

Supplemental Table S1. Biological process of upregulated differentially expressed genes

Term	Count	PValue	Genes
microtubule-based movement	8	4.83E-05	CENPE, KIF18A, DYNC1L12, KIF5B, KIF21A, KIF20A, KIF11, KIF20B
mRNA splicing, via spliceosome	8	0.000737	SNW1, SYF2, TRA2B, METTL3, TRA2A, CWC22, PRPF40A, BCAS2
protein folding	8	0.003469	DNAJC1, PPWD1, PFDN2, CCT8, PPIG, CWC27, PPIL4, PDRG1
regulation of alternative mRNA splicing, via spliceosome	6	0.000259	RBM25, SF3A1, RBM8A, TRA2B, NSRP1, RBM5
mRNA processing	6	0.000367	SON, RBM8A, AKAP8L, RBBP6, SMNDC1, QKI
double-strand break repair via homologous recombination	6	0.001674	RAD50, WDR48, RBBP8, NABP2, RAD54L, SMC5
nucleosome assembly	6	0.005805	BRD2, LOC100510904, LOC100516295, LOC100738859, SMARCA5, RSF1
stem cell population maintenance	5	0.006131	DDX6, MED10, NKAP, SMC3, EIF4E
mitotic chromosome condensation	4	0.001099	AKAP8L, AKAP8, NCAPG, SMC4
positive regulation of transforming growth factor beta receptor signaling pathway	4	0.002495	STK11, SNW1, CITED2, THBS1
positive regulation of ubiquitin-protein transferase activity	4	0.003125	ARRDC4, TRIB3, BMI1, TOPORS
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	4	0.007675	SNW1, EP300, AEN, TOPORS

Supplemental Table S2. Cellular component of upregulated differentially expressed genes

