Supplementary Table 1. Differentially expressed genes in peripheral blood following methotrexate exposure in the GSE35455 cohort

Downregulated Genes

Gene.symbol	Gene.title	log2(fold change)
AAK1	AP2 associated kinase 1	-0.516
ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	-0.606
ABHD8	abhydrolase domain containing 8	-0.812
ABLIM3	actin binding LIM protein family, member 3	-0.576
ACBD4	acyl-Coenzyme A binding domain containing 4	-0.5
ACCN3	amiloride-sensitive cation channel 3	-0.626
ACHE	acetylcholinesterase (Yt blood group)	-0.78
ADAM11	ADAM metallopeptidase domain 11	-0.702
ADAM15	ADAM metallopeptidase domain 15	-0.505
ADAMTS3	ADAM metallopeptidase with thrombospondin type 1 motif, 3	-0.583
ADIPOR2	adiponectin receptor 2	-0.512
ADORA1	adenosine A1 receptor	-0.545
ADORA3	adenosine A3 receptor	-0.872
AGXT	alanine-glyoxylate aminotransferase	-0.859
AIM1L	absent in melanoma 1-like	-0.737
AKAP8L	A kinase (PRKA) anchor protein 8-like	-0.665
ALDH1A3	aldehyde dehydrogenase 1 family, member A3	-0.536
ALPPL2	alkaline phosphatase, placental-like 2	-0.501
ANAPC13	anaphase promoting complex subunit 13	-0.608
ANKRD39	ankyrin repeat domain 39	-0.538
ANKRD50	ankyrin repeat domain 50	-0.5
AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	-0.595
AP3B2	adaptor-related protein complex 3, beta 2 subunit	-0.623
APOL3	apolipoprotein L, 3	-0.556
APOM	apolipoprotein M	-0.757
APTX	aprataxin	-0.609
AQP2	aquaporin 2 (collecting duct)	-0.591
ARF1	ADP-ribosylation factor 1	-0.523
ARHGEF10L	Rho guanine nucleotide exchange factor (GEF) 10-like	-0.765
ARL4C	ADP-ribosylation factor-like 4C	-0.523
ARMC5	armadillo repeat containing 5	-0.7245
ARPC3B	actin related protein 2/3 complex, subunit 3B, 21kDa///staufen, RNA binding protein, homolog 1 (Drosophila)///CSE1 chromosome segregation 1-like (yeast)	-0.566
ARR3	arrestin 3, retinal (X-arrestin)	-0.569

ARRB2	arrestin, beta 2	-0.534
ARSA	arylsulfatase A	-0.634
ASCL1	achaete-scute complex homolog 1 (Drosophila)	-0.657
ATG2A	ATG2 autophagy related 2 homolog A (S. cerevisiae)	-0.51
ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-0.783
ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	-0.937
AVEN	apoptosis, caspase activation inhibitor	-0.639
B2M	beta-2-microglobulin	-0.549
BACE2	beta-site APP-cleaving enzyme 2	-0.578
BAT2D1	BAT2 domain containing 1	-0.849
BAX	BCL2-associated X protein	-0.519
BAZ2A	bromodomain adjacent to zinc finger domain, 2A	-0.639
BCL3	B-cell CLL/lymphoma 3	-0.583
BMP4	bone morphogenetic protein 4	-0.584
BMP6	bone morphogenetic protein 6	-0.93
BMP7	bone morphogenetic protein 7 (osteogenic protein 1)	-0.605
BPI	bactericidal/permeability-increasing protein	-0.778
BPIL2	bactericidal/permeability-increasing protein-like 2///chromosome 22 open reading frame 28///F-box protein 7///ret finger protein-like 3	-0.725
BRF1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	-0.61
BZW2	basic leucine zipper and W2 domains 2	-0.582
C10orf137	chromosome 10 open reading frame 137	-0.517
C10orf28	chromosome 10 open reading frame 28	-0.507
C10orf95	chromosome 10 open reading frame 95	-0.574
C12orf47	chromosome 12 open reading frame 47	-0.567
C13orf1	chromosome 13 open reading frame 1	-0.65
C14orf131	chromosome 14 open reading frame 131	-0.663
C19orf24	chromosome 19 open reading frame 24	-0.615
C1orf107	chromosome 1 open reading frame 107	-0.509
C1orf164	chromosome 1 open reading frame 164	-0.845
C1orf50	chromosome 1 open reading frame 50	-0.672
C20orf118	chromosome 20 open reading frame 118///chromosome 20 open reading frame 117///SAM domain and HD domain 1	-0.698
C20orf121	chromosome 20 open reading frame 121	-0.698

C20orf151	chromosome 20 open reading frame 151///Cdk5 and Abl enzyme substrate 2///ribosomal protein S21	-0.502
C20orf74	chromosome 20 open reading frame 74	-0.768
C22orf26	chromosome 22 open reading frame 26	-0.782
C2orf32	chromosome 2 open reading frame 32	-0.626
C6orf134	chromosome 6 open reading frame 134	-0.81
C6orf168	chromosome 6 open reading frame 168	-0.813
C6orf85	chromosome 6 open reading frame 85	-0.814
C8orf51	chromosome 8 open reading frame 51	-0.512
C9orf125	chromosome 9 open reading frame 125	-0.82
CA9	carbonic anhydrase IX	-0.553
CAB39L	calcium binding protein 39-like///cytidine and dCMP deaminase domain containing 1	-0.747
CACNB4	calcium channel, voltage-dependent, beta 4 subunit	-0.53
CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	-0.617
CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	-0.505
CARHSP1	calcium regulated heat stable protein 1, 24kDa	-0.557
CASP9	caspase 9, apoptosis-related cysteine peptidase	-0.644
CCDC40	coiled-coil domain containing 40	-0.775
CCDC81	coiled-coil domain containing 81	-0.951
CCL25	chemokine (C-C motif) ligand 25	-0.631
CCR10	chemokine (C-C motif) receptor 10	-0.571
CCR9	chemokine (C-C motif) receptor 9	-0.516
CD151	CD151 molecule (Raph blood group)	-0.58
CD300A	CD300a molecule	-0.681
CD300C	CD300c molecule	-0.65
CD320	CD320 molecule	-0.591
CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	-0.518
CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4	-0.521
CDCA7	cell division cycle associated 7	-0.63
CDH1	cadherin 1, type 1, E-cadherin (epithelial)	-0.679
CDH16	cadherin 16, KSP-cadherin	-0.533
CDH19	cadherin 19, type 2	-0.689
CDH2	cadherin 2, type 1, N-cadherin (neuronal)	-0.828
CDK6	cyclin-dependent kinase 6	-0.744
CDSN	corneodesmosin	-0.661

CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	-1.001
CENPK	centromere protein K	-0.51
CENTD3	centaurin, delta 3	-0.557
CERCAM	cerebral endothelial cell adhesion molecule	-0.589
CILP	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	-0.682
CIRH1A	cirrhosis, autosomal recessive 1A (cirhin)	-0.877
CKB	creatine kinase, brain	-0.699
CLDN11	claudin 11 (oligodendrocyte transmembrane protein)	-0.538
CLDN12	claudin 12	-0.583
CLDN6	claudin 6	-0.543
CLDND1	claudin domain containing 1	-0.786
CLPP	ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	-0.675
COL14A1	collagen, type XIV, alpha 1 (undulin)	-0.725
COL17A1	collagen, type XVII, alpha 1	-0.519
COL3A1	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	-0.814
COL4A5	collagen, type IV, alpha 5 (Alport syndrome)	-0.682
COX8A	cytochrome c oxidase subunit 8A (ubiquitous)	-0.606
CPEB3	cytoplasmic polyadenylation element binding protein 3	-0.76
CPNE3	copine III	-1.117
CPSF4	cleavage and polyadenylation specific factor 4, 30kDa	-0.829
CRYGS	crystallin, gamma S	-0.899
CRYZ	crystallin, zeta (quinone reductase)	-0.619
CSDA	cold shock domain protein A	-0.518
CUL5	cullin 5	-0.757
CUL7	cullin 7	-0.634
CUTA	cutA divalent cation tolerance homolog (E. coli)	-0.503
CX3CR1	chemokine (C-X3-C motif) receptor 1///chemokine (C-C motif) receptor 8	-0.562
CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	-0.52
CXorf26	chromosome X open reading frame 26	-0.613
CXXC4	CXXC finger 4	-0.688
CYB5R2	cytochrome b5 reductase 2	-0.664

CYP2W1	cytochrome P450, family 2, subfamily W, polypeptide 1	-0.56
CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	-0.618
D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	-0.524
DARS	aspartyl-tRNA synthetase	-0.542
DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	-0.6
DDEFL1	development and differentiation enhancing factor-like 1	-0.584
DERL3	Der1-like domain family, member 3	-0.582
DGCR2	DiGeorge syndrome critical region gene 2	-0.529
DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	-0.669
)KFZP434A06	DKFZP434A062 protein	-0.579
)KFZP564C19	DKFZP564C196 protein	-0.864
DKK3	dickkopf homolog 3 (Xenopus laevis)	-0.946
DMRTC2	DMRT-like family C2	-0.664
DNAH3	dynein, axonemal, heavy chain 3	-0.667
DNMT3L	DNA (cytosine-5-)-methyltransferase 3-like	-0.644
DOLPP1	dolichyl pyrophosphate phosphatase 1	-0.515
DOM3Z	dom-3 homolog Z (C. elegans)	-0.55
DPF2	D4, zinc and double PHD fingers family 2	-0.575
DPF3	D4, zinc and double PHD fingers, family 3	-0.738
DPP9	dipeptidyl-peptidase 9	-0.53
DPYD	dihydropyrimidine dehydrogenase	-0.689
DRD4	dopamine receptor D4	-0.608
DSCR6	Down syndrome critical region gene 6	-0.57
DUSP2	dual specificity phosphatase 2	-0.633
EBF2	early B-cell factor 2	-0.552
ECT2	epithelial cell transforming sequence 2 oncogene	-0.849
EDA	ectodysplasin A	-0.883
EDEM1	ER degradation enhancer, mannosidase alpha-like 1	-0.677
EFR3A	EFR3 homolog A (S. cerevisiae)	-0.749
EI24	etoposide induced 2.4 mRNA	-0.683
EIF3K	eukaryotic translation initiation factor 3, subunit K	-0.577
ELF4	E74-like factor 4 (ets domain transcription factor)	-0.719
ELOVL2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	-0.723

ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	-0.511
EMD	emerin (Emery-Dreifuss muscular dystrophy)	-0.553
ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	-0.602
ERGIC1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	-0.603
ETNK2	ethanolamine kinase 2	-0.543
ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	-1.238
EXOC7	exocyst complex component 7	-0.76
F3	coagulation factor III (thromboplastin, tissue factor)	-0.647
FA2H	fatty acid 2-hydroxylase	-0.733
FAM22B	family with sequence similarity 22, member B	-0.523
FAM3A	family with sequence similarity 3, member A	-0.509
FAM40A	family with sequence similarity 40, member A	-0.719
FAM89A	family with sequence similarity 89, member A	-0.924
FBXL8	F-box and leucine-rich repeat protein 8	-0.647
FBXO31	F-box protein 31	-0.666
FBXO6	F-box protein 6	-0.566
FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	-1.017
FCHSD2	FCH and double SH3 domains 2	-0.511
FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	-0.598
FIBP	fibroblast growth factor (acidic) intracellular binding protein	-0.714
FJX1	four jointed box 1 (Drosophila)	-0.622
FKBP10	FK506 binding protein 10, 65 kDa	-0.577
FLJ22222	hypothetical protein FLJ22222	-0.787
FLJ22662	hypothetical protein FLJ22662	-0.625
FLJ44790	hypothetical FLJ44790///adhesion regulating molecule 1///oxysterol binding protein-like 2///laminin, alpha 5	-0.761
FNTB	farnesyltransferase, CAAX box, beta	-0.623
FOXL2	forkhead box L2	-0.599
FOXM1	forkhead box M1	-1.024
FOXRED1	FAD-dependent oxidoreductase domain containing 1	-0.564

