Table S5 Gene promoters with differential H3K27me3 read counts in the foetal and lamb developmental states

RefSeq autosomal genes with differences in H3K27me3 read density within their promoters in the fetal and lamb states were identified using CLCBIO (n=3/ group; $P^{adj} <0.05$) . Also included are details of the DAVID Functional Annotation Clustering (Enrichment Score ≥ 1.0) and GO analyses (P ≤ 0.05) (CLCBIO).

A. Diff Modified Genes

Feature ID	Fold change	t-test: fetus vs lamb normalized values - P-value	t-test: fetus vs lamb normalized values - FDR p-value correction	fetus - Normalized means	lamb - Normalized means
EPN3	-16.9246	1.27E-06	0.005665	2.369444	0.14
MCM6	-18.95	1.05E-06	0.005665	1.895	0.1
MDN1	-18.7057	1.38E-06	0.005665	2.753889	0.147222
APOH	89.56667	3.18E-06	0.009778	0.1	8.956667
DCDC1	-35.55	5.43E-06	0.012524	3.555	0.1
ECHS1	-10.95	6.11E-06	0.012524	1.095	0.1
ELAC2	9.40617	1.91E-05	0.028989	0.216111	2.032778
FAM78B	-44.7285	1.68E-05	0.028989	7.231111	0.161667
PRR15	-2.61053	2.12E-05	0.028989	165.2828	63.31389
PPP1R32	107.4444	2.75E-05	0.033751	0.1	10.74444
CDKL3	-81.9611	3.64E-05	0.040023	8.196111	0.1
OLFML2B	282.8833	3.91E-05	0.040023	0.1	28.28833
MACROD2	-42.6278	4.26E-05	0.040316	4.262778	0.1
TPST2	-6.76485	5.42E-05	0.047592	3.164444	0.467778
BTBD17	11.01035	6.08E-05	0.049802	1.502778	16.54611
CRYAB	19.9979	7.49E-05	0.054165	0.793889	15.87611
RARG	-12.9321	7.45E-05	0.054165	63.71222	4.926667
CCDC94	65.92222	0.000106	0.066359	0.1	6.592222
KCTD1	-7.53069	0.0001	0.066359	55.13722	7.321667
S100A4	113.5167	0.000108	0.066359	0.1	11.35167
BHLHE40	-166.933	0.000123	0.071827	16.69333	0.1
IRX5	1.654697	0.000147	0.072074	51.73722	85.60944
PLEKHA3	-18.2833	0.000145	0.072074	1.828333	0.1
SEMA3B	21.47372	0.000144	0.072074	0.856111	18.38389
STARD5	-8.3258	0.00014	0.072074	4.500556	0.540556
C15H11orf57	-18.0167	0.000171	0.072127	1.801667	0.1
CDH18	-78.2778	0.000182	0.072127	7.827778	0.1
METTL21C	21.5852	0.000193	0.072127	0.397778	8.586111
PEX14	-11.0222	0.00019	0.072127	1.102222	0.1

