rare Allele	Result
DIO1	rs11206244	CC+	T	🟢
DIO1	rs12095080	Variant not found	G	⚪
DIO1	rs2235544	AC+	A,T	🟠

Regulation of Oxidative Phosphorylation in Skeletal Muscle

Gene	SNP	Genotype	Rare Allele	Result
NDUFB6	rs629566	Variant not found	C	⚪

Aerobic Resistance

Gene	SNP	Genotype	Rare Allele	Result
ADRB2	rs1042713	GG+	A	🟢
ADRB2	rs1800888	CC+	T	🟢
ADRB3	rs4994	TT-	G	🟢
AMPD1	rs17602729	CC-	A	🔴
AQP1	rs1049305	Variant not found	C	⚪
CDCA3	rs5443	CT+	T	🟡
GABPB1	rs7181866	AA+	G	🟢
GABPB1	rs8031031	Variant not found	T	⚪
GABPB1	rs12594956	Variant not found	A	⚪
HFE	rs1799945	GG+	G	🔴
KCNJ11	rs5219	CC+	T	🔴
NOS3	rs1799983	GG+	T	🟢
PPARA	rs4253778	GG+	C,T	🔴
PPARD	rs2016520	AA-	T	🟢
PPARD	rs1053049	Variant not found	C	⚪
PPARD	rs2267668	AA+	A,C	🔴
PPARGC1A	rs13117172	Variant not found	T	⚪
PPARGC1A	rs8192678	GG-	T	🟢
PPARGC1B	rs7732671	Variant not found	C	⚪
PPARGC1B	rs11959820	Variant not found	A,G,T	⚪
PPP3CA	rs3804358	Variant not found	C	⚪
PPP3CB	rs3763679	Variant not found	T	⚪
VEGFA	rs3024994	CC+	T	🟢
VEGFA	rs3025039	CC+	T	🟢
VEGFA	rs2010963	GG+	G	🟢

Physical resistance

Gene	SNP	Genotype	Rare Allele	Result
ACE	rs121912703	Variant not found	T	⚪
ACE	rs4341	CG+	C	🟠
ACOXL	rs7578982	CT+	C	🟢
ACTN3	rs1815739	CT+	T	🟢
ACTN3	rs2228325	Variant not found	T	⚪
ADRB1	rs1801252	Variant not found	G	⚪
ADRB1	rs1801253	CC+	C	🟢
ADRB2	rs1042713	GG+	A	🟢
ADRB3	rs4994	TT-	G	🟢
AGTR2	rs121917810	GG+	T	🟢
AGTR2	rs35474657	CC-	A	🟢
APOE	rs11083750	CC+	A,G,T	🟢
CAMK1D	rs10906142	Variant not found	A	⚪

Gene	SNP	Genotype	Rare Allele	Result
CDCA3	rs5443	CT+	T	🟡
CLSTN2	rs17411949	CC+	T	🟢
CPQ	rs17737465	AG+	G	🟢
CRP	rs1205	CT+	T	🟢
CRP	rs3093059	TT-	G	🟢
EPAS1	rs10187368	GG+	A	🟢
FMNL2	rs11675841	CC+	T	🟢
GABPB1	rs12594956	Variant not found	A	⚪
GALM	rs6741892	AT+	T	🟢
GNB3	rs140263599	CC+	T	🟢
GRM3	rs2228595	Variant not found	T	⚪
HFE	rs111033557	Variant not found	A	⚪
HFE	rs1799945	GG+	G	🔴
HFE	rs1800562	GG+	A	🟢
HFE	rs1800730	AA+	T	🟢
HIF1A	rs11549465	CC+	T	🟢
HIF1A	rs11549467	GG+	A	🟢
IL-15RA	rs2228059	Variant not found	G	⚪
ITPR1	rs397514535	Variant not found	A	⚪
ITPR1	rs7632000	Variant not found	G,T	⚪
KCNJ11	rs104894236	Variant not found	A,T	⚪
KCNJ11	rs5219	CC+	T	🟢
L3MBTL4	rs1539808	CC+	T	🟢
MCT1	rs1049434	Variant not found	T	⚪
NALCN-AS1	rs9513851	Variant not found	A	⚪
NFATC4	rs10141896	GG+	A,T	🟢
NFIA-AS2	rs1572312	CC-	A	🟢
NRF2	rs1962142	Variant not found	G,T	⚪
PPARA	rs1800206	CC+	G	🟢
PPARA	rs4253778	GG+	C,T	🔴
PPARD	rs2267668	AA+	A,C	🟢
PPARGC1B	rs741581	Variant not found	A	⚪
PPARGC1B	rs7732671	Variant not found	C	⚪
RBFOX1	rs1057521725	Variant not found	A	⚪
RBFOX1	rs1064794750	Variant not found	G	⚪
SGMS1	rs2574975	GG-	C	🟢
SLC2A4	rs121434581	GG+	A,C	🟢
SOD2	rs4516970	GG+	A	🟢
SOD2	rs4880	CT-	G	🟢
SPOCK1	rs17170899	CC+	T	🟢
TPK1	rs371271054	TT+	C	🟢
TPK1	rs387906935	Variant not found	G	⚪
TSHR	rs1085307573	Variant not found		⚪
TSHR	rs12101255	Variant not found	T	⚪
TSHR	rs179247	Variant not found	G	⚪
UCP2	rs660339	CT-	T	🟢
UCP3	rs1800849	CT-	A,T	🟢
VEGFA	rs3024994	CC+	T	🟢
VEGFA	rs3025039	CC+	T	🟢
VEGFR2	rs1870377	TT+	A	🟢

Bone Strength

Gene	SNP	Genotype	Rare Allele	Result
P2RX7	rs3751143	AC+	C	🟡

Resveratrol

Gene	SNP	Genotype	Rare Allele	Result
ABCA1	rs1883025	AG-	T	🟢
ABCG8	rs6544713	CC+	C	🟢
ABI3BP	rs9848726	Variant not found	T	⚪
APOC1	rs4420638	AA+	G	🟢
APOE	rs7412	TT+	T	🔴
AR	rs5031002	GG+	A	🟢
ARVCF	rs5993891	Variant not found	T	⚪
B3GALT1	rs13020412	AA+	G	🟢
BRCA2	rs1801406	Variant not found	C,G	⚪
BRCA2	rs4942486	CT+	C	🟢
CASC17	rs1859962	GG+	T	🟡

Gene	SNP	Genotype	Rare Allele	Result
CASC21	rs16902104	CC+	G,T	
CASC8	rs1447295	CC+	C,T	
CASC8	rs6983267	GG+	T	
CDH1	rs16260	AC+	A	
CDKN1B	rs34330	CT+	C	
CHEK2	rs17879961	TT-	C,G	
CPS1	rs1047891	CC+	A	
CR1L	rs4844614	GT+	T	
CYP17A1	rs2486758	Variant not found	C	
CYP1A1	rs1048943	AA-	A,C,G	
CYP24A1	rs2296241	GG+	A	
CYP24A1	rs480995	Variant not found	G	
CYP3A4	rs2740574	AA-	T	
CYP3A4	rs4646438	---		
CYP3A4	rs55785340	AA+	G	
DAB2IP	rs1571801	AC-	T	
DEF8	rs4268748	CT+	C	
DNAH11	rs12670798	TT+	C	
EHBP1	rs2710646	Variant not found	A	
ELAC2	rs4792311	GG+	A,C	
ERI1	rs96621	CT+	C	
ESR2	rs2987983	Variant not found	G	
FABP2	rs1799883	GG-	A,C,G	
FADS2	rs174570	CC+	T	
FAM124A	rs10492519	Variant not found	C,G	
FCHSD1	rs251177	Variant not found	C	
FGFR4	rs2011077	Variant not found	T	
FGFR4	rs351855	CC-	A	
FYCO1	rs1545985	Variant not found	A	
FYCO1	rs7652331	Variant not found	A,C	
GPX1	rs1050450	CC-	A	
HDAC4	rs3791406	CT+	C	
HNF1A	rs2650000	GT-	A	
HNF1B	rs3760511	Variant not found	A,T	
IL-10	rs1800896	AG-	C	
INTERGENIC	rs10086908	Variant not found	C	
INTERGENIC	rs10445747	Variant not found	G	
INTERGENIC	rs10505483	AG-	T	
INTERGENIC	rs10896449	AA+	G	
INTERGENIC	rs12661968	TT+	C	
INTERGENIC	rs4054823	Variant not found	C	
INTERGENIC	rs428668	Variant not found	C	
INTERGENIC	rs5945572	AG+	G	
INTERGENIC	rs7965399	TT+	A,C	
IRF4	rs12203592	CC+	T	
ITGA2	rs1126643	CC+	T	
ITGA6	rs10207654	Variant not found	G	
JAZF1	rs10486567	AG+	A	
KIAA1211	rs629242	Variant not found	T	
KLF6	rs3750861	CC+	T	
LDLR	rs6511720	GG+	T	
MAGEC3	rs176026	Variant not found	A	
MC1R	rs1805005	GG+	T	
MC1R	rs1805007	CC+	T	
MC1R	rs1805008	CC+	T	
MC1R	rs1805009	GG+	A,C	
MGMT	rs2308327	AA+	G	
MSMB	rs10993994	AA-	G	
MTHFR	rs2066470	Variant not found	A,C	
NAF1	rs7675998	GG+	G,T	
OR4A46P	rs7395662	GG+	A	
PCAT19	rs11672691	AA+	T	
PCIF1	rs7679	TT+	C	
RNASEL	rs486907	Variant not found	T	
SELENON	rs11247735	Variant not found	A,C	
SELENOP	rs3877899	Variant not found		
SIRT1	rs144124002	Variant not found	G	
SIRT1	rs3758391	Variant not found	C	

Gene	SNP	Genotype	Rare Allele	Result
SLC45A2	rs185146	CT+	T	🟠
TCF2	rs4430796	AG+	G	🟢
TCF7L2	rs12255372	GG+	T	🟢
TGFBR1	rs334348	Variant not found	G,T	⚪
TGFBR1	rs334349	Variant not found	A	⚪
TMPRSS2	rs12329760	CT+	T	🟢
VDR	rs2107301	Variant not found	A	⚪
VDR	rs2238135	Variant not found	G	⚪
XRCC1	rs25489	GG-	G,T	🟢
ZNF827	rs13149290	TT+	T	🟢

Muscle stiffness

Gene	SNP	Genotype	Rare Allele	Result
DMD	rs370644567	AA+	G	🟢
ESR1	rs2234693	CT+	A,T	🟢

Achilles Tendinopathy Risk

Gene	SNP	Genotype	Rare Allele	Result
MMP3	rs650108	Variant not found	A	⚪
MMP3	rs679620	AG-	C	🟢

Ligament Rupture

Gene	SNP	Genotype	Rare Allele	Result
COL1A1	rs1800012	GT-	A	🟢

Selenium

Gene	SNP	Genotype	Rare Allele	Result
A2M	rs669	AA-	C	🟢
ABCA1	rs1883025	AG-	T	🟢
ABCA2	rs908832	Variant not found	C,G	⚪
ABCA7	rs113809142	Variant not found	G	⚪
ABCA7	rs115550680	AA+	G	🟢
ABCA7	rs200538373	Variant not found	A,C	⚪
ABCA7	rs3752246	Variant not found	C,T	⚪
ABCA7	rs3764650	TT+	G	🟢
ABCA7	rs78117248	Variant not found	G	⚪
ABCB1	rs1128503	CT-	G	🟢
ABCB1	rs3213619	TT-	G	🟢
ACE	rs1799752	Variant not found		⚪
ACE	rs4343	AG+	A	🟠
ADD1	rs4961	GT+	A,T	🟠
ADH1C	rs283413	Variant not found	A,T	⚪
ADRB2	rs1800888	CC+	T	🟢
AGAP2	rs12368653	GG+	A,T	🟢
AHI1	rs117447608	Variant not found	A	⚪
AHI1	rs121434349	Variant not found	A,T	⚪
AHI1	rs121434350	Variant not found	T	⚪
ALDH2	rs16941667	Variant not found	T	⚪
ALDH2	rs671	GG+	A	🟠
ALK	rs7577363	Variant not found	A	⚪
ANKRD1	rs10975200	Variant not found	C,G	⚪
AOC1	rs10156191	Variant not found	T	⚪
APH1B	rs1047552	Variant not found	A,G	⚪
APOC1	rs4420638	AA+	G	🟢
APOE	rs7412	TT+	T	🔴
APOE4	rs429358	TT+	C	🟢
APP	rs193922916	Variant not found	A,C	⚪
APP	rs281865161	Variant not found	A,G	⚪
APP	rs63749964	Variant not found	C	⚪
APP	rs63750064	Variant not found	G,T	⚪
APP	rs63750151	Variant not found	G,T	⚪
APP	rs63750399	Variant not found	A,C	⚪
APP	rs63750643	Variant not found	C	⚪
APP	rs63750734	Variant not found	T	⚪
APP	rs63750847	Variant not found	T	⚪
APP	rs63750868	Variant not found	C,G	⚪
APP	rs63751039	Variant not found	C	⚪
APP	rs63751122	Variant not found	G	⚪

Gene	SNP	Genotype	Rare Allele	Result
ARHGAP20	rs326946	TT-	C	🟢
ASIC2	rs9901756	Variant not found	C	⚪
ATM	rs664143	CC-	G,T	🟢
ATP2B1	rs2681472	CT-	G	🟢
ATP8B4	rs10519262	Variant not found	A	⚪
AURKA	rs2273535	Variant not found	T	⚪
BACE1	rs638405	Variant not found	G	⚪
BAG3	rs2234962	CT+	C	🟢
BATF	rs2300603	TT+	C	🟢
BCKDK	rs147210405	Variant not found	A	⚪
BCKDK	rs397514573	Variant not found	G,T	⚪
BCO1	rs12934922	AA+	G,T	🟢
BDNF	rs2049045	Variant not found	A,C	⚪
BDNF	rs6265	GG-	T	🟢
BIN1	rs744373	CT-	G	🟠
BRAP	rs3782886	AA-	C	🟢
BRCA2	rs1801406	Variant not found	C,G	⚪
BTD	rs104893686	TT+	G	🟢
BTD	rs104893687	CC+	T	🟢
C1ORF106	rs7522462	AG+	A	🟢
CACNB2	rs2228645	Variant not found	A,T	⚪
CALHM1	rs2986017	Variant not found	G	⚪
CAPZB	rs1472565	Variant not found	A,C	⚪
CAV3	rs1008642	Variant not found	A,G,T	⚪
CBLB	rs12487066	Variant not found	C	⚪
CCDC62	rs12817488	Variant not found	A	⚪
CCHCR1	rs130067	Variant not found	G	⚪
CCL2	rs1024611	CT-	G	🟠
CD2AP	rs10948363	AA+	G	🟢
CD2AP	rs9349407	GG+	C	🟢
CD58	rs12044852	CC+	A	🟡
CD86	rs1129055	GG+	A	🟢
CD86	rs9282641	GG+	A	🟢
CDH13	rs8055236	GG+	A,C,T	🟠
CDKN1A	rs1801270	CC+	A,T	🟢
CDKN2B-AS1	rs10116277	TT+	T	🔵
CDKN2B-AS1	rs1011970	GT+	T	🟢
CDKN2B-AS1	rs1063192	TT-	A,T	🔵
CDKN2B-AS1	rs10757272	TT+	T	🟠
CDKN2B-AS1	rs10757274	GG+	G	🟠
CDKN2B-AS1	rs1537375	Variant not found	C,G	⚪
CDKN2B-AS1	rs2383206	Variant not found	G	⚪
CETP	rs2303790	AA+	G	🟢
CETP	rs5882	AG+	A	🔵
CHAT	rs733722	CC+	A,G,T	🟢
CHRDL1	rs387906713	Variant not found	A	⚪
CHRDL1	rs387906714	Variant not found	A	⚪
CHST12	rs6952809	CC+	C	🟢
CLEC16A	rs6498169	Variant not found	A	⚪
CLEC16A	rs725613	Variant not found	G	⚪
CLPTM1L	rs401681	CT+	T	🟡
CLSTN2	rs17411949	CC+	T	🟢
CLU	rs11136000	CC+	C	🟢
CNKSR3	rs2275336	GG+	A	🟢
CNTNAP2	rs1057520549	Variant not found	T	⚪
CNTNAP2	rs1057520743	Variant not found	G	⚪
CNTNAP2	rs1085307838	Variant not found	C	⚪
CPS1	rs1047891	CC+	A	🟢
CR1	rs3818361	CC-	G	🟢
CR1	rs6656401	GG+	G,T	🟢
CRP	rs3091244	Variant not found	A,T	⚪
CTC1	rs199473673	Variant not found	A	⚪
CTC1	rs3027247	TT-	C	🟢
CTLA4	rs231775	AG+	G	🟡
CTNNA3	rs2306402	Variant not found	T	⚪
CYP1A1	rs1048943	AA-	A,C,G	🟢
CYP1A1	rs1800031	TT-	G	🟢
CYP1A1	rs41279188	CC-	A,T	🟢

Gene	SNP	Genotype	Rare Allele	Result
CYP1A1	rs56313657	GG-	A,T	🟢
CYP1A1	rs72547509	TT-	G,T	🟢
CYP1B1	rs1056836	CC-	C	🟢
CYP24A1	rs2296241	GG+	A	🟢
CYP24A1	rs4809957	AG+	G	🟢
CYP24A1	rs6068816	CT+	T	🟢
CYP2E1	rs2070673	TT+	T	🟢
CYP2R1	rs117913124	Variant not found	A	⚪
CYP3A4	rs2740574	AA-	T	🟢
CYP3A5	rs776746	AG-	C	🟠
DAPK1	rs4877365	Variant not found	A	⚪
DAPK1	rs4878104	Variant not found	T	⚪
DBC1	rs10984447	AA+	G	🟠
DHFR	rs1643649	Variant not found	C	⚪
DIO1	rs11206244	CC+	T	🟢
DIO1	rs2235544	AC+	A,T	🟡
DIRC3	rs966423	CT+	G,T	🟠
DKK1	rs1881747	Variant not found	C	⚪
DKKL1	rs2303759	TT+	G	🟢
DLEU1	rs2762051	CC+	T	🟢
DLG2	rs10501570	Variant not found	C	⚪
DLG2	rs17148090	AA+	C,G	🔵
DLG2	rs3885683	Variant not found	C	⚪
DMD	rs104894788	GG-	T	🟢
DMD	rs1800278	AA-	C	🟢
DMD	rs1801187	GG-	T	🟢
DMGDH	rs921943	AG-	T	🔵
DNAJC5B	rs13279522	TT+	C	🟢
DPYD	rs1801266	CC-	A	🟢
DPYD	rs1801267	GG-	T	🟢
DPYD	rs1801268	GG-	A	🟢
DSG2	rs2230234	AA+	G,T	🟢
E2F3	rs1570155	AG+	A,T	🟢
EIF2AK2	rs2254958	Variant not found	A	⚪
ENTPD7	rs911541	Variant not found	A	⚪
EPHX1	rs1051740	TT+	C	🟢
EPHX1	rs2234922	AG+	G,T	🔵
ERG	rs989554	Variant not found	A	⚪
EVI5	rs10735781	Variant not found	C	⚪
EVI5	rs6680578	Variant not found	A	⚪
F12	rs1801020	CT-	G	🟡
F7	rs6046	CT-	A	🟢
FAM171A2	rs5848	Variant not found	T	⚪
FAM47E	rs6812193	CC+	T	🟢
FAM69A	rs11164838	Variant not found	T	⚪
FAM69A	rs7536563	Variant not found	G	⚪
FASLG	rs763110	TT+	T	🔵
FGF20	rs12720208	Variant not found	A,C,T	⚪
FGF20	rs1721082	Variant not found	T	⚪
FGF20	rs1721100	Variant not found	G,T	⚪
FGF7	rs4338740	CT+	C	🟡
FLJ25967	rs2331291	Variant not found	T	⚪
FMN2	rs17672135	TT+	C	🟠
FOXE1	rs10984009	Variant not found	A	⚪
FOXE1	rs28937575	Variant not found	A	⚪
FRMD4A	rs10906466	AG+	C,G	🟢
G6PD	rs1050828	CC+	T	🟢
GAB2	rs2373115	GG-	A	🟢
GALNT3	rs16851009	Variant not found	T	⚪
GATA2	rs3803	Variant not found	A	⚪
GATA4	rs104894073	Variant not found	A,G,T	⚪
GATA4	rs104894074	Variant not found	A	⚪
GBF1	rs3758549	Variant not found	A	⚪
GCKR	rs1260326	CT+	C	🟡
GLUD2	rs9697983	Variant not found	G	⚪
GNAI3	rs6692804	Variant not found	A	⚪
GOLM1	rs10868366	GT+	T	🟢
GOLM1	rs7019241	CT+	G,T	🟢

