

Table 4. Enriched KEGG pathways in each subtypes of MCC

Enriched KEGG pathways by genes over-expressed in Subtype I MCC

Category	Term	Count	%	PValue	Genes	List	Tota	Pop	Hits	Pop	Total	Fold	Enrichmen	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	hsa03040:Spliceosome	33	3.886926	4.71E-18	SRSF1, CHERP, CRNKL1, 256		133	6879	6.667263863	7.81E-16	7.81E-16	5.72E-15				
KEGG_PATHWAY	hsa03030:DNA replication	17	2.002356	3.00E-14	MCM2, RNASEH2A, MC 256		36	6879	12.6891276	4.98E-12	2.49E-12	3.64E-11				
KEGG_PATHWAY	hsa04110:Cell cycle	27	3.180212	2.76E-13	CDC7, ANAPC1, CDC6, I 256		124	6879	5.850963962	4.59E-11	1.53E-11	3.36E-10				
KEGG_PATHWAY	hsa03430:Mismatch repair	10	1.177856	5.95E-08	EXO1, RFC5, POLD3, RP 256		23	6879	11.68308424	9.88E-06	2.47E-06	7.23E-05				
KEGG_PATHWAY	hsa03460:Fanconi anemia pathway	12	1.413428	2.80E-06	FANCL, RAD51C, RPA2, 256		53	6879	6.084021226	4.65E-04	9.30E-05	0.003403				
KEGG_PATHWAY	hsa03013:RNA transport	19	2.237927	6.15E-05	CLNS1A, NUP160, RAN, 256		172	6879	2.968318496	0.01015418	0.0016996	0.074678				
KEGG_PATHWAY	hsa03420:Nucleotide excision repair	9	1.060071	2.86E-04	RFC5, POLD3, RPA2, RF 256		47	6879	5.14552859	0.04639391	0.0067634	0.347118				
KEGG_PATHWAY	hsa03410:Base excision repair	7	0.824499	0.001166	POLD3, POLE2, UNG, P 256		33	6879	5.699928977	0.17603308	0.0239126	1.407289				
KEGG_PATHWAY	hsa00240:Pyrimidine metabolism	11	1.295642	0.004055	POLD3, PRIM1, TYMS, I 256		101	6879	2.926554765	0.49056714	0.0722006	4.816974				
KEGG_PATHWAY	hsa03018:RNA degradation	9	1.060071	0.007365	DIS3, EXOSC9, LSM8, E 256		77	6879	3.140777192	0.70684424	0.1154755	8.590158				
KEGG_PATHWAY	hsa04115:p53 signaling pathway	8	0.942285	0.011562	CCNB1, CCNE2, PPM1D 256		67	6879	3.208488806	0.85492666	0.1609638	13.17789				
KEGG_PATHWAY	hsa03015:mRNA surveillance pathway	9	1.060071	0.019135	CSTF3, ALYREF, HBS1L, 256		91	6879	2.657580701	0.95953309	0.2345356	20.92426				
KEGG_PATHWAY	hsa03440:Homologous recombination	5	0.588928	0.021122	POLD3, RAD51C, RPA2, 256		29	6879	4.632947198	0.97109518	0.2385996	22.84804				
KEGG_PATHWAY	hsa05016:Huntington's disease	14	1.648999	0.025784	NDUFB11, NDUFA8, SL 256		192	6879	1.959350586	0.98691499	0.2663585	27.19643				
KEGG_PATHWAY	hsa00670:One carbon pool by folate	4	0.471143	0.035999	TYMS, MTHFD2L, DHFR 256		20	6879	5.37421875	0.99772574	0.3335167	35.94879				
KEGG_PATHWAY	hsa05012:Parkinson's disease	11	1.295642	0.037697	NDUFB11, NDUFA8, SL 256		142	6879	2.0815636	0.99830261	0.3287855	37.30585				
KEGG_PATHWAY	hsa04114:Oocyte meiosis	9	1.060071	0.053264	CCNB1, ANAPC1, CCNE 256		111	6879	2.178737331	0.99988675	0.4140184	48.57612				
KEGG_PATHWAY	hsa00563:Glycosylphosphatidylinositol (GP)	4	0.471143	0.063502	PIGM, PIXG, PGAP1, PIC 256		25	6879	4.299375	0.99998137	0.4539558	54.94081				
KEGG_PATHWAY	hsa05166:HTLV-I infection	15	1.766784	0.088682	ANAPC1, SLC25A4, RAN 256		254	6879	1.586875615	0.99999998	0.5557361	67.6439				

