

Supplementary Table 12: Gene-wide p-values in TRACK-HD, REGISTRY, the TRACK-REGISTRY meta-analysis and GeM for all genes in the top 14 pathways from GeM

Pathway	Entrez	Gene Symbol	Chr	Start	End	p(TRACK)	p(REGISTRY)	p(META)	p(GeM)	Description
GO: 32300	4437	MSH3	5	79950467	80172634	2.94E-08	9.52E-04	8.88E-11	2.03E-02	mismatch repair complex
GO: 30983	4437	MSH3	5	79950467	80172634	2.94E-08	9.52E-04	8.88E-11	2.03E-02	mismatched DNA binding
GO: 6298	4437	MSH3	5	79950467	80172634	2.94E-08	9.52E-04	8.88E-11	2.03E-02	mismatch repair
KEGG 3430	4437	MSH3	5	79950467	80172634	2.94E-08	9.52E-04	8.88E-11	2.03E-02	KEGG_MISMATCH_REPAIR
KEGG 3430	5425	POLD2	7	44154279	44163169	7.21E-04	3.12E-01	2.75E-03	5.20E-01	KEGG_MISMATCH_REPAIR
KEGG 3430	3978	LIG1	19	48618703	48673560	1.65E-02	8.28E-02	5.35E-04	6.51E-02	KEGG_MISMATCH_REPAIR
KEGG 3430	27030	MLH3	14	75480467	75518235	1.69E-02	6.69E-01	1.47E-01	6.59E-03	KEGG_MISMATCH_REPAIR
GO: 6298	27030	MLH3	14	75480467	75518235	1.69E-02	6.69E-01	1.47E-01	6.59E-03	mismatch repair
GO: 32407	27030	MLH3	14	75480467	75518235	1.69E-02	6.69E-01	1.47E-01	6.59E-03	MutSalpha complex binding
GO: 32300	27030	MLH3	14	75480467	75518235	1.69E-02	6.69E-01	1.47E-01	6.59E-03	mismatch repair complex
GO: 30983	27030	MLH3	14	75480467	75518235	1.69E-02	6.69E-01	1.47E-01	6.59E-03	mismatched DNA binding
GO: 10822	5534	PPP3R1	2	68405989	68479651	1.82E-02	4.76E-01	6.12E-01	8.40E-01	positive regulation of mitochondrion organization
GO: 33683	2068	ERCC2	19	45854649	45873845	2.03E-02	8.83E-01	3.45E-01	7.45E-01	nucleotide-excision repair, DNA incision
GO: 90200	84334	APOPT1	14	104029299	104057236	2.51E-02	8.19E-01	4.40E-01	8.18E-01	positive regulation of release of cytochrome c from mitochondria
GO: 10822	84334	APOPT1	14	104029299	104057236	2.51E-02	8.19E-01	4.40E-01	8.18E-01	positive regulation of mitochondrion organization
GO: 32389	5395	PMS2	7	6012870	6048737	2.58E-02	3.66E-01	8.84E-03	1.91E-05	MutLalpha complex
GO: 32300	5395	PMS2	7	6012870	6048737	2.58E-02	3.66E-01	8.84E-03	1.91E-05	mismatch repair complex
GO: 30983	5395	PMS2	7	6012870	6048737	2.58E-02	3.66E-01	8.84E-03	1.91E-05	mismatched DNA binding
KEGG 3430	5395	PMS2	7	6012870	6048737	2.58E-02	3.66E-01	8.84E-03	1.91E-05	KEGG_MISMATCH_REPAIR
GO: 6298	5395	PMS2	7	6012870	6048737	2.58E-02	3.66E-01	8.84E-03	1.91E-05	mismatch repair
GO: 32407	5395	PMS2	7	6012870	6048737	2.58E-02	3.66E-01	8.84E-03	1.91E-05	MutSalpha complex binding
GO: 30983	4439	MSH5	6	31707725	31730455	4.35E-02	8.54E-01	7.73E-01	5.14E-01	mismatched DNA binding
GO: 6298	4439	MSH5	6	31707725	31730455	4.35E-02	8.54E-01	7.73E-01	5.14E-01	mismatch repair
KEGG 3430	5982	RFC2	7	73645832	73668738	4.80E-02	5.91E-01	2.02E-02	4.46E-01	KEGG_MISMATCH_REPAIR
GO: 30983	7508	XPC	3	14186647	14220172	5.52E-02	1.04E-01	2.77E-02	5.53E-01	mismatched DNA binding
