

**Table S1.** Details of the 47 differentially expressed genes between harvest mice from a high-altitude environment (H) and acclimated to a low-altitude environment (L), as detected respectively by Affymetrix Rat Clariom S Array with filter criteria of fold change of L/H > 4 or < -4, and ANOVA  $p < 0.05$ . The filtered genes were sorted in ascending order based on the FDR  $p$ -value [36]. The only one gene (*Tnfrsf12a*) with FDR  $p < 0.05$  was marked in bold.

Gene	ID	Fold Change	$p$	FDR $p$	Description
<b><i>Tnfrsf12a</i></b>	<b>TC1000002359.rn.2</b>	<b>13.0</b>	<b>1.06E-06</b>	<b>0.0246</b>	<b>Tumor necrosis factor receptor superfamily, member 12a</b>
<i>Arhgap20</i>	TC0800000694.rn.2	4.6	0.0005	0.3997	Rho GTPase activating protein 20
<i>Cd53</i>	TC0200004423.rn.2	7.3	0.0007	0.3997	Cd53 molecule; INVOLVED IN positive regulation of myoblast fusion (ortholog) AND FOUND IN cell surface AND cell-cell junction (ortholog) AND extracellular vesicular exosome (ortholog) AND INTERACTS WITH 17alpha-ethynylestradiol AND 2,3,7,8-tetrachlorodibenzodioxine AND 3H-1,2-dithiole-3-thione
<i>Ucp2</i>	TC0100002142.rn.2	5.0	0.0008	0.3997	Uncoupling protein 2 (mitochondrial, proton carrier)
<i>Slc25a25</i>	TC0300002876.rn.2	-25.6	0.001	0.4313	Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25
<i>Ankrd23</i>	TC0900001821.rn.2	-4.4	0.0011	0.4328	Ankyrin repeat domain 23
<i>Hbb</i>	TC0100006234.rn.2	14.5	0.0014	0.4659	Hemoglobin, beta
<i>RGD1565183</i>	TC0X00002652.rn.2	6.5	0.0017	0.4659	ENCODES a protein that exhibits structural constituent of ribosome (inferred) AND INVOLVED IN translation (inferred) AND FOUND IN ribosome (inferred) AND INTERACTS WITH C60 fullerene
<i>Slc7a2</i>	TC1600001707.rn.2	-4.2	0.0021	0.4659	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 2
<i>Cdkn1a</i>	TC2000000249.rn.2	4.9	0.0023	0.4659	Cyclin-dependent kinase inhibitor 1A
<i>Dusp14l1</i>	TC0200001120.rn.2	-4.1	0.0027	0.4659	Dual specificity phosphatase 14-like 1 [Source: RGD Symbol; Acc: 1590821]; ENCODES a protein that exhibits MAP kinase tyrosine/serine/threonine phosphatase

					activity (inferred) AND protein tyrosine phosphatase activity (inferred) AND INVOLVED IN inactivation of MAPK activity (inferred) AND INTERACTS WITH (S)-colchicine (ortholog) AND 3-methylcholanthrene (ortholog) AND 5-fluorouracil (ortholog)
<i>Hbb-b1</i>	TSUnmapped0000011 2.rn.2	4.2	0.0028	0.4659	Hemoglobin, beta adult major chain
<i>Cacng6</i>	TC0100004649.rn.2	-4.7	0.0031	0.4659	Calcium channel, voltage-dependent, gamma subunit 6
<i>Rpl35</i>	TC0300003018.rn.2	4.4	0.0037	0.4845	Ribosomal protein L35
<i>LOC100134871</i>	TC0100002239.rn.2	12.1	0.0037	0.4845	Beta globin minor gene
<i>LOC100361705</i>	TC0300000347.rn.2	4.7	0.0046	0.4845	rCG64259-like [Source: RGD Symbol; Acc: 2319569]
<i>Arhgap15</i>	TC0300000497.rn.2	6.8	0.0061	0.4924	Rho GTPase activating protein 15
<i>Ighg; Igh-6</i>	TC0600003269.rn.2	6.1	0.0069	0.5032	Immunoglobulin heavy chain (gamma polypeptide); immunoglobulin heavy chain 6
<i>Plek</i>	TC1400002279.rn.2	4.8	0.0072	0.5032	Pleckstrin
<i>Ikzf1</i>	TC1400001003.rn.2	7.3	0.0083	0.5065	IKAROS family zinc finger 1
<i>Cyp2f4</i>	TC0100001106.rn.2	7.8	0.0087	0.5082	Cytochrome P450, family 2, subfamily f, polypeptide 4
<i>Hbb-b1; LOC689064</i>	TCUn_AABR0702404 1v100000002.rn.2	20.2	0.0091	0.5084	Hemoglobin, beta adult major chain [Source: RGD Symbol; Acc: 1595848]; beta-globin hemoglobin, beta adult major chain; ENCODES a protein that exhibits heme binding (inferred) AND iron ion binding (inferred) AND oxygen binding (inferred) AND INVOLVED IN oxygen transport (inferred) AND PARTICIPATES IN Plasmodium infection pathway AND <i>Trypanosoma brucei</i> infection pathway AND FOUND IN hemoglobin complex (inferred) AND INTERACTS WITH (-)-demecolcine (ortholog) AND 17beta-estradiol (ortholog) AND 2,2',4,4',5,5'-hexachlorobiphenyl (ortholog); hemoglobin,

