

Supplementary table 1: List of sequences of primers used in sequenom assay

	SNP_ID	2nd-PCR Sequence	1st-PCR Sequence	Allele specific (iPLEX) primer Direction	iPLEX primer
ROCK2					
1	rs978906	ACGTTGGATGATAAAGCTCTCTCGGCAGTC	ACGTTGGATGACCTCTCTGTTGAAGCTAGA	F	cGCAGTCGCTCACACTACA
2	rs6753921	ACGTTGGATGGAACCCAACTGAAAAGCTCC	ACGTTGGATGCCAATCCCTTACTGAAAGAC	R	TCCATGTACACTGTGCT
3	rs2290156	ACGTTGGATGTTTTCTGGGAGAGACTGTTT	ACGTTGGATGGCTGTTACCCAGTTTTCTGT	F	tcacAATAATCACTTGAAGAAATGTG
4	rs10495582	ACGTTGGATGGATGTATCTGCAGGCTTACC	ACGTTGGATGCCCTTACTTCATGAGCAAC	F	TCTGCAGGCTTACCATAACA
5	rs2230774	ACGTTGGATGTTCTCCCCCTTCCATGTAG	ACGTTGGATGCGTACTTCATTTTTCCTTG	F	ACTCTCCATCTTGTAGAGAAA
6	rs10167277	ACGTTGGATGAGACTCACTTGTAAAGGCC	ACGTTGGATGGACTGTCTTGTGTATGTAGC	F	AAGTAGGTCATACTATGACA
7	rs13393192	ACGTTGGATGGCAAACCATGGGAGTAACAC	ACGTTGGATGTGCCTTTTGAAGTCAGGCAC	F	GTAACACTTTGTGTGGATTA
8	rs10929727	ACGTTGGATGTGAATGTTTGTCTCAACTGGG	ACGTTGGATGCACCAGCATTAAACAGATGAG	R	tGTCCACAATTAGTGTTCCT
9	rs6716817	ACGTTGGATGTGGGATCAGAATGAGGTTGG	ACGTTGGATGGGAGCACCCTGTTACATCAC	R	gCTTAATAATCTTTGATAGCTTGC
10	rs4477886	ACGTTGGATGGGAGCAGGAATGAGGATCAA	ACGTTGGATGATCCCCCCCCAAAAAAACC	F	gGAGGATCAATCTTATAAAAAAGC
11	rs41264193	ACGTTGGATGGGCAGAATCTGATCTTTTT	ACGTTGGATGAAAATCAACAGGTTTCGTAC	F	ccAGCTTCATAGCATAAACCTTCTG
12	rs12622447	ACGTTGGATGCCTAACTGCAGAATTTACAAG	ACGTTGGATGCCTTAATTGGAGTCATTTTTC	F	cGGGGGCAGGAGTACAGATGA
13	rs10929728	ACGTTGGATGAGGTAGGAAAACCTGAGCTG	ACGTTGGATGATAACTGGTCCCCTGCAAG	R	aGGTGGTCAAGTCAGACA
MYLK					
1	rs11717814	ACGTTGGATGAAGTGCACAAGAGTCTCTGG	ACGTTGGATGAGAGTAAACGTGGACTTGCC	F	ccccGCATTGAAGGTCAGCTT
2	rs1343700	ACGTTGGATGCAAAGGTTGTCAAATATGGG	ACGTTGGATGTAGAAGGTCCAGGATTTGCC	F	tAATATGGGGAGACTGGAGA
3	rs16834817	ACGTTGGATGGAGTTCTGCATTCTAATGGC	ACGTTGGATGAGGCATTTTCTGCACATTCC	F	cccTGGCTTTCAAAGTGCTT
4	rs2700408	ACGTTGGATGGATTGTGTATTAGGAAGG	ACGTTGGATGGAATCCATCTTTTATCATGC	R	TTCTTCAAAATTAACAGAAACCAATT
5	rs28497577	ACGTTGGATGTTGCCTCGTCACACATTTCC	ACGTTGGATGGGGCAAAATGAAAGCAGGG	R	ccacAACCTCCCTCAGTGTGGATC
6	rs3796164	ACGTTGGATGTTCTATTCTCCCCTCTCCTC	ACGTTGGATGCTGACATCTGAATTGGTGGC	R	CCACCACACAGGTCATTTG
7	rs40305	ACGTTGGATGTGTAGCCAAGAATGACGCTG	ACGTTGGATGTGTATGGGTGGCGGCGATG	F	TGCTCCTGCCAAGTCAC
8	rs820336	ACGTTGGATGTTGATCTAAGCCCCGAAGAC	ACGTTGGATGCAGCCCAGAACAAGCTGTTA	F	ccccGGGCCCCGCAGCAGCAGAGGC
9	rs936170	ACGTTGGATGACTCCTCTGAGGCTTTGGTG	ACGTTGGATGAAGTGACAGAAGCCCTTACC	F	GTGGTGGACAGCCCTGTGCC
10	rs9422	ACGTTGGATGAAGCCAGAGTCATCCATGAG	ACGTTGGATGCTCTCAACTGTTCATGAGTG	R	ggaaCAGGGACCTGTCTTCAGAATC
JNK1					
1	rs10857561	ACGTTGGATGTAATTGCCTACTAGGCAGTC	ACGTTGGATGCATTCTCATGCTCTCTCCAG	R	ACTAGGCAGTCTGCATGT
2	rs59115521	ACGTTGGATGGTGGCATGCTTGTTAATTTT	ACGTTGGATGAAGTGATGACTAAGTGAAGC	F	cttcCATGTATACATGTATTCCCATAG
3	rs3827680	ACGTTGGATGAACTAAGGCAACACCACCAC	ACGTTGGATGATCCTGTCCATGGATAGAGC	R	CACCACTGCCATGGAAGTCTG
4	rs10857565	ACGTTGGATGGCATCTGTAGATTGCTTAGG	ACGTTGGATGGAAGAGAAGGAAGGAAATGG	F	ccTAGTCTTCCAATTCACAAACATAG
5	rs9888128	ACGTTGGATGCAGCAAGAGAGGTGCATTTG	ACGTTGGATGTGTTTTGCCATGGCTTCCAG	R	GTCATTATAAAAGATCCTCAA
6	rs10508901	ACGTTGGATGCTTTGCTGTTAGCTTTGATG	ACGTTGGATGACAGTGCATTTGTGTTGTGG	R	GATGAATACTATTATAAGCCAAAG
7	rs45483593	ACGTTGGATGAACCAACCTAAAGGAGAGGG	ACGTTGGATGATATAAGGAAGTTATGGAC	R	CCCGTATAACTCCATTCTTGTTCTCT
8	rs28395809	ACGTTGGATGAGGAAGTTATGGACTTGGAG	ACGTTGGATGAACCAACCTAAAGGAGAGGG	F	tTGTATGGACTTGGAGGAGAGA
9	rs4838590	ACGTTGGATGTGAATGGGCTTCAGGGTATG	ACGTTGGATGTCTCTGTCCAAAAAAGGCC	R	gtaCAGGGTATGTGTGAATACTGC
10	rs9284	ACGTTGGATGGGTCTCCTAACACGTTTCATC	ACGTTGGATGAATAACCCAGAGGAGTGAG	R	atatgCCTGAATATAACTGGCTACA

