

NutraHacker

Fitness VO2 Report for Customer: 84adea33-9194-4753-925f-529a87656048

Instructions:

This report analyzes polymorphisms that have been found to influence activity related to the heart, the lungs and VO2 max.

PEP - Performance Enhancing Polymorphism

When one PEP allele is written, each allele provides a benefit, when two are listed then both alleles have to be present for the benefit.

NOTICE: NutraHacker reports are for scientific, educational and nutritional information only and are not intended to diagnose, cure, treat or prevent any disease, disorder or condition. Consult your doctor before beginning any treatment.

Thank you for using NutraHacker. To your health!

Gender of customer: Male

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs4646994	ACE	N/A	I	N/A	N/A	endurance/ power, VO2	Whilst the mechanism underpinning the association between the ACE I/D polymorphism and mountaineering performance has yet to be fully established, the I allele has been associated with enhanced endurance performance at sea level [28], greater hypoxic ventilatory drive [29], enhanced arterial oxygenation at altitude [30], and enhanced training-related gains in metabolic efficiency [31].
<p>Variant D carriers make more ACE protein which results in a more active RAS system than that of variant I carriers. A more active RAS system results in a heightened sensitivity to sodium intake and a higher risk for hypertension with high sodium intake. When sodium intake is low, the risk for hypertension in variant D carriers is equivalent to that of non-carriers. When it comes to exercise, variant D carriers respond more favorably to short sessions of strength and power-oriented exercise while variant I carriers respond more favorably to endurance exercise. Long-term endurance exercise for variant D carriers actually increases the risk for increased left ventricular mass, which is associated with increased cardiovascular mortality.</p> <p>Furthermore, if you are a variant D carrier and already have a medical condition like hypertension, diabetes, overweight, obesity, or kidney disease, the harmful effects of high sodium are even more detrimental. In this case, sodium restriction, either with a low sodium and/or high potassium diet, is especially important.</p> <p>http://www.gbhealthwatch.com/GND-Hypertension-ACE.php</p> <p>http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4544548/</p>							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1042713	ADRB2	Arg16Gly	G	AG	47.2603%	endurance, VO2, BMI	The beta-2 adrenergic receptor (encoded by ADRB2; location: 5q31-q32) is a member of the G protein-coupled receptor superfamily, expressed in many cell types throughout the body and plays a pivotal role in the regulation of the cardiac, pulmonary, vascular, endocrine and central nervous system.
<p>G encodes gly, A encodes Arg</p> <p>Positive association between the tested Gly16Arg polymorphism and endurance performance. Furthermore, in a study of 316 Mount Olympus marathon runners Tsianos et al. (2010) had shown an association between the 16Arg allele and the fastest time of athletes. The results of these studies were in agreement with the previous work in which an association of the 16Arg allele with higher peak VO2 in heart failure patients was reported (Wagoner et al., 2000).</p> <p>Influences regulation of glucose and mobilisation of fat stores. Plays a part in cardiac, pulmonary & vascular functions. G allele associates with elite endurance performance in males (p=0.03) - A allele associates with increased BMI and decreased VO2 max (p<.001)</p> <p>http://web.stanford.edu/class/gene210/files/projects/Gene210-AthleticsPresentation-Roos.pdf</p> <p>Lower VO2 max capacity, ADRB2 (rs4994 & rs1042713) NOT AA or TT: HIIT the only successful exercise for weight loss.</p> <p>Ahmetov II, Fedotovskaya ON. (2012) Sports genomics: Current state of knowledge and future directions. 1(1): e1. doi:10.7457/cmep.v1i1.e1</p>							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1800795	IL6	G-174C	CG	CC	15.1043%	VO2 max, endurance	During physical exercise the concentration of plasma IL-6 increases because of its release from muscles, which mediates metabolic processes. The IL-6 is relevant to many diseases such as diabetes (Kristiansen and Mandrup-Poulsen, 2005), atherosclerosis (Schuett et al., 2009; Huber et al., 1999), depression (Dowlati et al., 2010) and rheumatoid arthritis (Nishimoto, 2006). The IL-6 was linked to the regulation of glucose homeostasis during exercise. There was a relationship between the IL-6 release at the end of exercise and muscle glycogen concentration after exercise, which suggested that IL-6 acts as a carbohydrate sensor (Helge et al., 2003). The IL-6 plays an important role in the regulating fat metabolism in the muscle, increasing rates of fatty acid oxidation, and attenuating insulin's lipogenic effects (Bruce and Dyck, 2004). The IL-6 also plays a role in the hypertrophic muscle growth with a contribution of satellite cells to this process (Serrano et al., 2008).