Gene	SNP	Genotype	Rare Allele	Result
GPX1	rs1050450	CC-	A	
GPX4	rs713041	Variant not found	A,C	
GSTP1	rs1695	GG+	G	
HLA	rs2517532	CT-	G	
HLA-DRA	rs3135391	CC-	A	
HLA-DRA	rs61731956	GG+	A	
HLA-DRB1	rs3135388	CC-	A	
HLA-DRB1	rs660895	GG+	G	
HNF1A	rs1169300	Variant not found	A	
HNF1A	rs2464196	Variant not found	A	
HSPD1	rs2340690	Variant not found	G	
HSPD1	rs2565163	Variant not found	A,C	
HSPD1	rs788016	Variant not found	A	
HSPE1	rs2305560	Variant not found	T	
IDE	rs4646954	Variant not found	A	
IL-2RA	rs12722489	AG-	T	
IL-2RA	rs12722561	Variant not found	A,T	
IL-2RA	rs2104286	AG-	C	
IL-4	rs2243250	CC+	T	
IL-6	rs1800795	CG+	G	
IL-7R	rs6897932	CC+	T	
IL4R	rs1801275	Variant not found	G	
INTERGENIC	rs10162002	AG+	A	
INTERGENIC	rs10757278	GG+	G	
INTERGENIC	rs13192841	GG+	A	
INTERGENIC	rs1333049	CC+	C	
INTERGENIC	rs2119704	CC+	A	
INTERGENIC	rs2279420	Variant not found	G	
INTERGENIC	rs2313982	Variant not found	C,G,T	
INTERGENIC	rs2383207	GG+	G	
INTERGENIC	rs3129934	Variant not found	C	
INTERGENIC	rs383830	Variant not found	T	
INTERGENIC	rs4728142	AG+	A	
INTERGENIC	rs501120	AG-	C	
INTERGENIC	rs6847679	Variant not found	T	
INTERGENIC	rs7250581	Variant not found	G	
INTERGENIC	rs7850258	Variant not found	G	
INTERGENIC	rs9886784	Variant not found	C,T	
INTERGENIC	rs679582	AG+	G	
IRF5	rs3807306	Variant not found	A,T	
ITGB3	rs5918	TT+	C	
IYD	rs121918139	TT+	C	
IYD	rs121918140	Variant not found	A	
JAG1	rs28939668	Variant not found	T	
KCNE1	rs1805127	AG-	A,C,G	
KCNE2	rs2234916	AA+	G	
KCNE3	rs2270676	CT-	G	
KCNQ1	rs1057128	Variant not found	A	
KL	rs9527025	Variant not found	C,T	
KL	rs9536314	TT+	A,G	
KLC1	rs8702	Variant not found	G	
KLRB1	rs4763655	Variant not found	A	
LAG3	rs870849	CT+	C	
LDLR	rs688	CC+	T	
LIPA	rs1051338	Variant not found	G	
LIPA	rs1131706	Variant not found	T	
LIPA	rs3802656	Variant not found	A	
LRP6	rs2160525	AG+	G	
LRP8	rs5174	GG-	T	
LRRK2	rs11564148	AT+	A	
LRRK2	rs34637584	GG+	A	
LRRK2	rs34778348	GG+	A	
LTA	rs1799724	CT+	T	
MALT1	rs587777337	Variant not found	C	
MAOA	rs1137070	TT+	C	
MAOA	rs3027399	GG+	C	
MAOA	rs909525	GG-	T	
MAOB	rs1799836	AA-	A,C	

Gene	SNP	Genotype	Rare Allele	Result
MAPT	rs393152	AA+	G	
MC1R	rs1805008	CC+	T	
MCCC1	rs10513789	GG+	G	
MDM2	rs2279744	Variant not found	G	
MERTK	rs119489105	Variant not found	T	
MERTK	rs527236083	Variant not found		
MME	rs1836915	Variant not found	C	
MMP3	rs3025058	DI+	G	
MMP9	rs17576	Variant not found	G	
MMP9	rs3918242	Variant not found	T	
MPO	rs12316150	Variant not found	T	
MPO	rs2333227	TT+	T	
MPV17L2	rs874628	TT-	G,T	
MRAS	rs2306374	TT+	C	
MS4A6A	rs610932	CC-	G	
MTF1	rs3748682	TT+	C	
MTHFD1	rs1076991	AG-	C,G	
MTHFD1L	rs11754661	GG+	A,T	
MTHFD1L	rs17349743	TT+	C	
MTHFD1L	rs6922269	AG+	A	
MTHFD1L	rs803422	Variant not found	C,G	
MTHFR	rs1476413	AG-	G,T	
MTHFR	rs17037390	Variant not found	A	
MTHFR	rs1801131	AC-	G	
MTHFR	rs1801133	CC-	A	
MTHFR	rs2066470	Variant not found	A,C	
MTHFR	rs4846049	Variant not found	A,G	
MTRR	rs1801394	AA+	G	
MYBPC3	rs11570112	CC-	A,C	
NAF1	rs7675998	GG+	G,T	
NCKAP5	rs10193871	Variant not found	C	
NFE2L2	rs35652124	CT+	C	
NLRP1	rs115799546	Variant not found	G,T	
NOS3	rs1800779	AA+	G	
NOS3	rs1800783	Variant not found	C,G,T	
NOS3	rs207044	Variant not found	T	
NOS3	rs3918188	Variant not found	A,T	
NPPA	rs5065	AA+	G	
OLR1	rs1050283	Variant not found	A	
OLR1	rs11053646	Variant not found	G	
PCDH11X	rs5984894	AA+	G	
PCK1	rs8192708	AG+	G	
PDE4B	rs1321172	Variant not found	G	
PDE8B	rs4704397	AG+	A	
PECAM1	rs281865545	Variant not found	G,T	
PEX6	rs387906809	Variant not found	G	
PEX6	rs61753224	Variant not found	A	
PHACTR1	rs9349379	AA+	A	
PHTF1	rs6679677	CC+	A	
PICALM	rs10792832	AG+	G	
PICALM	rs3851179	AG-	C	
PIK3CA	rs104886003	GG+	A,C	
PIK3CA	rs1057518041	Variant not found		
PIK3CA	rs1057519699	Variant not found	A	
PIK3CA	rs1057519925	Variant not found	A,C	
PIK3CA	rs1057519926	Variant not found	T	
PIK3CA	rs1057519927	Variant not found	C,G,T	
PIK3CA	rs1057519928	Variant not found	C	
PIK3CA	rs1057519929	Variant not found	A	
PIK3CA	rs1057519930	Variant not found	T	
PIK3CA	rs1057519931	Variant not found	C	
PIK3CA	rs1057519932	Variant not found	G	
PIK3CA	rs1057519933	Variant not found	G	
PIK3CA	rs1057519934	Variant not found	C	
PIK3CA	rs1057519935	Variant not found	G	
PIK3CA	rs1057519936	Variant not found	G,T	
PIK3CA	rs1057519937	Variant not found	C	
PIK3CA	rs1057519938	Variant not found	C,T	

Gene	SNP	Genotype	Rare Allele	Result
PIK3CA	rs1057519939	Variant not found	C	
PIK3CA	rs1057519940	Variant not found	T	
PIK3CA	rs1057519941	Variant not found	C,G	
PIK3CA	rs1057519942	GG+	A	
PIK3CA	rs1064793349	Variant not found	A	
PIK3CA	rs1064793663	Variant not found	A	
PIK3CA	rs1064793732	Variant not found	A	
PIK3CA	rs1064793838	Variant not found	G	
PIK3CA	rs1064795304	Variant not found	G	
PIK3CA	rs121913272	Variant not found	C,G	
PIK3CA	rs121913273	Variant not found	A,C	
PIK3CA	rs121913274	Variant not found	C,G,T	
PIK3CA	rs121913275	Variant not found	A,C,T	
PIK3CA	rs121913277	Variant not found	A,C	
PIK3CA	rs121913279	Variant not found	G,T	
PIK3CA	rs121913281	Variant not found	T	
PIK3CA	rs121913282	Variant not found	C	
PIK3CA	rs121913283	Variant not found	A,T	
PIK3CA	rs121913284	Variant not found	A,G	
PIK3CA	rs121913285	Variant not found	G	
PIK3CA	rs121913286	Variant not found	A,G	
PIK3CA	rs121913287	Variant not found	A	
PIK3CA	rs121913288	Variant not found	G	
PIK3CA	rs12494623	Variant not found	G,T	
PIK3CA	rs141178472	Variant not found	C	
PIK3CA	rs17849071	Variant not found	G	
PIK3CA	rs17849079	Variant not found	T	
PIK3CA	rs2699887	CT+	T	
PIK3CA	rs3729679	Variant not found	G	
PIK3CA	rs3729687	Variant not found	A	
PIK3CA	rs397514565	Variant not found	A	
PIK3CA	rs397517200	Variant not found		
PIK3CA	rs397517201	Variant not found	C,G,T	
PLAU	rs2227562	GG+	A	
PLAU	rs2227564	TT+	C	
PLCL2	rs10510468	Variant not found	A,T	
PLD3	rs145999145	GG+	A	
PLPP3	rs17114036	AA+	G	
POLN	rs1923775	TT+	T	
PPP1R3B	rs3748140	GG-	T	
PPP1R3B	rs9987289	GG+	G	
PRDM2	rs2697962	Variant not found	A,C	
PRRC2C	rs2421847	AA+	G	
PSEN1	rs121917807	Variant not found	A	
PSEN1	rs63749805	Variant not found	G,T	
PSEN1	rs63749824	CC+	G,T	
PSEN1	rs63749911	Variant not found	C	
PSEN1	rs63749962	Variant not found	G	
PSEN1	rs63749967	Variant not found	C	
PSEN1	rs63750004	Variant not found	A,C	
PSEN1	rs63750218	Variant not found	C,G	
PSEN1	rs63750299	Variant not found	G	
PSEN1	rs63750306	Variant not found	C,G,T	
PSEN1	rs63750325	Variant not found	A	
PSEN1	rs63750391	Variant not found	A,C,T	
PSEN1	rs63750450	Variant not found	G	
PSEN1	rs63750526	Variant not found	A	
PSEN1	rs63750550	Variant not found	G,T	
PSEN1	rs63750730	Variant not found	T	
PSEN1	rs63750907	Variant not found	T	
PSEN1	rs63751106	Variant not found	A,C	
PSEN1	rs63751272	Variant not found	C,T	
PSEN1	rs63751441	Variant not found	G,T	
PSEN1	rs63751484	Variant not found	C	
PSEN2	rs150400387	Variant not found	G,T	
PSEN2	rs574125890	Variant not found	A,T	
PSEN2	rs61757781	Variant not found	G	
PSEN2	rs63750197	CC+	T	

Gene	SNP	Genotype	Rare Allele	Result
PSEN2	rs63750812	Variant not found	A	
PSEN2	rs775145486	Variant not found	G	
PSMA6	rs1048990	CG+	G,T	
PSRC1	rs599839	AA+	A,C	
PTCSC2	rs925489	CT+	C,T	
PTEN	rs121909229	GG+	A,C,T	
PTEN	rs121909232	CC+	G	
PTEN	rs371387815	Variant not found	G,T	
RAB25	rs34372695	CC+	G,T	
RNASEL	rs3738579	CT-	G	
RNASEL	rs486907	Variant not found	T	
RPL5	rs6604026	Variant not found	C,G	
RPS6KB1	rs630923	CC+	A	
RYR2	rs34967813	AA+	G	
SAMD12	rs17749211	Variant not found	T	
SCN5A	rs1805124	GG-	T	
SELENOF	rs5845	Variant not found	A	
SELENOP	rs3877899	Variant not found		
SEMA5A	rs6896702	Variant not found	C	
SEZ6L	rs688034	Variant not found	T	
SH2B3	rs3184504	CC+	A,C,G	
SH3GL2	rs1536076	Variant not found	G	
SLC30A7	rs11581062	AA+	G	
SLC39A11	rs891684	Variant not found	A	
SLC39A6	rs1050631	CT-	A	
SMAD3	rs17228212	TT+	C	
SNCA	rs104893875	Variant not found	A	
SNCA	rs356168	Variant not found	A	
SNCA	rs356219	AA+	G	
SOD2	rs1799725	Variant not found		
SOD2	rs2758331	Variant not found	A	
SORL1	rs12285364	Variant not found	T	
SORL1	rs2070045	Variant not found	G	
SORL1	rs641120	Variant not found	A	
SORL1	rs661057	Variant not found	C	
SORL1	rs668387	Variant not found	A,T	
SORL1	rs689021	Variant not found	A	
STAT4	rs10181656	CG+	C	
SYK	rs10993738	Variant not found	C	
TAP2	rs241448	Variant not found	G	
TERT	rs2736098	AG-	T	
TET1	rs5030882	Variant not found	T	
TG	rs11535853	Variant not found		
TG	rs180223	Variant not found	A,C,G	
TG	rs2069561	Variant not found	A	
TG	rs35301433	AA+	G	
TG	rs853326	Variant not found	G	
THBS2	rs8089	Variant not found	C	
TLR4	rs4986790	AA+	G,T	
TLR4	rs4986791	CC+	T	
TM2D3	rs139709573	Variant not found	A	
TMPO	rs17028450	CC+	T	
TNF	rs1800629	GG+	A	
TNFSF14	rs2291667	CC-	A	
TNFSF14	rs344560	GG-	C	
TNFSF4	rs1234313	AG+	G	
TNFSF4	rs1234315	Variant not found	T	
TNFSF4	rs3850641	Variant not found	G	
TNFSF4	rs3861950	TT+	C	
TPO	rs104893669	Variant not found	G,T	
TPO	rs1057518950	Variant not found	T	
TREM2	rs28937876	Variant not found	A	
TREM2	rs5143332484	Variant not found		
TREM2	rs75932628	CC+	A,T	
TSHR	rs2288493	Variant not found	T	
TTN	rs16866412	Variant not found	A	
TTN	rs2244492	GG-	T	
TTR	rs1800458	Variant not found	A	

Gene	SNP	Genotype	Rare Allele	Result
TXNRD2	rs5748469	AA+	A	🟢
TYR	rs28940879	Variant not found	A,C	⚪
USP24	rs287235	Variant not found	A,C	⚪
USP40	rs838552	Variant not found	G	⚪
VAV3	rs4915077	TT+	C	🟢
XPC	rs2228000	CC-	A	🟢
XPC	rs2228001	AA-	T	🟢
XRCC1	rs1799782	CT-	A	🟡
ZNF767P	rs354033	CC-	A	🟢

Pain Sensitivity

Gene	SNP	Genotype	Rare Allele	Result
COMT	rs6269	AG+	G	🟢
COMT	rs4680	AG+	A	🟡
COMT	rs4818	CC+	G,T	🔴
OPRM1	rs1799971	GG+	G	🔴

Vegetarian Protein Shake

Gene	SNP	Genotype	Rare Allele	Result
ACVR2B	rs2276541	Variant not found	A	⚪
CAPN3	rs12441700	Variant not found	T	⚪
DLK1	rs2273608	Variant not found	T	⚪
FTO	rs9939609	TT+	A	🟢
GCH1	rs104894433	Variant not found	A,C,T	⚪
GCH1	rs104894434	Variant not found	G	⚪
MCM6	rs4988235	AG+	A	🟢
MCM6	rs182549	TT+	T	🟢
PPARG	rs1801282	CG+	C	🔴
TRIM63	rs2275950	AA-	C,G	🟢

Brugada Syndrome

Gene	SNP	Genotype	Rare Allele	Result
CACNB2	rs2228645	Variant not found	A,T	⚪
GPD1L	rs72552293	Variant not found	G	⚪
KCNE3	rs2270676	CT-	G	🟠
SCN5A	rs1805124	GG-	T	🔴
SCN5A	rs28937318	GG-	A,T	🟢
SCN5A	rs7626962	GG+	A,T	🟢
TRPM4	rs172149856	GG+	A	🟢

Jervell and Lange-Nielsen Syndrome

Gene	SNP	Genotype	Rare Allele	Result
KCNE1	rs1805127	AG-	A,C,G	🟡
KCNQ1	rs1057128	Variant not found	A	⚪

Romano-Ward Syndrome

Gene	SNP	Genotype	Rare Allele	Result
CAV3	rs1008642	Variant not found	A,G,T	⚪
KCNE1	rs1805127	AG-	A,C,G	🟡
KCNE1	rs1805128	Variant not found	T	⚪
KCNH2	rs189014161	Variant not found	A,C	⚪
KCNH2	rs28928904	TT-	A,C,G	🟢
KCNH2	rs9333649	GG-	A,C,T	🟢
KCNQ1	rs1057128	Variant not found	A	⚪
SCN5A	rs1805124	GG-	T	🟢
SCN5A	rs7626962	GG+	A,T	🟢

Wolff-Parkinson-White Syndrome

Gene	SNP	Genotype	Rare Allele	Result
NODAL	rs121909283	GG-	T	🟢
PRKAG2	rs121908987	GG-	T	🟢
PRKAG2	rs121908990	CC-	G	🟢

Dopamine Synthesis

Gene	SNP	Genotype	Rare Allele	Result
DDC	rs11575461	Variant not found	A	⚪
DDC	rs11761683	Variant not found	G,T	⚪
DDC	rs11974297	Variant not found	A	⚪

Gene	SNP	Genotype	Rare Allele	Result
DDC	rs12540874	AG+	C,G	●
DDC	rs12718541	AG+	G	●
DDC	rs137853207	Variant not found	T	○
DDC	rs137853208	Variant not found	A	○
DDC	rs137853209	Variant not found	G	○
DDC	rs137853210	Variant not found	G	○
DDC	rs137853211	Variant not found	A,T	○
DDC	rs137853212	Variant not found	G,T	○
DDC	rs1451371	Variant not found	C	○
DDC	rs1451375	Variant not found	A	○
DDC	rs1470750	Variant not found	G	○
DDC	rs201951824	Variant not found	T	○
DDC	rs2044859	Variant not found	A	○
DDC	rs2060762	Variant not found	G	○
DDC	rs2242041	Variant not found	G	○
DDC	rs2329340	Variant not found	T	○
DDC	rs3735273	AG-	T	●
DDC	rs3757472	GT-	C	●
DDC	rs3779084	Variant not found	G	○
DDC	rs3837091	Variant not found		○
DDC	rs6592961	GG+	A	●
DDC	rs771317809	Variant not found	T	○
DDC	rs7809234	AA+	T	●
DDC	rs7809758	Variant not found	G	○
DDC	rs880028	Variant not found	G	○
DDC	rs921451	CT+	C	●
DDC	rs998850	Variant not found	C	○
IGF2	rs1003483	Variant not found	G	○
IGF2	rs1003484	Variant not found	G,T	○
IGF2	rs1004446	TT-	A	●
IGF2	rs10770125	AG+	G	●
IGF2	rs3741204	Variant not found	C	○
IGF2	rs3741205	Variant not found	A,T	○
IGF2	rs3741206	AA-	A,C,G	●
IGF2	rs3741208	CC-	G,T	●
IGF2	rs3741211	Variant not found	G	○
IGF2	rs4320932	AA-	C	●
IGF2	rs4366464	Variant not found	A,C	○
IGF2	rs7924316	Variant not found	G	○
TH	rs1057516491	Variant not found		○
TH	rs1057516736	Variant not found	T	○
TH	rs1057516819	Variant not found	T	○
TH	rs1057517162	Variant not found		○
TH	rs1057520384	Variant not found	A,T	○
TH	rs11564717	Variant not found	A,C	○
TH	rs121917762	CC-	A,T	●
TH	rs121917764	Variant not found	A,C	○
TH	rs121917765	Variant not found	A	○
TH	rs2070762	CT-	G	●
TH	rs28934580	Variant not found	T	○
TH	rs28934581	Variant not found	G	○
TH	rs3842727	Variant not found	T	○
TH	rs45471299	CC-	A	●
TH	rs587776767	Variant not found	T	○
TH	rs771351747	Variant not found	C	○
TH	rs786204540	Variant not found	A	○

