

Table 3. Biological process enriched in each subtypes of MCC

Enriched GO BP terms by genes over-expressed in Subtype I MCC

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_	GO:0006260-DNA replication	43	5.064782	1.14E-22	INGS, DBF4, TIPIN, KIAA0101, CHEK: 715	155	16792	6.515280848	2.27E-19	2.27E-19	1.96E-19	
GOTERM_BP_	GO:0000398-mRNA splicing, via spliceosome	46	5.418139	9.41E-19	SRSF1, PRPF4B, LSM8, CNRKL1, SRSI 715	222	16792	4.866326466	1.87E-15	9.37E-16	1.62E-15	
GOTERM_BP_	GO:0051301-cell division	56	6.595995	2.31E-17	CCNT2, CDK19, AURKA, ANKLE2, CCI 715	250	16792	3.75765035	4.61E-14	1.54E-14	3.98E-14	
GOTERM_BP_	GO:0000082-G1/S transition of mitotic cell cycle	27	3.180212	8.38E-14	DBF4, MCM10, PPAT, CCNE2, PRIM1 715	102	16792	6.216700946	1.67E-10	4.17E-11	1.44E-10	
GOTERM_BP_	GO:0007062-sister chromatid cohesion	26	3.062426	8.40E-13	RAD51C, KIF22, NUP810, SPC25, SEI 715	103	16792	5.928331862	1.67E-10	3.34E-10	1.44E-09	
GOTERM_BP_	GO:0006270-DNA replication initiation	15	1.766784	1.29E-11	CDCT, CDC6, TOPBP1, MCM2, CCM2 715	32	16792	11.00874126	2.57E-08	4.28E-09	2.22E-08	
GOTERM_BP_	GO:0006351-transcription, DNA-templated	144	16.96113	2.79E-11	XRCC5, ARNT2, NAA15, CBX3, CBX7 715	1955	16792	1.729864611	5.55E-08	7.93E-09	4.79E-08	
GOTERM_BP_	GO:0006355-regulation of transcription, DNA-templated	119	14.01649	3.03E-11	ARNT2, ZNF253, CNOT6, ZNF829, K1 715	1504	16792	1.858213064	6.02E-08	7.53E-09	5.20E-08	
GOTERM_BP_	GO:0000722-telomere maintenance via recomb	11	1.648999	2.19E-10	RAD51C, SMC5, RAD51, PRIM1, POL 715	32	16792	10.27482517	4.36E-07	4.85E-08	3.77E-07	
GOTERM_BP_	GO:00007067-mitotic nuclear division	36	4.240283	4.14E-10	KIF22, HAUS6, HAUS5, HAUS1, TIPIN 715	248	16792	3.409158583	8.24E-07	8.24E-08	7.11E-07	
GOTERM_BP_	GO:0006281-DNA repair	34	4.004711	1.51E-09	KIF22, RAD51C, ERCC6L2, UNG, CHE 715	235	16792	3.397875316	3.00E-06	2.73E-07	2.59E-06	
GOTERM_BP_	GO:1901796-regulation of signal transduction b	24	2.826855	2.16E-09	EXO1, INGS, SSRP1, CDK5R1, TAF5, 715	124	16792	4.545544778	4.30E-06	3.58E-07	3.71E-06	
GOTERM_BP_	GO:0016925-protein sumoylation	22	2.591284	1.98E-08	KIAA1586, NUP160, TRIM28, SMC5, 715	117	16792	4.416042078	3.94E-05	3.03E-06	3.40E-05	
GOTERM_BP_	GO:0000731-DNA synthesis involved in DNA rep	12	1.413428	1.25E-07	EXO1, POLD3, RAD51C, RFC3, RAD5: 715	35	16792	8.052107892	2.48E-04	1.77E-05	2.14E-04	
GOTERM_BP_	GO:0006369-termination of RNA polymerase II	15	1.766784	3.69E-07	SRSF1, CSTF3, UZF2F, ALYREF, SRSF: 715	64	16792	5.504370629	7.35E-04	4.90E-05	6.35E-04	
GOTERM_BP_	GO:0006406-mRNA export from nucleus	18	2.120141	9.80E-07	ENY2, SRSF1, SRSF10, NUP160, UZA 715	100	16792	4.227356643	0.0019495	1.22E-04	0.001684	
GOTERM_BP_	GO:0000086-G2/M transition of mitotic cell cyc	20	2.355713	5.46E-06	KHDRBS1, HAUS6, HAUS5, CCP110, I 715	137	16792	3.428513093	0.018051	6.39E-04	0.009376	
GOTERM_BP_	GO:0042276-error-prone translation synthesis	8	0.942285	7.86E-06	RFC5, RPA2, RFC3, RFC4, POLE2, RFC 715	19	16792	9.888555552	0.0155178	8.68E-04	0.013497	
GOTERM_BP_	GO:0000732-strand displacement	9	1.060071	8.12E-06	EXO1, RAD51C, USP91, BRIP1, R 715	26	16792	8.129532006	0.0160321	8.50E-04	0.013948	
GOTERM_BP_	GO:0034080-CENP-A-containing nucleosome as:	11	1.295642	9.72E-06	CENPO, CENPL, RSF1, CENPA, HJURP 715	43	16792	6.007871199	0.0191712	9.67E-04	0.016706	
GOTERM_BP_	GO:0000730-chromosome segregation	13	1.531213	2.60E-05	DSN1, NUF2, NDC80, BRCA1, SPC25 715	68	16792	4.489839572	0.0503996	0.00246	0.046424	
GOTERM_BP_	GO:0008380-RNA splicing	21	2.473498	2.63E-05	RBFOX1, SNRPA3, PRPF4B, RBM4, SI 715	166	16792	2.971033785	0.0509899	0.002376	0.04516	
GOTERM_BP_	GO:0000287-regulation of transcription involv	8	0.942285	3.29E-05	CDC1, TYMS, CDC45, DHFR, PCNA, N 715	23	16792	8.168805108	0.0634559	0.002864	0.056567	
GOTERM_BP_	GO:0006297-nucleotide-excision repair, DNA g	8	0.942285	4.48E-05	RFC5, POLD3, RPA2, RFC3, RFC4, RFI 715	24	16792	7.828438228	0.0853144	0.003709	0.076936	
