

ID	Descriptio	setSize	enrichment	NES	pvalue	p.adjust	qvalues
hsa05165	Human papi	321	0.4535176	1.5168867	0.001001	0.0102477	0.0054098
hsa05016	Huntingtor	269	0.4404965	1.4626777	0.001006	0.0102477	0.0054098
hsa05131	Shigellosi	212	0.4757418	1.5658992	0.001007	0.0102477	0.0054098
hsa05132	Salmonella	212	0.479945	1.579734	0.001007	0.0102477	0.0054098
hsa05020	Prion dise	240	0.4396212	1.4531522	0.0010081	0.0102477	0.0054098
hsa05166	Human T-ce	215	0.5028772	1.6542871	0.0010081	0.0102477	0.0054098
hsa04144	Endocytosi	233	0.4833499	1.5943948	0.0010091	0.0102477	0.0054098
hsa04810	Regulator	209	0.4567972	1.5006145	0.0010091	0.0102477	0.0054098
hsa05170	Human immu	198	0.4541426	1.4872467	0.0010111	0.0102477	0.0054098
hsa05169	Epstein-Ba	192	0.5056904	1.6547689	0.0010121	0.0102477	0.0054098
hsa05130	Pathogenic	182	0.4960999	1.616796	0.0010132	0.0102477	0.0054098
hsa04621	NOD-like r	167	0.4721422	1.5300177	0.0010194	0.0102477	0.0054098
hsa05152	Tuberculos	168	0.5362255	1.7376987	0.0010194	0.0102477	0.0054098
hsa05203	Viral carc	161	0.4844461	1.5674392	0.0010235	0.0102477	0.0054098
hsa04218	Cellular s	153	0.489643	1.5808431	0.0010246	0.0102477	0.0054098
hsa05164	Influenza	158	0.4596661	1.487073	0.0010246	0.0102477	0.0054098
hsa05206	MicroRNAs	158	0.5086495	1.6455401	0.0010246	0.0102477	0.0054098
hsa03013	RNA transp	152	0.4779992	1.5435713	0.0010256	0.0102477	0.0054098
hsa04145	Phagosome	145	0.6062024	1.9532161	0.0010256	0.0102477	0.0054098
hsa03040	Spliceosom	132	0.5179121	1.6556848	0.0010406	0.0102477	0.0054098
hsa04110	Cell cycle	123	0.6030942	1.9167031	0.0010406	0.0102477	0.0054098
hsa03010	Ribosome	127	0.5559621	1.7708309	0.0010417	0.0102477	0.0054098
hsa04380	Osteoclast	122	0.5291945	1.6810332	0.0010417	0.0102477	0.0054098
hsa04142	Lysosome	128	0.5245409	1.6687912	0.0010449	0.0102477	0.0054098
hsa04512	ECM-recept	86	0.5554744	1.706101	0.0010684	0.0102477	0.0054098
hsa05323	Rheumatoic	88	0.6431027	1.9764459	0.0010695	0.0102477	0.0054098
hsa04666	Fc gamma F	87	0.5544505	1.7004796	0.001073	0.0102477	0.0054098
hsa03008	Ribosome b	71	0.5534781	1.6709042	0.0010834	0.0102477	0.0054098
hsa05140	Leishmania	71	0.6154584	1.8580177	0.0010834	0.0102477	0.0054098
hsa04612	Antigen pr	65	0.5894278	1.762247	0.0010893	0.0102477	0.0054098
hsa05100	Bacterial	65	0.5467699	1.6347101	0.0010893	0.0102477	0.0054098
hsa03460	Fanconi ar	48	0.5505983	1.585471	0.0011236	0.0102477	0.0054098
hsa04672	Intestinal	45	0.5937936	1.6978776	0.0011261	0.0102477	0.0054098
hsa05320	Autoimmune	45	0.5664258	1.6196231	0.0011261	0.0102477	0.0054098
hsa04940	Type I dia	41	0.5848803	1.6441119	0.0011494	0.0102477	0.0054098
hsa05219	Bladder ca	41	0.6465432	1.8174476	0.0011494	0.0102477	0.0054098
hsa03030	DNA replic	36	0.655346	1.7971769	0.0011587	0.0102477	0.0054098
hsa05310	Asthma	28	0.693903	1.8476145	0.0011765	0.0102477	0.0054098
hsa05200	Pathways i	516	0.3894626	1.3218613	0.001998	0.0147347	0.0077785
hsa05010	Alzheimer	332	0.4097425	1.3726759	0.002002	0.0147347	0.0077785
hsa05014	Amyotrophi	327	0.4074267	1.3630543	0.002004	0.0147347	0.0077785
hsa04060	Cytokine-c	282	0.4042104	1.3434671	0.0020101	0.0147347	0.0077785
hsa05012	Parkinson	214	0.4258017	1.4006152	0.0020182	0.0147347	0.0077785
hsa04668	TNF signal	111	0.4872861	1.5355801	0.0020921	0.0147347	0.0077785
hsa05145	Toxoplasma	108	0.4948755	1.5555628	0.0020964	0.0147347	0.0077785
hsa04658	Th1 and Th	90	0.5134139	1.5834196	0.0021299	0.0147347	0.0077785
hsa04657	IL-17 sigr	93	0.5235706	1.6220295	0.0021322	0.0147347	0.0077785
hsa04640	Hematopoie	92	0.5200986	1.6056066	0.0021368	0.0147347	0.0077785
hsa03050	Proteasome	44	0.5568883	1.5869139	0.0022624	0.015283	0.008068
hsa03440	Homologous	37	0.5646549	1.5551169	0.0023202	0.0153596	0.0081084

hsa05163	Human cytochrome	212	0.433618	1.427249	0.0030211	0.0189634	0.0100109
hsa04015	Rap1 signaling	207	0.4326736	1.4197072	0.0030303	0.0189634	0.0100109
hsa04062	Chemokine	189	0.4439228	1.4521324	0.0030364	0.0189634	0.0100109
hsa04933	AGE-RAGE signaling	99	0.4951643	1.5477114	0.0031546	0.0193364	0.0102078
hsa00232	Caffeine metabolism	5	-0.952029	-1.882854	0.0037594	0.0226247	0.0119437
hsa04510	Focal adhesion	197	0.4361227	1.4274144	0.0040445	0.0233386	0.0123206
hsa04141	Protein processing	163	0.4516493	1.4620669	0.0040858	0.0233386	0.0123206
hsa00072	Synthesis	10	-0.811109	-2.051631	0.0041322	0.0233386	0.0123206
hsa05135	Yersinia infection	125	0.4638739	1.4738078	0.0041797	0.0233386	0.0123206
hsa05120	Epithelial	69	0.5148075	1.5571464	0.0043011	0.0233386	0.0123206
hsa05230	Central carbon	69	0.5144033	1.5559238	0.0043011	0.0233386	0.0123206
hsa05416	Viral myocytolysis	57	0.5256095	1.5498304	0.0044248	0.0236226	0.0124705
hsa05332	Graft-versus	36	0.573052	1.5714994	0.004635	0.0243521	0.0128556
hsa05162	Measles	132	0.4554392	1.4559685	0.0052029	0.0267047	0.0140976
hsa00120	Primary biliary	17	-0.904342	-2.607291	0.0053191	0.0267047	0.0140976
hsa04620	Toll-like	95	0.4829092	1.4992889	0.0053248	0.0267047	0.0140976
hsa00220	Arginine biosynthesis	21	-0.810452	-2.507095	0.0054645	0.0267453	0.0141119
hsa00053	Ascorbate	19	-0.707744	-2.120635	0.0054945	0.0267453	0.0141119
hsa00340	Histidine	22	-0.821071	-2.594334	0.005618	0.02695	0.0142271
hsa00040	Pentose	24	-0.517127	-1.672129	0.005848	0.0276525	0.0145979
hsa00591	Linoleic acid	25	-0.773121	-2.487519	0.0059524	0.0277498	0.0146493
hsa00650	Butanoate	26	-0.805173	-2.627552	0.006135	0.0278175	0.014685
hsa04950	Maturity onset	26	-0.516514	-1.685561	0.006135	0.0278175	0.014685
hsa00410	beta-Alanine	29	-0.720841	-2.388366	0.0067114	0.0282809	0.0149297
hsa00630	Glyoxylate	29	-0.692604	-2.29481	0.0067114	0.0282809	0.0149297
hsa00250	Alanine, aspartate	34	-0.544471	-1.879822	0.0068493	0.0282809	0.0149297
hsa00020	Citrate cycle	30	-0.470949	-1.57461	0.0068966	0.0282809	0.0149297
hsa05340	Primary immunodeficiency	34	0.5583156	1.5179755	0.0070093	0.0282809	0.0149297
hsa00640	Propanoate	33	-0.697913	-2.365583	0.0070423	0.0282809	0.0149297
hsa00760	Nicotinate	33	-0.440816	-1.49415	0.0070423	0.0282809	0.0149297
hsa00860	Porphyrin	33	-0.441138	-1.495241	0.0070423	0.0282809	0.0149297
hsa00350	Tyrosine metabolism	36	-0.764205	-2.665297	0.0071942	0.0282809	0.0149297
hsa04625	C-type lectin	102	0.4637085	1.4536796	0.0073222	0.0282809	0.0149297
hsa00260	Glycine, serine	38	-0.812756	-2.8379	0.0074074	0.0282809	0.0149297
hsa00620	Pyruvate	38	-0.547086	-1.910261	0.0074074	0.0282809	0.0149297
hsa00380	Tryptophan	42	-0.789632	-2.851053	0.0074627	0.0282809	0.0149297
hsa04975	Fat digestion	42	-0.545201	-1.968511	0.0074627	0.0282809	0.0149297
hsa00071	Fatty acid	43	-0.860306	-3.151222	0.0075188	0.0282809	0.0149297
hsa04914	Progesterone	91	0.4628383	1.4273774	0.0085562	0.0310216	0.0163765
hsa00270	Cysteine	49	-0.507322	-1.896175	0.0086957	0.0310216	0.0163765
hsa00140	Steroid hormone	51	-0.737302	-2.763698	0.0088496	0.0310216	0.0163765
hsa00830	Retinol metabolism	52	-0.836335	-3.151115	0.0088496	0.0310216	0.0163765
hsa04979	Cholesterol	50	-0.556904	-2.086402	0.0088496	0.0310216	0.0163765
hsa00330	Arginine	48	-0.502682	-1.853957	0.0089286	0.0310216	0.0163765
hsa04623	Cytosolic	53	0.524409	1.5277511	0.0089586	0.0310216	0.0163765
hsa05110	Vibrio cholerae	49	0.52018	1.4935103	0.0090192	0.0310216	0.0163765
hsa00280	Valine, leucine	47	-0.75276	-2.758385	0.0090909	0.0310216	0.0163765
hsa04064	NF-kappa B	99	0.4607527	1.4401526	0.0094637	0.0317415	0.0167565
hsa04061	Viral protein	97	0.4650014	1.4485724	0.0094937	0.0317415	0.0167565
hsa05150	Staphylococcus	84	0.4758035	1.4592894	0.009636	0.0318951	0.0168376
hsa05205	Proteoglycan	198	0.4209615	1.3785838	0.0101112	0.0327918	0.017311

hsa00590	Arachidoni	56	-0.48698	-1.834197	0.0102041	0.0327918	0.017311
hsa01212	Fatty acid	56	-0.538917	-2.029814	0.0102041	0.0327918	0.017311
hsa00982	Drug metab	58	-0.806647	-3.093366	0.0103093	0.0328031	0.017317
hsa04650	Natural ki	114	0.450367	1.424513	0.0104058	0.0328031	0.017317
hsa00360	Phenylalar	17	-0.66264	-1.910445	0.0106383	0.0332196	0.0175368
hsa05321	Inflammatc	63	0.4983318	1.4835685	0.0109529	0.0336793	0.0177795
hsa00310	Lysine deg	60	-0.425712	-1.643743	0.010989	0.0336793	0.0177795
hsa00980	Metabolism	64	-0.760185	-2.972792	0.0114943	0.0349046	0.0184263
hsa00010	Glycolysis	65	-0.477323	-1.878179	0.0119048	0.0357318	0.018863
hsa05211	Renal cell	66	0.4888732	1.4653312	0.0119826	0.0357318	0.018863
hsa05204	Chemical c	67	-0.794663	-3.129247	0.0121951	0.0360409	0.0190262
hsa04114	Oocyte mei	118	0.4516066	1.4317428	0.012487	0.0365769	0.0193092
hsa00983	Drug metab	68	-0.522893	-2.056139	0.0126582	0.0367533	0.0194023
hsa04664	Fc epsilon	65	0.4921575	1.4714322	0.0130719	0.0375454	0.0198204
hsa03320	PPAR signa	75	-0.685438	-2.73843	0.0131579	0.0375454	0.0198204
hsa01230	Biosynthes	69	-0.397162	-1.543291	0.0138889	0.0386321	0.0203941
hsa03015	mRNA surve	92	0.4575021	1.4123635	0.0138889	0.0386321	0.0203941
hsa04920	Adipocytok	69	-0.436383	-1.695697	0.0138889	0.0386321	0.0203941
hsa04659	Th17 cell	104	0.4479328	1.4060178	0.0146597	0.0404363	0.0213466
hsa04976	Bile secre	82	-0.61826	-2.489994	0.0149254	0.0404448	0.021351
hsa04540	Gap juncti	84	0.4671779	1.4328346	0.0149893	0.0404448	0.021351
hsa02010	ABC transp	43	-0.433901	-1.589341	0.0150376	0.0404448	0.021351
hsa04146	Peroxisome	81	-0.653444	-2.622469	0.0151515	0.0404448	0.021351
hsa05202	Transcript	167	0.423414	1.3721098	0.0152905	0.0404893	0.0213745
hsa04514	Cell adhes	138	0.4333077	1.3911269	0.0155119	0.0407495	0.0215119
hsa04670	Leukocyte	109	0.4449478	1.4001649	0.0157068	0.0409366	0.0216107
hsa04610	Complement	83	-0.690815	-2.769248	0.015873	0.0410466	0.0216688
hsa04260	Cardiac mu	80	0.4625944	1.4134818	0.01606	0.0412081	0.021754
hsa05330	Allograft	35	0.5370848	1.469554	0.0162791	0.041449	0.0218812
hsa04151	PI3K-Akt s	344	0.3751756	1.2584184	0.0180361	0.0453411	0.0239358
hsa05222	Small cell	92	0.4509947	1.3922744	0.0181624	0.0453411	0.0239358
hsa05167	Kaposi sar	185	0.4085907	1.3343302	0.0182186	0.0453411	0.0239358
hsa05161	Hepatitis	156	0.4176635	1.350271	0.0184615	0.0456028	0.024074
hsa00520	Amino suga	46	0.5129374	1.4715624	0.0191226	0.0468858	0.0247513
hsa04217	Necroptosi	124	0.428601	1.3626916	0.0198123	0.0482197	0.0254554
hsa04931	Insulin re	105	-0.400815	-1.736655	0.0212766	0.0510902	0.0269708
hsa00600	Sphingolip	47	0.5046469	1.4527467	0.0213004	0.0510902	0.0269708
hsa04390	Hippo sigr	153	0.4156388	1.3419161	0.0215164	0.0512369	0.0270482
hsa04922	Glucagon s	102	-0.401346	-1.707105	0.0217391	0.0513975	0.0271331
hsa04926	Relaxin si	128	0.4229212	1.3454949	0.0219436	0.0515129	0.027194
hsa04961	Endocrine	53	0.4940943	1.4394356	0.0223964	0.0522057	0.0275597
hsa04066	HIF-1 sigr	105	0.4368019	1.3718093	0.0230366	0.0533226	0.0281493
hsa03430	Mismatch r	22	0.5815784	1.4663912	0.0242718	0.055677	0.0293922
hsa01200	Carbon met	114	-0.405064	-1.756154	0.0243902	0.055677	0.0293922
hsa04120	Ubiquitin	132	0.4190255	1.3395596	0.024974	0.0566191	0.0298896
hsa04152	AMPK signa	119	-0.316338	-1.343334	0.0263158	0.0592553	0.0312812
hsa00770	Pantothena	20	-0.542418	-1.660635	0.0265957	0.059481	0.0314004
hsa04210	Apoptosis	134	0.4168494	1.3338149	0.026999	0.0599776	0.0316625
hsa00500	Starch and	30	-0.443917	-1.484229	0.0275862	0.0608736	0.0321355
hsa04923	Regulator	54	-0.397144	-1.503375	0.0277778	0.0608904	0.0321444
hsa00561	Glycerolip	58	-0.363224	-1.392908	0.0309278	0.0673494	0.0355542