The interleukin-6 was produced in larger amounts than any other cytokine in the relation to strenuous exercise. Strenuous exercise leads to a significant elevation of IL-6 in the serum, thereby eliciting an acute phase response (Northoff and Berg, 1991). In resting muscle the IL6 gene was silent, but it was rapidly activated by the muscle contractions (Pedersen et al., 2003).

Moreover, during the 8-week training period, a tendency for increased plasma IL-6 was observed in subjects with this genotype. VO2max values increased in all genotype groups, but subjects with genotype CG made the greatest gains in VO2max. Training significantly decreased BMI only in subjects with genotype CG.

This gene plays a role in glucose and lipid metabolism. Individuals with this genotype (GG) tend to have higher plasma IL6 levels and higher insulin levels, which are associated with higher levels of body fat. These individuals may benefit from lowering the level of saturated fats in their diet.

There was a genetically determined difference in the degree of the IL-6 response to stressful stimuli between individuals, with C allele found to be associated with significantly lower levels of plasma IL-6. Individuals with the C allele had significantly reduced IL-6 levels in serum after long-term exercise training program (Oberbach et al., 2008). C alleles linked to increased muscle fatigue and damage, feeling low after exercise - OTS.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3761487/>

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs2402970	NRF1	N/A	C	CC	73.0867%	lung capacity	Role in exercise adaptation: mitochondrial biogenesis, heme biosynthesis
CC genotype associated w/ increased VO2 max + RE w/ training [p=0.004]							
https://web.stanford.edu/class/gene210/files/projects/Gene210-AthleticsPresentation-Roos.pdf							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs6949152	NRF1	N/A	A	AA	70.0178%	lung capacity	Role in exercise adaptation: mitochondrial biogenesis, heme biosynthesis
AA genotype associated w/ increased VO2 max w/ training [p=0.047]							
https://web.stanford.edu/class/gene210/files/projects/Gene210-AthleticsPresentation-Roos.pdf							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1799983	NOS3	G894T, glu298asp	G	N/A	N/A		The NOS3 gene is involved in the production of nitric oxide, which helps to relax the walls of your blood vessels.
vasodilation and vo2, There was a tendency of the NOS3 Glu298 allele combined with a BDKRB2 -9/-9 genotype to be over-represented in the fastest finishing triathletes (n = 40, 28.6%) compared with the control subjects (n = 28, 17.3%; P = 0.028) (Saunders et al., 2006).							
https://www.ncbi.nlm.nih.gov/pubmed/28526204							
https://www.ncbi.nlm.nih.gov/pubmed/23681449							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1801253	ADRB1	Arg389Gly	C	CG	36.3535%		- beta-adrenergic receptors 1/2/3: G-protein coupled receptors in cardiac and adipose tissue that regulate cardiac function and metabolism - cardiac tissue: activated receptor -> increased cardiac output - adipose tissue: activated receptor -> increased lipid mobilization for energy production
- C allele associates with increased VO2 max and exercise time/endurance (p=0.002) - G allele associates with decreased VO2 max (p=0.006)							
http://web.stanford.edu/class/gene210/files/projects/Gene210-AthleticsPresentation-Roos.pdf							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1042713	ADBR2	Arg16Gly	G	AG	47.2603%		- beta-adrenergic receptors 1/2/3: G-protein coupled receptors in cardiac and adipose tissue that regulate cardiac function and metabolism - cardiac tissue: activated receptor -> increased cardiac output - adipose tissue: activated receptor -> increased lipid mobilization for energy production
G encodes gly, A encodes Arg							
G allele associates with elite endurance performance in males (p=0.03) - A allele associates with increased BMI and decreased VO2 max (p<.001)							
http://web.stanford.edu/class/gene210/files/projects/Gene210-AthleticsPresentation-Roos.pdf							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1042714	ADBR2	Gln27Glu	C	CG	46.3545%		- beta-adrenergic receptors 1/2/3: G-protein coupled receptors in cardiac and adipose tissue that regulate cardiac function and metabolism - cardiac tissue: activated receptor -> increased cardiac output - adipose tissue: activated receptor -> increased lipid mobilization for energy production
- C allele associates with elite distance running in middle age women (p=0.05) - G allele associates with increased BMI and decreased VO2 max (p=0.0001)							
http://web.stanford.edu/class/gene210/files/projects/Gene210-AthleticsPresentation-Roos.pdf							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs11549465	HIF-1a	P582S	C	CT	19.3437%		Hypoxia-inducible factor-1-alpha (HIF-1-alpha; encoded by HIF1A; location: 14q23.2) is a transcription factor regulating several genes in response to hypoxic stimuli. HIF-1-alpha mRNA and protein levels were found to be constitutively higher in the more glycolytic muscles compared with the more oxidative muscles (Pisani and Dechesne, 2005). A lower proportion of type IIA fibres in the soleus muscles of HIF-1-alpha knockout mice was detected as well as a metabolic shift away from glycolysis toward oxidation, and as a consequence, improved endurance capacity (Mason et al., 2004). Lunde et al. (2011) had shown that when HIF-1-alpha was overexpressed for 14 days after somatic gene transfer in adult rats, a slow-to-fast transformation was observed.
