

Table S3 Biological Processes of FGWYD-VD PPI Network

Cluster	Term	Pathway	Count	%	Pvalue
1	GO:0043066	negative regulation of apoptotic proce	21	36.84211	9.18E-18
	GO:0006954	inflammatory response	17	29.82456	6.06E-14
	GO:0007568	aging	12	21.05263	5.99E-12
	GO:0001666	response to hypoxia	11	19.29825	2.32E-10
	GO:0051092	positive regulation of NF-kappaB tran	10	17.54386	5.16E-10
	GO:0071456	cellular response to hypoxia	9	15.78947	9.62E-10
	GO:0001525	angiogenesis	11	19.29825	2.91E-09
	GO:0008284	positive regulation of cell proliferation	14	24.5614	3.12E-09
	GO:0043065	positive regulation of apoptotic proce	10	17.54386	5.97E-07
	GO:0034097	response to cytokine	6	10.52632	7.93E-07
	GO:0043524	negative regulation of neuron apoptoti	7	12.2807	4.95E-06
	GO:0042542	response to hydrogen peroxide	5	8.77193	2.47E-05
	GO:0006979	response to oxidative stress	6	10.52632	3.22E-05
	GO:0043536	positive regulation of blood vessel enc	4	7.017544	3.28E-05
	GO:0042127	regulation of cell proliferation	7	12.2807	3.39E-05
	GO:0045766	positive regulation of angiogenesis	6	10.52632	3.99E-05
	GO:0050679	positive regulation of epithelial cell pr	5	8.77193	4.71E-05
	GO:0035924	cellular response to vascular endotheli	4	7.017544	5.93E-05
	GO:0071677	positive regulation of mononuclear ce	3	5.263158	6.53E-05
	GO:0001938	positive regulation of endothelial cell	5	8.77193	8.16E-05
	GO:0050729	positive regulation of inflammatory re	5	8.77193	1.02E-04
	GO:2000352	negative regulation of endothelial cell	4	7.017544	1.08E-04
	GO:0045907	positive regulation of vasoconstrictor	4	7.017544	1.63E-04
	GO:0006919	activation of cysteine-type endopeptid	5	8.77193	1.68E-04
	GO:0043123	positive regulation of I-kappaB kinase	6	10.52632	1.96E-04
	GO:0032930	positive regulation of superoxide anio	3	5.263158	3.87E-04
	GO:0043525	positive regulation of neuron apoptoti	4	7.017544	3.94E-04
	GO:0030168	platelet activation	5	8.77193	5.83E-04
	GO:0090026	positive regulation of monocyte chem	3	5.263158	0.001272
	GO:0030949	positive regulation of vascular endothe	3	5.263158	0.001272
	GO:0043066	negative regulation of apoptotic proce	11	23.91304	2.64E-07
	GO:0045766	positive regulation of angiogenesis	6	13.04348	1.36E-05
	GO:0006986	response to unfolded protein	4	8.695652	1.92E-04
	GO:0050999	regulation of nitric-oxide synthase act	3	6.521739	0.002191
	GO:0006366	transcription from RNA polymerase II	7	15.21739	0.002339
	GO:0006954	inflammatory response	6	13.04348	0.00332
	GO:0051402	neuron apoptotic process	3	6.521739	0.003517
	GO:0030968	endoplasmic reticulum unfolded prote	3	6.521739	0.006461
	GO:0001666	response to hypoxia	4	8.695652	0.010936
	GO:0050727	regulation of inflammatory response	3	6.521739	0.012364
	GO:0030512	negative regulation of transforming gr	3	6.521739	0.012741
	GO:0038033	positive regulation of endothelial cell	2	4.347826	0.013329
	GO:2001028	positive regulation of endothelial cell	2	4.347826	0.013329

