

Figure S1. Correlation plot of the EXO.index with the expression of 10 proliferation-associated genes in 123 mantle cell lymphoma samples. The data were analyzed using the Pearson's correlation test. The data from the EXO.index and the expression levels of the 10 genes were log₂ transformed.

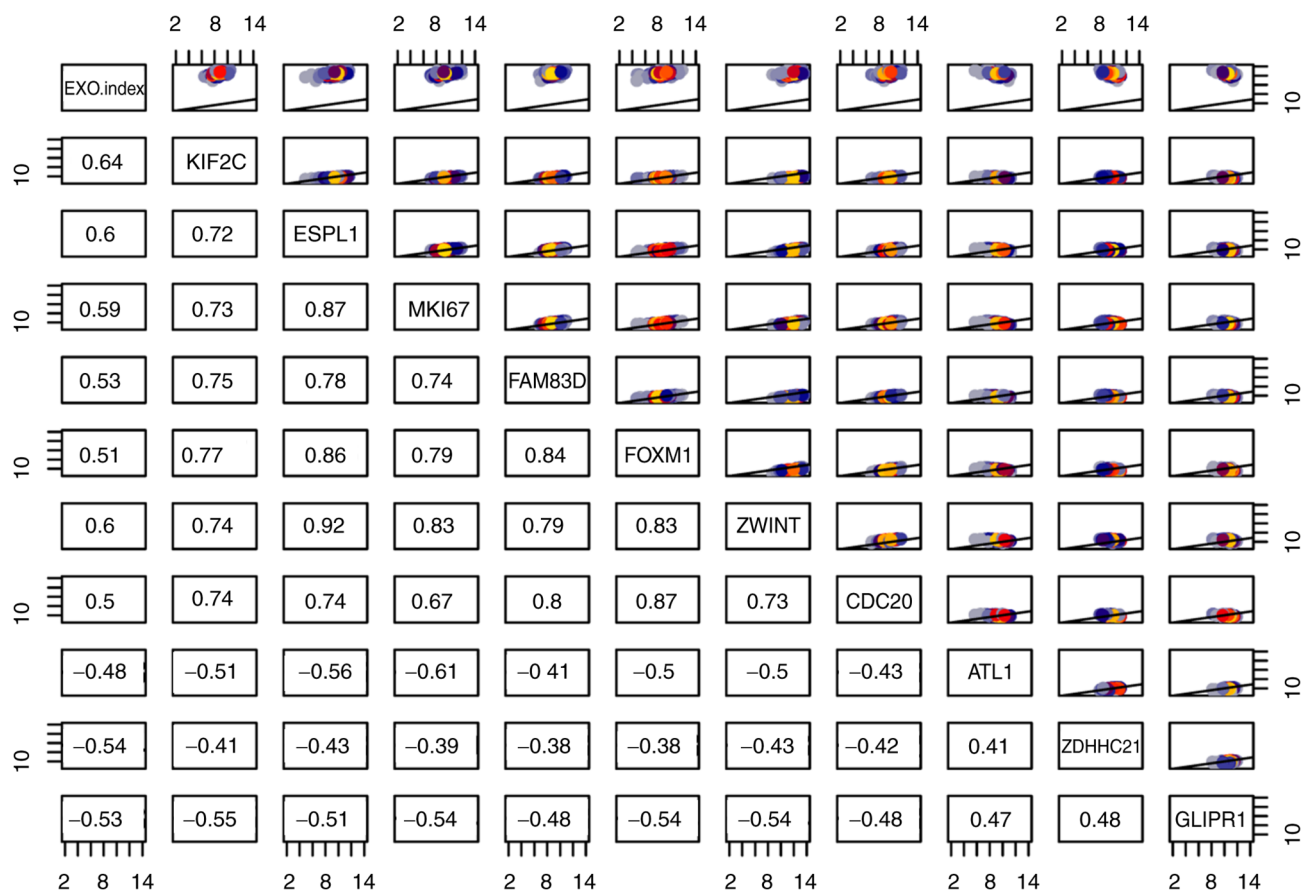


Table S1. GO pathway analysis of differentially expressed genes.

Term BP	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0050871~positive regulation of B cell activation	9	2.472527	1.15x10 ⁻⁰⁸	IGHG1, IGHG2, IGHG3, IGHG4, IGHD, IGHA1, IGHA2, IGHM, IGLC1	302	26	16792	1.92x10 ⁰¹	1.86x10 ⁻⁰⁵	1.86x10 ⁻⁰⁵
GO:0006910~phagocytosis, recognition	9	2.472527	2.21x10 ⁻⁰⁸	IGHG1, IGHG2, IGHG3, IGHG4, IGHD, IGHA1, IGHA2, IGHM, IGLC1	302	28	16792	1.79x10 ⁰¹	3.58x10 ⁻⁰⁵	1.79x10 ⁻⁰⁵
GO:0006911~phagocytosis, engulfment	9	2.472527	1.50x10 ⁻⁰⁷	IGHG1, IGHG2, IGHG3, IGHG4, IGHD, IGHA1, IGHA2, IGHM, IGLC1	302	35	16792	1.43x10 ⁰¹	2.43x10 ⁻⁰⁴	8.11x10 ⁻⁰⁵
GO:0050853~B cell receptor signaling pathway	10	2.747253	4.44x10 ⁻⁰⁷	IGHG1, IGHG2, PTPRC, IGHG3, IGHG4, IGHD, IGHA1, IGHA2, IGHM, IGLC1	302	54	16792	1.03x10 ⁰¹	7.20x10 ⁻⁰⁴	1.80x10 ⁻⁰⁴
GO:0007067~mitotic nuclear division	17	4.67033	1.08x10 ⁻⁰⁵	NEK1, TPX2, ANLN, CDC25C, CDK2, CDC25A, SMC3, DCTN2, PLK1, FIGN, BUB1, SKA1, MIS18BPI, WASL, TPR, CDCA5, ASPM	302	248	16792	3.81x10 ⁰	1.74x10 ⁻⁰²	3.50x10 ⁻⁰³
GO:0006958~complement activation, classical pathway	11	3.021978	1.12x10 ⁻⁰⁵	IGHG1, IGHG2, IGHG3, IGLV3-19, IGHG4, IGLV1-44, IGHD, IGHA1, IGHA2, IGHM, IGLC1	302	99	16792	6.18x10 ⁰	1.81x10 ⁻⁰²	3.03x10 ⁻⁰³
GO:0051301~cell division	20	5.494505	1.94x10 ⁻⁰⁵	KIF14, KIFC1, NEK1, TPX2, SYCE1, CDC25C, SMC3, CDC25A, CDK2, NCAPH, CDCA8, ATAD3B, FIGN, ZWINT, BUB1, SKA1, MIS18BPI, WASL, TPR, CDCA5	302	350	16792	3.18x10 ⁰	3.09x10 ⁻⁰²	4.48x10 ⁻⁰³
GO:0007062~sister chromatid cohesion	10	2.747253	9.74x10 ⁻⁰⁵	ESCO1, CDCA8, DDX11, PLK1, ZWINT, BUB1, RANGAP1, SKA1, CDCA5, SMC3	302	103	16792	5.40x10 ⁰	1.46x10 ⁻⁰¹	1.95x10 ⁻⁰²

