

Table S3. Pearson correlation coefficients of PD-GBO drug response score and specific inter-individual KEGG pathway enrichment levels from RNA-seq of glioblastoma tumor tissue.

	Patient ID			
	MA01	MA02	MA03	MA04
N_GLYCAN_BIOSYNTHESIS	-0.575057848	1.439325655	-0.097342393	-0.766925414
OTHER_GLYCAN_DEGRADATION	0.108933002	-0.261672798	1.282188339	-1.129448543
O_GLYCAN_BIOSYNTHESIS	-0.6064274	-0.506166616	1.493609241	-0.381015225
GLYCOSAMINOGLYCAN_DEGRADATION	-0.28818805	-0.126198375	1.39360873	-0.979222306
GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE	0.163788922	-0.032738805	1.151749416	-1.282799533
GLYCEROLIPID_METABOLISM	0.484891581	0.318766881	0.67991343	-1.483571892
GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	-0.807092358	-0.904789107	1.035787229	0.676094235
GLYCEROPHOSPHOLIPID_METABOLISM	0.458856872	0.846101862	0.12921858	-1.434177314
ETHER_LIPID_METABOLISM	-0.694294278	-0.148602199	1.456009886	-0.613113409
ARACHIDONIC_ACID_METABOLISM	-0.550610942	0.058327646	1.380217054	-0.887933758
LINOLEIC_ACID_METABOLISM	1.29336618	-0.517374964	0.227815194	-1.00380641
ALPHA_LINOLENIC_ACID_METABOLISM	-0.331681031	1.487682653	-0.643644329	-0.512357293
SPHINGOLIPID_METABOLISM	0.161265938	-1.193721475	1.228983028	-0.196527491
GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	-0.245763043	-1.292928521	0.564223256	0.974468308
GLYCOSPHINGOLIPID_BIOSYNTHESIS_GLOBO_SERIES	-0.979853933	0.639918677	1.056706701	-0.716771446
GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	-0.046390879	-0.224392121	1.341798219	-1.07101522
RIBOFLAVIN_METABOLISM	-0.866089182	-0.787779502	1.188633232	0.465235452
NICOTINATE_AND_NICOTINAMIDE_METABOLISM	-0.453035563	1.148670766	0.43747218	-1.133107383
PANTOTHENATE_AND_COA_BIOSYNTHESIS	-0.592613981	0.684824599	0.996864619	-1.089075236
AMINOACYL_TRNA_BIOSYNTHESIS	0.934070134	0.510744386	-1.363854319	-0.080960201
BASAL_TRANSCRIPTION_FACTORS	-0.006598709	1.000850067	-1.364301474	0.370050116
NON_HOMOLOGOUS_END_JOINING	0.120717757	0.735760943	-1.447382416	0.590903716
SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	-0.832386664	0.085379249	1.378698412	-0.631690996
LYSOSOME	-0.006928037	-0.003313716	1.229843003	-1.21960125
CARDIAC_MUSCLE_CONTRACTION	0.630025264	0.021489719	-1.419002769	0.767487786
RENIN_ANGIOTENSIN_SYSTEM	-0.555677024	0.321968448	1.248280272	-1.014571696
CIRCADIAN_RHYTHM_MAMMAL	0.057360381	0.476155473	0.879467655	-1.412983509
TASTE_TRANSDUCTION	-0.615506676	1.098039899	-1.047194883	0.56466166
PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	0.956767941	-0.339838488	-1.25154583	0.634616376
PATHOGENIC_ESCHERICHIA_COLI_INFECTION	0.134886696	0.701596219	0.616098064	-1.452580979
SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.376308432	0.886586153	-1.429853702	0.166959118
PRIMARY_IMMUNODEFICIENCY	-0.841748028	0.314989765	1.276666991	-0.749908728
HYPERTROPHIC_CARDIOMYOPATHY_HCM	-0.242761243	0.362857251	1.123630598	-1.243726607
ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	0.053451961	0.109793727	1.13734468	-1.300590368

