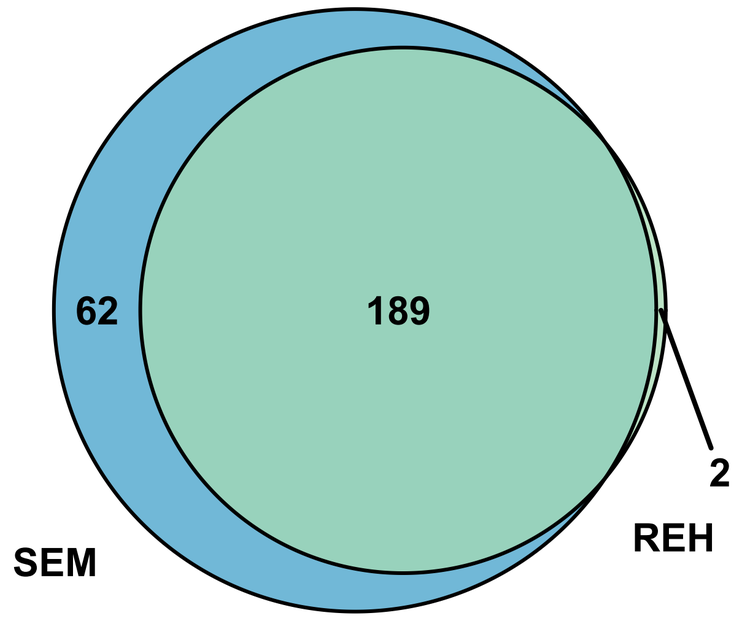
a

SEM and REH xenograft gene expression CNS vs Spleen

Genes with adjusted p-value <0.05 and Log2 fold-change > 0.6



b

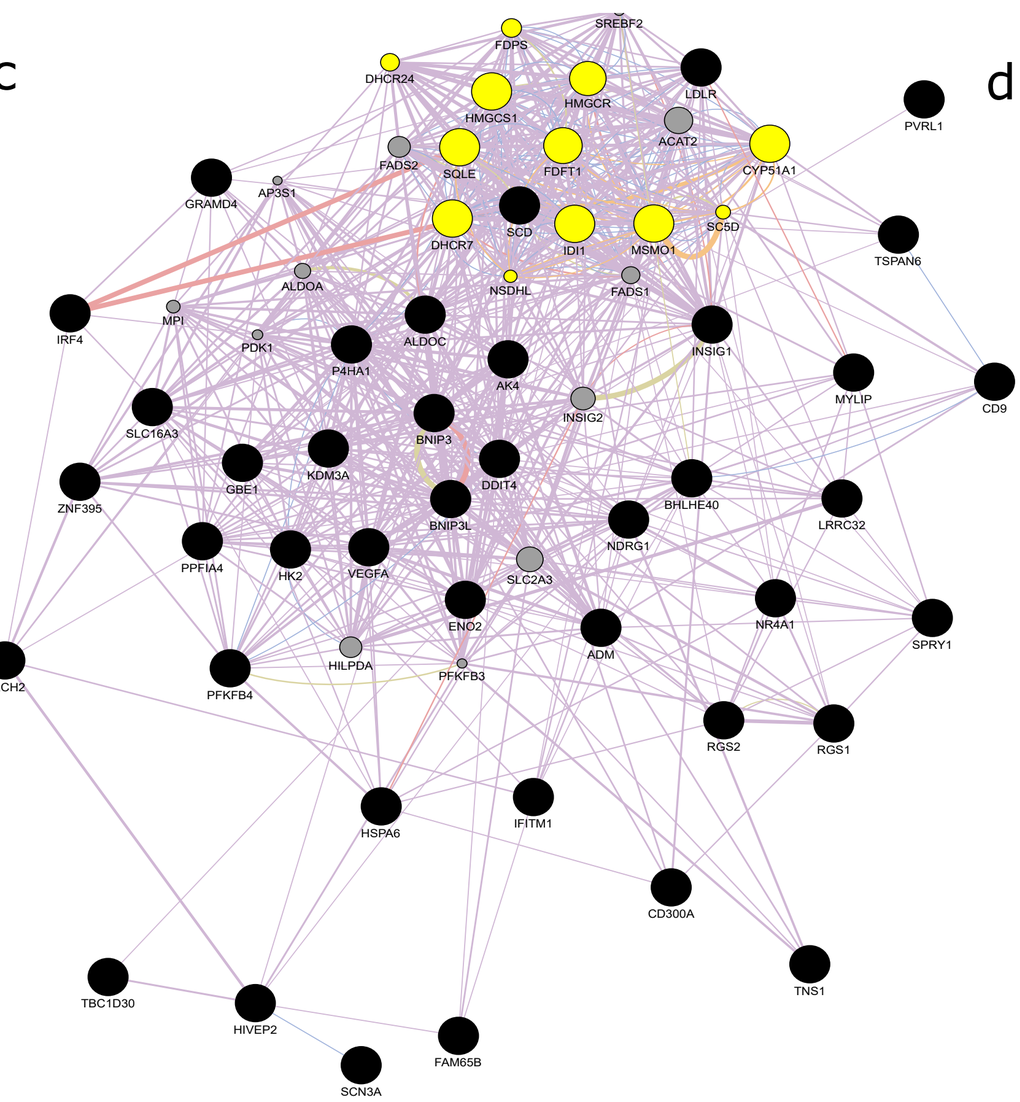
SEM cells. Gene expression in xenografted ALL cells retreived from CNS vs Spleen