hsa04330	Notch sigr	52	0.4814323	1.3951404	0.0326209	0.0705721	0.0372554
hsa04974	Protein di	99	0.4298129	1.3434458	0.0336488	0.0723231	0.0381798
hsa04115	p53 signal	72	0.4525861	1.3664272	0.0346696	0.0740363	0.0390842
hsa04915	Estrogen s	133	0.4063425	1.3002431	0.0353063	0.0749128	0.0395469
hsa01210	2-Oxocarbo	18	-0.54227	-1.595333	0.0378378	0.0797728	0.0421125
hsa05133	Pertussis	73	0.4446337	1.3450983	0.0389189	0.0815327	0.0430416
hsa00601	Glycosphir	26	0.5378422	1.4071277	0.0417163	0.0865679	0.0456997
hsa05235	PD-L1 expr	87	0.4347953	1.3335014	0.0418455	0.0865679	0.0456997
hsa00061	Fatty acid	17	-0.54679	-1.576441	0.0425532	0.0869451	0.0458988
hsa00430	Taurine ar	9	-0.679078	-1.660291	0.0425532	0.0869451	0.0458988
hsa05168	Herpes sin	452	0.3466833	1.1736636	0.045045	0.0914718	0.0482885
hsa04137	Mitophagy	64	0.4483534	1.3367962	0.0469945	0.0948487	0.0500712
hsa04071	Sphingolip	114	0.4088892	1.2933187	0.0489074	0.0981112	0.0517935

rank	leading_eccore_enricgeneSymbol
4207	tags=36%, 6696/5315/SPP1/PKM/E2F1/COL1A1/IKBKE/BAK1/ITGA3/CCNA2/CCNE1
5288	tags=45%, 2877/8479GPX2/TUBA1C/NDUFA4L2/TUBA4A/COX7B2/TUBA1B/TUBA3C/
4847	tags=45%, 80201/291CHKDC1/PYCARD/CXCL8/PFN2/ARPC1B/ITPR3/MAPK12/MAPK1
5388	tags=48%, 29108/2364PYCARD/LY96/CXCL8/ANXA2/PFN2/ARPC1B/BAK1/MAPK12/M
5344	tags=48%, 1535/8479CYBA/TUBA1C/NCF2/NDUFA4L2/TUBA4A/COX7B2/ITPR3/MAP
5351	tags=52%, 991/4316/9CDC20/MMP7/PTTG1/CCNB2/SLC2A1/E2F1/IL2RG/ICAM1/BU
6921	tags=64%, 10095/3561ARPC1B/IL2RG/DAB2/SRC/DNM1/FOLR1/CYTH4/RAB31/HRAS
3797	tags=35%, 3984/5217/LIMK1/PFN2/ARPC1B/ITGA3/ITGB4/RAC2/LPAR2/ENAH/SRC
5851	tags=47%, 10053/891/AP1M2/CCNB1/CCNB2/LIMK1/CDK1/BAK1/ITPR3/MAPK12/RA
5143	tags=52%, 1869/9641/E2F1/IKBKE/BAK1/ICAM1/CCNA2/CCNE1/MAPK12/CD3D/MAP
4182	tags=43%, 1364/29108CLDN4/PYCARD/TUBA1C/CXCL8/TUBA4A/ARPC1B/BAK1/MAPK
4189	tags=37%, 2919/29108CXCL1/PYCARD/CYBA/CXCL8/IKBKE/ITPR3/MAPK12/MAPK13
4185	tags=44%, 8877/2207/SPHK1/FCER1G/MAPK12/MAPK13/FCGR3A/SRC/RIPK2/ITGAM
5764	tags=57%, 5315/991/9PKM/CDC20/CDK1/BAK1/CCNA2/CCNE1/SRC/YWHAZ/CDKN2A/
3826	tags=40%, 4605/891/9MYBL2/CCNB1/CCNB2/FOXO1/E2F1/CXCL8/CDK1/ITPR3/CCN
5796	tags=47%, 29108/3576PYCARD/CXCL8/KPNA2/IKBKE/BAK1/ICAM1/HLA-DMA/HLA-D
2724	tags=34%, 4318/6659/MMP9/SOX4/CDCA5/E2F1/STMN1/BAK1/KIF23/CCNE1/CDC25
6495	tags=61%, 10460/5491TACC3/RPP25/EIF4EBP1/NUP62/ALYREF/RAN/NUP210/RANG
3917	tags=57%, 1535/8479CYBA/TUBA1C/NCF2/TUBA4A/TUBA1B/TUBA3C/FCGR3A/ITGA
6588	tags=70%, 6628/10262SNRPB/SF3B4/ALYREF/HSPA6/SNRPD2/SNRPD1/SNRPA1/HSP
2874	tags=50%, 991/2810/5CDC20/SFN/PLK1/CCNB1/PTTG1/CCNB2/CDC6/E2F1/CDK1/P
6453	tags=78%, 6132/6173/RPL8/RPL36A/MRPL17/MRPS12/RPS2/MRPL9/RPL17/RPSA/R
3126	tags=36%, 54209/1535TREM2/CYBA/NCF2/MAPK12/MAPK13/TYROBP/FCGR3A/CSF1/
4487	tags=51%, 10053/5535AP1M2/LAPTM4B/CTSC/GLA/LAPTM5/PPT1/CTSV/ACP5/ATP6
3494	tags=38%, 6696/1277/SPP1/COL1A1/ITGA3/ITGB4/COL1A2/HMMR/COL9A2/CD44/A
2888	tags=52%, 6364/2919/CCL20/CXCL1/CXCL6/CXCL8/CXCL5/ICAM1/CSF1/HLA-DMA/
3764	tags=46%, 8612/8877/PLPP2/SPHK1/LIMK1/MARCKSL1/ARPC1B/RAC2/FCGR3A/MAR
4903	tags=62%, 54913/6949RPP25/TCOF1/NOP56/RAN/DKC1/NXT1/GTPBP4/NHP2/POP7/
2881	tags=46%, 1535/65108CYBA/MARCKSL1/NCF2/MAPK12/MAPK13/FCGR3A/ITGAM/CYB
5731	tags=68%, 3108/972/3HLA-DMA/CD74/HLA-DRB1/HLA-DQA1/HLA-DRA/TAP1/HLA-D
5486	tags=60%, 10095/6714ARPC1B/SRC/DNM1/RHOG/WASF2/ITGA5/ARPC4/CLTA/MAD2L
4647	tags=46%, 29089/116CUBE2T/RMI2/RAD51/FANCI/FANCD2/EME1/FANCG/FAAP24/F
2867	tags=42%, 3108/7040/HLA-DMA/TGFB1/HLA-DRB1/HLA-DQA1/HLA-DRA/IL15RA/HL
3537	tags=38%, 3108/3123/HLA-DMA/HLA-DRB1/HLA-DQA1/HLA-DRA/HLA-DPA1/HLA-DQ
3537	tags=51%, 3108/3123/HLA-DMA/HLA-DRB1/HLA-DQA1/HLA-DRA/HLA-DPA1/HLA-DQ
2542	tags=46%, 4318/1869/MMP9/E2F1/CXCL8/SRC/CDKN2A/HRAS/CDK4/TYMP/MMP1/UP
4703	tags=78%, 4171/4173/MCM2/MCM4/RFC4/RNASEH2A/MCM6/FEN1/POLD1/MCM7/MCM3
2162	tags=39%, 2207/3108/FCER1G/HLA-DMA/HLA-DRB1/HLA-DQA1/HLA-DRA/HLA-DPA1
4212	tags=32%, 4318/11239MMP9/EGLN3/BIRC5/NQO1/SLC2A1/E2F1/CXCL8/EPO/IL2RG
5455	tags=41%, 25825/8479BACE2/TUBA1C/NDUFA4L2/TUBA4A/COX7B2/ITPR3/TUBA1B/
7364	tags=55%, 2877/8479GPX2/TUBA1C/NDUFA4L2/TUBA4A/PFN2/COX7B2/ITPR3/MAP
5019	tags=33%, 6364/2919/CCL20/CXCL1/CXCL6/TNFRSF21/CXCL8/EPO/CXCL5/IL2RG/
5664	tags=47%, 7345/8479UCHL1/TUBA1C/NDUFA4L2/TUBA4A/COX7B2/ITPR3/TUBA1B/
3096	tags=33%, 4318/6364/MMP9/CCL20/CXCL1/CXCL6/CXCL5/ICAM1/MAPK12/MAPK13/
4098	tags=42%, 23643/630CLY96/MAPK12/MAPK13/HLA-DMA/TGFB1/IRAK1/BIRC3/HLA-
6866	tags=60%, 3561/6300/IL2RG/MAPK12/CD3D/MAPK13/NFKBIE/HLA-DMA/HLA-DRB1/
5764	tags=48%, 4318/6280/MMP9/S100A9/CCL20/CXCL1/LCN2/CXCL6/CXCL8/CXCL5/IK
3500	tags=37%, 100133941/CD24/EPO/ITGA3/CD3D/CSF1/ITGAM/HLA-DMA/CD7/CD44/H
5664	tags=73%, 10213/5698PSMD14/PSMB9/PSMD2/PSMB2/PSME3/PSMB4/ADRM1/PSMB8/
4568	tags=57%, 5888/8438/RAD51/RAD54L/POLD1/EME1/RBBP8/BRCA1/XRCC2/XRCC3/B

6148 tags=47%, 1869/3576/E2F1/CXCL8/BAK1/ITPR3/MAPK12/RAC2/MAPK13/SRC/CDKN
 4809 tags=36%, 5909/5217/RAP1GAP/PFN2/VEGFB/MAPK12/RAC2/MAPK13/LPAR2/ENAH/
 6104 tags=49%, 6364/2919/CCL20/CXCL1/CXCL6/CXCL8/CXCL5/RAC2/SRC/HCK/PRKCD/
 3551 tags=37%, 3576/1277/CXCL8/COL1A1/ICAM1/VEGFB/MAPK12/MAPK13/COL1A2/CYB
 201 tags=100%, 10/7498/1ENAT2/XDH/CYP1A2/CYP2A6
 4373 tags=35%, 6696/1277/SPP1/COL1A1/VEGFB/ITGA3/ITGB4/RAC2/SRC/COL1A2/FLN
 5965 tags=50%, 1410/578/1CRYAB/BAK1/CKAP4/TUSC3/HSPA6/TRAF2/DDIT3/SSR2/DDO
 1005 tags=60%, 56898/3157BDH2/HMGCS1/HMGCL/ACAT1/BDH1/HMGCS2
 2911 tags=30%, 29108/3984PYCARD/LIMK1/CXCL8/MAPK12/RAC2/MAPK13/SRC/IRAK1/P
 2911 tags=36%, 2919/3576/CXCL1/CXCL8/MAPK12/MAPK13/SRC/ATP6V1F/GIT1/ATP6V0
 2385 tags=32%, 2539/5315/G6PD/PKM/SLC16A3/SLC1A5/HKDC1/PFKP/SLC2A1/HK2/GLS
 6179 tags=67%, 3383/5880/ICAM1/RAC2/HLA-DMA/ITGB2/HLA-DRB1/HLA-DQA1/HLA-DR
 3537 tags=47%, 3108/3123/HLA-DMA/HLA-DRB1/HLA-DQA1/HLA-DRA/HLA-DPA1/HLA-DQ
 5143 tags=43%, 9641/3561/IKBKE/IL2RG/BAK1/CCNE1/CD3D/IRAK1/MX2/CDK4/HSPA6/
 483 tags=71%, 3295/1109/HSD17B4/AKR1C4/AMACR/SCP2/CYP39A1/CYP27A1/BAAT/AC
 5150 tags=40%, 6696/2364SPP1/LY96/CXCL8/IKBKE/MAPK12/MAPK13/IRAK1/CTSK/CC
 893 tags=67%, 435/2805/ASL/GOT1/ACY1/GLUD1/ASS1/GLUL/GOT2/GPT2/ARG1/NAGS
 974 tags=58%, 7367/219/UGT2B17/ALDH1B1/ALDH3A2/ALDH9A1/UGT2B4/ALDH7A1/UG
 1168 tags=68%, 3067/3034/HDC/HAL/MAOA/ALDH1B1/ALDH3A2/ASPA/ALDH9A1/HNMT/MA
 974 tags=42%, 7367/9942/UGT2B17/XLB/UGP2/UGT2B4/CRYL1/UGT2B7/DCXR/UGT2B1
 358 tags=28%, 1573/84647CYP2J2/PLA2G12B/CYP1A2/CYP2E1/CYP2C9/CYP2C8/CYP3A
 1005 tags=69%, 79944/5689L2HGDH/BDH2/HMGCS1/HMGCL/ACSM1/HADH/ACADS/ECHS1/A
 734 tags=31%, 3171/3375/FOXA3/IAPP/FOXA2/NR5A2/HNF4A/GCK/PKLR/SLC2A2
 940 tags=55%, 23417/2627MLYCD/HIBCH/ALDH1B1/ALDH3A2/ALDH9A1/ACADS/ECHS1/A
 1191 tags=55%, 55902/509ACSS2/PCCA/AMT/PCCB/ACO1/MCEE/GLUL/ACAT1/HOGA1/GL
 1053 tags=47%, 8659/435/ALDH4A1/ASL/GOT1/ASPA/GLUD1/ASS1/GLUL/GOT2/GPT2/G
 1520 tags=27%, 2271/6392/FH/SDHD/ACO1/SUCLG2/PC/OGDHL/PCK2/PCK1
 6180 tags=65%, 3561/915/IL2RG/CD3D/ADA/TAP1/JAK3/CD3E/RFXANK/RFX5/CD79A/L
 1191 tags=58%, 593/55902/BCKDHA/ACSS2/PCCA/PCCB/DBT/MLYCD/HIBCH/ACACB/SUCL
 1500 tags=30%, 23410/549SIRT3/NMRK1/SIRT1/NT5E/SIRT5/NNT/ENPP1/NADK2/AOX1
 974 tags=24%, 7367/1356/UGT2B17/CP/UGT2B4/ALAS1/ALAD/UGT2B7/UGT2B15/UGT2B
 875 tags=50%, 128/1644/4ADH5/DDC/MAOA/FAH/GOT1/MAOB/GSTZ1/GOT2/DBH/HGD/AD
 4182 tags=37%, 29108/2207PYCARD/FCER1G/IKBKE/ITPR3/MAPK12/MAPK13/SRC/RELB/
 1128 tags=58%, 23464/275/GCAT/AMT/MAOA/CBS/MAOB/GAMT/GLYCTK/ALDH7A1/ALAS1/
 1191 tags=45%, 55902/98/ACSS2/ACYP2/ALDH1B1/ALDH3A2/ACACB/ALDH9A1/PC/ACAT
 952 tags=60%, 169355/111IDO2/INMT/MAOA/ALDH1B1/ALDH3A2/ALDH9A1/HADH/ECHS1
 834 tags=31%, 948/8613/CD36/PLPP3/GOT2/ACAT1/DGAT2/PLA2G12B/MTP/APOB/FA
 1242 tags=74%, 128/37/30ADH5/ACADVL/HADHB/CPT2/ALDH1B1/ALDH3A2/ALDH9A1/HA
 5072 tags=40%, 5347/891/PLK1/CCNB1/CCNB2/CDK1/PKMYT1/BUB1/CCNA2/MAPK12/MA
 824 tags=29%, 2729/2805/GCLC/GOT1/CBS/GOT2/TST/ADI1/BHMT2/SDS/CTH/AGXT2/M
 771 tags=45%, 7367/1583/UGT2B17/CYP11A1/CYP17A1/SULT1E1/HSD17B2/HSD17B8/C
 974 tags=56%, 7367/54884UGT2B17/RETSAT/DHRS4/CYP2C18/ALDH1A1/CYP26A1/CYP3
 1075 tags=46%, 1071/5590CETP/ANGPTL8/LDLR/CD36/APOE/APOC2/LIPG/ANGPTL4/LI
 1229 tags=44%, 6303/1124SAT1/SAT2/ALDH4A1/AGMAT/MAOA/ALDH1B1/GOT1/ALDH3A2
 6248 tags=55%, 29108/9641PYCARD/IKBKE/IL18/CCL5/POLR3K/IRF3/POLR2H/IRF7/CC
 5661 tags=55%, 11015/929KDELRL3/ATP6V1F/ATP6V0B/SLC12A2/SEC61A1/SEC61G/ATP
 1166 tags=66%, 64087/303MCCC2/HADHB/PCCA/PCCB/DBT/HMGCS1/HMGCL/HIBCH/ALDH
 4112 tags=42%, 2919/2364CXCL1/LY96/CXCL8/ICAM1/IRAK1/BIRC3/BCL2A1/RELB/SY
 2913 tags=32%, 6364/2919/CCL20/CXCL1/CXCL6/CXCL8/CXCL5/IL2RG/CSF1/IL18/CSF
 2162 tags=35%, 3880/3383/KRT19/ICAM1/FCGR3A/ITGAM/KRT23/C1QB/HLA-DMA/C1QC/
 3339 tags=31%, 4318/1277/MMP9/COL1A1/ITPR3/MAPK12/PLAUR/MAPK13/SRC/GPC3/CO