Term	Count	PValue	Genes
cytoplasm	77	5.43E-07	TES, AKAP8L, NKAP, ADM, PHAX, KIF11, SMC3, CHD1, SMC4, ETS2, PHTF1, NUDT4, PTTG1, EME1, PCF11, DPF2, EP300, DLGAP5, IER2, CEP68, BRD2, USP47, TSC22D2, PRPF40A, PPP4R3B, WDR35, LRRC41, ENAH, KCTD9, DMTF1, DDIT3, FAM185A, BIRC5, TERF2IP, TXNIP, PPIG, SGK1, ERGIC2, SLU7, GTF2A1, GGNBP2, CDCA2, RBM8A, SRF, NCAPG, CCNB1, UBB, FLRT2, UBC, MBIP, FLNC, SMNDC1, SOCS7, EIF4E, ATF7IP, TSNAX, NOP58, MAP3K1, GADD45B, BDNF, FUS, PLK1, RDX, UPF3B, EIF2S1, QKI, CENPE, SNRNP40, KIF18A, CDK7, NABP2, RLIM, ID3, PPIL4, ZCCHC2, CDKN3, METAP2
nucleus	69	5.36E-05	LTV1, WDR48, TES, CITED2, CCNF, ARID4A, PHAX, BMI1, CHD1, ETS2, NUDT4, PSMD8, STK11, PTTG1, CREB3L1, TLK2, PHACTR1, DLGAP5, CEP68, BRD2, USP47, PRKCI, OSR1, TSC22D2, ARID5B, LRRC41, RHOB, PHF20L1, DNAJC1, DMTF1, MORF4L2, CRY2, BIRC5, SRFBP1, TRIB3, KIF20A, SGK1, ZMYND11, VGLL3, GGNBP2, LOC100510904, BAZ2B, CCNB2, CCNB1, PABPN1, UBB, UBC, RBBP8, SAFB2, RBBP6, SMNDC1, ZKSCAN1, TSNAX, AKIRIN2, POU2F1, GADD45B, GADD45A, CCDC59, DONSON, EIF2S1, PHC3, QKI, PNRC2, CENPE, KIF18A, ID3, ESF1, CALM2, CDKN3
nucleoplasm	46	3.91E-08	CDCA2, PPP1R10, BOD1L1, AKAP8, NKAP, HNRNPU, PHAX, SMC3, SMC4, CLINT1, ETS2, EXOSC9, DPF2, SAFB2, RAD54L, UBXN7, RBBP6, CCT8, RBM5, IER2, ATF7IP, USP8, TIA1, POU2F1, FUS, PRPF40A, AEN, PPP4R3B, MRPL46, PHC3, SGO2, SNRNP40, RAD50, RYBP, DMTF1, FUBP1, WAC, NABP2, RLIM, LUC7L3, PFDN2, PPIG, KIF20B, SGK1, ZMYND11, PPIL4
membrane	31	1.32E-04	DIRAS3, DDX6, AKAP8, HNRNPU, NCAPG, HMMR, KIF11, CLINT1, CCNB2, CCNB1, STK11, KIF5B, NOP58, PRRC2C, PRPF40A, DDX52, GNL2, MED4, EIF2S1, LRRC41, HCFC1, HNRNPM, CENPE, RAD50, DYNC1L12, DRG1, OCIA1, DCP1A, ERGIC2, SLU7, EIF3A
nucleolus	28	6.96E-07	LOC100516295, PHTF1, MTDH, RPF1, EXOSC9, TRA2A, MBIP, BRIX1, LLPH, RBM34, RAB8A, NGDN, PLK1, SMARCA5, DNMTIP2, UPF3B, AEN, DDX52, GNL2, FTSJ3, EWSR1, MORF4L2, RPL7L1, FRG1, PFDN2, KIF20B, ERGIC2, EIF3A
centrosome	19	3.13E-06	CEP68, PLK1, CKAP2, NCAPG, PHAX, PPP4R3B, WDR35, AURKA, IFT20, CCNB2, DYNC1L12, CCNB1, DPF2, TRIM59, CCT8, KIF20B, CALM2, RAB8A, PAFAH1B1
catalytic step 2 spliceosome	13	3.88E-09	SF3A1, RBM8A, HNRNPU, CWC27, CDC40, HNRNPM, SNRNP40, SNW1, SYF2, CWC22, FRG1, SLU7, BCAS2
nuclear speck	9	1.34E-04	RBM25, SON, RBM8A, METTL3, AKAP8L, CWC22, NSRP1, SLU7, TOPORS
kinesin complex	7	1.14E-04	CENPE, KIF18A, KIF5B, KIF21A, KIF20A, KIF11, KIF20B
nuclear matrix	7	2.30E-04	HNRNPM, SNW1, CFL2, AKAP8L, AKAP8, PRPF40A, SMC3
spindle pole	6	0.001803	CCNB1, PLK1, KIF11, SMC3, CALM2, TOPORS
spindle microtubule	5	0.001832	PLK1, BIRC5, KIF11, CALM2, AURKA
small-subunit processome	5	0.004001	NOP56, UTP6, NOP58, NGDN, MPHOSPH10
condensed chromosome	4	0.003261	AKAP8, SMARCA5, NCAPG, BAZ1B
precatalytic spliceosome	4	0.008703	PRPF38B, SNRNP40, SON, BCAS2
mitotic spindle midzone	3	0.005988	CENPE, KIF18A, KIF20B

Supplemental Table S3. Molecular function of upregulated differentially expressed genes

