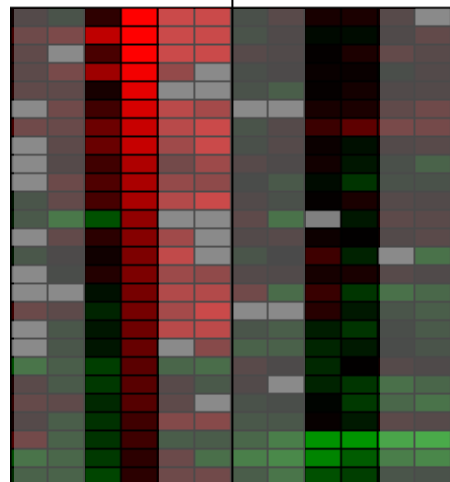


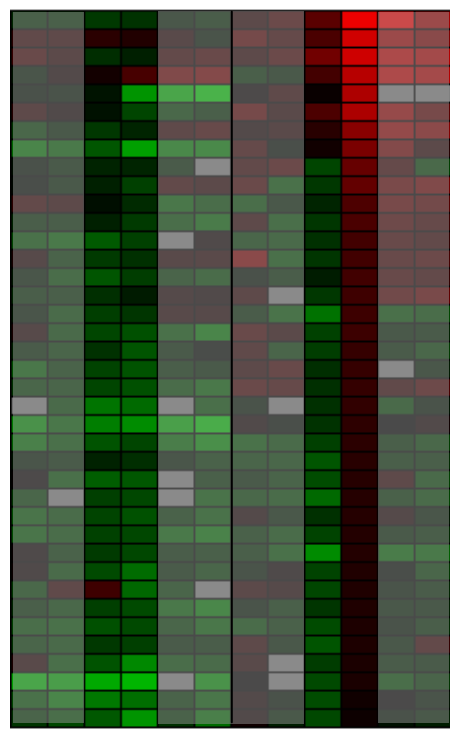
A



NM_005276
NM_006227
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XM_051191
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NM_006763
AC022015.4.64404.92131.1
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D43948
NM_002045
AF277315.2.1.94456.2
XM_030577
NM_001878
NM_018154
NM_005662

glycerol-3-phosphate dehydrogenase 1 (soluble); gpd1
phospholipid transfer protein; pltp
aquaporin 7; aqp7
hypothetical protein xp_098048; loc151361
apolipoprotein e; apoe
hypothetical protein flj22104; flj22104
likely ortholog of mouse polydom; polydom
nuclear receptor subfamily 1, group h, member 3; nr1h3
nuclear factor of activated t-cells, cytoplasmic, calcineurin-dependent 1; nfatc1
type 1 tumor necrosis factor receptor shedding aminopeptidase regulator; arts-1
hypothetical protein flj22104; flj22104
ensembl gencode prediction mwg oligo matches these RefSeq numbers NM_005063
btg family, member 2; btg2
ensembl gencode prediction
semaphorin sem2; loc56920
cyclin-dependent kinase inhibitor 2c; cdkn2c
peroxisomal long-chain acyl-coa thioesterase; zap128
orphan seven-transmembrane receptor, chemokine related; vshk1
guanylate binding protein 2, interferon-inducible; gbp2
kiaa0097 ha00943 cDNA clone for has a 1-bp insertion between 1475-1476 of the sequence kiaa0097.
growth associated protein 43; gap43
ensembl gencode prediction
atpase class ii type 9a; atp9a
cellular retinoic acid-binding protein 2; crabp2
hypothetical protein flj10604; flj10604
voltage-dependent anion channel 3; vdac3

B



NM_020351
NM_005654
XM_002704
AC024651.10.6973.97702.2
NM_002727
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AB051502
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AC025878.3.44634.48747.1
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AF117106
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NM_018188
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AC009716.4.1.68084.3
NM_007274

smooth muscle cell-expressed and macrophage conditioned medium-i; loc57086
nuclear receptor subfamily 2, group f, member 1; nr2f1
hypothetical protein flj10044; flj10044
ensembl gencode prediction
proteoglycan 1, secretory granule; prg1
atpase, na+/k+ transporting, beta 1 polypeptide; atp1b1
kiaa1715 protein; kiaa1715
oxytocin receptor; oxt
sex gene; hssexgene
atpase, ca++ transporting, plasma membrane 1; atp2b1
ensembl gencode prediction
hypothetical protein flj10337; kiaa1437
ensembl gencode prediction
htop1 topoisomerase 5'end
rec; loc51201
atpase, h+ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70kd, isoform 1; atp6a1
valosin-containing protein; vcp
ensembl prediction
n-acetylglucosamine-phosphate mutase; agm1
lysophospholipase i; lypla1
nucleoporin 50kd; nup50
rad51 homolog (reca homolog, e. coli) (s. cerevisiae); rad51
eti protein; eti
vascular endothelial growth factor c; vegfc
excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping
unknown
similar to unknown protein for image:4299322; loc90853
osteoclast stimulating factor 1; ostf1
deoxythymidylate kinase thymidylate kinase; dtymk
udp-galactose transporter related; ugtrel1
unknown (protein for mgo:16212)
m-phase phosphoprotein 6; mphosph6
igf-ii mRNA-binding protein 1; imp-1
v-ets erythroblastosis virus e26 oncogene homolog 1 (avian); ets1
similar to eukaryotic translation initiation factor 4e; eukaryotic translation initiation factor 4e-like 1 (h. sapiens);
hypothetical protein flj10709; flj10709
h3 histone family member d; h3fd
ensembl gencode prediction
cytosolic acyl coenzyme a thioester hydrolase; hbach