FRAG1	FGF receptor activating protein 1	-0.627
FRMD1	FERM domain containing 1	-1.595
FUT10	fucosyltransferase 10 (alpha (1,3) fucosyltransferase)	-0.568
FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group)	-0.5755
FXN	frataxin	-0.594
FZD7	frizzled homolog 7 (Drosophila)	-0.584
GABRD	gamma-aminobutyric acid (GABA) A receptor, delta	-0.601
GAL3ST1	galactose-3-O-sulfotransferase 1	-1.139
GALE	UDP-galactose-4-epimerase	-0.878
GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA)	-0.755
GC	group-specific component (vitamin D binding protein)	-0.715
GDF1	growth differentiation factor 1	-0.661
GFRA4	GDNF family receptor alpha 4	-0.704
GJC2	gap junction protein, gamma 12, 47kDa	-0.844
GLI3	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)	-0.892
GMEB2	glucocorticoid modulatory element binding protein 2	-0.675
GMPPA	GDP-mannose pyrophosphorylase A	-0.669
GNG13	guanine nucleotide binding protein (G protein), gamma 13	-0.597
GNMT	glycine N-methyltransferase	-0.613
GNPDA1	glucosamine-6-phosphate deaminase 1	-0.815
GNRHR	gonadotropin-releasing hormone receptor	-0.553
GOLGA2	golgi autoantigen, golgin subfamily a, 2	-0.605
GORASP2	golgi reassembly stacking protein 2, 55kDa	-0.585
GOSR1	golgi SNAP receptor complex member 1	-0.656
GP5	glycoprotein V (platelet)	-0.717
GPR109B	G protein-coupled receptor 109B	-0.827
GPR12	G protein-coupled receptor 12	-0.942
GPR143	G protein-coupled receptor 143	-0.629
GPR182	G protein-coupled receptor 182	-0.683
GPSM3	G-protein signaling modulator 3 (AGS3-like, C. elegans)	-0.617
GRID2	glutamate receptor, ionotropic, delta 2	-0.895
GRIN2D	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	-0.555
GRN	granulin	-0.548

GTDC1	glycosyltransferase-like domain containing 1	-0.619
GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa	-0.849
GTF3C2	general transcription factor IIIC, polypeptide 2, beta 110kDa	-0.771
GTF3C4	general transcription factor IIIC, polypeptide 4, 90kDa	-0.604
H3F3A	H3 histone, family 3A	-0.591
HAAO	3-hydroxyanthranilate 3,4-dioxygenase	-0.509
HBA1	hemoglobin, alpha 1	-0.635
HBD	hemoglobin, delta	-0.782
HBE1	hemoglobin, epsilon 1	-0.555
HBQ1	hemoglobin, theta 1	-0.953
HCG4	HLA complex group 4	-0.574
HDAC11	histone deacetylase 11	-0.82
HEXA	hexosaminidase A (alpha polypeptide)	-1.211
HHAT	hedgehog acyltransferase	-0.548
HMBOX1	homeobox containing 1	-0.561
HOXA11	homeobox A11	-0.635
HOXB6	homeobox B6	-0.584
HSF4	heat shock transcription factor 4	-0.584
HTR4	5-hydroxytryptamine (serotonin) receptor 4	-0.671
HTRA3	HtrA serine peptidase 3	-0.565
HYAL1	hyaluronoglucosaminidase 1	-0.505
ICAM1	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	-0.886
IFITM2	interferon induced transmembrane protein 2 (1-8D)	-0.741
IK	IK cytokine, down-regulator of HLA II	-0.506
IL10RB	interleukin 10 receptor, beta	-0.74
IL12B	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)	-0.642
IL17RC	interleukin 17 receptor C	-0.508
IL1F10	interleukin 1 family, member 10 (theta)	-0.604
IL1F5	interleukin 1 family, member 5 (delta)	-0.676
ILVBL	ilvB (bacterial acetolactate synthase)-like	-0.658
IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	-0.508
INPP5F	inositol polyphosphate-5-phosphatase F	-0.777
IQSEC2	IQ motif and Sec7 domain 2	-0.822
ISY1	ISY1 splicing factor homolog (S. cerevisiae)	-0.647
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	-0.728

ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	-0.592
ITIH5	inter-alpha (globulin) inhibitor H5	-0.557
ITIH5L	inter-alpha (globulin) inhibitor H5-like	-0.547
ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	-0.574
IWS1	IWS1 homolog (S. cerevisiae)	-0.536
JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	-0.514
KARS	lysyl-tRNA synthetase	-0.7516
KCNG1	potassium voltage-gated channel, subfamily G, member 1	-0.563
KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member 6	-0.516
KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member 7	-0.539
KCNIP2	Kv channel interacting protein 2	-0.537
KCNJ11	potassium inwardly-rectifying channel, subfamily J, member 11	-0.533
KCNK15	potassium channel, subfamily K, member 15	-0.523
KCNK3	potassium channel, subfamily K, member 3	-0.57
KDELR1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	-0.609
KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	-0.99
KIAA0831	KIAA0831	-0.736
KIAA1128	KIAA1128	-0.618
KIAA1394	KIAA1394 protein	-0.567
KIAA1604	KIAA1604 protein	-0.586
KIAA1618	KIAA1618	-0.748
KIAA1632	KIAA1632	-0.579
KIAA1727	KIAA1727 protein	-0.83
KIAA1843	KIAA1843 protein	-1.702
KIF25	kinesin family member 25	-0.712
KIRREL	kin of IRRE like (Drosophila)	-0.55
KLF6	Kruppel-like factor 6	-0.61
KLF7	Kruppel-like factor 7 (ubiquitous)	-0.89
KLF8	Kruppel-like factor 8	-0.637
KLK2	kallikrein-related peptidase 2	-0.679
KLK7	kallikrein-related peptidase 7	-0.864
KRT31	keratin 31	-0.567
KRT32	keratin 32	-0.798
KRT35	keratin 35	-0.786
KRT9	keratin 9 (epidermolytic palmoplantar keratoderma)	-0.781
KRTAP3-2	keratin associated protein 3-2	-0.64

KRTAP4-4	keratin associated protein 4-4	-0.64
KRTAP4-8	keratin associated protein 4-8	-0.717
LEPRE1	leucine proline-enriched proteoglycan (leprecan) 1	-0.983
LETMD1	LETM1 domain containing 1	-0.624
LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	-0.589
LIN7C	lin-7 homolog C (C. elegans)	-1.022
LIPE	lipase, hormone-sensitive	-0.559
LMLN	leishmanolysin-like (metallopeptidase M8 family)	-0.824
LOC51252	hypothetical protein LOC51252	-0.82
LOC554202	hypothetical LOC554202	-0.788
LOC651900	hypothetical protein LOC651900	-0.791
LOC652231	L1 protein///v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	-0.687
LOC90113	hypothetical protein BC009862	-0.553
LONRF1	LON peptidase N-terminal domain and ring finger 1	-0.598
LPIN3	lipin 3	-0.624
LPPR2	lipid phosphate phosphatase-related protein type 2	-0.505
LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	-0.692
LRCH1	leucine-rich repeats and calponin homology (CH) domain containing 1	-1.354
LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	-0.742
LST1	leukocyte specific transcript 1	-0.644
LTBP3	latent transforming growth factor beta binding protein 3	-0.537
LTF	lactotransferrin	-0.804
LYRM1	LYR motif containing 1	-0.617
MACF1	microtubule-actin crosslinking factor 1	-0.612
MAK10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	-0.816
MAOB	monoamine oxidase B	-0.546
MAP1S	microtubule-associated protein 1S	-0.853
MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	-0.619
MAP7D1	MAP7 domain containing 1	-0.628
MAPK12	mitogen-activated protein kinase 12	-0.54