This substitution increases HIF-1-alpha protein stability and transcriptional activity (Tanimoto et al., 2003), and therefore, may improve glucose metabolism and lower the risk of type 2 diabetes (Nagy et al., 2009). Prior et al. (2003) had shown that HIF1A Pro/Pro homozygotes showed preservation of the ability to increase VO2max through aerobic exercise training at each age (55, 60 and 65 yr) level evaluated.							
Contrary to this, subjects carrying the 582Ser allele were able to increase VO2max to a similar extent as Pro/Pro homozygotes at 55 yr of age, but showed significantly less increase in VO2max to aerobic exercise training than Pro/Pro homozygotes at 60 and 65 yr of age. However, McPhee et al. (2011) had shown that the HIF1A 582Ser allele was associated with greater gains in VO2max following endurance training in young women who completed a 6-week laboratory-based endurance training programme. Döring et al. (2010a) by studying 316 Caucasian male elite endurance athletes from the Genathlete cohort and 304 Caucasian male sedentary controls have found that the Pro582 allele was associated with endurance athlete status. Homozygotes of the Pro582 allele were significantly more frequent in athletes than in controls (84.0% vs. 75.0%, P = 0.006).							
The rare T allele is predicted to result in a proline to serine change in the amino acid sequence of the protein. This substitution increases HIF-1-alpha protein stability and transcriptional activity, and therefore, may improve glucose metabolism. Recently, Ahmetov et al. (2008a) investigated a hypothesis that HIF1A Pro582Ser genotype distribution may differ for controls and Russian sprint/strength athletes, for which anaerobic glycolysis is one of the most important sources of energy for power performance. The frequency of the HIF1A 582Ser allele was significantly higher in weightlifters (n = 53) than in 920 controls (17.9% vs. 8.5%; P = 0.001) and increased with their levels of achievement (sub-elite (14.7%) ? elite (18.8%) ? highly elite (25.0%)). These results were replicated in a cohort of Polish power-orientated athletes (n = 158; the frequency of the HIF1A 582Ser allele: 17.1% vs. 9.1%; P = 0.01; in comparison with 254 sedentary controls) (Cieszczyk et al., 2011a), but not in 81 Israeli sprinters (Eynon et al., 2010a). Furthermore, the 582Ser allele was significantly associated with an increased proportion of fast-twitch muscle fibres in m. vastus lateralis of all-round speed skaters (Ahmetov et al., 2008a).							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs12594956	GABPB1	N/A	A	N/A	N/A		Training response of VO2 at running economy was associated with GABPB1 rs12594956 A/C, rs8031031 C/T and rs7181866 A/G polymorphisms, and individuals carrying the A-T-G haplotype had 57.5 % elevated running economy in response to 18-wk endurance training than non-carriers.
Ahmetov 2012							
https://www.researchgate.net/publication/40759436_Interaction_between_SNPs_in_the_NRF2_gene_and_elite_endurance_performance							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1800849	UCP3	N/A	A	AG	34.1415%		The expression of UCP3 mainly in skeletal muscle mitochondria made UCP3 an attractive target for studies toward manipulation of energy expenditure to fight disorders such as obesity and type 2 diabetes. Overexpressing human UCP3 in mice resulted in lean, hyperphagic mice (Clapham et al., 2000). In humans, acute exercise induces up-regulation of UCP3, most likely because of elevated plasma free fatty acid levels (Schrauwen et al., 2002; Pilegaard et al., 2000).
Several polymorphisms in the UCP3 gene (location: 11q13.4) have been identified and related to markers of energy metabolism, aerobic capacity and obesity (Ahmetov et al., 2008e; Schrauwen and Hesselink, 2002; Halsall et al., 2001). One of the early detected observations was 5'UTR -55 C/T polymorphism (rs1800849), of which the T allele was reported to be associated with increased skeletal muscle UCP3 mRNA expression (Schrauwen et al., 1999), reduced BMI (Halsall et al., 2001) and increased aerobic capacity in Russian female rowers (Ahmetov et al., 2008e). The frequency of the UCP3 T allele was significantly higher in 694 Russian elite endurance athletes compared to 1,132 controls (Ahmetov et al., 2009b).							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs17602729	AMPD1	Gln12X	G	AG	20.6326%		Adenosine monophosphate deaminase 1 (AMPD1) catalyzes the deamination of adenosine monophosphate to inosine monophosphate in skeletal muscle. Deficiency of the AMPD1 is apparently a common cause of exercise-induced myopathy and probably the most common cause of metabolic myopathy in the human. In the overwhelming majority of cases, AMPD1 deficiency is due to a 34C/T transition in exon 2 (rs1760272934 C/T) of the AMPD1 gene (location: 1p13), which creates a nonsense codon (Gln12X) that prematurely terminates translation. AMPD1 deficiency individuals exhibit a low AMP deaminase activity and reduced submaximal aerobic capacity (VO ₂ at the ventilatory threshold) (Rubio et al., 2008). In a study of Rico-Sanz et al. (2003), subjects with the AMPD1 XX genotype had diminished exercise capacity and cardiorespiratory responses to exercise in the sedentary state. Furthermore, the training response of ventilatory phenotypes during maximal exercise was more limited in XX (Rico-Sanz et al., 2003). In a study of 935 coronary artery disease patients the carriers of the X allele had a significantly lower relative increase in peak VO ₂ after three months of aerobic training (Thomaes et al., 2011). Finally, two studies reported low frequency of the mutant X allele in a group of top-level Spanish male endurance athletes (cyclists and runners, n = 104) (Rubio et al., 2005) and 127 Polish rowers (Cieszczyk et al., 2011c) compared with controls.

