

Qiagen 84-Gene Microarray for Glucose Metabolism		Average Fold Change of Cold Ischemic Group Compared to Normal Control	
Gene Symbol	Gene Name	6 HOURS Post Reperfusion	24 HOURS Post Reperfusion
Acly	ATP citrate lyase	2.1457	-1.666
Aco1	Aconitase 1	2.201	5.137
Aco2	Aconitase 2, mitochondrial	2.0389	-1.3389
Agl	Amylo-1,6-glucosidase, 4-alpha-glucanotransferase	1.8139	-1.4553
Aldoa	Aldolase A, fructose-bisphosphate	2.2087	-1.3672
Aldob	Aldolase B, fructose-bisphosphate	1.0908	1.6008
Aldoc	Aldolase C, fructose-bisphosphate	1.6594	-2.5372
Bpgm	2,3-bisphosphoglycerate mutase	1.9381	-1.2499
Cs	Citrate synthase	1.8954	-1.0509
Dlat	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	1.8364	-1.1726
Dld	Dihydrolipoamide dehydrogenase	1.4427	-1.2231
Dlst	Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	1.5266	-1.1586
Eno1	Enolase 1, alpha non-neuron	2.2505	-1.0269
Eno2	Enolase 2, gamma neuronal	1.8524	-1.649
Eno3	Enolase 3, beta muscle	2.1339	-1.1574
Fbp1	Fructose bisphosphatase 1	1.0908	1.0516
Fbp2	Fructose bisphosphatase 2	1.1672	1.0516
Fh1	Fumarate hydratase 1	1.866	-1.5206
G6pc	Glucose-6-phosphatase, catalytic	1.0908	1.7382
G6pc3	Glucose 6 phosphatase, catalytic, 3	2.0452	-1.5047
G6pdx	Glucose-6-phosphate dehydrogenase X-linked	1.4477	-1.2669
Galm	Galactose mutarotase	1.7074	-1.223
Gapdhs	Glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	1.0908	1.0516
Gbe1	Glucan (1,4-alpha-), branching enzyme 1	1.1499	-1.6553
Gck	Glucokinase	1.0908	1.1863
Gpi1	Glucose phosphate isomerase 1	1.7688	-1.3107
Gsk3a	Glycogen synthase kinase 3 alpha	1.7959	-1.2064
Gsk3b	Glycogen synthase kinase 3 beta	1.4127	-1.2834
Gys1	Glycogen synthase 1, muscle	1.6422	-1.2808

Gys2	Glycogen synthase 2	1.0908	1.0516
H6pd	Hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	1.5477	-1.6296
Hk2	Hexokinase 2	1.8798	1.1414
Hk3	Hexokinase 3	1.0908	1.0516
ldh1	Isocitrate dehydrogenase 1 (NADP+), soluble	1.0294	-2.4725
ldh2	Isocitrate dehydrogenase 2 (NADP+), mitochondrial	1.1021	-1.8027
ldh3a	Isocitrate dehydrogenase 3 (NAD+) alpha	1.1786	-1.1376
ldh3b	Isocitrate dehydrogenase 3 (NAD+) beta	1.378	-1.3094
ldh3g	Isocitrate dehydrogenase 3 (NAD+), gamma	1.3516	-1.342
Mdh1	Malate dehydrogenase 1, NAD (soluble)	1.3536	-1.5706
Mdh1b	Malate dehydrogenase 1B, NAD (soluble)	1.0908	-1.4093
Mdh2	Malate dehydrogenase 2, NAD (mitochondrial)	1.6008	-1.316
Ogdh	Oxoglutarate dehydrogenase (lipoamide)	1.513	-1.4663
Pck1	Phosphoenolpyruvate carboxykinase 1, cytosolic	1.0908	1.2964
Pck2	Phosphoenolpyruvate carboxykinase 2 (mitochondrial)	-1.0304	-1.3099
Pcx	Pyruvate carboxylase	-1.0051	-1.4735
Pdha1	Pyruvate dehydrogenase E1 alpha 1	1.3086	-1.3282
Pdhb	Pyruvate dehydrogenase (lipoamide) beta	-1.0064	-1.2681
Pdk1	Pyruvate dehydrogenase kinase, isoenzyme 1	-1.4652	-1.6224
Pdk2	Pyruvate dehydrogenase kinase, isoenzyme 2	-1.6837	-2.5321
Pdk3	Pyruvate dehydrogenase kinase, isoenzyme 3	1.1862	-1.2999
Pdk4	Pyruvate dehydrogenase kinase, isoenzyme 4	-1.0653	-1.4314
Pdp2	Pyruvate dehydrogenase phosphatase catalytic subunit 2	1.0603	-1.0831
Pdpr	Pyruvate dehydrogenase phosphatase regulatory subunit	1.1214	-1.55
Pfkl	Phosphofructokinase, liver, B-type	1.3092	-1.2818
Pgam2	Phosphoglycerate mutase 2	1.4603	-1.57
Pgk1	Phosphoglycerate kinase 1	1.3522	-1.1222
Pgk2	Phosphoglycerate kinase 2	1.0908	1.0516