Term	Count	PValue	Genes
poly(A) RNA binding	61	1.47E-22	TES, PPP1R10, AKAP8L, NKAP, HNRNPU, FAM208A, THUMPDP1, MRPL32, RBM34, DNTTIP2, PRPF40A, DDX52, GNL2, CDC40, FTSJ3, EWSR1, SYF2, RPL7L1, FRG1, SRFBP1, PPIG, DDX6, MRPS35, LOC100516295, AKAP8, MRPS30, MTDH, RPF1, PABPN1, EXOSC9, UBC, TRA2A, SAFB2, BRIX1, RBBP6, LLPH, SMNDC1, EIF4E, TRMT1L, NOP58, PRPF38B, TIA1, FUS, FAM46A, CCDC59, RDX, PRRC2C, RSRC2, EIF2S1, ARCN1, HNRNPM, SNRNP40, SON, SNW1, CMSS1, FUBP1, TRMT6, MPHOSPH10, ESF1, PPIL4, METAP2
ATP binding	34	0.007809	DDX6, ROCK1, DDX1, TWF1, KIF11, SMC3, SMC4, CHD1, AURKA, STK11, KIF5B, CHORDC1, TLK2, RAD54L, ABL2, KIF21A, CCT8, PMS1, DDX18, PRKCI, MAP3K1, HSPA4, PLK1, SMARCA5, DDX52, CENPE, KIF18A, CDK7, DNAJA2, TRIB3, KIF20A, KIF20B, SGK1, CFTR
zinc ion binding	33	4.16E-04	PHF3, TES, JADE1, RSF1, BAZ2B, PRICKLE1, BMI1, RBM4, UBR5, CHORDC1, DPF2, EP300, RBBP6, LONRF3, RBM5, MORC3, MAP3K1, FUS, CNBP, SREK1IP1, BAZ1B, PHC3, TOPORS, PHF20L1, EWSR1, G2E3, RUM, BIRC5, TRIM59, ZMYND11, CBLL1, SLU7, ZCCHC2
nucleotide binding	17	3.73E-05	RBM27, RBM25, TIA1, RBM8A, NIFK, FUS, UPF3B, HNRNPM, RBM4, PABPN1, EWSR1, TRA2B, TRA2A, SAFB2, RBM34, PPIL4, RBM5
RNA binding	13	7.28E-04	DDX18, SF3A1, PRPF40A, THUMPDP1, QKI, SON, EWSR1, FUBP1, UBR5, CWC22, BRIX1, SMNDC1, EIF4G2
mRNA binding	11	2.96E-06	RBM25, RBM8A, PCF11, TRA2B, LUC7L3, UPF3B, DCP1A, NSRP1, QKI, EIF3A, RBM5
ATPase activity	7	0.005128	ATF7IP, CENPE, SMARCA5, KIF21A, KIF20A, KIF20B, PMS1
microtubule motor activity	6	0.002196	CENPE, DYNC1L2, KIF5B, KIF21A, KIF20A, KIF20B
ATP-dependent microtubule motor activity, plus-end-directed	4	0.001059	KIF18A, KIF5B, KIF11, KIF20B

Supplemental Table S4. Biological process of downregulated differentially expressed genes

Term	Count	PValue	Genes
translation	26	2.32E-14	SLC25A1, RPL3, RPL10, RPL12, RPL8, RPS4X, RPS14, RPL18A, RPL13, RPS11, RPL18, RPL39, SLC25A24, RPS9, RPS5, LOC100623540, RPSA, EEF2, MRPS6, RPS27, RPS29, RPL27A, ATM, RPS20, SLC25A5, SLC25A6
oxidation-reduction process	12	2.47E-04	LDHA, SH3PXD2A, GPX4, SCD, FTH1, ME1, CYBA, MSMO1, TXN, PGD, GAPDH, CYP51
cell adhesion	11	5.16E-04	FERMT1, TINAGL1, NOV, ITGA2, CD9, ITGA6, ITGAV, IGFBP7, RPSA, ATP1B1, CTGF
cell-matrix adhesion	8	6.51E-05	BCAM, ITGB4, ITGA2, EMP2, ITGA6, ITGAV, NID2, CTGF
positive regulation of apoptotic process	8	0.006305545	BNIP3L, BCL2L11, ITGA6, APBB2, ATG7, DUSP6, BCL2L1, TGM2
glycolytic process	6	6.31E-05	GPI, TPI1, PGK1, ENO1, GAPDH, HK1
cytoplasmic translation	5	0.001542102	RPLP1, RPLP2, RPL15, RPL8, RPL29
cellular response to oxidative stress	5	0.002470359	PARP1, LONP1, TXN, NFE2L1, SLC25A24
translational elongation	4	2.10E-04	EEF1G, RPLP1, RPLP2, EEF2
ribosomal small subunit assembly	4	0.003343141	RPS27, RPS5, RPSA, RPS10
cell adhesion mediated by integrin	3	0.009696745	NOV, ITGA2, ITGA6

