Supplementary table

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Table 1- Sample details in each datasets

	gse121233				
s.no.	File Name	Hybridization Controls Threshold	Pos vs Neg AUC Threshold	Condition	group
1	GSM3428207_Control_1.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
2	GSM3428209_Control_3.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
3	GSM3428210_Control_4.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
4	GSM3428211_Control_5.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
5	GSM3428212_FSGS_1.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
6	GSM3428213_FSGS_2.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
7	GSM3428214_FSGS_3.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
8	GSM3428216_FSGS_5.sst-rma-combined-dabg.chp	Out	Pass	A	fsgs
	gse125779				
s.no.	File Name	Hybridization Controls Threshold	Pos vs Neg AUC Threshold	Condition	group
1	GSM3581796_C1T.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
2	GSM3581797_C2T.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
3	GSM3581798_C3T.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
4	GSM3581799_C4T.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
5	GSM3581800_C5T.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
6	GSM3581801_C6T.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
7	GSM3581803_C8T.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
8	GSM3581804_F1T.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
9	GSM3581805_F2T.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
10	GSM3581806_F3T.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
11	GSM3581807_F4T.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
12	GSM3581808_F5T.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
13	GSM3581809_F6T.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
14	GSM3581810_F7T.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
15	GSM3581811_F8T.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs

	gse129973				
s.no.	File Name	Hybridization Controls Threshold	Pos vs Neg AUC Threshold	Condition	
1	GSM3728791_N01.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
2	GSM3728792_N02.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
3	GSM3728793_N03.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
4	GSM3728794_N04.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
5	GSM3728795_N05.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
6	GSM3728796_N06.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
7	GSM3728797_N07.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
8	GSM3728798_N08.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
9	GSM3728799_N09.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
10	GSM3728800_N10.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
11	GSM3728801_N11.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
12	GSM3728802_N12.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
13	GSM3728803_N13.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
14	GSM3728804_N14.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
15	GSM3728805_N15.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
16	GSM3728806_N16.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
17	GSM3728807_N17.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
18	GSM3728808_N18.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
19	GSM3728809_N19.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
20	GSM3728810_N20.sst-rma-combined-dabg.chp	Pass	Pass	C	cnt
21	GSM3728811_F01.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
22	GSM3728812_F02.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
23	GSM3728813_F03.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
24	GSM3728814_F04.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
25	GSM3728815_F05.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
26	GSM3728816_F06.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
27	GSM3728817_F07.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
28	GSM3728818_F08.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs

29	GSM3728819_F09.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
30	GSM3728820_F10.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
31	GSM3728821_F11.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
32	GSM3728822_F12.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
33	GSM3728823_F13.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
34	GSM3728824_F14.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
35	GSM3728825_F15.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
36	GSM3728826_F16.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
37	GSM3728827_F17.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
38	GSM3728828_F18.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
39	GSM3728829_F19.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs
40	GSM3728830_F20.sst-rma-combined-dabg.chp	Pass	Pass	A	fsgs

Table 2- Differentially regulated DEGs in dataset GSE121233

upregulated	**Gene Symbol**	**fsgs Avg (log2)**	**Cnt Avg (log2)**	**Fold Change**	**P-val**	**FDR P-val**
1	ABCA1	6.26	5.12	2.2	0.0027	0.1389
2	ABCG1	6.31	5.17	2.21	0.0009	0.0822
3	ADAMTS1	9.46	7.06	5.28	0.0004	0.0558
4	ANPEP	13.94	12.21	3.32	0.0402	0.4151
5	AXL	8.65	6.66	3.99	0.0013	0.0967
6	B2M	10.66	9.6	2.08	0.0016	0.1064
7	BIRC5	5.84	4.15	3.23	0.0061	0.1921
8	BMP2	8.1	7.01	2.14	0.0371	0.4026
9	C3	5.61	4.43	2.28	0.0069	0.2038
10	C7	9.86	7.82	4.11	0.0043	0.1658
11	CCDC85C	5.98	4.93	2.07	0.0007	0.0755
12	CD68	10.81	9.17	3.12	0.011	0.2508
13	CDH6	8.91	6.36	5.82	0.0237	0.3372
14	CHD3	9.59	8.3	2.45	0.0001	0.0346
15	CLDN1	8.49	6.74	3.36	0.0077	0.2134
16	CLIP3	8.12	7.09	2.04	0.0009	0.0843
17	COL4A1	7.02	5.95	2.1	0.0167	0.2933
18	DNM1P46	5.38	4.31	2.1	0.0041	0.1627
19	ECM1	8.87	6.65	4.65	0.0093	0.2335
20	FAM101B	7.38	6.07	2.48	0.0023	0.128
21	FBLN5	7.97	6.58	2.62	0.015	0.2805

22	FN1	6.97	4.89	4.22	0.0152	0.2825
23	GADD45A	12	10.98	2.02	0.0002	0.0417
24	GNAO1	7.48	6.47	2.02	0.0045	0.1674
25	HAVCR1	5.2	4.16	2.06	0.0361	0.3981
26	HIST1H3B	5	3.58	2.67	0.0092	0.2329
27	HNF1A-AS1	5.36	4.35	2.02	0.006	0.1913
28	IGFBP1	5.84	4.66	2.27	0.0414	0.42
29	ISX	4.66	3.57	2.13	0.0042	0.1649
30	ITGB6	5.39	4.06	2.51	0.003	0.1433
31	KDELR3	9.09	6.75	5.05	0.0013	0.0957
32	KLK6	14.51	13.07	2.71	0.0376	0.404
33	LINC01314	5.02	3.75	2.42	0.0164	0.2907
34	LRRC55	9.14	5.18	15.61	0.0002	0.0477
35	LUM	6.52	5.17	2.56	0.0213	0.3225
36	LYVE1	6.65	4.28	5.19	0.0026	0.135
37	MFGE8	6.48	5.28	2.3	0.001	0.0881
38	MIR1299	9.05	7.44	3.06	0.0406	0.4173
39	MIR3192	5.82	4.58	2.36	0.002	0.1197
40	MIR3911	6.37	4.68	3.24	0.0045	0.1672
41	MIR4440	5.71	4.67	2.05	0.0006	0.0687
42	MIR4454	11.39	10.23	2.24	5.68E-05	0.029
43	MIR4521	6.56	4.57	3.99	0.0387	0.4088
44	MLXIP	7.89	6.85	2.05	7.50E-05	0.0309
45	MYBPH	7.29	5.45	3.58	5.85E-05	0.0292
46	MYOF	10.01	8.57	2.72	0.0062	0.1932
47	NEAT1; MIR612	9.09	7.54	2.93	0.0011	0.0918
48	NID1	6.58	5.28	2.48	0.0048	0.1728
49	NPIPB11	10.83	9.48	2.55	0.0007	0.0714
50	NPIPB4; NPIPB3	13.79	12.35	2.71	0.0019	0.1176
51	NPIPB5; NPIPB4; NPIPB3	14.17	12.6	2.97	0.0409	0.418
52	NR1D1	7.82	5.6	4.65	0.0035	0.1523
53	NRIP2	11.29	9.63	3.16	0.0003	0.0507
54	OBFC1	11.91	10.86	2.06	0.0186	0.3064
55	OLFML2A	8.09	6.69	2.64	0.0008	0.0781
56	PARD3	10.48	9.48	2	0.0213	0.3225
57	PAX8	7.88	6.64	2.37	0.005	0.1747
58	PCDHGA10	8.07	6.91	2.24	0.0146	0.2778
59	PIGR	7.73	6.04	3.21	0.011	0.2509
60	PLK2	6.75	5.7	2.07	0.0032	0.1465
61	PRO0611	4.55	3.51	2.05	0.0023	0.1266
62	PTP4A3	7.48	6.43	2.07	0.0002	0.0417

63	PTPRQ	10.55	9.46	2.13	0.0135	0.2717
64	REN	14.56	8.88	51.35	0.0049	0.1746
65	RERG	9.52	8.32	2.29	0.0494	0.4545
66	RNA5SP313	6.29	4.64	3.14	0.0006	0.0693
67	RNA5SP314	7.27	5.38	3.72	4.73E-05	0.0276
68	RNA5SP316	6.79	5.4	2.62	0.0022	0.1254
69	SCD	8.64	7.22	2.67	0.003	0.1434
70	SEMA4G	7.2	5.8	2.65	4.31E-05	0.0271
71	SERPINA3	4.97	3.51	2.74	0.003	0.1425
72	SERPINE2	5.34	4.33	2.01	0.0143	0.2762
73	SHISA2	7.26	5.97	2.45	0.0016	0.1083
74	SLC7A5P2; SMG1P3; SMG1P1	9.24	8.23	2.02	0.0497	0.4554
75	SLC7A8	14.23	13.21	2.02	0.0135	0.2715
76	SMG1P1	8.27	7.17	2.14	0.0154	0.2842
77	SMG1P2	9.19	8.05	2.21	0.0155	0.2853
78	SNORD59A	4.4	3.29	2.16	0.0047	0.1701
79	SULF2	12.86	11.57	2.45	0.0023	0.1282
80	TNFRSF21	10.12	8.48	3.13	0.0041	0.163
81	TRAM2	13.42	12.17	2.38	0.0089	0.2281
down regulated	**Gene Symbol**	**FSGS Avg (log2)**	**CNT Avg (log2)**	**Fold Change**	**P-val**	**FDR P-val**
1	ABRACL	5.62	7.06	-2.72	0.0005	0.0658
2	ADIRF	7.53	9.17	-3.1	0.0004	0.0542
3	AFM	7.09	8.18	-2.12	0.0195	0.3109
4	ALB	5.25	7.31	-4.15	6.77E-05	0.0306
5	ALKBH7	6.73	8.24	-2.85	3.29E-05	0.0241
6	ANG; RNASE4	5.83	6.86	-2.04	0.0002	0.0477
7	APOH	4.7	5.89	-2.29	0.0044	0.1663
8	APOM	8.98	10.21	-2.34	0.0121	0.2595
9	AQP2	4.45	5.84	-2.62	0.0009	0.0843
10	ART4	4.16	7.37	-9.25	2.90E-06	0.0162
11	ASPA	6.06	7.35	-2.44	0.005	0.1758
12	ATP6V1F	8.25	9.6	-2.54	3.22E-05	0.0239
13	ATP6V1G3	5.32	7.11	-3.46	0.0162	0.2896
14	B3GALT2	7.56	10.16	-6.08	0.0001	0.0379
15	BLVRB	6.17	7.3	-2.19	7.67E-05	0.031
16	BRE-AS1	4.31	7.34	-8.16	0.0007	0.0755
17	BST1	7.32	8.93	-3.07	6.55E-05	0.0303
18	BTG2	10.12	12.32	-4.62	0.0091	0.2317
19	C1orf54	6.62	7.77	-2.21	0.0016	0.1076
20	C6orf48; SNORD52; SNORD48	5.78	6.9	-2.17	6.27E-05	0.0296
21	CA12	8.84	9.94	-2.14	0.0124	0.2631

22	CALB1	5.9	7.44	-2.91	0.0028	0.1402
23	CARD16	5	6.13	-2.18	5.99E-05	0.0293
24	CCDC148	5.81	7.52	-3.29	1.54E-06	0.0149
25	CETN3	8.27	9.31	-2.07	0.0006	0.0663
26	CHRDL1	7.43	8.66	-2.35	0.0057	0.1854
27	CLCNKB	6.27	7.32	-2.07	0.0136	0.2721
28	CLDN8	4.56	7.16	-6.04	0.0003	0.0487
29	CLEC3B	8.66	9.98	-2.51	0.0021	0.1223
30	CLYBL	6.39	7.67	-2.42	0.0033	0.147
31	COX5B	7.09	8.12	-2.04	1.53E-05	0.0187
32	COX6A1	14.6	15.62	-2.03	0.0004	0.056
33	COX7A1	11.52	12.59	-2.11	3.02E-05	0.0232
34	CPNE4	3.82	5.07	-2.37	0.0172	0.2962
35	CR1	11.38	12.56	-2.26	0.0003	0.0492
36	CRIM1	13.96	15.14	-2.26	0.0002	0.0453
37	CSRP2	6.92	7.95	-2.04	0.0004	0.0557
38	CTGF	13.53	15.86	-5.02	0.0003	0.0489
39	CTSV	6.89	8.24	-2.56	0.0086	0.2253
40	CTXN3	6.25	7.95	-3.26	0.0037	0.1567
41	CYP2B6	4.91	6.38	-2.78	0.0052	0.1777
42	DCXR	10.28	11.9	-3.07	0.0047	0.1697
43	DDTL; DDT	5.07	6.11	-2.06	2.53E-05	0.0216
44	DEFB1	13.76	16.93	-9.01	0.0003	0.049
45	DPP6	7.74	8.75	-2.01	0.0079	0.2161
46	DUSP1	6.37	7.39	-2.03	0.0047	0.171
47	EGF	5	7.08	-4.23	0.0003	0.0509
48	EGR1	8.17	12.94	-27.43	0.0141	0.2751
49	EMC6	4.92	5.99	-2.09	1.85E-05	0.0196
50	ERRFI1	9.97	11.06	-2.12	0.0242	0.3413
51	ERVFRD-1	5.05	6.19	-2.21	0.0133	0.2696
52	ESM1	5.46	8.96	-11.31	3.72E-05	0.0254
53	ETHE1	7.49	8.65	-2.23	0.0002	0.0464
54	EXPH5	11.1	12.45	-2.55	0.0013	0.0971
55	FABP4	3.79	5.34	-2.92	0.0093	0.2334
56	FAM200B	6.82	8.03	-2.31	2.03E-05	0.0197
57	FAM24B	5.81	6.92	-2.16	0.003	0.1424
58	FAM96B	8.28	9.49	-2.3	0.0001	0.035
59	FAU	8.6	9.66	-2.08	4.82E-06	0.0162
60	FMO2	4.65	6.45	-3.49	0.028	0.359
61	FOS	6	9.01	-8.05	0.008	0.2169
62	FRY	6.69	8.45	-3.39	0.0012	0.0948