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs5443	GNB3	N/A	T	CC	45.3757%	vo2	The proportion of the TT genotype was significantly higher in the group of endurance athletes (18.9%) than in sprinters (4.9%, P = 0.014) and controls (8.5%, P = 0.026). These results were even more pronounced when the subgroups of 20 top-level endurance athletes (50.0%) and 24 top-level sprinters (4.0%, P = 0.0009) were compared.
In a study of 95 healthy African American university students significant association of the rs5443 T allele with peak oxygen consumption was observed (Faruque et al., 2009). The GNB3 C825T polymorphism plays a role in the heart rate and body fatness regulation in African Americans and in responsiveness of resting blood pressure to endurance training in African American women (Rankinen et al., 2002).							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs5219	KCNJ11	Glu23	C	CT	45.7066%		The encoded protein, which has a greater tendency to allow potassium to flow into a cell rather than out of a cell, is controlled by G-proteins (Smith et al., 2007). The KCNJ11 gene is expressed in several tissues, including cardiac and skeletal muscle, where it is involved in the coupling of cell metabolism to cell electrical activity.
The E23K SNP at codon 23 of the KCNJ11 gene (rs5219) results in substitution of glutamic acid to lysine, and may cause modest reductions in ATP sensitivity, which could influence muscle response to exercise.							
Yi et al. (2008) had shown that the Glu/Glu genotype was associated with the highest values of VO2max and maximal minute ventilation in women in untrained state than in Glu/Lys heterozygotes. Furthermore, two independent case-control studies have demonstrated that the KCNJ11 Glu23 was significantly over-represented in endurance-oriented athletes compared to controls in mixed Caucasian (184 male endurance-oriented athletes with VO2max > 75 ml/kg/min; 61.0% vs. 50.0%, P = 0.01) (González et al., 2003) and Spanish (98 marathon runners; 68.0% vs. 53.0%, P = 0.04) (Ortiz et al., 2005) cohorts.							
The metabolic risk allele/genotype in rs5219 is T/TT.							
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4320608/							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs660339	UCP2	Ala55Val	A	GG	33.7688%		Val/Val genotype has been reported to be associated with higher exercise efficiency (Buemann et al., 2001), enhanced metabolic efficiency and physical activity (Astrup et al., 1999) and higher VO2max in 27 male Russian rowers (Ahmetov et al., 2008e). Recently, it has been shown that the frequency of the 55Val allele was over-represented in 694 Russian elite endurance athletes (Ahmetov et al., 2009b) compared to 1,132 controls. On the other hand, Sessa et al. (2011) found an increased frequency of the Ala55 allele in 29 Italian power-oriented athletes.
A is val, G is ala							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1870377	VEGFR2	His472Gln	A	N/A	N/A	vo2	In a study of 182 endurance-oriented Russian athletes the significantly higher frequency of the VEGFR2 472Gln allele compared to controls was reported (Ahmetov et al., 2009a). Furthermore, the 472Gln allele was also shown to be significantly associated with a higher proportion of type I fibres of m. vastus lateralis (determined by immunohistochemistry) in both athletes (all-round speed skaters, n = 23; age 20.4 ± 0.5 years) and physically-active men (n = 45; age 23.5 ± 0.4 years), and with a greater VO2max in female rowers (Ahmetov et al., 2009a).
A is gln, T is his							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs2229309	NFATC4	Gly160Ala	G	N/A	N/A		In a study of 1,423 Russian athletes, the frequency of the Gly160 allele of the NFATC4 gene was significantly higher in endurance-oriented athletes (n = 694) than in the control group (n = 1,132) (Ahmetov et al., 2009b). Furthermore, NFATC4 Gly allele was associated with high values of aerobic performance (VO2max and AT in % of VO2max values) both in male and female Russian rowers (Popov et al., 2008).
Allele A carriers were less frequent in the patient than in the control group (P=0.04). Although the strength of the associations was rather weak, these observations raise the hypothesis that the G160A polymorphism of the NFATC4 gene plays a role in the development of human cardiac hypertrophy.							
Gly160Ala (rs2229309 G/C). Gly160							