GOTERM_BP_	GO:0006396-RNA processing	15	1.766784	5.90E-05	CSTF3, HERR, EXOSC9, CNRKL1, UZ 715	97	16792	3.631749694	0.1108624	0.004689	0.101365	
GOTERM_BP_	GO:0006283-transcription-coupled nucleotide-e	13	1.531213	6.20E-05	RFC5, POLD3, USP7, RPA2, RFC3, RF 715	74	16792	4.125798526	0.1161191	0.004736	0.064777	
GOTERM_BP_	GO:0000245-spliceosomal complex assembly	8	0.942285	7.90E-05	CNRKL1, USPP9, SNRNP1, SART3, SN 715	26	16792	7.226250672	0.1455939	0.005811	0.135714	
GOTERM_BP_	GO:0008334-histone mRNA metabolic process	6	0.706714	8.46E-05	ZNF473, LSM11, SSB, SNRPF, SNRP 715	12	16792	11.74265734	0.1549918	0.005997	0.145247	
GOTERM_BP_	GO:1900264-positive regulation of DNA-direct	5	0.588928	1.02E-04	RFC5, RFC3, RFC4, RFC2, DSCC1 715	7	16792	16.77522478	0.1843976	0.007004	0.175768	
GOTERM_BP_	GO:0042769-DNA damage response, detection i	9	1.060071	1.08E-04	RFC5, POLD3, MRPS26, RPA2, RFC3, 715	36	16792	5.871328671	0.1932486	0.007132	0.185168	
GOTERM_BP_	GO:0019985-translesion synthesis	9	1.060071	1.08E-04	RFC5, POLD3, RPA2, RFC3, RFC4, RFI 715	36	16792	5.871328671	0.1932486	0.007132	0.185168	
GOTERM_BP_	GO:0000287-spliceosomal snRNP assembly	8	0.942285	1.32E-04	CLNS1A, SNRNP1, SART3, SNRPF, SN 715	28	16792	6.71008991	0.2312391	0.008447	0.226714	
GOTERM_BP_	GO:0031124-mRNA 3'-end processing	10	1.177856	2.26E-04	SRSF3, SRSF1, SARNP, CSTF3, UZF2 715	50	16792	4.697062937	0.3624559	0.013968	0.387756	
GOTERM_BP_	GO:0007076-mitotic chromosome condensati	6	0.706714	2.88E-04	NCAPH, NCAPG, CDC45, SMC2, NCA 715	15	16792	9.394125874	0.4367566	0.017245	0.494227	
GOTERM_BP_	GO:0006271-DNA strand elongation involved i	6	0.706714	2.88E-04	POLD3, PRIMP1, RFC3, RFC4, POLD1, 715	15	16792	9.394125874	0.4367566	0.017245	0.494227	
GOTERM_BP_	GO:0045892-negative regulation of transcription	39	4.59364	3.85E-04	XRCC5, CDK5R1, HMG82, ELF2, RSYF1 715	499	16792	1.835525597	0.5366424	0.022309	0.659891	
GOTERM_BP_	GO:0007049-cell cycle	22	2.591284	3.91E-04	CCNT2, LINS2, GMNN, SNRP, DTYM1 715	217	16792	2.380999664	0.5413658	0.022025	0.670524	
GOTERM_BP_	GO:0051297-centrosome organization	8	0.942285	3.96E-04	HAUS6, HAUS5, CEP120, CNAPS, HAI 715	33	16792	5.693409621	0.5455137	0.021667	0.678312	
GOTERM_BP_	GO:0042769-DNA damage response, detection i	9	0.824499	5.12E-04	MAD2L1, CEP57, SSB, SNRPF, SPA 715	25	16792	6.575888112	0.5935175	0.027185	0.676282	
GOTERM_BP_	GO:0006268-DNA unwinding involved in DNA r	5	0.588928	5.54E-04	MCM2, MCM4, TOP2A, RAD51, MCF 715	10	16792	11.74265734	0.6684249	0.028632	0.948243	
GOTERM_BP_	GO:0006298-mismatch repair	8	0.942285	5.79E-04	EXO1, POLD3, RPA2, MSH6, POLD1, 715	35	16792	5.368071928	0.6843165	0.029132	0.990222	
GOTERM_BP_	GO:0051170-nuclear import	6	0.706714	7.40E-04	SNRNP1, SNRPF, SNRPE, SMN2, SM 715	18	16792	7.828438228	0.7707794	0.036157	1.263347	
GOTERM_BP_	GO:0006296-nucleotide-excision repair, DNA int	8	0.942285	8.23E-04	RFC5, POLD3, RPA2, RFC3, RFC4, RF 715	37	16792	5.077905878	0.8060158	0.03921	1.405481	
GOTERM_BP_	GO:0007087-error-free translation synthesis	6	0.706714	9.69E-04	RFC5, RPA2, RFC3, RFC4, PCN1 715	19	16792	7.146415164	0.8548485	0.044912	1.65195	
GOTERM_BP_	GO:0003368-nucleotide-excision repair, DNA int	8	0.942285	9.73E-04	RFC5, POLD3, RPA2, RFC3, RFC4, RF 715	38	16792	4.944276776	0.8595688	0.040463	1.685827	
GOTERM_BP_	GO:0000734-double-strand break repair via hom	11	1.295642	0.001113	RAD51C, RPA2, NABP2, RAD51AP1, 715	74	16792	3.491060291	0.9101584	0.049128	1.894901	
GOTERM_BP_	GO:0007052-mitotic spindle organization	7	0.824499	0.001433	CENB1, SPC25, KHNTD1, NDC80, AI 715	30	16792	5.47990676	0.9424001	0.061458	2.43337	
GOTERM_BP_	GO:0006397-mRNA processing	18	2.120141	0.001663	SRSF1, RBFOX1, KHDRBS1, UZF2F, R 715	179	16792	2.361651756	0.6796276	0.069508	2.81972	
GOTERM_BP_	GO:0006409-RNA export from nucleus	7	0.824499	0.002034	NDC1, NUP160, SEH1L, RAE1, RAN, I 715	32	16792	5.137412587	0.9826454	0.082638	3.438381	