	baseMean expression level	log_2 Fold Change	Adj p-value	Rank in genelist
LDLR	1988.39	1.58	4.13E-16	25
HMGCS1	5900.98	1.59	4.86E-13	35
SQLE	2936.86	1.34	1.33E-11	41
CYP51A1	2836.84	1.19	3.41E-10	49
MSMO1	1933.47	1.22	4.19E-10	50
DHCR24	6110.11	1.07	2.02E-08	70
HMGCR	5194.64	1.10	6.8E-08	74
FDFT1	8908.53	0.92	2.43E-06	109
SREBF2	10944.15	0.81	1.40E-04	184
DHCR7	655.89	1.07	3.26E-04	212
MVK	532.85	0.80	2.87E-03	334
LSS	2074.06	0.74	3.21E-03	350
SC5D	901.36	0.91	4.26E-03	364
SREBF1	2585.07	0.63	0.03	738
HSD17B7	551.51	0.62	0.04	768
IDI1	4977.17	0.57	0.05	951
TM7SF2	102.92	0.63	0.16	1959
MVD	1037.95	0.42	0.29	3017
PMVK	1252.94	-0.44	0.29	3045
NSDHL	646.68	0.20	0.63	7263
FDPS	4124.33	0.14	0.74	9058
EBP	2398.54	-0.10	0.84	10898
IDI2	0.77	0.02	NA	NA

REH cells. Gene expression in xenografted ALL cells retreived from CNS vs Spleen

	baseMean expression level	log_2 Fold Change	Adj p-value	Rank in genelist
LDLR	1972.60	3.10	4.77E-90	3
SREBF1	3593.84	2.26	1.09E-67	7
SREBF2	8210.10	1.94	9.54E-66	9
FDFT1	6521.64	2.13	2.17E-54	12
SQLE	2604.02	1.87	3.92E-30	33
HMGCS1	4108.04	1.35	6.81E-22	59
MSMO1	1150.96	1.44	2.60E-18	78
SC5D	724.05	1.19	1.54E-14	122
DHCR7	1691.78	1.19	5.85E-13	150
HMGCR	3294.02	0.97	2.09E-11	178
CYP51A1	2344.26	1.06	3.69E-11	189
LSS	3029.86	0.49	5.75E-05	601
HSD17B7	443.24	0.66	9.06E-05	646
IDI1	9118.73	0.54	1.67E-04	693
MVD	1797.47	0.41	9.77E-03	1702
TM7SF2	1077.63	0.39	0.01	1754
PMVK	1609.09	-0.45	0.02	2010
NSDHL	703.24	0.30	0.17	4578
MVK	572.13	0.33	0.19	4886
FDPS	7172.24	0.12	0.64	10117
EBP	2717.29	-0.10	0.75	11717
DHCR24	0.00	NA	NA	NA
IDI2	0.39	-0.01	NA	NA