	GO:0045454 cell redox homeostasis	3	6.521739	0.018091
	GO:0071639 positive regulation of monocyte chem	2	4.347826	0.018612
	GO:1903071 positive regulation of ER-associated u	2	4.347826	0.021243
	GO:0071456 cellular response to hypoxia	3	6.521739	0.027306
	GO:1902176 negative regulation of oxidative stress	2	4.347826	0.036885
	GO:0043536 positive regulation of blood vessel enc	2	4.347826	0.049734
	GO:2000352 negative regulation of endothelial cell	2	4.347826	0.072439
	GO:0001937 negative regulation of endothelial cell	2	4.347826	0.074929
2	GO:0043542 endothelial cell migration	2	4.347826	0.074929
	GO:0006940 regulation of smooth muscle contracti	4	25	3.21E-07
	GO:0071880 adenylate cyclase-activating adrenergi	4	25	5.54E-07
	GO:0071883 activation of MAPK activity by adren	3	18.75	4.46E-06
	GO:0032811 negative regulation of epinephrine sec	3	18.75	4.46E-06
	GO:0035625 epidermal growth factor-activated rec	3	18.75	4.46E-06
	GO:0007186 G-protein coupled receptor signaling p	8	50	5.43E-06
	GO:0007187 G-protein coupled receptor signaling p	4	25	8.55E-06
	GO:0010700 negative regulation of norepinephrine	3	18.75	1.56E-05
	GO:0007200 phospholipase C-activating G-protein	4	25	2.55E-05
	GO:0019229 regulation of vasoconstriction	3	18.75	1.40E-04
	GO:0007268 chemical synaptic transmission	4	25	0.001155
	GO:0007198 adenylate cyclase-inhibiting serotonin	2	12.5	0.002678
	GO:0007218 neuropeptide signaling pathway	3	18.75	0.003574
	GO:0030168 platelet activation	3	18.75	0.004606
	GO:0051967 negative regulation of synaptic transm	2	12.5	0.008013
	GO:0050795 regulation of behavior	2	12.5	0.008013
	GO:0007399 nervous system development	3	18.75	0.026397
3	GO:0007271 synaptic transmission, cholinergic	2	12.5	0.03256
	GO:0001994 norepinephrine-epinephrine vasoconst	3	14.28571	8.07E-06
	GO:0007271 synaptic transmission, cholinergic	4	19.04762	1.09E-05
	GO:0008283 cell proliferation	6	28.57143	5.67E-05
	GO:0060079 excitatory postsynaptic potential	3	14.28571	5.00E-04
	GO:0042135 neurotransmitter catabolic process	2	9.52381	0.009491
	GO:0050804 modulation of synaptic transmission	2	9.52381	0.020065
	GO:0048169 regulation of long-term neuronal syna	2	9.52381	0.021234
	GO:0055114 oxidation-reduction process	4	19.04762	0.031803
4	GO:0007268 chemical synaptic transmission	3	14.28571	0.032636
	GO:0006750 glutathione biosynthetic process	3	37.5	1.78E-05
	GO:1901687 glutathione derivative biosynthetic pro	3	37.5	3.43E-05
	GO:2001237 negative regulation of extrinsic apopto	3	37.5	1.04E-04
	GO:0006749 glutathione metabolic process	3	37.5	2.27E-04
	GO:0097069 cellular response to thyroxine stimulu	2	25	8.34E-04
	GO:0006979 response to oxidative stress	3	37.5	8.74E-04
	GO:0051409 response to nitrosative stress	2	25	0.001667