358 tags=18%, 1573/84647CYP2J2/PLA2G12B/EPHX2/CYP4F3/CYP4F2/CYP2B6/CYP2E1
 1313 tags=43%, 79071/37/εELOVL6/ACADVL/HADHB/CPT2/CBR4/HADH/CPT1A/ACADS/EC
 1242 tags=59%, 128/4257/εADH5/MGST1/GSTM5/FMO2/GSTO1/MGST2/UGT2B17/MAOA/MA
 6866 tags=46%, 2207/3383/FCER1G/ICAM1/RAC2/TYROBP/FCGR3A/ITGB2/SYK/HRAS/IF
 875 tags=53%, 1644/4128/DDC/MAOA/GOT1/MAOB/GOT2/PAH/HPD/GLYAT/TAT
 3615 tags=37%, 3561/3108/IL2RG/HLA-DMA/TGFB1/HLA-DRB1/HLA-DQA1/IL18/HLA-DR
 843 tags=25%, 219/224/2εALDH1B1/ALDH3A2/ALDH9A1/HADH/ECHS1/BBOX1/AADAT/AC
 610 tags=52%, 128/4257/εADH5/MGST1/GSTM5/GSTO1/MGST2/UGT2B17/AKR7L/UGT2B4
 922 tags=29%, 5236/219/εPGM1/ALDH1B1/ALDH3A2/ALDH9A1/GCK/ALDH7A1/ENO3/PKL
 4490 tags=41%, 112399/651EGLN3/SLC2A1/TGFB1/HRAS/ARNT2/HIF1A/MAP2K2/MAPK3/
 1242 tags=55%, 128/4257/εADH5/MGST1/NAT1/GSTM5/SULT1A1/GSTO1/MGST2/UGT2B17
 2951 tags=28%, 991/5347/εCDC20/PLK1/CCNB1/PTTG1/CCNB2/CDK1/PKMYT1/BUB1/ITP
 1211 tags=35%, 4257/9/294MGST1/NAT1/GSTM5/GSTO1/MGST2/UGT2B17/TPMT/UGT2B4/
 2881 tags=29%, 2207/6300/FCER1G/MAPK12/ALOX5AP/RAC2/MAPK13/SYK/HRAS/VAV1/A
 948 tags=45%, 3157/1376/HMGCS1/CPT2/CD36/AQP7/PPARA/CPT1A/ACAA1/ACADM/ACO
 999 tags=33%, 48/435/28CACO1/ASL/GOT1/CBS/ACY1/ASS1/PC/GLUL/GOT2/GPT2/ARG
 6224 tags=53%, 23381/101εSMG5/ALYREF/CSTF2/UPF3B/PPP2R1A/PELO/PABPC1/PPP2R
 834 tags=22%, 948/32/514CD36/ACACB/PRKAG2/PPARA/CPT1A/IRS1/IRS2/ACSL6/PPA
 3551 tags=34%, 3561/6300/IL2RG/MAPK12/CD3D/MAPK13/NFKBIE/HLA-DMA/TGFB1/HLA
 974 tags=38%, 7367/8671/UGT2B17/SLC4A4/NROB2/ABCC2/CA2/SLC01A2/AQP8/LDLR/
 2322 tags=26%, 84790/983/TUBA1C/CDK1/TUBA4A/ITPR3/TUBA1B/TUBA3C/SRC/HRAS/T
 445 tags=28%, 23461/1034ABCA5/ABCA10/ABCC2/ABCA9/ABCC9/ABCG2/ABCA8/ABCB11
 1830 tags=53%, 83594/582εNUDT12/ABCD3/MPV17L/PAOX/PEX13/PEX1/NOS2/PEX12/PE
 2986 tags=25%, 4318/6692/MMP9/SPINT1/ETV4/SSX1/CXCL8/BAK1/CCNA2/ETV5/ITGAM
 3537 tags=30%, 1364/3383/CLDN4/ICAM1/MPZL1/ITGAM/HLA-DMA/MPZ/ITGB2/SDC3/VC
 3779 tags=32%, 1364/4318/CLDN4/MMP9/CYBA/NCF2/ICAM1/MAPK12/RAC2/MAPK13/ITG
 1103 tags=60%, 1191/2157/CLU/F8/C8G/C1R/SERPINA1/C2/PROS1/VWF/CFI/C5/C1S/S
 5288 tags=38%, 486/483/17FXDY2/ATP1B3/COX7B2/ATP1A1/TPM4/ASPH/UQCRH/TPM2/T
 6818 tags=71%, 3108/3123/HLA-DMA/HLA-DRB1/HLA-DQA1/HLA-DRA/HLA-DPA1/HLA-DQ
 4212 tags=32%, 6696/2056/SPP1/EPO/COL1A1/IL2RG/VEGFB/ITGA3/CCNE1/ITGB4/LPA
 3826 tags=37%, 1869/578/εE2F1/BAK1/ITGA3/CCNE1/CKS2/BIRC3/ITGAV/COL4A5/LAM
 4462 tags=34%, 2919/1869/CXCL1/E2F1/CXCL8/IKBKE/BAK1/ITPR3/ICAM1/MAPK12/MA
 4093 tags=32%, 4318/332/1MMP9/BIRC5/E2F1/CXCL8/IKBKE/CCNA2/CCNE1/MAPK12/MA
 4370 tags=57%, 80201/597εHKDC1/RENB/UP1L1/GNPDA1/HK2/NPL/CHIT1/HK3/GPI/G
 4882 tags=38%, 29108/153εPYCARD/CYBB/PYGB/SQSTM1/BIRC3/IFNGR2/SLC25A6/TRAFF
 917 tags=20%, 84699/583εCREB3L3/PYGL/CD36/ACACB/PRKAG2/PPARA/CPT1A/FOXO1/
 4259 tags=34%, 8612/8877/PLPP2/SPHK1/GLA/GAL3ST1/SGPP2/NEU1/CERS5/DEGS1/SM
 3461 tags=29%, 332/174/84BIRC5/AFP/TEAD2/TGFB1/YWHAZ/ITGB2/TEAD4/BIRC3/FZD
 917 tags=20%, 84699/583εCREB3L3/PYGL/PDE3B/ACACB/PRKAG2/CAMK2B/PPARA/CPT1
 3396 tags=27%, 4318/1277/MMP9/COL1A1/VEGFB/MAPK12/MAPK13/SRC/COL1A2/TGFB1/
 5086 tags=43%, 486/483/17FXDY2/ATP1B3/DNM1/ATP1A1/PLCB1/CLTA/PLCB3/CLTB/AP
 3129 tags=30%, 112399/22εEGLN3/ALDOA/HKDC1/ENO2/PFKP/SLC2A1/ENO1/EPO/TIMP1
 4451 tags=59%, 5984/9156/RFC4/EXO1/POLD1/PCNA/RFC2/LIG1/MSH2/POLD3/RPA2/SS
 1024 tags=33%, 128/55902/ADH5/ACSS2/PCCA/AMT/PCCB/ACO1/HIBCH/GOT1/SUCLG2/M
 8241 tags=65%, 991/27338/CDC20/UBE2S/BIRC3/SAE1/UBE2M/UBE2Z/UBE2I/UBE2Q2/B
 940 tags=17%, 23417/846εMLYCD/CREB3L3/CD36/ACACB/PRKAG2/ADRA1A/HNF4A/CPT1
 843 tags=45%, 1806/7964εDPYD/PANK3/ALDH1B1/ALDH3A2/ENPP1/PANK1/ALDH2/DPYS
 3099 tags=31%, 332/84790/BIRC5/TUBA1C/CTSC/TUBA4A/BAK1/ITPR3/TUBA1B/LMNB2/
 926 tags=33%, 178/5236/εAGL/PGM1/PYGL/ENPP1/TREH/UGP2/GCK/GBA3/GYS2/G6PC
 1865 tags=28%, 196883/364ADCY4/INSR/NPY1R/ADCY8/ADRB1/NPR1/ADCY1/PDE3B/AQP
 843 tags=26%, 219/224/2εALDH1B1/ALDH3A2/ALDH9A1/LPIN2/PNPLA3/PLPP3/LIPG/T

6359 tags=58%, 196403/306DTX3/HDAC1/PSENEN/NUMBL/HDAC2/DVL3/HEYL/DTX2/JAG2
3544 tags=28%, 6510/486/4SLC1A5/FXYD2/ATP1B3/COL1A1/SLC7A7/COL1A2/ATP1A1/C
3512 tags=36%, 2810/891/9SFN/CCNB1/CCNB2/RRM2/CDK1/CCNE1/CDKN2A/CDK4/GTSE1
5072 tags=33%, 4318/3880/MMP9/KRT19/ITPR3/SRC/KRT23/KRT17/PRKCD/TFF1/HRAS/
999 tags=44%, 48/2805/9EAC01/GOT1/ACY1/AADAT/GOT2/GPT2/NAGS/GPT
2196 tags=27%, 29108/2364PYCARD/LY96/CXCL6/CXCL8/CXCL5/MAPK12/MAPK13/ITGAM
3485 tags=46%, 10331/2526B3GNT3/FUT4/B3GNT5/B4GALT3/B3GALNT1/ST3GAL4/FUT3/
6866 tags=53%, 6300/915/5MAPK12/CD3D/MAPK13/NFKBIE/BATF/HRAS/IFNGR2/CD3E/H
794 tags=35%, 32/84869/7ACACB/CBR4/HSD17B8/ACSL6/ACSL5/ACSL1
360 tags=33%, 51380/570/CSAD/BAAT/CD01
8379 tags=51%, 9641/578/6IKBKE/BAK1/SRC/HLA-DMA/IRAK1/CD74/BIRC3/HLA-DRB1/
6747 tags=58%, 1869/6714/E2F1/SRC/SQSTM1/HRAS/FUNDC1/HIF1A/RAB7B/RRAS/TFE3
3975 tags=32%, 8877/2207/SPHK1/FCER1G/MAPK12/RAC2/MAPK13/S1PR2/SGPP2/HRAS/