Serotonin Synthesis

Gene	SNP	Genotype	Rare Allele	Result
DDC	rs1085307991	Variant not found	G	○
DDC	rs11761683	Variant not found	G,T	○
DDC	rs11974297	Variant not found	A	○
DDC	rs12540874	AG+	C,G	●
DDC	rs12718541	AG+	G	●
DDC	rs137853207	Variant not found	T	○
DDC	rs137853208	Variant not found	A	○
DDC	rs137853209	Variant not found	G	○
DDC	rs137853210	Variant not found	G	○

Gene	SNP	Genotype	Rare Allele	Result
DDC	rs137853211	Variant not found	A,T	○
DDC	rs137853212	Variant not found	G,T	○
DDC	rs1451371	Variant not found	C	○
DDC	rs1451375	Variant not found	A	○
DDC	rs1470750	Variant not found	G	○
DDC	rs201951824	Variant not found	T	○
DDC	rs2044859	Variant not found	A	○
DDC	rs2060762	Variant not found	G	○
DDC	rs2242041	Variant not found	G	○
DDC	rs2329340	Variant not found	T	○
DDC	rs3735273	AG-	T	●
DDC	rs3757472	GT-	C	●
DDC	rs3779084	Variant not found	G	○
DDC	rs3837091	Variant not found		○
DDC	rs6264	Variant not found	C	○
DDC	rs6592961	GG+	A	●
DDC	rs771317809	Variant not found	T	○
DDC	rs7809234	AA+	T	●
DDC	rs7809758	Variant not found	G	○
DDC	rs880028	Variant not found	G	○
DDC	rs921451	CT+	C	●
DDC	rs998850	Variant not found	C	○
PLEKHA7	rs366590	Variant not found	A	○
PTPRR	rs11178998	AG+	G	●
PTPRR	rs2175711	Variant not found	T	○
PTPRR	rs2203231	Variant not found	C	○
PTPRR	rs4341581	Variant not found	T	○
PTPRR	rs4489789	Variant not found	C	○
PTPRR	rs78162420	Variant not found	A	○
TPH1	rs1799913	AC-	A,T	●
TPH1	rs1800532	AC-	T	●
TPH1	rs2108977	Variant not found	C	○
TPH1	rs211105	Variant not found	G	○
TPH1	rs623580	Variant not found	T	○
TPH1	rs684302	Variant not found	T	○
TPH1	rs7933505	Variant not found	A	○
TPH2	rs1007023	Variant not found	T	○
TPH2	rs10506645	Variant not found	T	○
TPH2	rs10748185	Variant not found	A	○
TPH2	rs10879357	Variant not found	G	○
TPH2	rs11178997	AT+	A	●
TPH2	rs11179000	Variant not found	T	○
TPH2	rs11179002	Variant not found	T	○
TPH2	rs11179027	Variant not found	C	○
TPH2	rs11615016	Variant not found	G	○
TPH2	rs120074175	GG+	A	●
TPH2	rs120074176	CC+	T	●
TPH2	rs1386482	Variant not found	G	○
TPH2	rs1386483	Variant not found	C	○
TPH2	rs1386486	Variant not found	G	○
TPH2	rs1386493	Variant not found	G,T	○
TPH2	rs1386494	GG-	C,G	●
TPH2	rs1386496	Variant not found	A	○
TPH2	rs1386497	Variant not found	A	○
TPH2	rs1386498	Variant not found	G,T	○
TPH2	rs1473473	Variant not found	A,T	○
TPH2	rs1487275	Variant not found	A	○
TPH2	rs1487276	Variant not found	C	○
TPH2	rs1487278	TT+	C	●
TPH2	rs17110563	CC+	T	●
TPH2	rs17110690	Variant not found	A	○
TPH2	rs17110747	Variant not found	A	○
TPH2	rs1843809	TT+	T	●
TPH2	rs2171363	Variant not found	C,G	○
TPH2	rs4290270	AT+	T	●
TPH2	rs4469933	Variant not found	T	○
TPH2	rs4565946	CT+	A,G,T	●
TPH2	rs4570625	GT+	G	●

Gene	SNP	Genotype	Rare Allele	Result
TPH2	rs4760816	Variant not found	T	⚪
TPH2	rs4760820	Variant not found	G	⚪
TPH2	rs7305115	AG+	C,G,T	🟢
TPH2	rs7954758	Variant not found	G	⚪
TPH2	rs7955501	Variant not found	A	⚪
TPH2	rs7963720	Variant not found	G,T	⚪

Ventricular Tachycardia

Gene	SNP	Genotype	Rare Allele	Result
CASQ2	rs146664754	GG+	C	🟢
INTERGENIC	rs11970286	CT+	T	🟡
RYR2	rs16835237	Variant not found	C	⚪
RYR2	rs34967813	AA+	G	🟢
RYR2	rs186906598	GG+	A	🟢
RYR2	rs121918597	CC+	T	🟢
RYR2	rs200236750	CC+	T	🟢
RYR2	rs397516510	GG+	A	🟢
RYR2	rs3765097	Variant not found	T	⚪

Resting Metabolic Rate

Gene	SNP	Genotype	Rare Allele	Result
CRY2	rs11605924	AC+	C	🟠
LEPR	rs1805094	CG+	C	🟢

Trend towards Higher Carbohydrate Consumption

Gene	SNP	Genotype	Rare Allele	Result
FGF21	rs838133	CT-	A	🟢
FTO	rs9939609	TT+	A	🟢
FTO	rs8050136	CC+	A	🟢
GCK	rs4607517	GG+	A,C	🟢
RARB	rs7619139	AA+	A,T	🟡
SLC2A2	rs5400	TT-	A	🔴

Tendency to Higher Fat Intake

Gene	SNP	Genotype	Rare Allele	Result
FTO	rs8050136	CC+	A	🟢

Addiction tendency (eating, gambling, alcohol, smoking)

Gene	SNP	Genotype	Rare Allele	Result
ANKK1	rs1800497	CT-	A	🔴
DRD2	rs1076560	AC+	A	🟢
DRD2	rs12364283	AA+	G	🟢
DRD2	rs1799978	AA-	C	🟢
DRD2	rs4648317	CC-	A	🟢
OPRM1	rs1799971	GG+	G	🔵

Trend to Exercise During Leisure

Gene	SNP	Genotype	Rare Allele	Result
GABRG3	rs8036270	Variant not found	G	⚪
MC4R	rs17782313	CT+	C	🔵

Trend of Polyunsaturated Fat Intake and Weight Gain

Gene	SNP	Genotype	Rare Allele	Result
AATK	rs7220048	TT+	C	🟢
ACMSD	rs387906598	Variant not found	T	⚪
ADCYAP1	rs1893154	CC-	G	🟢
ADIPOQ	rs6444175	Variant not found	A	⚪
ADRA2A	rs553668	Variant not found	G,T	⚪
ADRB3	rs4994	TT-	G	🟢
ADSS	rs3102460	CT+	T	🟢
AK8	rs12552369	Variant not found	A	⚪
ALLC	rs387907075	Variant not found	C	⚪
ANKAR	rs12053254	TT+	C	🟢
ANKK1	rs1800497	CT-	A	🔴
ARHGAP11A	rs555387669	Variant not found		⚪
ARHGAP24	rs11732231	Variant not found	C,T	⚪
ARMC4	rs587777047	AA+	C	🟢
ARMC4	rs587777049	GG+	T	🟢

Gene	SNP	Genotype	Rare Allele	Result
ASIC2	rs28936	Variant not found	C	○
ASTN2	rs111033570	Variant not found	A	○
AUTS2	rs1057517708	Variant not found	T	○
AUTS2	rs1057518198	Variant not found		○
BDNF	rs12273539	Variant not found	T	○
BDNF	rs6265	GG-	T	●
BICC1	rs11006263	AA+	G	●
BICD1	rs2630578	Variant not found	C	○
C2CD4C	rs12978500	AC+	A	●
C8ORF34	rs1517114	CC+	A,G,T	●
CA8	rs267606695	Variant not found	C,G	○
CADM1	rs6589488	Variant not found	T	○
CAMK2A	rs2053053	Variant not found	A,C	○
CCDC33	rs2930291	Variant not found	A,C	○
CCDC77	rs1048466	AG+	A,C	●
CD46	rs35366573	CC+	T	●
CD46	rs7144	Variant not found	C	○
CDCA3	rs5443	CT+	T	◉
CDHR3	rs6967330	GG+	A	●
CELF2	rs3740194	Variant not found	C	○
COL4A1	rs113994104	Variant not found	A,T	○
COL4A1	rs3742207	AC-	A,G	●
COLEC12	rs16944558	Variant not found	T	○
CSMD1	rs995322	Variant not found	C,G	○
CYP2E1	rs2031920	CC+	T	●
CYP2E1	rs2070672	AA+	G	●
DAPL1	rs16843372	TT+	C	●
DDX60L	rs17612333	Variant not found	A,G	○
DLC1	rs121908500	Variant not found	C	○
DLG2	rs10501570	Variant not found	C	○
DMRT1	rs1057519638	Variant not found	T	○
DOCK8	rs112321280	Variant not found	G	○
DOCK8	rs192864327	GG+	C,T	●
ECT2	rs7646507	AG+	A	●
EEPD1	rs4302748	AG+	A	●
EHF	rs286913	CC-	G,T	●
EVA1A	rs17011455	TT+	C	●
FAM129A	rs147815528	Variant not found	A,C	○
FAM19A2	rs10784285	Variant not found	T	○
FAM209B	rs6024938	CT+	T	●
FAM71F1	rs6971091	GG+	A	●
FARP1	rs688872	TT-	G	●
FLJ33534	rs16857178	GG+	A	●
FSIP1	rs10152640	AG+	G	●
FTO	rs1121980	CC-	A	●
FTO	rs121918214	GG+	A	●
FTO	rs1421085	TT+	C	●
FTO	rs17817449	TT+	A,G	●
FTO	rs3751812	GG+	T	●
FTO	rs9930506	AA+	G	●
GCH1	rs10483639	Variant not found	C	○
GCH1	rs104894433	Variant not found	A,C,T	○
GCH1	rs104894434	Variant not found	G	○
GHRL	rs696217	Variant not found	T	○
GMDS	rs9378688	Variant not found	A	○
GPC5	rs2352028	CT+	G,T	◉
GSG1L	rs205391	CT+	C,G	●
HDAC9	rs11984041	CC+	T	●
IFI16	rs6940	Variant not found	T	○
IFNGR2	rs74315444	Variant not found	A	○
IL-1A	rs1800587	CT-	A,C	◉
IL-1B	rs1143634	CT-	A	●
INSIG2	rs7566605	GG+	C	●
INTERGENIC	rs10207060	GT+	A,G	●
INTERGENIC	rs11070098	TT+	C	●
INTERGENIC	rs11845134	Variant not found	T	○
INTERGENIC	rs12986207	Variant not found	A,C	○
INTERGENIC	rs17054265	CC+	G,T	●

Gene	SNP	Genotype	Rare Allele	Result
INTERGENIC	rs17468244	AA+	G	🟢
INTERGENIC	rs2153299	AA-	C	🟢
INTERGENIC	rs2575029	CC+	C	🟢
INTERGENIC	rs5767992	CC+	C	🟢
INTERGENIC	rs6486986	GT+	T	🟢
JDP2	rs741846	Variant not found	A,T	⚪
KCNB1	rs1057518621	Variant not found	T	⚪
KCNB1	rs1057521887	Variant not found	C	⚪
KIF6	rs20455	Variant not found	G	⚪
KIF6	rs9380880	GG+	A	🟢
KIRREL	rs6427419	Variant not found	A	⚪
LEPR	rs1137101	AA+	G	🟢
LGALS17A	rs8103033	AG+	A	🟢
LHPP	rs12773846	GG+	A,C	🟢
LINC00704	rs1391511	Variant not found	G	⚪
LINC01299	rs6981992	GT+	A,T	🟢
LINC01500	rs405460	AC-	A,T	🟢
LIPC	rs113298164	Variant not found	T	⚪
LIPC	rs1800588	CC+	T	🟡
LIPC	rs261332	GG+	G	🟢
LPP	rs1152846	AG-	C	🟢
LPP	rs4686484	Variant not found	A	⚪
MC4R	rs1057517991	Variant not found	G	⚪
MC4R	rs10871777	AG+	G	🟠
MC4R	rs12970134	AG+	A	🟢
MDFIC	rs7784447	GG+	A	🟢
NDUFA8	rs3818638	AG-	C	🟢
NIPSNAP3B	rs2472476	AG-	T	🟢
NLRP8	rs306450	Variant not found	G	⚪
NMNAT2	rs4652795	CT+	T	🟢
NPM2	rs11776272	GG+	G	🟢
NXPH1	rs765855	GG+	G	🟢
PCDH9	rs17081231	AA+	G	🟢
PCSK1	rs6232	AG-	C	🟠
PIP4K2A	rs746203	Variant not found	T	⚪
PKNOX2	rs10893366	CT+	T	🟢
PLEKHG1	rs17427389	GG+	A,T	🟢
POC5	rs2112347	GT+	G	🟢
PPARG	rs13306747	Variant not found	A,G,T	⚪
PPM1H	rs2029721	Variant not found	A	⚪
PTPRD	rs10116682	Variant not found	A	⚪
PTPRD	rs1975197	CC-	A	🔵
PTPRN2	rs10274279	TT+	C	🟢
PVALB	rs2022068	AA+	G	🟢
RAB17	rs2292873	AG-	T	🟢
RASEF	rs10867921	AG+	A	🟢
RBBP6	rs11860248	Variant not found	G	⚪
RBFOX1	rs1057521725	Variant not found	A	⚪
RBFOX1	rs1064794750	Variant not found	G	⚪
RIC3	rs1528133	Variant not found	C,G	⚪
RLN3	rs123277666	Variant not found		⚪
RPTOR	rs2289759	Variant not found	G	⚪
RSU1	rs11254160	AG+	A	🟢
RYR2	rs1057517873	AA+	G	🟢
S100P	rs3822262	AA-	G	🟢
SCG3	rs16964476	Variant not found	G	⚪
SCG3	rs3764220	Variant not found	G,T	⚪
SDC3	rs2282440	Variant not found	A,C	⚪
SERPINA12	rs61757459	Variant not found	A	⚪
SLC22A23	rs4959235	Variant not found	C	⚪
SLC29A3	rs1084004	CC+	C,G	🟢
SLC29A3	rs121912583	GG+	A	🟢
SLC29A3	rs869025176	Variant not found	C	⚪
SMYD3	rs11800820	CC+	A,T	🟢
SNRPN	rs220030	Variant not found	A,C	⚪
SORBS1	rs11188352	Variant not found	G	⚪
SPAG16	rs16851771	AA+	G	🟢
SPOCK3	rs9312517	AA+	G	🟢

Gene	SNP	Genotype	Rare Allele	Result
STON2	rs6574644	AA+	A	🟢
SYT1	rs17005598	Variant not found	A	⚪
TBC1D1	rs35859249	CC+	A,T	🟢
TCF4	rs613872	TT+	T	🟢
TCF4	rs9960767	CC+	C,G	🟡
TM9SF2	rs9513627	AA+	A	🟢
TMEM18	rs6548238	CC+	C	🟢
TMEM229B	rs1077989	AC+	C	🟢
TMEM45B	rs10894147	CC+	T	🟢
TMOD1	rs1475545	AG-	T	🟢
TNFRSF1B	rs5746059	Variant not found	G	⚪
TPTE2P1	rs2483374	AC+	C,T	🟢
TRABD2B	rs946836	Variant not found	G,T	⚪
TRAPPC9	rs267607137	CC-	A	🟢
TRIM66	rs4929923	CC+	C	🟢
TUB	rs2272382	Variant not found	C	⚪
UGT2B7	rs12233719	GG+	A,C,T	🟢
UNC13A	rs12608932	AC+	C	🟡
UNC5C	rs12643654	Variant not found	G	⚪
VSIG10	rs7957470	GG+	G	🟢
WDPCP	rs11683229	Variant not found	G,T	⚪
WDPCP	rs200322968	Variant not found	T	⚪
WDR11-AS1	rs10937273	Variant not found	A	⚪
WDR11-AS1	rs318240760	Variant not found	A,C	⚪
WDR11-AS1	rs4783244	GG+	T	🟢
ZBTB46	rs6062314	TT+	G,T	🟢
ZNF536	rs3786800	AA-	C	🟢

Trend of Higher Protein Consumption

Gene	SNP	Genotype	Rare Allele	Result
DRAM1	rs77694286	AA+	G	🟢
FTO	rs1421085	TT+	C	🟢

Testosterone

Gene	SNP	Genotype	Rare Allele	Result
CYP17A1	rs6162	GG+	A	🟠
CYP19A1	rs700518	AA-	C	🟢
FAM9B	rs5934505	CT+	G	🟢
FSHR	rs6166	AG-	T	🟢
HSD17B2	rs1424151	Variant not found	G	⚪
HSD17B3	rs9409407	GG+	T	🟢
PDE7B	rs7774640	Variant not found	A	⚪
SHBG	rs12150660	GG+	T	🔵
SHBG	rs6258	CC+	T	🟢
SHBG	rs727428	AG-	T	🟠

Tetrahydropiobterine (BH4)

Gene	SNP	Genotype	Rare Allele	Result
NOS3	rs1800779	AA+	G	🟢
NOS3	rs1800783	Variant not found	C,G,T	⚪
NOS3	rs3918188	Variant not found	A,T	⚪

Transport of MnSOD to Mitochondria

Gene	SNP	Genotype	Rare Allele	Result
SOD2	rs4880	CT-	G	🔵

Vitamin A (Retinol)

Gene	SNP	Genotype	Rare Allele	Result
BCO1	rs119478057	CC+	T	🟢
BCO1	rs12934922	AA+	G,T	🟢
BCO1	rs6564851	TT+	G	🟢
BCO1	rs7501331	CC+	T	🟢

Vitamin B1 (Thiamin)

Gene	SNP	Genotype	Rare Allele	Result
PNPLA3	rs738409	GG-	G	🔴
SLC19A2	rs28937595	GG-	A	🟢
SLC19A2	rs121908540	CC-	T	🟢

Gene	SNP	Genotype	Rare Allele	Result
SLC19A2	rs74315373	Variant not found	T	⚪
SLC19A2	rs74315374	GG-	A	🟢
SLC19A2	rs74315375	Variant not found	A	⚪
SLC19A3	rs121917884	Variant not found	G	⚪
SLC19A3	rs121917882	GG-	A	🟢
SLC25A19	rs119473030	Variant not found	C	⚪
SLC25A19	rs387906944	Variant not found	A	⚪
SLC35F3	rs34032258	CC+	G	🟢
TPK1	rs371271054	TT+	C	🟢

B12 vitamin

Gene	SNP	Genotype	Rare Allele	Result
ABCD4	rs3742801	TT+	T	🔴
APTX	rs12377462	TT+	C	🟢
CD320	rs2336573	CC+	T	🟠
CLYBL	rs41281112	CC+	T	🟢
CUBN	rs1801222	CT-	A	🟠
FUT2	rs492602	CT-	A,G	🟢
FUT2	rs602662	AG+	G	🟡
FUT2	rs1047781	Variant not found	T	⚪
FUT2	rs601338	AG+	A	🟠
FUT6	rs3760775	CC-	G	🟢
FUT6	rs3760776	CC-	G	🟢
FUT6	rs708686	GG-	T	🟢
INTERGENIC	rs4619337	Variant not found	C	⚪
INTERGENIC	rs12272669	Variant not found	A	⚪
MMAA	rs2270655	Variant not found	C	⚪
MS4A3	rs2298585	CC+	T	🟢
MTHFR	rs1801133	CC-	A	🟢
PRELID2	rs10515552	TT+	C	🟢
TCN1	rs34324219	CC+	A	🟢
TCN1	rs526934	AA+	A	🟢
TCN2	rs1801198	GG+	A,C	🟠
TCN2	rs9606756	AA+	G	🟢