5	GO:0018916 nitrobenzene metabolic process	2	25	0.001667
	GO:0051900 regulation of mitochondrial depolariza	2	25	0.001667
	GO:0007568 aging	3	37.5	0.001951
	GO:0008152 metabolic process	3	37.5	0.002022
6	GO:1902476 chloride transmembrane transport	4	50	5.66E-06
	GO:0007214 gamma-aminobutyric acid signaling p	3	37.5	3.43E-05
	GO:0034220 ion transmembrane transport	4	50	6.50E-05
	GO:0007165 signal transduction	4	50	0.009342
	GO:0006821 chloride transport	2	25	0.016559
	GO:0043524 negative regulation of neuron apoptoti	2	25	0.053755
7	GO:0007268 chemical synaptic transmission	2	25	0.095875
	GO:0007268 chemical synaptic transmission	5	55.55556	2.72E-06
	GO:0015844 monoamine transport	3	33.33333	5.55E-06
	GO:0042493 response to drug	5	55.55556	6.96E-06
	GO:0045471 response to ethanol	3	33.33333	0.001058
	GO:0051583 dopamine uptake involved in synaptic	2	22.22222	0.00238
	GO:0055085 transmembrane transport	3	33.33333	0.005558
	GO:0042136 neurotransmitter biosynthetic process	2	22.22222	0.005704
	GO:0048265 response to pain	2	22.22222	0.008072
	GO:0051412 response to corticosterone	2	22.22222	0.008545
	GO:0001975 response to amphetamine	2	22.22222	0.014677
	GO:0007611 learning or memory	2	22.22222	0.017026
	GO:0035094 response to nicotine	2	22.22222	0.017496
	GO:0060291 long-term synaptic potentiation	2	22.22222	0.017965
	GO:0019233 sensory perception of pain	2	22.22222	0.024512
	GO:0007613 memory	2	22.22222	0.029165
	GO:0007626 locomotory behavior	2	22.22222	0.039333
	GO:0001666 response to hypoxia	2	22.22222	0.079081
	GO:0007190 activation of adenylate cyclase activit	4	50	4.35E-07
	GO:0007189 adenylate cyclase-activating G-protein	3	37.5	1.81E-04
	GO:0046960 sensitization	2	25	8.34E-04
	GO:0002025 vasodilation by norepinephrine-epineph	2	25	0.00125
	GO:0031649 heat generation	2	25	0.00125
	GO:0071870 cellular response to catecholamine sti	2	25	0.002915
	GO:0002024 diet induced thermogenesis	2	25	0.003746
	GO:0010579 positive regulation of adenylate cyclase	2	25	0.003746
	GO:0060158 phospholipase C-activating dopamine	2	25	0.004162
	GO:0040015 negative regulation of multicellular or	2	25	0.004993
	GO:0007191 adenylate cyclase-activating dopamine	2	25	0.004993
	GO:0001963 synaptic transmission, dopaminergic	2	25	0.005408
	GO:0060292 long term synaptic depression	2	25	0.006652
	GO:0001659 temperature homeostasis	2	25	0.007895
	GO:0071880 adenylate cyclase-activating adrenergic	2	25	0.007895

8	GO:0019226 transmission of nerve impulse	2	25	0.008309
	GO:0046627 negative regulation of insulin receptor	2	25	0.012029
	GO:0001975 response to amphetamine	2	25	0.012854
	GO:0050873 brown fat cell differentiation	2	25	0.013266
	GO:0009409 response to cold	2	25	0.014914
	GO:0030819 positive regulation of cAMP biosynthesis	2	25	0.016559
	GO:0007612 learning	2	25	0.023525
	GO:0007416 synapse assembly	2	25	0.025158
	GO:0006874 cellular calcium ion homeostasis	2	25	0.038137
	GO:0030168 platelet activation	2	25	0.046974
9	GO:0018105 peptidyl-serine phosphorylation	2	25	0.050968
	GO:0007268 chemical synaptic transmission	2	25	0.095875
	GO:0032469 endoplasmic reticulum calcium ion homeostasis	2	25	0.006237
	GO:2001234 negative regulation of apoptotic signaling	2	25	0.006652
	GO:0006509 membrane protein ectodomain proteolysis	2	25	0.009137
	GO:0051402 neuron apoptotic process	2	25	0.013678
10	GO:0043066 negative regulation of apoptotic process	3	37.5	0.014056
	GO:0001764 neuron migration	2	25	0.042966
	GO:0008202 steroid metabolic process	4	80	6.25E-08
	GO:0042574 retinal metabolic process	3	60	2.81E-06
	GO:0008210 estrogen metabolic process	2	40	0.002618
	GO:0055114 oxidation-reduction process	3	60	0.007101
11	GO:0042572 retinol metabolic process	2	40	0.007128
	GO:0001523 retinoid metabolic process	2	40	0.014453
	GO:0007596 blood coagulation	3	100	1.19E-04
	GO:0010544 negative regulation of platelet activation	2	66.66667	9.53E-04
12	GO:0051918 negative regulation of fibrinolysis	2	66.66667	0.001191
	GO:0042730 fibrinolysis	2	66.66667	0.0025
	GO:0007598 blood coagulation, extrinsic pathway	2	66.66667	5.95E-04
	GO:0017187 peptidyl-glutamic acid carboxylation	2	66.66667	0.00131
	GO:0006465 signal peptide processing	2	66.66667	0.002975
	GO:0051897 positive regulation of protein kinase B	2	66.66667	0.00998
12	GO:0006888 ER to Golgi vesicle-mediated transport	2	66.66667	0.018966
	GO:0007596 blood coagulation	2	66.66667	0.021796
	GO:0030335 positive regulation of cell migration	2	66.66667	0.021796
	GO:0019430 removal of superoxide radicals	2	33.33333	0.003568
	GO:0060291 long-term synaptic potentiation	2	33.33333	0.011265
	GO:0009636 response to toxic substance	2	33.33333	0.025058
12	GO:0045471 response to ethanol	2	33.33333	0.03088
	GO:0007417 central nervous system development	2	33.33333	0.035228
	GO:0007605 sensory perception of sound	2	33.33333	0.038984