MAST1	microtubule associated serine/threonine kinase 1	-0.672
MATN2	matrilin 2	-0.923
MATN4	matrilin 4	-0.531
MBD2	methyl-CpG binding domain protein 2	-0.566
MCTP2	multiple C2 domains, transmembrane 2	-0.591
MDM2	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	-0.772
MED16	mediator complex subunit 16	-0.701
MED22	mediator complex subunit 22	-0.944
MEX3A	mex-3 homolog A (C. elegans)	-0.732
MFGE8	milk fat globule-EGF factor 8 protein	-0.656
MFSD2	major facilitator superfamily domain containing 2	-0.612
MGAT5	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	-0.549
MGC16025	hypothetical protein MGC16025	-0.874
MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	-0.789
MIF4GD	MIF4G domain containing	-0.535
MKRN2	makorin, ring finger protein, 2	-0.551
MLLT1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	-0.999
MN1	meningioma (disrupted in balanced translocation) 1	-0.794
MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	-0.557
MOSPD1	motile sperm domain containing 1	-0.69
MRPS10	mitochondrial ribosomal protein S10	-0.65
MS4A12	membrane-spanning 4-domains, subfamily A, member 12	-0.586
MTF1	metal-regulatory transcription factor 1	-0.727
MUC1	mucin 1, cell surface associated	-0.514
MVK	mevalonate kinase (mevalonic aciduria)	-0.61
MXRA8	matrix-remodelling associated 8	-0.532
MYBPC1	myosin binding protein C, slow type	-0.521
MYCNOS	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) opposite strand	-0.704
MYF5	myogenic factor 5	-0.693
MYF6	myogenic factor 6 (herculin)	-0.522
MYL2	myosin, light chain 2, regulatory, cardiac, slow	-0.559
NAPSA	napsin A aspartic peptidase	-0.844

NAV1	neuron navigator 1	-0.774
NCR2	natural cytotoxicity triggering receptor 2	-1
NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	-0.786
NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)	-0.606
NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	-0.525
NEK6	NIMA (never in mitosis gene a)-related kinase 6	-1.136
NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	-0.566
NEXN	nexilin (F actin binding protein)	-0.623
NF2	neurofibromin 2 (bilateral acoustic neuroma)	-0.605
NIBP	NIK and IKK{beta} binding protein	-0.577
NIN	ninein (GSK3B interacting protein)	-0.561
NIP30	NEFA-interacting nuclear protein NIP30	-0.507
NKD1	naked cuticle homolog 1 (Drosophila)	-0.733
NKX2-8	NK2 homeobox 8	-0.577
NLRP3	NLR family, pyrin domain containing 3	-0.794
NLRX1	NLR family member X1	-0.568
NMUR1	neuromedin U receptor 1	-0.723
NOVA1	neuro-oncological ventral antigen 1	-0.585
NPFFR1	neuropeptide FF receptor 1	-0.653
NPHS2	nephrosis 2, idiopathic, steroid-resistant (podocin)	-0.985
NPY6R	neuropeptide Y receptor Y6 (pseudogene)	-0.561
NR4A2	nuclear receptor subfamily 4, group A, member 2	-1.025
NR4A3	nuclear receptor subfamily 4, group A, member 3	-0.624
NRG1	neuregulin 1	-0.566
OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	-0.879
OBSCN	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	-0.679
ODF1	outer dense fiber of sperm tails 1	-1.117
OGFR	opioid growth factor receptor	-0.8145
OLFM1	olfactomedin 1	-0.704
ONECUT1	one cut homeobox 1	-0.935
ONECUT2	one cut homeobox 2	-0.578
OSBPL2	oxysterol binding protein-like 2	-0.593
OSTM1	osteopetrosis associated transmembrane protein 1	-0.519
OTOF	otoferlin	-0.547

OTUD4	OTU domain containing 4	-0.619
OTUD5	OTU domain containing 5	-0.528
OXA1L	oxidase (cytochrome c) assembly 1-like	-0.576
PACRG	PARK2 co-regulated	-0.509
PACS1	phosphofurin acidic cluster sorting protein 1	-0.566
PADI2	peptidyl arginine deiminase, type II	-0.664
PANK4	pantothenate kinase 4	-0.666
PAQR6	progestin and adipoQ receptor family member VI	-0.581
PCDHGA7	protocadherin gamma subfamily A, 7	-0.523
PCID2	PCI domain containing 2	-0.664
PCNX	pecanex homolog (Drosophila)	-1.028
PCTK3	PCTAIRE protein kinase 3	-0.636
PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	-1.137
PDZK1	PDZ domain containing 1	-0.546
PEA15	phosphoprotein enriched in astrocytes 15	-0.606
PELI2	pellino homolog 2 (Drosophila)	-0.574
PERP	PERP, TP53 apoptosis effector	-0.587
PEX26	peroxisome biogenesis factor 26	-0.592
PFDN6	prefoldin subunit 6	-0.528
PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-0.666
PFN1	profilin 1	-0.6
PHC2	polyhomeotic homolog 2 (Drosophila)	-0.594
PHF1	PHD finger protein 1	-0.928
PHLDB3	pleckstrin homology-like domain, family B, member 3	-0.648
PHPT1	phosphohistidine phosphatase 1	-0.755
PIGL	phosphatidylinositol glycan anchor biosynthesis, class L	-0.682
PIGO	phosphatidylinositol glycan anchor biosynthesis, class O///KIAA1539///stomatin (EPB72)-like 2///valosin-containing protein///Fanconi anemia, complementation group G	-0.524
PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	-0.621
PKD2	polycystic kidney disease 2 (autosomal dominant)	-0.557
PKM2	pyruvate kinase, muscle	-0.561
PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	-0.92
PLA2G4B	phospholipase A2, group IVB (cytosolic)	-0.583

