

**Supplementary**

**Table S1** Seventy-eight DECRGs

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GNAI3  
 F2R  
 MAPK3  
 VASP  
 TLN2  
 ITPR1  
 TFPI  
 PRKACB  
 RHOA  
 PPP1CC  
 GNAI2  
 COL3A1  
 PIK3CB  
 GNA13  
 PROCR  
 FCER1G  
 ITGB1  
 PROS1  
 PLAU  
 MAPK1  
 ADCY1  
 PRKCZ  
 RAP1B  
 SNAP23  
 FCGR2A  
 ITGB3  
 ORAI1  
 GNAQ  
 VAMP8  
 F2RL3  
 ADCY5  
 ACTB  
 VSIG4  
 MYL12A  
 SERPIND1  
 CFI

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**Table S1** (*continued*)

**Table S1** (*continued*)

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SERPINE1  
 SERPINA5  
 PLCB1  
 GNAI1  
 C1QC  
 C1QB  
 C1R  
 AKT3  
 TBXA2R  
 COL1A1  
 C1QA  
 A2M  
 LYN  
 F2RL2  
 MAPK11  
 COL1A2  
 F7  
 SERPINA1  
 PLAT  
 C5AR1  
 PLA2G4A  
 PRKG2  
 RASGRP1  
 GP6  
 SERPING1  
 FERMT3  
 BTK  
 LCP2  
 PLAUR  
 C3AR1  
 PTGS1  
 PIK3R6  
 ITGB2  
 PIK3R5  
 PLA2G4C  
 SYK

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**Table S1** (*continued*)

**Table S1** (*continued*)

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CD55  
 MASP1  
 C1S  
 C2  
 VWF  
 PLCB4

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**Table S2** Results of Cox proportional-hazards analysis of 78 DECRGs