KEGG 3430	6119	RPA3	7	7676575	7758238	6.55E-02	7.22E-01	9.17E-02	4.40E-01	KEGG_MISMATCH_REPAIR
GO: 32300	4292	MLH1	3	37034841	37092337	6.98E-02	3.97E-04	1.28E-04	4.13E-04	mismatch repair complex
GO: 6298	4292	MLH1	3	37034841	37092337	6.98E-02	3.97E-04	1.28E-04	4.13E-04	mismatch repair
KEGG 3430	4292	MLH1	3	37034841	37092337	6.98E-02	3.97E-04	1.28E-04	4.13E-04	KEGG_MISMATCH_REPAIR
GO: 30983	4292	MLH1	3	37034841	37092337	6.98E-02	3.97E-04	1.28E-04	4.13E-04	mismatched DNA binding
GO: 32407	4292	MLH1	3	37034841	37092337	6.98E-02	3.97E-04	1.28E-04	4.13E-04	MutSalpha complex binding
GO: 32389	4292	MLH1	3	37034841	37092337	6.98E-02	3.97E-04	1.28E-04	4.13E-04	MutLalpha complex
GO: 33683	2067	ERCC1	19	45910591	45927177	7.32E-02	3.96E-01	2.69E-01	3.30E-01	nucleotide-excision repair, DNA incision
GO: 32407	545	ATR	3	142168077	142297668	7.62E-02	7.94E-01	2.71E-01	2.97E-01	MutSalpha complex binding
GO: 90140	79594	MUL1	1	20825941	20834674	8.94E-02	5.22E-01	5.27E-01	4.68E-01	regulation of mitochondrial fission
GO: 90141	79594	MUL1	1	20825941	20834674	8.94E-02	5.22E-01	5.27E-01	4.68E-01	positive regulation of mitochondrial fission

GO: 10822	79594	MUL1	1	20825941	20834674	8.94E-02	5.22E-01	5.27E-01	4.68E-01	positive regulation of mitochondrion organization
GO: 90200	26355	FAM162A	3	122103023	122128961	1.32E-01	7.57E-01	6.93E-01	8.40E-01	positive regulation of release of cytochrome c from mitochondria
GO: 10822	26355	FAM162A	3	122103023	122128961	1.32E-01	7.57E-01	6.93E-01	8.40E-01	positive regulation of mitochondrion organization
GO:1900063	56947	MFF	2	228192228	228222549	1.52E-01	9.63E-01	5.92E-01	3.29E-01	regulation of peroxisome organization
GO: 10822	56947	MFF	2	228192228	228222549	1.52E-01	9.63E-01	5.92E-01	3.29E-01	positive regulation of mitochondrion organization
GO: 90200	56947	MFF	2	228192228	228222549	1.52E-01	9.63E-01	5.92E-01	3.29E-01	positive regulation of release of cytochrome c from mitochondria
GO: 32389	7486	WRN	8	30890778	31031277	1.66E-01	5.59E-01	6.60E-01	3.60E-01	MutLalpha complex
GO: 32300	7486	WRN	8	30890778	31031277	1.66E-01	5.59E-01	6.60E-01	3.60E-01	mismatch repair complex
GO: 10822	637	BID	22	18216906	18257431	1.77E-01	2.99E-02	7.33E-02	2.11E-01	positive regulation of mitochondrion organization
GO: 90200	637	BID	22	18216906	18257431	1.77E-01	2.99E-02	7.33E-02	2.11E-01	positive regulation of release of cytochrome c from mitochondria
GO: 90141	54708	MARCH_	10	94050920	94113721	1.81E-01	8.26E-03	4.51E-01	5.33E-02	positive regulation of mitochondrial fission
GO: 10822	54708	MARCH_	10	94050920	94113721	1.81E-01	8.26E-03	4.51E-01	5.33E-02	positive regulation of mitochondrion organization
GO: 90140	54708	MARCH_	10	94050920	94113721	1.81E-01	8.26E-03	4.51E-01	5.33E-02	regulation of mitochondrial fission
KEGG 3430	29935	RPA4	23	96138907	96140466	1.81E-01	N/A	N/A	N/A	KEGG_MISMATCH_REPAIR