DILATED_CARDIOMYOPATHY	-0.433575213	0.325484343	1.215990068	-1.107899198
GLYCOLYSIS_GLUONEOGENESIS	0.966052474	-0.194436708	0.544579546	-1.316195313
CITRATE_CYCLE_TCA_CYCLE	0.477538893	1.128870435	-1.125177243	-0.481232084
PENTOSE_PHOSPHATE_PATHWAY	0.583826661	0.995383912	-0.330582258	-1.248628315
PENTOSE_AND_GLUCURONATE_INTER CONVERSIONS	-0.571307765	0.070152349	1.378209676	-0.87705426
FRUCTOSE_AND_MANNOSE_METABOL ISM	1.370911296	-0.933916783	0.05801636	-0.495010873
GALACTOSE_METABOLISM	0.717505951	0.576955891	0.163475986	-1.457937828
ASCORBATE_AND_ALDARATE_METAB OLISM	-0.667337578	0.174344137	1.342567752	-0.849574311
FATTY_ACID_METABOLISM	0.441271629	-0.938665897	1.197508273	-0.700114005
STEROID_BIOSYNTHESIS	-0.131556609	1.441068575	-0.498865915	-0.810646051
PRIMARY_BILE_ACID_BIOSYNTHESIS	-0.633997106	-0.225526325	1.473264299	-0.613740868
STEROID_HORMONE_BIOSYNTHESIS	-0.624347641	-0.187600721	1.465541527	-0.653593165
OXIDATIVE_PHOSPHORYLATION	0.636781135	0.862204997	-0.146321193	-1.352664939
PURINE_METABOLISM	-1.347387155	-0.115357586	0.506173134	0.956571607
PYRIMIDINE_METABOLISM	0.266200994	0.832335118	-1.452862126	0.354326015
ALANINE_ASPARTATE_AND_GLUTAM ATE_METABOLISM	-0.205619403	1.047658133	-1.28866517	0.44662644
GLYCINE_SERINE_AND_THREONINE_ METABOLISM	0.483176388	-0.223863684	1.028532771	-1.287845475
CYSTEINE_AND_METHIONINE_METAB OLISM	0.741076605	0.483461064	-1.468809731	0.244272062
VALINE_LEUCINE_AND_ISOLEUCINE_ DEGRADATION	1.05572676	0.413534682	-1.298131157	-0.171130286
VALINE_LEUCINE_AND_ISOLEUCINE_ BIOSYNTHESIS	0.543772034	1.132595587	-0.928834267	-0.747533354
LYSINE_DEGRADATION	0.210351392	0.740966147	-1.464147245	0.512829705
ARGININE_AND_PROLINE_METABOLIS M	-0.199938433	0.633549915	0.893291027	-1.326902509
HISTIDINE_METABOLISM	-1.127104345	-0.079973861	1.308777034	-0.101698829
TYROSINE_METABOLISM	-0.622154593	-0.480037101	1.493187875	-0.390996181
PHENYLALANINE_METABOLISM	-0.842616366	1.214288529	0.425077549	-0.796749713
TRYPTOPHAN_METABOLISM	-0.924005774	0.462728739	1.186072239	-0.724795204
BETA_ALANINE_METABOLISM	-0.49448818	-0.583550782	-0.418546685	1.496585647
TAURINE_AND_HYPOTAURINE_META BOLISM	0.002878292	0.36845834	-1.367887568	0.996550936
SELENOAMINO_ACID_METABOLISM	1.109627873	0.404819687	-1.235800471	-0.27864709
GLUTATHIONE_METABOLISM	-0.528627157	1.273720984	0.268001984	-1.01309581
STARCH_AND_SUCROSE_METABOLIS M	-0.489426631	0.046229936	1.37487904	-0.931682345
AMINO_SUGAR_AND_NUCLEOTIDE_SU GAR_METABOLISM	0.619786023	-0.122246606	0.864142758	-1.361682175
GLYCOSAMINOGLYCAN_BIOSYNTHES IS_CHONDROITIN_SULFATE	0.313262933	0.620719043	0.552914164	-1.48689614
GLYCOSAMINOGLYCAN_BIOSYNTHES IS_HEPARAN_SULFATE	1.008447893	-1.161324892	0.634413255	-0.481536255
INOSITOL_PHOSPHATE_METABOLISM	0.654871142	-1.489399355	0.369229328	0.465298884
PYRUVATE_METABOLISM	0.159035873	0.672784369	-1.45900799	0.627187748
GLYOXYLATE_AND_DICARBOXYLATE _METABOLISM	1.4114758	-0.532858741	-0.850291291	-0.028325768

PROPANOATE_METABOLISM	1.390872252	-0.520387983	-0.891202273	0.020718004