/ITGB4/COL1A2/COL9A2/TUBG1/EIF4EBP1/ITGAV/COL4A5/LAMB1/HES6/MX2/HRAS/ATP6V1F/CDKLC2/TUBB/PLCB1/SLC25A6/CREB3L1/IFT57/PSMD14/TUBB4B/TRAF2/UQCRH/BAX/CREB3/PSMD23/SRC/RIPK2/CD44/HK2/SQSTM1/ARHGEF2/CYTH4/IL18/PRKCD/CASP4/PLCD3/PLCB1/TRAF2/CCAPK13/RIPK2/GAPDH/FLNC/IRAK1/FLNA/BIRC3/KLC2/PKN1/CYTH4/IL18/HRAS/CASP4/S100A10K12/TUBA1B/RAC2/MAPK13/TUBA3C/CYBB/C1QB/STIP1/C1QC/C1QA/KLC2/PRNP/PRKCD/TUBB/NCB1B/CCNA2/CCNE1/CD3D/TSP0/SPI1/HLA-DMA/TGFB1/ITGB2/CDKN2A/HLA-DRB1/RELB/HLA-DQA/GIT1/ASAP1/HSPA6/DNAJC6/TFRC/CXCR4/GRK6/CHMP4B/RAB11FIP5/WIPF3/HSPA8/VPS37C/AR/ITGAM/IQGAP3/ITGB2/ITGAV/HRAS/GIT1/TMSB4X/EZR/FGD3/CFL1/WASF2/CXCR4/VAV1/BDKRB2/CD3D/MAPK13/CDC25C/IRAK1/APOBEC3B/TAP1/HRAS/CHEK1/CFL1/TRAF2/APOBEC3C/CXCR4/K13/NFKBIE/HLA-DMA/IRAK1/CD44/HLA-DRB1/RELB/HLA-DQA1/HLA-DRA/SYK/TAP1/CDK4/HLA-12/TUBA1B/MAPK13/TUBA3C/LPAR2/SRC/GAPDH/IRAK1/ARHGEF2/CYTH4/IL18/NCK2/CASP4/TUB/RIPK2/CYBB/BIRC3/PKN1/IL18/PRKCD/CASP4/PLCB1/TRPV2/TRPM2/GBP5/TRAF2/CCL5/GBP2/HLA-DMA/TGFB1/IRAK1/COR01A/FCGR2A/ITGB2/CD74/HLA-DRB1/HLA-DQA1/IL18/HLA-DRA/SYHDAC11/SYK/HRAS/CDK4/HDAC7/CHEK1/CREB3L1/SCRIB/TRAF2/JAK3/MAPKAPK2/BAX/NFKB2/CRA2/CCNE1/MAPK12/MAPK13/TGFB1/E2F5/SQSTM1/CDKN2A/EIF4EBP1/CDC25A/HRAS/CDK4/CHEK1RB1/HLA-DQA1/IL18/HLA-DRA/MX2/CDK4/HLA-DPA1/IFNGR2/HLA-DQB1/SLC25A6/HLA-DMB/CCLB/MARCKS/EFNA3/CDC25C/CD44/SLC7A1/CDKN2A/GLS/IGF2BP1/EFNA4/CDC25A/HRAS/DNMT1/EZAP1/EIF3B/UBE2I/UPF3B/EIF2S2/PABPC1/NUP93/NUP37/RNPS1/NDC1/NXT1/NUP205/NUP188/NM/CYBB/HLA-DMA/COR01A/FCGR2A/ITGB2/HLA-DRB1/ITGAV/HLA-DQA1/HLA-DRA/TAP1/ATP6V1FA8/SNRPA/SF3A2/LSM4/PPIH/EFTUD2/PUF60/SNRPE/SNRPF/NCBP2/LSM7/TXNL4A/SF3B5/SNRPCKMYT1/CDC45/MCM2/BUB1/BUB1B/CCNA2/ORC6/MCM4/CCNE1/CDC25B/ORC1/TTK/TGFB1/YWHAZ/CPLP2/RPL10L/RPL39/RPL28/RPS5/MRPL12/RPL7/MRPL13/RPS21/RPL35A/RPS20/RPS3/RPL27/RSP11/TGFB1/FCGR2A/SQSTM1/RELB/ACP5/SYK/CSF1R/IFNGR2/NCF4/CTSK/NCF1/TNFRSF11B/TRVOB/CTSK/CTSA/CLTA/GM2A/TCIRG1/ATP6VOD2/NEU1/ATP6AP1/FUCA2/AP4M1/SORT1/CD63/NPCGRN/ITGAV/COL4A5/LAMB1/COMP/LAMC1/ITGA5/RELN/LAMC2/LAMA5/FRAS1/COL6A3/TNC/ITGB5TGFB1/ITGB2/HLA-DRB1/HLA-DQA1/ACP5/IL18/HLA-DRA/ATP6V1F/HLA-DPA1/HLA-DQB1/ATP6VCKS/HCK/SYK/VASP/PRKCD/ASAP1/NCF1/CFL1/WASF2/VAV1/LIMK2/ARPC4/MAPK3/ARPC3/ARPC2FBL/NOP58/RRP7A/UTP14A/UTP18/EMG1/POP1/GNL2/SNU13/DROSHA/UTP4/GNL3/UTP6/POP5/NOB/HLA-DMA/TGFB1/IRAK1/FCGR2A/ITGB2/HLA-DRB1/HLA-DQA1/HLA-DRA/HLA-DPA1/IFNGR2/NCPA1/HLA-DQB1/IFI30/HSPA6/HLA-DMB/HLA-DPB1/HSPA8/HLA-A/HSP90AB1/RFXANK/CTSS/PSME2/ARPC3/ARPC2/HCLS1/PIK3CD/ACTG1/ARPC5L/SHC1/RAC1/BCAR1/ACTB/WASF1/CLTB/CTTN/CDANCE/BRCA1/BLM/FANCA/USP1/RAD51C/TELO2/EME2/RPA2/ERCC1/FANCF/RPA1/MUS81/ATRA-DPA1/HLA-DQB1/HLA-DMB/CD86/CXCR4/HLA-DPB1/HLA-DQA2/CCL28/HLA-DRB5/IL15/TNFSF1B1/HLA-DMB/CD86/HLA-DPB1/HLA-A/CTLA4/HLA-DQA2/HLA-B/HLA-DRB5/GZMB/HLA-DOA/HLA-FB1/HLA-DMB/CD86/HLA-DPB1/HLA-A/HLA-DQA2/HLA-B/HLA-DRB5/IL1B/ICA1/GAD1/CPE/GZMB/K3A/MMP2/MAP2K2/MAPK3/E2F3/DAPK3/NRAS/FGFR3/RASSF1/E2F2/MCM5/POLA2/PCNA/RFC2/LIG1/PRIM1/POLA1/POLE4/PRIM2/POLD3/DNA2/RPA2/SSBP1/RFC5/RHLA-DQB1/HLA-DMB/HLA-DPB1/HLA-DQA2/HLA-DRB5/BAK1/VEGFB/ITGA3/CCNA2/CCNE1/RAC2/CKS2/LPAR2/RAD51/SPI1/TXNRD1/GSTP1/TGFB1/CDKTUBA3C/CSF1/GAPDH/CYBB/KLC2/HRAS/DKK1/TUBB/FZD6/PLCB1/SLC25A6/PSMD14/FZD7/TUBB4K12/TUBA1B/MAPK13/TUBA3C/SQSTM1/KLC2/NUP62/TUBB/ALYREF/TOMM40/PSMD14/TUBB4B/TRACSF1/LIF/TNFRSF12A/OSMR/TGFB1/GDF15/CLCF1/IL18/CSF1R/CSF3R/IL15RA/REL/IFNGR2/LTUBA3C/KLC2/TUBB/SLC25A6/PSMD14/TUBB4B/DDIT3/UQCRH/BAX/PSMD2/TUBA1A/CYC1/TUBB6/MMP14/CSF1/LIF/BIRC3/CREB3L1/TRAF2/CCL5/CREB3/TRAF5/MAPK3/IRF1/SOCS3/RPS6KA4/PIDRB1/LAMB1/HLA-DQA1/HLA-DRA/HLA-DPA1/IFNGR2/HLA-DQB1/HSPA6/HLA-DMB/LAMC1/HLA-DPHLA-DQA1/HLA-DRA/HLA-DPA1/IFNGR2/HLA-DQB1/HLA-DMB/JAK3/HLA-DPB1/CD3E/MAPK3/STATBKE/MAPK12/MAPK13/S100A8/MMP1/TRAF2/TRAF5/MAPK3/HSP90AB1/CCL2/CXCL3/IL1B/MAPK11LA-DRB1/HLA-DQA1/HLA-DRA/CSF1R/CSF3R/HLA-DPA1/HLA-DQB1/HLA-DMB/TFRC/CD37/ITGA5/PSMA5/PSMC4/PSMB10/PSMD13/PSMD11/PSMA7/PSMD1/PSMD7/PSMB3/PSMD4/PSMD3/PSMD9/PSMDLM/TOPBP1/BARD1/POLD3/RAD51C/BABAM1/RPA2/SSBP1/NBN/RAD51D/UIMC1/RPA1/MUS81

2A/EIF4EBP1/ITGAV/TAP1/HRAS/CDK4/PLCB1/CREB3L1/TRAF2/CCL5/CXCR4/BAX/CREB3/HLA-A
SRC/CSF1/ITGAM/EFNA3/ITGB2/EFNA4/VASP/HRAS/CSF1R/PGF/PLCB1/VAV1/APBB1IP/EFNA5/R
HRAS/PLCB1/NCF1/CCL5/JAK3/CXCR4/VAV1/GRK6/CCL26/MAPK3/GNGT1/CXCL13/STAT1/PAK1/C
B/TGFB1/COL4A5/PRKCD/HRAS/PLCD3/CDK4/COL3A1/PLCB1/BAX/SERPINE1/MMP2/MAPK3/STAT1

C/FLNA/COL9A2/BIRC3/ITGAV/COL4A5/LAMB1/VASP/HRAS/PGF/ZYX/COMP/LAMC1/VAV1/ITGA5/
ST/BAX/DNAJC5/HSPA8/SEC61A1/SEC61G/HSP90AB1/HYOU1/HSPH1/NPLOC4/MAN1B1/HSPBP1/UB

KN1/IL18/RHOG/RPS6KA1/TRAF2/WASF2/VAV1/ITGA5/WIPF3/MAP2K2/MAPK3/WIPF1/PIP5K1C/I
B/CCL5/ATP6V1C1/TCIRG1/ATP6VOD2/ATP6AP1/PAK1/ATP6V1H/LYN/CXCL3/RAC1/ATP6V1E1/AT
/SLC7A5/HRAS/SIRT6/HIF1A/MAP2K2/MAPK3/HK3/FGFR1/PIK3CD/LDHA/NRAS/PFKM/FGFR3
A/HLA-DPA1/HLA-DQB1/HLA-DMB/CD86/HLA-DPB1/HLA-A/HLA-DQA2/ACTG1/HLA-B/RAC1/HLA-D
B1/HLA-DMB/CD86/HLA-DPB1/HLA-A/HLA-DQA2/HLA-B/HLA-DRB5/IL1B/GZMB/HLA-DOA/HLA-F
JAK3/MSN/BAX/HSPA8/CD3E/STAT1/IRF3/IRF7/PIK3CD/CDK2/BBC3/CD209/BID/IL1B/IL2RA/C
OX2/CYP7A1/AKR1D1/SLC27A5/CYP8B1

L5/CD86/MAP2K2/MAPK3/STAT1/IRF3/IRF7/CCL4/PIK3CD/RAC1/IL1B/CXCL9/CCL3/MAPK11/CX
/GLS2/GPT/CPS1/OTC

T2B7/ALDH2/UGT2B15/RGN/UGT2B10

OB/ALDH7A1/CNDP1/ALDH2/AMDHD1/FTCD/UROC1

5/SORD/UGT2B10

4

CAT1/ACSM3/ALDH5A1/BDH1/ABAT/ACSM5/EHHADH/HMGCS2/ACSM2B/ACSM2A

COX1/ALDH7A1/CNDP1/ALDH2/ALDH6A1/ABAT/DPYS/EHHADH/UPB1

YCTK/GRHPR/SHMT1/CAT/HAO2/HAO1/AGXT

LS2/GPT/ALDH5A1/AGXT2/ABAT/CPS1/AGXT

CK/CD8A/BTK/IKBKG/CIITA/TAP2/PTPRC/CD4/DCLRE1C/ICOS/UNG/CD19/CD8B

G2/BCKDHB/MCEE/ACADS/ECHS1/ACSS3/ACAT1/ACOX1/ALDH6A1/ABAT/EHHADH

/ASPDH

10

H6/AOX1/HPD/ADH1A/ADH1C/TAT/ADH4/ADH1B

SYK/PRKCD/HRAS/LSP1/MAPKAPK2/NFKB2/CARD9/MAPK3/RRAS/STAT1/PAK1/IRF1/PIK3CD/BCL3

GRHPR/SDS/SHMT1/SARDH/CTH/GATM/AGXT2/PIPOX/DMGDH/DAO/AGXT/GNMT/BHMT

1/HAGH/ALDH7A1/GRHPR/LDHD/PKLR/ACOT12/ALDH2/PCK2/PCK1

/MAOB/AADAT/KMO/ACMSD/ACAT1/GCDH/ALDH7A1/TDO2/DHTKD1/CAT/HAAO/ALDH2/CYP1A1/ALDH

BP1/ABCG8/ABCG5/APOA1/MOGAT2

DH/CPT1A/ACADS/ECHS1/ECI2/ACAA1/ACADM/ACAT1/ACOX1/GCDH/ACAA2/ACSL6/ALDH7A1/ACSL

PK13/CDC25B/AURKA/CDC25C/MAD2L1/CDC25A/RPS6KA1/MAPK3/HSP90AB1/MAD2L2/ANAPC7/PIK

AT1A/CD01/BHMT/TAT

YP3A7/SRD5A1/UGT2B4/AKR1C4/UGT2B7/SRD5A2/CYP3A5/CYP1A1/UGT2B15/CYP7A1/UGT2B10/A

A7/UGT2B4/RDH5/UGT2B7/CYP3A5/CYP1A1/UGT2B15/ADH6/AOX1/UGT2B10/RDH16/CYP1A2/HSD1

PC/CYP27A1/APOB/APOC1/ABCB11/ABCG8/LPA/APOH/ABCG5/APOA2/LCAT/ANGPTL3/CYP7A1/APO

/ALDH9A1/PRODH/MAOB/GAMT/GOT2/HOGA1/ALDH7A1/ARG1/CNDP1/PRODH2/ALDH2/GATM/DAO

L4/CASP1/IL1B/POLR2K/IKBKG/POLR2L/POLR3C/POLR3D/POLR3H/MAVS/NFKBIB/CXCL10/POLR2

6V1C1/TCIRG1/ATP6VOD2/ATP6AP1/ATP6V1H/ACTG1/KCNQ1/KDELRL1/ACTB/ATP6V1E1/ATP6VOC/

1B1/ALDH3A2/ALDH9A1/BCKDHB/HADH/MCEE/ACADS/HIBADH/ECHS1/ACAA1/ACADM/ACAT1/IVD/A

K/LTB/TRAF2/PLAU/NFKB2/UBE2I/TRAF5/EDA/CARD10/TNFRSF11A/CCL13/LYN/CCL4/CARD11/C

1R/CCL5/CXCR4/CCL26/IL34/CXCL13/CCL13/CCL4/CCL2/CCL28/CXCL3/TNFRSF10C/IL2RA/CXC

FCGR2A/ITGB2/KRT17/C1QA/HLA-DRB1/PTAFR/HLA-DQA1/HLA-DRA/HLA-DPA1/HLA-DQB1/HLA-D

L1A2/FLNC/TGFB1/FLNA/CD44/ITGAV/HRAS/GPC1/FZD6/EZR/FZD7/PLAU/VAV1/MSN/ITGA5/IQG

/CYP4A11/CYP2C9/CYP2C8

HS1/ELOVL2/HSD17B8/ACAA1/ACADM/HSD17B4/ACAT1/ACOX1/ACAA2/ACSL6/SCP2/ACSL5/ACADL
OB/UGT2B4/GSTA2/FMO4/UGT2B7/FMO5/CYP3A5/GSTM1/UGT2B15/CYP2D6/ADH6/GSTA1/AOX1/UG
NGR2/HGST/VAV1/HLA-A/MAP2K2/MAPK3/PAK1/ULBP2/PIK3CD/SHC1/LCP2/HLA-B/RAC1/BID/NR

A/HLA-DPA1/IFNGR2/HLA-DQB1/HLA-DMB/HLA-DPB1/STAT1/HLA-DQA2/TGFB2/HLA-DRB5/IL1B/
AT1/GCDH/ALDH7A1/DHTKD1/AASS/ALDH2/PIPOX/EHHADH

/CYP2A13/EPHX1/GSTA2/UGT2B7/CYP3A5/CYP1A1/GSTM1/UGT2B15/AKR7A3/CYP2D6/ADH6/GSTA
R/ALDH2/PCK2/ADH6/FBP1/G6PC/ADH1A/ALDOB/ADH1C/PCK1/ADH4/ADH1B

PAK1/TFE3/PAK4/PIK3CD/TGFA/TGFB2/RAC1/NRAS/PRCC/GRB2/TGFB3/CDC42/RBX1/VHL/BAD/P
/SULT1A2/CYP2C18/CYP3A7/UGT2B4/CYP2A13/EPHX1/GSTA2/CYP3A43/UGT2B7/NAT2/CYP3A5/C
R3/CCNE1/MAPK12/MAPK13/AURKA/YWHAZ/CDC25C/MAD2L1/RPS6KA1/ESPL1/PPP2R1A/MAPK3/SG
UPP2/CES1/GSTA2/UGT2B7/NAT2/CES2/XDH/GSTM1/UGT2B15/GSTA1/DPYS/UGT2B10/UPB1/CYP2
LOX5/MAP2K2/MAPK3/LYN/PIK3CD/LCP2/RAC1/NRAS/GRB2/BTK/MAPK11

X1/ANGPTL4/ACSL6/PLIN5/SCP2/ACSL5/PLIN1/CYP27A1/ACADL/ACSL1/FABP1/ACOX2/APOA2/S
1/NAGS/SDS/SHMT1/GPT/ENO3/PKLR/CTH/MAT1A/PAH/CPS1/OTC/ALDOB

2C/RNPS1/NXT1/NCBP2/PPP1CA/PPP1CC/DAZAP1/CPSF1/EIF4A3/CPSF6/PABPC4/MSI2/FUS/CPS
RGC1A/ACSL5/LEPR/ACSL1/PCK2/G6PC/PCK1

-DRB1/HLA-DQA1/HLA-DRA/HLA-DPA1/IFNGR2/HLA-DQB1/HLA-DMB/JAK3/HLA-DPB1/CD3E/HIF1
ADCY1/UGT2B4/ABCG2/EPHX1/BAAT/UGT2B7/ABCB11/ABCG8/SLC51A/ABCG5/UGT2B15/SLC01B3/
UBB/PLCB1/TUBB4B/TUBA1A/MAP2K2/MAPK3/TUBB6/TUBB2A/PLCB3/CSNK1D/TUBB4A/TUBB2B/NR
/ABCG8/ABCG5/ABCA6/ABCB4