GOTERM_BP_	GO:0016032-viral process	25	2.944641	0.002216	USP7, MSH6, SLC25A4, NUP160, TAI 715	299	16792	1.963655074	0.9879276	0.087911	3.740385	
GOTERM_BP_	GO:0007077-mitotic nuclear envelope disassem	8	0.942285	0.002369	NDC1, CCNB1, CCN2B, NUP160, SEH 715	44	16792	4.270057216	0.9911099	0.091885	3.994267	
GOTERM_BP_	GO:0045893-positive regulation of transcription	37	4.358068	0.002448	ENY2, INGS, RAI1, HMG82, ELF2, RSI 715	515	16792	1.687294453	0.9923972	0.092974	4.123786	
GOTERM_BP_	GO:0006310-DNA recombination	11	1.295642	0.002677	EXO1, XRCC5, LIG3, RPAIN, END 715	83	16792	3.112511585	0.9951948	0.029976	4.502705	
GOTERM_BP_	GO:0042795-siRNA transcription from RNA pol	10	1.177856	0.002759	TAF11, CCNT2, PHAX, NABP2, ICE2, I 715	70	16792	3.355044955	0.9959194	0.100394	4.637341	
GOTERM_BP_	GO:2000001-regulation of DNA damage checkp	4	0.471143	0.003651	RPA2, WDR76, FEM1B, RNASEH2B 715	8	16792	11.74265734	0.9993129	0.128391	6.092397	
GOTERM_BP_	GO:0000076-DNA replication checkpoint	4	0.471143	0.003651	CDC6, CDC45, TIPIN, RAD17 715	8	16792	11.74265734	0.9993129	0.128391	6.092397	
GOTERM_BP_	GO:0000467-exonucleolytic trimming to genera	4	0.471143	0.003651	EXOSC9, EXOSC2, ERIZ, ER13 715	8	16792	11.74265734	0.9993129	0.128391	6.092397	
GOTERM_BP_	GO:0010569-regulation of double-strand break	5	0.588928	0.003918	KDM1A, RPA2, RAD51AP1, CHEK1, R 715	16	16792	7.339160839	0.9995965	0.134744	6.522958	
GOTERM_BP_	GO:0007051-spindle organization	5	0.588928	0.003918	CKAP5, SPAG5, TTK, AURKA, RANBP: 715	16	16792	7.339160839	0.9995965	0.134744	6.522958	
GOTERM_BP_	GO:0036297-interstrand cross-link repair	8	0.942285	0.004423	FANCL, RPA2, RAD51AP1, FANCI, RN 715	49	16792	3.834337091	0.9998531	0.148253	7.334404	
GOTERM_BP_	GO:0006376-mRNA splice site selection	5	0.588928	0.004953	SRSF1, C7ORF955-LUC12, SRSF10, L 715	17	16792	6.907445496	0.9999491	0.161826	8.178351	
GOTERM_BP_	GO:0006303-double-strand break repair via non	9	1.060071	0.005041	XRCC5, SUMO1, RIF1, MDC1, SMC5, 715	63	16792	3.355044955	0.9995974	0.161831	8.138441	
GOTERM_BP_	GO:0051383-kinetochore organization	3	0.353357	0.005264	SMC2, CENPH, SMC4 715	3	16792	23.48531469	0.9999727	0.165699	8.66972	
GOTERM_BP_	GO:0075733-intracellular transport of virus	8	0.942285	0.005542	NDC1, NUP160, SEH1L, RAE1, RAN, I 715	51	16792	3.683970931	0.9998843	0.17099	9.017343	
GOTERM_BP_	GO:0043928-exonucleolytic nuclear-transcrib	6	0.706714	0.006965	DIS3, EXOSC9, EXOSC2, LSM5, LSM2 715	29	16792	4.859030625	0.9999991	0.207001	11.31752	
GOTERM_BP_	GO:0045724-positive regulation of cilium assem	4	0.471									

GOTERM_BP	GO:0008053	mitochondrial fusion	4	0.471143	0.038794	USP30, OPA1, GDAP1, AFG3L2	715	18	16792	5.218958819	1	0.571329	49.33418
GOTERM_BP	GO:0008020	protein K6-linked ubiquitination	3	0.353357	0.042631	UBE2S, BRCA1, UBE2T	715	8	16792	8.806993007	1	0.602584	52.6995
GOTERM_BP	GO:0008156	negative regulation of DNA replication	4	0.471143	0.044654	CDC6, GMNN, TTF1, RAD17	715	19	16792	4.944276776	1	0.616109	54.38826
GOTERM_BP	GO:0007094	mitotic spindle assembly checkpoint	4	0.471143	0.050926	MAD2L1, TTK, BUB1B, MAD2L2	715	20	16792	4.697062937	1	0.66177	59.26948
GOTERM_BP	GO:0010389	regulation of G2/M transition of m3	3	0.353357	0.053295	CDKN2A, RNASEH2B, PKIA	715	9	16792	7.828438228	1	0.675075	60.98195
GOTERM_BP	GO:0042754	negative regulation of circadian rhythm	3	0.353357	0.053295	SIN3A, SFPQ, SUV39H2	715	9	16792	7.828438228	1	0.675075	60.98195
GOTERM_BP	GO:0010388	cullin neddylation	3	0.353357	0.053295	COP53, COP57B, COP58	715	9	16792	7.828438228	1	0.675075	60.98195
GOTERM_BP	GO:0006353	DNA-templated transcription, term	3	0.353357	0.053295	TTF1, SMN2, SMN1	715	9	16792	7.828438228	1	0.675075	60.98195
GOTERM_BP	GO:0016573	histone acetylation	5	0.588928	0.054798	ING5, WDR75, EPC2, TAF5, GTF3C4	715	34	16792	3.453722748	1	0.681762	62.03246