63	FRY-AS1	4.92	6.48	-2.93	5.86E-06	0.0162
64	FRZB	8.23	10.08	-3.61	0.0011	0.0913
65	FXYD4	5.51	8.09	-5.98	0.0011	0.0925
66	G0S2	6.31	7.68	-2.59	0.0042	0.1651
67	G6PC	6.41	11.37	-31.16	8.65E-07	0.0146
68	GADD45B	7.39	8.62	-2.35	0.0046	0.1697
69	GAS2	5.28	6.59	-2.48	0.0005	0.0613
70	GBP4	8.69	10.53	-3.56	0.0002	0.0421
71	GCNT4	4.88	6.97	-4.24	2.56E-05	0.0216
72	GIMAP2	5.11	6.27	-2.23	0.0004	0.0561
73	GIMAP7	9.05	10.68	-3.09	0.0007	0.071
74	GIMAP8	8.18	9.28	-2.13	0.0024	0.1295
75	GIPC2	7.24	8.45	-2.31	0.0263	0.3517
76	GJA5	9.66	10.74	-2.11	0.0141	0.2751
77	GLYATL1	7.25	8.85	-3.03	0.0007	0.0743
78	GMFG	11.35	12.43	-2.12	0.0021	0.1215
79	GNA14	6.13	7.19	-2.08	0.0051	0.1768
80	GPX8	7.56	8.71	-2.22	0.0327	0.3815
81	GSTA1	13.03	14.77	-3.34	0.0004	0.0588
82	GSTA2	10.54	13.48	-7.66	2.37E-05	0.0216
83	GSTA3	3.89	5.08	-2.28	1.24E-05	0.0173
84	GSTA5	3.84	4.92	-2.12	0.0001	0.035
85	GSTM3	7.78	9.35	-2.97	0.0044	0.167
86	GTF2A2	7.58	8.8	-2.34	7.80E-05	0.031
87	GTF2H5	6.96	8.09	-2.18	0.0015	0.1036
88	H2AFJ	7.26	8.85	-3.01	0.0002	0.0432
89	HAO2	7.49	9.51	-4.05	0.0037	0.1571
90	HBA1; HBA2	11.25	13.74	-5.65	0.0187	0.307
91	HBA2; HBA1	11.7	13.39	-3.24	0.0163	0.2905
92	HBB	8.91	12.24	-10.07	0.0047	0.1709
93	HCP5	8.42	10.53	-4.32	0.0256	0.3473
94	HES1	7.27	8.41	-2.21	0.0134	0.2701
95	HIGD2A	10.38	11.69	-2.48	0.0008	0.0801
96	HLA-DMA	8.62	10.04	-2.67	0.0173	0.2969
97	HLA-DOA	5.37	6.45	-2.11	0.0143	0.2762
98	HLA-DPB1	5.28	6.37	-2.13	0.0033	0.1481
99	HLA-DRB1	8.48	10.23	-3.37	0.0069	0.2037
100	HLA-DRB1; HLA-DRB5	14.8	16.16	-2.56	0.001	0.0849
101	HLA-DRB6	14.65	15.67	-2.02	0.0097	0.2393
102	HPGD	6.83	8.49	-3.15	0.0249	0.3445
103	HPS5; H6PD	7.02	8.56	-2.9	1.55E-06	0.0149

104	HRSP12	9.51	10.82	-2.48	0.0148	0.2799
105	HSBP1L1	8.22	9.5	-2.44	0.0001	0.035
106	IFI27	12.55	14.79	-4.73	0.0057	0.1858
107	IGF1	6.99	10.77	-13.74	0.0037	0.1555
108	IGIP	8.34	9.54	-2.3	0.0008	0.0775
109	ITGA1; PELO	9.51	10.69	-2.27	0.0133	0.2698
110	ITM2A	7.12	8.63	-2.85	0.0119	0.2581
111	JUN	5.07	6.19	-2.18	0.0014	0.0996
112	JUNB	5.26	7.46	-4.61	0.0137	0.2727
113	KCNJ1	5.42	6.98	-2.95	0.0002	0.0453
114	KIAA1551	7.77	9.52	-3.36	0.0009	0.0843
115	KLF9	8.99	10.64	-3.14	0.0004	0.0547
116	KLK1	4.68	6.29	-3.04	0.0084	0.2229
117	KLK7	11.08	12.21	-2.19	0.0015	0.103
118	KNG1	9.55	13.58	-16.36	8.68E-05	0.0322
119	L3MBTL3	6.53	8.49	-3.88	1.00E-05	0.0162
120	LAMTOR5	4.93	5.97	-2.06	3.08E-05	0.0234
121	LIFR	10.02	11.06	-2.06	0.0392	0.4107
122	LINC00052	4.93	6.3	-2.59	0.0198	0.3127
123	LINC00339	4.87	5.92	-2.07	0.0086	0.2253
124	LINC00493	11.54	12.83	-2.44	0.0007	0.0718
125	LINC01186	4.15	5.51	-2.56	0.0002	0.0442
126	LOC729970	6.09	7.14	-2.08	0.0021	0.1215
127	LPCAT2	9.39	11.04	-3.13	0.0007	0.0714
128	LPL	4.79	5.94	-2.2	0.0017	0.1101
129	LSM3	6.59	7.73	-2.2	7.38E-05	0.0309
130	LSM7	7.13	8.67	-2.91	0.0005	0.0617
131	LST1	5.45	6.48	-2.04	0.0001	0.035
132	MBNL3	6.33	7.38	-2.07	4.66E-05	0.0276
133	MGP	13.58	14.81	-2.34	0.0046	0.1697
134	MIOX	8.49	9.71	-2.32	0.0021	0.121
135	MIR3198-1	7.92	9.04	-2.17	6.91E-06	0.0162
136	MIR3685	5.34	6.47	-2.19	0.0023	0.1282
137	MNDA	5.84	7.06	-2.33	0.0064	0.1973
138	MORN2	6.46	7.58	-2.17	0.0005	0.063
139	MRLN	4.89	6.57	-3.2	0.0004	0.0542
140	MRO	4.67	5.78	-2.15	0.0079	0.2156
141	MRPL52	6.99	8.54	-2.95	0.0005	0.0643
142	MRPL54	8.61	9.69	-2.12	0.0004	0.055
143	MRPS21	8.28	9.34	-2.09	4.28E-06	0.0162
144	MT1G	17.65	18.69	-2.06	0.0132	0.2688

145	MT1H	17.07	18.14	-2.11	0.0289	0.3631
146	MT1L	11.63	12.88	-2.38	0.0114	0.2535
147	MTHFD2	5.71	6.73	-2.02	0.0042	0.1649
148	MUC15	4.32	5.41	-2.13	0.0023	0.1263
149	MYCT1	8.57	11.18	-6.08	0.0002	0.0456
150	MYLIP; MIR4639	10.49	11.71	-2.33	0.0001	0.0356
151	NAT8B	9.76	10.77	-2.01	0.0164	0.2907
152	NDUFA11	7.07	8.29	-2.33	1.83E-05	0.0196
153	NDUFA2	9.29	10.31	-2.03	6.84E-06	0.0162
154	NDUFAB1	12.07	13.1	-2.05	0.0003	0.0506
155	NDUFB6	9.58	10.66	-2.13	0.0003	0.0525
156	NDUFS4	9.92	11.18	-2.39	0.0001	0.035
157	NELL1	6.21	9.28	-8.4	0.0231	0.3331
158	NQO1	10.14	11.59	-2.73	0.0003	0.052
159	NTN4	10.84	12.34	-2.84	0.005	0.1758
160	NUPR2	3.52	4.55	-2.04	8.97E-05	0.0326
161	PCK1	6.55	8.22	-3.19	0.0006	0.0668
162	PDCD1LG2	5.07	6.58	-2.85	0.0316	0.3756
163	PDK4	8.43	12.08	-12.54	0.0017	0.1106
164	PLA1A	7.16	8.74	-3	0.0135	0.2715
165	PLGLA	6.45	7.71	-2.4	0.043	0.4277
166	POLR2G	10.74	12.41	-3.19	5.86E-06	0.0162
167	PPBP	4.2	5.35	-2.22	0.0311	0.3735
168	PPM1K	6.71	7.93	-2.33	0.0025	0.1324
169	PREX2	6.19	7.33	-2.21	0.0089	0.2295
170	PRODH2	6.62	8.11	-2.79	0.0005	0.0627
171	PTGS2	3.73	5.05	-2.49	9.66E-05	0.0326
172	PTPRB	10.73	12.66	-3.8	0.0037	0.1552
173	PVALB	4.83	6.79	-3.91	1.92E-07	0.0065
174	RAB11A	10.98	12.05	-2.11	0.0058	0.1883
175	RABAC1	12.14	13.63	-2.81	8.88E-05	0.0326
176	RARRES2	10.67	11.95	-2.44	0.0004	0.0566
177	RASD1	3.39	5.37	-3.95	0.0012	0.0948
178	RBP7	9.12	10.71	-3	0.0131	0.2686
179	RFTN2	5.53	6.6	-2.11	0.0093	0.2335
180	RNA5-8S5	10.8	12.48	-3.22	0.0002	0.0469
181	RNA5S1	4.79	5.91	-2.17	0.0104	0.2447
182	RNA5S10	4.79	5.91	-2.17	0.0104	0.2447
183	RNA5S11	4.79	5.91	-2.17	0.0104	0.2447
184	RNA5S12	4.79	5.91	-2.17	0.0104	0.2447
185	RNA5S13	4.79	5.91	-2.17	0.0104	0.2447

