

S7 Table The statistically enriched GO terms of Sub 2

GO	Style	Term	Pvalue	Gene count	The involved genes
Biological processes	Metabolic	positive regulation of RNA metabolic process	1.50E-10	155/424 (36.5%)	ARID1A,BCL11B,CTCF,ELK1,GATAG,KLF12,KLF13,KLF14,MK12,MES1,NOTCH1,PKNOX1 etc
		positive regulation of macromolecule metabolic process	4.00E-10		ARID1A,BCL11B,CTCF,ELK1,GATAG,KLF12,KLF13,KLF14,MK12,MES1,NOTCH1,PKNOX1,SMAD7,SOX9,SMARCA4,TRX3,ATXN1 etc
		positive regulation of nitrogen compound metabolic process	2.40E-09		TRX3,TEAD3,ZEB3,ABLNB,APP,ATXN1,BRPF1,CREB1,ESRRB,RYR1,GDF6,HAND2 etc
		negative regulation of nitrogen compound metabolic process	1.60E-05		CTCF,DNMT3A,KLF12,KLF14,MES2,NRIF,NRHP1,SMAD7,SOX9,SMARCA4,TRX3,ATXN1 etc
		regulation of phosphorus metabolic process	2.40E-05		HMGR,KSR,SMAD6,SMAD7,ADCY6,APP,APLF2,ATXN1,CAV3,CCND1,CCND2,CCNT2,CDKSR1 etc
		regulation of cellular protein metabolic process	3.70E-05		NRHP1,SMAD6,SMAD7,TRIP9,BOLL,CCND1,CCND2,CPB1,CPEB1,DU,CL1 etc
		negative regulation of RNA metabolic process	7.20E-05		CTCF,DNMT3A,KLF12,KLF14,MES2,NRIF,NRHP1,SMAD7,SOX9,SMARCA4,TRX3,BAZ2A,CBFA2T1 etc
		phosphorus metabolic process	1.80E-04		MAR1,NRKSACM1,SMAD7,NRIF,APP,CREB1,CAMK1D,CAMK2G,CAV2,CTTNBP2 etc
		phosphate metabolic process	1.80E-04		MAR1,NRKSACM1,SMAD7,NRIF,APP,CREB1,CAMK1D,CAMK2G,CAV2,CTTNBP2 etc
		negative regulation of macromolecule metabolic process	2.20E-04		CTCF,DNMT3A,KLF12,KLF14,MES2,NRIF,NRHP1,SMAD6,SMAD7,SOX9,SMARCA4 etc
positive regulation of protein metabolic process	2.10E-02	NRHP1,SMAD7,BOLL,CCND1,CCND2,DU,CL1,GAL1,GCL1,GDF6,GHR,HDAC4,PPARGC1A etc			
regulation of glucose metabolic process	2.30E-02	DYRK2,HDAC4,IRS1,PPARGC1A,PGAM1,TGFR1,IGFBP3,ZFP91 etc			
regulation of carbohydrate metabolic process	3.30E-02	DYRK2,HDAC4,IRS1,PPARGC1A,PGAM1 etc			
Biological processes	Transcription	regulation of transcription from RNA polymerase II promoter	1.20E-11	137/424 (32.3%)	BCL11B,DNMT3A,ELK1,GATAG,KLF12,KLF13,KLF14,MK12,MES1,NOTCH1,PKNOX1,PKNOX2 etc
		positive regulation of transcription, DNA dependent	1.10E-10		ABLNB,APP,ATXN1,CREB1,ESRRB,HAND2,HDAC4,JUNB,MITF,NEUROD1,NFAT5,NR2F1 etc
		regulation of transcription	3.80E-10		BRF1,HDHR53,KLF12,KLF13,KLF14,MK12,MES1,MES2,NRIF,NRHP1,SMAD7,SOX9,SMARCA4,TRX3,ATXN1,BAZ2A etc
		positive regulation of transcription from RNA polymerase II promoter	4.20E-10		JUNB,MITF,NEUROD1,NFAT5,PA3,PPARGC1A,RARB,RXR,RUNX1,SRE,STAT5 etc
		positive regulation of transcription	7.60E-10		SF1,TRX3,TEAD3,ZEB3,ABLNB,APP,ATXN1,BRPF1,CREB1,ESRRB,GDF6 etc