Supplemental Table S5. Cellular component of downregulated differentially expressed genes

Term	Count	PValue	Genes
extracellular exosome	80	4.62E-13	SLC25A1, LAD1, GPI, TINAGL1, RPL3, SLC44A1, ITGB4, RPLP1, DBI, ENO1, ACTB, ACTG1, RPS4X, CDH6, LGALS1, LAMP1, PLAUI, RPLP2, TIMP3, SH3BGRL2, ITGAV, RPS11, GLUL, RPS10, SPTAN1, TGM2, BCAS1, RPS9, TPI1, RPS5, TUBB, ANO6, MIF, ATP1B1, PGD, SDCBP2, EEF1G, BCAM, PKM, GPRC5A, PSME1, S100A4, TAGLN2, TNIK, PABPC1, SLC25A5, CD46, B4GALT5, CSTB, GRN, AHCY, MVK, MGST3, RPL12, TACSTD2, TXN, NID2, NDRG1, PPL, ACACA, ACAT2, LDHA, IGFBP7, SFN, ST3GAL1, VAT1, ST14, GALNT2, GOLM1, IDH1, MSN, BAIAP2, EEF2, PTPN13, DAB2, KRT19, CALM3, RPS20, CALR, ITM2B
cytoplasm	64	0.006371148	GPI, VEZT, TINAGL1, ACY1, YBX3, TMEM189, CCND2, FTH1, GRB10, TNS3, TNPO3, APOBEC1, SREBF1, SERPINB1, CXADR, PARP1, HMGCS1, MIF, PGD, SDCBP2, DUSP6, EEF1G, ACLY, TUBB2B, NOV, ELMO1, PSME1, S100A6, SELENOW, TNIK, PABPC1, GAPDH, CSNK1G2, MT1D, FTL, CSTB, ZNF395, AHCY, ACSS2, TXN, NDRG1, NPAS2, LDHA, GRK5, MT-2B, PGK1, SMYD2, EIF4EBP2, SFN, APBB2, METTL8, ATG7, IVNS1ABP, FDP5, SRD5A1, IRX3, MACC1, MSN, EEF2, PTPN13, SSH1, PTPRE, FABP3, BCL2L1
focal adhesion	28	9.72E-13	RPL3, RPL12, RPLP1, HACD3, RPL8, ACTB, ACTG1, RPS4X, GRK5, PLAUI, RPLP2, ITGAV, RPS11, RPL18, RPS1, TNS3, TGM2, RPS9, RPS5, ITGA2, HMGA1, MSN, FERMT1, DAB2, ITGA6, PABPC1, CALR, CD46
endoplasmic reticulum	20	3.60E-04	TPD52, CDS1, USP25, BNIP3L, MGST3, SSR2, BNIP3, ATP10A, ELOVL6, DHCR24, DBI, SGPP2, CYP51, EEF1B2, EEF1G, EBP, RCN1, P4HA2, FDFT1, TGM2
cell surface	16	5.07E-04	IGSF5, CXADR, ITGB4, F2R, EMP2, ANO6, MIF, MST1R, BCAM, PLAUI, CD109, LIPG, ITGAV, ADAM8, CD46, LDLR
cytosolic large ribosomal subunit	12	2.16E-08	RPL3, RPL10, RPL18A, RPL27A, RPL12, RPLP1, RPLP2, RPL13, RPL15, RPL8, RPL29, RPL18
ribosome	10	3.47E-07	RPS14, RPS29, RPL27A, LOC100623540, RPLP2, ATM, RPL8, RPL18, RPS10, RPL39
myelin sheath	10	8.98E-04	GPI, PKM, MSN, MIF, SLC25A5, ATP1B1, GLUL, NDRG1, ACTB, ACTG1
cytosolic small ribosomal subunit	9	1.55E-06	RPS4X, RPS9, RPS27, RPS29, RPS5, RPS20, RPSA, RPS11, RPS10
nuclear envelope	6	0.008395067	BNIP3L, PARP1, BNIP3, MGST3, SIGMAR1, S100A6
polysome	5	0.001397223	RPS4X, RPL10, CALR, EEF2, YBX3
integrin complex	4	0.004615113	ITGB4, ITGA2, ITGA6, ITGAV