186	RNA5S14	4.79	5.91	-2.17	0.0104	0.2447
187	RNA5S15	4.79	5.91	-2.17	0.0104	0.2447
188	RNA5S16	4.79	5.91	-2.17	0.0104	0.2447
189	RNA5S17	4.79	5.91	-2.17	0.0104	0.2447
190	RNA5S2	4.79	5.91	-2.17	0.0104	0.2447
191	RNA5S3	4.79	5.91	-2.17	0.0104	0.2447
192	RNA5S4	4.79	5.91	-2.17	0.0104	0.2447
193	RNA5S5	4.79	5.91	-2.17	0.0104	0.2447
194	RNA5S6	4.79	5.91	-2.17	0.0104	0.2447
195	RNA5S7	4.79	5.91	-2.17	0.0104	0.2447
196	RNA5S8	4.79	5.91	-2.17	0.0104	0.2447
197	RNF114	10.64	12.24	-3.02	1.15E-05	0.0171
198	RNF144B	6.5	7.69	-2.28	0.0063	0.1952
199	RNF152	8.03	9.16	-2.19	0.0048	0.1737
200	RNF212B	4.41	5.7	-2.45	0.0155	0.2853
201	RNU5B-1	3.65	4.84	-2.28	0.0006	0.0699
202	RNU6-1	9.2	10.47	-2.42	0.0033	0.1465
203	RNU6-2	9.2	10.47	-2.42	0.0033	0.1465
204	RNU6-33P	9.08	10.22	-2.2	0.0038	0.1587
205	RNU6-7	9.2	10.47	-2.42	0.0033	0.1465
206	RNU6-8	9.2	10.47	-2.42	0.0033	0.1465
207	RNU6-9	9.2	10.47	-2.42	0.0033	0.1465
208	RPL17; SNORD58B; RPL17-C18orf32	12.59	13.59	-2	0.0015	0.1031
209	RPL18	10.95	12.16	-2.31	9.83E-06	0.0162
210	RPL23AP4	11.17	12.42	-2.38	0.0018	0.1138
211	RPS19	14.42	15.96	-2.91	5.16E-05	0.0283
212	RPS28	14.77	15.87	-2.14	1.70E-05	0.0195
213	RPS5	15.01	16.41	-2.63	0.0003	0.0503
214	RRAS	7.88	9.02	-2.21	0.0002	0.0477
215	SAT2	8.51	9.85	-2.52	0.0009	0.0822
216	SDHC	5.7	6.85	-2.22	0.0053	0.1788
217	SEC61B	9.63	11.1	-2.77	1.01E-05	0.0162
218	SELP	4.04	5.86	-3.52	0.0002	0.0417
219	SEMA3B-AS1	8.85	10.48	-3.08	5.96E-06	0.0162
220	SEPW1	7.19	8.29	-2.15	0.0003	0.0525
221	SGIP1	5.99	7.23	-2.36	0.0002	0.0399
222	SH3BGRL2	14.1	15.61	-2.84	0.0006	0.0671
223	SLC12A3	6.93	10.07	-8.84	0.0334	0.386
224	SLC25A33	5.88	7.04	-2.23	0.0024	0.1305
225	SLC2A12	7.84	8.92	-2.1	0.0003	0.0525
226	SMCO3	7.84	8.99	-2.22	0.0006	0.0671

227	SMDT1	9.21	10.39	-2.28	4.21E-05	0.0271
228	SMIM20	5.18	6.25	-2.1	0.0001	0.035
229	SNAI2	5.11	6.17	-2.08	0.0224	0.329
230	SNHG8	10.51	13.28	-6.82	1.36E-05	0.0178
231	SNORA31	4.46	5.48	-2.02	0.0142	0.276
232	SNORD108; SNORD64; PWAR5	8.48	9.83	-2.55	0.0134	0.2709
233	SNORD14E	3.77	5.52	-3.38	0.0341	0.3888
234	SNORD3A	6.51	10.18	-12.68	0.0002	0.0477
235	SNORD3B-1	6.29	10.04	-13.47	0.0002	0.0477
236	SNORD3B-2	6.29	10.04	-13.47	0.0002	0.0477
237	SNORD3C	6.33	9.63	-9.82	0.0003	0.0528
238	SNORD3D	6.28	9.81	-11.57	0.0003	0.0498
239	SNORD94	5.87	7.38	-2.84	0.0149	0.2799
240	SPATA18	5.24	6.56	-2.51	4.73E-06	0.0162
241	STK17B	5.25	6.57	-2.5	6.21E-05	0.0295
242	STYXL1	6	7.14	-2.19	0.0003	0.0498
243	SURF1	6.24	7.38	-2.2	0.0071	0.2059
244	TCEB2	6.79	7.85	-2.08	7.01E-06	0.0162
245	TGFBR2	13.09	14.24	-2.21	0.023	0.3325
246	TM4SF1	9.33	10.4	-2.09	0.0144	0.2778
247	TM4SF18	7.64	8.84	-2.3	0.0297	0.3674
248	TM4SF5	7.37	8.65	-2.43	0.002	0.1189
249	TMEM130	6.51	7.64	-2.18	0.0012	0.0948
250	TMEM174	9	10.41	-2.65	0.0291	0.3645
251	TMEM178A	7.4	8.5	-2.15	0.0001	0.0375
252	TMEM185A	5.64	6.65	-2.02	5.87E-05	0.0292
253	TMEM207	5.43	6.56	-2.19	0.0395	0.4125
254	TMEM213	4.94	6.13	-2.29	0.0265	0.3519
255	TMEM244	4.5	6.41	-3.75	0.0033	0.147
256	TMEM256	7.03	8.16	-2.19	0.0006	0.0686
257	TMEM52B	8.53	10.56	-4.09	0.0012	0.095
258	TMOD2	7.84	8.87	-2.05	9.28E-05	0.0326
259	TNNC1	8.04	11.17	-8.78	9.67E-05	0.0326
260	TP53TG1	6.73	7.83	-2.14	0.0015	0.1046
261	TPM2	8.32	9.47	-2.22	0.0015	0.1051
262	TSPAN2	12.24	14.1	-3.65	0.0137	0.2722
263	TSPAN7	8.61	9.87	-2.4	0.032	0.3783
264	TTR	6.11	8.7	-6.01	7.11E-06	0.0162
265	TYROBP	7.63	8.7	-2.1	0.0072	0.2067
266	UBL5	11.64	13.2	-2.95	0.0007	0.0729
267	UQCR10	9.17	10.93	-3.4	1.13E-05	0.0171

268	UQCR11	9.36	11.7	-5.07	3.78E-07	0.0085
269	XPOT	8.16	9.17	-2.02	0.0025	0.132

Table 3- Differentially regulated DEGs in dataset GSE129973

Upregulated	Gene Symbol	FSGS Avg (log2)	CNT Avg (log2)	Fold Change	P-val	FDR P-val
1	A2M	14.62	12.94	3.21	0.0001	0.0092
2	ABCG1	8.24	6.54	3.26	2.06E-05	0.0044
3	ACSL4	11.18	9.96	2.32	0.0169	0.1128
4	ACSM3	5.78	4.5	2.43	0.0053	0.0598
5	ACTG1	17.14	16.09	2.08	0.0001	0.0088
6	ACTN1	8.59	7.54	2.07	4.14E-05	0.0062
7	ACTR3	12.64	11.54	2.14	3.31E-05	0.0055
8	ADAM9	11.51	10.23	2.42	0.0082	0.0761
9	ADAMTS1	10.61	6.99	12.3	0.0009	0.0241
10	ADAMTS9	9.2	7.99	2.3	0.0001	0.0092
11	ADH1B	9.76	8.52	2.36	0.0004	0.0154
12	AEBP1; MIR4649	8.59	7.51	2.12	0.0003	0.0139
13	AKAP12	7.9	6.65	2.38	0.0229	0.1332
14	ANXA2	8.6	6.7	3.72	9.47E-05	0.0083
15	ANXA2; ANXA2P2	11.18	9.11	4.2	0.0002	0.0124
16	C14orf105	13.56	12.54	2.03	0.0002	0.0105
17	C1R	7.32	6.16	2.24	0.0001	0.0092
18	C3	10.02	6.76	9.6	0.0002	0.0119
19	C6	5.92	4.25	3.17	0.0008	0.023
20	C7	16.37	14.93	2.7	0.001	0.0245
21	CAPN6	5.49	4.3	2.28	0.0427	0.1894
22	CCL2	9.19	6.65	5.83	0.0197	0.1227
23	CDH6	13.72	10.98	6.67	0.0008	0.022
24	CFH	8.28	7.02	2.39	0.0006	0.0194
25	CLDN1	7.57	6.02	2.92	0.0003	0.0141
26	COL1A1	6.3	5.18	2.17	1.45E-05	0.0039
27	COL1A2	7.73	6.42	2.48	0.0003	0.0129
28	COL3A1; MIR3606	7.88	5.69	4.56	7.24E-06	0.0027
29	COL4A1	8.77	6.74	4.11	4.40E-05	0.0063
30	COL4A2	8.18	6.87	2.48	0.0001	0.0092
31	COL6A3	7.1	5.75	2.54	6.62E-06	0.0026
32	CYBB	8.88	7.72	2.23	0.0087	0.0788

33	CYP1B1	10	8.73	2.41	0.0014	0.0301
34	CYP24A1	10.06	8.4	3.16	0.031	0.1581
35	DCDC2	11.63	9.82	3.52	0.0004	0.0168
36	DOCK11	7.8	6.63	2.25	0.0019	0.0346
37	EMP1	8.63	7.51	2.17	0.0369	0.1746
38	EPHA7	10.17	9.16	2.02	0.0001	0.0088
39	ERAP2	7.33	4.85	5.56	0.0007	0.021
40	F13A1	10.59	9.42	2.25	0.0055	0.0608
41	FBN1	7.31	6.09	2.33	2.84E-05	0.0051
42	FN1	9.4	6.74	6.35	1.74E-05	0.004
43	FSTL1; MIR198	9.17	7.83	2.53	3.38E-05	0.0056
44	GBP2	7.06	5.95	2.15	0.0015	0.0303
45	GCNT3	5.6	4.54	2.09	0.0006	0.0188
46	GPC4	9.57	8.43	2.2	0.0196	0.1225
47	GPR135	7.87	6.62	2.39	0.0004	0.017
48	HAO2-IT1	8.85	7.75	2.14	0.0117	0.0926
49	HAVCR1	11.92	7.75	17.97	0.0011	0.0256
50	HAVCR1P1	6.29	5	2.44	0.0009	0.0237
51	HAVCR2	8.77	7.47	2.46	0.0002	0.011
52	HIF1A	14.86	12.17	6.46	0.0001	0.009
53	HSP90B1; MIR3652	17.21	16.05	2.23	0.0004	0.0155
54	HSPA5	14.42	13.2	2.33	0.011	0.0895
55	IFITM1	9.23	8.19	2.05	0.0185	0.1186
56	IFITM2	13.8	12.54	2.4	0.0033	0.0468
57	IFNAR2	7.71	6.59	2.17	8.70E-05	0.0081
58	ITGAV	12.56	11.53	2.04	0.0044	0.0541
59	ITGB1	13	11.79	2.3	5.26E-06	0.0023
60	ITGB3	10.31	7.43	7.34	0.0006	0.0196
61	ITGB6	9.34	5.57	13.72	0.0004	0.0151
62	ITGB8	12	10.01	3.97	0.0049	0.0575
63	KCNIP4	6.51	5.29	2.32	0.0005	0.0177
64	KIAA0754; MACF1	9.05	7.39	3.16	0.0003	0.0145
65	KIAA1033	12.8	11.77	2.04	0.0017	0.0325
66	LAMA2	6.54	5.27	2.42	6.85E-06	0.0026
67	LAMC2	6.32	5.16	2.24	0.0002	0.0116
68	LAPTM5	9.21	7.74	2.76	0.0107	0.0881
69	LINC00152; MIR4435-2HG	6.85	5.5	2.54	0.0002	0.0107
70	LINC00641	7.04	5.99	2.08	2.40E-05	0.0047
71	LINC00837	7.07	6.05	2.03	0.0013	0.0281

72	LINC01320	10.09	8.86	2.35	0.0104	0.0867
73	LRRK2	10.5	9.14	2.55	0.0025	0.0403
74	LRRN4	6.08	4.78	2.46	0.0015	0.0307
75	LTF	7.34	4.91	5.4	0.0011	0.0256
76	LUM	7.72	6.58	2.21	0.0079	0.0743
77	LYG1	8.36	6.4	3.87	0.0306	0.157
78	LYZ	9.84	7.86	3.93	0.0112	0.0902
79	MACC1	8.9	7.02	3.69	0.0051	0.0589
80	MALT1	10.14	8.88	2.39	7.97E-05	0.0078
81	MGP	9.41	8.23	2.26	0.0111	0.0896
82	MIR181B1	5.51	4	2.86	4.61E-09	2.60E-05
83	MIR204	5.83	4.37	2.75	0.0002	0.0099
84	MIR21	6.81	4.57	4.73	0.0004	0.0169
85	MIR29A	6.16	4.06	4.3	1.32E-05	0.0037
86	MIR30A	4.15	2.89	2.39	7.03E-06	0.0026
87	MIR30C2	8.19	7.14	2.07	0.0003	0.0147
88	MIR30E	5.31	4.15	2.22	1.54E-05	0.0039
89	MIR4435-2HG	6.16	5.13	2.05	0.0001	0.0088
90	MIR4521	6.96	4.4	5.91	1.11E-09	7.50E-06
91	MIR573	5.72	4.6	2.17	0.0025	0.04
92	MIR590	7.61	6.37	2.36	1.21E-05	0.0035
93	MMP14	8.67	7.57	2.15	0.0042	0.0527
94	MMP7	10.3	7	9.8	0.0011	0.0256
95	MOXD1	7.28	5.97	2.48	0.0011	0.0262
96	MYOF	8.79	7.26	2.9	0.0012	0.0267
97	NPY1R	9	7.94	2.09	0.0007	0.0212
98	NR1D1	7.53	6.13	2.64	0.0015	0.0301
99	NRP1	11.38	9.43	3.89	0.0002	0.011
100	OLFM4	6.6	5.34	2.39	0.0287	0.1516
101	OSMR	8.87	6.78	4.26	3.80E-05	0.0058
102	PAPPA	9.24	7.61	3.1	0.0155	0.1076
103	PAPPA2	8.08	6.79	2.45	0.0083	0.0764
104	PIGR	14.56	11.91	6.28	0.0003	0.0135
105	PLTP	7.62	6.29	2.53	0.0296	0.1539
106	POSTN	6.64	4.81	3.54	0.0027	0.0412
107	PPFIBP1	11.95	10.32	3.09	0.0008	0.0219
108	PROM1	7.93	6.81	2.18	0.0143	0.1033
109	RCN1P2	10.67	8.55	4.36	3.12E-06	0.0019