BUTANOATE_METABOLISM	0.86467464	-0.335944815	-1.264290218	0.735560394
ONE_CARBON_POOL_BY_FOLATE	0.075565674	1.1145528	-1.317510237	0.127391763
FOLATE_BIOSYNTHESIS	0.659596739	-1.450043457	0.668996173	0.121450545
RETINOL_METABOLISM	-0.40005026	-0.348121883	1.478370946	-0.730198802
PORPHYRIN_AND_CHLOROPHYLL_ME TABOLISM	-0.555946963	0.11622094	1.355806712	-0.916080688
TERPENOID_BACKBONE_BIOSYNTHES IS	0.149095649	0.875871251	-1.430454437	0.405487537
LIMONENE_AND_PINENE_DEGRADATI ON	-1.34378239	0.96074394	-0.123012762	0.506051212
NITROGEN_METABOLISM	1.115410275	-0.91094323	-0.774966368	0.570499323
SULFUR_METABOLISM	-0.356473229	0.558994659	1.025669705	-1.228191135
METABOLISM_OF_XENOBIOTICS_BY_ CYTOCHROME_P450	-0.551637168	-0.080324149	1.431677058	-0.799715741
DRUG_METABOLISM_CYTOCHROME_P 450	-0.401264737	-0.101007491	1.413600178	-0.91132795
DRUG_METABOLISM_OTHER_ENZYME S	-0.418610854	-0.149598056	1.433224704	-0.865015793
BIOSYNTHESIS_OF_UNSATURATED_FA TTY_ACIDS	0.886755378	0.577019145	-1.368045999	-0.095728523
ABC_TRANSPORTERS	1.418526216	-0.930258063	-0.204131473	-0.28413668
RIBOSOME	-1.166945585	0.45922198	1.120972233	-0.413248627
RNA_DEGRADATION	-0.106739471	0.4578519	-1.341175868	0.990063439
RNA_POLYMERASE	1.020243495	-0.685188447	-1.014135184	0.679080136
DNA_REPLICATION	-0.10409618	0.786681442	-1.375056379	0.692471117
SPLICEOSOME	-0.303043324	0.761218626	-1.283542165	0.825366863
PROTEASOME	0.119592033	1.364622169	-0.637087618	-0.847126583
PROTEIN_EXPORT	0.932846871	0.425987883	-1.395348622	0.036513868
PPAR_SIGNALING_PATHWAY	-0.312585618	-0.117864093	1.397543512	-0.967093801
BASE_EXCISION_REPAIR	-0.038516298	0.937460876	-1.375656105	0.476711527
NUCLEOTIDE_EXCISION_REPAIR	-0.112498953	0.942653075	-1.351605553	0.521451431
MISMATCH_REPAIR	0.123222837	0.607722776	-1.449065999	0.718120386
HOMOLOGOUS_RECOMBINATION	0.203186025	0.640092258	-1.468882716	0.625604433
MAPK_SIGNALING_PATHWAY	-0.481881891	0.164777578	1.318371241	-1.001266929
ERBB_SIGNALING_PATHWAY	0.280191199	-1.478079771	0.697190323	0.500698248
CALCIUM_SIGNALING_PATHWAY	0.371691361	-1.35779269	1.008825144	-0.022723815
CYTOKINE_CYTOKINE_RECEPTOR_INT ERACTION	-0.566683501	0.180792644	1.326904853	-0.941013996
CHEMOKINE_SIGNALING_PATHWAY	-0.615449076	0.035672004	1.397110108	-0.817333035
PHOSPHATIDYLINOSITOL_SIGNALING _SYSTEM	1.14338741	-1.184383654	0.400669297	-0.359673053
NEUROACTIVE_LIGAND_RECEPTOR_I NTERACTION	-0.110064399	-1.360840688	0.570805098	0.900099989
CELL_CYCLE	-0.171595535	0.596380118	-1.335927951	0.911143368
OOCYTE_MEIOSIS	-0.253106099	0.790570795	-1.309525548	0.772060852
P53_SIGNALING_PATHWAY	-1.011252676	0.62599804	-0.676649368	1.061904004
UBIQUITIN_MEDIATED_PROTEOLYSIS	-0.598660893	0.419050534	-1.016963054	1.196573413
REGULATION_OF_AUTOPHAGY	-0.937901217	0.577726841	1.107909966	-0.74773559
ENDOCYTOSIS	-0.001527888	-0.813599092	1.409021973	-0.593894993
PEROXISOME	0.687315796	0.709987612	0.024980171	-1.422283579
MTOR_SIGNALING_PATHWAY	-1.064694913	0.508149747	1.130721208	-0.574176042

APOPTOSIS	-0.403177734	0.045145891	1.35615571	-0.998123867