PLAGL1	pleiomorphic adenoma gene-like 1	-0.504
PLD1	phospholipase D1, phosphatidylcholine-specific	-0.561
PLEKHA3	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3	-0.509
PLEKHA9	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 9	-0.507
PLEKHG4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	-0.786
PLEKHQ1	pleckstrin homology domain containing, family Q member 1	-0.877
PLUNC	palate, lung and nasal epithelium carcinoma associated	-0.546
PLXNB1	plexin B1	-0.813
PML	promyelocytic leukemia	-0.759
POLD4	polymerase (DNA-directed), delta 4	-0.51
POLE	polymerase (DNA directed), epsilon	-0.707
POLR1A	polymerase (RNA) I polypeptide A, 194kDa	-0.509
POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	-0.692
PPAPDC2	phosphatidic acid phosphatase type 2 domain containing 2///cell division cycle 37 homolog (S. cerevisiae)-like 1///chromosome 9 open reading frame 68///adenylate kinase 3///solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	-0.979
PPP1R12C	protein phosphatase 1, regulatory (inhibitor) subunit 12C	-0.747
PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	-0.518
PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	-0.549
PQLC1	PQ loop repeat containing 1	-0.591
PQLC2	PQ loop repeat containing 2	-0.525
PRB1	proline-rich protein BstNI subfamily 1	-0.656
PRH1	proline-rich protein HaeIII subfamily 1	-0.708
PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	-0.619
PRKCDBP	protein kinase C, delta binding protein	-0.529
PRKD1	protein kinase D1	-0.797
PRLH	prolactin releasing hormone	-0.648
PRLR	prolactin receptor	-0.542

PRMT2	protein arginine methyltransferase 2	-0.524
PRMT7	protein arginine methyltransferase 7	-0.595
PRR3	proline rich 3	-0.511
PRR5	proline rich 5 (renal)	-0.582
PRR7	proline rich 7 (synaptic)	-0.568
PRSS21	protease, serine, 21 (testisin)	-0.561
PSORS1C2	psoriasis susceptibility 1 candidate 2	-0.849
PSPHL	phosphoserine phosphatase-like	-0.72
PTCH2	patched homolog 2 (Drosophila)	-0.597
PTGES	prostaglandin E synthase	-0.596
PTGFR	prostaglandin F receptor (FP)	-0.67
PTPRS	protein tyrosine phosphatase, receptor type, S	-0.641
PVR	poliovirus receptor	-0.623
PYCRL	pyrroline-5-carboxylate reductase-like	-0.598
R3HDM2	R3H domain containing 2	-0.618
RAB14	RAB14, member RAS oncogene family	-0.624
RAB25	RAB25, member RAS oncogene family	-0.55
RAB27A	RAB27A, member RAS oncogene family	-0.661
RAB33A	RAB33A, member RAS oncogene family	-0.598
RABGAP1L	RAB GTPase activating protein 1-like	-0.694
RAD9A	RAD9 homolog A (S. pombe)	-0.548
RADIL	Rap GTPase interactor	-0.619
RAP1A	RAP1A, member of RAS oncogene family	-0.964
RASA4	RAS p21 protein activator 4	-0.516
RASGRP4	RAS guanyl releasing protein 4	-0.609
RASSF1	Ras association (RalGDS/AF-6) domain family 1	-0.614
RB1	retinoblastoma 1 (including osteosarcoma)	-0.732
RBM35B	RNA binding motif protein 35B	-0.936
RBM44	RNA binding motif protein 44///leucine rich repeat (in FLII) interacting protein 1	-0.657
REC8	REC8 homolog (yeast)	-0.766
RGS20	regulator of G-protein signaling 20	-0.527
RGS6	regulator of G-protein signaling 6	-0.682
RIC8A	resistance to inhibitors of cholinesterase 8 homolog A (C. elegans)	-0.597
RIPK3	receptor-interacting serine-threonine kinase 3	-0.556
RND3	Rho family GTPase 3	-0.599
RNF157	ring finger protein 157	-0.562
RNF186	ring finger protein 186	-0.83
RNF39	ring finger protein 39	-0.572
RNPEPL1	arginyl aminopeptidase (aminopeptidase B)-like 1	-0.704

RP5-886K2.1	neuronal thread protein AD7c-NTP	-0.71
RPS15	ribosomal protein S15	-0.818
RSAD1	radical S-adenosyl methionine domain containing 1	-0.653
S100A9	S100 calcium binding protein A9	-0.502
SALL3	sal-like 3 (Drosophila)	-0.571
SCAMP3	secretory carrier membrane protein 3	-0.798
SCAND1	SCAN domain containing 1	-0.662
SDCCAG1	serologically defined colon cancer antigen 1	-0.766
SEC23A	Sec23 homolog A (S. cerevisiae)	-0.526
SELPLG	selectin P ligand	-0.51
SERF1A	small EDRK-rich factor 1A (telomeric)	-0.617
SERPINC1	serpin peptidase inhibitor, clade C (antithrombin), member 1	-0.692
SETBP1	SET binding protein 1	-0.644
SEZ6L	seizure related 6 homolog (mouse)-like	-0.787
SF3B5	splicing factor 3b, subunit 5, 10kDa	-0.536
SFXN1	sideroflexin 1	-0.629
SH2B3	SH2B adaptor protein 3	-0.689
SIM2	single-minded homolog 2 (Drosophila)	-0.532
SIRT5	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	-0.519
SIX1	SIX homeobox 1	-0.59
SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	-0.549
SLC1A7	solute carrier family 1 (glutamate transporter), member 7	-0.5
SLC22A17	solute carrier family 22 (organic cation transporter), member 17	-0.705
SLC22A8	solute carrier family 22 (organic anion transporter), member 8	-0.923
SLC25A3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	-0.545
SLC25A39	solute carrier family 25, member 39	-0.721
SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	-0.664
SLC2A6	solute carrier family 2 (facilitated glucose transporter), member 6	-0.571
SLC34A1	solute carrier family 34 (sodium phosphate), member 1	-0.96
SLC38A1	solute carrier family 38, member 1	-0.708
SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	-0.65

SLC4A1	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	-0.893
SLC6A7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	-0.506
SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	-0.511
SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	-0.712
SLC8A2	solute carrier family 8 (sodium-calcium exchanger), member 2	-0.897
SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), member 1 (antiporter, Na+/H+, amiloride sensitive)	-0.608
SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	-0.679
SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	-0.575
SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	-0.56
SNAI1	snail homolog 1 (Drosophila)	-0.795
SNAPC4	small nuclear RNA activating complex, polypeptide 4, 190kDa	-0.57
SNX15	sorting nexin 15	-0.565
SOCS2	suppressor of cytokine signaling 2	-0.809
SOCS3	suppressor of cytokine signaling 3	-0.794
SORBS2	sorbin and SH3 domain containing 2	-0.633
SOX15	SRY (sex determining region Y)-box 15	-0.877
SOX17	SRY (sex determining region Y)-box 17	-0.509
SOX7	SRY (sex determining region Y)-box 7	-0.53
SPEG	SPEG complex locus	-0.816
SPEN	spen homolog, transcriptional regulator (Drosophila)	-0.56
SPINT2	serine peptidase inhibitor, Kunitz type, 2	-2.203
SPINT4	serine peptidase inhibitor, Kunitz type 4///WAP four-disulfide core domain 10B///WAP four-disulfide core domain 13	-0.603
SPTBN4	spectrin, beta, non-erythrocytic 4	-0.604
SREBF1	sterol regulatory element binding transcription factor 1	-0.595
SRF	serum response factor (c-fos serum response element-binding transcription factor)	-0.575
ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	-0.521