GOTERM_BP	GO:0010212	response to ionizing radiation	6	0.706714	0.056154	RAD51C, NABP2, RRM1, RNF168, TC	715	49	16792	2.875752819	1	0.687221	62.95748
GOTERM_BP	GO:0006139	nucleobase-containing compound	6	0.706714	0.056154	TYMS, METTL4, CRMP1, CTP51, BRIP	715	49	16792	2.875752819	1	0.687221	62.95748
GOTERM_BP	GO:0001701	in utero embryonic development	14	1.648999	0.056346	SRSF1, TAPT1, C2CD3, KIF3A, COP3	715	187	16792	1.758258853	1	0.684485	63.08695
GOTERM_BP	GO:0048025	negative regulation of mRNA splicing	4	0.471143	0.0576	SRSF10, SRSF12, UZAF2, TRA2B	715	21	16792	4.473393273	1	0.689467	63.92063
GOTERM_BP	GO:0000132	establishment of mitotic spindle	4	0.471143	0.0576	CENPA, NDC80, SPD1L, CDK5RAP2	715	21	16792	4.473393273	1	0.689467	63.92063
GOTERM_BP	GO:0034501	protein localization to kinetochore	3	0.353357	0.064784	TTK, BUB1B, SPD1L	715	10	16792	7.045594406	1	0.729473	68.36667
GOTERM_BP	GO:0046785	microtubule polymerization	3	0.353357	0.064784	CKAP5, FBXO5, HDGFRP3	715	10	16792	7.045594406	1	0.729473	68.36667
GOTERM_BP	GO:0035871	protein K11-linked deubiquitination	3	0.353357	0.064784	USP30, OTUD7A, USP37	715	10	16792	7.045594406	1	0.729473	68.36667
GOTERM_BP	GO:0061351	neural precursor cell proliferation	3	0.353357	0.064784	KIF3A, DBN1, ORC3	715	10	16792	7.045594406	1	0.729473	68.36667
GOTERM_BP	GO:0000723	telomere maintenance	5	0.588928	0.065192	XRCF5, POLD3, RPA2, POLD1, PCNA	715	36	16792	3.261849262	1	0.728315	68.60268
GOTERM_BP	GO:0071025	mitochondrial translational elongation	8	0.942285	0.069629	MRPL2, MRPL11, MRPL1, MRPS26, I	715	85	16792	2.210382559	1	0.74884	71.06747
GOTERM_BP	GO:0007080	mitotic metaphase plate congression	5	0.588928	0.070746	CENB1, KIF22, SEH1L, SPD1L, CDCA5	715	37	16792	3.173691174	1	0.751249	71.65908
GOTERM_BP	GO:0043044	ATP-dependent chromatin remodeling	4	0.471143	0.072103	HDAC2, ACTL6A, HNRNPCC, SMARCA4	715	23	16792	4.084402554	1	0.754783	72.36157
GOTERM_BP	GO:0000381	regulation of alternative mRNA splicing	5	0.588928	0.076535	RBFOX1, SRSF12, TRA2B, RBM4, NSF	715	38	16792	3.090172985	1	0.772721	74.54471
GOTERM_BP	GO:0035970	peptidyl-L-threonine dephosphorylation	3	0.353357	0.077008	PPM1D, PPM1E, PPM1B	715	11	16792	6.405085823	1	0.771745	74.76763
GOTERM_BP	GO:0033120	positive regulation of RNA splicing	3	0.353357	0.077008	SRSF1, UZAF2, HNRNPL	715	11	16792	6.405085823	1	0.771745	74.76763
GOTERM_BP	GO:0046811	rhythmic process	6	0.706714	0.078629	CDK5R1, SIN3A, SFPQ, CBX3, TOP2A	715	54	16792	2.609479409	1	0.775944	75.5187
GOTERM_BP	GO:0007088	regulation of mitotic nuclear division	4	0.471143	0.079906	MKI67, PDXP, FBXO5, PIN1	715	24	16792	3.914219114	1	0.778505	76.09504
GOTERM_BP	GO:0021997	neuronal plate axis specification	2	0.235571	0.083235	C2CD3, PTCH1	715	2	16792	23.48531469	1	0.78961	77.53862
GOTERM_BP	GO:0007057	spindle assembly involved in female meiosis	2	0.235571	0.083235	FBXO5, AURKA	715	2	16792	23.48531469	1	0.78961	77.53862
GOTERM_BP	GO:0006267	pre-replicative complex assembly	2	0.235571	0.083235	CDC45, ORC3	715	2	16792	23.48531469	1	0.78961	77.53862
GOTERM_BP	GO:0000354	cis assembly of pre-catalytic spliceosome	2	0.235571	0.083235	DDX23, SNRNP200	715	2	16792	23.48531469	1	0.78961	77.53862
GOTERM_BP	GO:0007346	regulation of mitotic cell cycle	5	0.588928	0.088798	CKS2, FBXO5, BIRC5, PTCH1, ZNF266	715	40	16792	2.935664336	1	0.808538	79.7691
GOTERM_BP	GO:0001833	inner cell mass cell proliferation	3	0.353357	0.089883	NCAPG2, CHEK1, PALB2	715	12	16792	5.871328671	1	0.809755	80.17932
GOTERM_BP	GO:0035518	histone H2A monoubiquitination	3	0.353357	0.089883	TRIM37, RNF168, PCGT1	715	12	16792	5.871328671	1	0.809755	80.17932
GOTERM_BP	GO:0000244	spliceosome tri-snRNP complex assembly	3	0.353357	0.089883	SRSF10, SRSF12, SRSF3	715	12	16792	5.871328671	1	0.809755	80.17932
GOTERM_BP	GO:0040015	negative regulation of multicellular organism growth	3	0.353357	0.089883	RAI1, ALMS1, PTCH1	715	12	16792	5.871328671	1	0.809755	80.17932