ID	HR	HR.95L	HR.95H	P value
<i>GNAI3</i>	0.551770053	0.273499215	1.113166603	0.096800072
<i>F2R</i>	0.775899099	0.593316252	1.014668669	0.063798715
<i>MAPK3</i>	1.21250931	0.696978822	2.109359394	0.495180377
<i>VASP</i>	1.438397342	0.853508034	2.424097762	0.172210576
<i>TLN2</i>	1.202281395	0.898716731	1.608382824	0.214700903
<i>ITPR1</i>	1.245164625	0.935128407	1.657991494	0.133390079
<i>TFPI</i>	1.054191263	0.86191657	1.289358226	0.607493658
<i>PRKACB</i>	0.758105566	0.485359399	1.18412057	0.223538073
<i>RHOA</i>	0.847491967	0.429475282	1.672372459	0.633259636
<i>PPP1CC</i>	0.527676003	0.311556254	0.893713288	0.017408849
<i>GNAI2</i>	1.146608514	0.618864695	2.124391801	0.663697631
<i>COL3A1</i>	1.011405679	0.89156794	1.14735109	0.860094618
<i>PIK3CB</i>	1.072420757	0.724656523	1.5870778	0.726633346
<i>GNA13</i>	0.835090365	0.479215382	1.455245268	0.524790899
<i>PROCR</i>	1.064800977	0.829362721	1.367075095	0.622384638
<i>FCER1G</i>	1.160405459	0.945380961	1.424336732	0.154795878
<i>ITGB1</i>	1.192643305	0.784957593	1.812069934	0.409106447
<i>PROS1</i>	1.095814309	0.870640353	1.379225068	0.435612168
<i>PLAU</i>	1.140223894	0.967941119	1.343171091	0.116392432
<i>MAPK1</i>	0.790976093	0.512586469	1.220561246	0.289395426
<i>ADCY1</i>	1.120182416	0.947919955	1.323749583	0.182808448
<i>PRKCZ</i>	1.048887916	0.915807827	1.201306461	0.490512387
<i>RAP1B</i>	1.099820065	0.806733429	1.499385215	0.547348292
<i>SNAP23</i>	0.704044482	0.440094441	1.126300599	0.143243572
<i>FCGR2A</i>	1.208942818	0.974305851	1.500086175	0.084793591
<i>ITGB3</i>	1.158978788	0.982509453	1.367143926	0.080015335
<i>ORAI1</i>	0.990148795	0.726575676	1.349335891	0.950012344
<i>GNAQ</i>	1.432439583	0.899659137	2.280733973	0.129927305
<i>VAMP8</i>	1.034838477	0.864604733	1.238589882	0.708812853
<i>F2RL3</i>	1.13434333	0.953243653	1.349848789	0.155493485
<i>ADCY5</i>	1.034117236	0.907691474	1.178151926	0.614088273
<i>ACTB</i>	1.629194034	0.901268471	2.945041668	0.106131852
<i>VSIG4</i>	1.051569809	0.911837062	1.212715637	0.48941751
<i>MYL12A</i>	1.316815337	0.982354594	1.765149411	0.065638765
<i>SERPIND1</i>	1.036791486	0.884444382	1.215380648	0.655897601
<i>CFI</i>	1.176799568	0.987418243	1.402503178	0.068983353
<i>SERPINE1</i>	1.22194552	1.063369719	1.404169056	0.00470851
<i>SERPINA5</i>	1.15787248	1.026679917	1.305829262	0.016889347
<i>PLCB1</i>	0.990980912	0.844617267	1.162707899	0.911526095