X19/DECR2/CRAT/ECH1/SOD1/MLYCD/HMGCL/DHRS4/NUDT7/PEX11A/ECI2/PEX11G/ACAA1/HSD17
/SPI1/BIRC3/BCL2A1/CSF1R/ARNT2/TCF3/DDIT3/IGFBP3/PLAU/CD86/BAX/PROM1/MLLT3/HDAC
AN/HLA-DRB1/ITGAV/HLA-DQA1/HLA-DRA/HLA-DPA1/NECTIN1/HLA-DQB1/VTCN1/HLA-DMB/CD86
AM/CYBB/ITGB2/VASP/EZR/NCF4/NCF1/CXCR4/VAV1/MSN/MMP2/THY1/PIK3CD/ACTG1/RAC1/BCA
ERPING1/CFH/CFB/FGB/F10/C3/FGG/VTN/F5/C4BPB/CFHR1/FGA/PROC/SERPINA5/CFHR2/C7/MB
PM3/CYC1/SLC9A1/SLC9A7/ATP2A3/COX6B1/COX8A/ATP1B1/CACNG4/COX7B/TNNI3/UQCRB/CACN
B1/HLA-DMB/CD86/HLA-DPB1/HLA-A/HLA-DQA2/HLA-B/HLA-DRB5/GZMB/HLA-DOA/HLA-F/HLA-C
R2/CSF1/COL1A2/OSMR/EFNA3/YWHAZ/COL9A2/EIF4EBP1/PKN1/ITGAV/COL4A5/LAMB1/SYK/EFN
B1/CDK4/LAMC1/TRAF2/BAX/LAMC2/TRAF5/LAMA5/CKS1B/E2F3/CDKN2B/PIK3CD/CDK2/BIRC7/I
PK13/SRC/HCK/SYK/HRAS/CDK4/TRAF2/CD86/MAPKAPK2/BAX/HLA-A/HIF1A/MAP2K2/MAPK3/GNG
PK13/SRC/TGFB1/YWHAZ/IRAK1/HRAS/CREB3L1/JAK3/BAX/CREB3/MAP2K2/ATP6AP1/MAPK3/PCN
FPT2/TSTA3/UGDH/GNPDA2/UXS1/NAGK/NANS/HK1/GMDS/GMPPA/AMDHD2/HEXB/GMPPB/CYB5R1/G
2/JAK3/RBCK1/CHMP4B/BAX/TRAF5/CHMP4C/HSP90AB1/FTH1/SHARPIN/STAT1/PPIA/CASP1/FTL
IRS1/PIK3R1/IRS2/PPARGC1A/MLXIPL/PPP1R3B/SLC27A2/PCK2/GYS2/SLC2A2/G6PC/SLC27A5/
PD2/ASAHI/GBA/SMPD4/CERS6/PSAP/ACER3/UGCG

6/DLG3/AREG/SCRIB/FZD7/SERPINE1/FZD1/PPP2R1A/PPP2R2C/CSNK1E/DVL3/YWHAH/CSNK1D/A
A/SIK2/FOXO1/GCK/PPARGC1A/ITPR2/PFKFB1/PCK2/FBP1/GCGR/GYS2/SLC2A2/G6PC/PCK1
COL4A5/HRAS/COL3A1/PLCB1/GNA15/CREB3L1/MMP1/CREB3/MMP2/MAP2K2/MAPK3/GNGT1/PLCB3
2M1/AP2S1/PLCB2/ATP1B1/VDR/DNM2/CLTC/RAB11A/ATP2B4/ADCY6/AP2A2/AP2B1/AP2A1/BDKR
/GAPDH/CYBB/HK2/EIF4EBP1/PFKFB3/PGK1/IFNGR2/TFRC/HMOX1/SERPINE1/HIF1A/MAP2K2/MA
BP1/RFC5/MSH6/RPA1

CEE/ACADS/ECHS1/IDNK/GLUD1/PC/GOT2/ACAT1/ACOX1/GCK/TKFC/GLYCTK/GPT2/SDS/SHMT1/G
RCA1/SOCS1/UBE2J2/ANAPC7/SOCS3/BIRC7/UBE2D1/UBE2L3/UBE2E1/UBE2A/PIAS3/ANAPC11/U
A/FOXO1/IRS1/PIK3R1/IRS2/PPARGC1A/LEPR/PFKFB1/PCK2/FBP1/GYS2/G6PC/PCK1

/UPB1

TUBA3C/LMNB1/CTSV/BIRC3/BCL2A1/HRAS/CTSK/TRAF2/DDIT3/BAX/CASP2/TUBA1A/MAP2K2/MA

7/IRS1/PIK3R1/IRS2/ADRB2/PLIN1/FABP4

KFC/GLYCTK/DGAT2/ALDH7A1/LIPC/GPAM/ALDH2/MOGAT2

/JAG1/DVL2/KAT2A/APH1B/HEY1/NCOR2/MFNG/CTBP2/ADAM17/NOTCH3/NOTCH1/LFNG/PSEN2/RB
OL9A2/COL4A5/COL3A1/COL16A1/COL5A1/COL5A2/SLC7A8/MEP1A/COL6A3/SLC3A2/KCNQ1/SLC3
/CHEK1/IGFBP3/BAX/SERPINE1/PERP/AIFM2/PMAIP1/CDK2/BBC3/BID/CCND2/CYCS/GORAB/THB
PLCB1/HSPA6/CREB3L1/HSPA8/CREB3/MMP2/MAP2K2/MAPK3/HSP90AB1/PLCB3/KRT18/FKBP4/PI

/C1QB/C1QC/IRAK1/ITGB2/C1QA/CFL1/ITGA5/MAPK3/IRF1/IRF3/CASP1/IL1B
B4GALT2/A4GALT/FUT2/FUT1/FUT6
IF1A/MAP2K2/MAPK3/STAT1/PIK3CD/BATF2/PDCD1/NRAS/LCK/PTPN6/BATF3/MAPK11/IKBKG/RP

EIF4EBP1/HLA-DQA1/HLA-DRA/SYK/TAP1/ALYREF/HLA-DPA1/NECTIN1/IFNGR2/HLA-DQB1/ZNF8
/MITF/ATF4/NRAS/PGAM5/MRAS/RHOT2/RPS27A/CSNK2B/BNIP3L/CSNK2A1/OPTN/UBA52/BECN1/
PLCB1/ADORA1/TRAF2/BAX/PPP2R1A/MAP2K2/MAPK3/CERS5/NSMAF/GNA12/PPP2R2C/DEGS1/SMP

K4/FZD6/HES4/DLG3/ATP6V0B/CREB3L1/SCRIB/FZD7/COMP/LAMC1/ITGA5/RELN/BAX/CREB3/LA
/CLTA/TUBA1A/CYC1/STX1A/TUBB6/HDAC1/KLC3/GPX8/TUBB2A/PSMB2/POLR2G/GPX7/HDAC2/PL
L5/WASF2/RBCK1/ITGA5/BAX/RRAGD/ARPC4/RRAGC/TRAF5/MAPK3/SHARPIN/HK3/ARPC3/ARPC2/
/RHOG/TRAF2/BAX/ARPC4/MAP2K2/MAPK3/HSP90AB1/RAB7B/KLC3/DYNLL1/RRAS/DYNC1H1/ARPC
F4/HSPA6/SLC25A6/CREB3L1/PSMD14/NCF1/LAMC1/TUBB4B/DDIT3/CCL5/UQCRH/BAX/HSPA8/CR
1/MAD2L1/HLA-DRA/HRAS/CDK4/IL15RA/HLA-DPA1/HLA-DQB1/CHEK1/RAN/SLC25A6/CREB3L1/H
PC4/CLTA/HLA-A/CHMP4C/WIPF1/HGS/FGFR4/ARPC3/ARPC2/RAB35/PIP5K1C/ARF3/CYTH2/SH3K
1/MSN/ITGA5/IQGAP1/ITGAX/LIMK2/ARPC4/SLC9A1/MAP2K2/MAPK3/GNA12/FGFR4/RRAS/ARPC3
BAX/LIMK2/CD3E/HLA-A/TRAF5/MAP2K2/MAPK3/GNGT1/PAK1/IRF3/PAK4/PIK3CD/GNG5/GNB2/H
DPA1/HLA-DQB1/PSMD14/HLA-DMB/TRAF2/JAK3/HLA-DPB1/BAX/NFKB2/PSMD2/CD3E/ISG15/HLA
B/EZR/TUBB4B/TRAF2/WASF2/BAX/WIPF3/ARPC4/TUBA1A/MAPK3/BAIAP2L1/TUBB6/GNA12/WIPF
RBCK1/CARD9/TRAF5/MAPK3/HSP90AB1/SHARPIN/STAT1/IRF3/PLCB3/IRF7/MCU/PSTPIP1/CCL2
K/HLA-DPA1/LSP1/IFNGR2/HLA-DQB1/ATP6V0B/HLA-DMB/MRC2/HLA-DPB1/BAX/ITGAX/CARD9/T
EB3/HLA-A/TRAF5/ATP6VOD2/MAPK3/HDAC1/RBL1/IRF3/HDAC2/LYN/IRF7/CDKN2B/YWHAH/PMAI
/SLC25A6/IGFBP3/MAPKAPK2/SERPINE1/HLA-A/MAP2K2/MAPK3/E2F3/RRAS/RBL1/E2F4/CDKN2B
5/HLA-DPB1/BAX/MAP2K2/MAPK3/STAT1/NXT1/IRF3/HLA-DQA2/IRF7/SOCS3/PIK3CD/ACTG1/CC
H2/EZR/FSCN1/PLAU/ITGA5/HMOX1/EFNA5/UBE2I/MAP2K2/MAPK3/BRCA1/HDAC1/E2F3/ST14/BM
CBP2/POP7/EIF3I/KPNB1/XPOT/EIF3D/EEF1A2/GEMIN7/NUP85/THOC6/POP1/EIF4A3/NUP43/TH
/TUBB/HLA-DPA1/NCF4/HLA-DQB1/ATP6V0B/COMP/NCF1/HLA-DMB/TUBB4B/TFRC/ITGA5/MRC2/H
/PPIL1/SRSF9/SNRNP40/U2AF2/BUD31/LSM2/PQBP1/EIF4A3/PRPF3/ISY1/SF3A3/SNU13/PRPF6
DC25C/E2F5/MCM6/CDKN2A/MCM7/MAD2L1/MCM3/CDC25A/CDK4/CDKN2D/CDC7/CHEK1/MCM5/ESPL
PLP0/RPL18A/RPL35/RPS19/RPL38/RPL23/RPL18/RPL23A/MRPL10/RPS10/MRPS15/MRPS7/RPL5
AF2/NFKB2/MAPK3/TNFRSF11A/STAT1/SOCS1/MITF/SIRPG/SOCS3/PIK3CD/SIRPA/LCP2/TGFB2/
1/CTSS/NPC2/ATP6V1H/ASAHI/CTSE/SLC11A1/CD68/LAMP3/CLN3/GBA/AP3M2/CLTB/GNS/GALNS
/SV2A/ITGA2/COL6A2/COL4A2/LAMB3/CD47/IBSP/ITGB8/THBS1/THBS2/LAMA4
OB/CTSK/MMP1/HLA-DMB/LTB/CCL5/CD86/HLA-DPB1/ATP6V1C1/TCIRG1/ATP6VOD2/ATP6AP1/TN
/PAK1/PIP5K1C/LYN/BIN1/PIK3CD/ARPC5L/RAC1/WAS/WASF1/CDC42/FCGR3B/RPS6KB2/ARPC1A
P10/HEATR1/GAR1/REXO2/NAT10/CSNK2B/NVL/NOL6/CSNK2A1/BMS1/NOB1/WDR75/LSG1/RBM28/
F4/HLA-DQB1/NCF1/HLA-DMB/HLA-DPB1/MAPK3/STAT1/HLA-DQA2/EEF1A2/TGFB2/HLA-DRB5/IL
3/HLA-DQA2/HSPA4/HLA-B/HLA-DRB5/RFX5/CALR/CD8A/NFYC/HLA-DOA/CIITA/HSPA5/HSP90AA
C42/VCL/CBL/ARPC1A/ARPC5/CTNNA1/DNM2/PTK2/CD2AP/CLTC/RHOA/ELMO2/CAV1/PIK3CB/CAV

3B/MAP3K14/LTBR

HSPD1/HLA-DOA/HLA-F

NASEH2C/POLE3/RPA1/RNASEH1/POLE2

N2A/BIRC3/ITGAV/COL4A5/LAMB1/HRAS/CSF1R/PGF/CDK4/CSF3R/FZD6/IL15RA/PLCB1/IFNGR2
B/TRAF2/DDIT3/UQCRH/PSMD2/FZD1/TUBA1A/CYC1/MAP2K2/MAPK3/TUBB6/KLC3/TUBB2A/PSMB2
F2/DDIT3/UQCRH/BAX/NUP210/PSMD2/TUBA1A/CYC1/TUBB6/KLC3/GPX8/TUBB2A/NUP93/PSMB2/
TB/TNFRSF11B/CCL5/TNFRSF18/CXCR4/TNFSF9/CCL26/IL34/IL27RA/EDA/TNFRSF4/TNFRSF11A
KLC3/TUBB2A/PSMB2/UBE2J2/MCU/TUBB4A/ATF4/PSMB4/ADRM1/VDAC1/PSMA5/PSMC4/TUBB2B/P
K3CD/BCL3/CCL2/ATF4/CXCL3/IL1B/MLKL/JAG1/IL15/MAP3K14/DNM1L/PGAM5/MAPK11/IKBKG/
B1/HSPA8/LAMC2/AOX5/LAMA5/MAPK3/STAT1/SOCS1/HLA-DQA2/BIRC7/TGFB2/HLA-DRB5/LAMB
1/HLA-DQA2/JAG2/HLA-DRB5/IL2RA/LCK/JAG1/IL12RB1/IL2RB/MAPK11/IKBKG/IL4R/HLA-DOA
/IKBKG/TRAF3/FADD/MAPK7/TRAF4/S100A7/HSP90AA1/TRADD/HSP90B1/MUC5B/CASP8/TNFAIP3
HLA-DPB1/CD2/CD3E/HLA-DQA2/HLA-DRB5/IL1B/IL2RA/ITGA2/IL1R2/CD8A/IL4R/CSF2RA/CD3
8/PSMA1/PSMA4/PSMB5/PSMC5/PSMC3/POMP/PSMB1/PSMB6/PSMA3/IFNG/PSMB7

/TRAF5/MAP2K2/MAPK3/GNGT1/GNA12/E2F3/IRF3/PLCB3/CCL4/PIK3CD/CCL2/ATF4/GNG5/GNB2
GS14/MAP2K2/MAPK3/FPR1/FGFR4/RRAS/PLCB3/FGFR1/PIK3CD/ACTG1/LCP2/RAC1/BCAR1/NRAS
CL13/PLCB3/LYN/CCL4/PIK3CD/SHC1/CCL2/GNG5/CXCL16/CCL28/GNB2/CXCL3/RAC1/BCAR1/GN
/PLCB3/PIK3CD/CCL2/F3/TGFB2/RAC1/IL1B/NRAS/COL4A2/TGFB3/CDC42/MAPK11/VCAM1/PLCB

RELN/LAMC2/LAMA5/MAPK3/PAK1/PIP5K1C/COL6A3/PAK4/PIK3CD/ACTG1/SHC1/TNC/ITGB5/PPP
E2J2/BCAP31/TRAM1L1/ATF4/RPN2/CAPN1/UBE2D1/STT3A/DNAJC10/DNAJB2/WFS1/BAG2/SSR3/

RF3/PIK3CD/ACTG1/CCL2/LCP2/CASP1/RAC1/BCAR1/IL1B/ACTB/WAS/LCK/CD8A/CDC42/MAPK11
P6VOC/MAP3K14/CDC42/MAPK11/ATP6V0E1/IKBKG