110	REN	10.05	7.86	4.56	0.0455	0.1966
111	RNF213	10.96	9.93	2.05	0.0069	0.0694
112	SERPINA3	7.69	4.47	9.32	0.0003	0.013
113	SERPINE2	7.49	5.79	3.25	0.0003	0.0131
114	SERPING1	13.18	11.56	3.08	0.0082	0.0762
115	SLC13A1	15.6	14.19	2.67	0.0113	0.0906
116	SLC15A1	8.6	7.38	2.33	0.0364	0.1731
117	SLC34A2	8.94	5.54	10.53	0.0025	0.0401
118	SLC35F6	11.44	10.22	2.33	0.01	0.0849
119	SLC47A2	9.96	8.86	2.14	0.0005	0.0184
120	SLC7A5P2; SMG1P3; SMG1P1	13.37	12.34	2.04	0.0025	0.0396
121	SLPI	8.28	4.5	13.7	0.0004	0.0152
122	SMG1P1	13.47	12.47	2	0.0034	0.0475
123	SMG1P5	11.12	10.11	2.02	0.0005	0.0185
124	SMG1P7	8.84	7.83	2.01	0.0009	0.0233
125	SNORD113-1	6.08	4.91	2.25	0.0005	0.0184
126	SNORD78	7.61	6.47	2.21	0.0005	0.0185
127	SOX4	8.21	6.45	3.38	0.0009	0.024
128	SPTLC3	12.2	10.87	2.5	0.038	0.1775
129	STAT3	12.65	11.5	2.22	0.0027	0.0415
130	STEAP4	7.06	5.14	3.77	0.0002	0.0112
131	SULT1C4	8.43	7.37	2.08	0.0027	0.0416
132	SVEP1	7.02	5.86	2.24	0.0007	0.0215
133	TES	7.55	6.27	2.43	4.22E-05	0.0062
134	TGM2	8.14	6.56	2.99	0.0049	0.0574
135	THBS2	7.25	5.48	3.4	0.0002	0.0119
136	TIMP1	6.54	5.15	2.62	2.83E-05	0.0051
137	TMEM2	8.54	6.79	3.36	3.05E-05	0.0053
138	TMSB10	11.6	10.13	2.76	0.0065	0.0671
139	TNC	8.55	5.35	9.16	8.77E-05	0.0081
140	TNFRSF12A	10.35	8.89	2.75	0.0012	0.0275
141	TNFSF10	12.89	11.86	2.05	0.0153	0.1069
142	TOP2A	5.21	4.13	2.12	0.0009	0.0233
143	TPM1	9.33	7.91	2.68	8.17E-06	0.0029
144	TRIM38	10.35	9.29	2.08	0.0031	0.0449
145	UGCG	11.29	9.61	3.2	0.0014	0.0292
146	VCAM1	13.15	11.2	3.85	0.0042	0.053
147	VCAN	6.99	4.95	4.12	2.84E-05	0.0051
148	VIM	9.37	7.55	3.53	0.0005	0.0175

149	WFDC2	6.65	4.93	3.3	0.0005	0.0176
Downregulated	Gene Symbol	FSGS Avg (log2)	CNTAvg (log2)	Fold Change	P-val	FDR P-val
1	Mar-02	10.07	11.1	-2.04	0.0141	0.1027
2	ABO	7.82	8.99	-2.25	0.006	0.0642
3	ACSF2	9.83	10.93	-2.16	0.0004	0.0159
4	ACSM5	7.97	9.17	-2.3	0.0009	0.0236
5	ADI1	9.04	10.12	-2.12	8.93E-05	0.0082
6	ADSSL1	6.79	7.96	-2.24	0.0002	0.0109
7	AGMAT	15.31	16.55	-2.36	0.0013	0.0283
8	AHCY	8.64	9.87	-2.34	0.0002	0.011
9	ALB	8.8	12.81	-16.13	0.0016	0.0313
10	ALDH3A2	10.71	11.93	-2.33	0.0019	0.0346
11	ANKS4B	7.4	8.43	-2.05	0.0031	0.0451
12	AOC1	8.07	9.17	-2.14	0.0065	0.0671
13	APOH	6.08	10.5	-21.36	0.0007	0.0214
14	APOM	9.53	10.96	-2.69	0.0006	0.0192
15	ARG2	9.14	10.53	-2.62	0.0026	0.0408
16	ASPDH	7.3	8.55	-2.38	0.0004	0.0154
17	ATF3	5.06	6.21	-2.21	0.0123	0.0952
18	ATP12A	5.43	6.57	-2.21	0.0147	0.1047
19	ATP5D	6.74	8.08	-2.53	0.0014	0.0292
20	ATP6V1B1	8.3	9.68	-2.62	0.0002	0.0123
21	BRE-AS1	6.55	9.76	-9.27	0.0042	0.053
22	BTG2	7.33	12.46	-34.98	0.0005	0.0175
23	C19orf53	9.86	10.97	-2.16	0.0032	0.0454
24	C9orf66	4.8	5.83	-2.04	0.0103	0.0863
25	CA2	8.18	9.68	-2.83	0.0069	0.0694
26	CEL	5.48	7.1	-3.07	0.0017	0.0331
27	CES3	6.68	8.04	-2.57	0.0003	0.0142
28	CLCNKB	10.85	11.9	-2.07	0.0004	0.016
29	CLDN8	7.58	8.66	-2.11	0.002	0.0353
30	CLEC18C; CLEC18B	8.73	9.8	-2.1	9.65E-07	0.001
31	CNNM2	7.16	8.51	-2.54	2.90E-05	0.0052
32	COTL1	10.86	11.97	-2.15	0.0137	0.1009
33	COX8A	12.96	14.98	-4.06	0.0004	0.0164
34	CRABP1	4.53	5.99	-2.75	0.0003	0.013
35	CTGF	7.25	8.64	-2.63	0.0016	0.0314
36	CTH	7.05	8.42	-2.59	0.0012	0.0266
37	CTSF	6.15	7.21	-2.09	2.34E-05	0.0046

38	CUTA	6.66	7.71	-2.07	1.08E-05	0.0033
39	CYFIP2	12.01	13.14	-2.19	0.0061	0.0648
40	CYP17A1	10.58	12.02	-2.71	0.0425	0.1888
41	CYP27B1	5.43	6.65	-2.33	0.007	0.0697
42	CYP2B6	8.65	10.97	-5	0.0002	0.011
43	CYP2B7P	6.31	7.49	-2.28	0.0002	0.011
44	CYP4F2	9.92	12.31	-5.21	0.0037	0.0493
45	CYP4F3	9.29	10.36	-2.09	0.0082	0.0764
46	DAO	8.61	10.06	-2.73	0.0117	0.0925
47	DCXR	11.1	12.77	-3.17	0.0005	0.0172
48	DEFB1	11.68	13.99	-4.96	0.0002	0.011
49	DNAJB1	8.82	10.16	-2.53	1.33E-05	0.0037
50	DNAJB11	6.68	7.78	-2.15	0.0002	0.0102
51	DNASE1	6.13	7.4	-2.42	1.05E-05	0.0033
52	DNPH1	9.71	10.76	-2.07	2.21E-05	0.0046
53	DPEP1	13.46	14.78	-2.5	0.0133	0.0994
54	DRAIC	5.57	6.73	-2.23	1.88E-05	0.0041
55	DUSP1	5.49	9.97	-22.26	3.93E-05	0.006
56	DUSP6	7	8	-2	0.0174	0.1147
57	EEF1B2; SNORA41	8.23	9.29	-2.09	0.0023	0.0385
58	EGF	9.34	13.01	-12.73	7.18E-05	0.0075
59	EGR1	6.9	10.99	-17.03	0.0005	0.0185
60	EPHX1	9.4	10.58	-2.27	0.0002	0.0103
61	EPHX2	10.51	11.61	-2.15	0.0007	0.0208
62	ERRFI1	11.29	13.51	-4.64	0.0433	0.1911
63	ESM1	5.35	6.51	-2.23	0.0018	0.0333
64	FABP1	8.24	9.84	-3.03	0.0013	0.0283
65	FAM151A	11.62	13.52	-3.72	0.0032	0.0456
66	FAM96B	8.98	9.99	-2.01	0.0019	0.0347
67	FBP1	12.14	13.42	-2.43	0.0007	0.0203
68	FBXO21	10.1	11.42	-2.49	0.0005	0.0182
69	FER1L6	5.26	6.52	-2.4	0.0211	0.1275
70	FN3K	5.19	6.34	-2.22	2.37E-05	0.0047
71	FOS	4.77	7.03	-4.82	0.0002	0.0109
72	FTCD	7.47	8.64	-2.25	0.0393	0.181
73	G6PC	11.78	16.92	-35.24	1.84E-06	0.0014
74	GABARAPL1	9.94	11.22	-2.43	0.0001	0.0088
75	GADD45B	7.83	9.63	-3.49	0.01	0.0851

76	GAMT	7.84	8.99	-2.21	1.51E-05	0.0039
77	GDF15	6.29	8.42	-4.37	0.007	0.0697
78	GLB1L2	7.36	8.63	-2.4	8.86E-05	0.0081
79	GPAT3	10.4	11.61	-2.31	0.0026	0.0407
80	GRAMD1B	7.17	8.28	-2.15	0.0117	0.0926
81	GSTA1	12.97	15.41	-5.43	3.67E-05	0.0058
82	GSTA2	13.55	16.2	-6.26	0.0002	0.0119
83	GSTA3	5.23	7.06	-3.55	1.98E-06	0.0014
84	GSTA5	5.07	6.45	-2.6	9.23E-06	0.0031
85	GSTM3	8.9	10.66	-3.39	1.54E-05	0.0039
86	HAGH	8.18	9.22	-2.05	3.04E-06	0.0019
87	HAO2	13.81	14.94	-2.2	0.02	0.1236
88	HBA1; HBA2	6.36	9.22	-7.26	6.18E-07	0.0008
89	HBA2; HBA1	6.13	8.3	-4.53	4.99E-06	0.0023
90	HBB	4.64	6.42	-3.42	3.55E-06	0.002
91	HES1	7.33	8.51	-2.26	0.0038	0.0504
92	HIGD2A	8.8	10.1	-2.47	0.0004	0.0166
93	HIST1H1E	10.02	11.4	-2.62	0.0002	0.0116
94	HIST1H2BD	7.48	8.6	-2.18	0.0007	0.021
95	HIST1H4C	10.29	11.65	-2.58	0.0108	0.0887
96	HIST2H2AB	5.5	6.68	-2.27	0.0017	0.0322
97	HIST2H2AC	12.86	13.94	-2.11	7.15E-05	0.0075
98	HIST2H2BE	7.96	9.26	-2.45	1.07E-06	0.001
99	HLA-DRB1	9.54	11	-2.77	0.0176	0.1153
100	HLA-DRB5	6.81	10.87	-16.68	0.033	0.1637
101	HMGCS2	6.91	9.17	-4.76	0.01	0.0852
102	HPD	15.56	16.61	-2.07	0.0009	0.0242
103	HPGD	7.35	8.53	-2.27	0.0017	0.0324
104	HRG	9.59	11.05	-2.76	0.011	0.0895
105	HSD11B2	12.39	14.28	-3.7	0.0018	0.0338
106	HSD17B14	7.3	9.31	-4.01	3.33E-06	0.0019
107	HSPA1A	4.93	7.21	-4.84	8.19E-08	0.0002
108	HSPA1A; HSPA1B	11.12	13.24	-4.35	3.84E-07	0.0007
109	HSPA1B; HSPA1A	10.99	13.8	-7.01	4.64E-07	0.0007
110	IDH1	9.03	10.43	-2.63	0.0008	0.0227

