

S4 Table. Gene Ontology Enrichment Analysis_Biological Process

ID	Name	p-value	Hit in Query List
GO:2000819	Regulation of nucleotide-excision repair	0.00000322	ARID1A,SMARCA4,PBRM1
GO:0045597	Positive regulation of cell differentiation	0.0000127	ARID1A,KRAS,SMARCA4,PIK3R1,ZNF219,PBRM1,TCF12,ACVRL1
GO:0070316	Regulation of G0 to G1 transition	0.0000171	ARID1A,SMARCA4,PBRM1
GO:0045023	G0 to G1 transition	0.0000203	ARID1A,SMARCA4,PBRM1
GO:1903508	Positive regulation of nucleic acid-templated transcription	0.0000476	ARID1A,SMARCA4,PIK3R1,CHD4,KMT2D,ZNF219,PBRM1,TCF12,ACVRL1
GO:0045893	Positive regulation of DNA-templated transcription	0.0000476	ARID1A,SMARCA4,PIK3R1,CHD4,KMT2D,ZNF219,PBRM1,TCF12,ACVRL1
GO:1902680	Positive regulation of RNA biosynthetic process	0.0000488	ARID1A,SMARCA4,PIK3R1,CHD4,KMT2D,ZNF219,PBRM1,TCF12,ACVRL1
GO:0006338	Chromatin remodeling	0.0000497	ARID1A,SMARCA4,CHD4,KMT2D,PBRM1
GO:0045732	Positive regulation of protein catabolic process	0.0000763	AMER1,APC2,KEAP1,NKD1
GO:0006289	Nucleotide-excision repair	0.0000996	ARID1A,SMARCA4,PBRM1
GO:2000781	Positive regulation of double-strand break repair	0.000103	ARID1A,SMARCA4,PBRM1
GO:0030071	Regulation of mitotic metaphase/anaphase transition	0.000121	ARID1A,SMARCA4,PBRM1
GO:1902099	Regulation of metaphase/anaphase	0.000132	ARID1A,SMARCA4,PBRM1

	transition of cell cycle		
GO:0007091	Metaphase/anaphase transition of mitotic cell cycle	0.000136	ARID1A,SMARCA4,PBRM1
GO:0010965	Regulation of mitotic sister chromatid separation	0.000149	ARID1A,SMARCA4,PBRM1
GO:0044784	Metaphase/anaphase transition of cell cycle	0.000149	ARID1A,SMARCA4,PBRM1
GO:0051306	Mitotic sister chromatid separation	0.000162	ARID1A,SMARCA4,PBRM1
GO:0033045	Regulation of sister chromatid segregation	0.000191	ARID1A,SMARCA4,PBRM1
GO:0051247	Positive regulation of protein metabolic process	0.000208	KRAS,TKN2,PIK3R1,AMER1,APC2,KEAP1,NKD1,ACVRL1
GO:1905818	Regulation of chromosome separation	0.000228	ARID1A,SMARCA4,PBRM1
GO:0030518	Intracellular steroid hormone receptor signaling pathway	0.000323	ARID1A,SMARCA4,KMT2D
GO:2000779	Regulation of double-strand break repair	0.00036	ARID1A,SMARCA4,PBRM1
GO:0045739	Positive regulation of DNA repair	0.000367	ARID1A,SMARCA4,PBRM1
GO:0051983	Regulation of chromosome segregation	0.000391	ARID1A,SMARCA4,PBRM1
GO:0051304	Chromosome separation	0.000407	ARID1A,SMARCA4,PBRM1
GO:0006325	Chromatin organization	0.00051	ARID1A,SMARCA4,CHD4,KMT2D,PBRM1
GO:0043401	Steroid hormone mediated signaling pathway	0.000533	ARID1A,SMARCA4,KMT2D