Table S1. Continued.

Term BP	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0038096~Fc-gamma receptor signaling pathway involved in phagocytosis	10	2.747253	4.73x10 ⁻⁰⁴	IGHG1, IGHG2, IGHG3, IGLV3-19, IGHG4, IGLV1-44, WASF2, ARPC4, WASL, IGLC1	302	127	16792	4.38x10 ⁰	5.36x10 ⁻⁰¹	8.17x10 ⁻⁰²
GO:0006898~receptor-mediated endocytosis	12	3.296703	5.45x10 ⁻⁰⁴	EGFR, IGLV3-19, IGLV1-44, IGHA1, IGHA2, ARHGAP27, ACKR4, CALR, CD6, PLA2R1, IGLC1, TMPRSS3	302	186	16792	3.59x10 ⁰	5.86x10 ⁻⁰¹	8.45x10 ⁻⁰²
GO:0000086~G2/M transition of mitotic cell cycle	10	2.747253	8.20x10 ⁻⁰⁴	PLK1, FOXM1, TPX2, CEP290, PRKACA, PCM1, CDC25C, CDC25A, CDK2, DCTN2	302	137	16792	4.06x10 ⁰	7.35x10 ⁻⁰¹	1.14x10 ⁻⁰¹
GO:0006281~DNA repair	13	3.571429	1.13x10 ⁻⁰³	ATRX, UHRF1, ERCC6L2, DDX11, FOXM1, APTX, POLQ, INO80D, FANCA, SMC3, CDK2, BOD1L1, INO80B	302	235	16792	3.08x10 ⁰	8.40x10 ⁻⁰¹	1.42x10 ⁻⁰¹
GO:0042742~defense response to bacterium	10	2.747253	1.22x10 ⁻⁰³	IGHG1, IGHG2, IGHG3, IGHG4, S100A8, IGHD, S100A9, DEFB105B, DEFB105A, IGLC1	302	145	16792	3.83x10 ⁰	8.63x10 ⁻⁰¹	1.42x10 ⁻⁰¹
GO:0031297~replication fork processing	5	1.373626	1.28x10 ⁻⁰³	ATRX, FANCM, DDX11, TONSL, BOD1L1	302	27	16792	1.03x10 ⁰¹	8.75x10 ⁻⁰¹	1.38x10 ⁻⁰¹
GO:0000281~mitotic cytokinesis	5	1.373626	1.69x10 ⁻⁰³	CKAP2, KIF23, KIF4A, PLK1, ANLN	302	29	16792	9.59x10 ⁰	9.35x10 ⁻⁰¹	1.67x10 ⁻⁰¹
GO:0045087~innate immune response	18	4.945055	2.03x10 ⁻⁰³	IGHG1, IGHG2, IGHG3, HMGB3, IGHG4, S100A8, S100A9, DEFB105B, DEFB105A, IGHM, PTK2B, IGHD, IGHA1, JAK1, IGHA2, CD6, IGLC1, AKIRIN2	302	430	16792	2.33x10 ⁰	9.63x10 ⁻⁰¹	1.86x10 ⁻⁰¹
GO:0008283~cell proliferation	16	4.395604	2.59x10 ⁻⁰³	EGFR, MKI67, TPX2, PRKDC, CDC25C, CDC25A, TACC2, TNFSF8, DCTN2, TYMS, UHRF1, PLK1, BUB1, FOXC1, AREG, IGFBP4	302	366	16792	2.43x10 ⁰	9.85x10 ⁻⁰¹	2.19x10 ⁻⁰¹

Table S1. Continued.