	SNP_ID	2nd-PCR Sequence	1st-PCR Sequence	Allele specific (iPLEX) primer Direction	iPLEX primer
TH					
1	rs2070762	ACGTTGGATGGGTACAGATGAGAAAACCG	ACGTTGGATGTCCTTCTCACGGATGGTGTC	F	gggaAGAAAACCGACCCCTGG
2	rs7483056	ACGTTGGATGAGGGCAGCACAAGAGGCAG	ACGTTGGATGGTGACTAATGCAATCAGTGG	R	gCTCCCACCCACCCAGCACAG
3	rs6356	ACGTTGGATGTCAAACACCTTCACAGCTCG	ACGTTGGATGTGGCCTTTGAGGAGAAGGAG	R	GAAGAGCAGGTTTAGCA
4	rs10770141	ACGTTGGATGTCCAAGGGGAAGGCATCAG	ACGTTGGATGACTGCTAGCTCCTGGCTTC	R	GAGGGACGTGCGTGCTCTT
5	rs3842727	ACGTTGGATGCAGCCAGCACAGTTTGTGAC	ACGTTGGATGAGCCACGTGACAGTGGGAG	R	ACAGTTTGTGACCCCTGCTCCCT
GNA11					
1	rs4806907	ACGTTGGATGTTACAGCAGTGCCTGGTATC	ACGTTGGATGTGTCAATCAGGCCTTACTGC	F	cGGCATTTTCATGAATGCCGA
2	rs2238625	ACGTTGGATGAGGCGCTGTGTACATGTTTC	ACGTTGGATGGACATGAGGGATCCAGCACT	R	cctttTACATGTTTCCTGAGCGAACC
3	rs308063	ACGTTGGATGATGGCAGAAATGGGTATGTG	ACGTTGGATGCAGCTTCTGAAACACGCATC	R	CCAATAAAACTTTATCGACAAAA
4	rs411386	ACGTTGGATGACATCAGTCAAGGTCACAGC	ACGTTGGATGTGGGAGGTAGACACAACCTG	R	aaATCAGTCAAGGTCACAGCCAGTCA
5	rs4900	ACGTTGGATGGAGGAGAGCAAAGCCCTGTT	ACGTTGGATGTGTTGAGGAAGAGGATGACG	F	AAAGCCCTGTTCCGGAC
6	rs308040	ACGTTGGATGTCTGCAGAGGGACGGGGAA	ACGTTGGATGGGAAAAAGAACGCCTGACTC	R	gggaaGGACGGGGAACCCGCCATGA
GNB3					
1	rs1129649	ACGTTGGATGACTCCTGCAGCAGTTCTTTG	ACGTTGGATGAAGGTGGGTGCAGGGAATG	R	GCAGCAGTTCTTTGGCTTCT
2	rs2071057	ACGTTGGATGTTGGCTCTACCTTCCCTGT	ACGTTGGATGTCACCTGCCAGGCTCTGCT	F	CCCCCAACCCCCCGCC
3	rs2301339	ACGTTGGATGACGTGGTATGTGTTGGCAGG	ACGTTGGATGACCTGACAGCTCCAGGGCAA	F	ctTTCTACCCCAACCAAGG
4	rs5443	ACGTTGGATGTCTCCACGAGAGCATCATC	ACGTTGGATGTCGTAGCCAGCGAATAGTAG	F	ATCTGCGGCATCACGTC
5	rs5446	ACGTTGGATGAATAAGAAGAGGGCCAGGAC	ACGTTGGATGTGGGTGTTATAGGCGTTTG	R	aagAGAAGAGGGCCAGGACCCTAGT
ADRA1A					
1	rs1383914	ACGTTGGATGTCAAAGGCAGGACCGATG	ACGTTGGATGTAGAAGCTGGAGAGAGCAGG	R	GCCCGCAGTTACCTACA
2	rs1048101	ACGTTGGATGAGGGCATGTTTGGAAGACTG	ACGTTGGATGCAGCCAAGAGTTCAAAAAGG	R	aatgTGAAGACTGCTTTCTGC
3	rs3802241	ACGTTGGATGAAGTAGCTGTGATCAGAGTG	ACGTTGGATGGGTAAAGACCTGGTAGTGAG	F	ggagaTGTGATCAGAGTGAAAAATT
ADRA1B					
1	rs3729604	ACGTTGGATGTAGAAGGGTTCTTCGGTGAC	ACGTTGGATGTGTCCACCGTCATCTCCATC	R	TGGGTGCCGGCTCCTTCCA
2	rs952037	ACGTTGGATGTAGTCTTTGAGTGCCCAAGG	ACGTTGGATGTCCCTGTGTATATCTGCTC	R	caaAGGGACTGAGAAGTGCAAGG
ADRA1D					
1	rs2326478	ACGTTGGATGAGTCCCCTCGACTTTCTTTG	ACGTTGGATGAAGAAAGGCACTGCAGGTAG	F	ACTTCTTTGTATCACCTTCA
2	rs6116268	ACGTTGGATGCTGCCTTCCTCCAAATTGAG	ACGTTGGATGTGGCAGAAAGGCAGAGAAG	F	AAGCAGATCCTCCACA
3	rs6116275	ACGTTGGATGAGCGGGAAGGAACGCAAAG	ACGTTGGATGAGCAGCCACCCACGCCTCT	R	TAGGGGAGAGCGCGGGCTT

F: Forward, R: Reverse, PCR: Pre-amplification PCR primers, SNP_ID: single nucleotide polymorphism identification number. Rho-associated, coiled-coil containing protein kinase 2 (ROCK2), Myosin light chain kinase (MYLK), c-Jun N-terminal kinase1 (JNK1), Tyrosine hydroxylase (TH), guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11), guanine nucleotide binding protein (G protein), beta polypeptide 3 (GNB3), adrenoceptor alpha 1A (ADRA1A), adrenoceptor alpha 1B (ADRA1B), adrenoceptor alpha 1D (ADRA1D).

Supplementary table 2: Primers and cycling conditions for quantitative real time PCR

S.No.	Gene	Forward Primer 5'-3'	Reverse Primer 5'-3'	Product size (base pairs)	Transcript Id.	Nucleotide Id.	Length (base pairs)	Length (amino acids)
1.	<i>ROCK2</i>	GCAAATCTGTTAATACTCGCCT	ATTGGTTTCATCCAGTTGTCTC	296	ENST00000315872	NM_004850.3	8292	1388
2.	<i>MYLK</i>	AAGATTGAAGGATACCCAGAC	TCCATCGTTTCCACAATGAG	218	ENST00000360304	NM_053025.3	7834	1914
3.	<i>JNK1</i>	ACAAACTTAAAGCCAGTCAG	TCAGAAGGATCATAACCAGAC	127	ENST00000374182	NM_002750.3	5638	384
4.	<i>TH</i>	TGTTTGAGACGTTTGAAGCC	AGGTGATGACACTTGTCAG	232	ENST00000352909	NM_000360.3	1889	497
5.	<i>GNA11</i>	TCGTCTACCAGAACATCTTCAC	GTCGGTCAGGTAGTACTTGG	190	ENST00000078429	NM_002067.4	4147	359
6.	<i>GNB3</i>	GATTCTAAGCTGCTGGTAAGTG	GGGATTTGAGGTGTAGATGGA	257	ENST00000229264	NM_002075.2	1923	340
7.	<i>ADRA1A</i>	CCATTGGGTCTTTCTTCCT	CTTGGAGATCCTGTAGAAGGT	293	ENST00000276393	NM_000680.2	2281	466
8.	<i>ADRA1B</i>	AAGAACTTTCACGAGGACAC	CAGAACACCACCTTGAACAC	233	ENST00000306675	NM_000679.3	1738	520
9.	<i>ADRA1D</i>	CCACTCACTCAAGTACCCAG	AGTACATGACCACGATGACC	227	ENST00000379453	NM_000678.3	2677	572
10.	<i>RN18S5</i>	GCTTAATTGACTCAACAC	AGCTATCAATCTGTCAATC	69	ENST00000606783	--	1869	--

Cycling conditions: 95°C-5minutes (Meteor taq activation, initial denaturation),
95°C-15 seconds; 60°C-20 seconds; 72°C-40 seconds (40 cycles, PCR cycle, melt, anneal, extend)
95°C-30 seconds, 60°C-1 minute, 97°C-30 seconds (dissociation step; melt curve)
37°C-30 minutes (cooling)

Supplementary table 3: List of SNPs genotyped in the three groups

Gene	SNP	Chromosome position	Contig position	Allele change	Codon position	Residue change	Function	Call Rate (%)	HWE (p value)		
									HAPE-c	HAPE-p	HLs
Rho-associated, coiled-coil containing protein kinase 2 (<i>ROCK2</i>)	rs978906	11323276	6204488	A/G	--	--	UTR-3	98	0.27	0.65	0.16
	rs6753921	11326755	6207967	A/G	--	--	Intron	95	<0.05	0.40	0.66
	rs2290156	11333208	6214420	C/G	--	--	Intron	97	0.57	0.35	0.45
	rs10495582	11354308	6235520	C/G	--	--	Intron	98	0.39	0.73	0.19
	rs2230774	11359120	6240332	C/A	2	Thr431Asn	missense	90	0.19	0.39	0.54
	rs10167277	11366000	6247212	A/T	--	--	Intron	98	0.37	0.44	0.51
	rs13393192	11368666	6249878	C/T	--	--	Intron	79	0.54	0.04	0.14
	rs10929727	11384214	6265426	C/T	--	--	Intron	98	0.66	0.34	0.65
	rs6716817	11385834	6267046	A/G	--	--	Intron	97	0.78	0.59	0.26
	rs4477886	11388294	6269506	A/G	--	--	Intron	97	0.81	0.90	0.16
	rs41264193	11389907	6271119	C/T	3	Ser114Ser	cds-synon	98	Single major genotype (CC) call (HWE, cannot be calculated)		
Myosin light chain kinase (<i>MYLK</i>)	rs10929728	11411483	6292695	C/T	--	--	Intron	97	0.36	0.91	0.70
	rs12622447	11475445	6356657	A/G	--	--	Intron	no call	--		
	rs9422	123332340	29827486	A/C	--	--	UTR-3	97	0.43	0.02	0.78
	rs11717814	123408551	29903697	G/C	--	--	Intron	98	0.52	0.40	0.71
	rs40305	123411589	29906735	C/T	3	Thr1186Thr	cds-synon	98	0.37	0.15	0.69
	rs820336	123415781	29910927	A/G	--	--	Intron	98	0.36	0.45	0.80
	rs936170	123422817	29917963	C/G	--	--	Intron	97	<0.05	0.25	0.60
	rs3796164	123453061	29948207	A/G	2	Val261Ala	missense	97	0.60	<0.05	<0.05
	rs28497577	123512627	30007773	G/T	2	Pro21His	missense	98	0.59	0.91	0.65
	rs1343700	123571754	30066900	C/T	--	--	Intron	97	0.38	0.75	<0.05
c-Jun N-terminal kinase1 (<i>JNK1</i>)	rs16834817	123578033	30073179	A/G	--	--	Intron	97	0.82	0.38	<0.05
	rs2700408	123595432	123595432	A/G	--	--	UTR-5	87	0.18	0.91	<0.05
	rs10857561	49608638	413102	A/G	--	--	nearGene-5	97	0.23	0.15	0.39
	rs59115521	49610371	414835	A/G	--	--	Intron	81	Single major genotype (AA) call (HWE, cannot be calculated)		
	rs3827680	49614391	418855	A/G	--	--	Intron	98	0.57	0.96	0.87
	rs10857565	49619793	424257	A/G	--	--	Intron	96	0.67	0.18	0.34
	rs9888128	49620267	424731	A/G	--	--	Intron	16	Low call rate, HWE cannot be calculated		
	rs10508901	49627398	431862	C/A	--	--	Intron	97	0.20	0.18	0.29
	rs45483593	49639268	443732	G/A	1	Glu365Lys	missense	97	Single major genotype (GG) call (HWE, cannot be calculated)		
	rs28395809	49639274	443738	A/G	1	Thr367Ala	missense	99	Single major genotype (AA) call (HWE, cannot be calculated)		
	rs4838590	49642591	447055	A/C	--	--	Intron	97	0.44	0.62	0.76
	rs9284	49643570	448034	G/T	--	--	nearGene-3	96	0.38	0.98	0.58