111	JUNB	6.2	9.42	-9.34	9.49E-05	0.0083
112	KCNJ10	8.8	9.84	-2.06	0.0007	0.0206
113	KCNK5	8.98	10.21	-2.35	0.0094	0.0825
114	KHK	8.99	10.15	-2.23	0.001	0.0253
115	KIAA1191	13.13	14.3	-2.25	0.0184	0.1182
116	KLF9	8.15	9.52	-2.59	0.0092	0.0811
117	KLHL3	5.77	7.24	-2.77	2.30E-05	0.0046
118	KLK1	4.9	7.66	-6.76	7.17E-05	0.0075
119	KNG1	14.97	16.48	-2.85	0.0013	0.0279
120	LAMB4	4.62	5.69	-2.1	0.0263	0.1444
121	LDHD	7.35	8.48	-2.18	0.0013	0.0278
122	LGMN	14.48	15.66	-2.26	0.0041	0.0518
123	LINC00671	8.68	9.71	-2.04	0.0001	0.0097
124	LINC01558	5.06	6.08	-2.02	0.0016	0.031
125	LOC100422296	14.53	15.55	-2.04	7.32E-06	0.0027
126	MACROD1	5.3	6.31	-2	4.47E-05	0.0063
127	MALAT1	14.4	16	-3.05	0.0002	0.0103
128	MAPT	7.93	9.34	-2.66	0.0003	0.0137
129	MFSD4	7.36	8.8	-2.72	0.0016	0.0313
130	MGAM	11.04	12.09	-2.07	0.0245	0.1387
131	MIF	7.15	8.15	-2	0.0034	0.0476
132	MIOX	11.63	13.57	-3.84	0.002	0.0357
133	MIR3189	4.12	5.92	-3.48	0.0006	0.0191
134	MIR4461	12.99	15.91	-7.6	2.81E-05	0.0051
135	MME	13.49	14.88	-2.62	0.0036	0.0486
136	MRO	7.34	9.4	-4.16	0.0016	0.0319
137	MRPS18A	5.78	6.83	-2.08	0.0002	0.0101
138	MUC13	7	9.67	-6.37	1.33E-05	0.0037
139	NDRG1	11.15	12.34	-2.28	3.21E-05	0.0055
140	NDUFB10	6.89	8.08	-2.28	0.0225	0.1318
141	NDUFB11	6.92	8.03	-2.17	0.0005	0.0179
142	NDUFB7	6.22	7.3	-2.12	0.0001	0.0089
143	NR4A1	5.62	7.68	-4.18	0.0006	0.0194
144	NR4A2	4.68	7.66	-7.85	0.0015	0.0302
145	NR4A3	4.16	6.56	-5.3	0.0041	0.0518
146	OAT	8.5	10.28	-3.44	8.08E-05	0.0079
147	OXER1	5.97	7.14	-2.25	0.0001	0.0092
148	PCK1	14.07	15.59	-2.87	0.0011	0.0261

149	PCK2	8.97	10.33	-2.58	0.0015	0.0308
150	PDK4	7.26	9.84	-6	0.0012	0.0268
151	PER1	5.71	7.2	-2.81	0.0088	0.0791
152	PIPOX	10.92	12.05	-2.19	0.0028	0.0419
153	PLPP4	6	7.09	-2.14	0.0031	0.0451
154	PNPLA1	6.18	7.29	-2.16	0.0001	0.009
155	PPM1K	6.57	7.78	-2.33	6.52E-06	0.0025
156	PRDX5	10.38	11.93	-2.92	0.0002	0.0102
157	PRODH2	8.03	10.33	-4.93	3.88E-06	0.0021
158	PSMB6	9.98	11.04	-2.08	0.0004	0.0162
159	PVALB	5.55	6.84	-2.44	1.48E-05	0.0039
160	RGS1	3.63	5.45	-3.52	0.0017	0.0324
161	RGS2	5.02	6.78	-3.39	0.0007	0.0207
162	RHCG	7.42	9.88	-5.5	0.0088	0.0793
163	RMRP	15.83	17.15	-2.5	0.0011	0.0255
164	RNA5S1	11.14	12.78	-3.12	6.55E-05	0.0073
165	RNA5S10	11.14	12.78	-3.12	6.55E-05	0.0073
166	RNA5S11	11.14	12.78	-3.12	6.55E-05	0.0073
167	RNA5S12	11.14	12.78	-3.12	6.55E-05	0.0073
168	RNA5S13	11.14	12.78	-3.12	6.55E-05	0.0073
169	RNA5S14	11.14	12.78	-3.12	6.55E-05	0.0073
170	RNA5S15	11.14	12.78	-3.12	6.55E-05	0.0073
171	RNA5S16	11.14	12.78	-3.12	6.55E-05	0.0073
172	RNA5S17	11.14	12.78	-3.12	6.55E-05	0.0073
173	RNA5S2	11.14	12.78	-3.12	6.55E-05	0.0073
174	RNA5S3	11.14	12.78	-3.12	6.55E-05	0.0073
175	RNA5S4	11.14	12.78	-3.12	6.55E-05	0.0073
176	RNA5S5	11.14	12.78	-3.12	6.55E-05	0.0073
177	RNA5S6	11.14	12.78	-3.12	6.55E-05	0.0073
178	RNA5S7	11.14	12.78	-3.12	6.55E-05	0.0073
179	RNA5S8	11.14	12.78	-3.12	6.55E-05	0.0073
180	RNA5S9	11.19	12.75	-2.94	6.70E-05	0.0074
181	RNF152	13.97	15.13	-2.25	1.58E-05	0.004
182	RNF212B	5.06	7.24	-4.53	0.003	0.0443

183	RNU11	8.48	10.87	-5.23	1.78E-06	0.0013
184	RNU1-10P	14.89	16.09	-2.3	0.0001	0.0092
185	RNU1-12P	11.65	13.81	-4.46	2.79E-05	0.0051
186	RNU1-13P	11.65	13.81	-4.46	2.79E-05	0.0051
187	RNU4-1	10.52	11.75	-2.35	1.98E-05	0.0043
188	RNU4-2	12.7	14.39	-3.23	1.28E-05	0.0037
189	RNU6-1; RNU6-2	14.27	15.29	-2.03	0.012	0.0939
190	RNU6-16P	13.18	14.22	-2.06	0.01	0.085
191	RNU6-30P	10.26	11.39	-2.19	0.0126	0.0965
192	RNU6-31P	12.52	13.55	-2.03	0.0117	0.0924
193	RNU6-39P	14.06	15.08	-2.03	0.0097	0.0836
194	RNVU1-1	14.89	16.09	-2.3	0.0001	0.0092
195	RNVU1-14	7.99	9.88	-3.7	1.11E-05	0.0034
196	RNVU1-15	7.22	8.64	-2.68	0.0001	0.0092
197	RNVU1-17	11.63	13.43	-3.49	1.70E-05	0.004
198	RNVU1-6	6.54	8.42	-3.69	9.65E-06	0.0032
199	RNY1	13.13	14.2	-2.1	0.0037	0.0493
200	RNY4	6.97	8.08	-2.17	3.72E-05	0.0058
201	RNY4P11	3.97	5.34	-2.57	3.74E-06	0.0021
202	RNY4P22	5.08	6.35	-2.4	0.001	0.0255
203	RNY5	6.88	8.27	-2.62	5.36E-05	0.0068
204	RORC	5.62	7.48	-3.62	9.92E-06	0.0033
205	RPL13AP20	10.1	11.14	-2.06	0.0025	0.0397
206	RPPH1	6.31	7.66	-2.54	0.0003	0.0149
207	RPS28	13.47	14.59	-2.18	0.0052	0.0593
208	RPS5	9.5	10.63	-2.18	0.0029	0.0434
209	SAT2	12.05	13.98	-3.8	4.66E-05	0.0064
210	SCARNA10	6.02	7.99	-3.9	0.0002	0.0103
211	SCARNA12	9.02	10.43	-2.64	0.0017	0.0329
212	SCARNA17	11.24	13.17	-3.81	8.71E-07	0.0009
213	SCARNA2	9.18	11.19	-4.03	3.13E-07	0.0006
214	SCARNA5	7.36	9.11	-3.36	1.11E-06	0.001
215	SCARNA6	8.23	10.29	-4.19	1.94E-05	0.0042
216	SCARNA9; SCARNA9L	12.61	13.74	-2.19	0.0255	0.1418
217	SEMA6D	7.33	8.44	-2.15	0.0048	0.0572

218	SERPINA5	9.14	10.8	-3.15	9.17E-05	0.0082
219	SERPINA6	7.13	8.59	-2.75	0.0002	0.0122
220	SIK1	5.93	8.26	-5.03	0.0026	0.0407
221	SLC10A2	8	9.06	-2.08	0.0025	0.0396
222	SLC12A3	12.58	16.2	-12.25	0.0002	0.0111
223	SLC13A2	9.51	10.52	-2.01	0.0048	0.0569
224	SLC16A7	7.05	8.08	-2.03	0.0031	0.0445
225	SLC22A8	12.71	14.06	-2.54	0.0044	0.0545
226	SLC25A10	8.87	10.14	-2.43	0.0062	0.0657
227	SLC25A42	6.83	7.9	-2.1	4.87E-05	0.0064
228	SLC2A12	6.25	7.36	-2.16	0.0053	0.0597
229	SLC36A2	12.43	14.58	-4.43	0.0023	0.0383
230	SLC4A1	7.71	9.18	-2.78	0.0282	0.15
231	SLC5A2	10.96	12.16	-2.31	0.0021	0.0361
232	SLC6A13	12.92	13.97	-2.06	0.0071	0.0706
233	SLC6A19	11.79	13.79	-4.02	0.0008	0.0221
234	SLC9A4	6.06	7.11	-2.07	0.0155	0.1076
235	SMIM24	15.09	16.56	-2.78	1.02E-05	0.0033
236	SNHG8	7.47	8.64	-2.25	0.0017	0.0328
237	SNORA11	10.44	11.55	-2.16	0.0469	0.2
238	SNORA12	8.85	10.29	-2.71	3.10E-05	0.0054
239	SNORA14B	8.41	9.71	-2.47	0.0039	0.051
240	SNORA20	10.95	12.78	-3.55	2.35E-05	0.0046
241	SNORA36B; MIR664A	4.63	5.85	-2.32	2.87E-05	0.0051
242	SNORA49	10.15	11.2	-2.08	0.003	0.0441
243	SNORA53	5.12	6.46	-2.52	1.95E-06	0.0014
244	SNORA54	10.39	11.92	-2.88	0.0006	0.0193
245	SNORA57	10.6	11.6	-2	0.0012	0.0274
246	SNORA5A	6.21	7.39	-2.27	0.0004	0.0157
247	SNORA80E	6.37	7.85	-2.78	2.39E-05	0.0047
248	SNORD103A; SNORD103B	4.23	6.38	-4.43	1.72E-05	0.004
249	SNORD104	13.89	14.91	-2.03	0.0004	0.0166
250	SNORD115-1	9.77	12.05	-4.86	3.74E-05	0.0058
251	SNORD115-10	10.06	12.15	-4.25	0.0002	0.0103
252	SNORD115-11; SNORD115-36; SNORD115-43; SNORD115-29	10.04	12.58	-5.79	0.0001	0.009
253	SNORD115-14	4.62	6.47	-3.59	6.53E-05	0.0073
254	SNORD115-15	10.03	12.47	-5.41	7.10E-	0.0074

