

## Additional file 6

Significantly over-represented transcription factor binding sites (TFBS) of 26 genes with a specific profile for the adipogenic commitment.

Rank	Transcription Factor Name (Matrix ID)	Total	Found	P-Value	Q-Value	UniGeneID	Gene Symbol	Gene Name
1	COUPTF (V\$COUPTF_Q6)	1872	7	1.95474E-06	0.000662657	Hs.134974 Hs.515465 Hs.188591 Hs.446685 Hs.438863 Hs.201253 Hs.405662	GAP43 APOE FLJ22104 ZAP128 NR1H3 ch-TOG CRABP2	Growth associated protein 43 Apolipoprotein E Hypothetical protein FLJ22104 Acyl-CoA thioesterase 2 Nuclear receptor subfamily 1, group H, member 3 Cytoskeleton associated protein 5 Cellular retinoic acid binding protein 2
2	PPAR, HNF-4, COUP, RAR (V\$DR1_Q3) Direct repeat 1	1835	6	2.68424E-05	0.004549783	Hs.134974 Hs.455323 Hs.188591 Hs.59729 Hs.438863 Hs.405662	GAP43 AQP7 FLJ22104 LOC56920 NR1H3 CRABP2	Growth associated protein 43 Aquaporin 7 Hypothetical protein FLJ22104 Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G Nuclear receptor subfamily 1, group H, member 3 Cellular retinoic acid binding protein 2
3	KROX (V\$KROX_Q6)	1597	5	0.000176864	0.019985633	Hs.519162 Hs.534074 Hs.439312 Hs.515465 Hs.188591	BTG2 NFATC1 PLTP APOE FLJ22104	BTG family, member 2 Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 Phospholipid transfer protein Apolipoprotein E Hypothetical protein FLJ22104
4	TTF-1 (V\$TTF1_Q6)	1911	5	0.000405312	0.027480171	Hs.491597 Hs.439312 Hs.26516 Hs.188591 Hs.436186	VDAC3 PLTP ASF1B FLJ22104 ARTS-1	Voltage-dependent anion channel 3 Phospholipid transfer protein ASF1 anti-silencing function 1 homolog B (S. cerevisiae) Hypothetical protein FLJ22104 Type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
5	GATA-3 (V\$GATA3_Q3) GATA-binding factor 3	1871	5	0.000367819	0.031172661	Hs.188591 Hs.59729 Hs.438863 Hs.386567 Hs.405662	FLJ22104 LOC56920 NR1H3 GBP2 CRABP2	Hypothetical protein FLJ22104 Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G Nuclear receptor subfamily 1, group H, member 3 Guanylate binding protein 2, interferon-inducible Cellular retinoic acid binding protein 2
6	c-Rel (V\$CREL_Q1) c-Rel	1913	4	0.003833323	0.056499841	Hs.534074 Hs.188591 Hs.386567 Hs.436186	NFATC1 FLJ22104 GBP2 ARTS-1	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 Hypothetical protein FLJ22104 Guanylate binding protein 2, interferon-inducible Type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
7	Barbie Box (V\$BARBIE_Q1) barbiturate-inducible element	1898	4	0.003726897	0.0574281	Hs.134974 Hs.455323 Hs.201253 Hs.405662	GAP43 AQP7 ch-TOG CRABP2	Growth associated protein 43 Aquaporin 7 Cytoskeleton associated protein 5 Cellular retinoic acid binding protein 2
8	COUP-TF, HNF-4 (V\$COUP_Q1)	1896	4	0.003712863	0.05993621	Hs.455323 Hs.446685 Hs.386567 Hs.405662	AQP7 ZAP128 GBP2 CRABP2	Aquaporin 7 Acyl-CoA thioesterase 2 Guanylate binding protein 2, interferon-inducible Cellular retinoic acid binding protein 2
9	HNF-4 (V\$HNF4_Q1) hepatic nuclear factor 4	1892	4	0.003684902	0.062459089	Hs.519162 Hs.455323 Hs.438863 Hs.386567	BTG2 AQP7 NR1H3 GBP2	BTG family, member 2 Aquaporin 7 Nuclear receptor subfamily 1, group H, member 3 Guanylate binding protein 2, interferon-inducible
10	Elk-1 (V\$ELK1_Q1) Elk-1	1891	4	0.003677935	0.065622096	Hs.455323 Hs.188591 Hs.438863 Hs.524418	AQP7 FLJ22104 NR1H3 GPD1	Aquaporin 7 Hypothetical protein FLJ22104 Nuclear receptor subfamily 1, group H, member 3 Glycerol-3-phosphate dehydrogenase 1 (soluble)