		regulation of transcription, DNA dependent	2.20E-07		ARID1A,BCL11B,CTCF,DNMT3A,ELF5,ELK1,GATAG,KLF12,KLF13,KLF14,MK12 etc
		transcription	5.90E-07		ARID1A,BCL11B,CTCF,DNMT3A,ELF5,ELK1,GATAG,KLF12,KLF13,KLF14,MK12 etc
		negative regulation of transcription	7.60E-06		CTCF,DNMT3A,KLF12,KLF14,MES2,NRIF,NRHP1,SMAD7,SOX9,SMARCA4,TRX3,BAZ2A,CBFA2T1,DR1 etc
		negative regulation of transcription, DNA dependent	5.50E-05		CTCF,DNMT3A,KLF12,KLF14,MES2,NRIF,NRHP1,SMAD7,SOX9,SMARCA4,TRX3,BAZ2A,CBFA2T1,DR1 etc
		positive regulation of gene specific transcription	3.70E-04		GATAG,NOTCH1,SMARCA4,SMARCA4,CREB1,HDAC4,NR2F2,PPARGC1ASRE,TFEB,ETS1 etc
Biological processes	Gene expression	regulation of gene-specific transcription	1.00E-03	87/424 (20.5%)	GATAG,NOTCH1,SMARCA4,SMARCA4,CREB1,HDAC4,SRE,TFEB,ETS1 etc
		positive regulation of specific transcription from RNA polymerase II promoter	1.90E-03		GATAG,NOTCH1,SMAD7,SMARCA4,TAL1,CREB1,HDAC4,NR2F2,PPARGC1ASRE etc
		regulation of specific transcription from RNA polymerase II promoter	2.70E-03		GATAG,NOTCH1,SMAD7,SMARCA4,TAL1,CREB1,HDAC4,SRE,TFEB,ETS1 etc
		negative regulation of transcription from RNA polymerase II promoter	4.30E-03		GATAG,NOTCH1,SMAD7,SMARCA4,TAL1,CREB1,HDAC4,SRE,TFEB,ETS1 etc
		positive regulation of macromolecule biosynthetic process	4.00E-09		DNMT3A,KLF12,MES1,SMAD7,SMARCA4,DR1,HDAC4,HDAC9,HYPI1,JARID1,NR2F2 etc
		positive regulation of biosynthetic process	4.00E-09		ARID1A,BCL11B,CTCF,ELK1,GATAG,KLF12,KLF13,KLF14,MK12,MES1,NOTCH1,PKNOX1 etc
		positive regulation of cellular biosynthetic process	6.70E-09		BCL11B,RRF1,CREB1,DYRK2,IRX1,GDF6,HAND2,HDAC4,IRS1,JUNB,MITF,NEUROD1 etc
		negative regulation of cellular biosynthetic process	6.20E-06		NFAT5,NR2F2,PA3,PPARGC1A,RARB,RXR,RUNX1,SRE,STAT5,STRN3,THRB,TRF3 etc
		negative regulation of macromolecule biosynthetic process	5.60E-06		DNMT3A,KLF12,KLF14,MES2,NRIF,NRHP1,SMAD7,SOX9,SMARCA4,TRX3,ATXN1,BAZ2A,CBFA2T1 etc
		negative regulation of biosynthetic process	1.00E-05		NRIF,SMAD7,SOX9,SMARCA4,TRX3,ATXN1,BAZ2A,CBFA2T1,DR1,EDP,EIF2,CL,GCL1 etc
Biological processes	Apoptosis	positive regulation of gene expression	2.00E-09	43/424 (9.9%)	ARID1A,BCL11B,CTCF,ELK1,GATAG,KLF12,KLF13,KLF14,MK12,MES2,NOTCH1 etc
		negative regulation of gene expression	8.50E-06		MES1,NRIF,NRHP1,SMAD7,SOX9,SMARCA4,TRX3,ATXN1,BAZ2A,CBFA2T1,DR1,EDP etc
		posttranscriptional regulation of gene expression	1.10E-04		SMAD7,APP,BCL11,CPB1,CPEB1,EPF2,EIF4,EIF5,EIF71,IGFBP5,MEP9,NANOS1,PPARGC1A etc