Gene	SNP	Chromosome position	Contig position	Allele change	Codon position	Residue change	Function	Call Rate (%)	HWE (p value)		
									HAPE-c	HAPE-p	HLs
Tyrosine hydroxylase (<i>TH</i>)	rs3842727	2184848	2124848	A/C	--	--	nearGene-3	97	0.05	0.29	0.82
	rs2070762	2186335	2186335	C/T	--	--	Intron	97	<0.05	0.07	0.84
	rs7483056	2190519	2130519	A/G	--	--	Intron	95	0.17	0.80	0.71
	rs6356	2190951	2130951	A/G	1	Val81Met	missense	98	0.49	0.15	0.05
	rs10770141	2193840	2133840	A/G	--	--	nearGene-5	97	<0.05	0.58	0.88
guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (<i>GNA11</i>)	rs4806907	3093163	3033163	C/T	--	--	nearGene-5	97	0.25	0.34	0.25
	rs2238625	3104652	3044652	C/T	--	--	Intron	96	0.15	0.86	0.37
	rs308063	3112023	3052023	A/G	--	--	Intron	98	<0.05	<0.05	<0.05
	rs411386	3113903	3053903	G/T	--	--	Intron	96	0.53	<0.05	0.41
	rs4900	3119239	3059239	C/T	3	Thr257Thr	cds-synon	90	<0.05	0.82	0.10
	rs308040	3121908	3061908	C/G	--	--	nearGene-3	96	0.47	<0.05	0.78
guanine nucleotide binding protein (G protein), beta polypeptide 3 (<i>GNB3</i>)	rs1129649	6948468	6888468	C/T	--	--	nearGene-5	97	0.39	0.64	0.46
	rs2071057	6950052	6890052	A/G	--	--	UTR-5	98	<0.05	<0.05	0.80
	rs2301339	6954624	6894624	A/G	--	--	Intron	97	<0.05	0.31	0.46
	rs5443	6954875	6894875	C/T	3	Ser275Ser	cds-synon	97	0.08	0.35	0.31
	rs5446	6956462	6956462	C/T	--	--	UTR-3	97	<0.05	0.90	0.42
adrenoceptor alpha 1A (<i>ADRA1A</i>)	rs3802241	26623384	14481530	A/G	--	--	UTR-3	96	0.49	0.44	0.84
	rs1048101	26628028	14486174	C/T	1	Cys347Arg	missense	96	0.33	0.47	0.93
	rs1383914	26723049	14581195	A/G	--	--	nearGene-5	no call	--		
adrenoceptor alpha 1B (<i>ADRA1B</i>)	rs952037	159390877	4202150	C/T	--	--	Intron	96	0.38	0.66	0.85
	rs3729604	159344461	4155734	A/G	3	Gly183Gly	cds-synon	95	0.53	0.94	0.66
adrenoceptor alpha 1D (<i>ADRA1D</i>)	rs2326478	4208247	4148247	C/T	--	--	Intron	94	<0.05	<0.05	<0.05
	rs6116268	4211440	4151440	C/T	--	--	Intron	98	1.0	0.56	0.80
	rs6116275	4230136	4170136	C/G	--	--	nearGene-5	98	Single major genotype (CC) call (HWE, cannot be calculated)		

A total of 57 SNPs across 9 genes were studied. 21 SNPs were removed from further analysis owing to either of the reasons like no call, low call (<95%), single major genotype call and for controls not being in HWE. All outlier SNPs are shaded in pink. **SNP**: Single nucleotide polymorphism, **HWE**: Hardy Weinberg equilibrium. **HAPE-p**: HAPE-patients, **HAPE-c**: HAPE-controls, **HLs**: Highlanders.

Supplementary table 4: Statistical analysis on the genetic models of the studied SNPs in HAPE-p and HAPE-c datasets

Gene (rsID) (ROCK2)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs978906	AA		69 (32%)	46 (22%)	1			
	AG		109 (50%)	113 (54%)	0.80 (1.49-1.33)	0.713	-0.215	0.39
	GG		38 (18%)	51 (24%)	0.61 (0.34-1.11)	2.614	-0.492	0.11
	A		247 (57%)	205 (49%)	1			
	G		185 (43%)	215 (51%)	0.80 (0.59-1.07)	2.24	-0.222	0.14
	Dominant Model	AA	69 (31.9%)	46 (21.9%)	1			
		AG-GG	147 (68.1%)	164 (78.1%)	0.74 (0.46-1.19)	1.53	-0.297	0.22
	Recessive Model	AA-AG	178 (82.4%)	159 (75.7%)	1			
		GG	38 (17.6%)	51 (24.3%)	0.73 (0.44-1.20)	1.56	-0.320	0.21
	Overdominant Model	AA-GG	107 (49.5%)	97 (46.2%)	1			
		AG	109 (50.5%)	113 (53.8%)	0.99 (0.66-1.49)	0.003	-0.011	0.96
rs2290156	GG		67 (32%)	78 (38%)	1			
	GC		98 (47%)	100 (49%)	1.06 (0.67-1.67)	0.064	0.059	0.80
	CC		45 (21%)	27 (13%)	1.63 (0.87-3.03)	2.362	0.488	0.12
	G		232 (55%)	256 (62%)	1			
	C		188 (45%)	154 (38%)	1.25 (0.93-1.68)	2.096	0.220	0.15
	Dominant Model	GG	78 (38%)	67 (31.9%)	1			
		GC-CC	127 (62%)	143 (68.1%)	1.20 (0.78-1.85)	0.671	0.181	0.41
	Recessive Model	GG-GC	165 (78.6%)	178 (86.8%)	1			
		CC	45 (21.4%)	27 (13.2%)	1.60 (0.91-2.81)	2.694	0.470	0.10
	Overdominant Model	GG-CC	112 (53.3%)	105 (51.2%)	1			
		GC	98 (46.7%)	100 (48.8%)	0.91 (0.60-1.38)	0.197	-0.094	0.66
rs10495582	CC		75 (35%)	45 (22 %)	1			
	CG		103 (47%)	108 (53%)	0.69 (0.42-1.13)	2.138	-0.370	0.14
	GG		39 (18%)	51 (25%)	0.54 (0.30-0.97)	4.219	-0.613	0.04
	C		253 (58%)	198 (49%)	1			
	G		181 (42%)	210 (51%)	0.75 (0.56-1.00)	3.936	-0.295	0.05
	Dominant Model	CC	75 (34.6%)	45 (22.1%)	1			
		CG-GG	142 (65.4%)	159 (77.9%)	0.64 (0.40-1.02)	3.457	-0.442	0.06
	Recessive Model	CC-CG	178 (82%)	153 (75%)	1			
		GG	39 (18%)	51 (25%)	0.71 (0.43-1.16)	1.895	-0.350	0.17
	Overdominant Model	CC-GG	114 (52.5%)	96 (47.1%)	1			
		CG	103 (47.5%)	108 (52.9%)	0.90 (0.59-1.36)	0.260	-0.107	0.61
rs10167277	TT		63 (29%)	74 (36%)	1			
	TA		103 (47%)	104 (50%)	1.14 (0.72-1.79)	0.300	0.128	0.58
	AA		52 (24%)	28 (14%)	1.87 (1.01-3.48)	3.948	0.627	0.05
	T		229 (53%)	252 (61%)	1			
	A		207 (47%)	160 (39%)	1.34 (0.99-1.79)	3.738	0.289	0.05
	Dominant Model	TT	63 (28.9%)	74 (35.9%)	1			
		TA-AA	155 (71.1%)	132 (64.1%)	1.31 (0.85-2.03)	1.480	0.270	0.22
	Recessive Model	TT-TA	166 (76.2%)	178 (86.4%)	1			
		AA	52 (23.9%)	28 (13.6%)	1.74 (1.02-2.99)	4.052	0.555	0.04
	Overdominant Model	TT-AA	115 (52.8%)	102 (49.5%)	1			
		TA	103 (47.2%)	104 (50.5%)	0.92 (0.61-1.38)	0.173	-0.087	0.68
rs10929727	TT		69 (32%)	80 (38%)	1			
	TC		101 (46%)	101 (48%)	1.07 (0.68-1.69)	0.094	0.071	0.76
	CC		48 (22%)	28 (13%)	1.71 (0.93-3.15)	2.987	0.537	0.08
	T		239 (55%)	261 (62%)	1			
	C		197 (45%)	157 (38%)	1.28 (0.95-1.71)	2.675	0.245	0.102
	Dominant Model	TT	80 (38.3%)	69 (31.6%)	1			
		TC-CC	129 (61.7%)	149 (68.3%)	1.23 (0.80-1.88)	0.870	0.203	0.35
	Recessive Model	TT-TC	181 (86.6%)	170 (78%)	1			
		CC	28 (13.4%)	48 (22%)	1.67 (0.96-2.90)	3.339	0.513	0.07
	Overdominant Model	TT-CC	108 (51.7%)	117 (53.7%)	1			
		TC	101 (48.3%)	101 (46.3%)	0.90 (0.60-1.36)	0.239	-1.02	0.63