ST8SIA5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	-0.504
STAT2	signal transducer and activator of transcription 2, 113kDa	-0.782
STC1	stanniocalcin 1	-0.695
STK10	serine/threonine kinase 10	-0.798
STK40	serine/threonine kinase 40	-0.569
STX18	syntaxin 18	-0.569
STX5	syntaxin 5	-0.587
STX5	syntaxin 5	-0.516
TAPBP	TAP binding protein (tapasin)	-0.616
TAS2R1	taste receptor, type 2, member 1	-1.158
TASP1	taspase, threonine aspartase, 1	-0.596
TBC1D13	TBC1 domain family, member 13	-0.9
TBC1D4	TBC1 domain family, member 4	-0.593
TBX4	T-box 4	-0.606
TESK1	testis-specific kinase 1	-0.511
TETRAN	tetracycline transporter-like protein	-0.658
TG	thyroglobulin	-0.87
THSD4	thrombospondin, type I, domain containing 4	-0.559
THUMPD3	THUMP domain containing 3	-1.048
TIAF1	TGFB1-induced anti-apoptotic factor 1	-0.66
TIGD5	tigger transposable element derived 5	-0.512
TLOC1	translocation protein 1	-0.839
TMEM104	transmembrane protein 104	-0.747
TMEM132A	transmembrane protein 132A	-0.736
TMEM134	transmembrane protein 134	-0.594
TMEM140	transmembrane protein 140	-0.89
TMEM159	transmembrane protein 159	-0.679
TMEM176B	transmembrane protein 176B	-1.476
TMEM39B	transmembrane protein 39B	-0.707
TMEM63A	transmembrane protein 63A	-0.51
TMSB10	thymosin, beta 10	-0.577
TNFRSF25	tumor necrosis factor receptor superfamily, member 25	-0.734
TNIP1	TNFAIP3 interacting protein 1	-0.543
TNIP2	TNFAIP3 interacting protein 2	-0.63
TNRC6B	trinucleotide repeat containing 6B	-0.588
TOLLIP	toll interacting protein	-0.671
TP53AP1	TP53 activated protein 1	-0.583
TP53I11	tumor protein p53 inducible protein 11	-0.593
TPCN2	two pore segment channel 2	-0.663
TPST2	tyrosylprotein sulfotransferase 2	-0.712

TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	-0.71
TRAF4	TNF receptor-associated factor 4	-0.509
TRAM2	translocation associated membrane protein 2	-0.75
TRIM17	tripartite motif-containing 17	-0.552
TRIP13	thyroid hormone receptor interactor 13	-0.541
TRO	trophinin	-0.695
TSC22D3	TSC22 domain family, member 3	-0.534
TSPAN7	tetraspanin 7	-0.602
TXNDC15	thioredoxin domain containing 15	-0.718
UBC	ubiquitin C	-0.57
UBR4	ubiquitin protein ligase E3 component n-recognin 4	-1.364
UCHL5IP	UCHL5 interacting protein	-0.749
UCN3	urocortin 3 (stresscopin)	-1.447
UNC13B	unc-13 homolog B (C. elegans)	-0.55
USP52	ubiquitin specific peptidase 52	-0.616
UTF1	undifferentiated embryonic cell transcription factor 1	-0.778
UTS2	urotensin 2	-0.525
UTS2R	urotensin 2 receptor	-0.558
VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	-0.58
VIM	vimentin	-0.526
VIPR2	vasoactive intestinal peptide receptor 2	-0.849
VSIG4	V-set and immunoglobulin domain containing 4	-0.742
WDR59	WD repeat domain 59	-0.737
WDR60	WD repeat domain 60	-0.673
WNT4	wingless-type MMTV integration site family, member 4	-0.693
XCR1	chemokine (C motif) receptor 1	-0.542
ZBTB5	zinc finger and BTB domain containing 5	-0.657
ZC3H15	zinc finger CCCH-type containing 15	-0.556
ZCCHC2	zinc finger, CCHC domain containing 2	-0.5515
ZIC3	Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila)	-1.619
ZNF264	zinc finger protein 264	-0.875
ZNF395	zinc finger protein 395	-0.504
ZNF614	zinc finger protein 614	-0.519
ZNF646	zinc finger protein 646	-0.789

ZNF663	zinc finger protein 663///chromosome 20 open reading frame 157///engulfment and cell motility 2///makorin, ring finger protein, pseudogene 3	-0.536
ZNF768	zinc finger protein 768	-0.514
ZNF84	zinc finger protein 84	-0.902
ZP3	zona pellucida glycoprotein 3 (sperm receptor)	-0.587
ZRSR2	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	-0.605

Upregulated Genes

Gene.symbol	Gene.title	log2(fold change)
MARCH5	membrane-associated ring finger (C3HC4) 5	0.586
MARCH7	membrane-associated ring finger (C3HC4) 7	0.669
ABCF3	ATP-binding cassette, sub-family F (GCN20), member 3	0.521
ACTB	actin, beta	0.576
AFTPH	aftiphilin	0.617
AK1	adenylate kinase 1	0.51
AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	0.516
ALG2	asparagine-linked glycosylation 2 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase)	0.583
AP1S2	adaptor-related protein complex 1, sigma 2 subunit	0.697
AS3MT	arsenic (+3 oxidation state) methyltransferase	0.509
ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	0.627
ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	0.588
AZI2	5-azacytidine induced 2	0.638
C14orf104	chromosome 14 open reading frame 104	0.52
C1GALT1C1	C1GALT1-specific chaperone 1	0.573
C21orf66	chromosome 21 open reading frame 66	0.603
C7orf23	chromosome 7 open reading frame 23	0.584
C7orf30	chromosome 7 open reading frame 30	0.646
CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	0.67
CDC123	cell division cycle 123 homolog (S. cerevisiae)	0.545
CDC5L	CDC5 cell division cycle 5-like (S. pombe)	0.612
CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	0.646
CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	0.652
CKAP4	cytoskeleton-associated protein 4	0.669
CLDN10	claudin 10	0.554
CLIP4	CAP-GLY domain containing linker protein family, member 4	0.518
CLTCL1	clathrin, heavy chain-like 1	0.517