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255	SNORD115-16	9.73	12.09	-5.12	4.68E-05	0.0064
256	SNORD115-17; SNORD115-19; SNORD115-18	3.88	4.96	-2.1	0.0009	0.0233
257	SNORD115-21	10.44	12.78	-5.06	0.0002	0.0098
258	SNORD115-22	10.01	12.52	-5.68	0.0001	0.0089
259	SNORD115-24	6.84	8.32	-2.78	5.96E-06	0.0025
260	SNORD115-25	5.35	7.01	-3.16	9.15E-05	0.0082
261	SNORD115-27	4.85	5.94	-2.14	1.08E-05	0.0033
262	SNORD115-28	3.87	5.26	-2.62	5.34E-05	0.0068
263	SNORD115-29; SNORD115-43; SNORD115-11	10.04	12.58	-5.79	0.0001	0.009
264	SNORD115-3	3.86	4.94	-2.12	8.22E-05	0.0079
265	SNORD115-30	4.8	6.23	-2.7	0.0002	0.0107
266	SNORD115-31	4.32	5.79	-2.79	1.93E-05	0.0042
267	SNORD115-32	6.55	8.75	-4.6	0.0002	0.0109
268	SNORD115-33	8.43	10.18	-3.37	9.76E-05	0.0084
269	SNORD115-35	3.2	4.57	-2.58	5.57E-05	0.0069
270	SNORD115-38	3.99	5.45	-2.75	0.0003	0.0144
271	SNORD115-39	4.41	6.55	-4.43	3.45E-05	0.0057
272	SNORD115-4	3.21	5.41	-4.59	2.06E-05	0.0044
273	SNORD115-40	8.27	10.54	-4.81	0.0001	0.0092
274	SNORD115-41	3.14	4.71	-2.97	1.17E-05	0.0035
275	SNORD115-42; SNORD115-10	11.34	14.05	-6.56	4.77E-05	0.0064
276	SNORD115-43; SNORD115-29; SNORD115-11	10.04	12.58	-5.79	0.0001	0.009
277	SNORD115-43; SNORD115-36; SNORD115-11; SNORD115-29	10.04	12.58	-5.79	0.0001	0.009
278	SNORD115-44	8.35	10.32	-3.93	4.90E-05	0.0065
279	SNORD115-5; SNORD115-12; SNORD115-9; SNORD115-10	9.83	12.38	-5.86	9.09E-05	0.0082
280	SNORD115-6	11.19	14.05	-7.24	2.14E-05	0.0045
281	SNORD115-8	3.87	5.5	-3.1	0.0001	0.0093
282	SNORD116-1	9.44	10.91	-2.77	0.0005	0.0172
283	SNORD116-2	10.88	12.24	-2.58	0.0018	0.0332
284	SNORD116-2; SNORD116-6	10.89	12.19	-2.46	0.0018	0.0331
285	SNORD116-3; SNORD116-9	12.54	13.91	-2.58	0.001	0.0251
286	SNORD116-5; SNORD116-7	9.32	10.87	-2.93	0.0004	0.0161
287	SNORD116-7; SNORD116-5	9.32	10.87	-2.93	0.0004	0.0161

288	SNORD116-8	11.7	13.11	-2.65	0.001	0.0243
289	SNORD116-9; SNORD116-3	12.54	13.91	-2.58	0.001	0.0251
290	SNORD14E	5.94	8.66	-6.59	9.94E-07	0.001
291	SNORD15A	6.57	7.58	-2.01	0.0053	0.0598
292	SNORD17	9.71	13.83	-17.36	5.47E-08	0.0002
293	SNORD3A	11.38	12.99	-3.06	0.0007	0.0205
294	SNORD3B-1	10.66	12.26	-3.03	0.0006	0.0202
295	SNORD3B-2	10.66	12.26	-3.03	0.0006	0.0202
296	SNORD3C	10.93	12.68	-3.35	0.0002	0.011
297	SNORD3D	10.86	12.26	-2.64	0.0007	0.0205
298	SNORD41	10.77	12.69	-3.78	0.0275	0.1479
299	SNORD42A	6.19	7.36	-2.26	0.0362	0.1729
300	SNORD51	7.62	9.44	-3.55	7.32E-07	0.0009
301	SNORD59A	12.76	14.92	-4.47	6.22E-06	0.0025
302	SNORD60	12.37	14.01	-3.13	1.68E-05	0.004
303	SNORD61	16.73	17.8	-2.1	0.0372	0.1757
304	SNORD62A; SNORD62B	6.24	8.08	-3.57	0.0003	0.0139
305	SNORD62B; SNORD62A	6.24	8.08	-3.57	0.0003	0.0139
306	SNORD63	9.63	11.39	-3.39	0.0002	0.0118
307	SNORD70	5.19	6.27	-2.12	0.0018	0.0334
308	SNORD71	15.92	17	-2.11	0.0005	0.0177
309	SNORD8	10.82	12.86	-4.11	5.06E-06	0.0023
310	SNORD90	7.01	9.58	-5.96	7.10E-06	0.0026
311	SNORD91B	7.06	8.84	-3.45	6.09E-06	0.0025
312	SNORD94	8.85	10.64	-3.47	2.33E-06	0.0015
313	SNORD97	13.54	14.98	-2.72	1.87E-05	0.0041
314	SORCS1	4.91	7.77	-7.3	0.0362	0.1727
315	SSTR2	5.89	7.81	-3.8	0.0001	0.0086
316	STRA6	6.18	7.34	-2.25	0.0027	0.0412
317	SUCLG1	11.17	12.18	-2.02	0.0036	0.0487
318	TECRP1	9.76	11.46	-3.25	0.0003	0.0128
319	THY1	9.15	10.32	-2.25	0.0089	0.0796
320	TM4SF5	5.36	6.38	-2.04	2.13E-05	0.0045
321	TMEM174	11.34	12.98	-3.13	0.0011	0.0259
322	TMEM256	8.68	10.28	-3.03	4.97E-05	0.0065
323	TMEM52B	13.7	14.78	-2.12	0.0016	0.0317
324	TMEM72	7.63	8.76	-2.18	0.0003	0.0129

325	TOB1	9.7	10.77	-2.09	0.0007	0.0206
326	TRPM6	5.34	7.52	-4.55	7.67E-05	0.0077
327	TRPM7	11.19	12.21	-2.04	0.0027	0.0417
328	TSKU	8.3	9.53	-2.34	0.0031	0.0445
329	TSPAN33	9.33	10.84	-2.86	0.0005	0.0176
330	TTC38	10.21	11.24	-2.03	3.24E-05	0.0055
331	UBALD1	6	7.13	-2.2	8.47E-05	0.0081
332	UGT2A2; UGT2A1	4.62	5.64	-2.03	0.0358	0.1717
333	USP2	11.39	13.05	-3.17	0.0339	0.1664
334	UXT	6.11	7.16	-2.08	0.0081	0.0757
335	VDR	7.33	8.34	-2.01	0.0039	0.0505
336	WDR83OS	5.12	6.3	-2.28	0.0006	0.0191
337	WNK1	9.89	11.37	-2.79	0.001	0.0244
338	XPNPEP2	13.55	15.17	-3.07	0.0022	0.0375
339	ZBTB16	6.13	7.29	-2.24	0.0422	0.1883
340	ZFP36	8.36	12.26	-14.97	0.0004	0.0166
341	ZYG11A	5.77	6.94	-2.25	0.0238	0.1368

Table 4- Differentially regulated DEGs in dataset GSE125779

upregulated	Gene Symbol	FSGS Avg (log2)	CNT Avg (log2)	Fold Change	P-val	FDR P-val
1	ABCG1	6.35	5.34	2.01	2.35E-08	5.31E-06
2	NPIPB4	13.79	12.77	2.02	6.24E-09	2.00E-06
3	CCL21	5.26	4.24	2.03	2.26E-05	0.0007
4	ITGB6	4.93	3.9	2.03	2.73E-05	0.0009
5	KPNA2	8.81	7.78	2.04	1.06E-08	3.01E-06
6	ARRDC4	14.58	13.53	2.07	2.59E-05	0.0008
7	MIR3911	6.24	5.19	2.07	1.98E-06	0.0001
8	MIR548T	14.73	13.66	2.1	8.63E-07	6.69E-05
9	NID1	6.63	5.56	2.1	5.75E-07	4.99E-05
10	SEMA7A	5.7	4.62	2.11	5.60E-07	4.89E-05
11	FAM101B	6.96	5.87	2.12	2.50E-06	0.0001
12	C1QC	6.11	5.02	2.14	1.27E-08	3.43E-06
13	EMP1	9.09	7.99	2.14	0.0008	0.0105

14	CYP24A1	5.62	4.48	2.2	0.0005	0.0079
15	COL4A1	7.24	6.1	2.21	2.53E-07	2.73E-05
16	C3	5.5	4.35	2.23	0.0001	0.0023
17	GADD45A	12.15	10.99	2.23	2.05E-09	9.09E-07
18	ITGB3	11.6	10.45	2.23	1.17E-05	0.0004
19	KIAA0040	10.58	9.42	2.23	8.94E-05	0.0021
20	GNAO1	7.24	6.07	2.25	3.80E-07	3.65E-05
21	VTRNA2-1	5.38	4.21	2.25	0.0167	0.1014
22	CLDN1	7.93	6.75	2.27	1.96E-07	2.26E-05
23	MIR30C2	6.02	4.84	2.27	2.52E-06	0.0001
24	HIST1H3B	4.72	3.53	2.29	6.58E-05	0.0017
25	MYOF	9.74	8.54	2.3	4.86E-08	8.66E-06
26	HAVCR1	5.84	4.62	2.33	7.83E-06	0.0003
27	BMP2	7.71	6.44	2.42	3.05E-05	0.0009
28	MIR1299	8.74	7.45	2.45	0.0002	0.0032
29	SULF2	13.03	11.73	2.47	3.65E-08	7.13E-06
30	BIRC5	5.54	4.22	2.48	0.0002	0.0036
31	SPP1	16.96	15.64	2.5	0.0003	0.005
32	CDH6	7.67	6.32	2.55	9.04E-07	6.94E-05
33	CHD3	9.45	8.08	2.59	1.72E-10	1.55E-07
34	MIR297	6.74	5.36	2.6	4.21E-09	1.54E-06
35	MYOZ2	8.16	6.77	2.61	0.0003	0.0055
36	RERG	9.58	8.17	2.64	0.0001	0.0028
37	TRAM2	13.22	11.82	2.64	1.32E-09	6.59E-07
38	SEMA4G	6.83	5.38	2.72	1.20E-07	1.63E-05
39	LUM	6.63	5.18	2.74	1.28E-09	6.53E-07
40	PIGR	8.07	6.62	2.74	4.39E-05	0.0012
41	AXL	8.25	6.8	2.75	2.77E-08	5.84E-06
42	MYBPH	6.77	5.29	2.77	2.81E-07	2.93E-05
43	MIR4256	6.16	4.66	2.82	1.28E-05	0.0005
44	NR1D1	7.05	5.53	2.88	5.04E-05	0.0014
45	NRIP2	11.11	9.57	2.92	4.92E-13	1.33E-09

46	FN1	6.87	5.31	2.95	7.60E-08	1.16E-05
47	C1QL1	8.04	6.42	3.08	0.0003	0.0055
48	KDELR3	8.55	6.8	3.36	4.39E-07	4.06E-05
49	C7	10.02	8.04	3.94	7.82E-09	2.39E-06
50	LYVE1	6.39	4.24	4.44	6.68E-09	2.12E-06
51	ADAMTS1	9.48	7.22	4.8	4.36E-11	4.99E-08
52	MIR4521	6.32	3.96	5.16	1.19E-14	1.15E-10
53	VTRNA1-3	6.08	3.57	5.68	4.66E-11	5.25E-08
54	ECM1	8.45	5.78	6.36	3.36E-06	0.0002
55	LRRC55	8.25	5.31	7.66	5.38E-10	4.04E-07
56	ERAP2	8.72	5	13.15	0.0349	0.1649
57	REN	14.22	9.81	21.23	2.93E-06	0.0002
58	DEFA1B	9.15	4.5	25.18	0.0129	0.0848
Downregulated	Gene Symbol	FSGS Avg (log2)	CNT Avg (log2)	Fold Change	P-val	FDR P-val
1	AFM	6.66	8.29	-3.1	8.57E-07	6.66E-05
2	AGMAT	9.32	10.83	-2.85	0.0001	0.0031
3	AGXT2	8.58	9.83	-2.37	9.76E-05	0.0022
4	AK4P3	8.79	10.16	-2.58	0.0001	0.0025
5	ALB	5.63	8.05	-5.33	1.92E-08	4.61E-06
6	ALDH6A1	10.04	11.2	-2.24	4.06E-05	0.0012
7	APOH	4.02	5.36	-2.54	7.57E-07	6.14E-05
8	APOM	9.03	10.51	-2.8	9.71E-05	0.0022
9	ART4	4	6.47	-5.55	1.82E-11	2.32E-08
10	ASPA	6.38	7.8	-2.67	1.95E-09	8.78E-07
11	ATP6V1G3	5.41	6.48	-2.09	0.039	0.1776
12	B3GALT2	7.34	8.83	-2.8	3.40E-08	6.82E-06
13	BBOX1	9.84	10.86	-2.02	0.0025	0.0258
14	BHMT	11.52	12.56	-2.06	0.0233	0.1267
15	BRE-AS1	4.45	6.36	-3.74	4.22E-07	3.94E-05
16	BST1	7.58	8.73	-2.22	2.08E-08	4.85E-06
17	CCDC148	6.12	7.38	-2.41	5.86E-11	6.28E-08
18	CH17-340M24.3	6.47	7.58	-2.16	1.50E-07	1.90E-05