<i>GNAI1</i>	1.084724806	0.915479834	1.285258136	0.347394815
<i>C1QC</i>	1.056252626	0.876084726	1.273472275	0.566277912
<i>C1QB</i>	1.066678925	0.893126108	1.273956634	0.476184039
<i>C1R</i>	1.116567731	0.942705662	1.322494972	0.201688331
<i>AKT3</i>	0.84042205	0.61766966	1.143506422	0.268517613
<i>TBXA2R</i>	1.086996136	0.818365689	1.443805152	0.564637348
<i>COL1A1</i>	1.067437984	0.949188434	1.20041902	0.275961642
<i>C1QA</i>	1.065739815	0.891996249	1.273325258	0.483171115
<i>A2M</i>	1.053895194	0.814746253	1.363240489	0.689340313
<i>LYN</i>	1.042620925	0.809939016	1.342148447	0.745988088
<i>F2RL2</i>	1.216390579	1.046148037	1.414337157	0.010883047
<i>MAPK11</i>	1.299299648	0.949427288	1.778103069	0.101893236
<i>COL1A2</i>	1.078247385	0.94907661	1.224998499	0.247203968
<i>F7</i>	0.913839055	0.792231192	1.054113783	0.21621905
<i>SERPINA1</i>	1.161159229	0.986006034	1.367426475	0.073287221
<i>PLAT</i>	1.215937967	1.009971467	1.46390783	0.03894702
<i>C5AR1</i>	1.184148041	1.003044776	1.397950137	0.045948874
<i>PLA2G4A</i>	0.931709905	0.735289427	1.180600883	0.558171118
<i>PRKG2</i>	0.958917102	0.856329518	1.073794595	0.467430807
<i>RASGRP1</i>	0.896158711	0.765260815	1.049446697	0.173547667
<i>GP6</i>	1.300612143	1.015587159	1.665629514	0.037295673
<i>SERPING1</i>	1.197359491	0.996658022	1.438477109	0.054329274
<i>FERMT3</i>	1.168374024	0.933760928	1.461935084	0.173611413
<i>BTK</i>	1.063806864	0.887970977	1.274461749	0.502214504

Table S2 (continued)

**Table S2** (continued)

ID	HR	HR.95L	HR.95H	P value
<i>LCP2</i>	1.157082352	0.910147917	1.471013166	0.233551142
<i>PLAUR</i>	1.455616805	1.170014386	1.81093524	0.000754501
<i>C3AR1</i>	1.132863296	0.924156821	1.388702889	0.229841884
<i>PTGS1</i>	0.998495045	0.831250014	1.199389278	0.987152651
<i>PIK3R6</i>	1.120655221	0.914658803	1.373045469	0.271682048
<i>ITGB2</i>	1.152648747	0.943798615	1.407714646	0.163665488
<i>PIK3R5</i>	1.151532858	0.924807878	1.433841507	0.207229711
<i>PLA2G4C</i>	1.027679733	0.798267348	1.323022464	0.832231861
<i>SYK</i>	1.073535869	0.864615454	1.332938541	0.520490024
<i>CD55</i>	1.293774768	0.98100589	1.70626208	0.068129714
<i>MASP1</i>	0.938225623	0.81256062	1.083325105	0.384791553
<i>C1S</i>	1.126969364	0.962813124	1.319113662	0.136707911
<i>C2</i>	1.10031775	0.939986061	1.28799692	0.234150199
<i>VWF</i>	1.049546166	0.849709925	1.296380238	0.653627321
<i>PLCB4</i>	0.964133614	0.830116949	1.119786347	0.632415323