Vitamin B3 (Niacin)

Gene	SNP	Genotype	Rare Allele	Result
BST1	rs4698412	AA+	A	🔴
CD38	rs6449182	Variant not found	G	⚪
GAD1	rs2241165	AA-	T	🟢
NAMPT	rs61330082	CC-	A	🟢
SIRT1	rs12778366	TT+	C	🔴
SIRT3	rs511744	CC+	T	🔴
SIRT6	rs352493	TT+	C	🔴

Vitamin B5 (Pantothenic Acid)

Gene	SNP	Genotype	Rare Allele	Result
ABCA1	rs1883025	AG-	T	🟢
ABCG8	rs6544713	CC+	C	🟢
AHCY	rs13043752	Variant not found	A	⚪
AHCY	rs41301825	Variant not found	T	⚪
AIRE	rs1055311	Variant not found	G,T	⚪
AIRE	rs1800520	Variant not found	A,G,T	⚪
ANAPC4	rs3816587	Variant not found	T	⚪
ANXA3	rs2867461	AG+	G,T	🟢
AOC1	rs10156191	Variant not found	T	⚪
APOA5	rs2075291	Variant not found	A,T	⚪
APOA5	rs2266788	TT-	A	🟢
APOA5	rs3135506	GG+	C	🟢
APOC1	rs4420638	AA+	G	🟢
APOE	rs7412	TT+	T	🔴
AR	rs5031002	GG+	A	🟢
BRCA2	rs4942486	CT+	C	🟢
C5	rs10985112	GG+	A	🟢
CDK6	rs42041	Variant not found		⚪
CDK6	rs606231255	Variant not found	T	⚪
CPS1	rs1047891	CC+	A	🟢
CR1L	rs4844614	GT+	T	🟡

Gene	SNP	Genotype	Rare Allele	Result
CTLA4	rs3087243	AG+	G	🟡
DNAH11	rs12670798	TT+	C	🟢
DOCK7	rs10889353	AC+	C,T	🟢
EOMES	rs3806624	CT-	G	🟢
FABP2	rs1799883	GG-	A,C,G	🟢
FADS1	rs174547	TT+	C	🟢
FADS2	rs174570	CC+	T	🟢
FCRL3	rs7528684	AG+	G	🟢
GAD1	rs1978340	Variant not found	A	⚪
GAD1	rs3762555	Variant not found	A,G	⚪
GAD1	rs3791878	Variant not found	T	⚪
GCKR	rs1260326	CT+	C	🟡
GPX1	rs1050450	CC-	A	🟢
GUCY1B2	rs3790022	CC-	A	🟢
HLA-DQA1	rs12722051	Variant not found	T	⚪
HLA-DRB1	rs6457617	TT+	A,T	🟠
HLA-DRB1	rs660895	GG+	G	🔴
HTR2A	rs1328674	AG-	C,G	🔴
HTR2A	rs6314	CC-	A	🟡
HYKK	rs8034191	TT+	C	🟢
ICAM3	rs2304240	AG+	G	🟢
IL-2RA	rs2104286	AG-	C	🟡
IL-2RB	rs743777	AG+	G	🟢
INTERGENIC	rs11162922	Variant not found	G	⚪
INTERGENIC	rs11761231	CT+	C	🟢
INTERGENIC	rs13192841	GG+	A	🟢
INTERGENIC	rs2327832	AG+	G	🟡
INTERGENIC	rs2837960	GT+	A,G	🟢
INTERGENIC	rs2872507	AG+	A	🟢
INTERGENIC	rs6920220	AG+	A	🔴
INTERGENIC	rs9550642	Variant not found	A	⚪
IRF5	rs2004640	Variant not found	G	⚪
ITGAV	rs3738919	AA+	A	🔵
JMJD1C	rs10761731	Variant not found	T	⚪
KIAA1109	rs13119723	GG+	G	🔴
KIAA1109	rs6822844	GT+	T	🟢
LDLR	rs6511720	GG+	T	🟢
LPL	rs13702	AG-	A,C	🟢
LPL	rs285	CT+	T	🟢
LPL	rs320	GT+	G	🟢
LPL	rs328	Variant not found	G	⚪
MAT1A	rs118204001	TT-	C	🟢
MAT1A	rs2993763	Variant not found	A	⚪
MAT1A	rs72558181	Variant not found	T	⚪
MCT1	rs1049434	Variant not found	T	⚪
MLXIPL	rs1051921	Variant not found	A	⚪
MMEL1	rs3890745	Variant not found	C	⚪
MMEL1	rs6684865	Variant not found	A	⚪
MTHFR	rs2066470	Variant not found	A,C	⚪
NAF1	rs7675998	GG+	G,T	🟢
NFKBIE	rs2233434	TT-	G	🟢
NFKBIE	rs2233437	Variant not found	A	⚪
NOD2	rs2066845	GG+	C,T	🟢
OR4A46P	rs7395662	GG+	A	🟢
PADI4	rs11203366	AG+	A	🟢
PADI4	rs2240340	AG-	C	🟡
PCIF1	rs7679	TT+	C	🟢
PHF19	rs1953126	Variant not found	C	⚪
PHTF1	rs6679677	CC+	A	🟢
PHYHIP	rs4871976	Variant not found	A	⚪
PLD4	rs2841277	CT+	T	🟢
PSMA4	rs12901682	CC+	C,T	🟢
PTPN2	rs1893217	CC-	G	🟠
PTPN2	rs2542151	GG+	T	🟠
PTPN22	rs2476601	GG+	G	🟢
PTPN22	rs2488457	Variant not found	A,C	⚪
RAB11B	rs2967605	GG-	T	🟢
SLC6A11	rs1809529	CT+	T	🟢

Gene	SNP	Genotype	Rare Allele	Result
STAT4	rs10181656	CG+	C	🟡
STAT4	rs7574865	GT+	G	🔴
TMEM241	rs9949617	CC+	T	🟢
TNF	rs1800610	CT-	A	🟢
TRAF1	rs10818488	Variant not found	G	⚪
TRAF1/C5	rs3761847	AA+	A	🟢
UBASH3A	rs11203203	AG+	A	🟠
VARS2	rs4678	CC-	A	🟢
WDFY4	rs877819	AG+	G	🟢
ZNF175	rs1543922	CC+	T	🟢
ZPR1	rs964184	CC+	C	🟢

Vitamin B6 (Pyridoxine)

Gene	SNP	Genotype	Rare Allele	Result
ABCA1	rs1883025	AG-	T	🟢
ABCB1	rs10248420	AA+	G,T	🟠
ABCB1	rs1128503	CT-	G	🟢
ABCB1	rs11983225	TT+	C	🟠
ABCB1	rs2032583	TT-	G	🟠
ABCB1	rs2235015	GG-	A,T	🟠
ABCB1	rs2235040	GG-	A,G,T	🟠
ABCB1	rs2235067	GG-	T	🟠
ABCB1	rs3213619	TT-	G	🟢
ABCB1	rs4148739	AA-	C	🟠
ADA	rs73598374	GG-	A,G,T	🟢
ADORA2A	rs5751876	Variant not found	C	⚪
AHCY	rs13043752	Variant not found	A	⚪
AHCY	rs41312290	Variant not found	C	⚪
ALPL	rs1697421	GG-	T	🟢
ALPL	rs1780316	Variant not found	C	⚪
ALPL	rs1106357	Variant not found	T	⚪
ALPL	rs1256335	TT-	G	🟢
ARMS2	rs10490924	GT+	T	🔴
ARMS2	rs3750847	Variant not found	T	⚪
BCR	rs2156921	Variant not found	A	⚪
BCR	rs2267012	Variant not found	A	⚪
BCR	rs2267013	Variant not found	G	⚪
BCR	rs2267015	Variant not found	G,T	⚪
BCR	rs3313172	Variant not found		⚪
BCR	rs3761418	Variant not found	G	⚪
BDNF	rs6265	GG-	T	🟢
C2	rs547154	CC-	T	🟢
C2	rs9332739	GG+	A,C	🟢
C3	rs2230199	CG-	C,T	🟠
C3	rs2230201	Variant not found	G,T	⚪
C3	rs2230205	AG-	T	🟢
C3	rs2287845	Variant not found	A	⚪
CBS	rs121964972	CC-	A	🟢
CBS	rs1801181	Variant not found	A	⚪
CBS	rs2851391	CT+	C	🟢
CBS	rs28934891	GG-	T	🟢
CBS	rs5742905	TT-	G	🟢
CETP	rs1532624	TT-	A	🟢
CETP	rs17231520	Variant not found	A	⚪
CETP	rs1864163	GG+	A	🔵
CETP	rs2303790	AA+	G	🟢
CETP	rs5880	GG+	C	🟢
CETP	rs5882	AG+	A	🔵
CETP	rs708272	CT-	A	🟠
CFB	rs4151667	TT+	A	🟢
CFH	rs1061147	CC+	C	🔵
CFH	rs1061170	TT+	T	🔵
CFH	rs1065489	GT+	T	🟢
CFH	rs1329428	AG-	T	🟢
CFH	rs3753394	CT+	T	🟢
CFH	rs800292	CT-	A	🔵
CHRM2	rs1824024	GT-	A	🟢
CHRM2	rs2061174	CT-	A,C	🟢

Gene	SNP	Genotype	Rare Allele	Result
CHRM2	rs324650	AT+	A	
CLOCK	rs1801260	AA+	C,G,T	
COL8A1	rs13081855	GG+	T	
COL8A1	rs13095226	Variant not found	C	
COMT	rs4680	AG+	A	
CRYBB2	rs74315489	Variant not found		
CRYBB3	rs74315490	GG+		
CRYGD	rs28931605	Variant not found		
CX3CR1	rs3732378	AG+	A	
CX3CR1	rs3732379	CT+	T	
DAT	rs1064795122	Variant not found	T	
DCDC2	rs7765678	Variant not found	C	
DCDC2	rs793862	Variant not found	C,G,T	
DCDC2	rs807701	Variant not found	A	
DTNBP1	rs2619522	GT-	C	
EPHA2	rs116506614	CC+		
EPHA2	rs3754334	CC-	A	
FGD6	rs12310399	Variant not found	C	
FGF20	rs1721100	Variant not found	G,T	
FKBP5	rs1360780	CC+	A,C	
GAD1	rs10432420	Variant not found	A	
GAD1	rs12185692	Variant not found	A	
GAD1	rs1978340	Variant not found	A	
GAD1	rs2058725	Variant not found	C	
GAD1	rs2241165	AA-	T	
GAD1	rs3762555	Variant not found	A,G	
GAD1	rs3791850	Variant not found	A,C	
GAD1	rs3791851	Variant not found	C	
GAD1	rs3791878	Variant not found	T	
GAD1	rs3828275	Variant not found	T	
GAD1	rs701492	TT+	T	
GAD1	rs769407	Variant not found	C	
GJA8	rs2132397	Variant not found		
GJA8	rs6657114	Variant not found		
GJA8	rs6688578	Variant not found		
GJA8	rs7541950	Variant not found		
GJA8	rs864309684	Variant not found		
GPHN	rs104894470	CC+	T	
GPX4	rs713041	Variant not found	A,C	
GRIA3	rs3848874	GG+	A,T	
GRIA3	rs687577	CC+	C	
GSR	rs3594	Variant not found	A	
HTR2A	rs1328674	AG-	C,G	
HTR2A	rs6314	CC-	A	
HTR2C	rs3813929	CC+	G,T	
HTRA1	rs11200638	AG+	A	
HTRA1	rs932275	Variant not found	A	
IL-1B	rs16944	AG+	G	
INTERGENIC	rs1031681	Variant not found	C	
INTERGENIC	rs10468017	CC+	T	
INTERGENIC	rs12678919	AA+	G	
INTERGENIC	rs1545843	AG+	A	
INTERGENIC	rs493258	AG-	C	
KIAA0319	rs4504469	CC+	G,T	
KIAA0319	rs761100	TT-	C	
MAF	rs121917735	Variant not found	G,T	
MAF	rs121917736	Variant not found	C	
MAF	rs786205221	Variant not found	T	
MAOA	rs909525	GG-	T	
MTHFR	rs1476413	AG-	G,T	
MTHFR	rs17037390	Variant not found	A	
MTHFR	rs1801131	AC-	G	
MTHFR	rs1801133	CC-	A	
MTHFR	rs2066470	Variant not found	A,C	
MTHFR	rs4846049	Variant not found	A,G	
MTRR	rs1801394	AA+	G	
NBPF3	rs4654748	CT+	T	
NOTCH4	rs422951	AG-	C	

Gene	SNP	Genotype	Rare Allele	Result
NPAS2	rs11123857	Variant not found	G	⚪
NR3C1	rs6198	Variant not found	C	⚪
OXTR	rs2254298	GG+	A	🟢
OXTR	rs237899	GG+	A,C	🟢
PDE11A	rs3770018	Variant not found	C	⚪
PDE9A	rs729861	Variant not found	G	⚪
PITX2	rs6533526	GG+	A	🟢
REST	rs1713985	AC-	T	🟢
REST	rs2227902	GG+	T	🟢
REST	rs3796530	Variant not found	A	⚪
SERPINF1	rs1136287	CT+	T	🟡
SKIV2L	rs2734331	TT-	G	🟢
SKIV2L	rs429608	GG+	A	🟢
SLC64A	rs25531	Variant not found	C,G	⚪
SOD2	rs4880	CT-	G	🟢
TDP2	rs2143340	TT-	G,T	🟢
TLR3	rs3775291	GG-	G,T	🟠
TPH1	rs1799913	AC-	A,T	🟢
TPH1	rs7933505	Variant not found	A	⚪
TTRAP	rs3212236	Variant not found	C	⚪
VEGFA	rs3025039	CC+	T	🟢

Vitamin B7 (Biotin)

Gene	SNP	Genotype	Rare Allele	Result
ABCA1	rs1883025	AG-	T	🟢
ACHE	rs1799805	Variant not found	T	⚪
ACHE	rs2571598	Variant not found	G,T	⚪
ACP7	rs472265	AA+	G	🟢
ADRA2A	rs553668	Variant not found	G,T	⚪
AR	rs6152	GG+	A	🟢
ARL15	rs1694089	Variant not found	C	⚪
ARMS2	rs3750847	Variant not found	T	⚪
C2	rs547154	CC-	T	🟢
C3	rs2230199	CG-	C,T	🟠
C3	rs2230201	Variant not found	G,T	⚪
C3	rs2230205	AG-	T	🟢
C3	rs2287845	Variant not found	A	⚪
CAPN10	rs3792267	GG+	A	🟢
CDKAL1	rs4712523	AG+	G	🟢
CDKAL1	rs7756992	AG+	G,T	🟢
CDKN2A	rs10811661	TT+	T	🟠
CDKN2A/B	rs2383208	AA+	G,T	🟢
CDKN2B-AS1	rs2383206	Variant not found	G	⚪
CETP	rs1532624	TT-	A	🟢
CETP	rs17231520	Variant not found	A	⚪
CETP	rs1864163	GG+	A	🔵
CETP	rs2303790	AA+	G	🟢
CETP	rs5880	GG+	C	🟢
CETP	rs5882	AG+	A	🔵
CETP	rs708272	CT-	A	🟠
CFH	rs1061147	CC+	C	🔵
CFH	rs1061170	TT+	T	🔵
CFH	rs1065489	GT+	T	🟢
CFH	rs1329428	AG-	T	🟢
CFH	rs3753394	CT+	T	🟢
CFH	rs800292	CT-	A	🔵
COL8A1	rs13081855	GG+	T	🟢
COL8A1	rs13095226	Variant not found	C	⚪
CRYBB2	rs74315489	Variant not found		⚪
CRYGD	rs28931605	Variant not found		⚪
CX3CR1	rs3732378	AG+	A	🔵
CX3CR1	rs3732379	CT+	T	🟢
DNER	rs1861612	AG+	A,C	🟢
EPHA2	rs3754334	CC-	A	🟢
FGD6	rs12310399	Variant not found	C	⚪
FGFR3	rs121913482	CC+	T	🟢
FGFR3	rs121913483	CC+	A,G,T	🟢
FTO	rs1121980	CC-	A	🟢

Gene	SNP	Genotype	Rare Allele	Result
GAD1	rs10432420	Variant not found	A	○
GAD1	rs12185692	Variant not found	A	○
GAD1	rs2058725	Variant not found	C	○
GAD1	rs2241165	AA-	T	●
GAD1	rs3762555	Variant not found	A,G	○
GAD1	rs3791850	Variant not found	A,C	○
GAD1	rs3791851	Variant not found	C	○
GAD1	rs3791878	Variant not found	T	○
GAD1	rs3828275	Variant not found	T	○
GAD1	rs701492	TT+	T	●
GAD1	rs769407	Variant not found	C	○
GCKR	rs780094	AG-	C	●
GJA8	rs2132397	Variant not found		○
GJA8	rs6657114	Variant not found		○
GJA8	rs6688578	Variant not found		○
GRK5	rs17098707	Variant not found	T	○
GSR	rs3594	Variant not found	A	○
HHEX	rs1111875	Variant not found	T	○
HHEX	rs5015480	TT+	T	●
HTRA1	rs11200638	AG+	A	●
HTRA1	rs932275	Variant not found	A	○
IL-6	rs1800795	CG+	G	●
INTERGENIC	rs12678919	AA+	G	●
INTERGENIC	rs2223841	AA-	C	●
INTERGENIC	rs6113491	Variant not found	C	○
INTERGENIC	rs6625163	AA+	A	●
IRS1	rs2943641	CT+	C	●
JAZF1	rs1635852	CT+	C	●
KCNJ11	rs5215	TT+	T	●
KCNJ11	rs5219	CC+	T	●
KCNQ1	rs2283228	AA+	C	●
MAF	rs121917735	Variant not found	G,T	○
MAF	rs121917736	Variant not found	C	○
MTTP	rs3816873	Variant not found	C	○
NOS3	rs1800783	Variant not found	C,G,T	○
NOS3	rs3918188	Variant not found	A,T	○
NOTCH2	rs10923931	Variant not found	T	○
NOTCH2	rs2793831	Variant not found	C	○
NOTCH4	rs422951	AG-	C	●
PAX4	rs2233578	Variant not found	A,T	○
PAX4	rs2233580	GG-	T	●
PITX2	rs6533526	GG+	A	●
PPARG	rs13306747	Variant not found	A,G,T	○
PPARG	rs1801282	CG+	C	●
PPARG	rs2197423	Variant not found	A	○
RBMS1	rs6718526	Variant not found	C	○
REST	rs1713985	AC-	T	●
REST	rs2227902	GG+	T	●
REST	rs3796530	Variant not found	A	○
RHOU	rs6426514	GG+	A	●
RPSAP52	rs1531343	CC+	C,T	●
SKIV2L	rs2734331	TT-	G	●
SKIV2L	rs429608	GG+	A	●
SLC2A14	rs12815313	Variant not found	G,T	○
SLC30A8	rs13266634	CC+	A,T	●
SOD2	rs2758331	Variant not found	A	○
TCF7L2	rs12255372	GG+	T	●
TGFBR3	rs1805110	CC-	A	●
TLR3	rs3775291	GG-	G,T	●
TRIB3	rs2295490	AG+	G,T	●
TRPS1	rs1057518791	Variant not found	T	○
VEGFA	rs3025039	CC+	T	●
VPS26A	rs4812829	AG+	A	●
VPS33B	rs121434383	Variant not found	A	○

Vitamin C (Ascorbic acid)

