

Table S1 Enrichment analysis by Enrichr, “MGI Mammalian Phenotype 2017”, of 200 genes selected as bimodal genes for mouse. Top 5 ranked terms.

Term	Overlap	P-value	Adjusted P-value
MP:0001262_decreased_body_weight	27/1189	5.68E-05	4.58E-02
MP:0011100_prewaning_lethality_complete_penetrance	16/674	1.26E-03	1.54E-01
MP:0001265_decreased_body_size	16/774	4.94E-03	2.31E-01
MP:0011098_embryonic_lethality_during_organogenesis_complete_penetrance	13/559	4.23E-03	2.31E-01
MP:0001732_postnatal_growth_retardation	13/590	6.58E-03	2.31E-01

Table S2 Enrichment analysis by Enrichr, “Allen Brain Atlas down”, of 200 genes selected as bimodal genes for human. Top 5 ranked terms

Term	Overlap	P-value	Adjusted P-value
shell part of the anterobasal nucleus	17/300	9.73E-09	1.82E-05
suboptic nucleus	15/300	3.75E-07	2.34E-04
Paraflocculus, granular layer	14/300	2.10E-06	4.36E-04
layer 1 of FCx	15/300	3.75E-07	2.34E-04
medial trapezoid nucleus	14/300	2.10E-06	4.36E-04

Table S3 Enrichment analysis by Enrichr, “Allen Brain Atlas down”, of 200 genes selected as bimodal genes for mouse. Top 5 ranked terms.

Term	Overlap	P-value	Adjusted P-value
intermediate stratum of r10Ve	15/300	3.75E-07	2.51E-04
rhombomere 11	15/300	3.75E-07	2.51E-04
r10 part of spinal vestibular nucleus	15/300	3.75E-07	2.51E-04
r11 alar plate	13/300	1.09E-05	4.36E-03
Flocculus	13/300	1.09E-05	4.36E-03

Table S4 Enrichment analysis by Enrichr, “GTEx Tissue Sample Gene Expression Profiles down”, of 200 genes selected as bimodal gene for human. Top 5 ranked terms.

Term	Overlap	P-value	Adjusted P-value
GTEx-XBEC-1326-SM-4AT69_heart_male_50-59_years	150/7340	1.75E-28	1.33E-25
GTEx-Q734-0426-SM-48TZX_pancreas_female_40-49_years	139/6240	6.10E-29	1.33E-25
GTEx-XQ8I-1926-SM-4BOOK_pancreas_male_50-59_years	120/4696	1.50E-28	1.33E-25
GTEx-PX3G-1026-SM-48TZW_pancreas_female_20-29_years	105/3830	3.13E-26	1.79E-23
GTEx-WRHU-1226-SM-4E3IJ_heart_female_50-59_years	158/8581	1.14E-25	4.35E-23

Table S5 Enrichment analysis by Enrichr, “GTEx Tissue Sample Gene Expression Profiles down”, of 200 genes selected as bimodal genes for mouse. Top 5 ranked terms

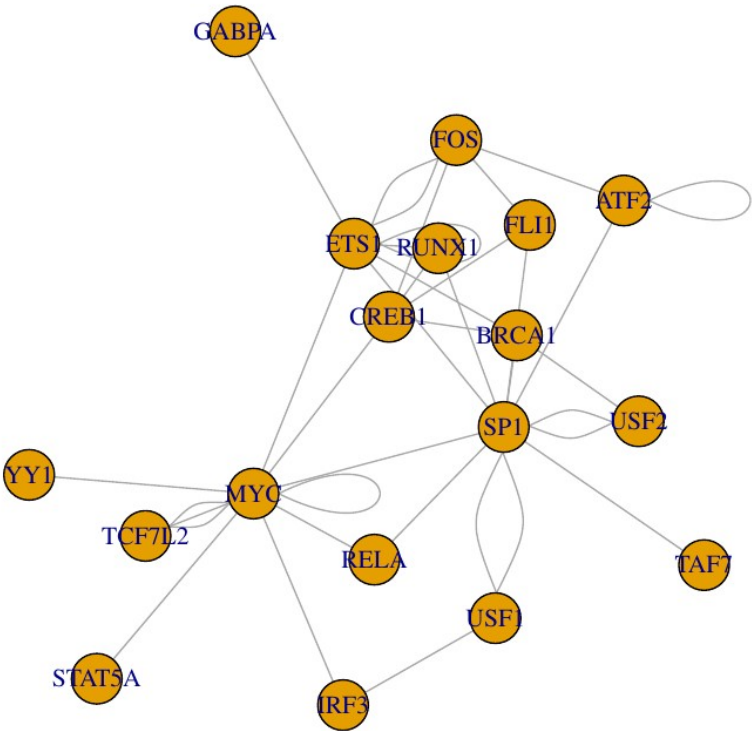
Term	Overlap	P-value	Adjusted P-value
GTEx-XBEC-1326-SM-4AT69_heart_male_50-59_years	147/7340	2.26E-26	4.98E-23
GTEx-WRHU-1226-SM-4E3IJ_heart_female_50-59_years	157/8581	5.71E-25	5.33E-22
GTEx-Q734-0426-SM-48TZX_pancreas_female_40-49_years	133/6240	7.26E-25	5.33E-22
GTEx-PX3G-1026-SM-48TZW_pancreas_female_20-29_years	100/3830	6.15E-23	3.38E-20
GTEx-T2IS-0426-SM-32QPE_heart_female_20-29_years	130/6360	3.89E-22	1.71E-19