RB5/BID/ACTB/CYCS/HLA-DOA/HLA-F/ABL1/CASP8/EIF4G3/CAV1/EIF4G2/HLA-C/CASP3/ITGAL

CND2/CYCS/IL2RB/EIF3H/IKBKG/TRAF3/FADD/RACK1/FCGR2B/CCND3/STAT5A/TLR2/TRADD/CSN

CL11/IKBKG/LBP/TRAF3/FADD/TLR5/TLR2/CASP8/IFNAR2/CCL3L3/IRF5/CXCL10/TLR7/PIK3CB

/CASP1/CD209/IL1B/NRAS/MAP3K14/MRAS/CLEC7A/MAPK11/IKBKG/CALM2/PLK3/NFATC4/BCL10

8A1/AOX1/EHHADH/CYP1A2

5/ACADL/ACSL1/ACADSB/ALDH2/ADH6/EHHADH/ADH1A/ADH1C/CYP4A11/ADH4/ADH1B
3CD/CDK2/ANAPC11/STK10/MAPK11/IGF1R/HSP90AA1/GNAI3/ADCY6/ANAPC5/KIF22/ADCY5/CDC

KR1D1/CYP1A2/HSD11B1/HSD17B6/CYP2E1/CYP3A4
7B6/ADH1A/CYP2B6/ADH1C/CYP4A11/CYP2C9/CYP2C8/ADH4/ADH1B/CYP2A6/CYP3A4
A1/APOC3

E/ADAR/POLR3F/AIM2/POLR1C/RELA/POLR3A/IKBKB/ZBP1
ATP6V0E1/ERO1A/ATP6V0D1/CFTR/ARF1/ADCY3/ATP6V1B2/PDIA4/PLCG1/GNAS
CAA2/ALDH7A1/ACADSB/ALDH2/AGXT2/ALDH6A1/ABAT/AOX1/EHHADH/HMGCS2
XCL3/IL1B/LCK/TNFSF13B/PARP1/MAP3K14/BTK/LTBR/IKBKG/LBP/TRAF3/TRIM25/VCAM1/PIDD
L9/CCR1/CXCR3/XCL2/IL2RB/CCL3/LTBR/CXCL11/CCR5/PF4V1
MB/SELPLG/HLA-DPB1/CFD/FPR1/C3AR1/KRT18/HLA-DQA2/FPR3/C5AR1/HLA-DRB5
AP1/FZD1/HIF1A/MMP2/SLC9A1/MAP2K2/MAPK3/CD63/RRAS/PAK1/FGFR1/HCLS1/PIK3CD/ACTG1

/ACSL1/ACADSB/EHHADH
T2B10/CYP1A2/FMO3/ADH1A/CYP2B6/CYP2E1/ADH1C/CYP2C9/CYP2C8/ADH4/ADH1B/CYP2A6/CYP
AS/LCK/PTPN6/GRB2/CD48/GZMB/FCGR3B/IFNAR2/CD247/HLA-C/ICAM2/PIK3CB/CASP3/ITGAL/
IL12RB1/TGFB3/IL4R/TLR5/HLA-DOA/TLR2

1/UGT2B10/CYP1A2/HSD11B1/SULT2A1/ADH1A/CYP2B6/CYP2E1/ADH1C/CYP2C9/ADH4/ADH1B/CY
AK2/VEGFA/RAPGEF1/EGLN2
YP1A1/GSTM1/UGT2B15/ADH6/GSTA1/UGT2B10/CYP1A2/HSD11B1/SULT2A1/ADH1A/CYP2E1/ADH1
O1/MAD2L2/FBXO5/ANAPC7/YWHAH/CDK2/PPP1CA/PPP1CC/YWHAQ/ANAPC11/YWHAB/MAPK11/IGF1
E1/CYP2A6/CYP3A4

LC27A2/PCK2/EHHADH/FABP4/CYP7A1/APOA1/APOA5/HMGCS2/APOC3/CYP4A11/SLC27A5/PCK1/C
F4/GSPT2/CPSF3/MSI1/PPP2R3A/SYMPK/ETF1/MAGOH/PPP2R5B/RNMT/FIP1L1/SSU72/MAGOH/N
A/IL27RA/MAPK3/HSP90AB1/STAT1/HLA-DQA2/HLA-DRB5/IL1B/IL2RA/LCK/IL12RB1/IL2RB/MA
SLC01B1/ABCB4/CYP7A1/SLC22A7/UGT2B10/SULT2A1/SLC22A1/SLC27A5/AQP9/SLC10A1/CYP3A
AS/PDGFA

B4/ACOX1/PXMP2/ACSL6/AMACR/PECR/PHYH/SCP2/ACSL5/ACSL1/CAT/BAAT/EPHX2/ACOX2/XDH/
1/NUPR1/ETV7/TFE3/HDAC2/MITF/PDGFA/MLF1/CDKN2C/CCND2/ETV6/PRCC/IL1R2/IL2RB/PAX8
/SELPLG/HLA-DPB1/CD2/HLA-A/CD276/NRCAM/CTLA4/CD58/HLA-DQA2/CNTNAP1/HLA-B/HLA-DR
R1/ACTB/CDC42/MAPK11/VCL/VCAM1/CLDN10/MYL9/SIPA1/CTNNA1/PTK2/GNAI3
L2/MASP1/C8B/F11/F2/F7/SERPINF2/F13B/MASP2/C4BPA/CPB2/KLKB1/C8A/CFHR3/SERPIND1/
B1/CACNB3/SLC9A6/COX7A2/CACNA1D/COX6C/ATP2A2/COX5A/TNNC1/COX4I1
/PRF1/HLA-DOB/IFNG/HLA-E/CD80/IL12A/FASLG/HLA-G
A4/HRAS/CSF1R/PGF/CDK4/CSF3R/G6PC3/AREG/CREB3L1/COMP/LAMC1/JAK3/ITGA5/RELN/EFNA
TGA2/COL4A2/LAMB3/E2F2/CYCS/ZBTB17/IKBK/ TRAF3/ TRAF4/LAMA4/PTK2/CCNE2
T1/E2F3/STAT1/IRF3/LYN/IRF7/PIK3CD/LEF1/GNG5/GNB2/HLA-B/CXCL3/RAC1/GNB1/BID/NRA
A/E2F3/STAT1/IRF3/IRF7/PIK3CD/CDK2/ATF4/TGFB2/BID/NRAS/YWHAQ/E2F2/CYCS/GRB2/TGF
FPT1/CYB5R3/PMM2
/VDAC1/BID/IL1B/CAPN1/MLKL/CHMP3/PARP1/DNM1L/CHMP1A/PGAM5/SLC25A5/FADD/VDAC2/HS
PCK1

CTG1/AXIN1/BBC3/LEF1/FZD2/WNT7B/PPP1CA/TGFB2/PPP1CC/ACTB/YWHAQ/RASSF1/CCND2/DVL
/PIK3CD/SHC1/ATF4/GNG5/GNB2/GNB1/NRAS/COL4A2/GRB2/MAPK11/ARRB2/GNB4/GNGT2/PLCB2
B2/ATP2B1
PK3/HK3/PIK3CD/LDHA/PFKM/HK1/LTBR/IGF1R/LDHB/ANGPT2/RBX1

PT/ENO3/PKLR/CAT/OGDHL/RGN/ALDH6A1/FBP1/EHHADH/HAO2/HAO1/CPS1/AGXT/ALDOB
BA1/PML/CUL4B/RBX1/CBL/RNF7/UBE20/UBE2L6/VHL/TRIM37/UBA2/PRPF19/RPS27A/UBE2D2/P

PK3/LMNA/CTSS/PMAIP1/PIK3CD/ACTG1/BBC3/ATF4/BID/CAPN1/NRAS/ACTB/PARP1/CYCS/MAP3

PJ/CTBP1/NOTCH2/NCSTN/MAML1/APH1A/DVL1/MAML2
6A1/CPA2/COL6A2/COL4A2/COL8A2/SLC36A4/COL11A1/PRSS3/KCNN4/ATP1B1
S1/CHEK2/CCND3/PIDD1
K3CD/TGFA/SHC1/ATF4/NRAS/GRB2/KRT20/CTSD/PLCB2/KRT10/CALM2/HSP90AA1/GNAI3/HSP90

S6KB2/TLR2/CSNK2B/CSNK2A1/CD247/NFKBIB/CD4/EGF/CSNK2A2/CD3G/PIK3CB/IFNG/PLCG1/R

3/HLA-DMB/TRAF2/CCL5/ITGA5/HLA-DPB1/BAX/ZNF320/CARD9/HLA-A/TRAF5/PILRA/ZNF93/ST
BCL2L1/CSNK2A2/MFN1/ATG9A/ULK1/TP53/RELA/TFEB/RAB7A/MAPK9/KRAS/SP1/GABARAP/RRAS
D2/PLCB3/ASAHI/PIK3CD/RAC1/BID/NRAS/MAPK11/CTSD/CERS6/PLCB2/PPP2R3A/TRADD/PLD2/

MC2/ATP6V1C1/ISG15/FZD1/HLA-A/TCIRG1/ATP6VOD2/PPP2R1A/LAMA5/MAP2K2/ATP6AP1/MAPK
CB3/POLR2H/SLC1A3/DCTN2/TUBB4A/BBC3/ATG101/PSMB4/ADRM1/VDAC1/TGM2/PSMA5/PSMC4/T
IRF3/PLCB3/HCLS1/CYTH2/CBX3/PIK3CD/ACTG1/ARPC5L/CASP1/CAPNS1/VDAC1/RAC1/BCAR1/I
3/ARPC2/DYNLRB1/PAK1/PLEKHM2/NCKAP1L/DYNLT1/CYTH2/CSE1L/STX10/PIK3CD/ACTG1/ARPC
EB3/PSMD2/TUBA1A/CYC1/MAPK3/TUBB6/KLC3/TUBB2A/PSMB2/MCU/PIK3CD/TUBB4A/ATF4/PSME
LA-DMB/TCF3/JAK3/HLA-DPB1/BAX/ESPL1/NFKB2/CREB3/CD3E/HLA-A/MAP2K2/MAPK3/E2F3/HL
BP1/BIN1/ARFGAP1/CAPZA1/ARPC5L/SNF8/RAB11FIP4/EHD1/HLA-B/IL2RA/FOLR2/SH3GLB2/RA
/ARPC2/PAK1/PIP5K1C/NCKAP1L/FGFR1/PAK4/PIK3CD/ACTG1/ARPC5L/ITGB5/PPP1CA/RAC1/BC
LA-B/RAC1/GNB1/BID/APOBEC3G/NRAS/CYCS/CALR/MAPK11/CCR5/IKBKG/AP1G2/GNB4/CUL4B/F
-A/TRAF5/HDAC1/E2F3/STAT1/CD58/IRF3/HDAC2/LYN/HLA-DQA2/IRF7/PIK3CD/CDK2/SAP30/A
1/ABCF2/TUBB2A/ARPC3/ARPC2/PAK1/NCKAP1L/HCLS1/CYTH2/MYO1F/MYO1G/SLC9A3R1/ACTG1/
/CASP1/IFI16/VDAC1/CXCL3/IL1B/TXN/CARD16/DNM1L/GSDMD/MAPK11/IKBKG/TRAF3/CARD18/
CIRG1/ATP6VOD2/ATP6AP1/MAPK3/RFXANK/STAT1/CTSS/ATP6V1H/HLA-DQA2/CD209/TGFB2/HLA
P1/PIK3CD/CDK2/ATF4/HLA-B/RAC1/NRAS/YWHAQ/CCND2/CHD4/GRB2/CDC42/YWHAB/KAT2A/LTE
/MCU/PIK3CD/CDK2/PPP1CA/TGFB2/HLA-B/VDAC1/PPP1CC/CAPN1/NRAS/CCND2/RBBP4/E2F2/TG
L2/CASP1/VDAC1/HLA-DRB5/BID/IL1B/ACTB/CYCS/RAE1/PML/IKBKG/SLC25A5/TRAF3/CPSF4/T
IF/SOCS1/HDAC2/DDIT4/PAK4/PIK3CD/SHC1/TNC/TGFB2/NRAS/DNMT3A/PDGFA/FGFR3/RASSF1/C
IOC5/EIF2S3/XPO5/RAE1/PABPC4/EIF3H/NUP107/NUP155/FUS/POP5/EIF2B5/SEC13/MAGOH/THC
LA-DPB1/COLEC12/SEC61A1/SEC61G/ATP6V1C1/HLA-A/TUBA1A/TCIRG1/ATP6VOD2/ATP6AP1/RA
/FUS/HNRNPM/HNRNPA3/RBM17/SNRPG/PRPF31/DDX23/SART1/SNRPB2/PRPF19/PRPF38A/HNRNPU
.1/PRKDC/PCNA/MAD2L2/HDAC1/E2F3/RBL1/E2F4/HDAC2/DBF4/CDKN2B/ANAPC7/YWHAH/CDK2/TG
/MRPS21/RPS23/RPS15/MRPL18/RPS12/RPS16/RPL7A/RPL36/RPS27A/RPL6/RPS7/RPL22L1/RPL
RAC1/IL1B/LCK/GRB2/MAP3K14/BTK/MAPK11/IKBKG/LILRB4/FCGR3B
/ATP6VOC/PLA2G15/AP1G2/CTSD/AP3D1/M6PR/AP1B1/NAGPA/SGSH/DNASE2/ATP6VOD1/AGA/MAN

IFRSF11A/CTLA4/ATP6V1H/HLA-DQA2/CCL2/TGFB2/CXCL3/HLA-DRB5/IL1B/ATP6V1E1/IL15/TNF
/ARPC5/INPPL1/FCGR2B/DNM2/PLD2
RPP30/EIF6/CSNK2A2/IMP4/RIOK1/AK6/NXT2
1B/PTPN6/TGFB3/MAPK11
1/HLA-F/CANX/HSPA2/TAPBP/LGMN/TAP2/PDIA3/CD4/HLA-C/NFYA/HLA-DOB/IFNG/CTSL/HLA-E
2/ELMO3/PXN

/ARNT2/MMP1/FZD7/LAMC1/TRAF2/GSTM3/JAK3/CXCR4/BDKRB1/HMOX1/BAX/NFKB2/LAMC2/TPM3
/CSNK1E/FRAT2/PSENEN/PLCB3/DVL3/MCU/PIK3CD/AXIN1/TUBB4A/ATF4/FZD2/ATG101/WNT7B/
NUP37/NDC1/GPX7/NXT1/NUP205/NUP188/DCTN2/MCU/ACTG1/TUBB4A/ATF4/CASP1/ATG101/PSM
/CXCL13/CCL13/CCL4/CCL2/CXCL16/CCL28/TGFB2/CXCL3/IL1B/TNFRSF10C/IL2RA/CXCL9/CCF
SMD13/TXN/PSMD11/UBE2L3/CYCS/PSMA7/PSMD1/UBA1/PSMD7/PSMB3/PSMD4/NDUFS6/PSMD3/SL
TRAF3/FADD
3/CYCS/TGFB3/MAPK11/CCR5/IKBKG/IL10RA/LAMA4/HLA-DOA/CIITA/TLR2/GNAI3/HSPA2/CASF
/STAT5A/NOTCH3/NOTCH1/RUNX3/CD247/NFKB1B/CD4/RBPJ/CD3G/NOTCH2/HLA-DOB/IFNG/PLCG
/ANAPC5/IL17D/IL17RA/CXCL10/SRSF1/CASP3/MAP3K7/IL17RB/IFNG/ELAVL1/MAPK15/RELA
3/HLA-DOA

HLA-B/RAC1/BCAR1/GNB1/BID/IL1B/NRAS/CCR1/E2F2/CYCS/CALR/GRB2/CCL3/MAPK11/CCR5/
ACTB/PDGFA/FGFR3/PFN1/RALA/SIPA1L2/CDC42/PRKCI/SIPA1L3/MRAS/PRKD2/MAPK11/IGF1R
B1/CXCL9/NRAS/FGR/CCR1/WAS/CXCR3/GSK3A/XCL2/GRB2/CDC42/CCL3/CXCL11/CCR5/IKBKG/F
2/PLCD4/STAT5A