VASCULAR_SMOOTH_MUSCLE_CONTRACTION	-0.59077067	0.071623384	1.380087622	-0.860940336
WNT_SIGNALING_PATHWAY	-1.18444026	0.933601696	0.714498713	-0.463660148
DORSO_VENTRAL_AXIS_FORMATION	0.083889114	-1.113215538	1.296953868	-0.267627444
NOTCH_SIGNALING_PATHWAY	0.518047112	-1.306122224	-0.203934323	0.992009435
HEDGEHOG_SIGNALING_PATHWAY	-0.030239825	0.218088318	-1.30509713	1.117248638
TGF_BETA_SIGNALING_PATHWAY	-0.926182445	-0.155963339	1.41638477	-0.334238986
AXON_GUIDANCE	0.221411079	-0.98895265	1.29984659	-0.532305019
VEGF_SIGNALING_PATHWAY	-0.020432105	0.11596032	1.173213557	-1.268741772
FOCAL_ADHESION	-0.230878637	0.304160673	1.157405927	-1.230687963
ECM_RECEPTOR_INTERACTION	-0.276988094	0.648421501	0.917425573	-1.28885898
CELL_ADHESION_MOLECULES_CAMS	-0.144801638	-0.425297397	1.433014708	-0.862915672
ADHERENS_JUNCTION	-0.071077522	-0.356142002	1.391924788	-0.964705264
TIGHT_JUNCTION	-0.912688742	0.907693682	0.821972656	-0.816977596
GAP_JUNCTION	-0.418608482	-0.91499536	1.407848757	-0.074244914
COMPLEMENT_AND_COAGULATION_CASCADES	-0.2062586	-0.219217053	1.39993758	-0.974461927
ANTIGEN_PROCESSING_AND_PRESENTATION	-0.124325456	0.018893954	1.273090345	-1.167658843
TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	-0.138802556	0.111974206	1.231575853	-1.204747503
NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	-0.207314427	-0.078621504	1.349193423	-1.063257492
RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	-0.155607542	0.27089918	1.145631756	-1.260923394
CYTOSOLIC_DNA_SENSING_PATHWAY	0.135327037	-0.354264834	1.29947229	-1.080534493
JAK_STAT_SIGNALING_PATHWAY	-0.507669086	0.070238079	1.367990442	-0.930559435
HEMATOPOIETIC_CELL_LINEAGE	-0.550919364	0.168600777	1.330233014	-0.947914427
NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	-0.382662515	-0.063914609	1.3958432	-0.949266076
T_CELL_RECEPTOR_SIGNALING_PATHWAY	-0.789051319	0.321198883	1.27430748	-0.806455045
B_CELL_RECEPTOR_SIGNALING_PATHWAY	-0.027948041	-0.217312022	1.33133143	-1.086071368
FC_EPSILON_RI_SIGNALING_PATHWAY	-0.337091564	0.416558718	1.124244644	-1.203711798
FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	0.00998236	-0.426193775	1.376789422	-0.960578006
LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	-0.030077588	-0.171183278	1.315031243	-1.113770377
INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	-0.104291667	0.163321679	1.18718278	-1.246212792
LONG_TERM_POTENTIATION	0.283858874	-1.365159092	0.055284415	1.026015803
NEUROTROPHIN_SIGNALING_PATHWAY	-0.402266619	-0.28228617	1.465706371	-0.781153583
LONG_TERM_DEPRESSION	0.318687133	-1.461812893	0.338997484	0.804128276
OLFACTORY_TRANSDUCTION	0.374687179	-1.356476584	1.009366291	-0.027576885
REGULATION_OF_ACTIN_CYTOSKELETON	-0.377154266	-0.048253566	1.388488833	-0.963081001
INSULIN_SIGNALING_PATHWAY	0.413649766	0.690848383	0.380934805	-1.485432953
GNRH_SIGNALING_PATHWAY	-0.710893743	0.942019053	0.773403243	-1.004528553

PROGESTERONE_MEDIATED_OOCYTE_MATURATION	-0.709300295	0.561265811	-0.967836077	1.115870561
MELANOGENESIS	-1.125098755	0.50227884	1.11388003	-0.491060115