13	GO:0007568 aging	2	33.33333	0.04818
	GO:0043065 positive regulation of apoptotic process	2	33.33333	0.086203

Genes	Fold Enrichment	Bonferroni
IL10, CDKN1A, NGF, MPO, MMP9, EGFR, IL2, R	13.59676113	1.39E-14
IL10, CRP, CD40, TGFB1, CXCL8, FOS, PTGS2, T	13.21409064	9.21E-11
IL10, CASP9, IL6, JUN, TGFB1, VCAM1, CAT, CC	21.42519936	9.10E-09
TGFB1, VCAM1, NOS2, PLA2, CASP3, MMP2, C	18.84047328	3.52E-07
AR, IL6, CD40, TGFB1, CD40LG, IL1B, CAT, TNF	22.15011212	7.84E-07
CCNB1, MDM2, HMOX1, AKT1, PTGS2, HIF1A, 5	27.61842105	1.46E-06
JUN, CXCL8, EGF, MMP2, SERPINE1, HMOX1, C	14.53166549	4.42E-06
TGFB1, EGF, EGFR, IL2, RELA, VEGFA, CXCL10	8.850538363	4.74E-06
IL6, MAPK8, TGFB1, HMOX1, AKT1, NGF, PTGS	9.819883041	9.06E-04
IL4, JUN, STAT1, FOS, BCL2L1, MCL1	33.99190283	0.001203234
JUN, BDNF, HMOX1, CCL2, APOE, NGF, BCL2L1	15.6225412	0.007493541
JUN, STAT1, CASP3, CAT, HMOX1	28.88200894	0.036779447
HMOX1, AKT1, APOE, PTGS2, MPO, EGFR	16.06889952	0.04777968
TGFB1, AKT1, MAPK14, VEGFA	62.02031394	0.048571195
CXCL10, JUN, CD40, NOS2, PLA2, TNF, TNFRSF	11.14689426	0.05017187
CXCL8, IL1B, SERPINE1, HMOX1, HIF1A, VEGF	15.37025172	0.058821308
IL6, TGFB1, MYC, EGFR, VEGFA	24.5497076	0.069015142
VCAM1, AKT1, MAPK14, VEGFA	51.23417239	0.086200355
IL4, TGFB1, TNF	220.9473684	0.094380335
JUN, CCL2, AKT1, HIF1A, VEGFA	21.34757183	0.116613151
SERPINE1, CCL2, EGFR, IL2, TNFRSF1A	20.17784186	0.143220834
IL10, IL4, SERPINE1, ICAM1	42.08521303	0.151930483
AKT1, PTGS2, EGFR, ICAM1	36.8245614	0.218985901
CASP8, CASP3, PPARG, NGF, TNF	17.74677658	0.22478281
CD40, CASP8, HMOX1, TNF, RELA, TNFRSF1A	10.97875123	0.257522196
CRP, TGFB1, EGFR	98.19883041	0.444877291
CASP9, JUN, CASP3, TP53	27.40432477	0.450785754
IL6, CD40, CD40LG, MAPK1, AKT1	12.8085431	0.587425322
CXCL10, SERPINE1, CCL2	55.23684211	0.855366298
IL1B, HIF1A, VEGFA	55.23684211	0.855366298
NFKBIA, IKBKB, GSK3B, HSPA5, PTEN, CDK1, I	8.825226947	2.52E-04
IL1A, NOS3, KDR, HSPB1, F3, NFE2L2	19.04574669	0.012873202
HSP90AA1, HSPB2, HSPB1, HSPB3	34.76604555	0.167630009
HSP90AA1, NOS3, CAV1	42.12040134	0.877133439
PARP1, IRF1, AHR, NR3C1, ESR1, RUNX2, NFE2	4.981100093	0.893367212
IKBKB, IL1A, SELE, AGER, CXCL2, NFE2L2	5.779052426	0.958396169
RB1, APP, CASP7	33.18577075	0.965547778
CCND1, HSPA5, NFE2L2	24.33623188	0.997964688
ADAM17, CAV1, RAF1, AGER	8.489383215	0.999972791
XIAP, SELE, ESR1	17.38302277	0.999993165
ADAM17, HSPA5, CAV1	17.11141304	0.999995256
KDR, HSPB1	146.0173913	0.999997317
HSPB1, MET	146.0173913	0.999997317