Gene	SNP	Genotype	Rare Allele	Result
ABCA1	rs1883025	AG-	T	●

Gene	SNP	Genotype	Rare Allele	Result
ABCB1	rs1128503	CT-	G	
ABCB1	rs3213619	TT-	G	
ABI3BP	rs9848726	Variant not found	T	
ALDH2	rs671	GG+	A	
AOC1	rs10156191	Variant not found	T	
APOB	rs1367117	GG+	A	
APOB	rs676210	AG+	A,T	
ATM	rs664143	CC-	G,T	
AURKA	rs2273535	Variant not found	T	
B3GALT1	rs13020412	AA+	G	
BCO1	rs12934922	AA+	G,T	
CCHCR1	rs130067	Variant not found	G	
CDKN1A	rs1801270	CC+	A,T	
CDKN2A	rs3731249	GG-	A,G,T	
CETP	rs5882	AG+	A	
CFH	rs1061147	CC+	C	
CFH	rs1061170	TT+	T	
CLPTM1L	rs401681	CT+	T	
CYP1A1	rs1048943	AA-	A,C,G	
CYP1A1	rs1800031	TT-	G	
CYP1A1	rs41279188	CC-	A,T	
CYP1A1	rs56313657	GG-	A,T	
CYP1A1	rs72547509	TT-	G,T	
CYP1B1	rs1056836	CC-	C	
CYP2E1	rs2070673	TT+	T	
CYP3A4	rs2740574	AA-	T	
CYP3A5	rs776746	AG-	C	
DEF8	rs4268748	CT+	C	
DHFR	rs1643649	Variant not found	C	
DIRC3	rs966423	CT+	G,T	
DPYD	rs1801266	CC-	A	
DPYD	rs1801267	GG-	T	
DPYD	rs1801268	GG-	A	
E2F3	rs1570155	AG+	A,T	
EPHX1	rs1051740	TT+	C	
EPHX1	rs2234922	AG+	G,T	
ERI1	rs96621	CT+	C	
FASLG	rs763110	TT+	T	
FOXE1	rs10984009	Variant not found	A	
G6PD	rs1050828	CC+	T	
GPX1	rs1050450	CC-	A	
GSTP1	rs1695	GG+	G	
HDAC4	rs3791406	CT+	C	
HLA-DRA	rs3135391	CC-	A	
HLA-DRB1	rs660895	GG+	G	
HNF1A	rs1169300	Variant not found	A	
HNF1A	rs2464196	Variant not found	A	
HTRA1	rs11200638	AG+	A	
IGF1R	rs3743262	Variant not found	T	
IL4R	rs1801275	Variant not found	G	
INTERGENIC	rs10445747	Variant not found	G	
INTERGENIC	rs12661968	TT+	C	
INTERGENIC	rs428668	Variant not found	C	
INTERGENIC	rs4698048	Variant not found	G	
INTERGENIC	rs9287638	CC+	A	
IRF4	rs12203592	CC+	T	
KL	rs9536314	TT+	A,G	
LMNA	rs553016	GG-	G,T	
MC1R	rs1805005	GG+	T	
MC1R	rs1805007	CC+	T	
MC1R	rs1805008	CC+	T	
MC1R	rs1805009	GG+	A,C	
MDM2	rs2279744	Variant not found	G	
MTHFR	rs1476413	AG-	G,T	
MTHFR	rs17037390	Variant not found	A	
MTHFR	rs1801131	AC-	G	
MTHFR	rs1801133	CC-	A	
MTHFR	rs4846049	Variant not found	A,G	

Gene	SNP	Genotype	Rare Allele	Result
MTRR	rs1801394	AA+	G	
PIK3CA	rs104886003	GG+	A,C	
PIK3CA	rs1057518041	Variant not found		
PIK3CA	rs1057519699	Variant not found	A	
PIK3CA	rs1057519925	Variant not found	A,C	
PIK3CA	rs1057519926	Variant not found	T	
PIK3CA	rs1057519927	Variant not found	C,G,T	
PIK3CA	rs1057519928	Variant not found	C	
PIK3CA	rs1057519929	Variant not found	A	
PIK3CA	rs1057519930	Variant not found	T	
PIK3CA	rs1057519931	Variant not found	C	
PIK3CA	rs1057519932	Variant not found	G	
PIK3CA	rs1057519933	Variant not found	G	
PIK3CA	rs1057519934	Variant not found	C	
PIK3CA	rs1057519935	Variant not found	G	
PIK3CA	rs1057519936	Variant not found	G,T	
PIK3CA	rs1057519937	Variant not found	C	
PIK3CA	rs1057519938	Variant not found	C,T	
PIK3CA	rs1057519939	Variant not found	C	
PIK3CA	rs1057519940	Variant not found	T	
PIK3CA	rs1057519941	Variant not found	C,G	
PIK3CA	rs1057519942	GG+	A	
PIK3CA	rs1064793349	Variant not found	A	
PIK3CA	rs1064793663	Variant not found	A	
PIK3CA	rs1064793732	Variant not found	A	
PIK3CA	rs1064793838	Variant not found	G	
PIK3CA	rs1064795304	Variant not found	G	
PIK3CA	rs121913272	Variant not found	C,G	
PIK3CA	rs121913273	Variant not found	A,C	
PIK3CA	rs121913274	Variant not found	C,G,T	
PIK3CA	rs121913275	Variant not found	A,C,T	
PIK3CA	rs121913277	Variant not found	A,C	
PIK3CA	rs121913279	Variant not found	G,T	
PIK3CA	rs121913281	Variant not found	T	
PIK3CA	rs121913282	Variant not found	C	
PIK3CA	rs121913283	Variant not found	A,T	
PIK3CA	rs121913284	Variant not found	A,G	
PIK3CA	rs121913285	Variant not found	G	
PIK3CA	rs121913286	Variant not found	A,G	
PIK3CA	rs121913287	Variant not found	A	
PIK3CA	rs121913288	Variant not found	G	
PIK3CA	rs12494623	Variant not found	G,T	
PIK3CA	rs141178472	Variant not found	C	
PIK3CA	rs17849071	Variant not found	G	
PIK3CA	rs17849079	Variant not found	T	
PIK3CA	rs2699887	CT+	T	
PIK3CA	rs3729679	Variant not found	G	
PIK3CA	rs3729687	Variant not found	A	
PIK3CA	rs397514565	Variant not found	A	
PIK3CA	rs397517200	Variant not found		
PIK3CA	rs397517201	Variant not found	C,G,T	
PPARG	rs17036170	GG+	A	
PPARGC1A	rs3774923	Variant not found	T	
PTEN	rs121909229	GG+	A,C,T	
PTEN	rs121909232	CC+	G	
PTEN	rs371387815	Variant not found	G,T	
RNASEL	rs3738579	CT-	G	
SIRT1	rs3758391	Variant not found	C	
SIRT1	rs4746720	Variant not found	C	
SLC23A1	rs1279683	Variant not found	A,C	
SLC23A1	rs33972313	GG-	A,G,T	
SLC2A14	rs10846086	Variant not found	G	
SLC2A14	rs2889504	Variant not found	A	
SLC39A6	rs1050631	CT-	A	
SLC45A2	rs185146	CT+	T	
SOD2	rs1799725	Variant not found		
SOD2	rs4880	CT-	G	
SOD3	rs1799895	CC+	G	

Gene	SNP	Genotype	Rare Allele	Result
SPIRE2	rs35096708	Variant not found	A	⚪
STAT4	rs10181656	CG+	C	🟡
TERT	rs2736098	AG-	T	🟢
TERT	rs2736100	TT-	A	🟠
TYR	rs28940879	Variant not found	A,C	⚪
XPC	rs2228000	CC-	A	🟢
XPC	rs2228001	AA-	T	🟢
XRCC1	rs1799782	CT-	A	🟡

Vitamin D (Cholecalciferol)

Gene	SNP	Genotype	Rare Allele	Result
ABCA1	rs1883025	AG-	T	🟢
ABCB1	rs1128503	CT-	G	🟢
ABCB1	rs3213619	TT-	G	🟢
ABI3BP	rs9848726	Variant not found	T	⚪
ACE	rs1799752	Variant not found		⚪
ACE	rs4343	AG+	A	🟠
ACHE	rs1799805	Variant not found	T	⚪
ACHE	rs2571598	Variant not found	G,T	⚪
ACP7	rs472265	AA+	G	🟢
ADCY5	rs11708067	AA+	G	🟢
ADD1	rs4961	GT+	A,T	🟠
ADD1	rs4963	CG+	G,T	🟢
ADD2	rs3755351	CC-	T	🟢
ADIPOQ	rs17366743	TT+	C	🟢
ADRA2A	rs553668	Variant not found	G,T	⚪
ADRB2	rs1800888	CC+	T	🟢
AGAP2	rs12368653	GG+	A,T	🟢
AGT	rs11568020	Variant not found	A,T	⚪
AGT	rs121912702	Variant not found	A	⚪
AGT	rs699	CT-	G	🟠
AGTR1	rs104893677	Variant not found	T	⚪
AGTR1	rs1492099	Variant not found	A,C	⚪
AGTR1	rs5186	AA+	C	🟢
AHI1	rs117447608	Variant not found	A	⚪
AHI1	rs121434349	Variant not found	A,T	⚪
AHI1	rs121434350	Variant not found	T	⚪
ALDH2	rs671	GG+	A	🟠
ALK	rs7577363	Variant not found	A	⚪
ANKRD1	rs10975200	Variant not found	C,G	⚪
AOC1	rs10156191	Variant not found	T	⚪
APOB	rs1367117	GG+	A	🟢
APOB	rs676210	AG+	A,T	🟢
APOE	rs7412	TT+	T	🔴
APOE4	rs429358	TT+	C	🟢
ARL15	rs1694089	Variant not found	C	⚪
ARL15	rs788517	Variant not found	T	⚪
ASIC2	rs9901756	Variant not found	C	⚪
ATM	rs664143	CC-	G,T	🟢
ATP2B1	rs2681472	CT-	G	🟢
ATP2B1	rs7965584	AG+	G	🟢
ATP6V1B1	rs2266917	Variant not found	T	⚪
AURKA	rs2273535	Variant not found	T	⚪
B3GALT1	rs13020412	AA+	G	🟢
BAG3	rs2234962	CT+	C	🟢
BAG6	rs3117583	TT-	G	🟢
BATF	rs2300603	TT+	C	🟢
BCAT1	rs7961152	Variant not found	C	⚪
BCO1	rs12934922	AA+	G,T	🟢
BDNF	rs13306221	Variant not found	T	⚪
BMPR1B	rs11097457	Variant not found	G	⚪
BMPR1B	rs121434417	Variant not found	A	⚪
BMPR1B	rs1434536	Variant not found	T	⚪
BMPR2	rs1006246556	Variant not found	A,T	⚪
BRAP	rs3782886	AA-	C	🟢
BRCA2	rs1801406	Variant not found	C,G	⚪
BTD	rs104893686	TT+	G	🟢
BTD	rs104893687	CC+	T	🟢

Gene	SNP	Genotype	Rare Allele	Result
C1ORF106	rs7522462	AG+	A	
CACNB2	rs2228645	Variant not found	A,T	
CALCA	rs3781719	Variant not found	G	
CAPN10	rs3792267	GG+	A	
CASZ1	rs880315	AA-	C	
CAV3	rs1008642	Variant not found	A,G,T	
CBLB	rs12487066	Variant not found	C	
CBS	rs1801181	Variant not found	A	
CBS	rs2851391	CT+	C	
CBS	rs28934891	GG-	T	
CBS	rs5742905	TT-	G	
CCHCR1	rs130067	Variant not found	G	
CCL2	rs1024611	CT-	G	
CD58	rs12044852	CC+	A	
CD86	rs1129055	GG+	A	
CD86	rs9282641	GG+	A	
CDH13	rs8055236	GG+	A,C,T	
CDKAL1	rs4712523	AG+	G	
CDKAL1	rs7756992	AG+	G,T	
CDKN1A	rs1801270	CC+	A,T	
CDKN2A	rs10811661	TT+	T	
CDKN2A	rs3731249	GG-	A,G,T	
CDKN2A/B	rs2383208	AA+	G,T	
CDKN2B-AS1	rs10116277	TT+	T	
CDKN2B-AS1	rs1011970	GT+	T	
CDKN2B-AS1	rs1063192	TT-	A,T	
CDKN2B-AS1	rs10757272	TT+	T	
CDKN2B-AS1	rs10757274	GG+	G	
CDKN2B-AS1	rs1537375	Variant not found	C,G	
CDKN2B-AS1	rs2383206	Variant not found	G	
CETP	rs2303790	AA+	G	
CETP	rs5882	AG+	A	
CFH	rs1061147	CC+	C	
CHRDL1	rs387906713	Variant not found	A	
CHRDL1	rs387906714	Variant not found	A	
CHST12	rs6952809	CC+	C	
CLCN6	rs13306560	Variant not found	T	
CLCN6	rs17376328	Variant not found	A	
CLCN6	rs3737964	Variant not found	A,C,G	
CLEC16A	rs6498169	Variant not found	A	
CLEC16A	rs725613	Variant not found	G	
CLPTM1L	rs401681	CT+	T	
CLSTN2	rs17411949	CC+	T	
CRP	rs3091244	Variant not found	A,T	
CYP1A1	rs1048943	AA-	A,C,G	
CYP1A1	rs1800031	TT-	G	
CYP1A1	rs41279188	CC-	A,T	
CYP1A1	rs56313657	GG-	A,T	
CYP1A1	rs72547509	TT-	G,T	
CYP1B1	rs1056836	CC-	C	
CYP24A1	rs2248359	CC+	T	
CYP24A1	rs2296241	GG+	A	
CYP24A1	rs2762932	Variant not found	C	
CYP24A1	rs4809957	AG+	G	
CYP24A1	rs6068812	AA+	G	
CYP24A1	rs6068816	CT+	T	
CYP27B1	rs1057520815	Variant not found	T	
CYP27B1	rs10877012	TT+	C,T	
CYP27B1	rs118204007	Variant not found	C	
CYP27B1	rs118204010	CC-	G	
CYP27B1	rs118204008	CC-	T	
CYP27B1	rs118204012	AA-	G	
CYP2E1	rs2070673	TT+	T	
CYP2R1	rs10741657	GG+	G	
CYP2R1	rs117913124	Variant not found	A	
CYP2R1	rs12794714	Variant not found	A	
CYP2R1	rs2060793	GG+	G	
CYP2R1	rs6013897	Variant not found	A	

Gene	SNP	Genotype	Rare Allele	Result
CYP2R1	rs61495246	TT-	G	
CYP3A4	rs2740574	AA-	T	
CYP3A5	rs776746	AG-	C	
CYP4A11	rs1126742	Variant not found	G	
DAPK1	rs11141915	AC+	C	
DBC1	rs10984447	AA+	G	
DEF8	rs4268748	CT+	C	
DHFR	rs1643649	Variant not found	C	
DIRC3	rs966423	CT+	G,T	
DKKL1	rs2303759	TT+	G	
DLEU1	rs2762051	CC+	T	
DMD	rs104894788	GG-	T	
DMD	rs1800278	AA-	C	
DMD	rs1801187	GG-	T	
DNAJC5B	rs13279522	TT+	C	
DNER	rs1861612	AG+	A,C	
DPYD	rs1801266	CC-	A	
DPYD	rs1801267	GG-	T	
DPYD	rs1801268	GG-	A	
DSG2	rs2230234	AA+	G,T	
E2F3	rs1570155	AG+	A,T	
ENPP1	rs997509	Variant not found	T	
EPHX1	rs1051740	TT+	C	
EPHX1	rs2234922	AG+	G,T	
ERG	rs989554	Variant not found	A	
ERI1	rs96621	CT+	C	
ESR1	rs11964281	Variant not found	T	
EVI5	rs10735781	Variant not found	C	
EVI5	rs6680578	Variant not found	A	
F12	rs1801020	CT-	G	
F7	rs6046	CT-	A	
FAM58A	rs1057521251	Variant not found	A	
FAM69A	rs11164838	Variant not found	T	
FAM69A	rs7536563	Variant not found	G	
FASLG	rs763110	TT+	T	
FGF20	rs1721100	Variant not found	G,T	
FLJ25967	rs2331291	Variant not found	T	
FMN2	rs17672135	TT+	C	
FOXE1	rs10984009	Variant not found	A	
FTO	rs10163409	Variant not found	T	
FTO	rs1121980	CC-	A	
G6PD	rs1050828	CC+	T	
GAD1	rs10432420	Variant not found	A	
GAD1	rs12185692	Variant not found	A	
GAD1	rs2058725	Variant not found	C	
GAD1	rs2241165	AA-	T	
GAD1	rs3762555	Variant not found	A,G	
GAD1	rs3791850	Variant not found	A,C	
GAD1	rs3791851	Variant not found	C	
GAD1	rs3791878	Variant not found	T	
GAD1	rs3828275	Variant not found	T	
GAD1	rs701492	TT+	T	
GAD1	rs769407	Variant not found	C	
GATA2	rs3803	Variant not found	A	
GATA4	rs104894073	Variant not found	A,G,T	
GATA4	rs104894074	Variant not found	A	
GC	rs2282679	AA-	G	
GC	rs4588	CC-	A,T	
GC	rs7041	GT-	G	
GC	rs1155563	TT+	C	
GCK	rs4607517	GG+	A,C	
GCKR	rs780094	AG-	C	
GPX1	rs1050450	CC-	A	
GPX4	rs713041	Variant not found	A,C	
GRK5	rs17098707	Variant not found	T	
GSTP1	rs1695	GG+	G	
GUCY1A3	rs587777320	Variant not found	A,T	
GUCY1A3	rs587777321	Variant not found	T	

Gene	SNP	Genotype	Rare Allele	Result
GUCY1A3	rs587777322	Variant not found		
HDAC4	rs3791406	CT+	C	
HHEX	rs1111875	Variant not found	T	
HHEX	rs5015480	TT+	T	
HIVEP2	rs761993070	CC+	A,G,T	
HIVEP2	rs878853251	Variant not found		
HLA-DRA	rs3135391	CC-	A	
HLA-DRA	rs61731956	GG+	A	
HLA-DRB1	rs3135388	CC-	A	
HLA-DRB1	rs660895	GG+	G	
HNF1A	rs1169300	Variant not found	A	
HNF1A	rs2464196	Variant not found	A	
HSPD1	rs2340690	Variant not found	G	
HSPD1	rs2565163	Variant not found	A,C	
HSPD1	rs788016	Variant not found	A	
HSPE1	rs2305560	Variant not found	T	
IFNL4	rs12979860	CC+	C	
IGF1R	rs3743262	Variant not found	T	
IGF2BP2	rs4402960	GG+	T	
IL-2RA	rs12722489	AG-	T	
IL-2RA	rs12722561	Variant not found	A,T	
IL-2RA	rs2104286	AG-	C	
IL-4	rs2243250	CC+	T	
IL-6	rs1800795	CG+	G	
IL-7R	rs6897932	CC+	T	
IL4R	rs1801275	Variant not found	G	
INSIG2	rs7566605	GG+	C	
INTERGENIC	rs10445747	Variant not found	G	
INTERGENIC	rs10757278	GG+	G	
INTERGENIC	rs12661968	TT+	C	
INTERGENIC	rs13192841	GG+	A	
INTERGENIC	rs1333049	CC+	C	
INTERGENIC	rs1937506	Variant not found	A	
INTERGENIC	rs198358	Variant not found	C	
INTERGENIC	rs2119704	CC+	A	
INTERGENIC	rs2383207	GG+	G	
INTERGENIC	rs2820037	AA+	T	
INTERGENIC	rs3129934	Variant not found	C	
INTERGENIC	rs383830	Variant not found	T	
INTERGENIC	rs428668	Variant not found	C	
INTERGENIC	rs4698048	Variant not found	G	
INTERGENIC	rs4728142	AG+	A	
INTERGENIC	rs501120	AG-	C	
INTERGENIC	rs632793	Variant not found	G	
INTERGENIC	rs6997709	Variant not found	A,T	
INTERGENIC	rs7250581	Variant not found	G	
INTERGENIC	rs751891	CC-	T	
INTERGENIC	rs791595	AG+	G	
INTERGENIC	rs7923837	AA+	A,T	
INTERGENIC	rs9287638	CC+	A	
IRF4	rs12203592	CC+	T	
IRF5	rs3807306	Variant not found	A,T	
IRS1	rs2943641	CT+	C	
ITGA11	rs7174755	TT+	C,G	
ITGB3	rs5918	TT+	C	
JAG1	rs28939668	Variant not found	T	
JAZF1	rs1635852	CT+	C	
KCNE1	rs1805127	AG-	A,C,G	
KCNE2	rs2234916	AA+	G	
KCNE3	rs2270676	CT-	G	
KCNJ11	rs5215	TT+	T	
KCNJ11	rs5219	CC+	T	
KCNQ1	rs104894252	GG+	A,C	
KCNQ1	rs1057128	Variant not found	A	
KCNQ1	rs2283228	AA+	C	
KL	rs9527025	Variant not found	C,T	
KL	rs9536314	TT+	A,G	
KLC1	rs8702	Variant not found	G	