GOTERM_BP	GO:0006379	mRNA cleavage	3	0.353357	0.089883	CSTF3, CPSF3, CSTF1	715	12	16792	5.871328671	1	0.809755	80.17932
GOTERM_BP	GO:0006259	DNA metabolic process	4	0.471143	0.096542	MKI67, RAN, TOPBP1, KPN2A	715	26	16792	3.613125336	1	0.830201	82.52911
GOTERM_BP	GO:0003048	tRNA methylation	4	0.471143	0.096542	LCMT2, THUMP2D, METTL2A, METT	715	26	16792	3.613125336	1	0.830201	82.52911
GOTERM_BP	GO:1900439	regulation of cellular response to hypoxia	7	0.824499	0.099205	NDC1, RPA2, NUP160, SEH1L, RAE1	715	75	16792	2.191962704	1	0.836154	83.39328

Enriched GO BP terms by genes over-expressed in Subtype II MCC

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP	GO:0051092	positive regulation of NF-kappaB transcription	15	2.29709	1.35e-05	BCL10, NFKBIA, TRAF3, TRIM15, MID2	451	133	16792	4.19918977	0.0326016	0.032602	0.023714
GOTERM_BP	GO:0002052	positive regulation of neuroblast proliferation	6	0.918836	1.50E-04	DCIT, SMO, SOX10, DRD2, CX3CR1, G	451	20	16792	11.16984479	0.3090411	0.061667	0.246168
GOTERM_BP	GO:0048661	positive regulation of smooth muscle cell proliferation	9	1.378254	1.88E-04	FGFR2, NAMPT, EREG, PTGS2, EDN1	451	60	16792	5.584922395	0.3711274	0.14325	0.331337
GOTERM_BP	GO:0002053	positive regulation of mesenchymal cell proliferation	6	0.918836	5.58E-04	FGFR2, SMO, TP63, CHRDL1, MYC, FOXD1	451	26	16792	8.5921883	0.74691	0.290718	0.978345
GOTERM_BP	GO:0045944	positive regulation of transcription	45	6.891271	5.65E-04	CSF3, FGFR2, NAMPT, HNF1B, CDX1	451	981	16792	1.707927338	0.75102	0.242761	0.989945
GOTERM_BP	GO:0006954	inflammatory response	23	3.522205	5.92E-04	SELP, NFKB1, C4A, PTGS2, C4B, C4B	451	379	16792	2.295911259	0.7669241	0.215518	1.036698
GOTERM_BP	GO:0046854	phosphatidylinositol phosphorylation	10	1.531394	9.34E-04	FGFR2, FGF7, EREG, PIK3C3, PDGFR	451	94	16792	3.960937869	0.6799226	0.280101	1.632639
GOTERM_BP	GO:0014066	regulation of phosphatidylinositol phosphorylation	10	1.378254	0.001136	FGFR2, FGF7, EREG, PDGFR, FGF23	451	78	16792	4.29609415	0.9390168	0.295601	1.981587
GOTERM_BP	GO:0043123	positive regulation of I-kappaB kinase activity	13	1.990812	0.001348	BCL10, PELL1, LPAR1, MID2, TRAF3	451	161	16792	3.006376444	0.9638592	0.308253	2.347838
GOTERM_BP	GO:0045007	innate immune response	24	3.675345	0.001368	IGHG1, MBL2, BCL10, CR1, C4A, C4B	451	430	16792	2.078110658	0.9655673	0.286002	2.381661
GOTERM_BP	GO:0005877	protein targeting to Golgi	5	0.765697	0.001753	RGPD6, RGPD5, RGPD8, RGPD4, RGF	451	45	16792	9.308203991	0.9866748	0.324671	3.042537
GOTERM_BP	GO:0048015	phosphatidylinositol-mediated signaling	10	1.531394	0.002178	FGFR2, FGF7, EREG, PIK3C3, PDGFR	451	106	16792	3.512529808	0.9953284	0.360576	3.766995
GOTERM_BP	GO:0071320	cellular response to cAMP	7	1.071975	0.00257	ZFP36L1, SLC8A1, STAR, AKAP7, PDE	451	52	16792	5.012109841	0.998224	0.385645	4.43064
GOTERM_BP	GO:0018108	peptidyl-tyrosine phosphorylation	12	1.837672	0.002798	EPHA5, FGF22, FLT1, FGF7, EREG, M	451	153	16792	2.92022086	0.998987	0.388896	4.813824
GOTERM_BP	GO:0042157	lipoprotein metabolic process	6	0.918836	0.003273	APOB, BMP1, LRP1, APOA5, APOLE	451	38	16792	5.878865679	0.9996862	0.415965	5.608776
GOTERM_BP	GO:0001819	positive regulation of cytokine production	5	0.765697	0.003533	CARD11, SLC11A1, PELL1, HNF1B, CDX1	451	24	16792	7.568363659	0.9998351	0.419802	6.042245
GOTERM_BP	GO:0032922	circadian regulation of gene expression	7	1.071975	0.004096	NAMPT, HNF1B, NPAS2, NCOA2, DR	451	57	16792	4.572451083	0.999959	0.447983	6.972681
GOTERM_BP	GO:0032496	response to lipopolysaccharide	12	1.837672	0.004747	TNFRSF9, SLC11A1, OTD5, SELP, PI	451	164	16792	2.742352388	0.9999918	0.478253	8.037753
GOTERM_BP	GO:0050679	positive regulation of epithelial cell proliferation	7	1.071975	0.005285	FGFR2, SMO, FGF7, NRAA3, MYC, FC	451	60	16792	4.343828529	0.9999978	0.496571	9.808551