NCF1, NOS3, NFE2L2	14.22247318	0.999999974
IL1A, AGER	104.2981366	0.999999984
CAV1, NFE2L2	91.26086957	0.999999999
CCNA2, PTEN, NFE2L2	11.4076087	1
HSPB1, NFE2L2	52.14906832	1
HSPB1, NFE2L2	38.42562929	1
KDR, NFE2L2	26.07453416	1
GJA1, CAV1	25.17541229	1
NOS3, PTEN	25.17541229	1
CHRM2, ADRA2C, ADRA2B, ADRA2A	262.375	9.17E-05
DRD2, ADRA2C, ADRA2B, ADRA2A	220.9473684	1.58E-04
ADRA2C, ADRA2B, ADRA2A	787.125	0.001275948
ADRA2C, ADRA2B, ADRA2A	787.125	0.001275948
ADRA2C, ADRA2B, ADRA2A	787.125	0.001275948
CHRM2, OPRD1, CXCL11, PTGER3, HTR1A, ADI	9.339265851	0.001550799
CHRM2, OPRD1, HTR1B, OPRM1	91.26086957	0.002443574
ADRA2C, ADRA2B, ADRA2A	449.7857143	0.004451839
OPRD1, PTGER3, HTR1B, OPRM1	63.60606061	0.007269939
ADRA2C, ADRA2B, ADRA2A	157.425	0.039307568
OPRD1, HTR1A, HTR1B, OPRM1	17.49166667	0.281517306
HTR1A, HTR1B	699.6666667	0.535514349
OPRD1, GAL, OPRM1	31.17326733	0.640843074
ADRA2C, ADRA2B, ADRA2A	27.37826087	0.732944289
HTR1B, DRD2	233.2222222	0.899829862
HTR1A, HTR1B	233.2222222	0.899829862
CHRM2, GAL, APOB	10.97038328	0.999524353
CHRM2, CHRM4	56.72972973	0.999922644
ADRA1D, ADRA1B, ADRA1A	599.7142857	0.002918842
CHRM3, CHRM1, CHRM5, HTR3A	86.44530245	0.003952586
CHRM3, CHRM1, CHRM5, CYP1A1, ADRA1D, A	13.10850898	0.020302666
PPP3CA, GRIN1, SNCA	85.67346939	0.165622518
MAOB, MAOA	199.9047619	0.968318973
PPP3CA, HRH1	94.07282913	0.999349356
GRIN1, SNCA	88.84656085	0.999577533
MAOB, MAOA, CYP1A1, SNCA	5.402831403	0.999991703
HTR2C, HTR2A, GRIN1	9.995238095	0.999993925
GCLC, GSS, GCLM	393.5625	0.002296881
GSTM2, GSTM1, GSTP1	286.2272727	0.004411586
GCLC, GSTP1, GCLM	165.7105263	0.013323649
GSTM2, GSTM1, GSTP1	112.4464286	0.028855502
GCLC, GCLM	2099	0.101992485
GCLC, GSS, GCLM	57.24545455	0.106672395
GCLC, GCLM	1049.5	0.193592839

