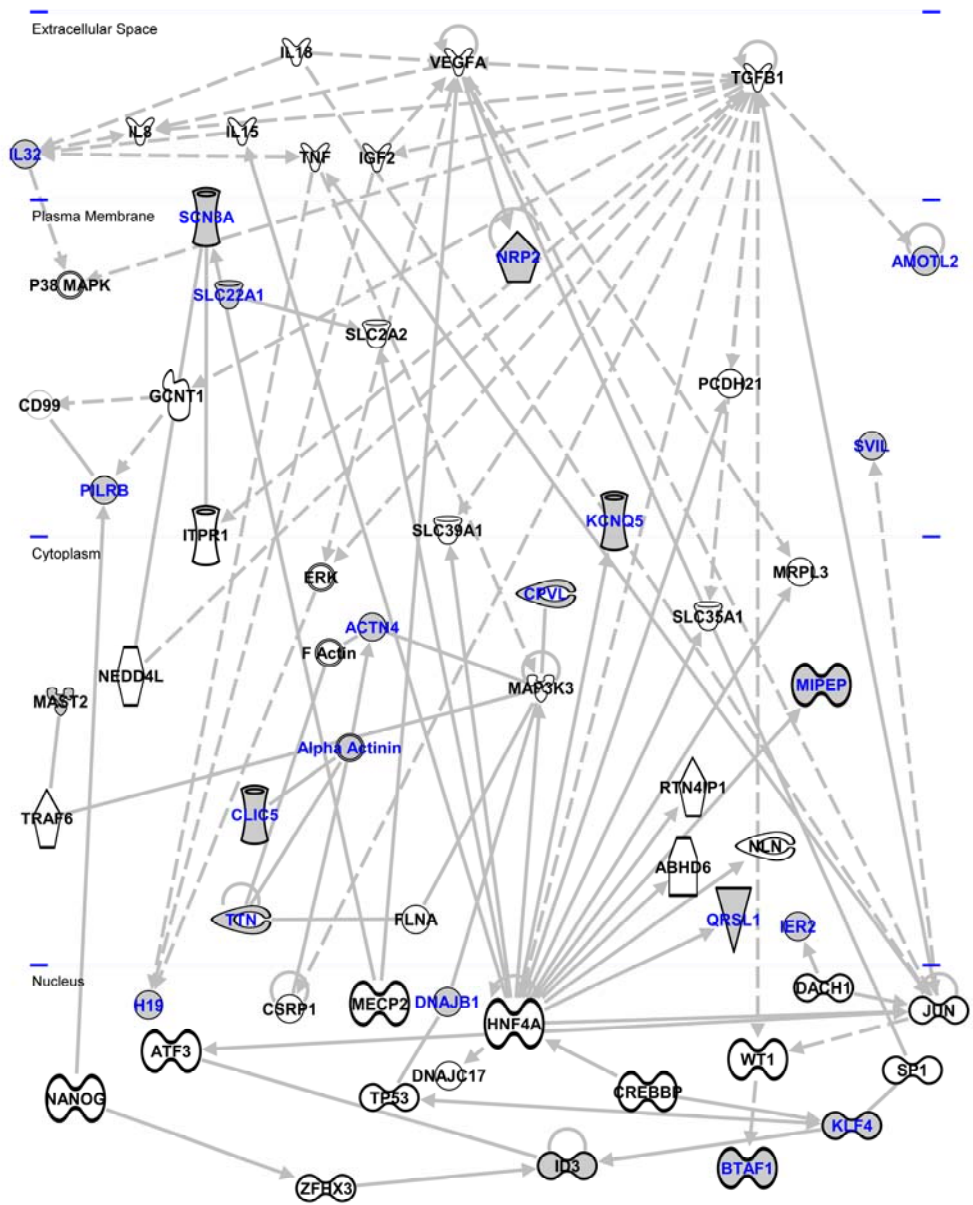


Figure S1. (a) Independent test of predictor gene set from study 1 applied to study 2 (young active subjects that underwent 12 wks intense interval based aerobic training. N=17, CC=0.51, $p=0.02$) Correlation was between predicted and observed response to exercise in terms of percent change in $\dot{V}O_2\text{max}$ (l/min). (b) The genes identified by QTL genotyping in 473 subjects (SVIL, TTN, NRP2 and MIPEP) 3 of which demonstrated a significant correlation with oxidative capacity changes following exercise, we used in the blind validation data set (Figure S2a). Addition of SVIL and NRP2 was found to improve the performance of the classifier (CC=0.64, $p=0.009$) while MIPEP did not alter this improved performance further.