Term BP	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0006956~complement activation	7	1.923077	4.73x10 ⁻⁰³	IGHG1, IGHG2, IGHG3, IGLV3-19, IGHG4, IGLV1-44, IGLC1	302	87	16792	4.47x10 ⁰	1.00x10 ⁰	3.47x10 ⁻⁰¹
GO:0000070~mitotic sister chromatid segregation	4	1.098901	9.79x10 ⁻⁰³	KIFC1, PLK1, ZWINT, ESPL1	302	25	16792	8.90x10 ⁰	1.00x10 ⁰	5.68x10 ⁻⁰¹
GO:0007018~microtubule-based movement	6	1.648352	1.52x10 ⁻⁰²	KIF23, KIF14, KIFC1, KIF1A, KIF4A, AP2A1	302	81	16792	4.12x10 ⁰	1.00x10 ⁰	7.10x10 ⁻⁰¹
GO:1903779~regulation of cardiac conduction	5	1.373626	1.79x10 ⁻⁰²	PLN, PRKACA, ATP1A2, FXYD7, ITPR2	302	56	16792	4.96x10 ⁰	1.00x10 ⁰	7.52x10 ⁻⁰¹
GO:0016311~dephosphorylation	6	1.648352	1.92x10 ⁻⁰²	PTPRC, SGPP2, NT5C1B, NT5DC2, APTX, G6PC3	302	86	16792	3.88x10 ⁰	1.00x10 ⁰	7.60x10 ⁻⁰¹
GO:0045669~positive regulation of osteoblast differentiation	5	1.373626	2.25x10 ⁻⁰²	SFRP2, IL6ST, JUNB, LTF, GNAS	302	60	16792	4.63x10 ⁰	1.00x10 ⁰	7.99x10 ⁻⁰¹
GO:0045787~positive regulation of cell cycle	4	1.098901	2.27x10 ⁻⁰²	RARA, CALR, TCF3, BCL2L11	302	34	16792	6.54x10 ⁰	1.00x10 ⁰	7.87x10 ⁻⁰¹
GO:0042384~cilium assembly	7	1.923077	2.43x10 ⁻⁰²	NEK1, CEP290, CELSR3, C5ORF42, PCMI1, NME8, IFT174	302	124	16792	3.14x10 ⁰	1.00x10 ⁰	7.97x10 ⁻⁰¹
GO:0018105~peptidyl-serine phosphorylation	7	1.923077	2.52x10 ⁻⁰²	PLK1, PRKDC, PRKACA, UHMK1, AKT3, CDK2, AKT2	302	125	16792	3.11x10 ⁰	1.00x10 ⁰	7.96x10 ⁻⁰¹
GO:0008584~male gonad development	6	1.648352	2.70x10 ⁻⁰²	SFRP2, BIK, AGO4, FANCA, BCL2L11, ASPM	302	94	16792	3.55x10 ⁰	1.00x10 ⁰	8.06x10 ⁻⁰¹
GO:0007080~mitotic metaphase plate congression	4	1.098901	2.83x10 ⁻⁰²	KIF14, KIFC1, CDCA8, CDCA5	302	37	16792	6.01x10 ⁰	1.00x10 ⁰	8.10x10 ⁻⁰¹
GO:0045947~negative regulation of translational initiation	3	0.824176	2.88x10 ⁻⁰²	EIF4EBP2, RARA, TPR	302	15	16792	1.11x10 ⁰¹	1.00x10 ⁰	8.05x10 ⁻⁰¹
GO:0006302~double-strand break repair	5	1.373626	3.06x10 ⁻⁰²	APTX, PRKDC, H2AFX, POLQ, CDCA5	302	66	16792	4.21x10 ⁰	1.00x10 ⁰	8.14x10 ⁻⁰¹
GO:0006275~regulation of DNA replication	3	0.824176	3.26x10 ⁻⁰²	ESCO1, CCDC88A, SMC3	302	16	16792	1.04x10 ⁰¹	1.00x10 ⁰	8.23x10 ⁻⁰¹
GO:0001895~retina homeostasis	4	1.098901	3.46x10 ⁻⁰²	IGHG3, IGHAI1, LTF, IGHAI2	302	40	16792	5.56x10 ⁰	1.00x10 ⁰	8.32x10 ⁻⁰¹
GO:0043066~negative regulation of apoptotic process	15	4.120879	3.55x10 ⁻⁰²	KIF14, EGFR, IL6ST, PRKDC, NOTCH2, BAG4, ATAD3A, CD44, PLK1, PTK2B, COMP, LTF, RARA, AGO4, ARHGDI1	302	455	16792	1.83x10 ⁰	1.00x10 ⁰	8.30x10 ⁻⁰¹
GO:0048563~post-embryonic organ morphogenesis	2	0.549451	3.55x10 ⁻⁰²	MYO7A, BCL2L11	302	2	16792	5.56x10 ⁰¹	1.00x10 ⁰	8.22x10 ⁻⁰¹

Table S1. Continued.

Term BP	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0070488~neutrophil aggregation	2	0.549451	3.55x10 ⁻⁰²	S100A8, S100A9	302	2	16792	5.56x10 ⁰¹	1.00x10 ⁰	8.22x10 ⁻⁰¹
GO:0030048~actin filament-based movement	3	0.824176	3.65x10 ⁻⁰²	MYO6, MYO7A, WASF2	302	17	16792	9.81x10 ⁰	1.00x10 ⁰	8.21x10 ⁻⁰¹
GO:0000082~G1/S transition of mitotic cell cycle	6	1.648352	3.65x10 ⁻⁰²	TYMS, CDC45, CDCA5, CDC25A, CDK2, CDT1	302	102	16792	3.27x10 ⁰	1.00x10 ⁰	8.13x10 ⁻⁰¹
GO:0008284~positive regulation of cell proliferation	15	4.120879	4.22x10 ⁻⁰²	TRPM4, KIF14, EGFR, FGF7, IL6ST, FOXM1, CALR, CDK2, PURA, CNOT6L, SFRP2, PTK2B, RARA, AREG, AKIRIN2	302	466	16792	1.79x10 ⁰	1.00x10 ⁰	8.48x10 ⁻⁰¹
GO:0019731~antibacterial humoral response	4	1.098901	4.40x10 ⁻⁰²	IGHA1, LTF, IGHA2, IGHM	302	44	16792	5.05x10 ⁰	1.00x10 ⁰	8.53x10 ⁻⁰¹
GO:0051493~regulation of cytoskeleton organization	3	0.824176	4.48x10 ⁻⁰²	CAPN6, S100A8, S100A9	302	19	16792	8.78x10 ⁰	1.00x10 ⁰	8.51x10 ⁻⁰¹
GO:0010881~regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	3	0.824176	4.48x10 ⁻⁰²	PLN, PRKACA, ATP1A2	302	19	16792	8.78x10 ⁰	1.00x10 ⁰	8.51x10 ⁻⁰¹
GO:0007623~circadian rhythm	5	1.373626	4.57x10 ⁻⁰²	EGFR, TOP1, TYMS, THRAP3, JUND	302	75	16792	3.71x10 ⁰	1.00x10 ⁰	8.49x10 ⁻⁰¹
GO:0007094~mitotic spindle assembly checkpoint	3	0.824176	4.92x10 ⁻⁰²	PLK1, BUB1, TPR	302	20	16792	8.34x10 ⁰	1.00x10 ⁰	8.64x10 ⁻⁰¹
GO:0007275~multicellular organism development	16	4.395604	4.98x10 ⁻⁰²	ZBTB7B, PLXNA3, HMGB3, ZFY, LTBP4, MINK1, SOX6, NME8, QRIC1, NOTCH2, PHF3, DDX11, SFRP2, RPS4Y1, LIMD1, SPATA24	302	521	16792	1.71x10 ⁰	1.00x10 ⁰	8.60x10 ⁻⁰¹
GO:0031532~actin cytoskeleton reorganization	4	1.098901	5.19x10 ⁻⁰²	FGF7, S100A9, CDC42BPA, MINK1	302	47	16792	4.73x10 ⁰	1.00x10 ⁰	8.66x10 ⁻⁰¹
GO:0097681~double-strand break repair via alternative nonhomologous end joining	2	0.549451	5.28x10 ⁻⁰²	PRKDC, POLQ	302	3	16792	3.71x10 ⁰¹	1.00x10 ⁰	8.64x10 ⁻⁰¹
GO:0032602~chemokine production	2	0.549451	5.28x10 ⁻⁰²	S100A8, S100A9	302	3	16792	3.71x10 ⁰¹	1.00x10 ⁰	8.64x10 ⁻⁰¹
GO:0098609~cell-cell adhesion	10	2.747253	5.60x10 ⁻⁰²	ARGLU1, COBLL1, MYO6, SH3GLB2, WASF2, HIST1H3B, RANGAPI1, ANLN, PERP, EHD4	302	271	16792	2.05x10 ⁰	1.00x10 ⁰	8.74x10 ⁻⁰¹
GO:0007219~Notch signaling pathway	6	1.648352	5.60x10 ⁻⁰²	NOTCH2, PLN, DTX3, FOXC1, PERP, IFT74	302	115	16792	2.90x10 ⁰	1.00x10 ⁰	8.69x10 ⁻⁰¹
GO:0090316~positive regulation of intracellular protein transport	3	0.824176	5.85x10 ⁻⁰²	CEP290, TPR, PCMI	302	22	16792	7.58x10 ⁰	1.00x10 ⁰	8.75x10 ⁻⁰¹