**Table S3** Five DECRGs for Constructing prognostic models

ID	coef	HR	HR.95L	HR.95H	P value
<i>PLAUR</i>	0.620525403	1.859904984	1.242161575	2.784860375	0.002587999
<i>F2RL2</i>	0.167867131	1.182779446	1.002057255	1.396095095	0.047227244
<i>SERPINA5</i>	0.167400635	1.182227812	1.023562128	1.365488778	0.022804205
<i>GP6</i>	0.41341397	1.511970808	1.128160826	2.026356234	0.005655756
<i>C5AR1</i>	-0.382499028	0.682154554	0.491188329	0.947365417	0.022451587

**Table S4** Results of the univariate Cox proportional-hazards regression of clinical phenotype data

ID	HR	HR.95L	HR.95H	P value
Riskscore	2.186119197	1.585121146	3.014985419	1.86E-06
Treatment_type	2.619332193	1.569358798	4.371786201	0.000229339
Age	1.389548365	0.828851743	2.329541652	0.212063665
Gender	1.109938841	0.674702538	1.825936855	0.681303975

**Table S5** Results of the multivariate Cox proportional-hazards regression of clinical phenotype data

ID	HR	HR.95L	HR.95H	P value
Riskscore	2.109099534	1.502707305	2.960191137	1.60E-05
Treatment_type	1.997626474	1.197266328	3.333019091	0.008066355

**Table S6** The annotation table of *PLAUR*, *SERPINA5*, *GP6*, *F2RL2*, and *C5AR1* in the Metascape database

MyList	Gene ID	Type	Tax ID	Homologene Gene ID	Homologene Gene Tax ID	Gene Symbol	Description	Biological Process (GO)	Protein Function (Protein Atlas)	Subcellular Location (Protein Atlas)	Drug (DrugBank)	Canonical Pathways	Hallmark Gene Sets	hsa04610 Complement and coagulation cas	R-HSA-109582 Hemostasis	GO:0001775 cell activation
PLAUR	5329	symbol	H. sapiens	5329	H. sapiens	PLAUR	plasminogen activator, urokinase receptor	GO:0038195 urokinase plasminogen activator signaling pathway;GO:2001268 negative regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway;GO:0034112 positive regulation of homotypic cell-cell adhesion	FDA approved drug targets:Biotech drugs; Predicted intracellular proteins; Cancer-related genes:Candidate cancer biomarkers; CD markers	Plasma membrane (Supported)	Alteplase; Urokinase; Tenecteplase; WX-UK1; Lanoteplase	(M120)PID ARF6 DOWNSTREAM PATHWAY; (M212)PID INTEGRIN5 PATHWAY; (M169)PID INTEGRIN2 PATHWAY	(M5916)HALLMARK APICAL SURFACE; (M5892)HALLMARK CHOLESTEROL HOMEOSTASIS; (M5890)HALLMARK TNFA SIGNALING VIA NFKB	1	1	0
F2RL2	2151	symbol	H. sapiens	2151	H. sapiens	F2RL2	coagulation factor II thrombin receptor like 2	GO:0070493 thrombin-activated receptor signaling pathway;GO:0051482 positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-coupled signaling pathway;GO:0035025 positive regulation of Rho protein signal transduction	G-protein coupled receptors:GPCRs excl olfactory receptors			(M138)PID THROMBIN PAR4 PATHWAY; (M193)PID NEPHRIN NEPH1 PATHWAY; (M238)PID THROMBIN PAR1 PATHWAY	(M5946)HALLMARK COAGULATION; (M5947)HALLMARK IL2 STAT5 SIGNALING	1	1	1
SERPINA5	5104	symbol	H. sapiens	5104	H. sapiens	SERPINA5	serpin family A member 5	GO:0007342 fusion of sperm to egg plasma membrane involved in single fertilization;GO:0045026 plasma membrane fusion;GO:0007009 plasma membrane organization	Predicted secreted proteins; Cancer-related genes:Candidate cancer biomarkers; Candidate cardiovascular disease genes		Urokinase; Drotrecogin alfa; Tifuvirtide; PPL-100	(M3468)NABA ECM REGULATORS; (M5885)NABA MATRISOME ASSOCIATED; (M5889)NABA MATRISOME	(M5944)HALLMARK ANGIOGENESIS; (M5907)HALLMARK ESTROGEN RESPONSE LATE	1	1	0
GP6	51206	symbol	H. sapiens	51206	H. sapiens	GP6	glycoprotein VI platelet	GO:1901731 positive regulation of platelet aggregation;GO:0034112 positive regulation of homotypic cell-cell adhesion;GO:0038065 collagen-activated signaling pathway	Disease related genes; Predicted intracellular proteins; Human disease related genes:Cardiovascular diseases:Hematologic diseases	Plasma membrane (Supported)				0	1	1
C5AR1	728	symbol	H. sapiens	728	H. sapiens	C5AR1	complement C5a receptor 1	GO:0038178 complement component C5a signaling pathway;GO:0002430 complement receptor mediated signaling pathway;GO:0032494 response to peptidoglycan	Transporters; G-protein coupled receptors:Chemokines and chemotactic factors receptors; CD markers; G-protein coupled receptors:GPCRs excl olfactory receptors; Predicted intracellular proteins	Golgi apparatus (Approved); Additional: Vesicles			(M5932)HALLMARK INFLAMMATORY RESPONSE	1	0	1