		regulation of gene expression, epigenetic	2.70E-03		ARID1A,CTCF,DNMT3A,SMARCA4,SMARCA4,ATXN1,BAZ2A,CBFA2T1,DR1,EDP etc
		positive regulation of apoptosis	2.90E-02		BRF1,CCL11,NOTCH1,TRIP3,ALDH1A1,APP,CDC82,DL1,CDP1,DYRK2,ING3 etc
		regulation of apoptosis	2.50E-03		DUSP1,DYRK2,RYA1,GCL1,GHR,HSP1,ING3,MITF,MAP2K,NRIF,NEUROD1,PREX1,PPM1 etc
		negative regulation of cell differentiation	1.50E-05		ARCA1,KLF4,NOTCH1,SMAD7,SOX9,TRX3,CCND1,CD86,EDP,HDAC4,HDAC9,NRIF,RRP1 etc
		neuron differentiation	4.90E-05		BD4,IFR1,MEP9,NRIF,NRHP1,NR2F2,OTX2,PA3,PAFAH1B1,EP3A,RAC1,SRE,CERS1B etc
		muscle cell differentiation	1.00E-04		ADAM12,GATAG,MK12,APP,CACNA1H,CACNB2,CAV2,CAV3,MBNL1,MPP,OKRAB3B etc
		cell morphogenesis involved in differentiation	2.40E-04		ATF1B1,BCL11B,NOTCH1,SOX9,APP,CREB1,CXCL12,CDK5R1,GAR3,LANE1,NRIF,NRHP1 etc
Biological processes	Differentiation	cell morphogenesis involved in neuron differentiation	3.10E-04	70/424 (16.5%)	ATF1B1,BCL11B,NOTCH1,APP,CREB1,CXCL12,CDK5R1,GAR3,NRIF,NRHP1 etc
		regulation of myoblast cell differentiation	3.10E-04		NRHP1,TAL1,CD86,MITF,PURR,RUNX1,TFEB,ETS1,MAP3B,ZFP64 etc
		striate muscle cell differentiation	1.70E-03		ADAM12,GATAG,APP,CACNA1H,CACNB2,CAV2,CAV3,MBNL1,MPP,OKRAB3B,TTN etc
		cerebellar granule cell differentiation	5.60E-03		ATF1B1,MEP9,SLK1
		regulation of muscle cell differentiation	7.00E-03		NOTCH1,TRX3,CAV3,EP3B,HDAC4,SRE etc
		negative regulation of muscle cell differentiation	1.30E-02		NOTCH1,TRX3,EP3B,HDAC4 etc
		regulation of striate muscle cell differentiation	1.70E-02		NOTCH1,TRX3,CAV3,EP3B,HDAC4 etc
		regulation of erythrocyte differentiation	1.70E-02		TAL1,CD86,ETS1,MAP3B etc
		positive regulation of cell differentiation	2.80E-02		GATAG,NOTCH1,TAL1,TGFB2,JUNB,JUND,NRIF,NEUROD1,RUNX1,SRE,SOC35 etc
		cardiac muscle cell differentiation	3.40E-02		GATAG,MAP3B,RYR1,TTN etc
Cellular component	Plasma membrane	plasma membrane	1.70E-03	237/336 (70.5%)	GATAG,MAP3B,RYR1,TTN etc
		plasma membrane part	2.50E-03		ADAM12,ADAM3,ABCA1,ATP2B2,ATP5V1B2,ATP1B1,ATP1B3,BCL2L11,HRM,CAP1 etc
		extrinsic to plasma membrane	9.70E-03		CACNB2,CACNG4,CNRI,CAV2,CAV3,CLDN3,CTTNBP2,CDK5R1,CPEB1,DL1,DCBLD2,DAG1 etc
		basal plasma membrane	3.00E-02		SMAD7,CAV2,GNB1,GNL3,RAC1 etc
		internal side of plasma membrane	3.90E-02		CAV2,CTTNBP2,HRH2B,MT etc
		vesicle membrane	4.50E-05		RAB14,RAB9B,RAB40,RAF2,RAF1,APF1,CACNB2,CAV3,CDK5R1,DRD4 etc
		cytoplasmic vesicle membrane	7.30E-05		SEC24,CACNG4,CAMK2G,CAV2,CTTNBP2,EPN2,GJA1,ITPR1,PHLDA1,SCAMP1,SLC32A1 etc