Enlarged version of figure 3b



Enlarged version of figure 3c

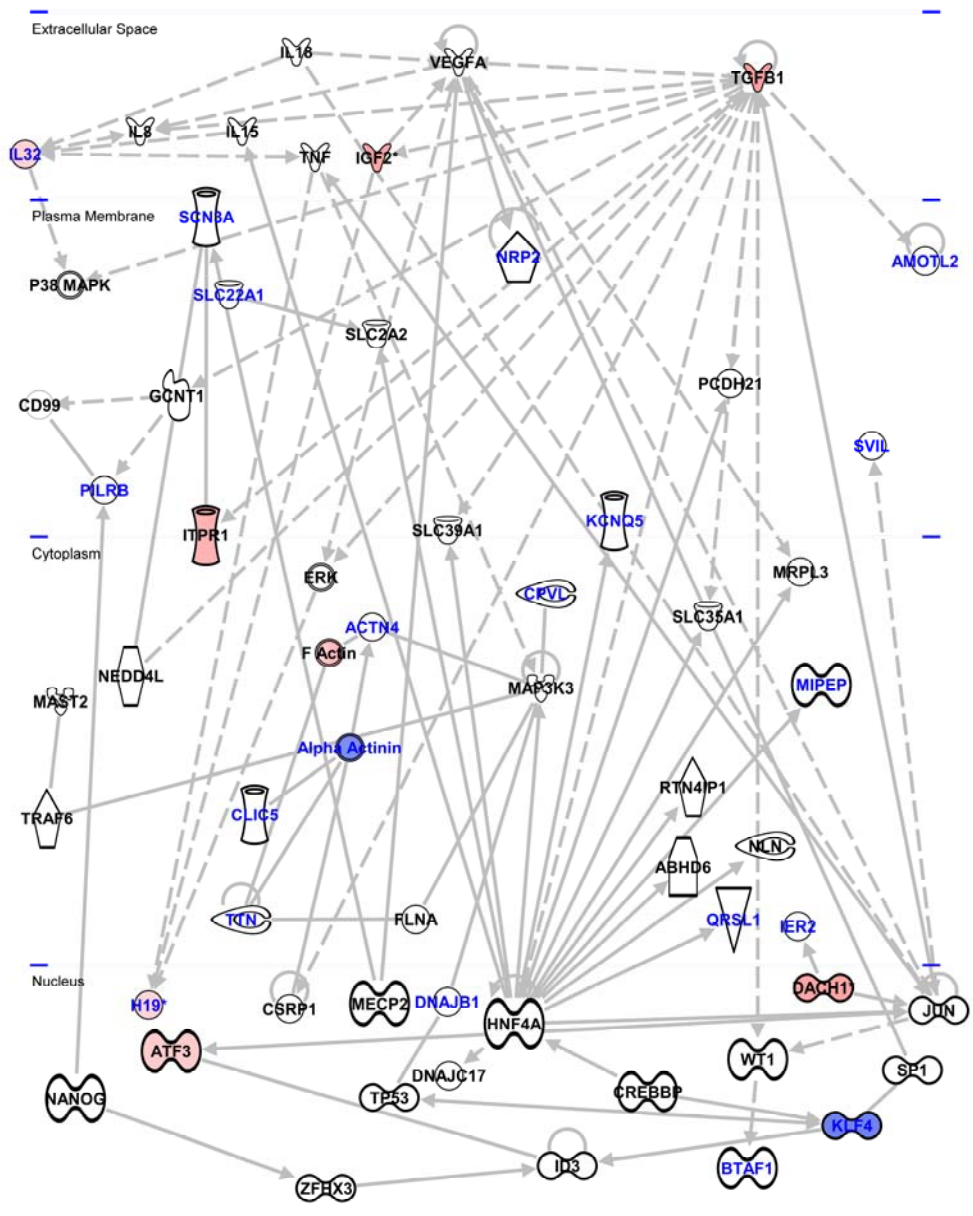


Table S1 Group 1 subject characteristics

	Pre-training (mean±sem)
Body Mass (kg)	78.6±2.7
Age (y)	23±1
Height (m)	1.82±0.02
$\dot{V}O_{2\max}$ (L·min ⁻¹)	3.71 ± 0.55

Values are mean (SE)

Table S2 Group 2 subject characteristics

	Pre-training (mean±SD)
Age (y)	29±6
Body Mass (kg)	81.8±9.0
Height (m)	1.8±0.5
$\dot{V}O_{2\max}$ (L·min ⁻¹)	4.1±0.5

Values are mean (SE)

Table S3. Baseline characteristics of the HERITAGE Family Study subjects.

	All	Men	Women
N	473	230	243
Age, years	35.7 (14.5)	36.7 (15.0)	34.8 (14.0)
BMI, kg/m ²	25.8 (4.9)	26.6 (4.9)	24.9 (4.8)
VO ₂ max, L/min	2.46 (0.7)	2.03 (0.6)	1.91 (0.4)
VO ₂ max, ml/kg/min	33.2 (8.8)	37.0 (9.0)	29.5 (6.9)

Values are mean (SD)

Table S4. SNPs set used in stepwise regression models described above. SNPs (n=35) showing strongest association with rdVO2mx from ALL genes were selected.

HERITAGE genes and SNPs chosen for regression models (n=10).

GENE	SNP	CHR	MAP
SLC4A5	rs828902	2	74,323,642
