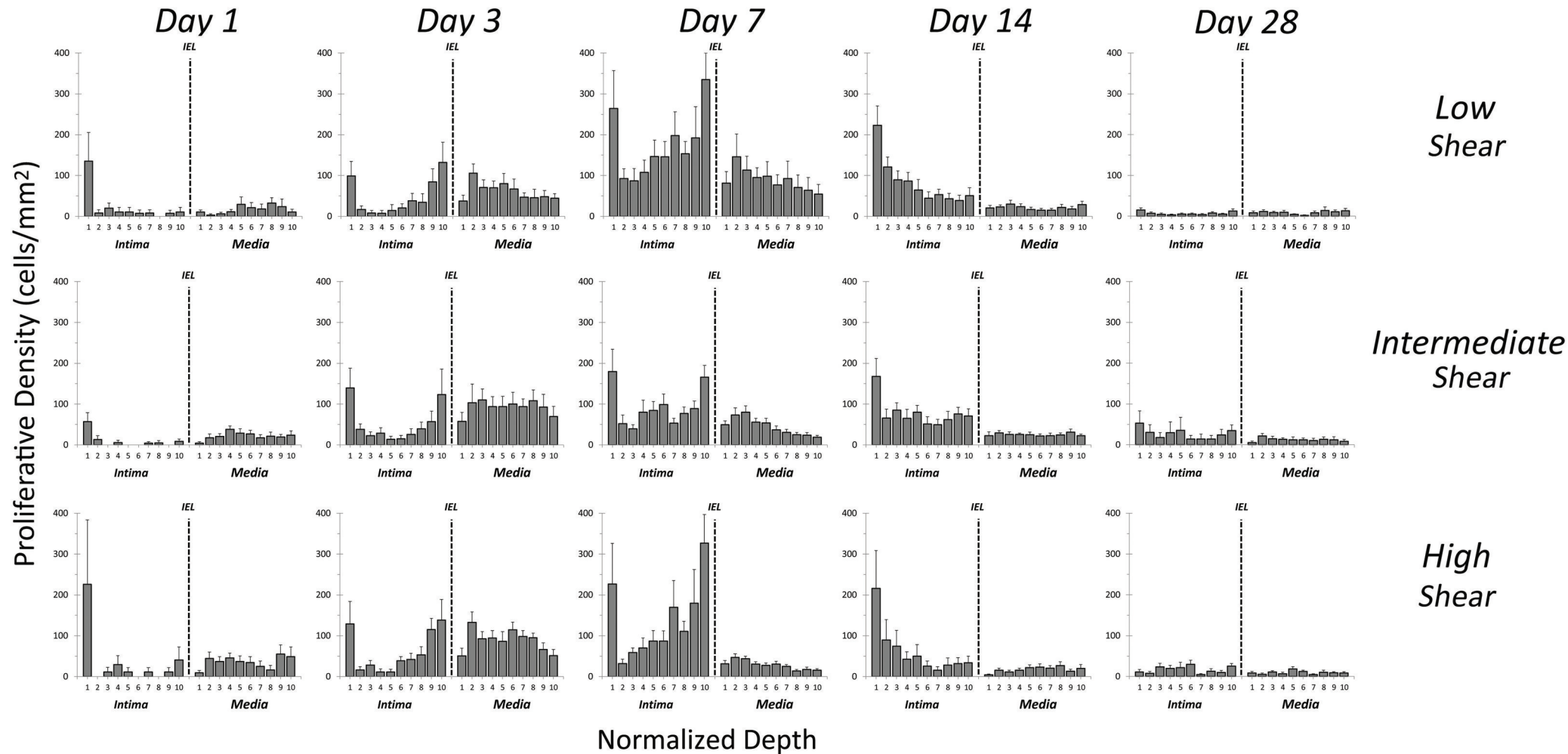
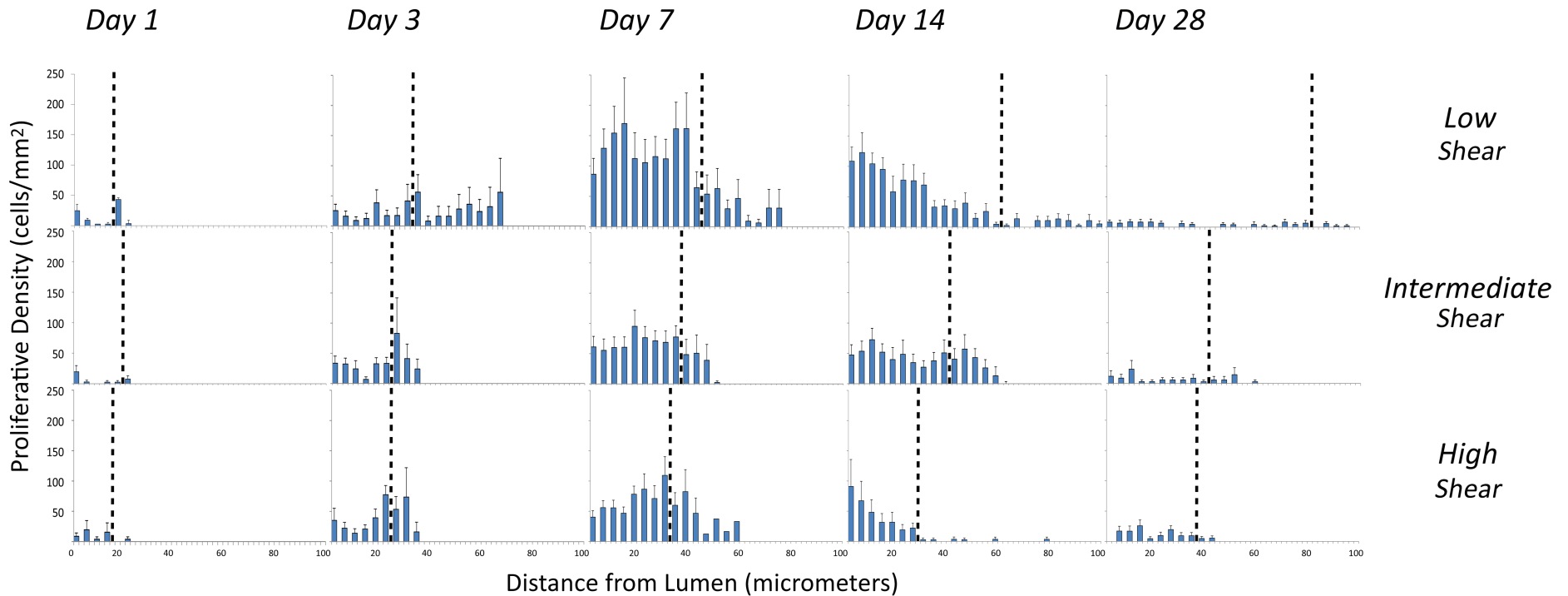


Intimal and Medial Proliferative Density - Normalized Dimensions



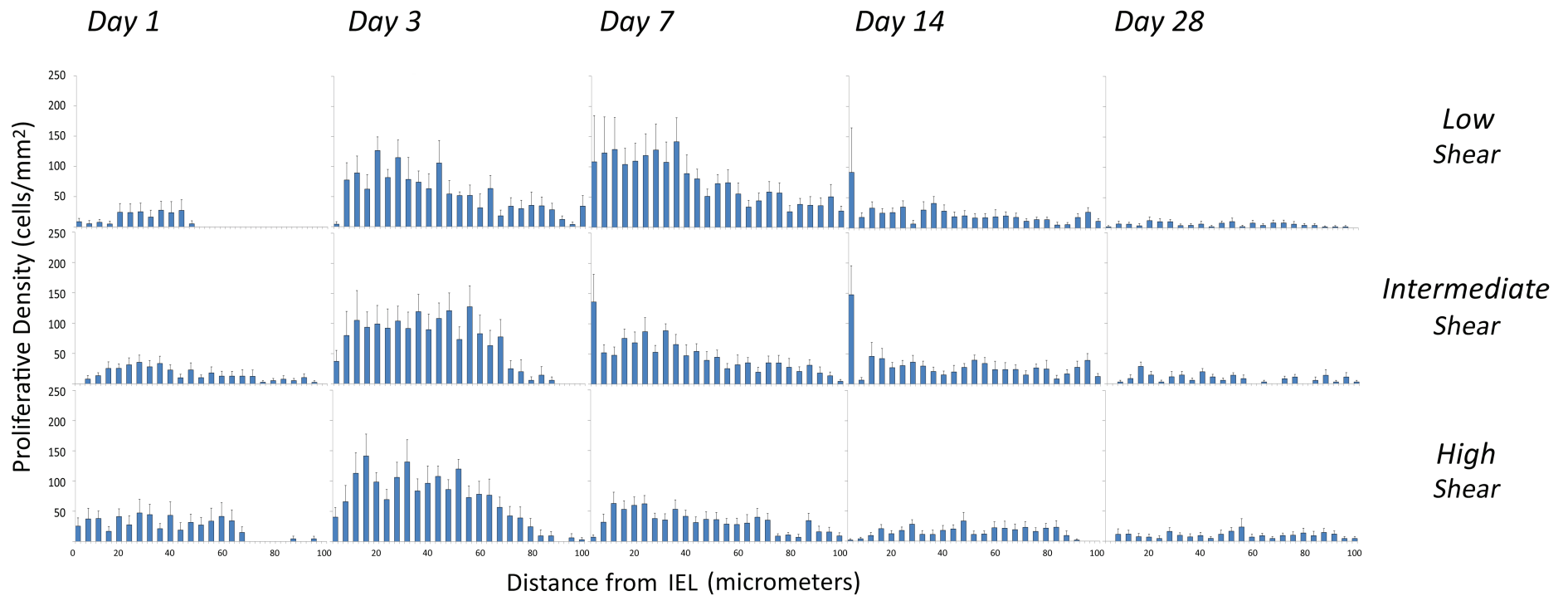
Supplemental Figure 1. Proliferative density within the intima and media as a function of normalized depth from the lumen or IEL, as a function flow condition, and time of implantation. Each compartment was divided into ten sections of equal thickness, with zero representing the lumen or IEL, in the intima or media respectively. The vertical dashed lines represent the location of the IEL. Note the proliferative density within the intima to be highly dependent on the depth within both the intimal and medial compartments ($p < .001$; three-way ANOVA). Focusing on the most active time point (Day 7), increased proliferation is observed in the intima adjacent to the IEL, an observation that is independent of the flow condition ($p < .001$, IEL Position 10 vs all other positions; post-hoc analysis).

Intimal Proliferative Density - Non-normalized Dimensions



Supplemental Figure 2. Proliferative density within the intima as a function of distance from the lumen, flow condition, and time of implantation. Each bar represents the proliferative densities in 4 μm intervals starting at the lumen and radiating outward. The dotted lines represent the average distance of the internal elastic lamina (IEL) from the lumen. In contrast to Figure 7, non-normalized (actual) dimensions are used to illustrate the distribution of positive cells in the context of a changing intimal thickness.

Medial Proliferative Density - Non-normalized Dimensions



Supplemental Figure 3. Proliferative density within the media as a function of distance from the lumen, flow condition, and time of implantation. Each bar represents the proliferative densities in 4 μm intervals starting at the internal elastic lamina and radiating outward.

Supplemental Table 1. mRNA expression levels, as a function of implantation time and flow condition, for the 42 upstream regulators that have an influence on TAGLN, MYH11, and ACTA gene expression.