Enriched KEGG pathways by genes over-expressed in Subtype II MCC

Category	Term	Count	%	PValue	Genes	List	Tota	Pop	Hits	Pop	Total	Fold	Enrichmen	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	hsa04668:TNF signaling pathway	13	1.990812	2.01E-04	RPS6KA4, PTGS2, CCL2 229		107	6879	3.649634739	0.04543532	0.0454353	0.257918				
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	20	3.062787	6.87E-04	FGFR2, FGF7, TAOK1, I 229		253	6879	2.374648325	0.1467121	0.0762642	0.877287				
KEGG_PATHWAY	hsa04810:Regulation of actin cytoskeleton	17	2.603369	0.001555	FGFR2, ENAH, FGF7, SS 229		210	6879	2.431752963	0.30197739	0.1129328	1.976815				
KEGG_PATHWAY	hsa04144:Endocytosis	17	2.603369	0.006146	SH3GL3, FGFR2, ARFGA 229		241	6879	2.118954864	0.75926088	0.2995346	7.604188				
KEGG_PATHWAY	hsa04622:RIG-I-like receptor signaling path	8	1.225115	0.008149	DDX58, IKBK, OTUD5, 229		70	6879	3.433063007	0.84894959	0.3147889	9.965283				
KEGG_PATHWAY	hsa04015:Rap1 signaling pathway	15	2.29709	0.009714	FGFR2, F2RL3, MAGI2, I 229		210	6879	2.145664379	0.895105	0.3132598	11.77034				
KEGG_PATHWAY	hsa00601:Glycosphingolipid biosynthesis -	5	0.765697	0.0099	B4GALT1, B3GALT1, FU 229		26	6879	5.776788713	0.89956374	0.2798666	11.98293				
KEGG_PATHWAY	hsa04912:GnRH signaling pathway	9	1.378254	0.01029	PLA2G4A, PLD1, PLA2G 229		91	6879	2.97091991	0.9083014	0.2581855	12.42672				
KEGG_PATHWAY	hsa05160:Hepatitis C	11	1.684533	0.012613	DDX58, CLDN17, IKBK 229		133	6879	2.484453492	0.94671496	0.2780424	15.02756				
KEGG_PATHWAY	hsa04724:Glutamatergic synapse	10	1.531394	0.01308	SLC17A7, PLA2G4A, PL 229		114	6879	2.635026431	0.95222819	0.2622365	15.54143				
KEGG_PATHWAY	hsa04024:cAMP signaling pathway	14	2.143951	0.014095	PLD1, DRD2, HTR4, NF 229		198	6879	2.123991002	0.9623348	0.2577674	16.64907				
KEGG_PATHWAY	hsa04623:Cytosolic DNA-sensing pathway	7	1.071975	0.018761	DDX58, IKBK, IFNA4, I 229		64	6879	3.285548581	0.98741192	0.3055143	21.57123				
KEGG_PATHWAY	hsa05200:Pathways in cancer	22	3.690666	0.020057	FGFR2, F2RL3, FGF7, PT 229		393	6879	1.681589386	0.99072273	0.3023337	22.88934				
KEGG_PATHWAY	hsa05161:Hepatitis B	11	1.684533	0.021894	DDX58, STAT6, IKBK, E 229		145	6879	2.278843548	0.99398564	0.3059821	24.72332				
KEGG_PATHWAY	hsa05144:Malaria	6	0.918836	0.022314	CSF3, SELP, CR1, LRP1, 229		49	6879	3.678281793	0.99455473	0.2935719	25.13775				
