

Supplemental Figure 1. Effects on glioblastoma gene expression subtype upon PROX1 overexpression or suppression. Calculations of expression changes of subtype classifier genes according to the RNA-seq data. The number of centroid genes with a relatively higher or lower expression for the specific centroid are represented in the first column. The genes with no available measurements are then subtracted from the total amount of classifier genes for each centroid in the second column. Shown are the number of genes corresponding to a fold change (FC) in gene expression higher or lower than 1. In the next the number of positively supporting genes for each subtype versus the total number of supporting genes is shown. Chi-square test was used to assess the significance of subtype changes.

TCGA subtypes		RNAseq data: U-343 MG PROX1 over U-343 MG							RNAseq data: U-343 MGa shPROX1 over U-343 MGa						
	# centroid genes per subtype	# non-available measurement	# with available measurement	# genes FC > 1	# genes FC < 1	supporting/total measurements	Chi-square p-value		# non-available measurement	# with available measurement	# genes FC > 1	# genes FC < 1	supporting/total measurements	Chi-square p-value	
Proneural	High: 137	42	137 – 42 = 95	52	43	52+31/95+63=	0.627		34	137 – 34 = 139	52	51	52+29/139+62=	0.733	
	Low: 73	10	73 – 10 = 63	32	31	0.52			11	73 – 11 = 62	33	29	0.40		
Neural	High: 81	22	81 – 22 = 59	39	24	39+59/59+103=	0.0164		23	81 – 23 = 58	23	35	23+49/58+103=	0.119	
	Low: 129	26	129 – 26 = 103	44	59	0.60			26	129 – 26 = 103	54	49	0.44		
Classical	High: 153	14	153 – 14 = 139	80	59	80+22/139+45=	0.45		16	153 – 16= 137	66	71	66+23/137+45=	0.732	
	Low: 57	12	57 – 12 = 45	23	22	0.55			10	57 – 10 = 45	24	23	0.45		
Mesenchymal	High: 164	36	164 – 36 = 128	35	93	35+12/128+33=	0.000095		37	164 – 37 = 127	81	46	81+20/127+12=	0.017	
	Low: 46	13	46 – 13 = 33	21	12	0.29			34	46 – 34 = 12	14	20	0.62		
Calculation of subtype index upon PROX1 overexpression in U-343 MG															
		% positively supporting *		subtype supporting index		rescaled subtype index**									
PN		52		2		4									
N		60		10		20									
CL		55		5		10									
MES		29		-21		-42									
Calculation of subtype index upon PROX1 suppression in U-343 MGa															
		% positively supporting *		subtype supporting index		rescaled subtype index**									
PN		40		-10		-20									
N		44		-6		-12									
CL		45		-5		-10									
MES		62		12		24									

* 0 is full negative change of subtype, 50 is neutral, and 100 is full subtype change in a positive direction, ** supporting index rescaled to have scale range from -100 to 100