Gene Symbol	Entrez Gene Name	Gene Accession Number	Post-operative Day / Flow condition											
			0.08 High	0.08 Low	1 High	1 Low	3 High	3 Low	7 High	7 Low	14 High	14 Low	28 High	28 Low
ACTA1	actin, alpha 1, skeletal muscle	NM_001100	-0.079	-0.551	-0.112	-0.683	-1.168	-0.706	-1.275	-1.327	-0.519	-0.277	-0.668	-0.454
MYH11	myosin, heavy chain 11, smooth muscle	NM_002474	-0.721	-0.647	-2.427	-2.127	-3.635	-2.833	-3.631	-3.569	-1.757	-0.635	-1.042	-0.466
TAGLN	transgelin	NM_001001522	-0.756	-0.561	-1.065	-1.010	-1.093	-1.012	-1.167	-0.853	-0.660	0.034	-0.584	-0.233
ABCB4	ATP binding cassette subfamily B member 4	NM_018849	0.195	0.199	0.038	0.388	-0.081	0.323	0.080	-0.071	0.033	-0.158	0.297	0.081
ABLIM1	actin binding LIM protein 1	NM_006720	-0.025	0.182	0.045	-0.066	-0.164	-0.201	-0.062	-0.074	-0.011	-0.176	-0.062	-0.058
AZIN1	antizyme inhibitor 1	NM_148174	0.476	0.283	0.008	-0.073	0.076	-0.197	-0.017	0.151	-0.012	-0.159	-0.054	-0.052
BMP6	bone morphogenetic protein 6	NM_001718	0.227	0.048	-0.072	0.030	-0.069	-0.110	0.189	0.107	0.109	-0.123	0.009	-0.022
BMPER	BMP binding endothelial regulator	NM_133468	-0.138	-0.152	-0.003	0.042	0.135	0.028	0.172	0.082	0.007	-0.093	-0.121	-0.164
CA4	carbonic anhydrase IV	NM_000717	-0.522	0.330	-0.801	-0.464	-0.123	-0.572	0.146	-0.151	-0.324	-0.448	-0.091	-0.242
CACNB4	calcium channel, voltage-dependent, beta 4 subunit	NM_001145798	-0.100	-0.176	-0.140	-0.092	-0.342	-0.258	-0.166	-0.147	-0.102	-0.273	-0.297	-0.190
CASZ1	castor zinc finger 1	NM_001079843	-0.137	-0.178	-0.027	-0.036	-0.003	-0.011	-0.194	-0.250	-0.063	0.092	-0.243	-0.182
CLIC5	chloride intracellular channel 5	NM_001114086	-0.005	-0.080	-0.032	0.083	-0.064	-0.030	-0.035	-0.160	0.003	0.139	-0.181	-0.279
DGCR8	DGCR8 microprocessor complex subunit	NM_022720	-0.096	-0.118	0.221	0.114	-0.095	0.042	-0.057	-0.124	-0.058	0.036	-0.118	-0.175
DNASE1	deoxyribonuclease I	NM_005223	-0.031	-0.179	0.095	0.268	-0.069	0.011	-0.032	-0.073	0.082	0.317	0.004	0.039
DOCK7	dedicator of cytokinesis 7	NM_033407	-0.264	0.022	-0.881	-0.717	0.428	0.104	0.455	0.672	0.489	0.438	0.902	0.961
FHL2	four and a half LIM domains 2	NM_001039492	-0.490	-0.884	-0.454	-0.767	-0.944	-0.452	-2.027	-1.810	-0.850	0.218	-1.140	-0.235
GATA6	GATA binding protein 6	NM_005257	-0.013	0.308	0.151	0.351	0.108	0.023	-0.107	-0.086	-0.305	0.031	-0.274	-0.035
GC	group-specific component (vitamin D binding protein)	NM_000583	0.314	0.235	0.239	0.437	0.248	0.231	0.342	0.372	0.328	0.049	0.221	0.165
HEY2	hes-related family bHLH transcription factor with YRPW motif 2	NM_012259	-0.426	-0.432	-0.334	-0.163	-0.365	-0.473	-0.594	-0.597	-0.362	-0.114	-0.530	-0.441
IPP	intracisternal A particle-promoted polypeptide	NM_001145349	-0.497	-0.304	-0.070	0.235	0.403	0.169	0.403	0.416	0.013	0.096	0.444	0.439
IRX4	iroquois homeobox 4	NM_016358	-0.106	-0.180	-0.092	-0.319	-0.178	-0.133	-0.181	-0.276	0.042	0.071	-0.199	-0.278