**Table S7** The enrichment results of *PLAUR*, *SERPINA5*, *GP6*, *F2RL2*, and *C5AR1* from the prediction of the Metascape database

GroupID	Category	Term	Description	LogP	Log(q-value)	InTerm_InList	Genes	Symbols
1_Summary	KEGG Pathway	hsa04610	Complement and coagulation cascades	-9.53519932	-5.188	4/85	728,2151,5104,5329	C5AR1,F2RL2,SERPINA5,PLAUR
1_Member	KEGG Pathway	hsa04610	Complement and coagulation cascades	-9.53519932	-5.188	4/85	728,2151,5104,5329	C5AR1,F2RL2,SERPINA5,PLAUR
1_Member	WikiPathways	WP558	Complement and coagulation cascades	-7.150945508	-3.105	3/59	728,5104,5329	C5AR1,SERPINA5,PLAUR
2_Summary	Reactome Gene Sets	R-HSA-109582	Hemostasis	-6.059852365	-2.190	4/621	2151,5104,5329,51206	F2RL2,SERPINA5,PLAUR,GP6
2_Member	Reactome Gene Sets	R-HSA-109582	Hemostasis	-6.059852365	-2.190	4/621	2151,5104,5329,51206	F2RL2,SERPINA5,PLAUR,GP6
2_Member	GO Biological Processes	GO:0007596	blood coagulation	-5.744571215	-2.138	3/172	2151,5329,51206	F2RL2,PLAUR,GP6
2_Member	GO Biological Processes	GO:0050817	coagulation	-5.729464215	-2.138	3/174	2151,5329,51206	F2RL2,PLAUR,GP6
2_Member	GO Biological Processes	GO:0007599	hemostasis	-5.707129015	-2.138	3/177	2151,5329,51206	F2RL2,PLAUR,GP6
2_Member	GO Biological Processes	GO:0042060	wound healing	-4.895389532	-1.393	3/330	2151,5329,51206	F2RL2,PLAUR,GP6
2_Member	GO Biological Processes	GO:0050878	regulation of body fluid levels	-4.743262959	-1.299	3/371	2151,5329,51206	F2RL2,PLAUR,GP6
2_Member	GO Biological Processes	GO:0009611	response to wounding	-4.536791776	-1.144	3/435	2151,5329,51206	F2RL2,PLAUR,GP6
3_Summary	GO Biological Processes	GO:0001775	cell activation	-4.023193713	-0.676	3/647	728,2151,51206	C5AR1,F2RL2,GP6
3_Member	GO Biological Processes	GO:0001775	cell activation	-4.023193713	-0.676	3/647	728,2151,51206	C5AR1,F2RL2,GP6