Table S1. Continued.

Term BP	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0016925~protein sumoylation	6	1.648352	5.95x10 ⁻⁰²	TRPM4, TOPI, CDCA8, RANGAPI, TPR, SMC3	302	117	16792	2.85x10 ⁰	1.00x10 ⁰	8.74x10 ⁻⁰¹
GO:0006260~DNA replication	7	1.923077	6.06x10 ⁻⁰²	TOPI, CDC45, CCDC88A, CDC25C, CDC25A, CDK2 CDT1	302	155	16792	2.51x10 ⁰	1.00x10 ⁰	8.74x10 ⁻⁰¹
GO:0000083~regulation of transcription involved in G1/S transition of mitotic cell cycle	3	0.824176	6.33x10 ⁻⁰²	TYMS, CDC45, CDT1	302	23	16792	7.25x10 ⁰	1.00x10 ⁰	8.80x10 ⁻⁰¹
GO:0030307~positive regulation of cell growth	5	1.373626	6.42x10 ⁻⁰²	EGFR, S100A8, SFRP2, PTK2B, S100A9	302	84	16792	3.31x10 ⁰	1.00x10 ⁰	8.78x10 ⁻⁰¹
GO:0034097~response to cytokine	4	1.098901	6.63x10 ⁻⁰²	TYMS, IL6ST, JUND, RARA	302	52	16792	4.28x10 ⁰	1.00x10 ⁰	8.82x10 ⁻⁰¹
GO:0006508~proteolysis	15	4.120879	6.78x10 ⁻⁰²	IGHG1, CAPN6, IGHG2, CTSZ, IGHG3, IGHG4, IGLV1-44, ESPL1, TMPRSS3, IGLV3-19, NAALAD2, PAPA, LTF, CPA3, IGLC1	302	500	16792	1.67x10 ⁰	1.00x10 ⁰	8.83x10 ⁻⁰¹
GO:0007126~meiotic nuclear division	3	0.824176	6.82x10 ⁻⁰²	MKI67, SMC3, CDK2	302	24	16792	6.95x10 ⁰	1.00x10 ⁰	8.80x10 ⁻⁰¹
GO:0007088~regulation of mitotic nuclear division	3	0.824176	6.82x10 ⁻⁰²	MKI67, FBXO43, CDC25C	302	24	16792	6.95x10 ⁰	1.00x10 ⁰	8.80x10 ⁻⁰¹
GO:0006338~chromatin remodeling	5	1.373626	6.87x10 ⁻⁰²	ATRX, TOPI, INO80B-WBP1, TAF6L, INO80B	302	86	16792	3.23x10 ⁰	1.00x10 ⁰	8.77x10 ⁻⁰¹
GO:0033152~immunoglobulin V(D)J recombination	2	0.549451	6.98x10 ⁻⁰²	PRKDC, TCF3	302	4	16792	2.78x10 ⁰¹	1.00x10 ⁰	8.77x10 ⁻⁰¹
GO:0032119~sequestering of zinc ion	2	0.549451	6.98x10 ⁻⁰²	S100A8, S100A9	302	4	16792	2.78x10 ⁰¹	1.00x10 ⁰	8.77x10 ⁻⁰¹
GO:0002326~B cell lineage commitment	2	0.549451	6.98x10 ⁻⁰²	PRKDC, TCF3	302	4	16792	2.78x10 ⁰¹	1.00x10 ⁰	8.77x10 ⁻⁰¹
GO:0002793~positive regulation of peptide secretion	2	0.549451	6.98x10 ⁻⁰²	S100A8, S100A9	302	4	16792	2.78x10 ⁰¹	1.00x10 ⁰	8.77x10 ⁻⁰¹
GO:0051726~regulation of cell cycle	6	1.648352	7.25x10 ⁻⁰²	PTPRC, PLK1, FOXM1, JUND, CDC25C, CDC25A	302	124	16792	2.69x10 ⁰	1.00x10 ⁰	8.82x10 ⁻⁰¹
GO:0048589~developmental growth	3	0.824176	7.33x10 ⁻⁰²	TYMS, GNAS, ASPM	302	25	16792	6.67x10 ⁰	1.00x10 ⁰	8.81x10 ⁻⁰¹
GO:0001816~cytokine production	3	0.824176	7.33x10 ⁻⁰²	S100A8, S100A9, PLA2R1	302	25	16792	6.67x10 ⁰	1.00x10 ⁰	8.81x10 ⁻⁰¹
GO:0006405~RNA export from nucleus	4	1.098901	7.57x10 ⁻⁰²	POM121L12, U2AF2, ZC3H11A, TPR	302	55	16792	4.04x10 ⁰	1.00x10 ⁰	8.85x10 ⁻⁰¹
GO:0006259~DNA metabolic process	3	0.824176	7.85x10 ⁻⁰²	FANCM, MKI67, IGFBP4	302	26	16792	6.42x10 ⁰	1.00x10 ⁰	8.90x10 ⁻⁰¹
GO:0021766~hippocampus development	4	1.098901	7.90x10 ⁻⁰²	KIF14, PLXNA3, RARA, OGDH	302	56	16792	3.97x10 ⁰	1.00x10 ⁰	8.88x10 ⁻⁰¹