GO:0090090	Negative regulation of canonical Wnt signaling pathway	0.000553	AMER1,APC2,NKD1
GO:0030111	Regulation of Wnt signaling pathway	0.000667	SMARCA4,AMER1,APC2,NKD1
GO:0042176	Regulation of protein catabolic process	0.00068	AMER1,APC2,KEAP1,NKD1
GO:0048729	Tissue morphogenesis	0.0007	ARID1A,KRAS,SMARCA4,KMT2D,NKD1,ACVRL1
GO:0030177	Positive regulation of Wnt signaling pathway	0.000728	SMARCA4,AMER1,NKD1
GO:2001022	Positive regulation of response to DNA damage stimulus	0.000854	ARID1A,SMARCA4,PBRM1
GO:0040029	Epigenetic regulation of gene expression	0.00111	ARID1A,SMARCA4,KMT2D
GO:0030178	Negative regulation of Wnt signaling pathway	0.00119	AMER1,APC2,NKD1
GO:2000045	Regulation of G1/S transition of mitotic cell cycle	0.00128	ARID1A,SMARCA4,PBRM1
GO:0000070	Mitotic sister chromatid segregation	0.00133	ARID1A,SMARCA4,PBRM1
GO:0009755	Hormone-mediated signaling pathway	0.00135	ARID1A,SMARCA4,KMT2D
GO:0032870	Cellular response to hormone stimulus	0.00147	ARID1A,SMARCA4,PIK3R1,KMT2D,KEAP1
GO:0030856	Regulation of epithelial cell differentiation	0.00149	KRAS,KEAP1,ACVRL1
GO:0006282	Regulation of DNA repair	0.00149	ARID1A,SMARCA4,PBRM1
GO:0009967	Positive regulation of signal transduction	0.00175	KRAS,SMARCA4,PIK3R1,KMT2D,AMER1,NKD1,ACVRL1

GO:0051090	Regulation of DNA-binding transcription factor activity	0.00177	KRAS,SMARCA4,CACNA1D,KEAP1
GO:0009725	Response to hormone	0.00189	ARID1A,KRAS,SMARCA4,PIK3R1,KMT2D,KEAP1
GO:0048646	Anatomical structure formation involved in morphogenesis	0.00192	ARID1A,SMARCA4,ZNF219,CAPN2,PBRM1,NKD1,ACVRL1
GO:1902806	Regulation of cell cycle G1/S phase transition	0.00192	ARID1A,SMARCA4,PBRM1
GO:0033043	Regulation of organelle organization	0.00195	ARID1A,SMARCA4,PIK3R1,CAPN2,APC2,PBRM1
GO:0000819	Sister chromatid segregation	0.00206	ARID1A,SMARCA4,PBRM1
GO:0071322	Cellular response to carbohydrate stimulus	0.0021	SMARCA4,CACNA1D,KEAP1
GO:0001678	Cellular glucose homeostasis	0.00215	SMARCA4,CACNA1D,PIK3R1
GO:0022411	Cellular component disassembly	0.00226	ARID1A,SMARCA4,PIK3R1,APC2
GO:0051240	Positive regulation of multicellular organismal process	0.0023	ARID1A,KRAS,SMARCA4,PIK3R1,ZNF219,PBRM1,ACVRL1
GO:0045944	Positive regulation of transcription by RNA polymerase II	0.00233	SMARCA4,PIK3R1,KMT2D,ZNF219,TCF12,ACVRL1
GO:0016055	Wnt signaling pathway	0.00237	SMARCA4,AMER1,APC2,NKD1
GO:0033044	Regulation of chromosome organization	0.0024	ARID1A,SMARCA4,PBRM1
GO:0198738	Cell-cell signaling by wnt	0.0024	SMARCA4,AMER1,APC2,NKD1
GO:0030155	Regulation of cell adhesion	0.00243	ARID1A,SMARCA4,PIK3R1,PBRM1,ACVRL1
GO:0035239	Tube morphogenesis	0.00268	ARID1A,KRAS,SMARCA4,PBRM1,NKD1,ACVRL1