**Table S8** Single-cell analysis results of signature genes (PLAUR, SERPINA5, GP6, F2RL2, and C5AR1)

Name	Gene	ExpID	Cancer	State	Correlation	Pvalue
F2RL2_EXP0057	F2RL2	EXP0057	GBM	Angiogenesis	-0.04	0.667
F2RL2_EXP0057	F2RL2	EXP0057	GBM	Apoptosis	-0.113	0.225
F2RL2_EXP0057	F2RL2	EXP0057	GBM	CellCycle	0.005	0.954
F2RL2_EXP0057	F2RL2	EXP0057	GBM	Differentiation	-0.025	0.788
F2RL2_EXP0057	F2RL2	EXP0057	GBM	DNAdamage	0.02	0.826
F2RL2_EXP0057	F2RL2	EXP0057	GBM	DNArepair	0.008	0.934
F2RL2_EXP0057	F2RL2	EXP0057	GBM	EMT	0.006	0.945
F2RL2_EXP0057	F2RL2	EXP0057	GBM	Hypoxia	0.012	0.897
F2RL2_EXP0057	F2RL2	EXP0057	GBM	Inflammation	0.037	0.693
F2RL2_EXP0057	F2RL2	EXP0057	GBM	Invasion	-0.049	0.601
F2RL2_EXP0057	F2RL2	EXP0057	GBM	Metastasis	0.012	0.893
F2RL2_EXP0057	F2RL2	EXP0057	GBM	Proliferation	0.084	0.368
F2RL2_EXP0057	F2RL2	EXP0057	GBM	Quiescence	-0.055	0.557
F2RL2_EXP0057	F2RL2	EXP0057	GBM	Stemness	0.04	0.668
F2RL2_EXP0058	F2RL2	EXP0058	GBM	Angiogenesis	0.055	0.253
F2RL2_EXP0058	F2RL2	EXP0058	GBM	Apoptosis	-0.111	0.022
F2RL2_EXP0058	F2RL2	EXP0058	GBM	CellCycle	-0.102	0.034
F2RL2_EXP0058	F2RL2	EXP0058	GBM	Differentiation	0.025	0.605
F2RL2_EXP0058	F2RL2	EXP0058	GBM	DNAdamage	-0.211	0
F2RL2_EXP0058	F2RL2	EXP0058	GBM	DNArepair	-0.208	0
F2RL2_EXP0058	F2RL2	EXP0058	GBM	EMT	-0.289	0
F2RL2_EXP0058	F2RL2	EXP0058	GBM	Hypoxia	-0.206	0
F2RL2_EXP0058	F2RL2	EXP0058	GBM	Inflammation	-0.103	0.033
F2RL2_EXP0058	F2RL2	EXP0058	GBM	Invasion	-0.351	0
F2RL2_EXP0058	F2RL2	EXP0058	GBM	Metastasis	-0.255	0
F2RL2_EXP0058	F2RL2	EXP0058	GBM	Proliferation	0.035	0.462
F2RL2_EXP0058	F2RL2	EXP0058	GBM	Quiescence	-0.094	0.051
F2RL2_EXP0058	F2RL2	EXP0058	GBM	Stemness	-0.166	0.001
C5AR1_EXP0057	C5AR1	EXP0057	GBM	Angiogenesis	-0.117	0.026
C5AR1_EXP0057	C5AR1	EXP0057	GBM	Apoptosis	0.021	0.685
C5AR1_EXP0057	C5AR1	EXP0057	GBM	CellCycle	-0.209	0
C5AR1_EXP0057	C5AR1	EXP0057	GBM	Differentiation	-0.029	0.578
C5AR1_EXP0057	C5AR1	EXP0057	GBM	DNAdamage	-0.11	0.036
C5AR1_EXP0057	C5AR1	EXP0057	GBM	DNArepair	-0.229	0
C5AR1_EXP0057	C5AR1	EXP0057	GBM	EMT	-0.082	0.12
C5AR1_EXP0057	C5AR1	EXP0057	GBM	Hypoxia	-0.007	0.888
C5AR1_EXP0057	C5AR1	EXP0057	GBM	Inflammation	0.086	0.102
C5AR1_EXP0057	C5AR1	EXP0057	GBM	Invasion	-0.184	0
C5AR1_EXP0057	C5AR1	EXP0057	GBM	Metastasis	-0.068	0.194
C5AR1_EXP0057	C5AR1	EXP0057	GBM	Proliferation	-0.125	0.017
C5AR1_EXP0057	C5AR1	EXP0057	GBM	Quiescence	0.049	0.352
C5AR1_EXP0057	C5AR1	EXP0057	GBM	Stemness	-0.172	0.001
C5AR1_EXP0058	C5AR1	EXP0058	GBM	Angiogenesis	0.046	0.339
C5AR1_EXP0058	C5AR1	EXP0058	GBM	Apoptosis	-0.055	0.25
C5AR1_EXP0058	C5AR1	EXP0058	GBM	CellCycle	-0.082	0.086
C5AR1_EXP0058	C5AR1	EXP0058	GBM	Differentiation	0.038	0.43
C5AR1_EXP0058	C5AR1	EXP0058	GBM	DNAdamage	-0.129	0.007
C5AR1_EXP0058	C5AR1	EXP0058	GBM	DNArepair	-0.117	0.015
C5AR1_EXP0058	C5AR1	EXP0058	GBM	EMT	-0.206	0
C5AR1_EXP0058	C5AR1	EXP0058	GBM	Hypoxia	-0.037	0.444
C5AR1_EXP0058	C5AR1	EXP0058	GBM	Inflammation	-0.059	0.217
C5AR1_EXP0058	C5AR1	EXP0058	GBM	Invasion	-0.252	0
C5AR1_EXP0058	C5AR1	EXP0058	GBM	Metastasis	-0.126	0.009
C5AR1_EXP0058	C5AR1	EXP0058	GBM	Proliferation	0.073	0.127
C5AR1_EXP0058	C5AR1	EXP0058	GBM	Quiescence	-0.103	0.032
C5AR1_EXP0058	C5AR1	EXP0058	GBM	Stemness	-0.181	0
PLAUR_EXP0057	PLAUR	EXP0057	GBM	Angiogenesis	0.23	0
PLAUR_EXP0057	PLAUR	EXP0057	GBM	Apoptosis	0.141	0.003
PLAUR_EXP0057	PLAUR	EXP0057	GBM	CellCycle	-0.031	0.527
PLAUR_EXP0057	PLAUR	EXP0057	GBM	Differentiation	0.069	0.151
PLAUR_EXP0057	PLAUR	EXP0057	GBM	DNAdamage	-0.03	0.534
PLAUR_EXP0057	PLAUR	EXP0057	GBM	DNArepair	0.015	0.763
PLAUR_EXP0057	PLAUR	EXP0057	GBM	EMT	0.253	0