GOTERM_BP	GO:0043547	positive regulation of GTPase activity	27	4.134763	0.005464	FGD2, FGFR2, RAB39A2, ARFGAP2	451	565	16792	1.779267312	0.9999986	0.490409	9.196848
GOTERM_BP	GO:0015721	bile acid and bile salt transport	5	0.765697	0.005478	NCOA2, ABCG3, SLC01C1, CEACAM1	451	27	16792	6.894965919	0.9999987	0.474655	9.219436
GOTERM_BP	GO:0001516	prostaglandin biosynthetic process	4	0.612557	0.005583	PTGDS, PTGS2, EDN1, PLA2G4F	451	14	16792	10.63794742	0.999999	0.465448	9.389117
GOTERM_BP	GO:0042060	wound healing	8	1.225115	0.005598	SLC11A1, EREG, ECLN2, PDGFR	451	80	16792	3.723281596	0.999999	0.451537	9.412092
GOTERM_BP	GO:0051482	positive regulation of cytosolic calcium ion concentration	5	0.765697	0.006258	F2RL3, AGTR1, DRD2, EDN1, LPAR1	451	28	16792	6.648717137	0.9999998	0.474649	10.46501
GOTERM_BP	GO:0035556	intracellular signal transduction	21	3.215926	0.006275	ZFP36, DRD2, MCF2, EDN1, MKRN2	451	403	16792	1.940171552	0.9999998	0.461887	10.49295
GOTERM_BP	GO:0009611	response to wounding	7	1.071975	0.006708	ZFP36, ZFP36L1, F2RL3, FGF7, POU5	451	63	16792	4.136979552	0.9999999	0.471165	11.17685
GOTERM_BP	GO:0050727	regulation of inflammatory response	7	1.071975	0.006708	CASP5, AGTR1, PTGS2, MGLL, BCL2	451	63	16792	4.136979552	0.9999999	0.471165	11.17685
GOTERM_BP	GO:0001525	angiogenesis	14	2.143951	0.007253	SAT1, FGFR2, FLT1, PTGS2, MMP19	451	223	16792	2.337486204	1	0.484971	12.03157
GOTERM_BP	GO:0051897	positive regulation of protein kinase activity	8	1.225115	0.007289	CSF3, AKR1C2, F7, ITSN1, NRG1, FGF	451	84	16792	3.545982473	1	0.474286	12.08729
GOTERM_BP	GO:0043087	regulation of GTPase activity	7	1.071975	0.007799	EPHA5, FGD2, RAB39A2, PROM2, S	451	65	16792	4.009687873	1	0.485456	12.87997
GOTERM_BP	GO:0044344	cellular response to fibroblast growth factor	5	0.765697	0.008031	ZFP36, ZFP36L1, EGR3, STAR, MYC	451	30	16792	6.205469327	1	0.483915	13.23752
GOTERM_BP	GO:0048525	negative regulation of viral process	3	0.459418	0.010007	MBL2, LTF, APOBEC3G	451	6	16792	18.61640798	1	0.549958	16.23063
GOTERM_BP	GO:0032680												

GOTERM_BP	GO:0045600	positive regulation of fat cell differ	5	0.765697	0.036706	ZFP36, ZFP36L1, MEDAG, ADIG, TMI	451	47	16792	3.960937869	1	0.7843	48.23873
GOTERM_BP	GO:2000145	regulation of cell motility	4	0.612557	0.038147	EREG, PKN2, EGF, NRG1	451	28	16792	5.318973709	1	0.791777	49.58598
GOTERM_BP	GO:0032715	negative regulation of interleukin-4	4	0.612557	0.038147	BPI, ARRB1, KLF2, GAS6	451	28	16792	5.318973709	1	0.791777	49.58598
GOTERM_BP	GO:0030728	ovulation	3	0.459418	0.039598	EREG, PTGS2, MYC	451	12	16792	9.308203991	1	0.798855	50.90796
GOTERM_BP	GO:0035815	positive regulation of renal sodium	3	0.459418	0.039598	DRD2, EDN1, NPR1	451	12	16792	9.308203991	1	0.798855	50.90796
GOTERM_BP	GO:1900004	negative regulation of serine-type	3	0.459418	0.039598	CR1, ANXA8, ANXA8L1	451	12	16792	9.308203991	1	0.798855	50.90796
GOTERM_BP	GO:0071260	cellular response to mechanical sti	6	0.918836	0.041631	CASP5, BCL10, PTGS2, TLR3, CNN2,	451	71	16792	3.146435152	1	0.810063	52.70625
GOTERM_BP	GO:0050766	positive regulation of phagocytosis	4	0.612557	0.041729	MBL2, SLC11A1, TUB, GAS6	451	29	16792	5.135560823	1	0.805833	52.7913
GOTERM_BP	GO:0036092	phosphatidylinositol-3-phosphate	5	0.765697	0.041843	FGFR2, FGF7, PIK3C3, FGF2, FGF2	451	49	16792	3.799266935	1	0.801775	52.89069
GOTERM_BP	GO:0016485	protein processing	6	0.918836	0.043795	PIK3C3, RHBDF1, CPXM2, F7, CPD,	451	72	16792	3.102734664	1	0.811727	54.55216
GOTERM_BP	GO:0032480	negative regulation of type I interfe	4	0.612557	0.045473	DDX58, IKBKE, OTUD5, UBA7	451	30	16792	4.964375462	1	0.819034	55.93616
GOTERM_BP	GO:0030449	regulation of complement activati	4	0.612557	0.045473	CR1, C4A, C4B, 2, C4B	451	30	16792	4.964375462	1	0.819034	55.93616
GOTERM_BP	GO:0051770	positive regulation of nitric-oxide	3	0.459418	0.045983	NAMPT, CCL20, MAP2K6	451	13	16792	8.5921883	1	0.817986	56.34939