Gene (rsID) (<i>ROCK2</i>)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs6716817	AA		69 (32%)	44 (21%)	1			
	AG		101 (47%)	105 (51%)	0.75 (0.45-1.23)	1.319	-0.294	0.25
	GG		43 (20%)	58 (28%)	0.56 (0.32-0.99)	3.867	-0.575	0.05
	A		239 (56%)	193 (51%)	1			
	G		187 (44%)	221 (49%)	0.75 (0.56-1.00)	3.771	-0.287	0.05
	Dominant Model	AA	69 (32.4%)	44 (21.3%)	1			
		AG-GG	144 (67.6%)	163 (78.7%)	0.68 (0.42-1.08)	2.676	-0.392	0.10
	Recessive Model	AA-AG	170 (79.8%)	149 (72%)	1			
		GG	43 (20.2%)	58 (28%)	0.69 (0.43-1.12)	2.285	-0.368	0.13
	Overdominant Model	AA-GG	112 (52.6%)	102 (49.3%)	1			
		AG	101 (47.4%)	105 (50.7%)	0.97 (0.65-1.47)	0.015	-0.026	0.90
rs4477886	AA		64 (30%)	47 (22%)	1			
	AG		108 (50%)	106 (51%)	0.89 (0.53-1.47)	0.218	-0.121	0.64
	GG		44 (20%)	56 (27%)	0.69 (0.39-1.22)	1.648	-0.377	0.19
	A		236 (55%)	200 (48%)	1			
	G		196 (45%)	218 (52%)	0.84 (0.63-1.12)	1.442	-0.178	0.23
	Dominant Model	AA	64 (29.6%)	47 (22.5%)	1			
		AG-GG	152 (70.4%)	162 (77.5%)	0.81 (0.51-1.31)	0.732	-0.207	0.39
	Recessive Model	AA-AG	153 (73.2%)	172 (79.6%)	1			
		GG	56 (26.8%)	44 (20.4%)	0.76 (0.47-1.23)	1.234	-0.272	0.27
	Overdominant Model	AA-GG	103 (49.3%)	108 (50%)	1			
		AG	106 (50.7%)	108 (50%)	1.05 (0.69-1.58)	0.045	0.044	0.83
rs10929728	TT		57 (27%)	76 (37%)	1			
	TC		104 (50%)	102 (50%)	1.23 (0.77-1.95)	0.747	0.204	0.39
	CC		49 (23%)	26 (13%)	2.04 (1.09-3.81)	4.939	0.711	0.03
	T		218 (52%)	254 (62%)	1			
	C		202 (48%)	154 (38%)	1.39 (1.04-1.87)	4.889	0.333	0.03
	Dominant Model	TT	57 (27.1%)	76 (37.2%)	1			
		TC-CC	153 (72.9%)	128 (62.8%)	1.41 (0.91-2.20)	2.378	0.347	0.12
	Recessive Model	TT-TC	161 (76.7%)	178 (87.2%)	1			
		CC	49 (23.3%)	26 (12.8%)	1.84 (1.06-3.21)	4.651	0.611	0.03
	Overdominant Model	TT-CC	106 (50.5%)	102 (50%)	1			
		TC	104 (49.5%)	102 (50%)	0.96 (0.64-1.45)	0.039	-0.041	0.84
Gene (rsID) (<i>MYLK</i>)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs9422	CC		103 (48%)	80 (39%)	1			
	CA		81 (38%)	93 (45%)	0.74 (0.47-1.15)	1.782	-0.305	0.18
	AA		32 (15%)	34 (16%)	0.77 (0.42-1.40)	0.746	-0.266	0.39
	C		287 (66%)	253 (61%)	1			
	A		145 (34%)	161 (39%)	0.82 (0.61-1.11)	1.639	-0.197	0.20
	Dominant Model	CC	80 (38.6%)	103 (47.7%)	1			
		CA-AA	127 (61.4%)	113 (52.3%)	0.74 (0.49-1.12)	2.064	-0.305	0.15
	Recessive Model	CC-CA	173 (83.6%)	184 (85.2%)	1			
		AA	34 (16.4%)	32 (14.8%)	0.88 (0.50-1.55)	0.199	-0.128	0.66
	Overdominant Model	CC-AA	135 (62.5%)	114 (55.1%)	1			
		CA	81 (37.5%)	93 (44.9%)	0.79 (0.52-1.20)	1.237	-0.237	0.27
rs11717814	GG		73 (33%)	101 (49%)	1			
	GC		101 (46%)	83 (40%)	1.59 (1.01-2.51)	4.074	0.467	0.04
	CC		44 (20%)	21 (10%)	2.86 (1.49-5.47)	10.07	1.050	0.002
	G		247 (57%)	285 (70%)	1			
	C		189 (43%)	125 (30%)	1.70 (1.26-2.31)	11.86	0.532	0.001
	Dominant Model	GG	73 (33.5%)	101 (49.3%)	1			
		GC-CC	145 (66.5%)	104 (50.7%)	1.84 (1.21-2.81)	7.996	0.611	0.005
	Recessive Model	GG-GC	174 (79.8%)	184 (89.8%)	1			
		CC	44 (20.2%)	21 (10.2%)	2.22 (1.23-4.02)	7.001	0.799	0.008
	Overdominant Model	GG-CC	117 (53.7%)	122 (59.5%)	1			
		GC	101 (46.3%)	83 (40.5%)	1.20 (0.79-1.81)	0.710	0.178	0.40

Gene (rsID) (MYLK)	Genotype/Alele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs40305	CC		81 (38%)	102 (49%)	1			
	CT		94 (44%)	84 (40%)	1.43 (0.91-2.25)	2.422	0.358	0.12
	TT		41 (19%)	23 (11%)	2.29 (1.22-4.33)	6.593	0.831	0.01
	C		256 (59%)	288 (69%)	1			
	T		176 (41%)	130 (31%)	1.53 (1.13-2.08)	7.613	0.428	0.006
	Dominant Model	CC	81 (37.5%)	102 (48.8%)	1			
		CT-TT	135 (62.5%)	107 (51.2%)	1.61 (1.06-2.45)	4.961	0.476	0.03
	Recessive Model	CC-CT	175 (81%)	186 (89%)	1			
		TT	41 (19%)	23 (11%)	1.92 (1.06-3.46)	4.649	0.650	0.03
	Overdominant Model	CC-TT	122 (56.5%)	125 (59.8%)	1			
		CT	94 (43.5%)	84 (40.2%)	1.15 (0.76-1.74)	0.440	0.141	0.51
rs820336	GG		74 (35%)	94 (46%)	1			
	GA		99 (46%)	84 (41%)	1.47 (0.93-2.32)	2.782	0.387	0.095
	AA		41 (19%)	25 (12%)	1.99 (1.06-3.74)	4.635	0.690	0.03
	G		247 (58%)	272 (67%)	1			
	A		181 (42%)	134 (33%)	1.45 (1.07-1.96)	5.791	0.371	0.02
	Dominant Model	GG	74 (34.6%)	94 (46.3%)	1			
		GA-AA	140 (65.4%)	109 (53.7%)	1.59 (1.04-2.44)	4.570	0.464	0.03
	Recessive Model	GG-GA	173 (80.8%)	178 (87.7%)	1			
		AA	41 (19.2%)	25 (12.3%)	1.62 (0.91-2.88)	2.736	0.484	0.098
	Overdominant Model	GG-AA	115 (53.7%)	119 (58.6%)	1			
		GA	99 (46.3%)	84 (41.4%)	1.21 (0.80-1.83)	0.779	0.187	0.38
rs3796164	AA		128 (61%)	90 (43%)	1			
	AG		61 (29%)	91 (44%)	0.44 (0.28-0.70)	12.194	-0.811	0.0005
	GG		20 (10%)	27 (13%)	0.58 (0.29-1.14)	2.482	-0.540	0.12
	A		317 (76%)	271 (65%)	1			
	G		101 (24%)	145 (35%)	0.61 (0.44-0.84)	9.071	-0.497	0.003
	Dominant Model	AA	128 (61.2%)	90 (43.3%)	1			
		AG-GG	81 (38.8%)	118 (56.7%)	0.47 (0.31-0.72)	12.154	-0.748	0.0005
	Recessive Model	AA-AG	189 (90.4%)	181 (87%)	1			
		GG	20 (9.6%)	27 (13%)	0.81 (0.42-1.56)	0.387	-0.207	0.53
	Overdominant Model	AA-GG	148 (70.8%)	117 (56.2%)	1			
		AG	61 (29.2%)	91 (43.8%)	0.49 (0.31-0.76)	10.306	-0.721	0.001
rs28497577	GG		137 (63%)	103 (50%)	1			
	GT		72 (33%)	83 (40%)	0.59 (0.39-0.92)	5.422	-0.515	0.02
	TT		9 (4%)	20 (10%)	0.37 (0.16-0.88)	5.081	-0.987	0.02
	G		346 (79%)	289 (70%)	1			
	T		90 (21%)	123 (30%)	0.60 (0.43-0.84)	9.050	-0.515	0.003
	Dominant Model	GG	137 (62.8%)	103 (50%)	1			
		GT-TT	81 (37.2%)	103 (50%)	0.55 (0.36-0.84)	7.856	-0.596	0.005
	Recessive Model	GG-GT	209 (95.9%)	186 (90.3%)	1			
		TT	9 (4.1%)	20 (9.7%)	0.46 (0.19-1.08)	3.185	-0.784	0.07
	Overdominant Model	GG-TT	146 (67%)	123 (59.7%)	1			
		GT	72 (33%)	83 (40.3%)	0.66 (0.43-1.00)	3.762	-0.423	0.05
rs1343700	CC		102 (48%)	128 (63%)	1			
	CT		90 (42%)	63 (31%)	1.55 (0.99-2.42)	3.670	0.436	0.06
	TT		22 (10%)	11 (5%)	2.21 (0.96-5.06)	3.553	0.794	0.06
	C		294 (69%)	319 (79%)	1			
	T		134 (31%)	85 (21%)	1.54 (1.09-2.15)	6.311	0.429	0.01
	Dominant Model	CC	102 (47.7%)	128 (63.4%)	1			
		CT-TT	112 (52.3%)	74 (36.6%)	1.65 (1.09-2.51)	5.510	0.501	0.02
	Recessive Model	CC-CT	192 (89.7%)	191 (94.5%)	1			
		TT	22 (10.3%)	11 (5.5%)	1.84 (0.83-4.11)	2.221	0.610	0.14
	Overdominant Model	CC-TT	124 (57.9%)	139 (68.8%)	1			
		CT	90 (42.1%)	90 (42.1%)	1.42 (0.92-2.18)	2.521	0.348	0.11