GSTM2, GSTM1	1049.5	0.193592839
GCLC, GCLM	1049.5	0.193592839
GCLC, GSS, GCLM	38.16363636	0.222711715
GSTM2, GSTM1, GSTP1	37.48214286	0.229773369
GABRA6, GABRA3, GABRE, GABRG3	90.27956989	3.96E-04
GABRA6, GABRA3, GABRG3	286.2272727	0.002396304
GRIA2, GABRA6, GABRA3, GABRG3	39.98095238	0.004542204
GRIA2, CLDN4, GABRA6, GABRE	7.231696813	0.481613899
GABRA6, GABRG3	104.95	0.689267851
SNCB, MT3	31.8030303	0.979094588
GRIA2, SNCB	17.49166667	0.999137033
GRIN2A, CHRNA4, CRH, SLC6A2, SLC6A4	38.87037037	4.87E-04
SLC6A2, SLC6A3, SLC6A4	699.6666667	9.94E-04
GRIN2A, CRH, SLC6A2, SLC6A3, SLC6A4	30.6871345	0.001245444
GRIN2A, CRH, SLC6A3	53.30793651	0.172630596
SLC6A2, SLC6A3	746.3111111	0.347240124
SLC6A2, SLC6A3, SLC6A4	22.93989071	0.631233037
CHAT, SLC6A3	310.962963	0.640817187
CRH, SLC6A2	219.503268	0.765611406
CRH, CALM1	207.308642	0.784794172
GRIN2A, CALM1	120.3727599	0.929110665
GRIN2A, CRH	103.654321	0.953762791
CHRNA4, SLC6A3	100.8528529	0.957551035
GRIN2A, CRH	98.19883041	0.961029104
GRIN2A, CHRNA4	71.76068376	0.988231166
GRIN2A, SLC6A4	60.18637993	0.994999269
CHRNA4, SLC6A3	44.42328042	0.99924053
CHRNA4, SLC6A4	21.69509044	0.999999606
ADRB1, DRD1, ADRB2, DRD5	209.9	8.10E-05
DRD1, ADRB2, DRD5	125.94	0.033062621
DRD1, DRD5	2099	0.143679704
ADRB1, ADRB2	1399.333333	0.207587448
ADRB1, ADRB2	1399.333333	0.207587448
DRD1, DRD5	599.7142857	0.418979157
ADRB1, ADRB2	466.4444444	0.502492252
DRD1, DRD5	466.4444444	0.502492252
DRD1, DRD5	419.8	0.539636476
ADRB1, ADRB2	349.8333333	0.605817815
DRD1, DRD5	349.8333333	0.605817815
DRD1, DRD5	322.9230769	0.635252753
DRD1, DRD5	262.375	0.711021816
ADRB1, DRD1	220.9473684	0.771060883
ADRB1, ADRB2	220.9473684	0.771060883

DRD1, DRD5	209.9	0.788163416
PRKCB, PRKCD	144.7586207	0.894697399
DRD1, DRD5	135.4193548	0.909851446
ADRB1, ADRB2	131.1875	0.916590488
ADRB1, ADRB2	116.6111111	0.938874461
ADRB1, DRD1	104.95	0.955208296
DRD1, DRD5	73.64912281	0.988060645
ACHE, DRD1	68.81967213	0.991254467
PRKCB, DRD5	45.13978495	0.999277123
PRKCB, PRKCD	36.50434783	0.999870136
PRKCB, PRKCD	33.584	0.999940535
GRIN2B, DRD5	17.49166667	0.999999993
BCL2, PSEN1	279.8666667	0.78409962
BCL2, PSEN1	262.375	0.805083262
BACE1, PSEN1	190.8181818	0.894471953
BCL2, PSEN1	127.2121212	0.965757047
BCL2, PSEN1, SQSTM1	13.83956044	0.968828286
MAPT, PSEN1	39.98095238	0.999978756
SULT1E1, NR1I2, AKR1C3, CYP1B1	312.4093023	5.62E-06
AKR1C1, AKR1C3, CYP1B1	839.6	2.53E-04
SULT1E1, CYP1B1	610.6181818	0.210160045
AKR1C1, AKR1C3, CYP1B1	17.01891892	0.473431333
AKR1C3, CYP1B1	223.8933333	0.474705482
AKR1C1, AKR1C3	110.1114754	0.730251162
THBD, PLAT, F2	91.26086957	0.005241166
THBD, F2	1399.333333	0.041068816
THBD, F2	1119.466667	0.05107269
PLAT, F2	533.0793651	0.104277443
F7, F10	2238.933333	0.017124888
F7, F10	1017.69697	0.037294631
F7, F10	447.7866667	0.082788841
F7, F10	133.2698413	0.25239085
F7, F10	69.96666667	0.426105943
F7, F10	60.84057971	0.472215655
F7, F10	60.84057971	0.472215655
NQO1, SOD1	466.4444444	0.337083232
S100B, GFAP	147.2982456	0.728242393
NQO1, MBP	65.85098039	0.945977373
NQO1, SOD1	53.30793651	0.972871797
MBP, S100B	46.64444444	0.983825919
MBP, SOD1	42.08521303	0.98967235

NQO1, SOD1	33.92323232	0.996581774
S100B, SOD1	18.65777778	0.999968542