19	CHRDL1	7.68	8.69	-2.01	8.98E-05	0.0021
20	CLDN8	5.1	6.43	-2.52	0.0002	0.0042
21	CR1	11.7	12.76	-2.08	6.73E-05	0.0017
22	CTGF	13.86	15.3	-2.73	1.40E-05	0.0005
23	CTSV	6.71	8.11	-2.64	4.23E-08	7.93E-06
24	CTXN3	6.01	8.22	-4.63	3.94E-09	1.49E-06
25	CXCL9	6.14	7.36	-2.33	0.0085	0.063
26	CYP2B6	4.85	6.5	-3.13	3.07E-11	3.77E-08
27	DAO	6.29	7.34	-2.08	0.0003	0.0051
28	DCXR	10.77	12.06	-2.45	1.02E-05	0.0004
29	DEFB1	14.83	16.99	-4.46	2.77E-05	0.0009
30	DUSP1	5.96	7.17	-2.31	2.67E-09	1.15E-06
31	ECM2	5.7	6.83	-2.19	7.29E-08	1.13E-05
32	EGF	4.89	6.41	-2.87	2.02E-05	0.0007
33	EGR1	7.83	11.61	-13.69	1.03E-05	0.0004
34	ERRFI1	10.32	11.32	-2	0.0021	0.0233
35	ESM1	5.74	9.21	-11.14	3.48E-10	2.80E-07
36	FAM96B	8.15	9.24	-2.13	1.19E-05	0.0005
37	FBP1	6.71	8.17	-2.75	3.71E-07	3.60E-05
38	FBXO21	9.4	10.43	-2.04	1.58E-10	1.46E-07
39	FMO2	4.92	6.05	-2.19	0.0003	0.005
40	FOS	5.22	8.1	-7.32	1.36E-07	1.77E-05
41	FPR1	4.69	6.01	-2.49	7.77E-08	1.18E-05
42	FRY-AS1	5.62	6.93	-2.49	5.42E-09	1.79E-06
43	G0S2	6.62	8.05	-2.7	0.0003	0.0048
44	G6PC	6.85	11.32	-22.24	2.57E-17	1.73E-12
45	GBA3	6.23	7.25	-2.02	7.18E-05	0.0018
46	GBP4	9.39	10.66	-2.41	3.91E-08	7.46E-06
47	GIPC2	6.75	8.28	-2.89	1.12E-07	1.56E-05
48	GK	7.26	8.42	-2.23	3.54E-09	1.37E-06
49	GLYAT	11.3	12.65	-2.55	0.0011	0.0139
50	GLYATL1	7.33	9.04	-3.27	1.36E-07	1.77E-05

51	GSTA1	13.15	15.08	-3.79	1.69E-08	4.30E-06
52	GSTA2	11.22	13.79	-5.95	4.85E-09	1.65E-06
53	GSTA3	3.87	5.11	-2.36	1.08E-10	1.06E-07
54	GSTA5	3.69	4.97	-2.43	1.25E-11	1.73E-08
55	GSTM3	8.04	9.14	-2.15	0.0004	0.006
56	HAO2	7.89	9.71	-3.53	4.18E-05	0.0012
57	HBA1; HBA2	11.73	12.97	-2.36	8.56E-05	0.002
58	HBB	10.14	11.78	-3.11	3.23E-05	0.001
59	HCP5	9.82	10.86	-2.06	5.48E-06	0.0003
60	HGD	7.43	8.47	-2.06	1.79E-05	0.0006
61	HIST2H2AA4; HIST2H2AA3	9.92	11.37	-2.72	0.001	0.0129
62	HLA-DRB1	9.56	10.95	-2.63	0.0007	0.0101
63	HLA-DRB4	4.39	5.5	-2.15	0.0159	0.0981
64	HPD	9.49	10.85	-2.56	0.0032	0.0313
65	HPGD	7.08	8.14	-2.07	0.0006	0.0085
66	HPS5; H6PD	7.27	8.33	-2.08	1.75E-08	4.40E-06
67	HRSP12	9.61	11.08	-2.76	2.15E-06	0.0001
68	IFI27	14.09	15.31	-2.33	0.0002	0.0037
69	IFI6	9.39	11.01	-3.08	0.0027	0.0278
70	IGF1	7.82	10.45	-6.19	0.0003	0.0057
71	JUNB	5.52	7.03	-2.85	5.21E-05	0.0014
72	KLF9	9.45	10.57	-2.16	1.07E-05	0.0004
73	KNG1	10.22	12.06	-3.58	0.0017	0.0193
74	L3MBTL3	6.88	8.21	-2.52	4.23E-07	3.94E-05
75	LOX	9.38	10.42	-2.05	6.90E-05	0.0017
76	LPL	5.1	6.21	-2.16	0.0003	0.0056
77	LSM7	7.81	8.84	-2.05	0.0005	0.0072
78	MIOX	8.61	10.08	-2.78	0.0003	0.005
79	MNDA	5.84	7.02	-2.28	2.03E-05	0.0007
80	MORN2	6.85	7.87	-2.03	3.16E-07	3.19E-05
81	MRLN	5.05	6.87	-3.54	7.27E-12	1.07E-08
82	MRO	4.52	5.85	-2.51	1.15E-06	8.25E-05
83	MUC13	4.81	6.08	-2.4	0.0048	0.0424
84	MYCT1	9.4	11.11	-3.26	7.16E-10	4.97E-07

85	NQO1	10.27	11.29	-2.03	7.58E-06	0.0003
86	PAH	10.31	12.02	-3.27	4.58E-05	0.0013
87	PCK1	6.46	8.02	-2.96	7.50E-07	6.10E-05
88	PDK4	9.31	11.13	-3.55	4.14E-07	3.88E-05
89	PLGLA	6.57	7.58	-2.02	0.0072	0.0562
90	POLR2G	11.22	12.37	-2.21	1.48E-06	9.88E-05
91	PPM1K	7.17	8.52	-2.56	5.72E-07	4.98E-05
92	PRODH2	6.43	8.25	-3.55	8.38E-11	8.84E-08
93	PSAT1	8.13	9.61	-2.79	6.24E-05	0.0016
94	PTGS2	4.17	5.23	-2.08	8.10E-05	0.002
95	PVALB	5.21	6.6	-2.61	6.06E-06	0.0003
96	RABAC1	12.75	13.78	-2.04	4.52E-05	0.0013
97	RNA5-8S5	11.53	12.97	-2.7	2.99E-13	1.06E-09
98	RNA5S1	5.15	6.28	-2.19	5.68E-08	9.34E-06
99	RNA5S10	5.15	6.28	-2.19	5.68E-08	9.34E-06
100	RNA5S11	5.15	6.28	-2.19	5.68E-08	9.34E-06
101	RNA5S12	5.15	6.28	-2.19	5.68E-08	9.34E-06
102	RNA5S13	5.15	6.28	-2.19	5.68E-08	9.34E-06
103	RNA5S14	5.15	6.28	-2.19	5.68E-08	9.34E-06
104	RNA5S15	5.15	6.28	-2.19	5.68E-08	9.34E-06
105	RNA5S16	5.15	6.28	-2.19	5.68E-08	9.34E-06
106	RNA5S17	5.15	6.28	-2.19	5.68E-08	9.34E-06
107	RNA5S2	5.15	6.28	-2.19	5.68E-08	9.34E-06
108	RNA5S3	5.15	6.28	-2.19	5.68E-08	9.34E-06
109	RNA5S4	5.15	6.28	-2.19	5.68E-08	9.34E-06
110	RNA5S5	5.15	6.28	-2.19	5.68E-08	9.34E-06
111	RNA5S6	5.15	6.28	-2.19	5.68E-08	9.34E-06
112	RNA5S7	5.15	6.28	-2.19	5.68E-08	9.34E-06
113	RNA5S8	5.15	6.28	-2.19	5.68E-08	9.34E-06
114	RNF114	10.84	12.06	-2.32	5.08E-08	8.94E-06
115	RNF152	7.97	9.34	-2.58	2.63E-	5.60E-06

					08	
116	RNF212B	4.12	5.8	-3.2	6.26E-12	1.02E-08
117	RNU4-2	4.05	5.24	-2.27	1.13E-06	8.14E-05
118	RPS5	15.33	16.34	-2.02	0.0006	0.009
119	S100A12	4.24	6.32	-4.22	6.14E-05	0.0016
120	S100A8	5.47	7.05	-2.98	5.06E-06	0.0002
121	S100A9	8.05	9.74	-3.24	0.0008	0.0115
122	SAT2	9.11	10.4	-2.45	1.52E-06	0.0001
123	SEC61B	9.58	10.88	-2.46	0.0003	0.005
124	SELP	4.18	5.18	-2.01	2.82E-07	2.93E-05
125	SLC12A3	7	8.37	-2.6	0.0418	0.186
126	SLC25A33	5.95	7.1	-2.21	2.70E-09	1.15E-06
127	SLC2A12	8.58	9.58	-2	2.08E-05	0.0007
128	SLC36A2	7.09	8.7	-3.04	5.32E-05	0.0014
129	SLC7A7	7.56	8.89	-2.51	2.78E-06	0.0002
130	SMCO3	8.09	9.3	-2.31	1.78E-07	2.10E-05
131	SNHG8	11.16	12.91	-3.36	7.49E-07	6.10E-05
132	SNORD13	12.6	13.92	-2.49	0.0015	0.018
133	SNORD14E	4.37	6.22	-3.62	1.47E-05	0.0005
134	SNORD3A	6.51	11.1	-24.17	1.56E-16	3.05E-12
135	SNORD3B-1	5.7	10.23	-23.09	2.15E-16	3.05E-12
136	SNORD3B-2	5.7	10.23	-23.09	2.15E-16	3.05E-12
137	SNORD3C	5.66	9.8	-17.63	9.59E-16	1.08E-11
138	SNORD3D	5.27	9.54	-19.36	2.26E-16	3.05E-12
139	SNORD41	3.51	4.67	-2.24	0.0002	0.0043
140	SNORD66	3.27	4.5	-2.33	6.54E-06	0.0003
141	SNORD71	4.74	6.93	-4.58	2.22E-07	2.49E-05
142	TM4SF5	7.06	8.38	-2.49	2.47E-07	2.68E-05
143	TMEM14A	12.13	13.2	-2.09	5.06E-08	8.94E-06
144	TMEM174	9.18	10.53	-2.54	0.0001	0.0026
145	TMEM52B	8.84	10.31	-2.79	0.0075	0.0578
146	TNNC1	8.55	10.36	-3.52	1.87E-08	4.54E-06
147	TTR	6.71	8.35	-3.12	1.43E-	9.68E-05

					06	
148	UACA	15.26	16.34	-2.1	9.47E-09	2.76E-06
149	UBL5	12.07	13.26	-2.28	3.95E-07	3.75E-05
150	UGT2B7	12.93	14.14	-2.32	0.0006	0.0087
151	UQCR11	10.22	11.61	-2.62	2.61E-08	5.60E-06
152	VNN1	4.77	5.81	-2.06	2.35E-05	0.0008
153	WDR49	6.75	7.79	-2.05	3.66E-05	0.0011
154	WDR83OS	10.28	11.4	-2.18	4.86E-06	0.0002
155	XPNPEP2	8.53	9.53	-2.01	0.0034	0.0326
156	ZFP36	8.99	10.06	-2.09	0.0018	0.0199

Table 5- Kegg Pathway Analysis

s.no	Functional Category name	Genes		Enrichment FDR p value
1	Transforming growth factor beta production	ITGB6 FN1 LUM		0.002248823
2	Regulation of transforming growth factor beta production	ITGB6 FN1 LUM		0.002248823
3	Extracellular matrix organization	ADAMTS1 COL4A1 LUM ITGB6 FN1		0.002554385
4	Extracellular structure organization	ADAMTS1 COL4A1 LUM ITGB6 FN1		0.002554385
5	Phospholipid homeostasis	ITGB6 ABCG1		0.014201254
6	Myeloid leukocyte activation	HAVCR1 ITGB6 NR1D1 C3 PIGR		0.014706438
7	Complement activation, alternative pathway	C7 C3		0.014706438
8	Integrin-mediated signaling pathway	ITGB6 FN1 ADAMTS1		0.014706438
9	Positive regulation of steroid biosynthetic process	NR1D1 ABCG1		0.014706438
10	Cell junction organization	CDH6 FN1 CLDN1 C3 COL4A1		0.014706438