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rs8111989	CKM	N/A	T	CT	39.9519%		The muscle isoform of creatine kinase (CKM) is a key enzyme of energy supply for muscle. In contracting muscles ADP formation triggers the creatine kinase mechanism of anaerobic ATP resynthesis which provides rephosphorylation between creatine phosphate and ADP.
Muscle-specific creatine kinase is thought to play an integral role in maintaining energy homeostasis by providing a supply of creatine phosphate.							
Participants with 2 copies of the T allele for rs8111989 variant had higher PFT scores for run time, pull-ups, and total PFT score. Specifically, participants with 2 copies of the TT allele (variant) (n = 97) demonstrated an overall higher total PFT score as compared with those with one copy of the C allele (n = 79) (TT: 250 ± 31 vs.							
A significantly lower VO2max response to endurance training program was detected in parents and offspring with CKM GG genotype. In a following study, Rivera et al. (1999) have confirmed these results in 277 full sib pairs from 98 Caucasian families. The association study of 102 male volunteers from northern China revealed significant association between the A/G CKM gene polymorphism and running economy response to endurance training (Zhou et al., 2006). AG genotype carriers showed larger running economy response than those with AA and GG genotypes. Furthermore, Heled et al. (2007) have demonstrated association between the A/G CKM gene polymorphism and susceptibility to exertional rhabdomyolysis.							
Furthermore, the CKM AA genotype was associated with higher values of VO2max (n = 85, P = 0.0097) in a group of rowers (Fedotovskaya et al., 2012b). It should be noted that Döring et al. (2011) by studying other CKM gene polymorphisms (rs344816, rs10410448, rs432979, rs1133190, rs7260359, rs7260463 and rs4884) in 316 male Caucasian elite endurance athletes and 304 sedentary controls found no association with athlete status.							
https://www.ncbi.nlm.nih.gov/pubmed/26327553							