Supplemental Table S6. Molecular function of downregulated differentially expressed genes

Term	Count	PValue	Genes
structural constituent of ribosome	30	1.15E-16	SLC25A1, RPL3, RPL10, RPL12, RPLP1, RPL8, RPS4X, RPS14, RPL18A, RPLP2, RPL13, RPL15, RPS11, RPL18, RPS10, RPL39, SLC25A24, RPS9, RPS5, LOC100623540, RPSA, MRPS6, RPS27, RPS29, RPL27A, ATM, RPS20, RPL29, SLC25A5, SLC25A6
poly(A) RNA binding	26	0.00600838	CSTB, GRN, POP7, RPL3, RPL12, TXN, ENO1, RPL8, RPS4X, LGALS1, RPL18A, RPL13, RPS11, RPS10, FDPS, RPS9, PARP1, PABPC4, EEF2, RPS27, PKM, RPS20, S100A4, PABPC1, RPL29, SLC25A5
calcium ion binding	20	0.008940336	TPD52, S100A2, DGKA, CETN2, ITPR3, LRP8, NID2, SYTL2, CDH6, RCN1, PRRG1, S100A6, CHP1, CALM3, ADAM8, S100A4, CALR, LDLR, SPTAN1, SLC25A24
NAD binding	5	0.003178343	AHCY, PARP1, IDH1, ME1, GAPDH

Supplemental Table S7. KEGG pathway of upregulated differentially expressed genes

Term	Count	PValue	Genes
Spliceosome	16	6.16187E-09	RBM25 PRPF38B SF3A1 RBM8A HNRNPU PRPF40A CDC40 HNRNPM SNRNP40 SNW1 SYF2 TRA2B TRA2A SLU7 SMNDC1 BCAS2
Cell cycle	11	3.27472E-05	CCNB2 CDK7 CCNB1 TGFβ2 PTTG1 GADD45B GADD45A RAD21 PLK1 EP300 SMC3
FoxO signaling pathway	10	0.000551038	CCNB2 STK11 CCNB1 TGFβ2 USP7 GADD45B GADD45A PLK1 EP300 SGK1
RNA transport	9	0.005401042	FXR1 RBM8A EIF3J UPF3B PHAX EIF4E EIF2S1 EIF3A EIF4G2
Oocyte meiosis	7	0.012570634	CCNB2 PPP3CB PTTG1 PLK1 SMC CALM2 AURKA
Ribosome biogenesis in eukaryotes	6	0.014823538	NOP56 UTP6 NOP58 MPHOSPH10 GNL2 WDR43
MAPK signaling pathway	10	0.028731975	TGFβ2 PPP3CB MAP3K1 GADD45B BDNF GADD45A DDIT3 SRF FLNC LAMTOR3
Vasopressin-regulated water reabsorption	4	0.037725291	DYNC1LI2 CREB3L1 DYNLL1 RAB5A
p53 signaling pathway	5	0.038328943	CCNB2 CCNB1 GADD45B GADD45A THBS1
TGF-beta signaling pathway	5	0.047175706	TGFβ2 ROCK1 EP300 ID3 THBS1