		cytoplasmic vesicle part	1.20E-04		CAMK2G,CAV2,CTTNBP2,EPN2,FGA,GJA1,ITPR1,PHLDA1,SCAMP1,SLC32A1,SVT1 etc
		membrane-bounded vesicle	2.10E-03		ARCA1,ATP8V1B2,DNAK5,NOTCH1,RAB14,SB24C,AP51,APP,CACNG4,CAMK2G,CAV2 etc
		cytoplasmic membrane-bounded vesicle	2.70E-03		RAB14,SB24C,AP51,APP,CACNG4,CAMK2G,CAV2,CTTNBP2,EPN2,FGA,GJA1,ITPR1 etc
Cellular component	Vesicle	cytoplasmic vesicle	3.10E-03	30/336 (8.9%)	RAB14,SB24C,AP51,APP,CACNG4,CAMK2G,CAV2,CTTNBP2,EPN2,FGA,GJA1,ITPR1 etc
		vesicle	5.50E-03		CACNG4,CAMK2G,CAV2,CLDN3,CTTNBP2,EPN2,FGA,GJA1,ITPR1,MAP3B etc
		transport vesicle	2.90E-02		RAB14,SB24C,AP51,CAV2,SVT1,VAMP2 etc
		coated vesicle membrane	4.20E-02		SEC24,EPN2,SCAMP1,SLC32A1,SVT1,VAMP2 etc
		clathrin coated vesicle membrane	5.00E-02		EPN2,SCAMP1,SLC32A1,SVT1,VAMP2 etc
		transcription regulator activity	1.90E-09		ARBP2,ARID1A,BCL11A,CTCF,ELF5,ELK1,GATAG,HRP1,KLF12,KLF13,KLF14 etc
		RNA polymerase II transcription factor activity	5.00E-08		PKNOX1,SOX12,SOX9,SF1,SP1,TRX3,TEAD3,CREB1,HDAC4,JUNB,JUND etc
		transcription factor activity	3.10E-07		CTCF,ELF5,ELK1,GATAG,KLF12,KLF14,MES1,MES2,NRIF,NOTCH1,PKNOX1,PKNOX2 etc
		transcription repressor activity	7.20E-06		CTCF,ELF12,KLF4,MES1,NRIF,TRX3,ATXN1,CBFA2T1,DR1,EDP,EP3B,HDAC4 etc
		transcription activator activity	9.50E-05		ARID1A,CTCF,ELK1,GATAG,KLF14,MK12,NOTCH1,SOX9,SMARCA4,SMARCA4,SP1,TEAD3 etc
Molecular function	Transcription activity	specific RNA polymerase II transcription factor activity	3.40E-04	90/408 (22.0%)	MES1,PKNOX1,SOX9,CREB1,NR2F2,RXR,SRF,FOX etc
		RNA polymerase II transcription factor activity, enhancer binding	7.10E-03		GATAG,PKNOX1,CREB1,MITF,PA3,TFAP4 etc
		transcription corepressor activity	1.60E-02		CBFA2T1,DR1,HDAC4,NRIF,NR2F2,THRB etc
		transcription cofactor activity	2.00E-02		ARBP2,BCL11A,CTCF,ELF12,MK12,SMARCA4,CREB1,CBFA2T1,DR1,HAND2 etc
		protein kinase activity	3.60E-04		MAR1,NRKSACM1,CAMK1D,CAMK2G,CAV2,CTTNBP2,CCND1,CDK5R1,CD86,CD93,CHRM1,DYRK1A etc
		protein serine/threonine kinase activity	4.90E-04		CAMK1D,CAMK2G,CDK5R1,CD93,DRK1,ADPRK1,PKM2,PKM3,MAP3B,MAP4K12,MAP4K13 etc
		protein tyrosine kinase activity	3.60E-02		CAV2,CTTNBP2,CREB1,DYRK2,MEP9,MAP2K,NR1,NR2F1,STK4,TTN etc
		metal ion binding	3.60E-02		RPNT1,ADAM1,ADAM3,ADAM18,ADAM56,ADAM59,ADAM15L3,ARBP2,ATP1B2,ATP1B3 etc
		ion binding	3.90E-02		NOX4,NOTCH1,PAPPA,PHF15,PHF3,REX1,SEC24C,SNRKBSP1,SP2,TFAP15,ZEB3,ABLNB etc
		inorganic ion binding	4.70E-02		ATF1B1,MAR1,NRKSACM1,ADCY6,DYRK2,RYA1,RYA4,GCL1,CKM,PKM3,MAP3B,MTLK etc