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rs2267668	PPARD	N/A	A	AA	68.6313%	metabolism, vo2 peak	Mitochondrial function is associated with aerobic physical fitness and insulin sensitivity and may play an important role in the pathophysiology of type 2 diabetes. Peroxisome proliferator-activated receptor (PPAR)-delta (gene PPARD) and PPARgamma coactivator 1alpha (gene PPARGC1A) are determinants of mitochondrial function in animals and in vitro.
<p>After 9 months of intervention, the minor G allele of SNP rs2267668 in PPARD and the minor serine-encoding allele of the common Gly482Ser SNP in PPARGC1A were independently associated with less increase in individual anaerobic threshold (n = 136, P = 0.002 and P = 0.005), a precise measurement of aerobic physical fitness.</p> <p>In addition, low skeletal muscle mitochondrial function in vitro was detected in young carriers of the G allele of the SNP rs2267668 in PPARD (n = 19, P = 0.02).</p> <p>https://www.ncbi.nlm.nih.gov/pubmed/17327385</p> <p>https://www.ncbi.nlm.nih.gov/pubmed/24118591</p>							

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rs2402970	NRF1	N/A	T	CC	73.0867%	lung capacity	Nuclear respiratory factor 1 (NRF-1) is a critical component of the energy-sensing mechanism in mammalian cells, and translates physiological signals (particularly those induced by exercise) into increased capacity for mitochondrial biogenesis and oxidative phosphorylation.
<p>NRF-1 genotypes and several phenotypes indicative of maximum (VO₂max) and submaximum aerobic capacity (ventilatory threshold (VT) and metabolic cost of submaximum running at 12 km/hour (running economy; RE)) both at baseline and in response to a 18-week endurance training programme in young Chinese men of Han origin (n = 102; 19 (SD 1) years).</p> <p>For rs2402970, a significant genotype effect was seen for VT (p = 0.004) and RE (p = 0.027).</p> <p>https://www.ncbi.nlm.nih.gov/pubmed/?term=rs2402970</p>							