1CA/RAC1/BCAR1/PPP1CC/ACTB/ITGA2/PDGFA/COL6A2/COL4A2/CCND2/LAMB3/PARVG/GRB2/CDC
CALR/PPP1R15A/DNAJB11/ERO1A/PDIA6/RBX1/HSPA4L/SSR4/VCP/SEC13/UBXN1/HSPA5/HSP90A
/IKBKG

PRF1/HLA-DOB/EIF4G1/HLA-E/RAC3/CD80/LAMA1

K2B/CCNE2/HSPA2/MAVS/CSNK2A1/OAS3/CASP8/BAD/TNFAIP3/IFNAR2/NFKBIB/BCL2L1/TLR7/F
MAP3K7/TLR8

KSR1/CASP8/RHOA

27/ADCY3/ANAPC4/ADCY7/PIK3CB

1/TRADD/BCL10/CSNK2B/CSNK2A1/PIAS4/TNFAIP3

ITGB5/FZD2/WNT7B/PPP1CA/TGFB2/RAC1/PPP1CC/NRAS/ACTB/ITGA2/PTPN6/CTTN/TFAP4/GRE

'3A4

'PRF1/IFNG/PLCG1/HLA-E/RAC3/PRKCB/NFATC1/VAV3/TNFRSF10A/PIK3R2/MICB/KRAS/FASLG/F

P2A6/CYP3A4

C/CYP2C9/CYP2C8/ADH4/ADH1B/CYP2A6/CYP3A4
R

.YP8B1

XT2/RBM8A/PABPC1L/SMG7/PABPN1/CASC3/CSTF3/PYM1/ACIN1/PPP1CB/PPP2R3B/PPP2R5D/PPF

.PK11/IKBKG/IL4R/HLA-DOA/HSP90AA1/STAT5A
.4

'SLC27A2/PIPOX/EHHADH/HAO2/DAO/HAO1/AGXT
:/PML/ZBTB17/IGF1R/FUS/GZMB
B5/PDCD1/SIGLEC1/CD6/CD8A/ITGB8/GLG1/VCAM1/CLDN10/PTPRF/HLA-DOA/HLA-F

'F12/F9/CFHR5/KNG1/C6/PLG/CFHR4/SERPINC1

.5/CREB3/LAMC2/PPP2R1A/LAMA5/MAP2K2/MAPK3/HSP90AB1/GNGT1/BRCA1/PPP2R2C/FGFR4/FGF

.S/CCR1/E2F2/CYCS/MAPK11/CCR5/IKBKG/TRAF3/GNB4/FADD/ANGPT2/GNGT2/CALM2/HLA-F/NFA
B3/YWHAB/MAPK11/IKBKG/TRAF3/FADD/STAT5A/TLR2/NFATC4/VDAC3/CCNE2/MAVS/CASP8/BAD

.P90AA1/STAT5A/TRADD/VDAC3/USP21/CASP8/TNFAIP3/IFNAR2/FAF1/PLA2G4A/SPATA2L/CAPN2

.2/TGFB3/YWHAB/PRKCI/PARD6B/LLGL1/PARD6G/WWC1/WNT4/NF2/CCND3

;

'TAS4/UBE2Q1/ANAPC5/UBA52/UBE2N/UBR5/UBE2E2/UBE2F/CDC27/STUB1/MAP3K1/UBE4B/ANAPC

K14/IKBKG/GZMB/CTSD/DFFA/FADD/CSF2RB

B1/HSPA2/ADCY6/ADCY5/CALM3/HBEGF/ADCY3/KRT15/ADCY7/PIK3CB

ELA/NFATC1/IKBKB/RASGRP1/PIK3R2/STAT3/CD274/TICAM1/KRAS/PPP3CB/MAP3K3/ZAP70

AT1/IRF3/HLA-DQA2/IRF7/SOCS3/PIK3CD/CCL2/SRSF9/PPP1CA/HCFC1/HLA-B/HLA-DRB5/PPP1
2/ATG9B
GNAI3/S1PR3/PPP2R5B

3/HDAC1/PPP2R2C/RBL1/STAT1/IRF1/ATP6V1H/IRF3/HDAC2/COL6A3/DVL3/HEYL/BCAP31/SLC9
CTN5/TUBB2B/PSMD13/PSMD11/CLTB/AP2M1/CYCS/PSMA7/AP2S1/PSMD1/PSMD7/POLR2K/PSMB3/
L1B/CAPN1/ACTB/UBE2D1/WASF1/GSK3A/PFN1/CYCS/CTTN/HK1/CDC42/MAPK11/IKBKG/VCL/AKT
5L/LEF1/CASP1/RAC1/IL1B/MLKL/ACTB/TXN/DYNC1LI1/PFN1/CYCS/FHOD1/RALA/RPS3/GSDMD/
4/ADRM1/VDAC1/RAC1/PSMA5/IL1B/PSMC4/TUBB2B/PSMD13/PSMD11/CYCS/PSMA7/PSMD1/PSMD7
A-DQA2/CDKN2B/ANAPC7/PIK3CD/CDK2/ATF4/TGFB2/HLA-B/VDAC1/HLA-DRB5/IL2RA/NRAS/LCK
B10/EHD2/FGFR3/ARF4/CHMP3/CLTB/AP2M1/EPS15L1/IL2RB/AP2S1/VPS28/CHMP1A/CDC42/PML
AR1/PPP1CC/PIP4K2A/NRAS/ACTB/ITGA2/PDGFA/FGFR3/WASF1/PFN1/PIP4K2C/CDC42/MRAS/IT
ADD/RBX1/AP1B1/APOBEC3D/RNF7/GNGT2/RPS6KB2/CALM2/HLA-F/TLR2/NFATC4/TRADD/PTK2/C
DRM1/HLA-B/RAC1/HLA-DRB5/BID/PSMC4/PSMD13/CCND2/PSMD11/E2F2/CYCS/PSMD1/CALR/MAF
ARPC5L/TUBB4A/CASP1/RAC1/IL1B/TUBB2B/ACTB/WASF1/PTPN6/CYCS/CTTN/RPS3/NCL/CDC42/
FADD/CARD6/TRIP6/VDAC2/PLCB2/HSP90AA1/VDAC3/MAVS/OAS3/CASP8/TNFAIP3/RHOA/IFNAR2
-DRB5/BID/IL1B/RFX5/CYCS/ATP6VOC/TGFB3/CLEC7A/MAPK11/LBP/CTSD/NFYC/FADD/FCGR3B/
R/RANBP1/CCR5/IKBKG/TRAF3/ATP6VOD1/CCND3/HLA-F/STAT5A/TRADD/VDAC3/CCNE2/GTF2E2/
FB3/MRAS/MAPK11/SLC25A5/CHEK2/VDAC2/RHEB/CCND3/RAD9A/CALM2/HLA-F/NBN/RAD1/NFATC
RIM25/FADD/PRSS3/CCND3/HLA-DOA/CIITA/TRADD/MAVS/OAS3/RAB11A/CASP8/IFNAR2/KPNA6/
CND2/E2F2/GRB2/VIM
C2/TGS1/EIF3E/STRAP/EIF3G/RPP30/SEH1L/MAGOH/THOC1/SUMO2/EIF4G3/EIF4G2/NXT2/RBM
B7B/TUBB6/HGS/TUBB2A/DYNC1H1/CTSS/MSR1/OLR1/ATP6V1H/HLA-DQA2/ACTG1/TUBB4A/ITGB5
I/LSM8/RBMX/HSPA2/MAGOH/PHF5A/THOC2/TCERG1/DHX15/HNRNPA1/SF3B3/PPIE/USP39/SF3B2/
FB2/CDKN2C/YWHAQ/CCND2/ANAPC11/E2F2/CDK7/RAD21/TGFB3/YWHAB/ZBTB17
.37/MRPS17/MRPL15/MRPL28/RPL27A/RPS11/RPS4X/RPL19/RPLP1/MRPL27/UBA52/RPL13A/RPL5
2B1/ABCA2/PSAP/GNPTAB/HEXB/CTSW/AP3B1/SLC17A5/CLTC/GGA1/GGA3/ABCB9/AP1S3/AP1S2/
SF13B/ATP6VOC/TGFB3/CCL3/ATP6V0E1

;

;/FZD1/TRAF5/HIF1A/MMP2/LAMA5/MAP2K2/MAPK3/HSP90AB1/GNGT1/CKS1B/HDAC1/GNA12/E2F2
PSMB4/ADRM1/VDAC1/BID/PSMA5/IL1B/CAPN1/PSMC4/TUBB2B/NRAS/RTN3/CDK5/PSMD13/APP/F
IB4/ANXA11/ATXN2L/ADRM1/VDAC1/RAC1/BID/PSMA5/PSMC4/DCTN5/TUBB2B/ACTB/NUP85/PSMD1
1/TNFSF12/IL15/CD27/TNFSF13B/CXCR3/IL12RB1/XCL2/IL1R2/IL2RB/TGFB3/CCL3/LTBR/CXC
.C25A5/NDUFS5/NDUFB9/COX6B1/MAPT/PSMD9/PSMD8/VDAC2/UBE2L6/PSMA1/COX8A/CALM2/HSPA
8/BAD/PIK3R5
1/RELA/STAT4/NFATC1/IKBKB/MAML1/MAML2/MAPK9/IL12A/PPP3CB/GATA3/ZAP70

'IKBKG/GNB4/FADD/IL10RA/GNGT2/RPS6KB2/RHEB/PLCB2/CALM2/HLA-F/NFATC4/TRADD/PTK2/C
!'/PARD6B/PARD6G/ANGPT2/RALGDS/THBS1/RALB/PLCB2/LPAR5/CALM2/SIPA1/GNAI3/FGFR2/TLN
'F4V1/ARRB2/GNB4/GRK2/GNGT2/PLCB2/PTK2/GNAI3/GNG4/CXCR6/BAD/PIK3R5/ADCY6/RHOA/DC

:42/IBSP/IGF1R/ITGB8/VCL/THBS1/THBS2/CCND3/LAMA4/MYL9/PTK2/TLN1/PPP1R12C/BAD/PAK
A1/ERP29/UBQLN4/NSFL1C/CANX/HSP90B1/HSPA2/EDEM2/UBE2D2/DAD1/SSR1/PDIA3/TRAM1/S1

:AB9A/CSNK2A2/MX1/CD3G/PIK3CB/CASP3/MAP3K7

:2/CDC42/LUM/MRAS/MAPK11/DROSHA/IGF1R/HPSE/CBL/THBS1/WNT4/RPS6KB2

'PP3CB/SH2D1A/HLA-G/ZAP70

'2CA/GSPT1/DDX19A/TARDBP

'R1/COL6A3/MLST8/GYS1/DDIT4/YWHAH/PIK3CD/CDK2/TGFA/TNC/ITGB5/ATF4/GNG5/GNB2/RAC1

TC4/TRADD/RPS27A/GNG4/CASP8/PIK3R5/IFNAR2/VEGFA/UBA52/BECN1/CLEC2B/PIK3R6

!/VPS4A

:4/RHOBTB2/HUWE1/CDC34/SKP2/DDB1/TRIM32/CDC23/UBE2E3/CUL7/WWP2/SKP1/UBE2J1/UBE2F

.CC/BID/IL1B/ZNF14/ZNF205/CYCS/CALR/PML/ZNF611/IKBKG/ZNF486/TRAF3/SRPK1/ZNF600/F

1A3R1/PIK3CD/AXIN1/CDK2/TNC/ITGB5/FZD2/WNT7B/HLA-B/NRAS/ATP6V1E1/ITGA2/COL6A2/J/
 'GPX1/PSMD4/NDUFS6/PSMD3/SLC25A5/POLR2L/NDUFS5/NDUFB9/DNAL4/WIPI1/COX6B1/PSMD9/I
 '1S1/RBX1/WIPI1/TLR5/RPS6KB2/ARPC1A/ARPC5/PLCB2/TNIP1/PLCD4/MYL9/TRADD/PTK2/BCL1
 'CDC42/MAPK11/IKBKG/FADD/M6PR/VPS18/TLR5/ARPC1A/ARPC5/HSP90AA1/MYL9/TLR2/DNM2/TF
 'PSMB3/PSMD4/NDUFS6/MAPK11/PSMD3/SLC25A5/NDUFS5/NDUFB9/COX6B1/PSMD9/PSMD8/VDAC2
 'CDKN2C/IL15/CCND2/ANAPC11/E2F2/IL1R2/IL2RB/CALR/MAP3K14/TGFB3/KAT2A/LTBR/RANBF
 ./CAPZB/PRKCI/AGAP1/SH3GL1/CCR5/VPS25/ARRB2/IGF1R/PARD6B/PARD6G/CBL/MVB12A/SNX12
 'GB8/VCL/FGD1/ABI2/ARPC1A/ARPC5/LPAR5/MYL9/PTK2/BRK1/FGFR2/SSH2
 'NAI3/GNG4/CASP8/BAD/AP1S3/AP1S2/PAK2/TAPBP/CD247/AP1S1/TAP2/PDIA3/CD4/BCL2L1/A1
 '3K14/PSMD7/VIM/BTK/PSMD4/MAPK11/IKBKG/PSMD3/TRAF3/FADD/NCOR2/PSMD8/CCND3/HLA-DC
 'MAPK11/IKBKG/MYO5A/FADD/TLR5/CLDN10/ARPC1A/ARPC5/LPAR5/TRADD/BRK1/ABL1/MYO6/TUF
 ?
 'HSPD1/IL10RA/ATP6VOD1/FCGR2B/HLA-DOA/CIITA/CALM2/VDR/TLR2/PLK3/TRADD/BCL10/RABF
 'YWHAG/HDAC10/SRF/CASP8/BAD/VAC14/RHOA/ACTN1/TBP/ACTN4/GTF2H1/SND1/RBPJ/HDAC8/HI
 '4/VDAC3/CCNE2
 'NFKB1B/CXCL10/TLR7/MX1/NXT2/PIK3CB/CASP3/PABPN1/HNRNPUL1/FDPS/HLA-DOB/ADAR/IFN
 18A/PABPC1L/EIF2B1/GEMIN2/CASC3/THOC7/EIF2B4/EIF3F/DDX20/AAAS/PYM1/THOC3/ACIN1/I
 '5/CD209/HLA-B/RAC1/HLA-DRB5/TUBB2B/ACTB/ATP6V1E1/ITGA2/DYNC1LI1/ATP6VOC/CALR/CLF
 'SRSF2/MAGOH/THOC1/SRSF1/PRPF4/DHX38/PRPF38B/SF3B6/RBM8A/SNRNP70/DHX8/RP9/SNRNP
 37A/MRPL4/RPL30/RPL32/MRPL33/MRPS5/RPS27/MRPL36/RPL13/RPS9/RPL41/RPS14/MRPL11/RI
 'LGMN/AP1S1/MANBA

3/FGFR4/PIM2/STAT1/FRAT2/HDAC2/PLCB3/FGFR1/PPARD/MITF/DVL3/DAPK3/CDKN2B/HEYL/PM/
 'PSMD11/CYCS/PSMA7/DVL2/PSMD1/PSMD7/PSMB3/PSMD4/NDUFS6/PSMD3/SLC25A5/APH1B/NDUFS5
 .3/NUP43/PSMD11/PFN1/CYCS/PSMA7/RAE1/PSMD1/PSMD7/PSMB3/GPX1/PSMD4/TOMM40L/NDUFS6
 'L11/CCR5/PF4V1/CXCL17/IL4R/CSF2RB/CSF2RA/IL10RA/INHA/GDF11/TNFRSF25/IL20RB/CXCF
 15/PSMA4/VDAC3/RPS27A/GNAI3/PSMB5/NDUFB3/TUBB3/COX7B/DAXX/PSMC5/NDUFA8/UBA52/UQC