PSAPL1	11.27884	0.000176	0.072127	1.362778	15.37056
RIN1	-26.7969	0.000154	0.072127	17.52222	0.653889
SCN5A	1.466453	0.000166	0.072127	61.29833	89.89111
SLC5A2	-22.6473	0.000194	0.072127	3.46	0.152778
HHEX	-1.78305	0.000219	0.076874	102.8272	57.66944
ZNF483	30.88965	0.000214	0.076874	0.568889	17.57278
FAM83D	-31.6941	0.000246	0.077433	2.993333	0.094444
FUT1	1.796303	0.000245	0.077433	15.92778	28.61111
PPP1R13L	-116.383	0.000241	0.077433	11.63833	0.1
TRIM25	-22.793	0.000234	0.077433	7.952222	0.348889
EML6	-4.32379	0.000255	0.078216	23.39889	5.411667
SIRPA	174.1611	0.000263	0.078776	0.1	17.41611
INSM1	-2.53575	0.000277	0.080947	28.21444	11.12667
RASL11B	-3.35574	0.000292	0.08169	8.542222	2.545556
SYNE2	-30.7768	0.000288	0.08169	5.745	0.186667
AQP1	150.3222	0.000319	0.082421	0.1	15.03222
CBY1	40.9	0.000362	0.082421	0.1	4.09
CDH8	-2.52089	0.00031	0.082421	50.98222	20.22389
IGLON5	2.469834	0.000352	0.082421	13.04833	32.22722
LIN28A	1.847622	0.000305	0.082421	36.62667	67.67222
MLXIPL	2.186318	0.000351	0.082421	14.51222	31.72833
NMBR	3.088122	0.000354	0.082421	17.77833	54.90167
PCGF1	-139.067	0.000351	0.082421	13.90667	0.1
PTGES	-1.95523	0.000362	0.082421	47.34056	24.21222
RAB11A	-6.89002	0.000338	0.082421	1.879444	0.272778
CACNB4	2.035516	0.000376	0.082462	36.25889	73.80556
ITGB5	-5.52423	0.00037	0.082462	15.83	2.865556
GPR84	9.776915	0.000416	0.083053	1.573889	15.38778
HEATR8	2.527242	0.000439	0.083053	4.292778	10.84889
IPO11	-15.6889	0.000411	0.083053	1.568889	0.1
LIMCH1	10.68645	0.000415	0.083053	0.561667	6.002222
MARCKS	36.96044	0.000421	0.083053	0.351111	12.97722
PPP1R1A	6.961028	0.000432	0.083053	1.297222	9.03
PRDM1	-16.0719	0.000413	0.083053	38.34944	2.386111
SCRT1	3.668676	0.000436	0.083053	17.14333	62.89333
TMEM180	-6.39825	0.000431	0.083053	3.650556	0.570556
DBNDD2	-11.2378	0.000469	0.084832	25.285	2.25
GNG2	19.37931	0.000462	0.084832	0.354444	6.868889
NEK6	41.36111	0.000466	0.084832	0.1	4.136111
FAM78A	-13.3556	0.000491	0.086177	20.55278	1.538889
HPCA	4.174969	0.000485	0.086177	24.90278	103.9683

PDK4	76.67222	0.000511	0.088519	0.1	7.667222
LRRC10B	1.968779	0.000525	0.089649	26.95833	53.075
GALNTL6	-2.38554	0.00054	0.090362	48.75778	20.43889
LIN7C	47.93333	0.000544	0.090362	0.1	4.793333
EMILIN2	3.681276	0.00062	0.101564	10.66056	39.24444
MC4R	-1.79966	0.000641	0.102257	14.28333	7.936667
RASGRP2	-27.5442	0.000639	0.102257	38.24056	1.388333
37316	-44.3648	0.000659	0.102499	3.918889	0.088333
RHOF	-170.994	0.000655	0.102499	17.09944	0.1
AFAP1L2	-11.2039	0.000724	0.104998	7.693333	0.686667
ARID3A	-14.9326	0.000712	0.104998	17.22222	1.153333
GABRA5	-10.772	0.000726	0.104998	48.905	4.54
GUCA2B	11.37561	0.000718	0.104998	0.792778	9.018333
NPAS2	-31.5268	0.000735	0.104998	5.885	0.186667
NUAK2	-4.12579	0.000743	0.104998	12.62722	3.060556
PXMP4	6.02109	0.00073	0.104998	4.241111	25.53611
RAPGEF4	-12.9519	0.000726	0.104998	8.972778	0.692778