GOTERM_BP	GO:0035810	positive regulation of urine volume	3	0.459418	0.045983	DRD2, EDN1, NPR1	451	13	16792	8.5921883	1	0.817986	56.34939
GOTERM_BP	GO:0032897	negative regulation of viral transcri	3	0.459418	0.045983	ZFP36, TRIM8, MID2	451	13	16792	8.5921883	1	0.817986	56.34939
GOTERM_BP	GO:0014032	neural crest cell development	3	0.459418	0.045983	EDN1, FOXC2, NRG1	451	13	16792	8.5921883	1	0.817986	56.34939
GOTERM_BP	GO:0031086	nuclear-transcribed mRNA catabol	2	0.306279	0.052888	ZFP36, ZFP36L1	451	2	16792	37.23281596	1	0.855974	61.58495
GOTERM_BP	GO:0060529	squamous basal epithelial stem cel	2	0.306279	0.052888	FGFR2, TP63	451	2	16792	37.23281596	1	0.855974	61.58495
GOTERM_BP	GO:0071378	cellular response to growth hormo	2	0.306279	0.052888	STAR, MYC	451	2	16792	37.23281596	1	0.855974	61.58495
GOTERM_BP	GO:1902172	regulation of keratinocyte apoptot	2	0.306279	0.052888	ZFP36, ZFP36L1	451	2	16792	37.23281596	1	0.855974	61.58495
GOTERM_BP	GO:0006583	melanin biosynthetic process from	2	0.306279	0.052888	DCT, TYR	451	2	16792	37.23281596	1	0.855974	61.58495
GOTERM_BP	GO:1904582	regulation of intracellular	2	0.306279	0.052888	ZFP36, ZFP36L1	451	2	16792	37.23281596	1	0.855974	61.58495
GOTERM_BP	GO:0007032	endosome organization	4	0.612557	0.053444	ANXA8, ANXA8L1, PIK3C3, ALS2CL	451	32	16792	4.654101996	1	0.854977	61.98274
GOTERM_BP	GO:0048146	positive regulation of fibroblast pr	5	0.765697	0.056371	FOSL2, EREG, PDGFRA, MYC, GAS6	451	54	16792	3.447482896	1	0.855974	62.00329
GOTERM_BP	GO:0015758	glucose transport	4	0.612557	0.057658	SLC2A9, SLC2A3, SLC5A1, EDN1	451	33	16792	4.513068602	1	0.868648	64.85799
GOTERM_BP	GO:0050829	defense response to Gram-negativ	5	0.765697	0.059563	SLC11A1, SELP, BPI, GSDMD, TLR5	451	55	16792	3.384801451	1	0.871385	66.08816
GOTERM_BP	GO:0042953	lipoprotein transport	3	0.459418	0.059774	MA2, APOB, LRP1	451	15	16792	7.446654931	1	0.871239	66.22228
GOTERM_BP	GO:0001649	osteoblast differentiation	7	1.071975	0.060803	SMO, RRBP1, CLTC, WWTR1, RUNX2	451	104	16792	2.506056129	1	0.872341	66.86731
GOTERM_BP	GO:0071346	cellular response to interferon-gam	5	0.765697	0.066228	CCL20, STAR, EDN1, TLR3, MYC	451	57	16792	3.266036488	1	0.89127	70.08042
GOTERM_BP	GO:1902187	negative regulation of viral release	3	0.459418	0.067134	TRIM8, TRIM15, MID2	451	16	16792	6.981152993	1	0.89151	70.58761
GOTERM_BP	GO:0035994	response to muscle stretch	3	0.459418	0.067134	SLC8A1, EDN1, NFKBIA	451	16	16792	6.981152993	1	0.89151	70.58761
GOTERM_BP	GO:0006936	muscle contraction	7	1.071975	0.067862	SLC8A1, DES, SLC6A8, MYL10, MYL1	451	107	16792	2.435791699	1	0.891092	70.98917
GOTERM_BP	GO:0007275	multicellular organism developme	21	3.215926	0.070071	CSF3, CDX1, H1FNT, BMP1, MCL1, S	451	521	16792	1.500746901	1	0.89597	72.17593
GOTERM_BP	GO:0060070	canonical Wnt signaling pathway	6	0.918836	0.071994	SMO, RARG, EGF, FZD4, MYC, TCF7L	451	83	16792	2.691528865	1	0.899589	73.17214
GOTERM_BP	GO:0030097	hemopoiesis	5	0.765697	0.073264	TTC7A, MKNK2, CNN2, RUNX1, RUN	451	59	16792	3.155232887	1	0.900909	73.81142
GOTERM_BP	GO:0070935	3'-UTR-mediated mRNA stabilizati	3	0.459418	0.074775	ZFP36, YBK3, BOLL	451	17	16792	6.070496935	1	0.902947	74.55327
GOTERM_BP	GO:2001240	negative regulation of extrinsic apr	4	0.612557	0.076021	EYA4, MCL1, CX3CR1, NRG1	451	37	16792	4.252169293	1	0.904092	75.15013
GOTERM_BP	GO:0007249	I-kappaB kinase/NF-kappaB signali	5	0.765697	0.076919	BCL10, IKBK, RPK3, TLR3, TRADD	451	60	16792	3.102734664	1	0.904146	75.57174
GOTERM_BP	GO:0045669	positive regulation of osteoblast di	5	0.765697	0.076919	LTF, TP63, GLI3, RUNX2, FGF2	451	60	16792	3.102734664	1	0.904146	75.57174
GOTERM_BP	GO:0032490	detection of molecule of bacterial	19	2.909648	0.077707	CSF3, FGFR2, NAMPT, NACCI, FLT1,	451	466	16792	1.518076187	1	0.903877	75.93648