Table 6- PPI string analysis with combined score 16 commonly upregulated degs. In all three datasets

#node1	node2	combined_score
ABCG1	PPARG	0.695
ABCG1	PPARA	0.624
ABCG1	GPS2	0.947
ADAMTS1	CFP	0.925
ADAMTS1	FN1	0.508
AGT	TBL1X	0.904
AGT	C3	0.419
AGT	REN	0.999
AGT	PPARG	0.542
AGT	HAVCR1	0.457
AGT	FN1	0.582
AGT	SPP1	0.438
AGT	PPARA	0.939
BCL6	HDAC4	0.966
BCL6	NCOR1	0.999
BCL6	HDAC3	0.423
BCL6	FN1	0.508
BCL6	HDAC1	0.965
BCL6	SIN3A	0.826
BCL6	PPARA	0.566
C3	VTN	0.636

C3	PIGR	0.41
C3	C7	0.46
C3	FN1	0.695
C3	CFHR1	0.999
C3	CFI	0.999
C3	CD46	0.999
C3	CFP	0.999
C3	CFH	0.999
C3	VSIG4	0.999
C3	CR1	0.999
C7	VTN	0.665
C7	CFP	0.92
C7	CFI	0.547
CD46	VTN	0.507
CD46	CFP	0.714
CD46	VSIG4	0.559
CD46	ITGB1	0.68
CD46	CR1	0.685
CD46	CFI	0.947
CFH	VTN	0.607
CFH	CFP	0.725
CFH	CFHR1	0.954
CFH	FN1	0.422
CFH	SDC4	0.428
CFH	SPP1	0.708
CFH	CFI	0.996
CFHR1	VTN	0.459
CFHR1	CFP	0.719
CFHR1	CFI	0.708
CFI	VTN	0.471
CFI	CFP	0.704
CFI	CR1	0.825
CFP	VTN	0.459
CFP	VSIG4	0.585
CFP	CR1	0.647
COL4A1	ITGB8	0.707
COL4A1	ITGAV	0.946
COL4A1	LUM	0.61
COL4A1	ITGB6	0.718
COL4A1	ITGA5	0.799
COL4A1	ITGB5	0.775

COL4A1	FN1	0.781
COL4A1	COL4A2	0.999
COL4A1	SDC4	0.649
COL4A1	SPP1	0.628
COL4A1	ITGA4	0.704
COL4A1	ITGB1	0.954
COL4A2	ITGB8	0.676
COL4A2	ITGAV	0.943
COL4A2	LUM	0.548
COL4A2	ITGB6	0.682
COL4A2	ITGA5	0.766
COL4A2	ITGB5	0.752
COL4A2	FN1	0.737
COL4A2	SPP1	0.612
COL4A2	SDC4	0.646
COL4A2	ITGA4	0.7
COL4A2	ITGB1	0.948
CR1	VSIG4	0.616
FN1	ITGB8	0.894
FN1	VTN	0.983
FN1	ITGAV	0.999
FN1	LUM	0.755
FN1	REN	0.639
FN1	ITGB6	0.974
FN1	PPARG	0.567
FN1	ITGA5	0.999
FN1	ITGB5	0.945
FN1	SPP1	0.983
FN1	SDC4	0.999
FN1	ITGA4	0.999
FN1	ITGB1	0.999
GPS2	TBL1X	0.997
GPS2	NCOR1	0.999
GPS2	HDAC3	0.988
GPS2	HDAC1	0.438
GPS2	PPARA	0.541
HAVCR1	REN	0.563
HAVCR1	SPP1	0.632
HDAC1	TBL1X	0.975
HDAC1	RARA	0.948
HDAC1	HDAC4	0.595

HDAC1	NCOR1	0.999
HDAC1	PPARG	0.929
HDAC1	HDAC3	0.937
HDAC1	SIN3A	0.999
HDAC3	TBL1X	0.999
HDAC3	NR1D1	0.956
HDAC3	RARA	0.932
HDAC3	HDAC4	0.993
HDAC3	NCOR1	0.999
HDAC3	PPARG	0.997
HDAC3	PPARA	0.737
HDAC3	SIN3A	0.978
HDAC4	TBL1X	0.755
HDAC4	RARA	0.402
HDAC4	PPARG	0.663
HDAC4	SIN3A	0.882
HDAC4	NCOR1	0.999
ITGA4	ITGB8	0.955
ITGA4	VTN	0.76
ITGA4	ITGAV	0.942
ITGA4	ITGB6	0.965
ITGA4	ITGA5	0.928
ITGA4	ITGB5	0.961
ITGA4	SPP1	0.933
ITGA4	ITGB1	0.999
ITGA5	ITGB8	0.959
ITGA5	VTN	0.884
ITGA5	ITGAV	0.91
ITGA5	ITGB6	0.971
ITGA5	SDC4	0.418
ITGA5	SPP1	0.806
ITGA5	ITGB5	0.984
ITGA5	ITGB1	0.999
ITGAV	ITGB8	0.999
ITGAV	VTN	0.999
ITGAV	SDC4	0.93
ITGAV	ITGB6	0.999
ITGAV	ITGB1	0.999
ITGAV	ITGB5	0.999
ITGAV	SPP1	0.999
ITGB1	ITGB8	0.907
ITGB1	VTN	0.969
ITGB1	LUM	0.759
ITGB1	ITGB6	0.994
ITGB1	PPARG	0.477
ITGB1	ITGB5	0.91
ITGB1	SDC4	0.676
ITGB1	SPP1	0.997
ITGB5	ITGB8	0.907
ITGB5	VTN	0.974
ITGB5	ITGB6	0.905
ITGB5	SPP1	0.905
ITGB6	ITGB8	0.907
ITGB6	VTN	0.952
ITGB6	SPP1	0.75
ITGB8	SPP1	0.658
ITGB8	VTN	0.948
LUM	VTN	0.478
LUM	SPP1	0.543
MYOF	TAB2	0.426
MYOF	VSIG4	0.667
NCOR1	TBL1X	0.999
NCOR1	NR1D1	0.999
NCOR1	RARA	0.999
NCOR1	PPARA	0.999
NCOR1	SIN3A	0.999
NCOR1	PPARG	0.999
NCOR1	TAB2	0.999
PIGR	VTN	0.423
PPARA	TBL1X	0.691
PPARA	REN	0.524
PPARA	SIN3A	0.638
PPARG	REN	0.624
PPARG	SPP1	0.603
REN	SPP1	0.517
SDC4	VTN	0.81
SDC4	SPP1	0.407
SIN3A	TBL1X	0.826
SPP1	VTN	0.79
TAB2	TBL1X	0.521

Table 7- Top 20 in network string_interactions (1).tsv ranked by Degree method- cytoscape –cytohubba

Rank	Name	degree
1	FN1	40
2	VTN	38
3	SPP1	36
4	ITGB1	30
5	C3	24
5	NCOR1	24
5	COL4A1	24
5	ITGAV	24
5	ITGA5	24
5	COL4A2	24
11	HDAC3	22
11	ITGB8	22
11	ITGB6	22
11	ITGB5	22
11	ITGA4	22
16	PPARG	20
16	CFP	20
18	PPARA	18
18	TBL1X	18
18	HDAC1	18

Table 8- pathways -cross validation enrichr

pathway					
Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	Integrin cell surface interactions Homo sapiens R-HSA-216083	3.73E-08	0.000004511	180.73	3091.42
2	Fibronectin matrix formation Homo sapiens R-HSA-1566977	0.003296	0.04229	399.68	2284.21
3	Activation of C3 and C5 Homo sapiens R-HSA-174577	0.003296	0.04229	399.68	2284.21
4	Defective CHST6 causes MCDC1 Homo sapiens R-HSA-3656225	0.003844	0.04229	333.05	1852.16
5	Defective ST3GAL3 causes MCT12 and EIEE15 Homo sapiens R-HSA-3656243	0.003844	0.04229	333.05	1852.16
6	Defective B4GALT1 causes B4GALT1-CDG (CDG-2d) Homo sapiens R-HSA-3656244	0.003844	0.04229	333.05	1852.16
7	Regulation of Complement cascade Homo sapiens R-HSA-977606	0.00008873	0.003579	184.86	1724.73
8	Terminal pathway of complement Homo sapiens R-HSA-166665	0.004392	0.04429	285.46	1549.44
9	Keratan sulfate degradation Homo sapiens R-HSA-2022857	0.006582	0.06126	181.62	912.35
10	Extracellular matrix organization Homo sapiens R-HSA-1474244	2.36E-07	0.00001427	59.09	901.63

Table 9- Metascape gene ontology and pathways interaction with combined score

Description	Enrichment	Hits	LogP	Z_score
Integrin cell surface interactions	120.4705882	COL4A1|FN1|ITGB6|LUM	-7.600337219	21.80640398
Extracellular matrix organization	42.52491694	COL4A1|FN1|ITGB6|LUM|ADAMTS1	-7.227952347	14.31801225
regulation of transforming growth factor beta production	187.3170732	FN1|ITGB6|LUM	-6.328977261	23.60033223
transforming growth factor beta production	178.6046512	FN1|ITGB6|LUM	-6.265569323	23.03973838
miRNA targets in ECM and membrane receptors	178.6046512	COL4A1|FN1|ITGB6	-6.265569323	23.03973838
ECM-receptor interaction	93.65853659	COL4A1|FN1|ITGB6	-5.413294694	16.61050167
ECM-receptor interaction	93.65853659	COL4A1|FN1|ITGB6	-5.413294694	16.61050167
integrin-mediated signaling pathway	70.4587156	FN1|ITGB6|ADAMTS1	-5.040951735	14.36280599
Focal adhesion	38.59296482	COL4A1|FN1|ITGB6	-4.259548846	10.52035119
angiogenesis	17.06666667	C3|COL4A1|FN1|ADAMTS1	-4.223483648	7.863850944
blood vessel morphogenesis	14.77633478	C3|COL4A1|FN1|ADAMTS1	-3.980714862	7.25885569
blood vessel development	13.28145266	C3|COL4A1|FN1|ADAMTS1	-3.801891528	6.835374446
cell junction organization	11.05035971	C3|COL4A1|FN1	-2.671646525	5.303440215
extracellular structure organization	25.34653465	COL4A1|LUM|ADAMTS1	-3.719176422	8.422960578
external encapsulating structure organization	25.18032787	COL4A1|LUM|ADAMTS1	-3.710762327	8.393324124
Degradation of the extracellular matrix	54.85714286	COL4A1|FN1|ADAMTS1	-4.715037929	12.62835359
ECM proteoglycans	134.7368421	COL4A1|FN1|ITGB6|LUM	-7.797719204	23.07819555
extracellular matrix organization	25.43046358	COL4A1|LUM|ADAMTS1	-3.723404853	8.437886579

Table 10- GSEA and ORA analysis results

geneSet	description	size	overlap	expect	enrichment Ratio	pValue	FDR	userId
R-HSA-3000178	**ECM proteoglycans**	**76**	**4**	**0.064816**	**61.71345**	**3.05E-07**	**4.14E-04**	**COL4A1;ITGB6;LUM;FN1**
R-HSA-216083	**Integrin cell surface interactions**	**85**	**4**	**0.072491**	**55.17908**	**4.79E-07**	**4.14E-04**	**COL4A1;ITGB6;LUM;FN1**
R-HSA-1474244	**Extracellular matrix organization**	**301**	**5**	**0.256704**	**19.47767**	**2.09E-06**	**0.001207**	**COL4A1;ITGB6;LUM;FN1;ADAMTS1**
R-HSA-1474228	Degradation of the extracellular matrix	140	3	0.119397	25.12619	1.81E-04	0.07822	COL4A1;FN1;ADAMTS1
R-HSA-2129379	Molecules associated with elastic fibres	38	2	0.032408	61.71345	4.47E-04	0.154608	ITGB6;FN1
R-HSA-1566948	Elastic fibre formation	45	2	0.038378	52.11358	6.28E-04	0.169139	ITGB6;FN1
R-HSA-977606	**Regulation of Complement cascade**	**47**	**2**	**0.040083**	**49.89598**	**6.85E-04**	**0.169139**	**C3;C7**
R-HSA-166658	Complement cascade	58	2	0.049465	40.43295	0.001043	0.207118	C3;C7
R-HSA-3000171	Non-integrin membrane-ECM interactions	59	2	0.050317	39.74765	0.001079	0.207118	COL4A1;FN1
R-HSA-8957275	Post-translational protein phosphorylation	108	2	0.092107	21.71399	0.003565	0.615972	C3;FN1