Table SI. Continued.

Term BP	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0021987~cerebral cortex development	4	1.098901	7.90x10 ⁻⁰²	KIF14, H2AFX, ASPM, TACC2	302	56	16792	3.97x10 ⁰	1.00x10 ⁰	8.88x10 ⁻⁰¹
GO:0016049~cell growth	4	1.098901	7.90x10 ⁻⁰²	NOTCH2, TYMS, ATP6V0E1, ATAD3A	302	56	16792	3.97x10 ⁰	1.00x10 ⁰	8.88x10 ⁻⁰¹
GO:0017148~negative regulation of translation	4	1.098901	8.57x10 ⁻⁰²	CNOT3, IGF2BP3, CALR, PURA	302	58	16792	3.83x10 ⁰	1.00x10 ⁰	9.04x10 ⁻⁰¹
GO:0003417~growth plate cartilage development	2	0.549451	8.65x10 ⁻⁰²	COMP, RARA	302	5	16792	2.22x10 ⁰¹	1.00x10 ⁰	9.02x10 ⁻⁰¹
GO:0051653~spindle localization	2	0.549451	8.65x10 ⁻⁰²	WASL, ASPM	302	5	16792	2.22x10 ⁰¹	1.00x10 ⁰	9.02x10 ⁻⁰¹
GO:0070201~regulation of establishment of protein localization	2	0.549451	8.65x10 ⁻⁰²	CEP290, WHSC1	302	5	16792	2.22x10 ⁰¹	1.00x10 ⁰	9.02x10 ⁻⁰¹
GO:0007283~spermatogenesis	12	3.296703	8.73x10 ⁻⁰²	ATRX, KIF1C, HSF1, BIK, H2AFX, RARA, CALR, CDC25C, NME8, BCL2L11, ASPM, SPATA24	302	385	16792	1.73x10 ⁰	1.00x10 ⁰	9.01x10 ⁻⁰¹
GO:0051216~cartilage development	4	1.098901	8.92x10 ⁻⁰²	TYMS, CD44, GNAS, SOX6	302	59	16792	3.77x10 ⁰	1.00x10 ⁰	9.03x10 ⁻⁰¹
GO:0060271~cilium morphogenesis	6	1.648352	9.80x10 ⁻⁰²	NEK1, CEP290, C5ORF42, PCM1, NME8, IFT74	302	136	16792	2.45x10 ⁰	1.00x10 ⁰	9.21x10 ⁻⁰¹
GO:0006977~DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	4	1.098901	9.99x10 ⁻⁰²	CNOT6L, CNOT3, CDC25C, CDK2	302	62	16792	3.59x10 ⁰	1.00x10 ⁰	9.22x10 ⁻⁰¹
Term CC	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0042571~immunoglobulin complex, circulating	6	1.648352	1.14x10 ⁻⁰⁵	IGHG1, IGHG2, IGHG3, IGHG4, IGHD, IGLC1	302	19	18224	1.91x10 ⁰¹	4.16x10 ⁻⁰³	4.16x10 ⁻⁰³
GO:0005634~nucleus	125	34.34066	1.26x10 ⁻⁰⁵	SCAF1, KIF1C, PLXNA3, NT5C1B-RDH14, S100A8, U2AF2, S100A9, CNOT3, LUZP1, RORA, TOPI1, CDCA8, PTGIS, DDX11, CEP290, PRKACA, RARA, H2AFX, CDCA5, ASPM, MTUS1, AKIRIN2, SPATA24, ARGLU1, EGFR, MYO6, EMX2, FOXN2, ESPL1,	302	5415	18224	1.39x10 ⁰	4.57x10 ⁻⁰³	2.29x10 ⁻⁰³

Table S1. Continued.