NAI3/PTGER4/GNG4/CASP8/ARHGEF11/ADCY6/RHOA/TAPBP/VEGFA/CCL3L3/TAP2/ADCY5/PDIA3/
I1/ADCY6/RHOA/VEGFA/KITLG/RAPGEF1/ADORA2B/ADCY5/PARD3/EPHA2/EGF/RASSF5/CALM3/AD
CK2/CCL3L3/PIK3R6/XCL1/ADCY5/PARD3/NFKBIB/CXCL10/CCL8/PREX1/ADCY3/CCR10/ADCY7/I

2/RHOA/VEGFA/RAPGEF1/ACTN1/ACTN4
UB1/UBE4B/CAPN2/P4HB/DNAJC1/LMAN2/PDIA4/ATF6B/SEC23B/FBX06/RPN1/UGGT1/SVIP/UBQI

./GNB1/IL2RA/NRAS/ITGA2/PDGFA/COL6A2/FGFR3/YWHAQ/COL4A2/CCND2/LAMB3/IL2RB/GRB2/

2/UBE2K/CDC16/RHOBTB1/ANAPC1/TRIP12/SMURF2/MID1/CDC26/FANCL/UBA3/FBXW11/CUL2/UF

ADD/ZNF589/ZNF544/ZNF195/ZNF354A/ZNF675/ZNF229/EIF2B5/RHEB/ZNF783/HLA-DOA/HLA-I

AG1/COL4A2/CCND2/LAMB3/ATP6V0C/DVL2/CHD4/GRB2/TUBG2/CDC42/PRKCI/ATP6V0E1/IKBKG/
PSMD8/VDAC2/PLCB2/PSMA1/COX8A/PSMA4/VDAC3/PSMB5/NDUFB3/TUBB3/DCTN1/COX7B/CLTC/C
LO/RPS27A/TLN1/UBE2D2/GLMN/RHOA/UBA52/UBE2N/TECPR1/ACTN1/BECN1/ACTN4/ARF1/NFKBII
RADD/BRK1/RAB5C/MYO6/HSP90B1/DYNC1I2/CASP8/RHOA/AHNAK2/VPS11/ARF1/PTPRC/VPS33A/I
2/PSMA1/COX8A/HSPA5/PSMA4/VDAC3/CSNK2B/PSMB5/HSPA2/NDUFB3/TUBB3/NOTCH1/CSNK2A1/C
P1/IKBKG/SLC25A5/MSX1/CHEK2/VDAC2/CCND3/HLA-D0A/HLA-F/STAT5A/NFATC4/VDAC3/CANX/C
2/GRK2/ARPC1A/ARPC5/SH3GLB1/HLA-F/ARAP1/RUFY1/VPS45/VPS35/SMAP1/DNM2/PLD2/RAB5C,

TR/CALM3/CD3G/HLA-C/TNFRSF1B/PIK3CB/CASP3/MAP3K7/DDB1/PXN/GNG2/PLCG1/HLA-E/RELA,
A/HLA-F/TLR2/TRADD/CCNE2/MAVS/OAS3/CASP8/TNFAIP3/PSMC5/IFNAR2/TAPBP/RUNX3/PSMC
3B3/CASP8/ARHGEF11/PAK2/RHOA

5C/KSR1/CASP8/BAD/RHOA/CYP27B1
A-C/PIK3CB/CASP3/SKP2/GTF2A2/EGR2/ATF6B/DDB1/GTF2E1/CCR3/PXN/TP53/HDAC5/HLA-E/I

3/PRSS1/RELA/PRKCB

PRMT5/SUMO3/EIF2B3/EIF4E2/EIF4G1/FXR1/EIF2B2/GEMIN8/PAIP1/EIF3C/EIF5B/GEMIN6/EII
C7A/STX18/ATP6V0E1/FCGR3B/M6PR/THBS1/STX7/ATP6V0D1/THBS2/FCGR2B/HLA-D0A/HLA-F/
P200/U2SURP/THOC3/ACIN1/HNRNPC/RBM22/SRSF3/SNRPD3/U2AF1L4/CCDC12/LSM3/TRA2B/HSP

L29/RPS3A/RPS6/MRPL14/RPS24/RPL10/RPL9/RPL4/MRPL3/RPL14/MRPS16/RPL24/RPL11/MRPI

AIP1/PIK3CD/AXIN1/CDK2/TGFA/BBC3/LEF1/BIRC7/FZD2/GNG5/WNT7B/JAG2/GNB2/TGFB2/RAC
5/FADD/NDUFB9/NAE1/WIPI1/ATP2A3/COX6B1/MAPT/PSMD9/WNT4/PSMD8/VDAC2/PLCB2/PSMA1/C
3/NUP107/NUP155/MAPK11/PSMD3/FUS/NDUFS5/NDUFB9/DNAL4/HNRNPA3/WIPI1/COX6B1/PSMD9,
R6/ACVR1/IL21R/IFNAR2/GDF10/CCL3L3/IL17D/IL20RA/ACVR1B/XCL1/IL32/OSM/CD4/IL17RA,
RB/NDUFA1/PSMC3/NDUFA13/NDUFS8/ADCY5/COX7A2/BCL2L1/COX6C/PSMB1/CALM3/MFN1/NDUF

/CALM3/ADCY3/GNA13/HLA-C/ADCY7/PIK3CB/CASP3/ATF6B/CCR3/PXN/TP53/GNG2/GNAS/HLA-E,
Y3
PIK3CB/CCL19/CCR3/PXN/GNG2/PLCG1/RELA/RAC3/PRKCB/ARRB1/CCR2/VAV3/IKBKB

N2/PRKCSH/MOGS/DERL1/SKP1/DERL3/UBE2J1/EIF2AK1/RAD23A/UGGT2

ITCP1/PKN3/YWHAB/IKBK/IBSP/IGF1R/IL4R/GNB4/ITGB8/ANGPT2/THBS1/GNGT2/RPS6KB2/THI

3C/XIAP/KEAP1/UBE2W/SMURF1/UBE3C/PIAS2/ANAPC13/ANAPC2/NEDD4L/UBOX5/CBLB/ERCC8/UI

3/TLR2/ZNF605/ZNF426/TRADD/MAVS/ZNF607/ZNF746/OAS3/ZNF7/ZNF623/CASP8/DAXX/BAD/II

IBSP/HEY1/TRAF3/PARD6B/ITGB8/LLGL1/PARD6G/FADD/THBS1/WNT4/RPS6KB2/MFNG/ATP6VOD1,
ASP8/MAP3K10/PSMC5/NDUFA8/POLR2I/UQCRB/NDUFA1/PSMC3/POLR2D/NDUFA13/BECN1/NRF1/TI
3/BCL2L1/ELMO2/RPTOR/CYTH3/CAPN2/FNBP1L
ELMO2/CYTH3/RAB9A/ACBD3/KLC1/PIK3CB/CASP3/MAP3K7/VPS16/NCKAP1/CASP7/KPNA4/RHOH/I
COX7B/BAD/PSMC5/NDUFA8/GRIN2D/UQCRB/NDUFA1/PSMC3/NDUFA13/NDUFS8/COX7A2/CACNA1D/C
CNE2/TLN1/SRF/VAC14/ADCY6/ANAPC5/TBP/ADCY5/CRTC2/CD4/CDC27/BCL2L1/ATR/RANBP3/M
/FGFR2/HSPA2/ACAP3/CLTC/RAB11A/RHOA/ARF1/AP2A2/WIPF2/SNX3/PARD3/ARF5/IST1/AP2B1,

/RAC3/PRKCB/SKP1
3/CD247/ENTPD1/TAP2/PDIA3/NFKBIB/CXCL10/RBPJ/CD3G/HLA-C/PIK3CB/CASP3/SKP2/MAP3K

RELA

71/NUP214/DDX19A/TARDBP/GEMIN5/RPP38/EIF3J/SMN2/TPR
FLR2/CANX/RAB5C/DYNC1I2/TUBB3
A1A/BCAS2/TRA2A/SRSF10/PRPF40A/DDX46/SRSF7/PRPF40B/SRSF4/CWC15

20/RPL10A/RPS18/MRPL21/RPL12/RPS28/MRPL24/RPL26L1/MRPS2/RPL22/RPS17/RPS15A/MRPI

1/GNB1/BID/IL2RA/NRAS/ITGA2/PDGFA/JAG1/IL15/FGFR3/RASSF1/COL4A2/CCND2/LAMB3/IL1:
COX8A/CALM2/ADAM17/PSMA4/VDAC3/CSNK2B/PSMB5/NDUFB3/TUBB3/CSNK2A1/COX7B/CASP8/BAI
/PSMD8/VCP/PSMA1/COX8A/SEC13/HSPA5/UBQLN4/PSMA4/PSMB5/FIG4/NDUFB3/TUBB3/DCTN1/C
/CXCL10/IL13RA2/CCL8/BMP8B/TNFSF15/CRLF2/TNFRSF14/CCR10/BMP2/TNFRSF1B
A12/COX5A/PSMB6/NDUFB4/KLC1/NDUFA9/CASP3/NDUFB11/PSMA3/COX4I1/KIF5B/HTRA2/TP53/I

/RELA/MYC/RAC3/PRKCB/NFATC1/IL10RB/IKBKB/TSC1/ELK1

3S2/RHEB/CCND3/LPAR5/LAMA4/HSP90AA1/TLR2/PPP2R3A/PTK2/FGFR2/HSP90B1/CCNE2/YWHAG,

ZNFAR2/TAPBP/ZNF415/ZNF404/ZNF813/TAP2/ZNF432/PDIA3/BCL2L1/SRSF2/ZNF251/SRSF1/ZNF

/THBS2/RHEB/CCND3/LAMA4/HLA-F/PPP2R3A/TRADD/PTK2/CCNE2/PTGER4/NOTCH3/NOTCH1/PPP2R3B/NDUFS8/POLR2J/ATG13/AP2A2/HTT/ACTR1A/COX7A2/AP2B1/COX6C/PSMB1/NDUFA12/COX5A/NDUFA13/NDUFB4/NDUFA9/PIK3CB/CASP3/NDUFA10/ATF6B/HLA-C/VPS26A/VPS29/STAM/

DYNC2LI1

COX6C/CSNK2A2/PSMB1/CAV1/NDUFA12/COX5A/PSMB6/NDUFB4/KLC1/NDUFA9/PIK3CB/CASP3/NDUFA10/ATF6B/HLA-C/VPS26A/VPS29/STAM/

7

L22/RPL31/MRPS11

2RB1/E2F2/CYCS/DVL2/MSH2/IL2RB/RALA/GRB2/PAX8/TGFB3/CDC42/PML/ZBTB17/IKBKG/IGF1R/PSMC5/NDUFA8/GRIN2D/UQCRB/NDUFA1/PSMC3/NDUFA13/BECN1/NDUFS8/ATG13/CDK5R1/COX7B/OPTN/DAXX/BAD/PSMC5/HNRNPA1/NDUFA8/GRIN2D/UQCRB/NDUFA1/PSMC3/NDUFA13/BECN1,

PLCG1/PARK7/GNAS/PSMB7

/PPP2R5B/CDC37/GNG4/BAD/PIK3R5/PRKAA2/IFNAR2/VEGFA/KITLG

F282/ZNF43/ZNF74/ZNF480/ZNF256/ZNF300/ZNF124/TNFRSF14/HLA-C/ZNF765/ZNF160/ZNF22:

2R5B/CASP8/BAD/IFNAR2/VEGFA/LFNG
PSMB6/NDUFB4/KLC1/AP2A1/POLR2E/NDUFA9/POLR2B/CASP3/NDUFB11/PSMA3/COX4I1

UFB11/PSMA3/CAV2/COX4I1/ATF6B
-DOB
CAV2/IGF2R/CAPZA2/ASAP3/KIF5B/HLA-E/ARRB1/MVB12B/VTG1/RAB22A/RAB11FIP1/RAB7A/TS

R/HEY1/TRAF3/IL4R/GNB4/FADD/CSF2RB/RBX1/CBL/RALGDS/CSF2RA/CCDC6/GNGT2/WNT4/RPS6
A2/PSEN2/CACNA1D/COX6C/APBB1/ATP2A2/CSNK2A2/PSMB1/CAPN2/CALM3/NDUFA12/COX5A/PSM
/NDUFS8/WDR41/ATG13/ACTR1A/COX7A2/BCL2L1/SEH1L/COX6C/PSMB1/RAB1A/NDUFA12/COX5A/

2/PIK3CB/ZNF267/CASP3/MAP3K7/EIF2B1/ZNF549/ZNF792/ZNF530/ZNF101/ZNF528/ZNF768/E

G101/SMAD2/HSPA1A/GIT2/TGFBR1/PLD1/PIP5K1A/RNF41/CHMP6/ACAP1/CHMP2B/SNX2/EPN1/A

KB2/RALB/TRAF4/PLCB2/CCND3/LPAR5/VHL/LAMA4/CALM2/HSP90AA1/STAT5A/CTBP2/CTNNA1/P
B6/NDUFB4/KLC1/NDUFA9/PIK3CB/CASP3/NDUFB11/PSMA3/COX4I1/NCSTN/CASP7/NOX1/KIF5B
PSMB6/NXT2/NDUFB4/KLC1/NDUFA9/TNFRSF1B/CASP3/NDUFB11/PSMA3/COX4I1/KIF5B/ULK1/TP

IF2B4/HLA-DOB/ZNF430/ZNF473/ZNF669/TP53/IFNG/ZNF587/ZNF682/EIF2B3/NECTIN2/PPP1C

RFGAP3/IQSEC2/SMURF2/ZFYVE27/GBF1/HLA-G/SMAD3/CHMP4A/SNX6/PARD6A

TK2/PLD2/ABL1/GNAI3/FGFR2/HSP90B1/CCNE2/PTGER4/NOTCH3/NOTCH1/GLI1/MSH6/GNG4/CAS
53/HNRNPA2B1/PSMB7/UBQLN2/SRSF3/DERL1/NDUFA7/NDUFB2/ATXN2/NUP214/NEFL/PSMD12/NE

B/SRSF3/ZNF785/HLA-E/EIF2B2/RELA/ZNF808/ZNF701/ZNF107/ZNF419/ZNF135/POU2F1/POU2

P8/ARHGEF11/BAD/ADCY6/RHOA/IFNAR2/VEGFA/KITLG

FH/TARDBP/SMCR8/DNAH14/CHMP2B/SRSF7/NDUFA6/TPR/COX6A1/COX7A2L/PSMD6/GABARAP/PPP

F2/EIF2AK1/ZFP69/ZNF257/ZFP82/ZNF845/ZNF841/ZNF347/IKBKB/ZNF766/TSC1/ZNF431/ZNF

'3CB/NUP133/UQCR10/NDUFA11/UQCRFS1/NUP50/NDUFS3/PSMC2/NDUFB10/NDUFB7/NCBP1/EIF2S

211/PIK3R2/ZNF506/ZNF8/ZNF714/ZNF331/SRSF7/ZNF439/ZNF84/ZNF57/ZNF550/ZNF736/TIC

;1/NDUFA3/NRG2/DCTN3/PSMA6/NDUFB5/RB1CC1/WIPI2/VAPB/NDUFAB1

AM1/ZNF614/SRSF4/IL12A/FASLG/ZNF85/HLA-G/ZNF777/ZFP69B/TAB1/ZNF226/ZNF250/ZNF12

2/EIF2S1/ZNF562/ZNF764/ZFP30/ZNF416/ZNF90/TYK2/ZNF559/ZNF26/CASP9/ZNF773/ZIK1/ZI

√F133/IRAK4/ZNF547/ZNF234/ZNF200/TNFRSF1A/TNFSF14/AKT3/ZNF786/TBK1/ZNF286A/ZNF28

34/ZNF551/ZNF182/ZNF778/ZNF613/JAK2/ZNF552/ZNF514/MTOR/ZNF517/ZNF285/ZNF667/ZNF

365/ZNF227/ZNF850/ZNF230/APAF1/ZNF713/ZNF630/ZNF77/ZNF708/BST2/EIF2AK2/ZNF670/Z

NF233/ZNF248/ZNF585B/NXF1/BCL2/ZNF350