Table S6 Enrichment of selected genes as bimodal genes in Embryonic brain by “Jensen TISSUES” by Enrichr.

Term	Overlap	P-value	Adjusted P-value
Human			
Embryonic_brain	150/4936	6.42E-51	8.15E-49
Mouse			
Embryonic_brain	122/4936	8.01E-28	2.36E-26

Table S7 TF enrichment enriched in “ENCODE and ChEA Consensus TFs from ChIP-X” by Enrichr for human and mouse bimodal gens. Bold TFs are common. Genes in red are also commonly selected between human and mouse in Table 7.

human	ATF2 , BRCA1 , CEBPD, CHD1 , CREB1 , E2F6, ELF1, ETS1, FLI1 , FOS , GABPA , IRF3 , KAT2A, MAX , MYC , NELFE, NFYA, NFYB, NR2C2, NRF1, PBX3 , PML , RELA , RUNX1, SIN3A, SIX5 , SP1 , SP2 , STAT5A, TAF1 , TAF7 , TCF3 , TCF7L2, USF1 , USF2 , YY1 , ZBTB33, ZBTB7A, ZMIZ1 , ZNF384
mouse	ATF2 , BHLHE40, BRCA1 , CHD1 , CREB1 , E2F1, E2F4, E2F6, ELF1, FLI1 , FOS , GABPA , IRF3 , KLF4, MAX , MYC , NFYA, NFYB, NR2C2, NRF1, PBX3 , PML , RCOR1, RUNX1, SIX5 , SP1 , SP2 , SPI1, TAF1 , TAF7 , TCF3 , TCF7L2, UBTF , USF1 , USF2 , YY1 , ZBTB33, ZBTB7A, ZMIZ1 , ZNF384



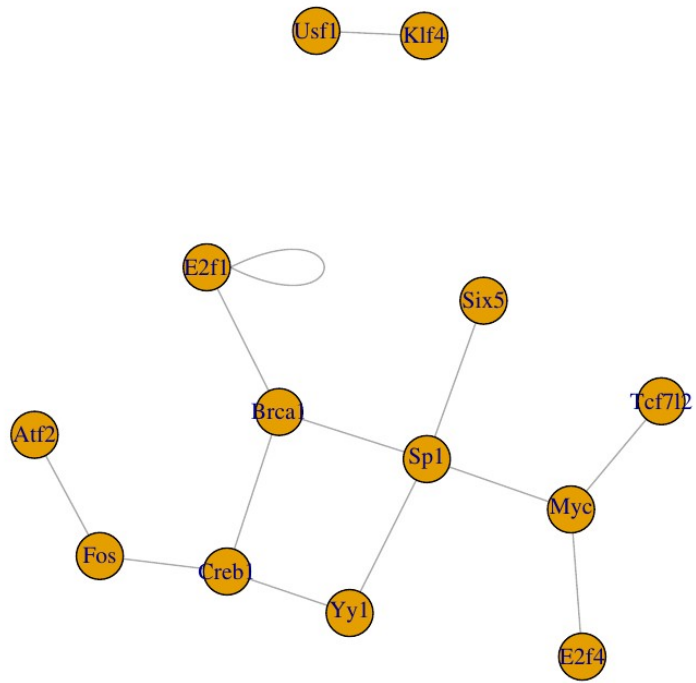


Figure S1 TF network identified by regnetworkweb for TFs in Table S7. Upper:human, lower: mouse.