<i>Rgs13</i>	TC1300001554.rn.2	4.2	0.0109	0.5084	beta adult major chain (Hbb-b1), mRNA. Regulator of G-protein signaling 13 [Source: RGD Symbol; Acc: 1562103]; INVOLVED IN G-protein coupled receptor signaling pathway (ortholog) AND negative regulation of G-protein coupled receptor protein signaling pathway (ortholog) AND FOUND IN cytosol (ortholog) AND nucleus (ortholog) AND plasma membrane (ortholog) AND INTERACTS WITH lead diacetate AND 17beta-estradiol (ortholog) AND 5-fluorouracil (ortholog)
<i>Laptm5</i>	TC0500001570.rn.2	4.3	0.0115	0.5084	Lysosomal protein transmembrane 5
<i>Blnk</i>	TC0100007686.rn.2	6.3	0.0137	0.5187	B-cell linker; ENCODES a protein that exhibits SH3/SH2 adaptor activity (ortholog) AND INVOLVED IN intracellular signal transduction (ortholog) AND positive regulation of signal transduction (ortholog) AND PARTICIPATES IN phosphatidylinositol 3-kinase class I signaling pathway AND B cell receptor signaling pathway AND primary immunodeficiency disease pathway AND ASSOCIATED WITH Agammaglobulinemia (ortholog) AND AGAMMAGLOBULINEMIA 4 AUTOSOMAL RECESSIVE (ortholog) AND FOUND IN cytoplasm (ortholog) AND INTERACTS WITH beta-naphthoflavone AND diuron AND indole-3-methanol
<i>Tcrb</i>	TC0400000725.rn.2	61.2	0.0144	0.5198	T-cell receptor beta chain
<i>Nr4a1</i>	TC0700001870.rn.2	-4.1	0.0156	0.5268	nuclear receptor subfamily 4, group A, member 1
<i>Il2rg</i>	TC0X00001947.rn.2	50.0	0.0156	0.5268	interleukin 2 receptor, gamma

<i>Alas2</i>	TC0X00001581.rn.2	52.2	0.0158	0.5268	5-aminolevulinate synthase 2
<i>Dnase1l3</i>	TC1500002466.rn.2	4.8	0.0171	0.5276	ENCODES a protein that exhibits DNA binding AND endodeoxyribonuclease activity AND endonuclease activity (ortholog) AND INVOLVED IN apoptotic DNA fragmentation (ortholog) AND developmentally programmed cell death (ortholog) AND FOUND IN nucleus AND INTERACTS WITH 3-chloropropane-1,2-diol AND ammonium chloride AND cadmium dichloride
<i>Hmgb2l1</i>	TC1100001483.rn.2	8.9	0.0183	0.5333	high mobility group box 2-like 1
<i>Dnase1l3</i>	TC1500002467.rn.2	4.8	0.019	0.5374	deoxyribonuclease 1-like 3
<i>Myom2</i>	TC1600001984.rn.2	-4.0	0.0209	0.5451	myomesin 2
<i>Hist1h2bcl1</i>	TC1700001825.rn.2	4.9	0.022	0.5477	Histone H2B; ENCODES a protein that exhibits DNA binding (inferred) AND protein heterodimerization activity (inferred) AND INVOLVED IN nucleosome assembly (inferred) AND PARTICIPATES IN systemic lupus erythematosus pathway AND FOUND IN nucleosome (inferred) AND nucleus (inferred) AND INTERACTS WITH (-)-demecolcine (ortholog) AND (S)-nicotine (ortholog) AND 2,3,7,8-tetrachlorodibenzodioxin (ortholog)
<i>Nnat</i>	TC0300002176.rn.2	-318.5	0.0224	0.5477	Neuronatin
<i>Cd79a</i>	TC0100001061.rn.2	5.1	0.0251	0.5598	Cd79a molecule, immunoglobulin-associated alpha
<i>Smco1</i>	TC1100001758.rn.2	-4.6	0.0261	0.5608	Single-pass membrane protein with coiled-coil domains 1
<i>Tcrb</i>	TC0400000714.rn.2	4.3	0.0275	0.5659	T-cell receptor beta chain
<i>Hist2h3c2</i>	TC0200001754.rn.2	4.8	0.0276	0.5659	Histone cluster 2, H3c2
<i>LOC100911042</i>	TC1100001759.rn.2	-4.8	0.0324	0.5702	Uncharacterized LOC100911042
<i>Alb</i>	TC1400001516.rn.2	-26.8	0.0329	0.573	Albumin

<i>Rbm3</i>	TC0X00000125.rn.2	-4.9	0.0329	0.573	RNA binding motif (RNP1, RRM) protein 3
<i>Ms4a6b</i>	TC0100003231.rn.2	5.4	0.0345	0.5816	Membrane-spanning 4-domains, subfamily A, member 6B
<i>LOC100360581</i>	TC0600003308.rn.2	5.1	0.0377	0.5826	Uncharacterized protein; rCG58847-like
<i>Neurl1</i>	TC0100003765.rn.2	-4.9	0.04	0.5826	Neuralized E3 ubiquitin protein ligase 1
<i>Tmsb10;</i> <i>LOC100364435</i>	TC0700001491.rn.2	4.2	0.0432	0.5905	Thymosin, beta 10 [Source: RGD Symbol; Acc: 62022]; thymosin beta 10-like
<i>Cyp2e1</i>	TC0100002862.rn.2	-9.2	0.0433	0.5905	Cytochrome P450, family 2, subfamily e, polypeptide 1

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