Gene (rsID) (MYLK)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs16834817	AA		150 (70%)	136 (65%)	1			
	AG		57 (27%)	65 (31%)	0.81 (0.51-1.27)	0.865	-0.216	0.35
	GG		8 (4%)	7 (3%)	0.98 (0.33-2.91)	0.001	-0.201	0.97
	A		357 (83%)	337 (81%)	1			
	G		73 (17%)	79 (19%)	0.87 (0.59-1.27)	0.544	-0.142	0.46
	Dominant Model	AA	150 (69.8%)	136 (65.4%)	1			
		AG-GG	65 (30.2%)	72 (34.6%)	0.82 (0.53-1.28)	0.769	-0.197	0.38
	Recessive Model	AA-AG	207 (96.3%)	201 (96.6%)	1			
		GG	8 (3.7%)	7 (3.4%)	1.03 (0.35-3.05)	0.002	0.027	0.96
	Overdominant Model	AA-GG	158 (73.5%)	143 (68.8%)	1			
		AG	57 (26.5%)	65 (31.2%)	0.81 (0.51-1.27)	0.861	-0.215	0.35
Gene (rsID) (JNK1)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs10857561	GG		75 (35%)	59 (28%)	1			
	GA		111 (52%)	112 (54%)	0.78 (0.49-1.24)	1.134	-0.251	0.29
	AA		27 (13%)	38 (18%)	0.55 (0.29-1.06)	3.218	-0.598	0.07
	G		261 (61%)	230 (55%)	1			
	A		165 (39%)	188 (45%)	0.77 (0.57-1.04)	2.971	-0.261	0.09
	Dominant Model	GG	75 (35.2%)	59 (28.2%)	1			
		GA-AA	138 (64.8%)	150 (71.8%)	0.72 (0.46-1.13)	2.040	-0.324	0.15
	Recessive Model	GG-GA	186 (87.3%)	171 (81.8%)	1			
		AA	27 (12.7%)	38 (18.2%)	0.64 (0.36-1.15)	2.193	-0.440	0.14
	Overdominant Model	GG-AA	102 (47.9%)	97 (46.4%)	1			
		GA	111 (52.1%)	112 (53.6%)	0.95 (0.63-1.43)	0.069	-0.056	0.79
rs3827680	AA		77 (36%)	92 (45%)	1			
	AG		103 (48%)	94 (46%)	1.28 (0.82-1.99)	1.186	0.245	0.28
	GG		35 (16%)	20 (10%)	1.71 (0.88-3.33)	2.531	0.538	0.11
	A		257 (60%)	278 (67%)	1			
	G		173 (40%)	134 (33%)	1.28 (0.95-1.73)	2.584	0.247	0.11
	Dominant Model	AA	77 (35.8%)	92 (44.7%)	1			
		AG-GG	138 (64.2%)	114 (55.3%)	1.36 (0.89-2.06)	2.020	0.304	0.16
	Recessive Model	AA-AG	180 (83.7%)	186 (90.3%)	1			
		GG	35 (16.3%)	20 (9.7%)	1.46 (0.78-2.71)	1.404	0.375	0.24
	Overdominant Model	AA-GG	112 (52.1%)	112 (54.4%)	1			
		AG	103 (47.9%)	94 (45.6%)	1.13 (0.75-1.71)	0.352	0.124	0.55
rs10857565	GG		95 (46%)	84 (41%)	1			
	GA		95 (46%)	96 (47%)	0.91 (0.59-1.41)	0.177	-0.093	0.67
	AA		15 (7%)	24 (12%)	0.57 (0.26-1.22)	2.128	-0.569	0.15
	G		285 (70%)	264 (65%)	1			
	A		125 (30%)	144 (35%)	0.83 (0.61-1.14)	1.368	-0.187	0.24
	Dominant Model	GG	95 (46.3%)	84 (41.2%)	1			
		GA-AA	110 (53.7%)	120 (58.8%)	0.85 (0.56-1.29)	0.604	-0.166	0.44
	Recessive Model	GG-GA	190 (92.7%)	180 (88.2%)	1			
		AA	15 (7.3%)	24 (11.8%)	0.61 (0.29-1.27)	1.751	-0.493	0.19
	Overdominant Model	GG-AA	110 (53.7%)	108 (52.9%)	1			
		GA	95 (46.3%)	96 (47.1%)	1.00 (0.66-1.52)	0.000	0.002	0.99
rs10508901	CC		74 (35%)	60 (29%)	1			
	CA		109 (52%)	110 (54%)	0.80 (0.51-1.27)	0.881	-0.221	0.35
	AA		27 (13%)	35 (17%)	0.62 (0.32-1.19)	2.070	-0.48	0.15
	C		257 (61%)	230 (56%)	1			
	A		163 (39%)	180 (44%)	0.81 (0.59-1.09)	1.966	-0.214	0.16
	Dominant Model	CC	74 (35.2%)	60 (29.3%)	1			
		CA-AA	136 (64.8%)	145 (70.7%)	0.76 (0.49-1.19)	1.449	-0.273	0.23
	Recessive Model	CC-CA	183 (87.1%)	170 (82.9%)	1			
		AA	27 (12.9%)	35 (17.1%)	0.71 (0.39-1.27)	1.330	-0.346	0.25
	Overdominant Model	CC-AA	101 (48.1%)	95 (46.3%)	1			
		CA	109 (51.9%)	110 (53.7%)	0.94 (0.62-1.42)	0.093	-0.065	0.76

Gene (rsID) (JNK1)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs4838590	AA		84 (39%)	98 (47%)	1			
	AC		98 (46%)	93 (45%)	1.19 (0.77-1.83)	0.582	0.170	0.45
	CC		33 (15%)	17 (8%)	1.89 (0.95-3.77)	3.289	0.638	0.07
	A		266 (62%)	289 (69%)	1			
	C		164 (38%)	127 (31%)	1.29 (0.96-1.76)	2.828	0.262	0.09
	Dominant Model	AA	84 (39.1%)	98 (47.1%)	1			
		AC-CC	131 (60.9%)	110 (52.9%)	1.30 (0.86-1.97)	1.534	0.262	0.22
	Recessive Model	AA-AC	182 (84.7%)	191 (91.8%)	1			
		CC	33 (15.3%)	17 (8.2%)	1.70 (0.89-3.27)	2.545	0.531	0.11
	Overdominant Model	AA-CC	117 (54.4%)	115 (55.3%)	1			
		AC	98 (45.6%)	93 (44.7%)	1.04 (0.69-1.57)	0.035	0.039	0.85
rs9284	TT		78 (38%)	95 (46%)	1			
	TG		98 (47%)	93 (45%)	1.24 (0.80-1.93)	0.924	0.216	0.34
	GG		31 (15%)	17 (8%)	2.01 (1.00-4.02)	3.868	0.696	0.05
	T		254 (61%)	283 (69%)	1			
	G		160 (39%)	127 (31%)	1.34 (0.98-1.81)	3.444	0.290	0.06
	Dominant Model	AA	78 (37.7%)	95 (46.3%)	1			
		AG-GG	129 (62.3%)	110 (53.7%)	1.36 (0.89-2.07)	2.075	0.308	0.15
	Recessive Model	AA-AG	176 (85%)	188 (91.7%)	1			
		GG	31 (15%)	17 (8.3%)	1.76 (0.91-3.39)	2.809	0.563	0.09
	Overdominant Model	AA-GG	109 (52.7%)	112 (54.6%)	1			
		AG	98 (47.3%)	93 (45.4%)	1.07 (0.71-1.62)	0.113	0.071	0.74
Gene (rsID) (TH)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs7483056	AA		72 (34%)	74 (37%)	1			
	AG		104 (49%)	88 (44%)	1.21 (0.76-1.91)	0.638	0.187	0.42
	GG		35 (17%)	39 (19%)	0.93 (0.51-1.70)	0.060	-0.076	0.81
	A		248 (59%)	236 (59%)	1			
	G		174 (41%)	166 (41%)	0.99 (0.74-1.34)	0.000	0.000	0.99
	Dominant Model	AA	72 (34.1%)	74 (36.8%)	1			
		AG-GG	139 (65.9%)	127 (63.2%)	1.12 (0.73-1.73)	0.264	0.113	0.61
	Recessive Model	AA-AG	176 (83.4%)	162 (80.6%)	1			
		GG	35 (16.6%)	39 (19.4%)	0.84 (0.49-1.43)	0.422	-0.179	0.52
	Overdominant Model	AA-GG	107 (50.7%)	113 (56.2%)	1			
		AG	104 (49.3%)	88 (43.8%)	1.23 (0.81-1.87)	0.985	0.210	0.32
rs6356	AA		82 (39%)	76 (36%)	1			
	AG		91 (43%)	96 (46%)	0.77 (0.49-1.23)	1.184	-0.256	0.28
	GG		38 (19%)	37 (18%)	0.94 (0.52-1.68)	0.047	-0.064	0.83
	A		255 (60%)	248 (59%)	1			
	G		167 (40%)	170 (41%)	0.93 (0.69-1.25)	0.221	-0.071	0.64
	Dominant Model	AA	82 (38.9%)	76 (36.4%)	1			
		AG-GG	129 (61.1%)	133 (63.6%)	0.82 (0.54-1.26)	0.793	-0.193	0.37
	Recessive Model	AA-AG	173 (82%)	172 (82.3%)	1			
		GG	38 (18%)	37 (17.7%)	1.08 (0.63-1.83)	0.074	0.074	0.79
	Overdominant Model	AA-GG	120 (56.9%)	113 (54.1%)	1			
		AG	91 (43.1%)	96 (45.9%)	0.80 (0.53-1.21)	1.165	-0.229	0.28
rs3842727	AA		155 (71%)	166 (81%)	1			
	AC		60 (28%)	34 (17%)	1.59 (0.96-2.63)	3.200	0.461	0.07
	CC		3 (1%)	5 (2%)	0.54 (0.11-2.65)	0.576	-0.615	0.45
	A		370 (85%)	366 (89%)	1			
	C		66 (15%)	44 (11%)	1.28 (0.83-1.98)	1.266	0.248	0.26
	Dominant Model	AA	155 (71.1%)	166 (81%)	1			
		AC-CC	63 (28.9%)	39 (19%)	1.46 (0.90-2.37)	2.383	0.381	0.12
	Recessive Model	AA-AC	215 (98.6%)	200 (97.6%)	1			
		CC	3 (1.4%)	5 (2.4%)	0.50 (0.11-2.35)	0.775	-0.696	0.38
	Overdominant Model	AA-CC	158 (72.5%)	171 (83.4%)	1			
		AC	60 (27.5%)	34 (16.6%)	1.62 (0.98-2.67)	3.537	0.481	0.06