GO: 10822	572	BAD	11	64037300	64052176	1.87E-01	2.48E-01	4.16E-01	1.79E-01	positive regulation of mitochondrion organization
GO: 90200	572	BAD	11	64037300	64052176	1.87E-01	2.48E-01	4.16E-01	1.79E-01	positive regulation of release of cytochrome c from mitochondria
GO: 33683	2071	ERCC3	2	128014866	128051752	1.97E-01	4.27E-01	8.61E-01	7.39E-03	nucleotide-excision repair, DNA incision
GO: 10822	708	C1QBP	17	5336099	5342471	2.05E-01	8.72E-01	2.59E-01	5.99E-01	positive regulation of mitochondrion organization
GO:1900063	57506	MAVS	20	3827446	3856770	2.13E-01	7.14E-02	2.31E-01	8.82E-01	regulation of peroxisome organization
GO: 10822	5366	PMAIP1	18	57567192	57571538	2.38E-01	1.05E-01	2.58E-02	1.10E-01	positive regulation of mitochondrion organization
GO: 90200	5366	PMAIP1	18	57567192	57571538	2.38E-01	1.05E-01	2.58E-02	1.10E-01	positive regulation of release of cytochrome c from mitochondria
GO: 90200	29108	PYCARD	16	31212807	31214097	2.44E-01	4.42E-01	1.57E-01	N/A	positive regulation of release of cytochrome c from mitochondria
GO: 10822	29108	PYCARD	16	31212807	31214097	2.44E-01	4.42E-01	1.57E-01	N/A	positive regulation of mitochondrion organization
GO: 30983	2956	MSH6	2	48010221	48034092	2.46E-01	3.15E-01	1.58E-01	9.36E-02	mismatched DNA binding
GO: 32300	2956	MSH6	2	48010221	48034092	2.46E-01	3.15E-01	1.58E-01	9.36E-02	mismatch repair complex
KEGG 3430	2956	MSH6	2	48010221	48034092	2.46E-01	3.15E-01	1.58E-01	9.36E-02	KEGG_MISMATCH_REPAIR
GO: 6298	2956	MSH6	2	48010221	48034092	2.46E-01	3.15E-01	1.58E-01	9.36E-02	mismatch repair
GO: 10822	51100	SH3GLB1	1	87170253	87213867	2.55E-01	7.63E-01	2.92E-01	5.27E-01	positive regulation of mitochondrion organization
GO: 90141	664	BNIP3	10	133781204	133795435	2.63E-01	1.17E-01	7.70E-01	7.19E-01	positive regulation of mitochondrial fission
GO: 90140	664	BNIP3	10	133781204	133795435	2.63E-01	1.17E-01	7.70E-01	7.19E-01	regulation of mitochondrial fission
GO: 10822	664	BNIP3	10	133781204	133795435	2.63E-01	1.17E-01	7.70E-01	7.19E-01	positive regulation of mitochondrion organization

GO: 90200	664	BNIP3	10	133781204	133795435	2.63E-01	1.17E-01	7.70E-01	7.19E-01	positive regulation of release of cytochrome c from mitochondria
GO: 32407	4595	MUTYH	1	45794914	45806142	2.75E-01	4.31E-01	1.97E-01	1.97E-01	MutSalpa complex binding
GO: 6298	4595	MUTYH	1	45794914	45806142	2.75E-01	4.31E-01	1.97E-01	1.97E-01	mismatch repair
GO: 10822	2810	SFN	1	27189633	27190947	2.78E-01	4.30E-01	2.23E-01	7.65E-01	positive regulation of mitochondrion organization
KEGG 3430	5424	POLD1	19	50887580	50921275	2.84E-01	6.48E-01	6.86E-01	2.11E-01	KEGG_MISMATCH_REPAIR
KEGG 3430	6118	RPA2	1	28218049	28241236	2.94E-01	2.04E-02	1.18E-01	7.45E-01	KEGG_MISMATCH_REPAIR
GO: 6298	2072	ERCC4	16	14014014	14046205	3.00E-01	5.58E-01	2.66E-01	6.21E-01	mismatch repair