GOTERM_BP	GO:0032765	positive regulation of mast cell cyt	2	0.306279	0.078265	BCL10, NRA43	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:0035276	oligopeptide transmembrane trans	2	0.306279	0.078265	SLC15A1, CDH17	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:0002282	microglial cell activation involved	2	0.306279	0.078265	CX3CR1, TLR3	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:0018879	biphenyl metabolic process	2	0.306279	0.078265	STAR, SRD5A2	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:0021769	orbitofrontal cortex development	2	0.306279	0.078265	FGFR2, DRD2	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:0021940	positive regulation of cerebellar gr	2	0.306279	0.078265	EGF, FGF2	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:0018894	dibenzo-p-dioxin metabolic proces	2	0.306279	0.078265	STAR, SRD5A2	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:0018963	phthalate metabolic process	2	0.306279	0.078265	STAR, SRD5A2	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:0032490	detection of molecule of bacterial	19	2.909648	0.077707	CSF3, FGFR2, NAMPT, NACCI, FLT1,	451	466	16792	1.518076187	1	0.903877	75.93648
GOTERM_BP	GO:0021847	ventricular zone neuroblast divisio	2	0.306279	0.078265	DCT, FGFR2	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:1900126	negative regulation of hyaluronan	2	0.306279	0.078265	AP2A1, CLTC	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:0046639	negative regulation of alpha-beta	2	0.306279	0.078265	GLI3, IHH	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:0071409	cellular response to cycloheximide	2	0.306279	0.078265	KLF2, MYC	451	3	16792	24.82187731	1	0.902913	76.19143
GOTERM_BP	GO:0019933	cAMP-mediated signaling	4	0.612557	0.080969	EPHA5, PDE4D, RAPGEF3, GLP1R	451	38	16792	3.919243786	1	0.908228	77.39184
GOTERM_BP	GO:0043623	cellular protein complex assembly	3	0.459418	0.082677	OOEP, PDE4DIP, LOC653513	451	18	16792	6.205469327	1	0.910483	78.12045
GOTERM_BP	GO:2000249	regulation of actin cytoskeleton re	3	0.459418	0.082677	PDGFRA, RHOD, RAPGEF3	451	18	16792	6.205469327	1	0.910483	78.12045
GOTERM_BP	GO:0033280	response to vitamin D	3	0.459418	0.082677	TYR, PTGS2, AQP3	451	18	16792	6.205469327	1	0.910483	78.12045
GOTERM_BP	GO:0048169	regulation of long-term neuronal	3	0.459418	0.082677	DRD2, GRIK2, CAMK2B	451	18	16792	6.205469327	1	0.910483	78.12045
GOTERM_BP	GO:0070266	necroptotic process	3	0.459418	0.082677	RIK3, TLR3, MLKL	451	18	16792	6.205469327	1	0.910483	78.12045
GOTERM_BP	GO:0046597	negative regulation of viral entry	3	0.459418	0.082677	TRIM8, GSN, MID2	451	18	16792	6.205469327	1	0.910483	78.12045
GOTERM_BP	GO:0071222	cellular response to lipopolysacche	7	1.071975	0.083347	ZFP36, CSF3, CCL20, STAR, CX3CR1,	451	113	16792	2.306457626	1	0.909862	78.40013
GOTERM_BP	GO:0008219	cell death	4	0.612557	0.086052	BCL10, FOSL2, PMXP2, EMP1	451	39	16792	3.818750355	1	0.914606	79.49543
GOTERM_BP	GO:0006895	Golgi to endosome transport	3	0.459418	0.09082	TGOLN2, VPS13C, AP2A1	451	19	16792	5.878865679	1	0.923839	81.29974
GOTERM_BP	GO:0046827	positive regulation of protein expo	3	0.459418	0.09082	RAPGEF3, TCF7L2, GAS6	451	19	16792	5.878865679	1	0.923839	81.29974
GOTERM_BP	GO:0060716	labyrinthine layer blood vessel dev	3	0.459418	0.09082	PLCD3, PLCD1, JUNB	451	19	16792	5.878865679	1	0.923839	81.29974
GOTERM_BP	GO:0032332	positive regulation of chondrocyte	3	0.459418	0.09082	GLI3, RUNX2, IHH	451	19	16792	5.878865679	1	0.923839	81.29974
GOTERM_BP	GO:0043280	positive regulation of cysteine-type	4	0.612557	0.091266	BCL10, NOD1, ARRB1, MYC	451	40	16792	3.723281596	1	0.9227	81.46082
GOTERM_BP	GO:0042742	defense response to bacterium	8	1.225115	0.095384	IGHG1, MBL2, SLC11A1, NOD1, CCL	451	145	16792	2.054224329	1	0.92954	82.88568
GOTERM_BP	GO:0014068	positive regulation of phosphatidy	5	0.765697	0.096516	CSF3, SELP, FLT1, PDGFRA, NRG1	451	65	16792	2.864062767	1	0.929862	83.25909
GOTERM_BP	GO:0060326	cell chemotaxis	5	0.765697	0.096516	AGTR1, CCL20, CXCL2, PDGFRA, LPA	451	65	16792	2.864062767	1	0.929862	