Gene	SNP	Genotype	Rare Allele	Result
KLRB1	rs4763655	Variant not found	A	⚪
LAG3	rs870849	CT+	C	🟢
LEPR	rs1137101	AA+	G	🟢
LIPA	rs1051338	Variant not found	G	⚪
LIPA	rs1131706	Variant not found	T	⚪
LIPA	rs3802656	Variant not found	A	⚪
LMNA	rs553016	GG-	G,T	🟢
LRP8	rs5174	GG-	T	🔵
M6PR	rs1805762	Variant not found	G,T	⚪
MACROD2	rs398124654	Variant not found	C	⚪
MALT1	rs587777337	Variant not found	C	⚪
MAOA	rs1137070	TT+	C	🟢
MAOA	rs3027399	GG+	C	🟢
MAOA	rs909525	GG-	T	🟠
MC1R	rs1805005	GG+	T	🟢
MC1R	rs1805007	CC+	T	🟢
MC1R	rs1805008	CC+	T	🟢
MC1R	rs1805009	GG+	A,C	🟢
MDM2	rs2279744	Variant not found	G	⚪
MERTK	rs119489105	Variant not found	T	⚪
MERTK	rs527236083	Variant not found		⚪
MMP3	rs3025058	DI+	G	🔴
MMP9	rs17576	Variant not found	G	⚪
MMP9	rs3918242	Variant not found	T	⚪
MOV10	rs2932538	CC-	C,G	🟢
MPV17L2	rs874628	TT-	G,T	🟢
MRAS	rs2306374	TT+	C	🟢
MTHFD1	rs1076991	AG-	C,G	🟢
MTHFD1L	rs11754661	GG+	A,T	🟢
MTHFD1L	rs17349743	TT+	C	🟢
MTHFD1L	rs6922269	AG+	A	🟡
MTHFD1L	rs803422	Variant not found	C,G	⚪
MTHFR	rs1476413	AG-	G,T	🟢
MTHFR	rs17037390	Variant not found	A	⚪
MTHFR	rs1801131	AC-	G	🟠
MTHFR	rs1801133	CC-	A	🟢
MTHFR	rs2066470	Variant not found	A,C	⚪
MTHFR	rs4846049	Variant not found	A,G	⚪
MTNR1B	rs10830963	CC+	G	🟢
MTRR	rs1801394	AA+	G	🟢
MTTP	rs3816873	Variant not found	C	⚪
MYBPC1	rs11110912	Variant not found	G	⚪
MYBPC3	rs11570112	CC-	A,C	🟢
MYO16	rs17485138	Variant not found	T	⚪
NADSYN1	rs12785878	GG+	G	🔴
NAF1	rs7675998	GG+	G,T	🟢
NCKAP5	rs10193871	Variant not found	C	⚪
NEDD4L	rs2288774	CT+	A,C	🟢
NEDD4L	rs3865418	CC+	C	🟢
NEDD4L	rs4149601	AA+	A	🟢
NFE2L2	rs35652124	CT+	C	🟢
NFE2L2	rs6721961	GG+	C,G	🟢
NGF	rs11466112	CC-	A	🟢
NGF	rs6330	CC-	A	🟢
NLRP1	rs115799546	Variant not found	G,T	⚪
NOS3	rs1799983	GG+	T	🟢
NOS3	rs1800779	AA+	G	🟢
NOS3	rs1800783	Variant not found	C,G,T	⚪
NOS3	rs207044	Variant not found	T	⚪
NOS3	rs3918188	Variant not found	A,T	⚪
NOTCH2	rs10923931	Variant not found	T	⚪
NOTCH2	rs2793831	Variant not found	C	⚪
NOV	rs2071518	CC+	T	🟢
NPPA	rs5065	AA+	G	🟢
NPPA	rs5068	Variant not found	G,T	⚪
NR2F2-AS1	rs2398162	Variant not found	G	⚪
NR3C1	rs6198	Variant not found	C	⚪
OLR1	rs11053646	Variant not found	G	⚪

Gene	SNP	Genotype	Rare Allele	Result
OPRM1	rs10485057	Variant not found	G	
OPRM1	rs17174794	Variant not found	G,T	
OPRM1	rs1799971	GG+	G	
PAX4	rs2233578	Variant not found	A,T	
PAX4	rs2233580	GG-	T	
PCK1	rs8192708	AG+	G	
PDE4B	rs1321172	Variant not found	G	
PECAM1	rs281865545	Variant not found	G,T	
PEX5L	rs7630877	GG+	A,C	
PHACTR1	rs9349379	AA+	A	
PIK3CA	rs104886003	GG+	A,C	
PIK3CA	rs1057518041	Variant not found		
PIK3CA	rs1057519699	Variant not found	A	
PIK3CA	rs1057519925	Variant not found	A,C	
PIK3CA	rs1057519926	Variant not found	T	
PIK3CA	rs1057519927	Variant not found	C,G,T	
PIK3CA	rs1057519928	Variant not found	C	
PIK3CA	rs1057519929	Variant not found	A	
PIK3CA	rs1057519930	Variant not found	T	
PIK3CA	rs1057519931	Variant not found	C	
PIK3CA	rs1057519932	Variant not found	G	
PIK3CA	rs1057519933	Variant not found	G	
PIK3CA	rs1057519934	Variant not found	C	
PIK3CA	rs1057519935	Variant not found	G	
PIK3CA	rs1057519936	Variant not found	G,T	
PIK3CA	rs1057519937	Variant not found	C	
PIK3CA	rs1057519938	Variant not found	C,T	
PIK3CA	rs1057519939	Variant not found	C	
PIK3CA	rs1057519940	Variant not found	T	
PIK3CA	rs1057519941	Variant not found	C,G	
PIK3CA	rs1057519942	GG+	A	
PIK3CA	rs1064793349	Variant not found	A	
PIK3CA	rs1064793663	Variant not found	A	
PIK3CA	rs1064793732	Variant not found	A	
PIK3CA	rs1064793838	Variant not found	G	
PIK3CA	rs1064795304	Variant not found	G	
PIK3CA	rs121913272	Variant not found	C,G	
PIK3CA	rs121913273	Variant not found	A,C	
PIK3CA	rs121913274	Variant not found	C,G,T	
PIK3CA	rs121913275	Variant not found	A,C,T	
PIK3CA	rs121913277	Variant not found	A,C	
PIK3CA	rs121913279	Variant not found	G,T	
PIK3CA	rs121913281	Variant not found	T	
PIK3CA	rs121913282	Variant not found	C	
PIK3CA	rs121913283	Variant not found	A,T	
PIK3CA	rs121913284	Variant not found	A,G	
PIK3CA	rs121913285	Variant not found	G	
PIK3CA	rs121913286	Variant not found	A,G	
PIK3CA	rs121913287	Variant not found	A	
PIK3CA	rs121913288	Variant not found	G	
PIK3CA	rs12494623	Variant not found	G,T	
PIK3CA	rs141178472	Variant not found	C	
PIK3CA	rs17849071	Variant not found	G	
PIK3CA	rs17849079	Variant not found	T	
PIK3CA	rs2699887	CT+	T	
PIK3CA	rs3729679	Variant not found	G	
PIK3CA	rs3729687	Variant not found	A	
PIK3CA	rs397514565	Variant not found	A	
PIK3CA	rs397517200	Variant not found		
PIK3CA	rs397517201	Variant not found	C,G,T	
PLCL2	rs10510468	Variant not found	A,T	
PLPP3	rs17114036	AA+	G	
PPARG	rs13306747	Variant not found	A,G,T	
PPARG	rs17036170	GG+	A	
PPARG	rs1801282	CG+	C	
PPARG	rs2197423	Variant not found	A	
PPARG	rs4684847	Variant not found	T	
PPARG	rs6802898	Variant not found	T	

Gene	SNP	Genotype	Rare Allele	Result
PPARGC1A	rs3774923	Variant not found	T	⚪
PPARGC1A	rs8192678	GG-	T	🟢
PSMA6	rs1048990	CG+	G,T	🟢
PSRC1	rs599839	AA+	A,C	🟡
PTEN	rs121909229	GG+	A,C,T	🟢
PTEN	rs121909232	CC+	G	🟢
PTEN	rs371387815	Variant not found	G,T	⚪
PTH	rs6256	AC-	A,T	🟠
PTPRD	rs10116682	Variant not found	A	⚪
PTPRD	rs10481625	Variant not found	A,C,G	⚪
PTPRS	rs1143699	Variant not found	A	⚪
RASGRP1	rs7403531	CC+	C,G	🟢
RBMS1	rs6718526	Variant not found	C	⚪
RHOU	rs6426514	GG+	A	🟢
RNASEL	rs3738579	CT-	G	🔵
RNASEL	rs486907	Variant not found	T	⚪
RPL5	rs6604026	Variant not found	C,G	⚪
RPS6KB1	rs630923	CC+	A	🟢
RPSAP52	rs1531343	CC+	C,T	🟢
RYR2	rs34967813	AA+	G	🟢
SAMD12	rs17749211	Variant not found	T	⚪
SCN5A	rs1805124	GG-	T	🟢
SDHAF4	rs1048886	AA+	G	🟢
SEZ6L	rs688034	Variant not found	T	⚪
SH2B3	rs3184504	CC+	A,C,G	🟢
SHMT1	rs1979277	AG+	A	🟢
SIRT1	rs3758391	Variant not found	C	⚪
SIRT1	rs4746720	Variant not found	C	⚪
SLC2A14	rs12815313	Variant not found	G,T	⚪
SLC30A7	rs11581062	AA+	G	🟢
SLC30A8	rs13266634	CC+	A,T	🔴
SLC39A6	rs1050631	CT-	A	🟠
SLC45A2	rs185146	CT+	T	🟠
SMAD3	rs17228212	TT+	C	🟢
SOD2	rs2758331	Variant not found	A	⚪
SOD2	rs4880	CT-	G	🟢
SPIRE2	rs35096708	Variant not found	A	⚪
STAT4	rs10181656	CG+	C	🟡
STK39	rs3754777	Variant not found	T	⚪
STK39	rs6749447	GT+	G	🟢
SYK	rs10993738	Variant not found	C	⚪
TAP2	rs1800454	GG-	T	🟢
TAP2	rs241428	AA-	A,C,G	🟢
TAP2	rs241448	Variant not found	G	⚪
TCF7L2	rs12255372	GG+	T	🟢
TCF7L2	rs7901695	TT+	C	🟢
TCF7L2	rs7903146	CC+	G,T	🟢
TERT	rs2736098	AG-	T	🟢
TERT	rs2736100	TT-	A	🟠
TGFBR3	rs1805110	CC-	A	🟢
THADA	rs7578597	TT+	C	🟢
THBS2	rs8089	Variant not found	C	⚪
TLR4	rs4986790	AA+	G,T	🟢
TLR4	rs4986791	CC+	T	🟢
TMPO	rs17028450	CC+	T	🟢
TNF	rs1800629	GG+	A	🟢
TNFSF14	rs2291667	CC-	A	🟢
TNFSF14	rs344560	GG-	C	🟢
TNFSF4	rs1234313	AG+	G	🟢
TNFSF4	rs1234315	Variant not found	T	⚪
TNFSF4	rs3850641	Variant not found	G	⚪
TNFSF4	rs3861950	TT+	C	🟢
TRIB3	rs2295490	AG+	G,T	🟡
TRPM6	rs11144134	CT+	C	🟠
TTN	rs16866412	Variant not found	A	⚪
TTN	rs2244492	GG-	T	🟢
TTR	rs1800458	Variant not found	A	⚪
TXNRD2	rs5748469	AA+	A	🟢

Gene	SNP	Genotype	Rare Allele	Result
TYR	rs28940879	Variant not found	A,C	⚪
UBE2E2	rs7612463	AC+	A,G	🟢
VDR	rs1057521095	Variant not found	A	⚪
VDR	rs11574010	Variant not found	T	⚪
VDR	rs1544410	AG-	C,T	🟡
VDR	rs2228570	CC-	C,T	🟢
VDR	rs731236	CT-	G	🟢
VDR	rs7975232	AC+	A	🟢
VPS26A	rs4812829	AG+	A	🟢
VPS33B	rs121434383	Variant not found	A	⚪
WFS1	rs10010131	Variant not found	G	⚪
WFS1	rs10012946	Variant not found	C	⚪
WSCD2	rs3794260	Variant not found	A	⚪
WSCD2	rs9739493	CC+	C,G	🟢
XPC	rs2228000	CC-	A	🟢
XPC	rs2228001	AA-	T	🟢
XRCC1	rs1799782	CT-	A	🟡
ZNF767P	rs354033	CC-	A	🟢

Vitamin E (Tocopherol)

Gene	SNP	Genotype	Rare Allele	Result
A2M	rs669	AA-	C	🟢
ABCA2	rs908832	Variant not found	C,G	⚪
ABCA7	rs113809142	Variant not found	G	⚪
ABCA7	rs115550680	AA+	G	🟢
ABCA7	rs200538373	Variant not found	A,C	⚪
ABCA7	rs3752246	Variant not found	C,T	⚪
ABCA7	rs3764650	TT+	G	🟢
ABCA7	rs78117248	Variant not found	G	⚪
ACE	rs1799752	Variant not found		⚪
ACE	rs4343	AG+	A	🟠
ADD1	rs4961	GT+	A,T	🟠
ADRB2	rs1800888	CC+	T	🟢
AGAP2	rs12368653	GG+	A,T	🟢
AHI1	rs117447608	Variant not found	A	⚪
AHI1	rs121434349	Variant not found	A,T	⚪
AHI1	rs121434350	Variant not found	T	⚪
ALK	rs7577363	Variant not found	A	⚪
ANKRD1	rs10975200	Variant not found	C,G	⚪
AOC1	rs10156191	Variant not found	T	⚪
APH1B	rs1047552	Variant not found	A,G	⚪
APOA5	rs12272004	CC+	A	🔴
APOC1	rs4420638	AA+	G	🟢
APOE	rs7412	TT+	T	🔴
APOE4	rs429358	TT+	C	🟢
APP	rs193922916	Variant not found	A,C	⚪
APP	rs281865161	Variant not found	A,G	⚪
APP	rs63749964	Variant not found	C	⚪
APP	rs63750064	Variant not found	G,T	⚪
APP	rs63750151	Variant not found	G,T	⚪
APP	rs63750399	Variant not found	A,C	⚪
APP	rs63750643	Variant not found	C	⚪
APP	rs63750734	Variant not found	T	⚪
APP	rs63750847	Variant not found	T	⚪
APP	rs63750868	Variant not found	C,G	⚪
APP	rs63751039	Variant not found	C	⚪
APP	rs63751122	Variant not found	G	⚪
ARHGAP20	rs326946	TT-	C	🟢
ARVCF	rs5993891	Variant not found	T	⚪
ASIC2	rs9901756	Variant not found	C	⚪
ATP2B1	rs2681472	CT-	G	🟢
ATP8B4	rs10519262	Variant not found	A	⚪
BACE1	rs638405	Variant not found	G	⚪
BAG3	rs2234962	CT+	C	🟢
BATF	rs2300603	TT+	C	🟢
BDNF	rs2049045	Variant not found	A,C	⚪
BDNF	rs6265	GG-	T	🟢
BIN1	rs744373	CT-	G	🟠

Gene	SNP	Genotype	Rare Allele	Result
BRAP	rs3782886	AA-	C	
BRCA2	rs1801406	Variant not found	C,G	
BTD	rs104893686	TT+	G	
BTD	rs104893687	CC+	T	
C1ORF106	rs7522462	AG+	A	
CACNB2	rs2228645	Variant not found	A,T	
CALHM1	rs2986017	Variant not found	G	
CASC17	rs1859962	GG+	T	
CASC21	rs16902104	CC+	G,T	
CASC8	rs1447295	CC+	C,T	
CASC8	rs6983267	GG+	T	
CAV3	rs1008642	Variant not found	A,G,T	
CBLB	rs12487066	Variant not found	C	
CCL2	rs1024611	CT-	G	
CD2AP	rs10948363	AA+	G	
CD2AP	rs9349407	GG+	C	
CD58	rs12044852	CC+	A	
CD86	rs1129055	GG+	A	
CD86	rs9282641	GG+	A	
CDH1	rs16260	AC+	A	
CDH13	rs8055236	GG+	A,C,T	
CDKN1B	rs34330	CT+	C	
CDKN2B-AS1	rs10116277	TT+	T	
CDKN2B-AS1	rs1011970	GT+	T	
CDKN2B-AS1	rs1063192	TT-	A,T	
CDKN2B-AS1	rs10757272	TT+	T	
CDKN2B-AS1	rs10757274	GG+	G	
CDKN2B-AS1	rs1537375	Variant not found	C,G	
CDKN2B-AS1	rs2383206	Variant not found	G	
CETP	rs2303790	AA+	G	
CETP	rs5882	AG+	A	
CFH	rs1061170	TT+	T	
CHAT	rs733722	CC+	A,G,T	
CHEK2	rs17879961	TT-	C,G	
CHRDL1	rs387906713	Variant not found	A	
CHRDL1	rs387906714	Variant not found	A	
CHST12	rs6952809	CC+	C	
CLEC16A	rs6498169	Variant not found	A	
CLEC16A	rs725613	Variant not found	G	
CLSTN2	rs17411949	CC+	T	
CLU	rs11136000	CC+	C	
CNTNAP2	rs1057520549	Variant not found	T	
CNTNAP2	rs1057520743	Variant not found	G	
CNTNAP2	rs1085307838	Variant not found	C	
COMT	rs4680	AG+	A	
CPS1	rs1047891	CC+	A	
CR1	rs3818361	CC-	G	
CR1	rs6656401	GG+	G,T	
CRP	rs3091244	Variant not found	A,T	
CTNNA3	rs2306402	Variant not found	T	
CYP17A1	rs2486758	Variant not found	C	
CYP24A1	rs2296241	GG+	A	
CYP24A1	rs480995	Variant not found	G	
CYP24A1	rs4809957	AG+	G	
CYP24A1	rs6068816	CT+	T	
CYP2R1	rs117913124	Variant not found	A	
CYP3A4	rs2740574	AA-	T	
CYP3A4	rs4646438	---		
CYP3A4	rs55785340	AA+	G	
CYP4F2	rs2108622	CC+	T	
DAB2IP	rs1571801	AC-	T	
DAPK1	rs4877365	Variant not found	A	
DAPK1	rs4878104	Variant not found	T	
DBC1	rs10984447	AA+	G	
DKK1	rs1881747	Variant not found	C	
DKKL1	rs2303759	TT+	G	
DLEU1	rs2762051	CC+	T	
DMD	rs104894788	GG-	T	