KEGG_PATHWAY	hsa04620:Toll-like receptor signaling pathv	9	1.378254	0.023997	IKBK, IFNA4, MAP3K8, 229		106	6879	2.550506715	0.99634242	0.2957941	26.77414				
KEGG_PATHWAY	hsa04064:NF-kappa B signaling pathway	8	1.225115	0.024824	DDX58, CARD11, BCL1 229		87	6879	2.762234603	0.99699299	0.2893512	27.56633				
KEGG_PATHWAY	hsa04726:Serotonergic synapse	9	1.378254	0.030567	PLA2G4A, PTGS2, HTR4 229		111	6879	2.435619025	0.99923154	0.3286037	32.85196				
KEGG_PATHWAY	hsa04977:Vitamin digestion and absorptior	4	0.612557	0.034769	FOLH1, APOB, SLC19A3 229		22	6879	5.461691147	0.99971828	0.3496486	36.49185				
KEGG_PATHWAY	hsa04270:Vascular smooth muscle contracti	9	1.378254	0.039965	AGTR1, PLA2G4A, PLA2 229		117	6879	2.310715485	0.99991904	0.3756705	40.7411				
KEGG_PATHWAY	hsa04723:Retrograde endocannabinoid sig	8	1.225115	0.049795	SLC17A7, PTGS2, MGL 229		101	6879	2.379350599	0.99999249	0.4298493	48.0709				
KEGG_PATHWAY	hsa05202:Transcriptional misregulation in	11	1.684533	0.050342	NFKB1, FLT1, ELK4, ME 229		167	6879	1.978636613	0.99999342	0.4186277	48.45324				
KEGG_PATHWAY	hsa04925:Aldosterone synthesis and secret	7	1.071975	0.051354	AGTR1, STAR, NPR1, CA 229		81	6879	2.595989002	0.99999486	0.4110924	49.15318				
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	18	2.756508	0.065006	FGFR2, CSF3, FLT1, FGF 229		345	6879	1.567267894	0.99999982	0.4763592	57.78218				
KEGG_PATHWAY	hsa05215:Prostate cancer	7	1.071975	0.071134	FGFR2, IKBK, PDGFRA, 229		88	6879	2.389489877	0.99999996	0.4943101	61.1977				
KEGG_PATHWAY	hsa04014:Ras signaling pathway	13	1.990812	0.071467	FGFR2, PLA2G4A, PLD1 229		226	6879	1.727924412	0.99999996	0.4825222	61.37554				
KEGG_PATHWAY	hsa04020:Calcium signaling pathway	11	1.684533	0.07328	AGTR1, SLC8A1, P2RX1, 229		179	6879	1.845990583	0.99999998	0.4785337	62.33198				
KEGG_PATHWAY	hsa04610:Complement and coagulation ca	6	0.918836	0.077872	MBL2, CR1, AZM, C4A, 229		69	6879	2.612113157	0.99999999	0.4876967	64.65764				
KEGG_PATHWAY	hsa04913:Ovarian steroidogenesis	5	0.765697	0.078179	PLA2G4A, PTGS2, STAR 229		49	6879	3.065234828	0.99999999	0.4771322	64.80826				
KEGG_PATHWAY	hsa05218:Melanoma	6	0.918836	0.085661	FGF7, MET, PDGFRA, F 229		71	6879	2.538532505	1	0.4982058	68.30191				
KEGG_PATHWAY	hsa04919:Thyroid hormone signaling pathv	8	1.225115	0.086757	NCOA2, DIO2, PFKFB2, 229		115	6879	2.089690526	1	0.4914823	68.78575				