Pgm1	Phosphoglucomutase 1	1.2227	-1.081
Pgm2	Phosphoglucomutase 2	-1.1031	-1.5252
Pgm3	Phosphoglucomutase 3	-1.2936	-1.6723
Phka1	Phosphorylase kinase alpha 1	-1.2574	-1.3725
Phkb	Phosphorylase kinase beta	-1.1414	-1.4538
Phkg1	Phosphorylase kinase gamma 1	-1.0625	1.3769
Phkg2	Phosphorylase kinase, gamma 2 (testis)	-1.0028	-1.4068
Pklr	Pyruvate kinase liver and red blood cell	1.0908	1.832
Prps1	Phosphoribosyl pyrophosphate synthetase 1	1.3527	-1.2059
Prps1l1	Phosphoribosyl pyrophosphate synthetase 1-like 1	1.0908	1.0516
Prps2	Phosphoribosyl pyrophosphate synthetase 2	1.2812	-1.2221
Pygl	Liver glycogen phosphorylase	1.0908	1.0516
Pygm	Muscle glycogen phosphorylase	1.3007	3.1081
Rbks	Ribokinase	1.1015	-1.358
Rpe	Ribulose-5-phosphate-3-epimerase	-1.3525	-1.2208
Rpia	Ribose 5-phosphate isomerase A	-1.1714	-1.0641
Sdha	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	-1.1282	-1.3445
Sdhb	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	-1.041	-1.3377
Sdhc	Succinate dehydrogenase complex, subunit C, integral membrane protein	-1.1211	-1.2971
Sdhd	Succinate dehydrogenase complex, subunit D, integral membrane protein	-1.0168	-1.1281
Sucla2	Succinate-Coenzyme A ligase, ADP-forming, beta subunit	1.0628	-1.3453
Suc1g1	Succinate-CoA ligase, GDP-forming, alpha subunit	1.0173	-1.5879
Suc1g2	Succinate-Coenzyme A ligase, GDP-forming, beta subunit	1.0388	-1.3646
Taldo1	Transaldolase 1	-1.0539	-1.2312
Tkt	Transketolase	-1.1531	-1.4542
Tpi1	Triosephosphate isomerase 1	-1.3177	-1.2562
Ugp2	UDP-glucose pyrophosphorylase 2	-1.7646	-1.5086

Table S1: Summary of Average Fold Change of 84 Genes for Glucose Metabolism at 6 and 24 Hours Postreperfusion (n=3).