Gene (rsID) (GNA11)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs4806907	TT		84 (40%)	59 (29%)	1			
	TC		93 (44%)	110 (53%)	0.67 (0.42-1.06)	2.983	-0.403	0.08
	CC		34 (16%)	37 (18%)	0.79 (0.43-1.45)	0.586	-0.238	0.44
	T		261 (62%)	228 (55%)	1			
	C		161 (38%)	184 (45%)	0.85 (0.63-1.15)	1.132	-0.160	0.29
	Dominant Model	TT	84 (39.8%)	59 (28.6%)	1			
		TC-CC	127 (60.2%)	147 (71.4%)	0.70 (0.45-1.09)	2.470	-0.351	0.12
	Recessive Model	TT-TC	177 (83.9%)	169 (82%)	1			
		CC	34 (16.1%)	37 (18%)	1.00 (0.58-1.72)	0.000	0.000	0.99
	Overdominant Model	TT-CC	118 (55.9%)	96 (46.6%)	1			
		TC	93 (44.1%)	110 (53.4%)	0.73 (0.49-1.11)	2.190	-0.312	0.14
rs2238625	TT		86 (40%)	107 (51%)	1			
	TC		99 (46%)	90 (43%)	1.34 (0.87-2.06)	1.741	0.290	0.187
	CC		30 (14%)	11 (5%)	3.82 (1.73-8.43)	11.037	1.341	0.001
	T		271 (63%)	304 (73%)	1			
	C		159 (37%)	112 (27%)	1.64 (1.19-2.24)	9.516	0.493	0.002
	Dominant Model	TT	86 (40%)	107 (51.4%)	1			
		TC-CC	129 (60%)	101 (48.6%)	1.59 (1.05-2.41)	4.859	0.465	0.03
	Recessive Model	TT-TC	185 (86%)	197 (94.7%)	1			
		CC	30 (13.9%)	11 (5.3%)	3.25 (1.53-6.93)	9.334	1.180	0.002
	Overdominant Model	TT-CC	116 (54%)	118 (56.7%)	1			
		TC	99 (46%)	90 (43.3%)	1.07 (0.71-1.62)	0.105	0.068	0.75
rs411386	TT		64 (30%)	72 (35%)	1			
	TG		88 (41%)	97 (47%)	0.97 (0.60-1.56)	0.021	-0.036	0.88
	GG		61 (29%)	39 (19%)	1.51 (0.85-2.66)	1.972	0.409	0.16
	T		216 (51%)	241 (58%)	1			
	G		210 (49%)	175 (42%)	1.24 (0.92-1.66)	2.019	0.212	0.16
	Dominant Model	TT	64 (30.1%)	72 (34.6%)	1			
		TG-GG	149 (70%)	136 (65.4%)	1.13 (0.73-1.76)	0.301	0.123	0.58
	Recessive Model	TT-TG	152 (71.4%)	169 (81.2%)	1			
		GG	61 (28.6%)	39 (18.8%)	1.55 (0.95-2.54)	3.078	0.440	0.08
	Overdominant Model	TT-GG	125 (58.7%)	111 (53.4%)	1			
		TG	88 (41.3%)	97 (46.6%)	0.81 (0.54-1.23)	0.954	-0.207	0.33
rs308040	GG		60 (28%)	62 (32%)	1			
	GC		89 (42%)	92 (47%)	0.84 (0.51-1.38)	0.470	-0.174	0.49
	CC		64 (30%)	42 (21%)	1.39 (0.79-2.46)	1.279	0.330	0.26
	G		209 (49%)	216 (55%)	1			
	C		217 (51%)	176 (45%)	1.19 (0.89-1.60)	1.366	0.176	0.24
	Dominant Model	GG	60 (28.2%)	62 (31.6%)	1			
		GC-CC	153 (71.8%)	134 (68.4%)	1.02 (0.65-1.61)	0.007	0.020	0.93
	Recessive Model	GG-GC	149 (70%)	154 (78.6%)	1			
		CC	64 (30.1%)	42 (21.4%)	1.55 (0.96-2.51)	3.193	0.438	0.07
	Overdominant Model	GG-CC	124 (58.2%)	104 (53.1%)	1			
		GC	89 (41.8%)	92 (46.9%)	0.72 (0.47-1.10)	2.261	-0.325	0.13
Gene (rsID) (GNB3)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs1129649	TT		94 (43%)	80 (39%)	1			
	TC		100 (46%)	102 (49%)	0.78 (0.50-1.21)	1.255	-0.251	0.26
	CC		23 (11%)	25 (12%)	0.71 (0.36-1.40)	0.979	-0.345	0.32
	T		288 (66%)	262 (63%)	1			
	C		146 (44%)	152 (37%)	0.82 (0.61-1.12)	1.566	-0.195	0.21
	Dominant Model	TT	94 (43.3%)	80 (38.6%)	1			
		TC-CC	123 (56.7%)	127 (61.4%)	0.76 (0.50-1.16)	1.639	-0.274	0.20
	Recessive Model	TT-TC	194 (89.4%)	182 (87.9%)	1			
		CC	23 (10.6%)	25 (12.1%)	0.80 (0.42-1.53)	0.456	-0.223	0.50
	Overdominant Model	TT-CC	117 (53.9%)	105 (50.7%)	1			
		TC	100 (46.1%)	102 (49.3%)	0.84 (0.56-1.27)	0.696	-0.176	0.40

Gene (rsID) (GNB3)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs5443	CC		123 (59%)	114 (55%)	1			
	CT		72 (34%)	73 (35%)	0.91 (0.58-1.41)	0.192	-0.100	0.66
	TT		15 (7%)	21 (10%)	0.75 (0.35-1.58)	0.582	-0.293	0.45
	C		318 (76%)	301 (72%)	1			
	T		102 (24%)	115 (28%)	0.88 (0.63-1.22)	0.609	-0.132	0.44
	Dominant Model	CC	123 (58.6%)	114 (54.8%)	1			
		CT-TT	87 (41.4%)	94 (45.2%)	0.88 (0.58-1.33)	0.386	-0.132	0.53
	Recessive Model	CC-CT	195 (92.9%)	187 (89.9%)	1			
		TT	15 (7.1%)	21 (10.1%)	0.79 (0.38-1.65)	0.391	-0.236	0.53
	Overdominant Model	CC-TT	138 (65.7%)	135 (64.9%)	1			
		CT	72 (34.3%)	73 (35.1%)	0.94 (0.61-1.45)	0.076	-0.061	0.78
Gene (rsID) (ADRA1A)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs3802241	AA		69 (33%)	58 (29%)	1			
	AG		99 (47%)	105 (52%)	0.70 (0.43-1.14)	2.072	-0.353	0.15
	GG		44 (21%)	39 (19%)	1.00 (0.55-1.84)	0.000	0.003	0.99
	A		237 (56%)	221 (55%)	1			
	G		187 (44%)	183 (45%)	0.96 (0.72-1.29)	0.071	-0.040	0.79
	Dominant Model	AA	69 (32.5%)	58 (28.7%)	1			
		AG-GG	143 (67.5%)	144 (71.3%)	0.78 (0.50-1.22)	1.202	-0.252	0.27
	Recessive Model	AA-AG	168 (79.2%)	163 (80.7%)	1			
		GG	44 (20.8%)	39 (19.3%)	1.23 (0.74-2.07)	0.631	0.210	0.43
	Overdominant Model	AA-GG	113 (53.3%)	97 (48%)	1			
		AG	99 (46.7%)	105 (52%)	0.70 (0.46-1.07)	2.735	-0.354	0.098
rs1048101	CC		68 (32%)	57 (28%)	1			
	CT		99 (47%)	107 (53%)	0.69 (0.43-1.12)	2.226	-0.365	0.14
	TT		44 (21%)	38 (19%)	1.04 (0.56-1.90)	0.013	0.035	0.91
	C		235 (56%)	221 (55%)	1			
	T		187 (44%)	183 (45%)	0.97 (0.73-1.31)	0.034	-0.027	0.85
	Dominant Model	CC	68 (32.2%)	57 (28.2%)	1			
		CT-TT	143 (67.8%)	145 (71.8%)	0.78 (0.49-1.22)	1.216	-0.253	0.27
	Recessive Model	CC-CT	167 (79.2%)	164 (81.2%)	1			
		TT	44 (20.9%)	38 (18.8%)	1.28 (0.77-2.15)	0.892	0.249	0.35
	Overdominant Model	CC-TT	112 (53.1%)	95 (47%)	1			
		CT	99 (46.9%)	107 (53%)	0.69 (0.45-1.04)	3.145	-0.378	0.08
Gene (rsID) (ADRA1B)	Genotype/Allele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs952037	CC		82 (40%)	77 (37%)	1			
	CT		93 (45%)	104 (50%)	0.83 (0.53-1.30)	0.648	-0.184	0.42
	TT		30 (15%)	27 (13%)	0.94 (0.49-1.80)	0.032	-0.059	0.86
	C		257 (63%)	258 (62%)	1			
	T		153 (37%)	158 (38%)	0.92 (0.68-1.25)	0.265	-0.079	0.61
	Dominant Model	CC	82 (40%)	77 (37%)	1			
		CT-TT	123 (60%)	131 (63%)	0.85 (0.56-1.30)	0.533	-0.158	0.47
	Recessive Model	CC-CT	175 (85.4%)	181 (87%)	1			
		TT	30 (14.6%)	27 (13%)	1.00 (0.55-1.83)	0.000	0.003	0.99
	Overdominant Model	CC-TT	112 (54.6%)	104 (50%)	1			
		CT	93 (45.4%)	104 (50%)	0.86 (0.57-1.30)	0.516	-0.151	0.47
rs3729604	GG		150 (74%)	145 (73%)	1			
	GA		50 (24%)	51 (26%)	0.95 (0.58-1.54)	0.046	-0.053	0.83
	AA		4 (2%)	3 (2%)	2.01 (0.43-9.52)	0.775	0.698	0.38
	G		350 (86%)	341 (86%)	1			
	A		58 (14%)	57 (14%)	1.05 (0.69-1.60)	0.057	0.051	0.81
	Dominant Model	GG	150 (73.5%)	145 (72.9%)	1			
		GA-AA	54 (26.5%)	54 (27.1%)	1.00 (0.62-1.60)	0.000	0.000	0.99
	Recessive Model	GG-GA	200 (98%)	196 (98.5%)	1			
		AA	4 (2%)	3 (1.5%)	2.01 (0.43-9.53)	0.779	0.700	0.38
	Overdominant Model	GG-AA	154 (75.5%)	148 (74.4%)	1			
		GA	50 (24.5%)	51 (25.6%)	0.93 (0.58-1.51)	0.078	-0.069	0.78