Rank	Transcription Factor Name (Matrix ID)	Total	Found	P-Value	Q-Value	UniGeneID	Gene Symbol	Gene Name
11	GF11 (V\$GF11_Q6)	1890	4	0.003670976	0.069136718	Hs.491597 Hs.188591 Hs.438863 Hs.386567	VDAC3 FLJ22104 NR1H3 GBP2	Voltage-dependent anion channel 3 Hypothetical protein FLJ22104 Nuclear receptor subfamily 1, group H, member 3 Guanylate binding protein 2, interferon-inducible
12	Poly A (V\$LSDSPOLYA_B) Lentiviral Poly A downstream element	1887	4	0.003650155	0.072788393	Hs.310512 Hs.491597 Hs.386567 Hs.524418	CCRL1 VDAC3 GBP2 GPD1	Chemokine (C-C motif) receptor-like 1 Voltage-dependent anion channel 3 Guanylate binding protein 2, interferon-inducible Glycerol-3-phosphate dehydrogenase 1 (soluble)
13	LXR (V\$LXR_Q3)	316	2	0.00536938	0.075842496	Hs.519162 Hs.188591	BTG2 FLJ22104	BTG family, member 2 Hypothetical protein FLJ22104
14	Pax-4 (V\$PAX4_01) Pax-4 binding sites	1885	4	0.00363632	0.077044531	Hs.134974 Hs.534074 Hs.439312 Hs.405662	GAP43 NFATC1 PLTP CRABP2	Growth associated protein 43 Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 Phospholipid transfer protein Cellular retinoic acid binding protein 2
15	PPAR (V\$PPARG_03) PPAR (peroxisome proliferator-activated receptor gamma)	1880	4	0.00360189	0.081402706	Hs.455323 Hs.188591 Hs.438863 Hs.405662	AQP7 FLJ22104 NR1H3 CRABP2	Aquaporin 7 Hypothetical protein FLJ22104 Nuclear receptor subfamily 1, group H, member 3 Cellular retinoic acid binding protein 2
16	v-Maf (V\$VMAF_01) v-Maf	1873	4	0.003554065	0.086059141	Hs.439312 Hs.438863 Hs.436186 Hs.405662	PLTP NR1H3 ARTS-1 CRABP2	Phospholipid transfer protein Nuclear receptor subfamily 1, group H, member 3 Type 1 tumor necrosis factor receptor shedding aminopeptidase regulator Cellular retinoic acid binding protein 2
17	E2F-1 (V\$E2F1_Q4) E2F-1	1856	4	0.003439742	0.089697888	Hs.519162 Hs.310512 Hs.534074 Hs.524418	BTG2 CCRL1 NFATC1 GPD1	BTG family, member 2 Chemokine (C-C motif) receptor-like 1 Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 Glycerol-3-phosphate dehydrogenase 1 (soluble)
18	E2 (V\$E2_Q6) papilloma virus regulator E2	1685	4	0.002427171	0.091423435	Hs.519162 Hs.439312 Hs.436186 Hs.405662	BTG2 PLTP ARTS-1 CRABP2	BTG family, member 2 Phospholipid transfer protein Type 1 tumor necrosis factor receptor shedding aminopeptidase regulator Cellular retinoic acid binding protein 2
19	PPAR direct repeat 1 (V\$PPAR_DR1_Q2)	1842	4	0.003347517	0.094567352	Hs.455323 Hs.188591 Hs.438863 Hs.405662	AQP7 FLJ22104 NR1H3 CRABP2	Aquaporin 7 Hypothetical protein FLJ22104 Nuclear receptor subfamily 1, group H, member 3 Cellular retinoic acid binding protein 2
20	E2 (V\$E2_Q6_01)	768	3	0.002280735	0.09664616	Hs.519162 Hs.439312 Hs.405662	BTG2 PLTP CRABP2	BTG family, member 2 Phospholipid transfer protein Cellular retinoic acid binding protein 2

CRSD: a comprehensive web server for composite regulatory signature discovery

P value threshold: 0.05

N value: 54576

There are 26 accession numbers in the request (transfer to UniGene ID):

Hs.525324(NM\_001262) Hs.439312(NM\_006227) Hs.201253(D43948) Hs.438863(NM\_005693) Hs.188591(NM\_022918) Hs.519162(NM\_006763) Hs.524418(NM\_005276) Hs.515465(NM\_000041) Hs.310512(NM\_016557) Hs.386567(NM\_004120) Hs.405662(NM\_001878) Hs.59729(NM\_020163) Hs.491597(NM\_005662) Hs.134974(NM\_002045) Hs.436186(NM\_016442) Hs.455323(NM\_001170) Hs.26516(NM\_018154) Hs.534074(NM\_006162) Hs.446685(NM\_006821)

There were 19 unique genes found.