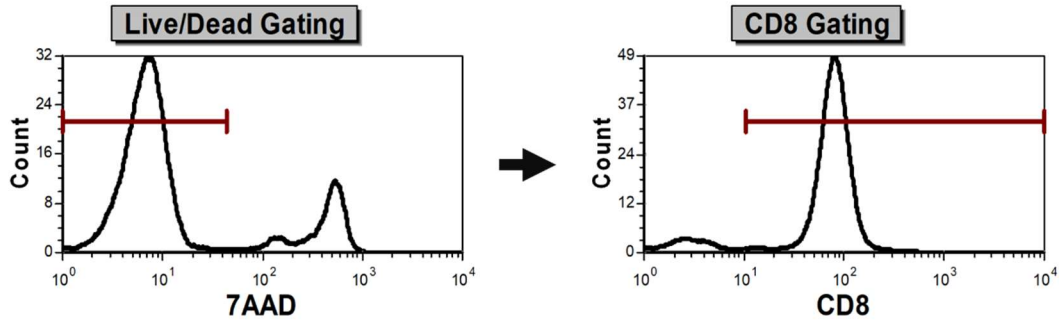
Qiagen 84-Gene Microarray for Antigen-Presenting Cells		Average Fold Change of Cold Ischemic Group Compared to Normal Control
Gene Symbol	Gene Name	6 HOURS Post-Reperfusion
Ccl11	Chemokine (C-C motif) ligand 11	-1.0403
Ccl12	Chemokine (C-C motif) ligand 12	-1.0403
Ccl17	Chemokine (C-C motif) ligand 17	1.0672
Ccl19	Chemokine (C-C motif) ligand 19	-1.1933
Ccl2	Chemokine (C-C motif) ligand 2	2.2477
Ccl20	Chemokine (C-C motif) ligand 20	-1.0844
Ccl3	Chemokine (C-C motif) ligand 3	-1.0403
Ccl4	Chemokine (C-C motif) ligand 4	-1.0403
Ccl5	Chemokine (C-C motif) ligand 5	1.4664
Ccl7	Chemokine (C-C motif) ligand 7	1.9803
Ccl8	Chemokine (C-C motif) ligand 8	1.2025
Ccr1	Chemokine (C-C motif) receptor 1	-1.0403
Ccr2	Chemokine (C-C motif) receptor 2	-1.0403
Ccr3	Chemokine (C-C motif) receptor 3	-1.0403
Ccr5	Chemokine (C-C motif) receptor 5	-1.0403
Ccr9	Chemokine (C-C motif) receptor 9	-1.0403
Cd1d1	CD1d1 antigen	-1.0799
Cd1d2	CD1d2 antigen	-1.0403
Cd2	CD2 antigen	-1.0403
Cd209a	CD209a antigen	-1.0403
Cd28	CD28 antigen	-1.0403
Cd33	CD33 antigen	-1.0403
Cd36	CD36 antigen	-1.3664
Cd4	CD4 antigen	-1.0403
Cd40	CD40 antigen	-1.0403
Cd40lg	CD40 ligand	-1.0403
Cd44	CD44 antigen	1.3568
Cd74	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	-1.5994
Cd80	CD80 antigen	1.4776
Cd86	CD86 antigen	-1.0403
Cd8a	CD8 antigen, alpha chain	-1.0403
Cdc42	Cell division cycle 42 homolog (<i>S. cerevisiae</i>)	1.0028
Cdkn1a	Cyclin-dependent kinase inhibitor 1A (P21)	-1.0688
Cebpa	CCAAT/enhancer binding protein (C/EBP), alpha	-1.051