Gene (rsID) (<i>ADRA1D</i>)	Genotype/Alele		HAPE-p (n=225)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs6116268	CC		111 (50%)	117 (56%)	1			
	CT		88 (40%)	78 (38%)	1.16 (0.75-1.79)	0.442	0.147	0.51
	TT		21 (10%)	13 (6%)	1.55 (0.72-3.34)	1.268	0.440	0.26
	C		310 (70%)	312 (75%)	1			
	T		130 (30%)	104 (25%)	1.20 (0.87-1.66)	1.239	0.184	0.27
	Dominant Model	CC	111 (50.5%)	117 (56.2%)	1			
		CT-TT	109 (49.5%)	91 (43.8%)	1.21 (0.81-1.82)	0.842	0.191	0.36
	Recessive Model	CC-CT	199 (90.5%)	195 (93.8%)	1			
		TT	21 (9.6%)	13 (6.2%)	1.42 (0.66-3.05)	0.809	0.351	0.37
	Overdominant Model	CC-TT	132 (60%)	130 (62.5%)	1			
		CT	88 (40%)	78 (37.5%)	1.10 (0.72-1.67)	0.191	0.093	0.66

HAPE-p vs. HAPE-c, Significant SNPs are marked in blue and corresponding p-values in yellow. Minor allele or the variant allele has been marked in pink. Cut-off level for significance was $p < 0.05$. p-values are adjusted with age and gender. Analysis has been performed by Multinomial Logistic Regression using SPSS version 16. n: number of samples, B: regression coefficient. OR: Odds ratio, CI: Confidence Interval, HAPE-p: HAPE-patients, HAPE-c: HAPE-controls, Rho-associated, coiled-coil containing protein kinase 2 (**ROCK2**), Myosin light chain kinase (**MYLK**), c-Jun N-terminal kinase1 (**JNK1**), Tyrosine hydroxylase (**TH**), guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (**GNA11**), guanine nucleotide binding protein (G protein), beta polypeptide 3 (**GNB3**), adrenoceptor alpha 1A (**ADRA1A**), adrenoceptor alpha 1B (**ADRA1B**), adrenoceptor alpha 1D (**ADRA1D**).

Supplementary table 5: Statistical analysis on the genetic models of the significantly associated SNPs (observed in HAPE-p vs HAPE-c) in HAPE-p and HLs datasets

Gene (rsID) (<i>ROCK2</i>)	Genotype/Allele		HAPE-p (n=225)	HLs (n=259)	OR(95%CI)	Chi-square	B	p-value
rs10929728	TT		57 (27%)	82 (32%)	1			
	TC		104 (50%)	122 (48%)	1.42 (0.82-2.47)	1.563	0.352	0.21
	CC		49 (23%)	50 (20%)	1.29 (0.66-2.52)	0.560	0.255	0.45
	T		218 (52%)	286 (56%)	1			
	C		202 (48%)	222 (44%)	1.17 (0.84-1.62)	0.847	0.153	0.36
	Dominant Model	TT	57 (27.1%)	82 (32.3%)	1			
		TC-CC	153 (72.9%)	172 (67.7%)	1.40 (0.84-2.35)	1.630	0.336	0.20
	Recessive Model	TT-TC	161 (76.7%)	204 (80.3%)	1			
		CC	49 (23.3%)	50 (19.7%)	1.05 (0.61-1.81)	0.035	0.051	0.85
	Overdominant Model	TT-CC	106 (50.5%)	132 (52%)	1			
		TC	104 (49.5%)	122 (48%)	1.26 (0.79-2.01)	0.975	0.234	0.32
Gene (rsID) (<i>MYLK</i>)	Genotype/Allele		HAPE-p (n=225)	HLs (n=259)	OR(95%CI)	Chi-square	B	p-value
rs11717814	GG		73 (33%)	175 (69%)	1			
	GC		101 (46%)	69 (27%)	4.13 (2.42-7.04)	27.182	1.418	1.85E-07
	CC		44 (20%)	8 (3%)	14.0 (5.03-39.0)	25.500	2.639	4.42E-07
	G		247 (57%)	419 (83%)	1			
	C		189 (43%)	85 (17%)	4.24 (2.85-6.32)	50.494	1.445	1.20E-12
	Dominant Model	GG	73 (33.5%)	175 (69.4%)	1			
		GC-CC	145 (66.5%)	77 (30.6%)	5.25 (3.16-8.70)	41.195	1.658	1.38E-10
	Recessive Model	GG-GC	174 (79.8%)	244 (96.8%)	1			
		CC	44 (20.2%)	8 (3.2%)	8.13 (2.99-22.1)	16.908	2.096	3.92E-05
	Overdominant Model	GG-CC	117 (53.7%)	183 (72.6%)	1			
		GC	101 (46.3%)	69 (27.4%)	2.75 (1.65-4.57)	15.043	1.010	0.0001
rs40305	CC		81 (38%)	181 (72%)	1			
	CT		94 (44%)	65 (26%)	3.45 (2.03-5.86)	21.061	1.238	4.45E-06
	TT		41 (19%)	7 (3%)	17.0 (5.6-51.98)	24.777	2.835	6.44E-07
	C		256 (59%)	427 (84%)	1			
	T		176 (41%)	79 (16%)	4.17 (2.78-6.27)	47.295	1.429	6.11E-12
	Dominant Model	CC	81 (37.5%)	181 (71.5%)	1			
		CT-TT	135 (62.5%)	72 (28.5%)	4.58 (2.77-7.56)	35.383	1.522	2.71E-09
	Recessive Model	CC-CT	175 (81%)	246 (97.2%)	1			
		TT	41 (19%)	7 (2.8%)	11.05 (3.7-32.9)	18.677	2.403	1.55E-05
	Overdominant Model	CC-TT	122 (56.5%)	188 (74.3%)	1			
		CT	94 (43.5%)	65 (25.7%)	2.36 (1.42-3.91)	11.055	0.858	0.001
rs820336	GG		74 (35%)	180 (71%)	1			
	GA		99 (46%)	67 (26%)	3.96 (2.32-6.75)	25.480	1.375	4.47E-07
	AA		41 (19%)	7 (3%)	18.19 (6.1-54.6)	26.770	2.901	2.29E-07
	G		247 (58%)	427 (84%)	1			
	A		181 (42%)	81 (16%)	4.45 (2.96-6.68)	51.819	1.493	6.09E-13
	Dominant Model	GG	74 (34.6%)	180 (70.9%)	1			
		GA-AA	140 (65.4%)	74 (29.1%)	5.2 (3.1-8.6)	40.532	1.649	1.93E-10
	Recessive Model	GG-GA	173 (80.8%)	247 (97.2%)	1			
		AA	41 (19.2%)	7 (2.8%)	11.36 (3.9-33.6)	19.338	2.430	1.09E-05
	Overdominant Model	GG-AA	115 (53.7%)	187 (73.6%)	1			
		GA	99 (46.3%)	67 (26.4%)	2.59 (1.56-4.29)	13.524	0.951	0.0002

HAPE-p vs. HLs, Significant SNPs are marked in blue and corresponding p-values in yellow. Minor allele or the variant allele has been marked in pink. Cut-off level for significance was $p < 0.05$. p-values are adjusted with age and gender. Analysis has been performed by Multinomial Logistic Regression using SPSS version 16. n: number of samples, B: regression coefficient. OR: Odds ratio, CI: Confidence Interval, HAPE-p: HAPE-patients, HAPE-c: HAPE-controls, HLs: Highlanders, Rho-associated, coiled-coil containing protein kinase 2 (*ROCK2*), Myosin light chain kinase (*MYLK*).