Term CC	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0005654~nucleoplasm	71	19.50549	1.58x10 ⁻⁰⁴	DEPDC1, PARP10, TAF6L, TACC2, UHRF1, ZWINT, C2CD4A, PDE4DIP, PRDM2, DST, ZIM3, HMGB3, NEK1, NT5C1B, IGF2BP3, SOX6, AFAP1L1, CALR, UHMK1, SESN3, CNOT6L, JUND, DDX3Y, FBXO43, TCF3, ARHGDI1, MKI67, PCNP, WHSC1, ZBTB45, TET2, NOTCH2, ZNF215, PLK1, HIST1H3B, PON2, AREG, HDAC9, KIF23, ERCC6L2, CDT1, BAG4, CDC45, MAZ, HSF1, LTF, TPR, FANCA, LOC653513, INO80D, AKT2, INO80B, KIF14, ZFY, TPX2, APTX, ARHGAP27, PALLD, CDK2, PURA, SERPINB6, RPS4Y1, GNAS, FOXO1, JMJD1C, WASL, TBX18, SRCAP, IFT74, FOXM1, THAP5, NFYC, RGS10, TYMS, CHD9, NCAPH, SH3GLB2, PTK2B, HJURP, FIGN, LARS, POU2F1, LIMD1, AGO4, SNRNP70, EHD4, ZBTB7B, ZNF264, CDC25C, SMC3, CDC25A, RGS13, ATRX, ZNF672, THRAP3, JAK1, KIF23, U2AF2, RORA, CDT1, BODIL1, TOPI1, FANCM, CDCA8, CDC45, DDX11, HSF1, SRRM2, H2AFX, RARA, PRKACA, TPR, FANCA, CDCA5, AKT3, AKT2, SPATA24, ARGLU1, TRPM4, ESCO1, MYO6, TPX2, APTX, ARHGAP27, DEPDC1, PARP10, CDK2, RPS4Y1, FOXO1, RPS11, JMJD1C, EP400, PMPA1, KIF4A, FOXM1, PRKDC, NFYC, ANLN, SOX6, TYMS, CHD9, AKT1S1, HJURP, PTK2B, BUB1, POU2F1, SNRNP70, POLQ, TCF3, ZBTB7B, TONSL, WHSC1, CELSRI, CDC25C, SMC3, CDC25A, QRICH1, NOTCH2, PLK1, THRAP3, HIST1H3B, ATP6V0A1, ZC3H11A, MIS18BP1, HDAC9, HPGD, GLYR1	302	2784	18224	1.54x10 ⁰	5.60x10 ⁻⁰²	1.90x10 ⁻⁰²

Table S1. Continued.

Term CC	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0009897~external side of plasma membrane	13	3.571429	2.30x10 ⁻⁰⁴	IGHG1, PTPRC, IGHG2, IGHG3, IGHG4, IL6ST, CALR, IGHM, ITGAX, IGHD, IGHA1, IGHA2, IGLC1	302	213	18224	3.68x10 ⁰	8.06x10 ⁻⁰²	2.08x10 ⁻⁰²
GO:0005694~chromosome	8	2.197802	1.79x10 ⁻⁰³	TOP1, KIF4A, HMGB3, WHSC1, POLQ, CDCA5, SMC3, BOD1L1	302	105	18224	4.60x10 ⁰	4.80x10 ⁻⁰¹	1.23x10 ⁻⁰¹
GO:0072562~blood microparticle	9	2.472527	3.81x10 ⁻⁰³	IGHG1, IGHG2, IGHG3, IGHG4, IGHD, IGHA1, IGHA2, IGHM, IGLC1	302	152	18224	3.57x10 ⁰	7.52x10 ⁻⁰¹	2.07x10 ⁻⁰¹
GO:0005813~centrosome	16	4.395604	5.04x10 ⁻⁰³	KIF23, CKAP2, NEK1, ESPL1, PCM1, CDK2, DCTN2, CDC45, DDX11, PLK1, CEP290, PDE4DIP, PRKACA, MARCKS, LOC653513, IFT74	302	426	18224	2.27x10 ⁰	8.42x10 ⁻⁰¹	2.32x10 ⁻⁰¹
GO:0000776~kinetochore	6	1.648352	1.10x10 ⁻⁰²	PLK1, ZWINT, BUB1, RANGAP1, TPR, DCTN2	302	81	18224	4.47x10 ⁰	9.82x10 ⁻⁰¹	3.96x10 ⁻⁰¹
GO:0005871~kinesin complex	5	1.373626	1.13x10 ⁻⁰²	KIF23, KIF14, KIFC1, KIF1A, KIF4A	302	53	18224	5.69x10 ⁰	9.84x10 ⁻⁰¹	3.70x10 ⁻⁰¹
GO:0000775~chromosome, centromeric region	5	1.373626	1.45x10 ⁻⁰²	CDCA8, MKI67, HJURP, CDCA5, SMC3	302	57	18224	5.29x10 ⁰	9.95x10 ⁻⁰¹	4.14x10 ⁻⁰¹
GO:0005615~extracellular space	34	9.340659	1.48x10 ⁻⁰²	IGHG1, IGHG2, IGHG3, IGHG4, S100A8, IL6ST, LTBP4, S100A9, IGHM, CALR, PTGIS, PAPA, COMP, IGHA1, LTF, CPA3, COL12A1, IGHA2, ANGPTL1, LECT2, PCSK5, ARHGDIA, MTUS1, SPON1, EGFR, CTSZ, TNFSF8, TNFAIP6, SERPINB6, SFRP2, F3, AREG, IGLC1, IGFBP4	302	1347	18224	1.52x10 ⁰	9.96x10 ⁻⁰¹	3.89x10 ⁻⁰¹
GO:0000785~chromatin	6	1.648352	1.60x10 ⁻⁰²	ESCO1, PLK1, JUND, APTX, JMJD1C, SMC3	302	89	18224	4.07x10 ⁰	9.97x10 ⁻⁰¹	3.88x10 ⁻⁰¹
GO:0005938~cell cortex	7	1.923077	1.64x10 ⁻⁰²	MYO6, PTK2B, MYO7A, MARCKS, DST, AKT2, ITPR2	302	123	18224	3.43x10 ⁰	9.98x10 ⁻⁰¹	3.72x10 ⁻⁰¹
GO:0016020~membrane	50	13.73626	1.78x10 ⁻⁰²	KIFC1, ATP6V0E1, PLXNA3, IL6ST, HBS1L, LUZP1, DIRAS1, CEP290, PRKACA, CALCR1, FNDC3A, EGFR, KIF14, CCDC88A, MYO6, NBAS, ARHGAP27, PCMI, DCTN2, RPS4Y1, GNAS, TOMM22, RPS11, KIF4A, GANAB, RAP1GAP, PRKDC, CALR, G6PC3, SLC29A1, NCAPH, ITGAX, DDX3Y, B3GNT6, BUB1, AGO4, CD6, EHD4, PTPRC, OSBP18, MKI67, ATP1A2, ITPR2, NOTCH2, AP2A1, CD300A, PLN, HIST1H3B, JAK1, TMOD1	302	2200	18224	1.37x10 ⁰	9.99x10 ⁻⁰¹	3.75x10 ⁻⁰¹

Table SI. Continued.

