

**S8 Table. List of Differentially Expressed Adipogenesis Network and Anchor Genes.**

<b>L<sub>path adipog</sub> Genes</b>				
<b>Probe Set ID</b>	<b>Gene Symbol</b>	<b>Gene Title</b>	<b>Log<sub>2</sub>FC</b>	<b>L<sub>anchor adipog Genes</sub></b>
1422651_at	Adipoq	adiponectin, C1Q and collagen domain containing	-0.421347	
1435077_at	ASXL1	additional sex combs like 1	-0.542604	
1422912_at	BMP4	bone morphogenetic protein 4	-1.195104	
1418982_at	CEBPa	CCAAT/enhancer binding protein (C/EBP), alpha	-1.055289	
1427844_a_at	CEBPb	CCAAT/enhancer binding protein (C/EBP), beta	-1.416855	L <sub>anchor</sub>
1418901_at	CEBPb	CCAAT/enhancer binding protein (C/EBP), beta	-0.727956	
1423233_at	CEBPd	CCAAT/enhancer binding protein (C/EBP), delta	-1.336919	
1456605_at	CEBPd	CCAAT/enhancer binding protein (C/EBP), delta	-0.516927	L <sub>anchor</sub>
1437745_at	CHD7	chromodomain helicase DNA binding protein 7	-1.441792	L <sub>anchor</sub>
1438992_x_at	CREB2	activating transcription factor 4	0.514875	
1448135_at	CREB2	activating transcription factor 4	-0.441271	L <sub>anchor</sub>
1424471_at	EPAC	Rap guanine nucleotide exchange factor (GEF) 3	-0.974207	L <sub>anchor</sub>
1427060_at	ERK1	mitogen-activated protein kinase 3	-0.883972	L <sub>anchor</sub>
1426585_s_at	ERK2	mitogen-activated protein kinase 1	-1.202173	
1416544_at	EZH2	enhancer of zeste homolog 2 (Drosophila)	-0.497959	
1448886_at	GATA3	GATA binding protein 3	-0.418089	L <sub>anchor</sub>
1421866_at	GR	nuclear receptor subfamily 3, group C, member 1	-0.788955	
1421867_at	GR	nuclear receptor subfamily 3, group C, member 1	-1.375725	
1433444_at	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	-0.797982	
1433445_x_at	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	-0.609106	L <sub>anchor</sub>
1424458_at	JMJDC2C	lysine (K)-specific demethylase 4C	-0.868275	
1417395_at	KLF4	Kruppel-like factor 4 (gut)	-2.299423	
1451022_at	LRP6	low density lipoprotein receptor-related protein 6	0.746302	L <sub>anchor</sub>
1427150_at	MLL3	lysine (K)-specific methyltransferase 2C	-0.518829	
1416572_at	MMP14	matrix metalloproteinase 14 (membrane-inserted)	-0.48744	

1448383_at	MMP14	matrix metalloproteinase 14 (membrane-inserted)	-1.078622	
1423202_a_at	NCOR1	nuclear receptor co-repressor 1	-0.722665	L_anchor
1448893_at	NCOR2	nuclear receptor co-repressor 2	-1.35313	
1456467_s_at	NLK	nemo like kinase	0.742247	
1425837_a_at	Nocturnin	CCR4 carbon catabolite repression 4-like ( <i>S. cerevisiae</i> )	-0.806877	
1426464_at	NR1D1	nuclear receptor subfamily 1, group D, member 1	-1.475204	L_anchor
1425615_a_at	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	-0.925597	
1425580_a_at	PIK3C3	phosphoinositide-3-kinase, class 3	-0.779372	
1429434_at	PIK3Ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	0.813153	
1429435_x_at	PIK3Ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	0.677044	
1460326_at	PIK3Ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	-0.837878	
1453069_at	PIK3Cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide	-1.025567	L_anchor
1443798_at	PIK3Cd	phosphatidylinositol 3-kinase catalytic delta polypeptide	2.096801	L_anchor
1420611_at	PKA	protein kinase, cAMP dependent, catalytic, beta	-0.948384	
1450519_a_at	PKA	protein kinase, cAMP dependent, catalytic, alpha	-1.385787	
1423302_a_at	PTIP	PAX interacting (with transcription-activation domain) protein 1	-0.622208	
1423303_at	PTIP	PAX interacting (with transcription-activation domain) protein 1	-1.382188	
1454943_a_at	PTIP	PAX interacting (with transcription-activation domain) protein 1	-0.423649	
1423734_at	RAC1	RAS-related C3 botulinum substrate 1	-0.736388	
1425762_a_at	RXRa	retinoid X receptor alpha	-0.5068	L_anchor
1454773_at	RXRa	retinoid X receptor alpha	-1.106345	
1416990_at	RXRb	retinoid X receptor beta	-0.675337	
1426406_at	SETD8	SET domain containing (lysine methyltransferase) 8	-0.902194	
1416670_at	SETDB1	SET domain, bifurcated 1	0.615873	
1451833_a_at	SETDB1	SET domain, bifurcated 1	-0.446396	
1423507_a_at	SIRT2	sirtuin 2	-0.733882	L_anchor
1415958_at	SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4	-1.523955	

1415959_at	SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4	-2.300591	
1459843_s_at	SMAD1	SMAD family member 1	0.881402	
1448994_at	SP1	trans-acting transcription factor 1	0.472075	
1426690_a_at	SREBF1	sterol regulatory element binding transcription factor 1	-1.385623	L_anchor
1450008_a_at	$\beta$ catenin	catenin (cadherin associated protein), beta 1	-2.198538	
1420811_a_at	$\beta$ catenin	catenin (cadherin associated protein), beta 1	-0.817598	
1426587_a_at	STAT3	signal transducer and activator of transcription 3	-1.599634	L_anchor
1459961_a_at	STAT3	signal transducer and activator of transcription 3	-1.049479	
1460700_at	STAT3	signal transducer and activator of transcription 3	-1.144656	
1421469_a_at	STAT5A	signal transducer and activator of transcription 5A	-1.101546	
1417440_at	SWI1	AT rich interactive domain 1A (SWI-like)	-1.505176	
1455979_at	SWI1	AT rich interactive domain 1B (SWI-like)	0.518932	
1426804_at	SWI2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	-1.263507	
1426805_at	SWI2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	-1.912802	
1450461_at	TCF7	transcription factor 7, T cell specific	0.461626	
1433471_at	TCF7	transcription factor 7, T cell specific	-0.295828	L_anchor
1423250_a_at	TGFB2	transforming growth factor, beta 2	-0.318399	L_anchor
1450922_a_at	TGFB2	transforming growth factor, beta 2	-0.711545	
1419089_at	TIMP3	tissue inhibitor of metalloproteinase 3	-1.475497	
1458512_at	TLE3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	-0.911589	L_anchor
1451006_at	XDH	xanthine dehydrogenase	-1.057305	