B. DAVID Cluster Analysis

Category	Term	Count	%	P-value	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benjamini P-value
Annotation Cluster 1 **Enrichment Score: 3.127263706769486**										
GOTERM_CC_FAT	GO:0005886~plasma membrane	16	20.77922	5.30E-05	GPR84, CRYAB, GABRA5, ITGB5, LIN7C, CACNB4, AQP1, CDH8, CDH18, RASGRP2, MC4R, RAB11A, MARCKS, GNG2, RHOF, SCN5A	32	1186	6966	2.936762	0.005236
SP_PIR_KEYWORDS	cell membrane	10	12.98701	8.22E-04	GPR84, CDH18, GABRA5, RASGRP2, MC4R, LIN7C, RAB11A, MARCKS, GNG2, RHOF	41	475	7349	3.773556	0.084946
SP_PIR_KEYWORDS	membrane	19	24.67532	0.009529	TPST2, GPR84, SLC5A2, GABRA5, ITGB5, LIN7C, AQP1, SIRPA, CDH8, TMEM180, PTGES, CDH18, PXMP4, RASGRP2, MC4R, RAB11A, MARCKS, GNG2, RHOF	41	1963	7349	1.734913	0.291556
Annotation Cluster 2 **Enrichment Score: 1.3881714905758415**										
GOTERM_BP_FAT	GO:0003001~generation of a signal involved in cell-cell signaling	3	3.896104	0.010418	MC4R, LIN7C, CACNB4	36	39	8785	18.77137	0.95943
GOTERM_BP_FAT	GO:0046903~secretion	3	3.896104	0.081067	MC4R, LIN7C, CACNB4	36	119	8785	6.151961	0.97517
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	3	3.896104	0.081067	MC4R, LIN7C, CACNB4	36	119	8785	6.151961	0.97517
Annotation Cluster 3 **Enrichment Score: 1.0175944387326201**										
GOTERM_CC_FAT	GO:0030054~cell junction	4	5.194805	0.059586	GABRA5, RASGRP2, LIN7C, SCN5A	32	202	6966	4.310644	0.7814
SP_PIR_KEYWORDS	synapse	3	3.896104	0.061032	GABRA5, RASGRP2, LIN7C	41	74	7349	7.266645	0.572649
GOTERM_CC_FAT	GO:0045202~synapse	3	3.896104	0.13545	GABRA5, RASGRP2, LIN7C	32	145	6966	4.503879	0.798306
SP_PIR_KEYWORDS	cell junction	3	3.896104	0.17264	GABRA5, RASGRP2, LIN7C	41	138	7349	3.896607	0.818344

C. DAVID GO Biological Process

Term	Count	%	P-Value	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benjamini P-value
GO:0003001~generation of a signal involved in cell-cell signaling	3	3.896104	0.010418	MC4R, LIN7C, CACNB4	36	39	8785	18.77137	0.95943
GO:0007610~behavior	4	5.194805	0.028304	NPAS2, GABRA5, MC4R, CACNB4	36	167	8785	5.844977	0.987636
GO:0007264~small GTPase mediated signal transduction	4	5.194805	0.029626	RASL11B, RASGRP2, RAB11A, RHOF	36	170	8785	5.74183	0.953465
GO:0045449~regulation of transcription	10	12.98701	0.035174	INSM1, HHEX, NPAS2, RARG, MLXIPL, PEX14, CBY1, ZNF483, PCGF1, MCM6	36	1166	8785	2.092863	0.935382
GO:0007242~intracellular signaling cascade	6	7.792208	0.045668	RASL11B, RARG, RASGRP2, RAB11A, RHOF, DCDC1	36	498	8785	2.940094	0.942772
GO:0007517~muscle organ development	3	3.896104	0.045751	CRYAB, CBY1, CACNB4	36	86	8785	8.512597	0.908222
GO:0007214~gamma-aminobutyric acid signaling pathway	2	2.597403	0.046804	GABRA5, CACNB4	36	12	8785	40.6713	0.876981

D. DAVID GO Cellular Component

Term	Count	%	P-Value	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benjamini P-value
GO:0005886~plasma membrane	16	20.77922	5.30E-05	GPR84, CRYAB, GABRA5, ITGB5, LIN7C, CACNB4, AQP1, CDH8, CDH18, RASGRP2, MC4R, RAB11A, MARCKS, GNG2, RHOF, SCN5A	32	1186	6966	2.936762	0.005236
GO:0044459~plasma membrane part	9	11.68831	0.010978	GABRA5, RASGRP2, LIN7C, ITGB5, GNG2, CACNB4, AQP1, SCN5A, RHOF	32	715	6966	2.740122	0.420979
GO:0019898~extrinsic to membrane	4	5.194805	0.028806	RASGRP2, LIN7C, RAB11A, GNG2	32	151	6966	5.766556	0.618845