Gene	SNP	Genotype	Rare Allele	Result
DMD	rs1800278	AA-	C	
DMD	rs1801187	GG-	T	
DNAJC5B	rs13279522	TT+	C	
DPP6	rs10239794	Variant not found	A,C	
DSG2	rs2230234	AA+	G,T	
EHBP1	rs2710646	Variant not found	A	
EIF2AK2	rs2254958	Variant not found	A	
ELAC2	rs4792311	GG+	A,C	
ENTPD7	rs911541	Variant not found	A	
ERG	rs989554	Variant not found	A	
ESR2	rs2987983	Variant not found	G	
EVI5	rs10735781	Variant not found	C	
EVI5	rs6680578	Variant not found	A	
F12	rs1801020	CT-	G	
F7	rs6046	CT-	A	
FAM124A	rs10492519	Variant not found	C,G	
FAM171A2	rs5848	Variant not found	T	
FAM69A	rs11164838	Variant not found	T	
FAM69A	rs7536563	Variant not found	G	
FCHSD1	rs251177	Variant not found	C	
FGF20	rs1721100	Variant not found	G,T	
FGFR4	rs2011077	Variant not found	T	
FGFR4	rs351855	CC-	A	
FLJ10986	rs10493256	Variant not found	T	
FLJ10986	rs1470407	CT+	C	
FLJ10986	rs333662	Variant not found	A	
FLJ10986	rs6587852	Variant not found	C	
FLJ25967	rs2331291	Variant not found	T	
FMN2	rs17672135	TT+	C	
FRMD4A	rs10906466	AG+	C,G	
FYCO1	rs1545985	Variant not found	A	
FYCO1	rs7652331	Variant not found	A,C	
GAB2	rs2373115	GG-	A	
GATA2	rs3803	Variant not found	A	
GATA4	rs104894073	Variant not found	A,G,T	
GATA4	rs104894074	Variant not found	A	
GCKR	rs1260326	CT+	C	
GOLM1	rs10868366	GT+	T	
GOLM1	rs7019241	CT+	G,T	
GPX1	rs1050450	CC-	A	
GRN	rs850713	Variant not found	A,T	
GRN	rs9897526	Variant not found	A,C	
GSTP1	rs1695	GG+	G	
HLA-DRA	rs3135391	CC-	A	
HLA-DRA	rs61731956	GG+	A	
HLA-DRB1	rs3135388	CC-	A	
HLA-DRB1	rs660895	GG+	G	
HNF1B	rs3760511	Variant not found	A,T	
HSPD1	rs2340690	Variant not found	G	
HSPD1	rs2565163	Variant not found	A,C	
HSPD1	rs788016	Variant not found	A	
HSPE1	rs2305560	Variant not found	T	
HTRA1	rs11200638	AG+	A	
IDE	rs4646954	Variant not found	A	
IL-10	rs1800896	AG-	C	
IL-18RAP	rs3771150	Variant not found	A	
IL-2RA	rs12722489	AG-	T	
IL-2RA	rs12722561	Variant not found	A,T	
IL-2RA	rs2104286	AG-	C	
IL-4	rs2243250	CC+	T	
IL-6	rs1800795	CG+	G	
IL-7R	rs6897932	CC+	T	
INTERGENIC	rs10086908	Variant not found	C	
INTERGENIC	rs10260404	CT+	C	
INTERGENIC	rs1027615	Variant not found	A	
INTERGENIC	rs10505483	AG-	T	
INTERGENIC	rs10757278	GG+	G	
INTERGENIC	rs10896449	AA+	G	

Gene	SNP	Genotype	Rare Allele	Result
INTERGENIC	rs12473579	GG+	A	🟢
INTERGENIC	rs13036957	Variant not found	A	⚪
INTERGENIC	rs13192841	GG+	A	🟢
INTERGENIC	rs1333049	CC+	C	🔴
INTERGENIC	rs16901979	AC+	A	🔴
INTERGENIC	rs17027230	Variant not found	T	⚪
INTERGENIC	rs2119704	CC+	A	🟢
INTERGENIC	rs2279420	Variant not found	G	⚪
INTERGENIC	rs2383207	GG+	G	🟠
INTERGENIC	rs2836061	CT+	T	🟡
INTERGENIC	rs3129934	Variant not found	C	⚪
INTERGENIC	rs383830	Variant not found	T	⚪
INTERGENIC	rs4054823	Variant not found	C	⚪
INTERGENIC	rs4728142	AG+	A	🟢
INTERGENIC	rs501120	AG-	C	🟡
INTERGENIC	rs5945572	AG+	G	🟡
INTERGENIC	rs6690993	Variant not found	A	⚪
INTERGENIC	rs6700125	Variant not found	A,C	⚪
INTERGENIC	rs7250581	Variant not found	G	⚪
INTERGENIC	rs7965399	TT+	A,C	🟢
INTERGENIC	rs905080	Variant not found	G	⚪
INTERGENIC	rs9886784	Variant not found	C,T	⚪
IRF5	rs3807306	Variant not found	A,T	⚪
ITGA2	rs1126643	CC+	T	🟢
ITGA6	rs10207654	Variant not found	G	⚪
ITGB3	rs5918	TT+	C	🟢
JAG1	rs28939668	Variant not found	T	⚪
JAZF1	rs10486567	AG+	A	🟡
KCNE1	rs1805127	AG-	A,C,G	🟡
KCNE2	rs2234916	AA+	G	🟢
KCNE3	rs2270676	CT-	G	🟢
KCNQ1	rs1057128	Variant not found	A	⚪
KIAA1211	rs629242	Variant not found	T	⚪
KL	rs9527025	Variant not found	C,T	⚪
KL	rs9536314	TT+	A,G	🟢
KLC1	rs8702	Variant not found	G	⚪
KLF6	rs3750861	CC+	T	🟢
KLRB1	rs4763655	Variant not found	A	⚪
LAG3	rs870849	CT+	C	🟢
LDLR	rs688	CC+	T	🟢
LIPA	rs1051338	Variant not found	G	⚪
LIPA	rs1131706	Variant not found	T	⚪
LIPA	rs3802656	Variant not found	A	⚪
LIPC	rs3825776	Variant not found	C	⚪
LOXHD1	rs988213	Variant not found	G	⚪
LRP6	rs2160525	AG+	G	🟢
LRP8	rs5174	GG-	T	🔵
LTA	rs1799724	CT+	T	🟠
MAGEC3	rs176026	Variant not found	A	⚪
MAGI2	rs757863	Variant not found	G	⚪
MALT1	rs587777337	Variant not found	C	⚪
MAOA	rs1137070	TT+	C	🟢
MAOA	rs3027399	GG+	C	🟢
MAOA	rs909525	GG-	T	🟠
MERTK	rs119489105	Variant not found	T	⚪
MERTK	rs527236083	Variant not found		⚪
MME	rs1836915	Variant not found	C	⚪
MMP3	rs3025058	DI+	G	🔴
MMP9	rs17576	Variant not found	G	⚪
MMP9	rs3918242	Variant not found	T	⚪
MPO	rs12316150	Variant not found	T	⚪
MPO	rs2333227	TT+	T	🟢
MPV17L2	rs874628	TT-	G,T	🟢
MRAS	rs2306374	TT+	C	🟢
MS4A6A	rs610932	CC-	G	🟢
MSMB	rs10993994	AA-	G	🟢
MTHFD1	rs1076991	AG-	C,G	🟢
MTHFD1L	rs11754661	GG+	A,T	🟢

Gene	SNP	Genotype	Rare Allele	Result
MTHFD1L	rs17349743	TT+	C	🟢
MTHFD1L	rs6922269	AG+	A	🟡
MTHFD1L	rs803422	Variant not found	C,G	⚪
MYBPC3	rs11570112	CC-	A,C	🟢
NAF1	rs7675998	GG+	G,T	🟢
NCKAP5	rs10193871	Variant not found	C	⚪
NKAIN3	rs7834588	CT+	T	🟢
NLRP1	rs115799546	Variant not found	G,T	⚪
NOS3	rs1800779	AA+	G	🟢
NOS3	rs1800783	Variant not found	C,G,T	⚪
NOS3	rs207044	Variant not found	T	⚪
NOS3	rs3918188	Variant not found	A,T	⚪
NPPA	rs5065	AA+	G	🟢
OLR1	rs1050283	Variant not found	A	⚪
OLR1	rs11053646	Variant not found	G	⚪
PCAT19	rs11672691	AA+	T	🟢
PCDH11X	rs5984894	AA+	G	🟢
PCK1	rs8192708	AG+	G	🟡
PDE4B	rs1321172	Variant not found	G	⚪
PECAM1	rs281865545	Variant not found	G,T	⚪
PEX6	rs387906809	Variant not found	G	⚪
PEX6	rs61753224	Variant not found	A	⚪
PHACTR1	rs9349379	AA+	A	🟢
PICALM	rs10792832	AG+	G	🟡
PICALM	rs3851179	AG-	C	🔵
PLAU	rs2227562	GG+	A	🟢
PLAU	rs2227564	TT+	C	🟢
PLCL2	rs10510468	Variant not found	A,T	⚪
PLD3	rs145999145	GG+	A	🔵
PLPP3	rs17114036	AA+	G	🟢
POLN	rs1923775	TT+	T	🟢
PON2	rs12704795	Variant not found	G	⚪
PPP1R3B	rs3748140	GG-	T	🟢
PPP1R3B	rs9987289	GG+	G	🟢
PRRC2C	rs2421847	AA+	G	🟢
PSEN1	rs121917807	Variant not found	A	⚪
PSEN1	rs63749805	Variant not found	G,T	⚪
PSEN1	rs63749824	CC+	G,T	🟢
PSEN1	rs63749911	Variant not found	C	⚪
PSEN1	rs63749962	Variant not found	G	⚪
PSEN1	rs63749967	Variant not found	C	⚪
PSEN1	rs63750004	Variant not found	A,C	⚪
PSEN1	rs63750218	Variant not found	C,G	⚪
PSEN1	rs63750299	Variant not found	G	⚪
PSEN1	rs63750306	Variant not found	C,G,T	⚪
PSEN1	rs63750325	Variant not found	A	⚪
PSEN1	rs63750391	Variant not found	A,C,T	⚪
PSEN1	rs63750450	Variant not found	G	⚪
PSEN1	rs63750526	Variant not found	A	⚪
PSEN1	rs63750550	Variant not found	G,T	⚪
PSEN1	rs63750730	Variant not found	T	⚪
PSEN1	rs63750907	Variant not found	T	⚪
PSEN1	rs63751106	Variant not found	A,C	⚪
PSEN1	rs63751272	Variant not found	C,T	⚪
PSEN1	rs63751441	Variant not found	G,T	⚪
PSEN1	rs63751484	Variant not found	C	⚪
PSEN2	rs150400387	Variant not found	G,T	⚪
PSEN2	rs574125890	Variant not found	A,T	⚪
PSEN2	rs61757781	Variant not found	G	⚪
PSEN2	rs63750197	CC+	T	🟢
PSEN2	rs63750812	Variant not found	A	⚪
PSEN2	rs775145486	Variant not found	G	⚪
PSMA6	rs1048990	CG+	G,T	🟢
PSRC1	rs599839	AA+	A,C	🟡
RNASEL	rs3738579	CT-	G	🔵
RNASEL	rs486907	Variant not found	T	⚪
RPL5	rs6604026	Variant not found	C,G	⚪
RPS6KB1	rs630923	CC+	A	🟢

Gene	SNP	Genotype	Rare Allele	Result
RYR2	rs34967813	AA+	G	🟢
SAMD12	rs17749211	Variant not found	T	⚪
SCN5A	rs1805124	GG-	T	🟢
SELENOP	rs3877899	Variant not found		⚪
SEZ6L	rs688034	Variant not found	T	⚪
SH2B3	rs3184504	CC+	A,C,G	🟢
SLC30A7	rs11581062	AA+	G	🟢
SMAD3	rs17228212	TT+	C	🟢
SOD1	rs17880487	Variant not found	T	⚪
SOD3	rs1799895	CC+	G	🟢
SOD3	rs2855262	TT+	C	🟢
SORL1	rs12285364	Variant not found	T	⚪
SORL1	rs2070045	Variant not found	G	⚪
SORL1	rs641120	Variant not found	A	⚪
SORL1	rs661057	Variant not found	C	⚪
SORL1	rs668387	Variant not found	A,T	⚪
SORL1	rs689021	Variant not found	A	⚪
SYK	rs10993738	Variant not found	C	⚪
TAP2	rs241448	Variant not found	G	⚪
TCF2	rs4430796	AG+	G	🟢
TCF7L2	rs12255372	GG+	T	🟢
TET1	rs5030882	Variant not found	T	⚪
THBS2	rs8089	Variant not found	C	⚪
TLR4	rs4986790	AA+	G,T	🟢
TLR4	rs4986791	CC+	T	🟢
TM2D3	rs139709573	Variant not found	A	⚪
TMPO	rs17028450	CC+	T	🟢
TMPRSS2	rs12329760	CT+	T	🟢
TNF	rs1800629	GG+	A	🟢
TNFSF14	rs2291667	CC-	A	🟢
TNFSF14	rs344560	GG-	C	🟢
TNFSF4	rs1234313	AG+	G	🟢
TNFSF4	rs1234315	Variant not found	T	⚪
TNFSF4	rs3850641	Variant not found	G	⚪
TNFSF4	rs3861950	TT+	C	🟢
TREM2	rs28937876	Variant not found	A	⚪
TREM2	rs5143332484	Variant not found		⚪
TREM2	rs75932628	CC+	A,T	🟢
TRPM7	rs8042919	Variant not found	A,T	⚪
TTN	rs16866412	Variant not found	A	⚪
TTN	rs2244492	GG-	T	🟢
TTPA	rs121917849	Variant not found	C	⚪
TTPA	rs121917850	GG-	T	🟢
TTPA	rs121917851	CC-	A	🟢
TTR	rs1800458	Variant not found	A	⚪
TXNRD2	rs5748469	AA+	A	🟢
VDR	rs2107301	Variant not found	A	⚪
VDR	rs2238135	Variant not found	G	⚪
XRCC1	rs25489	GG-	G,T	🟢
ZNF767P	rs354033	CC-	A	🟢
ZNF827	rs13149290	TT+	T	🟢
ZPR1	rs964184	CC+	C	🟢

Vitamin K

Gene	SNP	Genotype	Rare Allele	Result
ABCA1	rs1883025	AG-	T	🟢
ACE	rs4343	AG+	A	🟠
ADD1	rs4961	GT+	A,T	🟠
ADD1	rs4963	CG+	G,T	🟢
ADD2	rs3755351	CC-	T	🟢
AGT	rs11568020	Variant not found	A,T	⚪
AGT	rs121912702	Variant not found	A	⚪
AGT	rs699	CT-	G	🟠
AGTR1	rs104893677	Variant not found	T	⚪
AGTR1	rs1492099	Variant not found	A,C	⚪
AGTR1	rs5186	AA+	C	🟢
ARHGEF3	rs7646054	Variant not found	G	⚪
ARMS2	rs10490924	GT+	T	🔴

Gene	SNP	Genotype	Rare Allele	Result
ARMS2	rs3750847	Variant not found	T	⚪
ATP2B1	rs7965584	AG+	G	🟢
ATP6V1B1	rs2266917	Variant not found	T	⚪
BAG6	rs3117583	TT-	G	🟢
BCAT1	rs7961152	Variant not found	C	⚪
BDNF	rs13306221	Variant not found	T	⚪
BMP2	rs235754	Variant not found	A,G	⚪
BMPR1B	rs11097457	Variant not found	G	⚪
BMPR1B	rs121434417	Variant not found	A	⚪
BMPR1B	rs1434536	Variant not found	T	⚪
BMPR2	rs1006246556	Variant not found	A,T	⚪
C2	rs547154	CC-	T	🟢
C2	rs9332739	GG+	A,C	🟢
C3	rs2230199	CG-	C,T	🟠
C3	rs2230201	Variant not found	G,T	⚪
C3	rs2230205	AG-	T	🟢
C3	rs2287845	Variant not found	A	⚪
CALCA	rs3781719	Variant not found	G	⚪
CASZ1	rs880315	AA-	C	🟢
CBS	rs1801181	Variant not found	A	⚪
CBS	rs2851391	CT+	C	🟢
CBS	rs28934891	GG-	T	🟢
CBS	rs5742905	TT-	G	🟢
CETP	rs1532624	TT-	A	🟢
CETP	rs17231520	Variant not found	A	⚪
CETP	rs1864163	GG+	A	🔵
CETP	rs2303790	AA+	G	🟢
CETP	rs5880	GG+	C	🟢
CETP	rs5882	AG+	A	🔵
CETP	rs708272	CT-	A	🟠
CFB	rs4151667	TT+	A	🟢
CFH	rs1061147	CC+	C	🔵
CFH	rs1061170	TT+	T	🔵
CFH	rs1065489	GT+	T	🟢
CFH	rs1329428	AG-	T	🟢
CFH	rs3753394	CT+	T	🟢
CFH	rs800292	CT-	A	🔵
CLCN6	rs13306560	Variant not found	T	⚪
CLCN6	rs17376328	Variant not found	A	⚪
CLCN6	rs3737964	Variant not found	A,C,G	⚪
COL8A1	rs13081855	GG+	T	🟢
COL8A1	rs13095226	Variant not found	C	⚪
CX3CR1	rs3732378	AG+	A	🔵
CX3CR1	rs3732379	CT+	T	🟢
CYP19A1	rs12594287	Variant not found	A	⚪
CYP19A1	rs16964201	Variant not found	T	⚪
CYP19A1	rs17703883	Variant not found	C	⚪
CYP4A11	rs1126742	Variant not found	G	⚪
CYP4F2	rs2108622	CC+	T	🟢
DAPK1	rs11141915	AC+	C	🟢
F12	rs118204454	Variant not found	G,T	⚪
F12	rs118204455	Variant not found	C	⚪
FDPS	rs2297480	AC-	G	🟢
FGD6	rs12310399	Variant not found	C	⚪
FTCDNL1	rs12615435	Variant not found	G	⚪
GAD1	rs3762555	Variant not found	A,G	⚪
GGCX	rs11676382	CC+	G	🟢
GGCX	rs28928872	Variant not found	G	⚪
GPX1	rs1050450	CC-	A	🟢
GUCY1A3	rs587777320	Variant not found	A,T	⚪
GUCY1A3	rs587777321	Variant not found	T	⚪
GUCY1A3	rs587777322	Variant not found		⚪
HIVEP2	rs761993070	CC+	A,G,T	🟢
HIVEP2	rs878853251	Variant not found		⚪
HTRA1	rs11200638	AG+	A	🟠
HTRA1	rs932275	Variant not found	A	⚪
IL-1B	rs16944	AG+	G	🟠
INTERGENIC	rs10468017	CC+	T	🟢