Table S8 (continued)

Table S8 (continued)

Name	Gene	ExpID	Cancer	State	Correlation	Pvalue
PLAUR_EXP0057	PLAUR	EXP0057	GBM	Hypoxia	0.324	0
PLAUR_EXP0057	PLAUR	EXP0057	GBM	Inflammation	0.316	0
PLAUR_EXP0057	PLAUR	EXP0057	GBM	Invasion	0.152	0.002
PLAUR_EXP0057	PLAUR	EXP0057	GBM	Metastasis	0.344	0
PLAUR_EXP0057	PLAUR	EXP0057	GBM	Proliferation	-0.007	0.886
PLAUR_EXP0057	PLAUR	EXP0057	GBM	Quiescence	0.085	0.078
PLAUR_EXP0057	PLAUR	EXP0057	GBM	Stemness	-0.35	0
PLAUR_EXP0058	PLAUR	EXP0058	GBM	Angiogenesis	0.098	0.036
PLAUR_EXP0058	PLAUR	EXP0058	GBM	Apoptosis	-0.112	0.016
PLAUR_EXP0058	PLAUR	EXP0058	GBM	CellCycle	-0.052	0.269
PLAUR_EXP0058	PLAUR	EXP0058	GBM	Differentiation	-0.058	0.22
PLAUR_EXP0058	PLAUR	EXP0058	GBM	DNAdamage	-0.086	0.065
PLAUR_EXP0058	PLAUR	EXP0058	GBM	DNArepair	-0.084	0.072
PLAUR_EXP0058	PLAUR	EXP0058	GBM	EMT	-0.108	0.021
PLAUR_EXP0058	PLAUR	EXP0058	GBM	Hypoxia	-0.068	0.145
PLAUR_EXP0058	PLAUR	EXP0058	GBM	Inflammation	0.052	0.271
PLAUR_EXP0058	PLAUR	EXP0058	GBM	Invasion	-0.219	0
PLAUR_EXP0058	PLAUR	EXP0058	GBM	Metastasis	-0.052	0.265
PLAUR_EXP0058	PLAUR	EXP0058	GBM	Proliferation	0.034	0.471
PLAUR_EXP0058	PLAUR	EXP0058	GBM	Quiescence	-0.093	0.048
PLAUR_EXP0058	PLAUR	EXP0058	GBM	Stemness	-0.203	0
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	Angiogenesis	0.055	0.328
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	Apoptosis	-0.17	0.002
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	CellCycle	-0.214	0
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	Differentiation	0.055	0.328
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	DNAdamage	-0.244	0
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	DNArepair	-0.266	0
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	EMT	-0.179	0.001
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	Hypoxia	-0.177	0.002
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	Inflammation	0.043	0.449
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	Invasion	-0.294	0
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	Metastasis	-0.151	0.007
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	Proliferation	0.05	0.372
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	Quiescence	-0.008	0.893
SERPINA5_EXP0058	SERPINA5	EXP0058	GBM	Stemness	-0.174	0.002
GP6_EXP0057	GP6	EXP0057	GBM	Angiogenesis	0.053	0.559
GP6_EXP0057	GP6	EXP0057	GBM	Apoptosis	0.13	0.155
GP6_EXP0057	GP6	EXP0057	GBM	CellCycle	-0.046	0.618
GP6_EXP0057	GP6	EXP0057	GBM	Differentiation	0.056	0.543
GP6_EXP0057	GP6	EXP0057	GBM	DNAdamage	-0.052	0.57
GP6_EXP0057	GP6	EXP0057	GBM	DNArepair	-0.1	0.272
GP6_EXP0057	GP6	EXP0057	GBM	EMT	-0.079	0.387
GP6_EXP0057	GP6	EXP0057	GBM	Hypoxia	0.022	0.813
GP6_EXP0057	GP6	EXP0057	GBM	Inflammation	-0.02	0.83
GP6_EXP0057	GP6	EXP0057	GBM	Invasion	-0.125	0.171
GP6_EXP0057	GP6	EXP0057	GBM	Metastasis	-0.192	0.034
GP6_EXP0057	GP6	EXP0057	GBM	Proliferation	-0.012	0.898
GP6_EXP0057	GP6	EXP0057	GBM	Quiescence	-0.029	0.749
GP6_EXP0057	GP6	EXP0057	GBM	Stemness	0.104	0.256
GP6_EXP0058	GP6	EXP0058	GBM	Angiogenesis	0.138	0.013
GP6_EXP0058	GP6	EXP0058	GBM	Apoptosis	-0.148	0.008
GP6_EXP0058	GP6	EXP0058	GBM	CellCycle	-0.209	0
GP6_EXP0058	GP6	EXP0058	GBM	Differentiation	0.178	0.001
GP6_EXP0058	GP6	EXP0058	GBM	DNAdamage	-0.256	0
GP6_EXP0058	GP6	EXP0058	GBM	DNArepair	-0.312	0
GP6_EXP0058	GP6	EXP0058	GBM	EMT	-0.212	0
GP6_EXP0058	GP6	EXP0058	GBM	Hypoxia	-0.267	0
GP6_EXP0058	GP6	EXP0058	GBM	Inflammation	0.066	0.241
GP6_EXP0058	GP6	EXP0058	GBM	Invasion	-0.338	0
GP6_EXP0058	GP6	EXP0058	GBM	Metastasis	-0.172	0.002
GP6_EXP0058	GP6	EXP0058	GBM	Proliferation	0.123	0.027
GP6_EXP0058	GP6	EXP0058	GBM	Quiescence	-0.003	0.954
GP6_EXP0058	GP6	EXP0058	GBM	Stemness	-0.186	0.001