CMTM6	CKLF-like MARVEL transmembrane domain containing 6	0.818
COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	0.525
CSPP1	centrosome and spindle pole associated protein 1	0.57
CXCR4	chemokine (C-X-C motif) receptor 4	0.57
CYFIP2	cytoplasmic FMR1 interacting protein 2	0.535
DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	0.525
EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	0.55
ENOX1	ecto-NOX disulfide-thiol exchanger 1	0.673
ESD	esterase D/formylglutathione hydrolase	0.726
EYA4	eyes absent homolog 4 (Drosophila)	0.552
F12	coagulation factor XII (Hageman factor)	1.11
FAM49A	family with sequence similarity 49, member A	0.562
FAM49B	family with sequence similarity 49, member B	0.706
FAM57B	family with sequence similarity 57, member B	0.723
FASTKD3	FAST kinase domains 3	0.752
FLJ14959	hypothetical protein FLJ14959	0.501
FLJ20489	hypothetical protein FLJ20489	0.616
GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.590666667
GARS	glycyl-tRNA synthetase	0.512
GPR65	G protein-coupled receptor 65	0.556
HMGB1	high-mobility group box 1	0.735
HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	0.668
HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	0.536
HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	0.71
ICAM5	intercellular adhesion molecule 5, telencephalin	0.503
IRS2	insulin receptor substrate 2	0.57
ITCH	itchy homolog E3 ubiquitin protein ligase (mouse)	0.515
KIAA0265	KIAA0265 protein	0.512

LSM4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0.518
MGC70863	similar to RPL23AP7 protein	0.64
MIB1	mindbomb homolog 1 (Drosophila)	0.601
MSL3L1	male-specific lethal 3-like 1 (Drosophila)	0.543
MSLN	mesothelin	0.525
MSRB2	methionine sulfoxide reductase B2	0.704
NARFL	nuclear prelamin A recognition factor-like	0.703
NBR1	neighbor of BRCA1 gene 1	0.56
NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	0.714
NIF3L1	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	0.788
NMI	N-myc (and STAT) interactor	0.786
NONO	non-POU domain containing, octamer-binding	0.585
NOTCH2NL	Notch homolog 2 (Drosophila) N-terminal like	0.51
NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	0.505
NPTN	neuroplastin	0.867
NR1H4	nuclear receptor subfamily 1, group H, member 4	0.555
NR4A3	nuclear receptor subfamily 4, group A, member 3	0.689
PDK3	pyruvate dehydrogenase kinase, isozyme 3	0.596
PPP6C	protein phosphatase 6, catalytic subunit	0.761
PRDX4	peroxiredoxin 4	0.77
PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2	0.584
PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6	0.514
PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	0.501
PYGM	phosphorylase, glycogen; muscle (McArdle syndrome, glycogen storage disease type V)	0.695
QPCT	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	0.677
RAB24	RAB24, member RAS oncogene family	0.501
RBMS1	RNA binding motif, single stranded interacting protein 1	0.524
RDH16	retinol dehydrogenase 16 (all-trans)	0.699
RP5-1022P6.2	hypothetical protein KIAA1434	0.501
RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	0.554

SCFD1	sec1 family domain containing 1	0.553
SEBOX	SEBOX homeobox	0.644
SEMA6C	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	0.599
SETD3	SET domain containing 3	0.502
SF4	splicing factor 4	0.506
SFRS18	splicing factor, arginine/serine-rich 18	0.517
SIGLEC1	sialic acid binding Ig-like lectin 1, sialoadhesin	0.538
STX10	syntaxin 10	0.758
SYN3	synapsin III	0.656
TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	0.541
TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	0.521
TINP1	TGF beta-inducible nuclear protein 1	0.773
TLR5	toll-like receptor 5	0.517
TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	0.716
TPPP3	tubulin polymerization-promoting protein family member 3	0.665
TPST1	tyrosylprotein sulfotransferase 1	1.071
TUBA1B	tubulin, alpha 1b	0.607
UXT	ubiquitously-expressed transcript	0.57
VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	0.521
VAV1	vav 1 guanine nucleotide exchange factor	0.517
ZNF343	zinc finger protein 343	0.514

Supplementary Table 2. Enriched GO biological process terms among downregulated differentially expressed genes following methotrexate treatment in GSE35455

Term	Adjusted *P*-value	Odds Ratio	Genes
Negative Regulation of Receptor Signaling Pathway via JAK-STAT (GO:0046426)	0.0226	17.0918	*SOCS2; SOCS3; INPP5F; BCL3; NF2; SH2B3*
Amyloid Fibril Formation (GO:1990000)	0.0823	9.3961	*SERF1A; CDSN; RIPK3; MDM2; B2M; EMD*
Calcium-Mediated Signaling (GO:0019722)	0.0823	4.3282	*CX3CR1; PRKAA1; XCR1; PLA2G4B; CCR9; ATP2A2; NMUR1; MCTP2; SLC8A1; TPCN2; SLC9A1*
Negative Regulation of Receptor Signaling Pathway via STAT (GO:1904893)	0.0823	13.0345	*SOCS2; SOCS3; BCL3; NF2; SH2B3*
Positive Regulation of Bone Mineralization (GO:0030501)	0.0823	7.0798	*BMP4; ATP2B1; BMP7; SLC8A1; BMP6; WNT4; LTF*
Regulation of Receptor Signaling Pathway via JAK-STAT (GO:0046425)	0.0958	5.3410	*SOCS2; SOCS3; IL10RB; CAMK2A; BCL3; NF2; JAK3; SH2B3*
Regulation of Synaptic Vesicle Priming (GO:0010807)	0.0958	46.7971	*UNC13B; NAPSA; OSBPL2*
Regulation of Cardiac Conduction (GO:1903779)	0.0958	10.4260	*ATP2A2; ATP2B1; AGXT; SLC8A1; SLC8A2*
Positive Regulation of Biomineral Tissue Development (GO:0070169)	0.0958	6.0949	*BMP4; CEBPB; ATP2B1; BMP7; SLC8A1; BMP6; WNT4*
Myoblast Differentiation (GO:0045445)	0.0958	9.7738	*RB1; SRF; SOX15; NRG1; MAPK12*

Supplementary Table 3. Enriched disease annotations among 106 methotrexate-upregulated genes in GSE35455

Term	Adjusted *P*-value	Odds Ratio	Genes
LYMPHOMA	0.0372	54.6346	*CXCR4;ACTB*
IMMUNE SYSTEM CANCER	0.0372	54.6346	*CXCR4;ACTB*
NON-HODGKIN LYMPHOMA	0.0372	54.6346	*CXCR4;ACTB*
LYMPHATIC SYSTEM CANCER	0.0372	54.6346	*CXCR4;ACTB*
Abnormal Lymph Node B Cell Domain Morphology MP:0002344	0.0370	57.9145	*PTEN;CXCR4;TNFSF13B*

Supplementary Table 4. Gene set enrichment analysis of MSigDB Hallmark pathways in baseline synovial tissue (GSE45867)

Gene set enrichment analysis (fgsea) was performed using the MSigDB Hallmark gene set collection. Pathways are ordered by normalized enrichment score (NES). Adjusted P values were calculated using the Benjamini–Hochberg method. NES > 0 indicates relative enrichment in MTX responders, whereas NES < 0 indicates relative enrichment in MTX non-responders.