Term	CC	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0005913~cell-cell adherens junction		12	3.296703	1.89x10 ⁻⁰²	ARGLU1, COBLL1, EGFR, MYO6, SH3GLB2, CADM2, WASF2, HIST1H3B, DSC2, RANGAP1, ANLN, EHD4	302	323	18224	2.24x10 ⁰	9.99x10 ⁻⁰¹	3.71x10 ⁻⁰¹
GO:0030496~midbody		7	1.923077	2.03x10 ⁻⁰²	KIF23, KIF14, KIF4A, CDCA8, DDX11, PLK1, ASPM	302	129	18224	3.27x10 ⁰	9.99x10 ⁻⁰¹	3.74x10 ⁻⁰¹
GO:0031012~extracellular matrix		11	3.021978	2.58x10 ⁻⁰²	GANAB, SFRP2, F3, LTBP4, COMP, S100A9, COL12A1, PRKDC, RPS11, CALR, SPON1	302	296	18224	2.24x10 ⁰	1.00x10 ⁰	4.29x10 ⁻⁰¹
GO:0005829~cytosol		69	18.95604	2.98x10 ⁻⁰²	KIF23, NT5C1B-RDH14, S100A8, MYO7A, WASF2, S100A9, CNOT3, WWC2, RANGAP1, OGDH, CDT1, BAG4, CDCA8, HSF1, CEP290, PRKACA, FNDC3A, CDCA5, AKT2, KIF14, TRPM4, MYO6, CCDC88A, NBAS, TPX2, MINK1, ESPL1, PCM1, BCL2L1, CDK2, DCTN2, SERPINB6, ZWINT, AKAP5, RPS4Y1, GNAS, WASL, RPS11, DST, KIF4A, RAPIGAP, NT5C1B, PRKDC, ARPC4, IGF2BP3, CALR, TYMS, RGS10, NCAPH, AKT1S1, GMIP, PTK2B, CNOT6L, BUB1, LARS, AGO4, SKA1, ARHGDIA, CDC25C, CDC25A, SMC3, RGS13, PLK1, AP2A1, JAK1, RGS7, HPGD, FAMI26A, TMOD1	302	3315	18224	1.26x10 ⁰	1.00x10 ⁰	4.59x10 ⁻⁰¹
GO:0072686~mitotic spindle		4	1.098901	3.00x10 ⁻⁰²	KIF23, RANGAP1, ESPL1, TPR	302	41	18224	5.89x10 ⁰	1.00x10 ⁰	4.43x10 ⁻⁰¹
GO:0000922~spindle pole		6	1.648352	3.46x10 ⁻⁰²	CKAP2, DDX11, PLK1, TPX2, RANGAP1, SMC3	302	109	18224	3.32x10 ⁰	1.00x10 ⁰	4.74x10 ⁻⁰¹
GO:0005876~spindle microtubule		4	1.098901	3.59x10 ⁻⁰²	CAPN6, KIF4A, PLK1, SKA1	302	44	18224	5.49x10 ⁰	1.00x10 ⁰	4.71x10 ⁻⁰¹
GO:0051233~spindle midzone		3	0.824176	3.86x10 ⁻⁰²	KIF14, CDCA8, PLK1	302	19	18224	9.53x10 ⁰	1.00x10 ⁰	4.80x10 ⁻⁰¹
GO:0000242~pericentriolar material		3	0.824176	3.86x10 ⁻⁰²	NEK1, TUBE1, PCMI	302	19	18224	9.53x10 ⁰	1.00x10 ⁰	4.80x10 ⁻⁰¹

Table SI. Continued.

Term CC	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0070062~extracellular exosome	59	16.20879	4.03x10 ⁻⁰²	IGHG1, IGHG2, IGHG3, IGHG4, S100A8, IL6ST, LTBP4, HBS1L, S100A9, WASF2, LUZP1, IGHM, FCRL4, CD44, DDX11, LTF, COL12A1, H2AFX, PRKACA, CTSZ, MYO6, MINK1, TAF6L, DCTN2, SERPINB6, F3, IGHD, GNAS, RPS11, WASL, DST, GANAB, ARPC4, CALR, IGLV3-19, GPM6A, COMP, IGHA1, CD22, IGHA2, ANGPTL1, PLA2R1, ARHGDI1, EHD4, COBL1, PTPRC, TMC5, THSD7A, KRT72, CD300A, THRAP3, HIST1H3B, CDC42BPA, ATP6V0A1, DSC2, MARCKS, PMP2, IGLC1, HPGD	302	2811	18224	1.27x10 ⁰	1.00x10 ⁰	4.79x10 ⁻⁰¹
GO:000790~nuclear chromatin	8	2.197802	4.16x10 ⁻⁰²	UHRF1, DDX11, JUND, APTX, H2AFX, RARA, CDCA5, TCF3	302	193	18224	2.50x10 ⁰	1.00x10 ⁰	4.76x10 ⁻⁰¹
GO:0031410~cytoplasmic vesicle	9	2.472527	4.19x10 ⁻⁰²	CCDC88A, MYO6, DSC2, CEP290, SLC4A7, RAB12, WASL, DST, IFT74	302	235	18224	2.31x10 ⁰	1.00x10 ⁰	4.65x10 ⁻⁰¹
GO:0071752~secretory dimeric IgA immunoglobulin complex	2	0.549451	4.87x10 ⁻⁰²	IGHA1, IGHA2	302	3	18224	4.02x10 ⁰¹	1.00x10 ⁰	5.04x10 ⁻⁰¹
GO:0071748~monomeric IgA immunoglobulin complex	2	0.549451	4.87x10 ⁻⁰²	IGHA1, IGHA2	302	3	18224	4.02x10 ⁰¹	1.00x10 ⁰	5.04x10 ⁻⁰¹
GO:0071751~secretory IgA immunoglobulin complex	2	0.549451	4.87x10 ⁻⁰²	IGHA1, IGHA2	302	3	18224	4.02x10 ⁰¹	1.00x10 ⁰	5.04x10 ⁻⁰¹
GO:0005720~nuclear heterochromatin	3	0.824176	5.06x10 ⁻⁰²	ATRX, UHRF1, FOXC1	302	22	18224	8.23x10 ⁰	1.00x10 ⁰	5.04x10 ⁻⁰¹
GO:0030425~dendrite	11	3.021978	5.25x10 ⁻⁰²	RAP1GAP, CNTNAP4, PTK2B, IL6ST, ZWINT, MINK1, MAPK8IP3, RANGAP1, RARA, GNAS, PURA	302	335	18224	1.98x10 ⁰	1.00x10 ⁰	5.05x10 ⁻⁰¹
GO:0035869~ciliary transition zone	3	0.824176	5.91x10 ⁻⁰²	CEP290, C5ORF42, PCMI	302	24	18224	7.54x10 ⁰	1.00x10 ⁰	5.36x10 ⁻⁰¹
GO:0005925~focal adhesion	12	3.296703	6.07x10 ⁻⁰²	KIF23, EGFR, PTPRC, CD44, PTK2B, JAK1, LIMD1, MARCKS, RPS11, CALR, PALLD, DST	302	391	18224	1.85x10 ⁰	1.00x10 ⁰	5.33x10 ⁻⁰¹