GO: 33683	2072	ERCC4	16	14014014	14046205	3.00E-01	5.58E-01	2.66E-01	6.21E-01	nucleotide-excision repair, DNA incision
KEGG 3430	5983	RFC3	13	34392206	34540695	3.15E-01	7.80E-01	7.18E-01	6.12E-01	KEGG_MISMATCH_REPAIR
GO: 90200	7157	TP53	17	7571720	7590868	3.21E-01	5.79E-01	2.20E-01	2.47E-01	positive regulation of release of cytochrome c from mitochondria
GO: 10822	7157	TP53	17	7571720	7590868	3.21E-01	5.79E-01	2.20E-01	2.47E-01	positive regulation of mitochondrion organization
GO: 10822	207	AKT1	14	105235686	105262080	3.62E-01	4.10E-01	5.64E-01	3.96E-01	positive regulation of mitochondrion organization
KEGG 3430	5981	RFC1	4	39289069	39368001	3.64E-01	6.29E-01	7.60E-01	6.19E-01	KEGG_MISMATCH_REPAIR
GO: 90200	581	BAX	19	49458117	49465055	3.65E-01	1.25E-01	2.47E-01	8.13E-01	positive regulation of release of cytochrome c from mitochondria
GO: 10822	581	BAX	19	49458117	49465055	3.65E-01	1.25E-01	2.47E-01	8.13E-01	positive regulation of mitochondrion organization
GO: 90200	90427	BMF	15	40380091	40401075	3.71E-01	5.25E-02	3.21E-02	5.08E-01	positive regulation of release of cytochrome c from mitochondria
GO: 10822	90427	BMF	15	40380091	40401075	3.71E-01	5.25E-02	3.21E-02	5.08E-01	positive regulation of mitochondrion organization
GO: 10822	10891	PPARGC	4	23793644	23891700	3.79E-01	1.49E-01	1.47E-01	3.43E-01	positive regulation of mitochondrion organization
GO: 10822	65018	PINK1	1	20959948	20978004	3.83E-01	8.71E-01	5.33E-01	4.83E-01	positive regulation of mitochondrion organization
GO: 90200	65018	PINK1	1	20959948	20978004	3.83E-01	8.71E-01	5.33E-01	4.83E-01	positive regulation of release of cytochrome c from mitochondria
GO: 90200	10962	MLLT11	1	151032151	151040973	3.90E-01	7.62E-01	9.23E-01	4.75E-01	positive regulation of release of cytochrome c from mitochondria
GO: 10822	10962	MLLT11	1	151032151	151040973	3.90E-01	7.62E-01	9.23E-01	4.75E-01	positive regulation of mitochondrion organization
GO: 32300	4436	MSH2	2	47630206	47710367	3.98E-01	3.10E-01	7.03E-01	5.49E-01	mismatch repair complex
GO: 30983	4436	MSH2	2	47630206	47710367	3.98E-01	3.10E-01	7.03E-01	5.49E-01	mismatched DNA binding
GO: 6298	4436	MSH2	2	47630206	47710367	3.98E-01	3.10E-01	7.03E-01	5.49E-01	mismatch repair
KEGG 3430	4436	MSH2	2	47630206	47710367	3.98E-01	3.10E-01	7.03E-01	5.49E-01	KEGG_MISMATCH_REPAIR
GO: 10822	841	CASP8	2	202098166	202152434	4.15E-01	8.81E-01	4.49E-01	3.35E-01	positive regulation of mitochondrion organization
GO: 10822	7533	YWHAH	22	32340479	32353590	4.25E-01	7.16E-01	2.86E-01	6.25E-01	positive regulation of mitochondrion organization
GO: 10822	8655	DYNLL1	12	120907660	120936298	4.50E-01	3.11E-01	4.07E-01	4.21E-01	positive regulation of mitochondrion organization
GO: 32407	5378	PMS1	2	190648811	190742355	4.57E-01	8.23E-01	3.36E-01	7.24E-02	MutSalpa complex binding