TTN	rs10497520	2	179,353,100
NRP2	rs3770991	2	206,363,984
CREB1	rs2709356	2	208,120,337
PPARD	s2076167	6	35,499,765
SVIL	rs6481619	10	30,022,960
KIF5B	rs806819	10	32,403,990
ACTN3	s1815739	11	66,084,671
MIPEP	rs7324557	13	23,194,862
ACE	DI	17	58,919,622

Molecular predictor genes and SNPs chosen for regression models (n=25).

GENE	SNP	CHR	MAP
ID3	rs11574	1	23,758,085
MAST2	rs2236560	1	46,268,021
SYPL2	rs12049330	1	109,832,711
SCN3A	rs7574918	2	165,647,425
AMOTL2	rs13322269	3	135,569,834
BTNL9	rs888949	5	180,425,011
KCNQ5	rs10943075	6	73,776,703
RTN4IP1/QRSL1	rs898896	6	107,169,855
SLC22A3	rs2457571	6	160,754,818
CPVL	rs4257918	7	29,020,374
PILRB	rs13228694	7	99,778,243
DEPDC6	rs7386139	8	121,096,600
KLF4	rs4631527	9	109,309,857
TET1	rs12413410	10	70,055,236
BTAFL1	rs2792022	10	93,730,409
H19	rs2251375	11	1,976,072
METTL3	rs1263809	14	21,058,740
DIS3L	rs1546570	15	64,382,829
UNKL	rs3751894	16	1,426,876
IL32	rs13335800	16	3,052,198
SMTNL2	rs7217556	17	4,425,585
ZSWIM7	rs10491104	17	15,825,286
ENOSF1	rs3786355	18	671,962
IER2	rs892020	19	13,128,185
DNAJB1	rs4926222	19	14,488,050