Clec4b2	C-type lectin domain family 4, member b2	-1.0403
Csf1r	Colony stimulating factor 1 receptor	1.6177
Csf2	Colony stimulating factor 2 (granulocyte-macrophage)	3.3299
Cxcl1	Chemokine (C-X-C motif) ligand 1	1.5621
Cxcl10	Chemokine (C-X-C motif) ligand 10	1.9099
Cxcl12	Chemokine (C-X-C motif) ligand 12	-1.286
Cxcl2	Chemokine (C-X-C motif) ligand 2	-1.0403
Cxcr1	Chemokine (C-X-C motif) receptor 1	-1.0403
Cxcr4	Chemokine (C-X-C motif) receptor 4	-1.0403
ErbB2	V-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	-1.0563
Fas	Fas (TNF receptor superfamily member 6)	-1.0656
Fcgr1a	Fc receptor, IgE, high affinity I, alpha polypeptide	-1.0403
Fcgr2a	Fc receptor, IgE, low affinity II, alpha polypeptide	1.1399
Fcgr1	Fc receptor, IgG, high affinity I	-1.0403
Fcgrt	Fc receptor, IgG, alpha chain transporter	-1.639
Flt3	FMS-like tyrosine kinase 3	-1.0403
Flt3l	FMS-like tyrosine kinase 3 ligand	-1.0224
H2-DMa	Histocompatibility 2, class II, locus DMA	-1.0091
Icam1	Intercellular adhesion molecule 1	-1.4254
Icam2	Intercellular adhesion molecule 2	-1.0403
Ifng	Interferon gamma	-1.0403
Il10	Interleukin 10	-1.0403
Il12a	Interleukin 12A	-1.0403
Il12b	Interleukin 12b	-1.0403
Il16	Interleukin 16	-1.1702
Il2	Interleukin 2	-1.0403
Il6	Interleukin 6	1.0386
Irf7	Interferon regulatory factor 7	1.6751
Itgam	Integrin alpha M	-1.0403
Itgb2	Integrin beta 2	-1.0718
Lrp1	Low density lipoprotein receptor-related protein 1	-1.3849
Lyn	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	-1.2036
Mif	Macrophage migration inhibitory factor	-1.0246
Nfkb1	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1, p105	-1.0263
Ptpcr	Protein tyrosine phosphatase, receptor type, C	-1.0403
Rac1	RAS-related C3 botulinum substrate 1	-1.0384
Rag1	Recombination activating gene 1	-1.0403

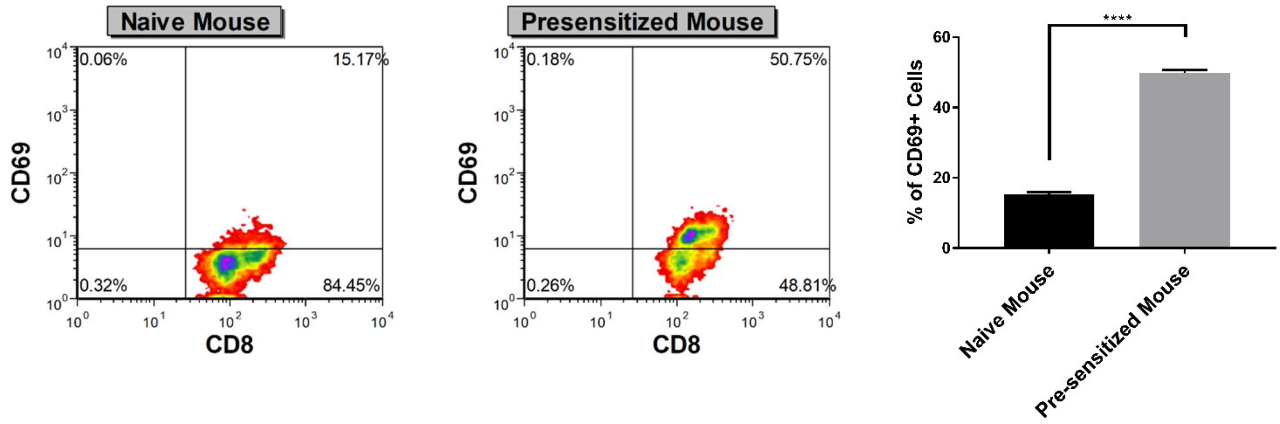
Rela	V-rel reticuloendotheliosis viral oncogene homolog A (avian)	1.05
Relb	Avian reticuloendotheliosis viral (v-rel) oncogene related B	1.3776
Stat3	Signal transducer and activator of transcription 3	-1.3253
Tap2	Transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	1.0434
Tapbp	TAP binding protein	-1.0779
Tgfb1	Transforming growth factor, beta 1	-1.0039
Thbs1	Thrombospondin 1	-1.2117
Tlr1	Toll-like receptor 1	-1.4638
Tlr2	Toll-like receptor 2	-1.0188
Tlr7	Toll-like receptor 7	-2.0244
Tlr9	Toll-like receptor 9	-1.0403
Tnf	Tumor necrosis factor	-1.0403
Tnfsf11	Tumor necrosis factor (ligand) superfamily, member 11	-1.0403

Table S2: Summary of Average Fold Change of 84 Genes for Antigen-Presenting Cells at 6 Hours Postreperfusion (n=3).