GO: 32389	5378	PMS1	2	190648811	190742355	4.57E-01	8.23E-01	3.36E-01	7.24E-02	MutLalpha complex
GO: 32300	5378	PMS1	2	190648811	190742355	4.57E-01	8.23E-01	3.36E-01	7.24E-02	mismatch repair complex
GO: 30983	5378	PMS1	2	190648811	190742355	4.57E-01	8.23E-01	3.36E-01	7.24E-02	mismatched DNA binding

GO: 6298	5378	PMS1	2	190648811	190742355	4.57E-01	8.23E-01	3.36E-01	7.24E-02	mismatch repair
GO: 33683	2073	ERCC5	13	103498191	103528351	4.73E-01	7.10E-01	3.43E-01	2.62E-01	nucleotide-excision repair, DNA incision
GO: 10822	7755	ZNF205	16	3162563	3170518	4.74E-01	9.01E-01	7.24E-01	9.47E-01	positive regulation of mitochondrion organization
GO: 90200	8743	TNFSF10	3	172223298	172241297	4.77E-01	6.95E-01	6.77E-01	6.09E-01	positive regulation of release of cytochrome c from mitochondria
GO: 10822	8743	TNFSF10	3	172223298	172241297	4.77E-01	6.95E-01	6.77E-01	6.09E-01	positive regulation of mitochondrion organization
KEGG 3430	6742	SSBP1	7	141438121	141450288	4.81E-01	8.18E-01	8.67E-01	5.17E-01	KEGG_MISMATCH_REPAIR
GO: 10822	28958	COA3	17	40949652	40950704	4.87E-01	1.75E-03	5.11E-01	N/A	positive regulation of mitochondrion organization
GO: 6298	11277	TREX1	3	48506919	48509044	4.91E-01	4.76E-01	7.94E-01	4.11E-01	mismatch repair
GO: 32407	11277	TREX1	3	48506919	48509044	4.91E-01	4.76E-01	7.94E-01	4.11E-01	MutSalpha complex binding
GO: 33683	22909	FAN1	15	31196055	31235311	5.30E-01	2.16E-06	1.15E-04	2.10E-09	nucleotide-excision repair, DNA incision
GO: 10822	10572	SIVA1	14	105219470	105225996	5.32E-01	1.48E-01	6.74E-01	8.89E-01	positive regulation of mitochondrion organization
GO: 6298	9156	EXO1	1	242011493	242053241	5.56E-01	9.35E-01	9.03E-01	2.23E-01	mismatch repair
KEGG 3430	9156	EXO1	1	242011493	242053241	5.56E-01	9.35E-01	9.03E-01	2.23E-01	KEGG_MISMATCH_REPAIR
GO: 90200	10105	PPIF	10	81107220	81115090	5.62E-01	2.02E-01	4.28E-01	4.88E-01	positive regulation of release of cytochrome c from mitochondria
GO: 10822	10105	PPIF	10	81107220	81115090	5.62E-01	2.02E-01	4.28E-01	4.88E-01	positive regulation of mitochondrion organization
GO: 6298	7161	TP73	1	3569129	3652765	5.69E-01	3.18E-01	4.40E-01	5.54E-01	mismatch repair
GO: 10822	7531	YWHAE	17	1247834	1303556	5.70E-01	8.16E-01	4.96E-01	5.15E-01	positive regulation of mitochondrion organization
GO: 10822	7532	YWHAG	7	75956108	75988342	5.78E-01	4.82E-01	9.74E-01	8.36E-02	positive regulation of mitochondrion organization
GO: 10822	7534	YWHAZ	8	101930804	101965623	5.89E-01	1.51E-01	1.89E-01	5.93E-02	positive regulation of mitochondrion organization
GO: 90140	64423	INF2	14	105155943	105185947	5.93E-01	2.11E-01	2.83E-01	5.52E-01	regulation of mitochondrial fission
GO: 10822	578	BAK1	6	33540323	33548070	5.98E-01	7.98E-01	7.78E-01	3.03E-01	positive regulation of mitochondrion organization