ADIPOCYTOKINE_SIGNALING_PATHWAY	0.341531899	-0.027676686	1.033311323	-1.347166535
TYPE_II_DIABETES_MELLITUS	-0.822087475	-0.902961584	0.760212674	0.964836386
TYPE_I_DIABETES_MELLITUS	-0.086758667	0.822600952	0.643283256	-1.379125542
MATURITY_ONSET_DIABETES_OF_THE_YOUNG	0.078252968	-1.415026623	0.446921001	0.889852655
ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	-0.88372673	0.055966879	1.381687135	-0.553927284
VASOPRESSIN_REGULATED_WATER_REABSORPTION	0.38913634	-1.278540063	1.084384878	-0.194981155
ALZHEIMERS_DISEASE	0.508268966	0.255362945	0.710174333	-1.473806243
PARKINSONS_DISEASE	0.502165132	1.055090295	-0.319230053	-1.238025373
AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	0.066802896	-0.916373991	1.372126711	-0.522555616
HUNTINGTONS_DISEASE	0.114075855	1.371458131	-0.779398144	-0.706135842
PRION_DISEASES	-0.360804174	-0.655154819	1.488924493	-0.4729655
VIBRIO_CHOLERAЕ_INFECTION	0.848217136	-0.954245546	0.878944624	-0.772916214
EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	0.058441482	-0.209150639	1.288096096	-1.137386939
LEISHMANIA_INFECTION	0.031522268	0.073832804	1.169616458	-1.274971531
PATHWAYS_IN_CANCER	-0.593591357	0.230546303	1.305932783	-0.942887729
COLORECTAL_CANCER	-1.138469405	1.291433438	0.033944638	-0.186908671
RENAL_CELL_CARCINOMA	-0.504503364	0.042573274	1.379218973	-0.917288884
PANCREATIC_CANCER	-1.215686328	1.067832717	0.504571494	-0.356717883
ENDOMETRIAL_CANCER	0.693594217	-1.480940996	0.482508495	0.304838284
GLIOMA	0.805274854	-1.411082445	0.005517411	0.600290181
PROSTATE_CANCER	-0.199160612	-0.150954151	1.374277487	-1.024162724
THYROID_CANCER	-0.555858107	-0.303451163	1.48552701	-0.626217741
BASAL_CELL_CARCINOMA	0.367190297	1.055651598	-1.319093335	-0.10374856
MELANOMA	-0.835450188	-0.464973779	1.437698847	-0.137274879
BLADDER_CANCER	-1.074286915	0.497647618	1.134486899	-0.557847602
CHRONIC_MYELOID_LEUKEMIA	-0.983945564	0.331955072	1.250416999	-0.598426507
ACUTE_MYELOID_LEUKEMIA	-0.353578166	-0.24189878	1.446470614	-0.850993668
SMALL_CELL_LUNG_CANCER	-0.560471941	0.815651021	0.869412575	-1.124591654
NON_SMALL_CELL_LUNG_CANCER	-0.913781211	0.118441274	-0.560112042	1.355451978
ASTHMA	0.103681206	0.388841627	0.919234835	-1.411757668
AUTOIMMUNE_THYROID_DISEASE	-0.138450103	0.054663904	1.261387536	-1.177601337
ALLOGRAFT_REJECTION	-0.027729161	0.681467694	0.750429634	-1.404168167
GRAFT_VERSUS_HOST_DISEASE	-0.144256999	0.384136965	1.063879579	-1.303759545
VIRAL_MYOCARDITIS	-0.417244488	0.889591754	0.744381715	-1.21672898
MAPK_SIGNALING_PATHWAY	-0.24587582	-0.122486808	1.379316568	-1.01095394
ERBB_SIGNALING_PATHWAY	0.037444441	-1.379668605	0.982824771	0.359399393
PI3KAKT_SIGNALING_PATHWAY	-0.257816757	-0.158080147	1.395815462	-0.979918559
HERPES_SIMPLEX_VIRUS_1_INFECTION	-0.202612444	0.601807728	0.922252886	-1.321448171
PROTEIN_DIGESTION_AND_ABSORPTION	-0.827646482	0.059224558	1.388267142	-0.619845218
STAPHYLOCOCCUS_AUREUS_INFECTION	-0.355348728	0.144314438	1.295187874	-1.084153584

HUMAN_PAPILLOMAVIRUS_INFECTION

-0.064583518 0.479861077 0.949801196 -1.365078754