GO:0009896	Positive regulation of catabolic process	0.00276	AMER1,APC2,KEAP1,NKD1
GO:0032984	Protein-containing complex disassembly	0.00282	ARID1A,SMARCA4,APC2
GO:0022407	Regulation of cell-cell adhesion	0.00293	ARID1A,SMARCA4,PIK3R1,PBRM1
GO:0000082	G1/S transition of mitotic cell cycle	0.00305	ARID1A,SMARCA4,PBRM1
GO:0040007	Growth	0.00329	KRAS,SMARCA4,CHD4,KMT2D,NKD1,ACVRL1
GO:0030855	Epithelial cell differentiation	0.00343	KRAS,SMARCA4,KEAP1,PBRM1,ACVRL1
GO:0071383	Cellular response to steroid hormone stimulus	0.00345	ARID1A,SMARCA4,KMT2D
GO:0006302	Double-strand break repair	0.00355	ARID1A,SMARCA4,PBRM1
GO:0045926	Negative regulation of growth	0.00358	SMARCA4,NKD1,ACVRL1
GO:0060828	Regulation of canonical Wnt signaling pathway	0.00361	AMER1,APC2,NKD1
GO:0051052	Regulation of DNA metabolic process	0.00363	ARID1A,SMARCA4,PBRM1,ACVRL1
GO:0051091	Positive regulation of DNA-binding transcription factor activity	0.00375	KRAS,SMARCA4,CACNA1D
GO:0051276	Chromosome organization	0.00392	ARID1A,SMARCA4,CHD4,PBRM1
GO:0045937	Positive regulation of phosphate metabolic process	0.00399	KRAS,TKN2,PIK3R1,CAPN2,ACVRL1
GO:0010562	Positive regulation of phosphorus metabolic process	0.00399	KRAS,TKN2,PIK3R1,CAPN2,ACVRL1
GO:0044843	Cell cycle G1/S phase transition	0.0042	ARID1A,SMARCA4,PBRM1
GO:0030522	Intracellular receptor signaling	0.00434	ARID1A,SMARCA4,KMT2D

	pathway		
GO:0000122	Negative regulation of transcription by RNA polymerase II	0.00455	ARID1A,SMARCA4,CC2D1B,CHD4,ZNF219
GO:2001020	Regulation of response to DNA damage stimulus	0.00487	ARID1A,SMARCA4,PBRM1
GO:0030163	Protein catabolic process	0.00495	AMER1,CAPN2,APC2,KEAP1,NKD1
GO:0098813	Nuclear chromosome segregation	0.00495	ARID1A,SMARCA4,PBRM1
GO:0051054	Positive regulation of DNA metabolic process	0.00507	ARID1A,SMARCA4,PBRM1
GO:0002684	Positive regulation of immune system process	0.00531	ARID1A,CSMD3,SMARCA4,PIK3R1,PBRM1
GO:1905114	Cell surface receptor signaling pathway involved in cell-cell signaling	0.00567	SMARCA4,AMER1,APC2,NKD1
GO:0060070	Canonical Wnt signaling pathway	0.00601	AMER1,APC2,NKD1
GO:0140014	Mitotic nuclear division	0.00628	ARID1A,SMARCA4,PBRM1
GO:0007155	Cell adhesion	0.0063	ARID1A,SMARCA4,LAMC2,PIK3R1,PBRM1,ACVRL1
GO:0031401	Positive regulation of protein modification process	0.00649	KRAS,TNK2,PIK3R1,AMER1,ACVRL1
GO:0044706	Multi-multicellular organism process	0.00651	ARID1A,KRAS,CAPN2
GO:0008284	Positive regulation of cell population proliferation	0.00683	KRAS,SMARCA4,LAMC2,KMT2D,ACVRL1
GO:0022409	Positive regulation of cell-cell	0.00689	ARID1A,SMARCA4,PBRM1

adhesion			
GO:0042593	Glucose homeostasis	0.00689	SMARCA4,CACNA1D,PIK3R1
GO:0033500	Carbohydrate homeostasis	0.00694	SMARCA4,CACNA1D,PIK3R1
GO:0045165	Cell fate commitment	0.00714	SMARCA4,CHD4,APC2
GO:0030334	Regulation of cell migration	0.00714	SMARCA4,LAMC2,PIK3R1,NKD1,ACVRL1
GO:0045934	Negative regulation of nucleobase- containing compound metabolic process	0.00725	ARID1A,SMARCA4,CC2D1B,CHD4,ZNF219,ACVRL1
GO:1901990	Regulation of mitotic cell cycle phase transition	0.00759	ARID1A,SMARCA4,PBRM1
GO:0007059	Chromosome segregation	0.00812	ARID1A,SMARCA4,PBRM1
GO:0010558	Negative regulation of macromolecule biosynthetic process	0.00838	ARID1A,SMARCA4,CC2D1B,CHD4,ZNF219,ACVRL1