GO: 90200	578	BAK1	6	33540323	33548070	5.98E-01	7.98E-01	7.78E-01	3.03E-01	positive regulation of release of cytochrome c from mitochondria
GO: 33683	4913	NTHL1	16	2089816	2097867	6.25E-01	5.50E-01	4.66E-01	6.35E-01	nucleotide-excision repair, DNA incision
GO: 90200	10018	BCL2L11	2	111878491	111926022	6.27E-01	8.58E-01	8.05E-01	1.51E-02	positive regulation of release of cytochrome c from mitochondria
GO: 10822	10018	BCL2L11	2	111878491	111926022	6.27E-01	8.58E-01	8.05E-01	1.51E-02	positive regulation of mitochondrion organization
GO: 10822	4836	NMT1	17	43138680	43186384	6.37E-01	9.42E-01	9.35E-01	4.65E-01	positive regulation of mitochondrion organization
GO: 10822	10971	YWHAQ	2	9724106	9771106	6.38E-01	1.92E-01	6.28E-01	7.69E-01	positive regulation of mitochondrion organization
GO: 10822	7529	YWHAB	20	43514344	43537161	6.50E-01	2.53E-01	4.98E-01	8.31E-01	positive regulation of mitochondrion organization
GO: 6298	10714	POLD3	11	74303575	74354105	6.51E-01	8.79E-01	6.36E-01	1.52E-01	mismatch repair
KEGG 3430	10714	POLD3	11	74303575	74354105	6.51E-01	8.79E-01	6.36E-01	1.52E-01	KEGG_MISMATCH_REPAIR
GO: 30983	6996	TDG	12	104359593	104382656	6.84E-01	1.83E-01	2.10E-01	4.78E-01	mismatched DNA binding
GO: 6298	6996	TDG	12	104359593	104382656	6.84E-01	1.83E-01	2.10E-01	4.78E-01	mismatch repair
GO: 90140	1723	DHODH	16	72042643	72059316	6.96E-01	9.59E-01	7.30E-01	4.85E-01	regulation of mitochondrial fission

GO: 6298	25	ABL1	9	133589268	133763062	6.97E-01	6.47E-01	9.21E-01	1.81E-01	mismatch repair
GO: 30983	4438	MSH4	1	76262556	76378923	7.24E-01	2.05E-01	2.13E-01	1.40E-01	mismatched DNA binding
KEGG 3430	5985	RFC5	12	118454506	118470044	7.38E-01	1.15E-01	2.33E-01	3.95E-01	KEGG_MISMATCH_REPAIR
GO:1900063	10059	DNM1L	12	32832137	32898584	7.55E-01	8.32E-01	6.94E-01	1.36E-03	regulation of peroxisome organization
GO: 90141	10059	DNM1L	12	32832137	32898584	7.55E-01	8.32E-01	6.94E-01	1.36E-03	positive regulation of mitochondrial fission
GO: 90200	10059	DNM1L	12	32832137	32898584	7.55E-01	8.32E-01	6.94E-01	1.36E-03	positive regulation of release of cytochrome c from mitochondria
GO: 10822	10059	DNM1L	12	32832137	32898584	7.55E-01	8.32E-01	6.94E-01	1.36E-03	positive regulation of mitochondrion organization
GO: 90140	10059	DNM1L	12	32832137	32898584	7.55E-01	8.32E-01	6.94E-01	1.36E-03	regulation of mitochondrial fission
KEGG 3430	6117	RPA1	17	1733273	1802848	7.75E-01	2.96E-01	5.51E-01	4.76E-01	KEGG_MISMATCH_REPAIR
GO: 10822	5533	PPP3CC	8	22298483	22398657	7.99E-01	4.58E-01	7.29E-01	3.38E-01	positive regulation of mitochondrion organization
KEGG 3430	5984	RFC4	3	186507681	186524484	8.08E-01	7.04E-01	7.95E-01	3.01E-01	KEGG_MISMATCH_REPAIR
GO: 4748	6240	RRM1	11	4115924	4160106	8.20E-01	6.60E-01	9.85E-01	3.40E-01	ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor
GO: 16728	6240	RRM1	11	4115924	4160106	8.20E-01	6.60E-01	9.85E-01	3.40E-01	oxidoreductase activity, acting on CH or CH2 groups, disulfide as acceptor
GO: 30983	5111	PCNA	20	5095599	5107268	8.29E-01	2.76E-01	6.40E-01	3.55E-01	mismatched DNA binding
KEGG 3430	5111	PCNA	20	5095599	5107268	8.29E-01	2.76E-01	6.40E-01	3.55E-01	KEGG_MISMATCH_REPAIR
GO: 6298	5111	PCNA	20	5095599	5107268	8.29E-01	2.76E-01	6.40E-01	3.55E-01	mismatch repair
GO: 90200	638	BIK	22	43506754	43525718	8.52E-01	6.42E-01	8.52E-01	1.19E-01	positive regulation of release of cytochrome c from mitochondria
GO: 10822	638	BIK	22	43506754	43525718	8.52E-01	6.42E-01	8.52E-01	1.19E-01	positive regulation of mitochondrion organization
GO: 10822	596	BCL2	18	60790579	60986613	8.65E-01	5.93E-01	4.81E-01	6.54E-01	positive regulation of mitochondrion organization
GO: 10822	3002	GZMB	14	25100160	25103432	8.84E-01	8.26E-01	8.18E-01	6.33E-01	positive regulation of mitochondrion organization
GO: 10822	27113	BBC3	19	47724079	47736023	8.89E-01	4.98E-01	7.87E-01	2.78E-01	positive regulation of mitochondrion organization
GO: 90200	27113	BBC3	19	47724079	47736023	8.89E-01	4.98E-01	7.87E-01	2.78E-01	positive regulation of release of cytochrome c from mitochondria
GO: 16728	6241	RRM2	2	10262695	10271546	8.96E-01	3.35E-01	3.69E-01	2.65E-01	oxidoreductase activity, acting on CH or CH2 groups, disulfide as acceptor
GO: 4748	6241	RRM2	2	10262695	10271546	8.96E-01	3.35E-01	3.69E-01	2.65E-01	ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor
GO: 10822	8398	PLA2G6	22	38507502	38577836	9.01E-01	2.91E-01	6.64E-01	1.80E-01	positive regulation of mitochondrion organization
GO: 90200	8398	PLA2G6	22	38507502	38577836	9.01E-01	2.91E-01	6.64E-01	1.80E-01	positive regulation of release of cytochrome c from mitochondria
GO: 90200	8739	HRK	12	117299027	117319232	9.10E-01	6.48E-01	8.21E-01	4.30E-01	positive regulation of release of cytochrome c from mitochondria
GO: 10822	8739	HRK	12	117299027	117319232	9.10E-01	6.48E-01	8.21E-01	4.30E-01	positive regulation of mitochondrion organization

GO: 10822	5599	MAPK8	10	49609687	49643183	9.32E-01	7.42E-01	8.49E-01	7.87E-01	positive regulation of mitochondrion organization
GO: 4748	50484	RRM2B	8	103216729	103251346	9.38E-01	6.29E-01	8.45E-01	6.44E-06	ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor
GO: 16728	50484	RRM2B	8	103216729	103251346	9.38E-01	6.29E-01	8.45E-01	6.44E-06	oxidoreductase activity, acting on CH or CH2 groups, disulfide as acceptor
GO: 10822	140735	DYNLL2	17	56160780	56167618	9.58E-01	8.08E-01	8.19E-01	8.93E-01	positive regulation of mitochondrion organization
KEGG 3430	57804	POLD4	11	67118236	67121067	9.59E-01	6.48E-01	9.21E-01	3.74E-01	KEGG_MISMATCH_REPAIR
GO: 10822	84709	MGARP	4	140187317	140201492	9.78E-01	8.81E-01	8.98E-01	1.51E-01	positive regulation of mitochondrion organization