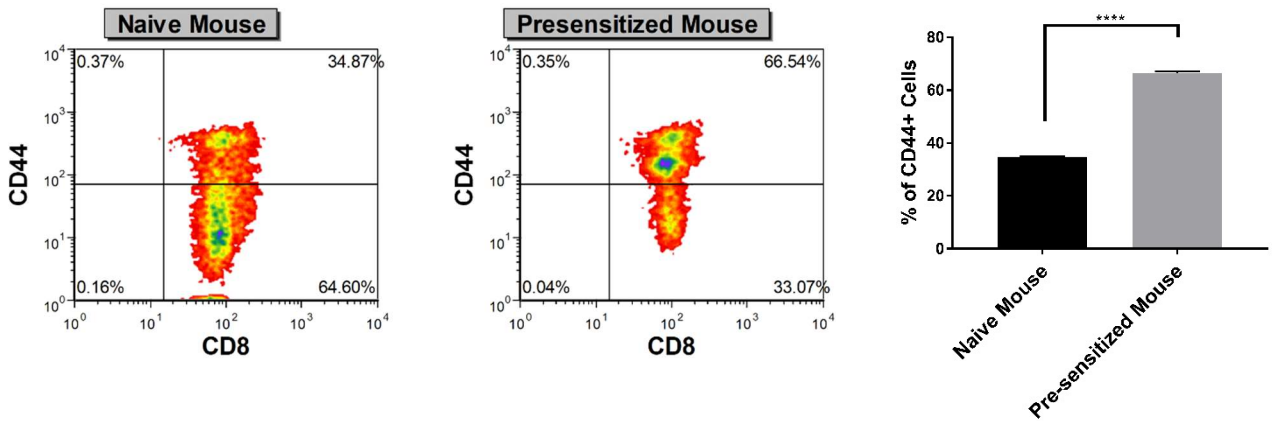
A.



B.



C.



D.

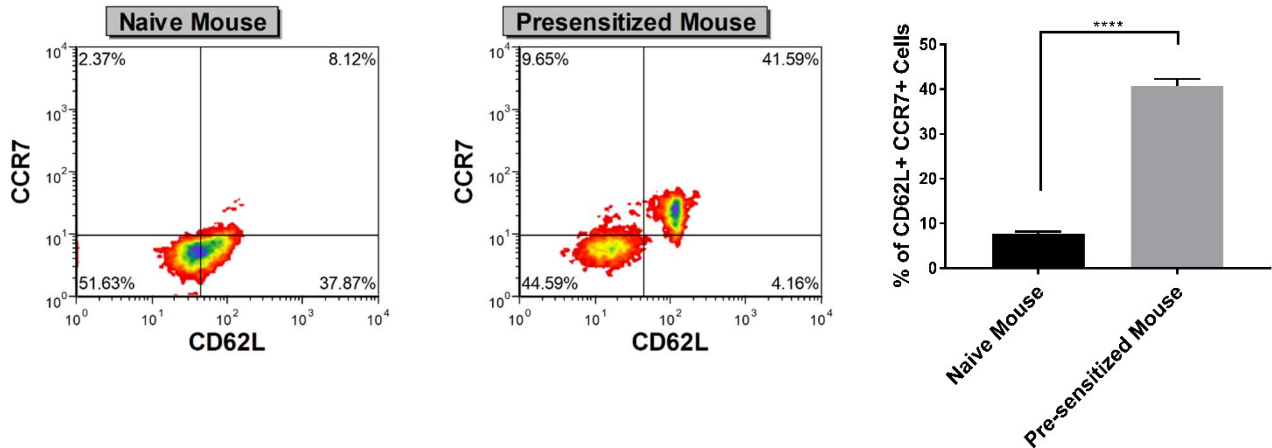


Figure S1: Phenotype of CD8⁺ T cells Isolated from Presensitized Mice. Live CD8⁺ T cells in the spleens are gated and included in the analysis (A). Presensitizing C57/BL6 mice with FVB mouse cardiac ECs increases the percentage of activated T cells (B), and of the central memory T cell phenotype (C)(D). (n=3, ****p<0.0001)