KCNMA1	potassium channel, calcium activated large conductance subfamily M alpha	NM_001014797	-0.004	0.086	0.117	0.416	0.060	0.306	-0.186	-0.027	-0.209	0.109	-0.089	0.008
KLF5	Kruppel-like factor 5	NM_001730	1.766	1.905	0.876	1.099	0.711	0.847	0.978	0.832	0.772	0.389	0.812	0.761
LAMA2	laminin subunit alpha 2	NM_001079823	0.140	0.382	-1.066	-1.010	-0.310	-0.614	0.111	-0.091	0.290	-0.127	0.450	0.356
LAMC1	laminin subunit gamma 1	NM_002293	-0.107	-0.475	-0.695	-0.722	-0.322	-0.194	-0.440	-0.228	-0.018	0.478	-0.156	0.016
LDB3	LIM domain binding 3	NM_001171610	-0.019	-0.076	-0.382	-0.269	-0.024	-0.111	0.047	-0.216	0.185	-0.133	-0.100	-0.137
MARCKSL1	MARCKS-like 1	NM_023009	1.179	0.492	1.494	1.330	0.509	0.831	-0.038	0.090	0.419	0.636	0.142	0.187
MDK	midkine (neurite growth-promoting factor 2)	NM_002391	0.203	-0.091	-0.066	-0.001	0.018	-0.064	0.061	-0.002	-0.026	-0.081	-0.124	-0.173
MKL2	MKL/myocardin-like 2	NM_014048	-0.581	-0.456	-0.608	-0.554	-0.124	-0.105	-0.342	-0.265	0.033	-0.037	-0.035	-0.079
MORF4L1	mortality factor 4 like 1	NM_006791	-0.428	-0.339	-0.125	-0.153	-0.255	-0.176	-0.691	-0.664	-0.327	-0.333	-0.288	-0.135
MYOC	myocilin, trabecular meshwork inducible glucocorticoid response	NM_000261	0.131	0.227	-0.095	0.038	-0.094	0.173	0.004	-0.076	0.139	0.065	0.077	0.099
MYOCD	myocardin	NM_001146313	-0.522	0.272	-0.635	-1.133	-1.117	-0.913	-1.339	-1.268	-1.025	-0.740	-0.889	-0.510
NOTCH3	notch 3	NM_000435	-0.927	-0.472	-1.817	-1.592	-1.104	-1.012	-0.831	-0.754	0.339	0.986	0.406	0.816
NUP155	nucleoporin 155kDa	NM_153485	0.024	0.187	0.309	0.240	0.095	-0.059	0.242	0.100	0.004	0.221	0.067	0.068
PALLD	palladin, cytoskeletal associated protein	NM_001166108	-0.258	-0.135	-0.262	-0.460	-0.322	-0.246	-0.383	-0.323	-0.267	-0.055	-0.272	-0.349
PDLIM5	PDZ and LIM domain 5	NM_006457	0.867	0.687	0.567	0.732	0.211	0.424	-0.021	-0.006	0.119	0.600	0.263	0.507
PINX1	PIN2/TERF1 interacting, telomerase inhibitor 1	NM_017884	0.011	-0.049	0.099	0.044	0.257	0.155	-0.102	-0.058	-0.013	0.070	-0.109	-0.081
PRKG1	protein kinase, cGMP-dependent, type I	NM_001098512	-0.258	-0.322	-0.132	0.041	-0.301	-0.240	-0.468	-0.426	-0.421	-0.315	-0.411	-0.435
RLN2	relaxin 2	NM_005059	-0.160	0.182	0.923	0.115	0.154	-0.606	1.421	0.828	0.277	-0.193	0.525	-0.029
RPS7	ribosomal protein S7	NM_001011	0.458	-0.011	0.946	0.524	0.428	0.737	-0.078	0.024	0.179	0.202	0.298	0.389
RFXP1	relaxin/insulin-like family peptide receptor 1	NM_021634	0.002	-0.182	-0.287	-0.433	-0.306	-0.263	-0.563	-0.614	-0.326	-0.230	-0.461	-0.530
SV2A	synaptic vesicle glycoprotein 2A	NM_014849	-0.173	0.114	-0.431	-0.071	-0.145	-0.089	-0.084	-0.169	-0.068	-0.028	-0.044	-0.123
TINF2	TERF1 (TRF1)-interacting nuclear factor 2	NM_001099274	-0.023	-0.151	-0.143	-0.172	-0.233	-0.246	-0.333	-0.479	-0.174	-0.157	-0.406	-0.327
TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	NM_003747	-0.157	0.014	-0.199	0.080	-0.215	-0.185	-0.006	-0.121	-0.007	0.128	-0.228	0.021
TPM1	tropomyosin 1 (alpha)	NM_001018020	-1.700	-1.678	-2.066	-2.106	-2.567	-1.724	-2.816	-2.262	-1.915	-0.875	-1.480	-0.831

