

Table E-1. Gene Lists from Beadstudio and Genespring

A. Beadstudio 2 fold, p<0.05 Gene List, 19 Genes

Gene	Diff Score*	Regulation
ARG1	44.13	up
BNIP3L	25.68	up
CA4	40.43	up
CCR7	-71.37	down
CEACAM6	16.8	up
CEACAM8	15.99	up
CSPG2	53.25	up
ECHDC3	17.85	up
FKBP5	15.1	up
IQGAP1	70.95	up
KCTD12	14.99	up
LY96	49.69	up
MMP9	30.01	up
OLFM4	18.97	up
ORM1	17.00	up
PDK4	102.71	up
S100A12	39.53	up
SDPR	41.33	up
TPST1	26.83	up

*Diff score: Using the Illumina Custom Algorithm a Diff score is calculated from the p-value of significance. {DiffScore = (10sgn(Icond-Iref)log10(p))} For each gene, Diff scores of corresponding probes are averaged and concordance between the probes is reported.

For a p-value of 0.05, Diff score = ± 13

For a p-value of 0.01, Diff score = ± 20

For a p-value of 0.001, Diff score = ± 30

Legend: ARG1=Arginase 1; BNIP3L= BCL2/adenovirus E1B 19kDa interacting protein 3-like; CA4= Carbonic anhydrase 4; CCR7=Chemokine receptor 7; CEACAM6= carcinoembryonic antigen-related cell adhesion molecule 6; CEAMCAM8= carcinoembryonic antigen-related cell adhesion molecule 8; CSPG2=Chondroitin sulfate proteoglycan 2; ECHDC3= Enoyl-CoA hydratase domain-containing protein 3; FKBP5= FK506 binding protein 5; IQGAP1= IQ motif containing GTPase activating protein 1; KCTD12= potassium channel tetramerisation domain containing 12; LY96= Lymphocyte antigen 96; MMP9=Matrix metalloproteinase 9; OLFM4= olfactomedin 4; ORM1= orosomucoid 1; PDK4= pyruvate dehydrogenase kinase, isozyme 4; S100A12= S100 calcium binding protein A12; SDPR= serum deprivation response; TPST1= tyrosylprotein sulfotransferase 1

B. GeneSpring 2 fold, p<0.05 Gene List, 16 Genes

Gene	p-value*	Regulation
ACSL1	4.03e-04	up
AKAP7	0.001	up
APOBEC3A	0.03	up
ARG1	2.84 E-07	up
CA4	2.00 E-04	up
CCR7	4.37 E-05	down
CRISPLD2	4.74 E-06	up
CSPG2	3.45 E-05	up
FCGR3B	0.024	up

FOLR3	9.23 E-04	up
IQGAP1	7.97 E-07	up
LY96	0.001	up
MMP9	1.11 E-05	up
ORM1	0.006	up
PADI4	4.70 E-06	up
S100A12	3.87 E-04	up

*Bonferroni Family wise error (FWER) corrected p-value

Legend: ACSL1= acyl-CoA synthetase long-chain family member 1; AKAP7=A-kinase anchor protein 7; APOBEC3A= apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A; ARG1=Arginase 1; CA4= Carbonic anhydrase 4; CCR7=Chemokine receptor 7; CRISPLD2= cysteine-rich secretory protein LCCL domain containing 2; CSPG2= Chondroitin sulfate proteoglycan 2; FCGR3B= Fc fragment of IgG, low affinity IIIb, receptor (CD16b); FOLR3= folate receptor 3; IQGAP1= IQ motif containing GTPase activating protein 1; LY96= Lymphocyte antigen 96; MMP9=Matrix metalloproteinase 9; ORM1= orosomucoid 1; PADI4= peptidyl arginine deiminase, type IV; S100A12= S100 calcium binding protein A12

For questions related to the material in this supplemental table contact Taura L. Barr at barrt@mail.nih.gov.