Supplementary table 6: Statistical analysis on the genetic models of the significantly associated SNPs (observed in HAPE-p vs HAPE-c) in HLs and HAPE-c datasets

Gene (rsID) (<i>ROCK2</i>)	Genotype/Alele		HLs (n=259)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs10929728	TT		82 (32%)	76 (37%)	1			
	TC		122 (48%)	102 (50%)	1.05 (0.56-1.97)	0.021	0.047	0.89
	CC		50 (20%)	26 (13%)	1.98 (0.86-4.58)	2.581	0.685	0.11
	T		286 (56%)	254 (62%)	1			
	C		222 (44%)	154 (38%)	1.37 (0.92-2.05)	2.340	0.314	0.13
	Dominant Model	TT	82 (32.3%)	76 (37.2%)	1			
		TC-CC	172 (67.7%)	128 (62.8%)	1.27 (0.69-2.32)	0.595	0.237	0.44
	Recessive Model	TT-TC	204 (80.3%)	178 (87.2%)	1			
		CC	50 (19.7%)	26 (12.8%)	1.95 (0.94-4.02)	3.231	0.665	0.07
	Overdominant Model	TT-CC	132 (52%)	102 (50%)	1			
		TC	122 (48%)	102 (50%)	0.82 (0.46-1.44)	0.484	-0.201	0.49
Gene (rsID) (<i>MYLK</i>)	Genotype/Alele		HLs (n=259)	HAPE-c (n=210)	OR(95%CI)	Chi-square	B	p-value
rs11717814	GG		175 (69%)	101 (49%)	1			
	GC		69 (27%)	83 (40%)	0.29 (0.15-0.58)	12.690	-1.230	0.0004
	CC		8 (3%)	21 (10%)	0.06 (0.01-0.29)	11.913	-2.864	0.001
	G		419 (83%)	285 (70%)	1			
	C		85 (17%)	125 (30%)	0.28 (0.16-0.47)	22.191	-1.286	2.47E-06
	Dominant Model	GG	175 (69.4%)	101 (49.3%)	1			
		GC-CC	77 (30.6%)	104 (50.7%)	0.25 (0.13-0.47)	18.100	-1.398	2.1E-05
	Recessive Model	GG-GC	244 (96.8%)	184 (89.8%)	1			
		CC	8 (3.2%)	21 (10.2%)	0.12 (0.03-0.53)	7.926	-2.118	0.005
	Overdominant Model	GG-CC	183 (72.6%)	122 (59.5%)	1			
		GC	69 (27.4%)	83 (40.5%)	0.37 (0.19-0.71)	9.014	-0.999	0.003
rs40305	CC		181 (72%)	102 (49%)	1			
	CT		65 (26%)	84 (40%)	0.36 (0.19-0.69)	9.228	-1.014	0.002
	TT		7 (3%)	23 (11%)	0.06 (0.01-0.29)	11.814	-2.826	0.001
	C		427 (84%)	288 (69%)	1			
	T		79 (16%)	130 (31%)	0.30 (0.18-0.51)	20.232	-1.207	6.86E-06
	Dominant Model	CC	181 (71.5%)	102 (48.8%)	1			
		CT-TT	72 (28.5%)	107 (51.2%)	0.29 (0.16-0.54)	15.098	-1.233	0.0001
	Recessive Model	CC-CT	246 (97.2%)	186 (89%)	1			
		TT	7 (2.8%)	23 (11%)	0.10 (0.02-0.45)	8.861	-2.353	0.003
	Overdominant Model	CC-TT	188 (74.3%)	125 (59.8%)	1			
		CT	65 (25.7%)	84 (40.2%)	0.46 (0.24-0.86)	5.940	-0.788	0.02
rs820336	GG		180 (71%)	94 (46%)	1			
	GA		67 (26%)	84 (41%)	0.31 (0.16-0.59)	12.376	-1.184	0.0005
	AA		7 (3%)	25 (12%)	0.05 (0.01-0.25)	13.462	-2.981	0.0002
	G		427 (84%)	272 (67%)	1			
	A		81 (16%)	134 (33%)	0.27 (0.16-0.45)	24.688	-1.324	6.74E-07
	Dominant Model	GG	180 (70.9%)	94 (46.3%)	1			
		GA-AA	74 (29.1%)	109 (53.7%)	0.25 (0.13-0.46)	19.160	-1.402	1.2E-05
	Recessive Model	GG-GA	247 (97.2%)	178 (87.7%)	1			
		AA	7 (2.8%)	25 (12.3%)	0.09 (0.02-0.42)	9.609	-2.391	0.002
	Overdominant Model	GG-AA	187 (73.6%)	119 (58.6%)	1			
		GA	67 (26.4%)	84 (41.4%)	0.40 (0.21-0.76)	7.987	-0.918	0.005

HAPE-c vs. HLs, Significant SNPs are marked in blue and corresponding p-values in yellow. Minor allele or the variant allele has been marked in pink. Cut-off level for significance was $p < 0.05$. p-values are adjusted with age and gender. Analysis has been performed by Multinomial Logistic Regression using SPSS version 16. n: number of samples, B: regression coefficient. OR: Odds ratio, CI: Confidence Interval, HAPE-p: HAPE-patients, HAPE-c: HAPE-controls, HLs: Highlanders, Rho-associated, coiled-coil containing protein kinase 2 (*ROCK2*), Myosin light chain kinase (*MYLK*).

Supplementary table 7: Haplotype distribution of the three studied groups.

HAPE-p vs HAPE-c					HAPE-p vs HLs				HLs vs HAPE-c			
Gene	Haplotypes	Chi-square	OR(95%CI)	p-value	Haplotypes	Chi-square	OR(95%CI)	p-value	Haplotypes	Chi-square	OR(95%CI)	p-value
ROCK2	ACCACAAC	2.44	1.24	0.11	ACCACAAC	0.063	1.03	0.80	ACCACAAC	1.73	0.19	0.19
	AGCTTAAT	0.06	1.06	0.81	AGCTTAAT	2.95	0.71	0.09	AGCTTAAT	4.93	1.58	0.03
	GGGTTGGT	10.95	0.64	0.0009	GGGTTGGT	0.151	1.05	0.70	GGGTTGGT	12.99	0.62	0.0003
MYLK	CTA	11.68	1.63	0.0006	CTA	90.95	4.23	<0.0000001	CTA	28.67	0.43	<0.0000001
	GCG	10.89	0.63	0.001	GCG	57.34	0.32	<0.0000001	GCG	31.06	2.35	<0.0000001
JNK1	AAGAAT	0.02	0.98	0.89	--							
	GAGCAT	1.10	1.40	0.29								
	AAAAAT	1.36	0.75	0.24								
	GGGCCG	0.15	1.06	0.70								
TH	AAG	9.04	0.32	0.003	AAG	Not found			AAG	Not found		
	AAA	0.01	0.99	1.00	AAA	14.74	0.61	0.0001	AAA	13.56	1.63	0.0002
	AGA	0.00	1.00	1.00	AGA	Not found			AGA	14.33	0.24	0.0002
	AGG	0.002	1.01	1.00	AGG	Not found			AGG	Not found		
	CAG	2.46	1.41	0.12	CAG	Not found			CAG	Not found		
GNA11	CC	2.17	2.05	0.15	--							
	CT	5.8	0.71	0.02								
	TC	6.05	0.99	0.01								
	TT	0.12	0.95	0.73								
GNB3	CC	0.04	0.97	0.85	--							
	CT	1.19	0.82	0.274								
	TC	2.02	1.22	0.16								
	TT	0.65	0.81	0.42								
ADRA1A	CA	0.09	1.04	0.76	--							
	TG	0.09	0.96	0.76								
ADRA1B	GC	0.02	0.98	0.88	--							
	AC	1.10	1.40	0.30								
	AT	1.36	0.75	0.24								
	GT	0.15	1.06	0.696								

Haplotypes with a cumulative frequency >2% were taken for statistical analysis. PHASE v2.1.1 software was used to generate haplotype combinations. A students T-test was performed by SISA to generate p-values and other statistical parameters. Significance cut off $p < 0.05$. Haplotypes found significant in HAPE-p vs HAPE-c were checked in HAPE-p vs HLs and HLs vs HAPE-c. Yellow marked values are significant parameters which are studied. *GNA11* SNPs rs411386 and rs308040 were removed from further analysis due to a flip in major and minor genotypes in the populations under study i.e. in HAPE-p vs. HAPE-c, the SNPs have major genotype as TT and GG while in HAPE-p vs. HLs and HLs vs. HAPE-c, the major genotypes were GG and CC. *GNA11* haplotypes CT and TC were observed to be marginally significant ($p < 0.05$), but were not studied further as there was not a marked change in odds ratio on alleles changes. The order of

SNPs is as follows: *ROCK2*: rs978906, rs2290156, rs10495582, rs10167277, rs10929727, rs6716817, rs4477886, rs10929728; *MYLK*: rs11717814, rs40305, rs820336; *JNK1*: rs10857561, rs3827680, rs10857565, rs10508901, rs4838590, rs9284; *TH*: rs3842727, rs7483056, rs6356; *GNA11*: rs4806907, rs2238625; *GNB3*: rs1129649, rs5443; *ADRA1A*: rs3802241, rs1048101; *ADRA1B*: rs952037, rs3729604. No haplotype could have been formed for *ADRA1D* as only a single SNP, rs6116268 was left after HWE analysis.