Pathway	NES	Adjusted *P* value
HALLMARK_PROTEIN_SECRETION	2.612	3.37×10^{-14}
HALLMARK_INTERFERON_GAMMA_RESPONSE	2.611	1.29×10^{-21}
HALLMARK_INTERFERON_ALPHA_RESPONSE	2.456	1.31×10^{-11}
HALLMARK_ALLOGRAFT_REJECTION	2.304	3.93×10^{-14}
HALLMARK_IL6_JAK_STAT3_SIGNALING	2.28	1.60×10^{-8}
HALLMARK_ANDROGEN_RESPONSE	2.163	6.20×10^{-8}
HALLMARK_COMPLEMENT	2.035	7.80×10^{-9}
HALLMARK_IL2_STAT5_SIGNALING	2.02	6.67×10^{-9}
HALLMARK_G2M_CHECKPOINT	1.991	2.91×10^{-8}
HALLMARK_MITOTIC_SPINDLE	1.979	5.47×10^{-8}
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	1.912	1.52×10^{-5}
HALLMARK_INFLAMMATORY_RESPONSE	1.875	7.38×10^{-7}
HALLMARK_TGF_BETA_SIGNALING	1.85	7.82×10^{-4}
HALLMARK_APOPTOSIS	1.828	1.25×10^{-5}
HALLMARK_KRAS_SIGNALING_UP	1.823	2.78×10^{-6}
HALLMARK_MTORC1_SIGNALING	1.8	4.68×10^{-6}
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	1.763	1.19×10^{-5}
HALLMARK_UV_RESPONSE_DN	1.753	1.05×10^{-4}
HALLMARK_PI3K_AKT_MTOR_SIGNALING	1.752	6.79×10^{-4}
HALLMARK_E2F_TARGETS	1.74	2.77×10^{-5}
HALLMARK_KRAS_SIGNALING_DN	−1.651	3.90×10^{-5}
HALLMARK_NOTCH_SIGNALING	1.604	1.55×10^{-2}
HALLMARK_TNFα_SIGNALING_VIA_NF-κB	1.56	1.05×10^{-3}
HALLMARK_MYC_TARGETS_V1	1.504	2.50×10^{-3}
HALLMARK_MYOGENESIS	−1.434	2.17×10^{-3}
HALLMARK_GLYCOLYSIS	1.394	1.61×10^{-2}
HALLMARK_APICAL_JUNCTION	1.284	8.49×10^{-2}
HALLMARK_OXIDATIVE_PHOSPHORYLATION	1.259	1.08×10^{-1}
HALLMARK_HEME_METABOLISM	1.224	1.50×10^{-1}
HALLMARK_UV_RESPONSE_UP	1.198	1.89×10^{-1}
HALLMARK_ESTROGEN_RESPONSE_EARLY	1.143	3.09×10^{-1}
HALLMARK_P53_PATHWAY	1.112	3.84×10^{-1}
HALLMARK_ANGIOGENESIS	1.112	4.38×10^{-1}
HALLMARK_HEDGEHOG_SIGNALING	1.109	4.38×10^{-1}
HALLMARK_HYPOXIA	1.105	3.84×10^{-1}
HALLMARK_COAGULATION	1.097	3.89×10^{-1}
HALLMARK_SPERMATOGENESIS	1.054	4.73×10^{-1}

HALLMARK_ADIPOGENESIS	1.014	5.81×10^{-1}
HALLMARK_PEROXISOME	1.012	5.81×10^{-1}
HALLMARK_XENOBIOTIC_METABOLISM	0.965	6.93×10^{-1}
HALLMARK_ESTROGEN_RESPONSE_LATE	0.935	7.44×10^{-1}
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	0.928	6.94×10^{-1}
HALLMARK_BILE_ACID_METABOLISM	0.896	7.64×10^{-1}
HALLMARK_WNT_BETA_CATENIN_SIGNALING	0.896	7.48×10^{-1}
HALLMARK_MYC_TARGETS_V2	−0.892	7.64×10^{-1}
HALLMARK_CHOLESTEROL_HOMEOSTASIS	0.859	7.64×10^{-1}
HALLMARK_APICAL_SURFACE	0.853	7.64×10^{-1}
HALLMARK_PANCREAS_BETA_CELLS	−0.824	8.49×10^{-1}
HALLMARK_DNA_REPAIR	0.813	8.96×10^{-1}
HALLMARK_FATTY_ACID_METABOLISM	0.78	9.21×10^{-1}

Supplementary Table 5. Leading-edge genes for significantly enriched Hallmark pathways in GSE45867

Leading-edge gene subsets were extracted from fgsea results for pathways with adjusted $P < 0.05$ and available leading-edge output.

Pathway	NES	Adjusted *P* value	Leading-edge genes
HALLMARK_ALLOGRAFT_REJECTION	2.304	3.93×10^{-14}	*CXCL9, FAS, JAK2, STAT1, TPD52, GCNT1, …*
HALLMARK_ANDROGEN_RESPONSE	2.163	6.20×10^{-8}	*MAF, CDK6, ELK4, UBE2J1, TPD52, TNFAIP8, …*
HALLMARK_APICAL_JUNCTION	1.284	8.49×10^{-2}	*CTNNA1, ADAM9, CD274, PTPRC, SKAP2, B4GALT1, …*
HALLMARK_ANGIOGENESIS	1.112	4.38×10^{-1}	*FSTL1, VCAN, NRP1, TNFRSF21, KCNJ8, SPP1*
HALLMARK_ADIPOGENESIS	1.014	5.81×10^{-1}	*ABCA1, UBQLN1, TANK, MTCH2, UCP2, SDHC, …*
HALLMARK_APICAL_SURFACE	0.853	7.64×10^{-1}	*CRYBG1, B4GALT1, NCOA6, ADAM10, GATA3, LYN, …*