Supplemental Table S8. KEGG pathway of downregulated differentially expressed genes

Term	Count	PValue	Genes
Metabolic pathways	54	4.97E-05	GPI PGAP1 ACY1 GALNT18 DGKA MSMO1 SAT1 HK1 LIPG ME1 HADH GLUL TPI1 HMGCS1 PGD LSS ACLY NDUFS8 PKM NME7 B3GNT3 PGP POLR1D ND1 GAPDH ND4 CD51 AHCY MVK ACSS2 AK4 ACACA ACAT2 POLD3 LDHA EBP PGK1 SC5D COX1 LOC100524239 ST3GAL1 FDFT1 GALNT7 FDPS RRM2 GALNT2 IDH1 MBOAT2 DHCR24 CYP51 SQLE P4HA2 FASN LPIN1
Biosynthesis of antibiotics	26	3.90E-11	GPI MVK ACSS2 ACY1 MSMO1 AK4 ACAT2 HK1 LDHA PGK1 SC5D HADH FDFT1 FDPS TPI1 HMGCS1 IDH1 PGD LSS CYP51 ACLY SQLE PKM NME7 PGP GAPDH
Ribosome	24	2.83E-12	RPS9 RPL3 RPL10 RPS5 RPL12 RPLP1 LOC100623540 RPSA RPL8 RPS4X RPS27 RPL18A RPS29 RPL27A RPLP2 RPL13 RPS20 RPL15 RPS2 RPS11 RPL29 RPL18 RPS10 RPL39
Carbon metabolism	12	9.96E-05	GPI PKM ACSS2 TPI1 IDH1 ME1 PGP PGK1 PGD GAPDH ACAT2 HK1
Proteoglycans in cancer	12	0.013996961	PLAU ITGA2 IGF2 TIMP3 MSN ITGAV ITPR3 CAMK2G HSPG2 EGFR ACTB ACTG1
Phagosome	11	0.00536717	TUBB2B LAMP1 ITGA2 TUBB SLA-2 LOC100624785 ITGAV CYBA CALR ACTB ACTG1
Regulation of actin cytoskeleton	11	0.04031857	ITGB4 ITGA2 F2R MSN ITGA6 ITGAV BAIAP2 EGFR ACTB ACTG1 SSH1
Steroid biosynthesis	8	8.18E-07	SQLE EBP SC5D MSMO1 DHCR24 LSS CYP51 FDFT1
Glycolysis / Gluconeogenesis	8	6.54E-04	GPI LDHA PKM ACSS2 TPI1 PGK1 GAPDH HK1
Fatty acid metabolism	7	0.001245585	ELOVL5 SCD FASN HADH HACD3 ACAT2 ACACA
Biosynthesis of amino acids	7	0.005937287	PKM TPI1 ACY1 IDH1 PGK1 GAPDH GLUL
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	7	0.006428675	TCF7L1 ITGB4 ITGA2 ITGA6 ITGAV ACTB ACTG1
Glucagon signaling pathway	7	0.043891441	LDHA PKM SLC2A1 CALM3 ITPR3 CAMK2G ACACA
Pyruvate metabolism	6	0.003005758	LDHA PKM ACSS2 ME1 ACAT2 ACACA
Mucin type O-Glycan biosynthesis	5	0.006460422	GALNT7 GALNT2 GALNT18 ST3GAL1 B4GALT5
Glutathione metabolism	5	0.048833489	RRM2 GPX4 IDH1 MGST3 PGD
Terpenoid backbone biosynthesis	4	0.015961228	FDPS MVK HMGCS1 ACAT2
Butanoate metabolism	4	0.023368492	HMGCS1 HADH ACAT2 AACS
Propanoate metabolism	4	0.029176619	LDHA ACSS2 ACAT2 ACACA