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rs16139	NPY	N/A	T	TT	92.946%	Heart capacity	Neuropeptide Y (NPY) is a molecule that may have both vasoconstrictive and vasodilatory actions. A common polymorphism in the human NPY gene that results in the Leucine7 to Proline7 substitution (Leu7Pro) in the signal peptide part of the NPY was recently identified. This substitution has been associated with elevated serum cholesterol levels and with slightly accelerated progression rate of carotid intima-media thickness, thus suggesting increased risk of atherosclerosis in carriers of Pro7 substitution.
Recent data also indicate that subjects with Pro7 substitution may have increased endothelial release of NPY. This study was undertaken to elucidate the effects of Leu7Pro polymorphism on arterial endothelial function. We measured flow-mediated endothelial-dependent dilatation (FMD) of the brachial artery in two separate populations: in 152 middle-aged men and in 95 prepubertal children. In both study populations, subjects with Pro7 substitution had 48-52% higher FMD compared with subjects having the wildtype (Leu7/Leu7) signal peptide sequence. We conclude that Pro7 substitution in signal peptide of the NPY is associated with enhanced endothelial-dependent vasodilation.							
https://www.ncbi.nlm.nih.gov/pubmed/12818415							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs211302	KIF5B	N/A	G	CC	56.1396%	Heart capacity	Kinesins are a superfamily of microtubule-based molecular motors that play an integral role in the movement of various cellular organelles and vesicles.
KIF5B encodes a common conserved isoform of kinesin heavy chain that is expressed in various tissues, including cardiac myocytes. KIF5B-containing kinesin motors have been shown to participate in transport of Kv1 K+ channels and active zone-components essential for presynaptic assembly in axons (10, 21), transport of mitochondria in neurons and other cell types (14, 19), and movement of glucose transporter 4 (Glut4) to the cell membrane after insulin stimulation in adipocytes and skeletal muscle cells (23).							
Essentially, the rs211302 C allele resulted in lower promoter activity. The same allele was associated with lower delta-SV50 in the linkage-positive families .							
Statistically significant differences in promoter activity among haplotypes were found. An independent effect of SNP rs211302 on promoter activity was found with constructs specifically testing this variant. The minor allele resulted in lower promoter activity, which is concordant with the observed association of the same allele with a lower SV50 training response.							
https://www.ncbi.nlm.nih.gov/pubmed/18984674							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs2253206	CREB1	N/A	G	GG	29.1079%	VO2	Induces transcription of genes in response to cAMP binding
<p>The CREB1 SNPs rs2360969 and rs2253206 were associated with temperature change during exercise (rs2360969, $r = .17$, $p = 0.02$; rs2253206, $r = .17$, $p = 0.02$) indicating that for rs2360969, individuals with the T allele had greater changes in temperature over the course of the exercise, and for rs2253206, individuals with the A allele had greater changes in temperature during exercise.</p> <p>for rs2253206, individuals with the G allele had higher VO2 max</p> <p>Our results indicate that for the CREB1 SNP rs2253206, individuals with the A allele (AG genotypes, and to a greater extent AA genotypes) have a greater change in temperature during exercise. If greater temperature change while exercising translates into a more unpleasant subjective exercise experience, then our findings suggest that the AA individuals (and to a lesser extent AG individuals) may have less pleasant subjective experiences of exercise than GG individuals. rs2253206 was shown to be strongly associated with heart rate (HR) change in response to a 20-week endurance training program, with GG and AG genotypes and showing 57% and 20% better change in HR than the AA participants [38].</p> <p>https://www.hindawi.com/journals/jce/2012/540563/</p> <p>https://www.hindawi.com/journals/jce/2012/540563/#B38</p>							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs2360969	CREB1	N/A	C	CC	35.5941%	VO2	Induces transcription of genes in response to cAMP binding
<p>The CREB1 SNPs rs2360969 and rs2253206 were associated with temperature change during exercise (rs2360969, $r = .17$, $p = 0.02$; rs2253206, $r = .17$, $p = 0.02$) indicating that for rs2360969, individuals with the T allele had greater changes in temperature over the course of the exercise, and for rs2253206, individuals with the A allele had greater changes in temperature during exercise.</p> <p>for rs2360969, individuals with the C allele had higher VO2 max.</p> <p>Additionally, we found that for rs2360969, TT individuals experienced greater change in temperature than did CT and CC individuals.</p> <p>https://www.hindawi.com/journals/jce/2012/540563/</p>							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs5370	EDN1	Lys198Asn	G	GG	60.7866%	VO2	endothelin 1: expressed in vascular endothelium; acts as a vasoconstrictor to regulate blood pressure
<p>However, we observed a significant ($P=0.0025$) interaction between the endothelin 1 rs5370 (G/T; Lys198Asn) genotype and cardiorespiratory fitness level on the risk of hypertension: among low-fit subjects, the rs5370 minor allele (T; 198Asn) was associated with higher risk of hypertension (odds ratio: 1.95; 95% CI: 1.36 to 2.81; $P=0.0003$), whereas the risk did not differ among genotypes in high-fit subjects. In the white Health, Risk Factors, Exercise Training and Genetics subjects ($N=480$), the rs5370 T allele was associated with blunted systolic blood pressure ($P=0.0046$) and pulse pressure ($P=0.0016$) responses to a 20-week endurance training program. The Lys198Asn variant of the endothelin 1 locus is associated with blood pressure phenotypes in whites. However, the expression of the genotype effect is modulated by physical activity or cardiorespiratory fitness level.</p>							
<p>G allele associates with increased cardiorespiratory fitness (OR=1.95; $p=0.00025$), i) T allele associates with increased hypertension ($p=.0003$), ii) for Caucasians only and not African Americans, iii) T allele decreases the VO2 max and pulse pressure response to training</p>							
<p>https://www.ncbi.nlm.nih.gov/pubmed/17938376</p>							