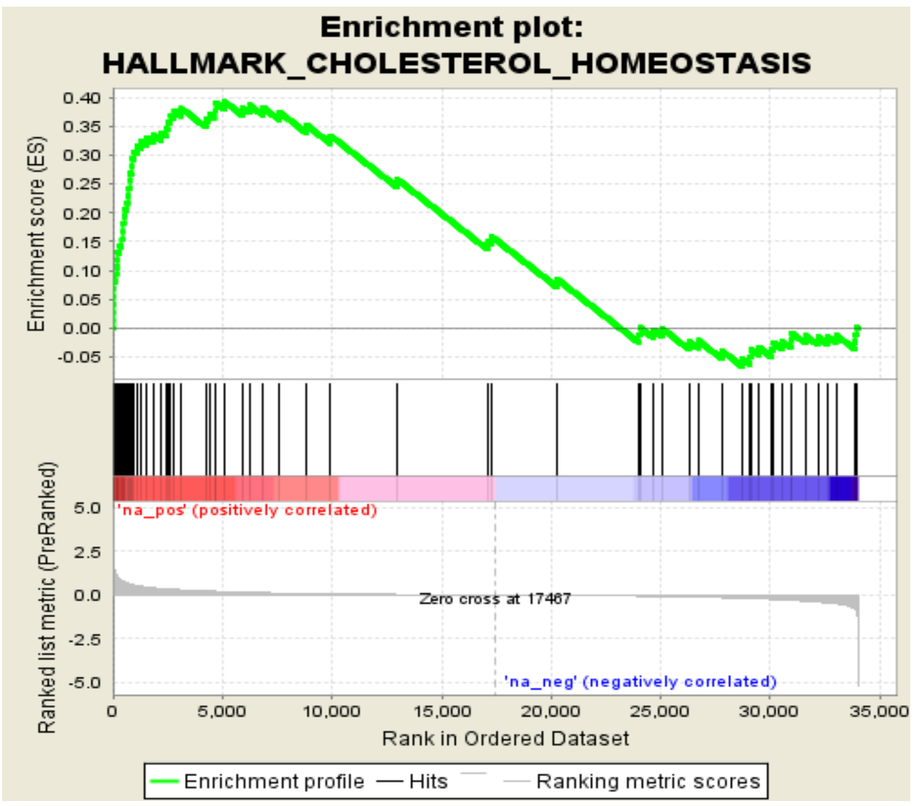
c



d

Gene Network	q-value	Occurences in Sample	Occurrences in Genome
cholesterol biosynthetic process	3.58E-18	12	33
sterol biosynthetic process	3.58E-18	12	34
cholesterol metabolic process	3.51E-14	12	69
steroid biosynthetic process	1.36E-13	13	107
sterol metabolic process	1.40E-13	12	80
alcohol biosynthetic process	2.19E-12	12	101
organic hydroxy compound biosynthetic process	2.61E-11	12	125
steroid metabolic process	2.02E-10	13	196
alcohol metabolic process	8.07E-09	13	264
glycolysis	2.43E-05	6	48
monosaccharide metabolic process	5.67E-05	9	209
glucose catabolic process	6.51E-05	6	58
glucose metabolic process	9.79E-05	8	161
hexose catabolic process	2.08E-04	6	72
hexose metabolic process	2.14E-04	8	182
monosaccharide catabolic process	2.14E-04	6	74
single-organism carbohydrate catabolic process	0.00101232	6	97
carbohydrate catabolic process	0.001285868	6	102
carbohydrate kinase activity	0.02429718	3	17
response to hypoxia	0.042823266	5	116
response to decreased oxygen levels	0.044260756	5	118
response to oxygen levels	0.045782348	5	120
cellular response to hypoxia	0.067890551	4	68
cellular response to decreased oxygen levels	0.072883279	4	70
cellular response to oxygen levels	0.078112169	4	72

e



f

Name of GeneSet	Number of Genes	Normalised Enrichment Score	False Discovery Rate q-value
HALLMARK_TNFA_SIGNALING_VIA_NFKB	190	5.2258525	0
HALLMARK_CHOLESTEROL_HOMEOSTASIS	72	3.9789872	0
HALLMARK_INTERFERON_GAMMA_RESPONSE	191	3.921294	0
HALLMARK_HYPOXIA	188	3.9108407	0
HALLMARK_UV_RESPONSE_DN	141	3.7583632	0
HALLMARK_MITOTIC_SPINDLE	198	3.657221	0
HALLMARK_ESTROGEN_RESPONSE_EARLY	183	3.4749246	0
HALLMARK_KRAS_SIGNALING_UP	170	3.4248111	0
HALLMARK_ALLOGRAFT_REJECTION	178	3.0722015	0
HALLMARK_IL2_STAT5_SIGNALING	197	2.9819734	1.02E-04
HALLMARK_INTERFERON_ALPHA_RESPONSE	93	2.902626	9.33E-05
HALLMARK_INFLAMMATORY_RESPONSE	181	2.6650493	8.62E-05
HALLMARK_ANDROGEN_RESPONSE	97	2.55135	1.75E-04
HALLMARK_KRAS_SIGNALING_DN	147	2.4090657	7.71E-04
HALLMARK_COMPLEMENT	172	2.2474463	0.001974049
HALLMARK_HEME_METABOLISM	191	2.0771627	0.005601735
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	174	2.044133	0.006376944
HALLMARK_ESTROGEN_RESPONSE_LATE	173	1.9561938	0.010122927
HALLMARK_BILE_ACID_METABOLISM	104	1.8099852	0.022086777
HALLMARK_IL6_JAK_STAT3_SIGNALING	74	1.7644167	0.02662824
HALLMARK_TGF_BETA_SIGNALING	52	1.7310841	0.029115979
HALLMARK_MYOGENESIS	177	1.7262442	0.028639007
HALLMARK_PROTEIN_SECRETION	96	1.5796239	0.056467623
HALLMARK_HEDGEHOG_SIGNALING	34	1.5261691	0.07021268
HALLMARK_ANGIOGENESIS	30	1.5202888	0.06925001