Gene	SNP	Genotype	Rare Allele	Result
INTERGENIC	rs12678919	AA+	G	🟢
INTERGENIC	rs1937506	Variant not found	A	⚪
INTERGENIC	rs198358	Variant not found	C	⚪
INTERGENIC	rs2820037	AA+	T	🟢
INTERGENIC	rs493258	AG-	C	🟠
INTERGENIC	rs632793	Variant not found	G	⚪
INTERGENIC	rs6997709	Variant not found	A,T	⚪
INTERGENIC	rs751891	CC-	T	🟢
ITGA11	rs7174755	TT+	C,G	🟢
LRP4	rs2306033	Variant not found	A	⚪
LRP5	rs3736228	CT+	T	🟠
LRP5	rs4988321	CT-	A,C	🟢
M6PR	rs1805762	Variant not found	G,T	⚪
MACROD2	rs398124654	Variant not found	C	⚪
MAOA	rs1137070	TT+	C	🟢
MAOA	rs3027399	GG+	C	🟢
MAOA	rs909525	GG-	T	🟠
MOV10	rs2932538	CC-	C,G	🟢
MTHFR	rs1476413	AG-	G,T	🟢
MTHFR	rs17037390	Variant not found	A	⚪
MTHFR	rs1801131	AC-	G	🟠
MTHFR	rs1801133	CC-	A	🟢
MTHFR	rs2066470	Variant not found	A,C	⚪
MTHFR	rs4846049	Variant not found	A,G	⚪
MTRR	rs1801394	AA+	G	🟢
MYBPC1	rs11110912	Variant not found	G	⚪
MYO16	rs17485138	Variant not found	T	⚪
NEDD4L	rs2288774	CT+	A,C	🟢
NEDD4L	rs3865418	CC+	C	🟢
NEDD4L	rs4149601	AA+	A	🟢
NFE2L2	rs35652124	CT+	C	🟢
NFE2L2	rs6721961	GG+	C,G	🟢
NGF	rs11466112	CC-	A	🟢
NGF	rs6330	CC-	A	🟢
NOS3	rs1799983	GG+	T	🟢
NOS3	rs1800779	AA+	G	🟢
NOS3	rs1800783	Variant not found	C,G,T	⚪
NOS3	rs3918188	Variant not found	A,T	⚪
NOTCH4	rs422951	AG-	C	🟢
NOV	rs2071518	CC+	T	🟢
NPPA	rs5068	Variant not found	G,T	⚪
NR2F2-AS1	rs2398162	Variant not found	G	⚪
NR3C1	rs2918419	Variant not found	C	⚪
NR3C1	rs6198	Variant not found	C	⚪
OPRM1	rs10485057	Variant not found	G	⚪
OPRM1	rs17174794	Variant not found	G,T	⚪
OPRM1	rs1799971	GG+	G	🔴
PPARG	rs4684847	Variant not found	T	⚪
PPARGC1A	rs8192678	GG-	T	🟢
QPCT	rs3770748	Variant not found	G	⚪
REST	rs1713985	AC-	T	🟢
REST	rs2227902	GG+	T	🟢
REST	rs3796530	Variant not found	A	⚪
SERPINF1	rs1136287	CT+	T	🟡
SHMT1	rs1979277	AG+	A	🟢
SKIV2L	rs2734331	TT-	G	🟢
SKIV2L	rs429608	GG+	A	🟢
STK39	rs3754777	Variant not found	T	⚪
STK39	rs6749447	GT+	G	🟢
TAP2	rs1800454	GG-	T	🟢
TAP2	rs241428	AA-	A,C,G	🟢
TAP2	rs241448	Variant not found	G	⚪
TLR3	rs3775291	GG-	G,T	🟠
TRPM6	rs11144134	CT+	C	🟠
VDR	rs7975232	AC+	A	🟢
VEGFA	rs3025039	CC+	T	🟢
VKORC1	rs9923231	CC+	A,G,T	🟢
WNT16	rs2707466	GG-	G,T	🟠

Gene	SNP	Genotype	Rare Allele	Result
WSCD2	rs3794260	Variant not found	A	⚪
WSCD2	rs9739493	CC+	C,G	🟢

Vitamin K2

Gene	SNP	Genotype	Rare Allele	Result
VKORC1	rs9934438	GG+	A	🟢

Oxygen Volume (O2) Max (VO2 Max)

Gene	SNP	Genotype	Rare Allele	Result
ACSL1	rs6552828	AA+	G	🟠
CREB1	rs2253206	GG+	G	🔴
CRP	rs1205	CT+	T	🔵
INTERGENIC	rs2360969	Variant not found	T	⚪
MYBPC3	rs1052373	Variant not found	T	⚪

Whey Protein

Gene	SNP	Genotype	Rare Allele	Result
ANOS1	rs5978942	Variant not found	C	⚪
GEMIN8	rs2158035	Variant not found	C	⚪
INTERGENIC	rs17616434	CC+	C	🔵
MCM6	rs4988235	AG+	A	🟢
MCM6	rs182549	TT+	T	🟢
PPARD	rs1053049	Variant not found	C	⚪
PPARD	rs2267668	AA+	A,C	🟢
PPARD	rs2016520	AA-	T	🟢
STAT6	rs324015	Variant not found	C	⚪
TLR6	rs35220466	Variant not found	T	⚪
TRIM63	rs2275950	AA-	C,G	🟢

Zeaxanthin

Gene	SNP	Genotype	Rare Allele	Result
ABCA1	rs1883025	AG-	T	🟢
ARMS2	rs10490924	GT+	T	🔴
ARMS2	rs3750847	Variant not found	T	⚪
BCO1	rs6564851	TT+	G	🟢
C2	rs547154	CC-	T	🟢
C2	rs9332739	GG+	A,C	🟢
C3	rs2230199	CG-	C,T	🟠
C3	rs2230201	Variant not found	G,T	⚪
C3	rs2230205	AG-	T	🟢
C3	rs2287845	Variant not found	A	⚪
CETP	rs1532624	TT-	A	🟢
CETP	rs17231520	Variant not found	A	⚪
CETP	rs1864163	GG+	A	🔵
CETP	rs2303790	AA+	G	🟢
CETP	rs5880	GG+	C	🟢
CETP	rs5882	AG+	A	🔵
CETP	rs708272	CT-	A	🟠
CFB	rs4151667	TT+	A	🟢
CFH	rs1061147	CC+	C	🔵
CFH	rs1061170	TT+	T	🔵
CFH	rs1065489	GT+	T	🟢
CFH	rs1329428	AG-	T	🟢
CFH	rs3753394	CT+	T	🟢
CFH	rs800292	CT-	A	🔵
COL8A1	rs13081855	GG+	T	🟢
COL8A1	rs13095226	Variant not found	C	⚪
CRYBB2	rs74315489	Variant not found		⚪
CRYBB3	rs74315490	GG+		🟢
CRYGD	rs28931605	Variant not found		⚪
CX3CR1	rs3732378	AG+	A	🔵
CX3CR1	rs3732379	CT+	T	🟢
EPHA2	rs116506614	CC+		🟢
EPHA2	rs3754334	CC-	A	🟢
FGD6	rs12310399	Variant not found	C	⚪
GJA8	rs2132397	Variant not found		⚪
GJA8	rs6657114	Variant not found		⚪
GJA8	rs6688578	Variant not found		⚪

Gene	SNP	Genotype	Rare Allele	Result
GJA8	rs7541950	Variant not found		
GJA8	rs864309684	Variant not found		
GSR	rs3594	Variant not found	A	
HTRA1	rs11200638	AG+	A	
HTRA1	rs932275	Variant not found	A	
INTERGENIC	rs10468017	CC+	T	
INTERGENIC	rs12678919	AA+	G	
INTERGENIC	rs493258	AG-	C	
KL	rs9536314	TT+	A,G	
MAF	rs121917735	Variant not found	G,T	
MAF	rs121917736	Variant not found	C	
MAF	rs786205221	Variant not found	T	
MC1R	rs1805005	GG+	T	
MC1R	rs1805007	CC+	T	
MC1R	rs1805008	CC+	T	
MC1R	rs1805009	GG+	A,C	
NOTCH4	rs422951	AG-	C	
PITX2	rs6533526	GG+	A	
REST	rs1713985	AC-	T	
REST	rs2227902	GG+	T	
REST	rs3796530	Variant not found	A	
SERPINF1	rs1136287	CT+	T	
SIRT1	rs3758391	Variant not found	C	
SKIV2L	rs2734331	TT-	G	
SKIV2L	rs429608	GG+	A	
SOD2	rs2758331	Variant not found	A	
SOD3	rs1799895	CC+	G	
SOD3	rs2855262	TT+	C	
TLR3	rs3775291	GG-	G,T	
VEGFA	rs3025039	CC+	T	

Zinc

Gene	SNP	Genotype	Rare Allele	Result
ABCA1	rs1883025	AG-	T	
ABCB1	rs10248420	AA+	G,T	
ABCB1	rs1128503	CT-	G	
ABCB1	rs11983225	TT+	C	
ABCB1	rs2032583	TT-	G	
ABCB1	rs2235015	GG-	A,T	
ABCB1	rs2235040	GG-	A,G,T	
ABCB1	rs2235067	GG-	T	
ABCB1	rs3213619	TT-	G	
ABCB1	rs4148739	AA-	C	
ACHE	rs1799805	Variant not found	T	
ACHE	rs2571598	Variant not found	G,T	
ACP7	rs472265	AA+	G	
ADA	rs73598374	GG-	A,G,T	
ADCY5	rs11708067	AA+	G	
ADIPOQ	rs17366743	TT+	C	
ADORA2A	rs5751876	Variant not found	C	
ADRA2A	rs553668	Variant not found	G,T	
AHCY	rs13043752	Variant not found	A	
AHCY	rs41312290	Variant not found	C	
ALDH2	rs671	GG+	A	
ARL15	rs1694089	Variant not found	C	
ARL15	rs788517	Variant not found	T	
ATM	rs664143	CC-	G,T	
AURKA	rs2273535	Variant not found	T	
BCO1	rs12934922	AA+	G,T	
BCR	rs2156921	Variant not found	A	
BCR	rs2267012	Variant not found	A	
BCR	rs2267013	Variant not found	G	
BCR	rs2267015	Variant not found	G,T	
BCR	rs3313172	Variant not found		
BCR	rs3761418	Variant not found	G	
BDNF	rs6265	GG-	T	
CA1	rs121909577	Variant not found	G,T	
CA1	rs7841425	Variant not found	A	

Gene	SNP	Genotype	Rare Allele	Result
CA1	rs1532423	CT-	A	
CAPN10	rs3792267	GG+	A	
CCHCR1	rs130067	Variant not found	G	
CDKAL1	rs4712523	AG+	G	
CDKAL1	rs7756992	AG+	G,T	
CDKN1A	rs1801270	CC+	A,T	
CDKN2A	rs10811661	TT+	T	
CDKN2A/B	rs2383208	AA+	G,T	
CDKN2B-AS1	rs2383206	Variant not found	G	
CFH	rs1061170	TT+	T	
CHRM2	rs1824024	GT-	A	
CHRM2	rs2061174	CT-	A,C	
CHRM2	rs324650	AT+	A	
CLOCK	rs1801260	AA+	C,G,T	
CLPTM1L	rs401681	CT+	T	
CTLA4	rs231775	AG+	G	
CYP1A1	rs1048943	AA-	A,C,G	
CYP1A1	rs1800031	TT-	G	
CYP1A1	rs41279188	CC-	A,T	
CYP1A1	rs56313657	GG-	A,T	
CYP1A1	rs72547509	TT-	G,T	
CYP1B1	rs1056836	CC-	C	
CYP2E1	rs2070673	TT+	T	
CYP3A4	rs2740574	AA-	T	
CYP3A5	rs776746	AG-	C	
DAT	rs1064795122	Variant not found	T	
DHFR	rs1643649	Variant not found	C	
DIRC3	rs966423	CT+	G,T	
DNER	rs1861612	AG+	A,C	
DPYD	rs1801266	CC-	A	
DPYD	rs1801267	GG-	T	
DPYD	rs1801268	GG-	A	
E2F3	rs1570155	AG+	A,T	
ENPP1	rs997509	Variant not found	T	
EPHX1	rs1051740	TT+	C	
ESR1	rs11964281	Variant not found	T	
FAM58A	rs1057521251	Variant not found	A	
FASLG	rs763110	TT+	T	
FGF20	rs1721100	Variant not found	G,T	
FKBP5	rs1360780	CC+	A,C	
FOXE1	rs10984009	Variant not found	A	
FTO	rs10163409	Variant not found	T	
FTO	rs1121980	CC-	A	
G6PD	rs1050828	CC+	T	
GAD1	rs10432420	Variant not found	A	
GAD1	rs12185692	Variant not found	A	
GAD1	rs1978340	Variant not found	A	
GAD1	rs2058725	Variant not found	C	
GAD1	rs2241165	AA-	T	
GAD1	rs3762555	Variant not found	A,G	
GAD1	rs3791850	Variant not found	A,C	
GAD1	rs3791851	Variant not found	C	
GAD1	rs3791878	Variant not found	T	
GAD1	rs3828275	Variant not found	T	
GAD1	rs701492	TT+	T	
GAD1	rs769407	Variant not found	C	
GCK	rs4607517	GG+	A,C	
GCKR	rs780094	AG-	C	
GPHN	rs104894470	CC+	T	
GPX1	rs1050450	CC-	A	
GPX4	rs713041	Variant not found	A,C	
GRK5	rs17098707	Variant not found	T	
GSTP1	rs1695	GG+	G	
HHEX	rs1111875	Variant not found	T	
HHEX	rs5015480	TT+	T	
HLA-DRA	rs3135391	CC-	A	
HLA-DRB1	rs660895	GG+	G	
HNF1A	rs1169300	Variant not found	A	

Gene	SNP	Genotype	Rare Allele	Result
HNF1A	rs2464196	Variant not found	A	⚪
HTR2A	rs1328674	AG-	C,G	🟢
HTR2A	rs6314	CC-	A	🟠
HTR2C	rs3813929	CC+	G,T	🟢
HTRA1	rs11200638	AG+	A	🟠
IGF2BP2	rs4402960	GG+	T	🟢
IL-1B	rs16944	AG+	G	🟡
IL4R	rs1801275	Variant not found	G	⚪
INSIG2	rs7566605	GG+	C	🟢
INTERGENIC	rs1031681	Variant not found	C	⚪
INTERGENIC	rs1545843	AG+	A	🟢
INTERGENIC	rs791595	AG+	G	🟡
INTERGENIC	rs7923837	AA+	A,T	🟢
IRS1	rs2943641	CT+	C	🟡
JAZF1	rs1635852	CT+	C	🟢
KCNJ11	rs5215	TT+	T	🟢
KCNJ11	rs5219	CC+	T	🟢
KCNQ1	rs104894252	GG+	A,C	🟢
KCNQ1	rs2283228	AA+	C	🟢
LEPR	rs1137101	AA+	G	🟢
MAOA	rs909525	GG-	T	🟠
MDM2	rs2279744	Variant not found	G	⚪
MT1A	rs11076161	Variant not found	G	⚪
MTHFR	rs1476413	AG-	G,T	🟢
MTHFR	rs17037390	Variant not found	A	⚪
MTHFR	rs1801131	AC-	G	🟠
MTHFR	rs4846049	Variant not found	A,G	⚪
MTNR1B	rs10830963	CC+	G	🟢
MTRR	rs1801394	AA+	G	🟢
MTTP	rs3816873	Variant not found	C	⚪
NAF1	rs7675998	GG+	G,T	🟢
NBDY	rs4826508	CT+	T	🟢
NOS3	rs1800783	Variant not found	C,G,T	⚪
NOS3	rs3918188	Variant not found	A,T	⚪
NOTCH2	rs10923931	Variant not found	T	⚪
NOTCH2	rs2793831	Variant not found	C	⚪
NPAS2	rs11123857	Variant not found	G	⚪
NR3C1	rs6198	Variant not found	C	⚪
OXTR	rs2254298	GG+	A	🟢
OXTR	rs237899	GG+	A,C	🟢
PAX4	rs2233578	Variant not found	A,T	⚪
PAX4	rs2233580	GG-	T	🟢
PDE11A	rs3770018	Variant not found	C	⚪
PDE9A	rs729861	Variant not found	G	⚪
PEX5L	rs7630877	GG+	A,C	🟢
PIK3CA	rs104886003	GG+	A,C	🟢
PIK3CA	rs1057518041	Variant not found		⚪
PIK3CA	rs1057519699	Variant not found	A	⚪
PIK3CA	rs1057519925	Variant not found	A,C	⚪
PIK3CA	rs1057519926	Variant not found	T	⚪
PIK3CA	rs1057519927	Variant not found	C,G,T	⚪
PIK3CA	rs1057519928	Variant not found	C	⚪
PIK3CA	rs1057519929	Variant not found	A	⚪
PIK3CA	rs1057519930	Variant not found	T	⚪
PIK3CA	rs1057519931	Variant not found	C	⚪
PIK3CA	rs1057519932	Variant not found	G	⚪
PIK3CA	rs1057519933	Variant not found	G	⚪
PIK3CA	rs1057519934	Variant not found	C	⚪
PIK3CA	rs1057519935	Variant not found	G	⚪
PIK3CA	rs1057519936	Variant not found	G,T	⚪
PIK3CA	rs1057519937	Variant not found	C	⚪
PIK3CA	rs1057519938	Variant not found	C,T	⚪
PIK3CA	rs1057519939	Variant not found	C	⚪
PIK3CA	rs1057519940	Variant not found	T	⚪
PIK3CA	rs1057519941	Variant not found	C,G	⚪
PIK3CA	rs1057519942	GG+	A	🟢
PIK3CA	rs1064793349	Variant not found	A	⚪
PIK3CA	rs1064793663	Variant not found	A	⚪

Gene	SNP	Genotype	Rare Allele	Result
PIK3CA	rs1064793732	Variant not found	A	
PIK3CA	rs1064793838	Variant not found	G	
PIK3CA	rs1064795304	Variant not found	G	
PIK3CA	rs121913272	Variant not found	C,G	
PIK3CA	rs121913273	Variant not found	A,C	
PIK3CA	rs121913274	Variant not found	C,G,T	
PIK3CA	rs121913275	Variant not found	A,C,T	
PIK3CA	rs121913277	Variant not found	A,C	
PIK3CA	rs121913279	Variant not found	G,T	
PIK3CA	rs121913281	Variant not found	T	
PIK3CA	rs121913282	Variant not found	C	
PIK3CA	rs121913283	Variant not found	A,T	
PIK3CA	rs121913284	Variant not found	A,G	
PIK3CA	rs121913285	Variant not found	G	
PIK3CA	rs121913286	Variant not found	A,G	
PIK3CA	rs121913287	Variant not found	A	
PIK3CA	rs121913288	Variant not found	G	
PIK3CA	rs12494623	Variant not found	G,T	
PIK3CA	rs141178472	Variant not found	C	
PIK3CA	rs17849071	Variant not found	G	
PIK3CA	rs17849079	Variant not found	T	
PIK3CA	rs2699887	CT+	T	
PIK3CA	rs3729679	Variant not found	G	
PIK3CA	rs3729687	Variant not found	A	
PIK3CA	rs397514565	Variant not found	A	
PIK3CA	rs397517200	Variant not found		
PIK3CA	rs397517201	Variant not found	C,G,T	
PPARG	rs13306747	Variant not found	A,G,T	
PPARG	rs1801282	CG+	C	
PPARG	rs2197423	Variant not found	A	
PPARG	rs6802898	Variant not found	T	
PPCDC	rs2120019	CT+	C	
PTEN	rs121909229	GG+	A,C,T	
PTEN	rs121909232	CC+	G	
PTEN	rs371387815	Variant not found	G,T	
PTPRD	rs10116682	Variant not found	A	
PTPRD	rs10481625	Variant not found	A,C,G	
PTPRS	rs1143699	Variant not found	A	
RASGRP1	rs7403531	CC+	C,G	
RBMS1	rs6718526	Variant not found	C	
RHOU	rs6426514	GG+	A	
RNASEL	rs3738579	CT-	G	
RPSAP52	rs1531343	CC+	C,T	
SDHAF4	rs1048886	AA+	G	
SLC2A14	rs12815313	Variant not found	G,T	
SLC30A3	rs11126936	Variant not found	T	
SLC30A3	rs73924411	Variant not found	T	
SLC30A8	rs13266634	CC+	A,T	
SLC39A6	rs1050631	CT-	A	
SLC64A	rs25531	Variant not found	C,G	
SOD2	rs2758331	Variant not found	A	
SOD3	rs1799895	CC+	G	
SOD3	rs2855262	TT+	C	
STAT4	rs10181656	CG+	C	
TCF7L2	rs12255372	GG+	T	
TCF7L2	rs7901695	TT+	C	
TCF7L2	rs7903146	CC+	G,T	
TERT	rs2736098	AG-	T	
TG	rs180223	Variant not found	A,C,G	
TGFBR3	rs1805110	CC-	A	
THADA	rs7578597	TT+	C	
TPH1	rs1799913	AC-	A,T	
TPH1	rs7933505	Variant not found	A	
TRIB3	rs2295490	AG+	G,T	
TYR	rs28940879	Variant not found	A,C	
UBE2E2	rs7612463	AC+	A,G	
VPS26A	rs4812829	AG+	A	
VPS33B	rs121434383	Variant not found	A	

Gene	SNP	Genotype	Rare Allele	Result
WFS1	rs10010131	Variant not found	G	○
WFS1	rs10012946	Variant not found	C	○
XPC	rs2228000	CC-	A	●
XPC	rs2228001	AA-	T	●
XRCC1	rs1799782	CT-	A	●

Alcohol

Gene	SNP	Genotype	Rare Allele	Result
ADH1B	rs1229984	GG-	C,G	●
ALDH2	rs671	GG+	A	●