Table SI. Continued.

Term CC	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0000942~condensed nuclear chromosome outer kinetochore	2	0.549451	6.45x10 ⁻⁰²	PLK1, BUB1	302	4	18224	3.02x10 ⁰¹	1.00x10 ⁰	5.44x10 ⁻⁰¹
GO:0005874~microtubule	10	2.747253	7.40x10 ⁻⁰²	KIF23, KIF14, KIFC1, KIF1A, KIF4A, FIGN, TPX2, TUBE1, MTUS1, DCTN2	302	311	18224	1.94x10 ⁰	1.00x10 ⁰	5.84x10 ⁻⁰¹
GO:0030016~myofibril	3	0.824176	7.76x10 ⁻⁰²	PDE4DIP, LOC653513, TMOD1	302	28	18224	6.47x10 ⁰	1.00x10 ⁰	5.91x10 ⁻⁰¹
GO:0008278~cohesin complex	2	0.549451	9.51x10 ⁻⁰²	CDCA5, SMC3	302	6	18224	2.01x10 ⁰¹	1.00x10 ⁰	6.58x10 ⁻⁰¹
Term MF	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0034987~immunoglobulin receptor binding	9	2.472527	8.01x10 ⁻⁰⁹	IGHG1, IGHG2, IGHG3, IGHG4, IGHD, IGHA1, IGHA2, IGHM, IGLC1	290	26	16881	2.01x10 ⁰¹	3.65x10 ⁻⁰⁶	3.65x10 ⁻⁰⁶
GO:0003823~antigen binding	11	3.021978	1.07x10 ⁻⁰⁵	IGHG1, IGHG2, IGHG3, IGLV3-19, IGHG4, IGLV1-44, IGHD, IGHA1, IGHA2, IGHM, IGLC1	290	103	16881	6.22x10 ⁰	4.89x10 ⁻⁰³	2.45x10 ⁻⁰³
GO:0005524~ATP binding	48	13.18681	3.27x10 ⁻⁰⁵	KIF23, KIFC1, PGS1, KIF4A, ERCC6L2, MYO7A, NEK1, PRKDC, UHMK1, FANCM, CHD9, ATAD3A, ATAD3B, DDX11, FIGN, MSH5-SAPCD1, PTK2B, DDX3Y, BUB1, LARS, PRKACA, POLQ, AKT3, AKT2, EHD4, KIF14, TRPM4, EGFR, MYO6, MKI67, TPX2, MINK1, ATP1A2, UBE2H, TTF2, SMC3, CDK2, ATRX, KIF1A, MAP4K5, PLK1, THRAP3, ROR1, CDC42BPA, JAK1, SRCAP, EP400, CLCN4	290	1495	16881	1.87x10 ⁰	1.48x10 ⁻⁰²	4.95x10 ⁻⁰³
GO:0005515~protein binding	182	50	1.61x10 ⁻⁰⁴	PLXNA3, S100A8, IL6ST, U2AF2, LTBP4, FST, S100A9, CNOT3, RANGAP1, RORA, IGHM, SLX4IP, TOP1, CDCA8, EIF4EBP2, PTGIS, CD44, DDX11, EIF1AY, CEP290, PRKACA, RARA, H2AFX, CDCA5, AKIRIN2, SPATA24, SPON1, ARGLU1, EGFR, MYO6, EMX2, FOXN2, ESPL1, PARP10, DEPD1, PCMI, TAF6L, BCL2L11, DCTN2, TNFAIP6, UHRF1, MAP4K5, F3, ZWINT, SPATA18, TMEM170A, ROR1, AKAP5, HHLA2,	290	8785	16881	1.21x10 ⁰	7.09x10 ⁻⁰²	1.82x10 ⁻⁰²

Table S1. Continued.

Term MF	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
				PDE4DIP, RAB12, RPS11, DST, EP400, KIF4A, HMGB3, NEK1, ARPC4, AFAP1L1, SOX6, IGF2BP3, CALR, FXVD7, UHMK1, AKT1S1, ITGAX, GMIP, CNOT6L, JUND, SKA1, POLQ, FCHO2, TCF3, ARHGDI1A, PHACTR2, MKI67, CELSR3, SYCE1, WHSC1, PCNP, TET2, QRICH1, NOTCH2, CD300A, PLK1, TROAP, HIST1H3B, CDC42BPA, AREG, PMP2, HDAC9, GLYR1, KIF23, IGHG1, IGHG2, FGF7, TTC23, MYO7A, WASF2, ANKRD10, FCRL4, CDT1, FANCM, BAG4, CDC45, C4ORF33, MAZ, HSF1, LTF, CALCRL, TPR, FANCA, AKT3, AKT2, INO80B, KIF14, CTSZ, TPX2, APTX, MINK1, UBE2H, ACKR4, PALLD, CDK2, TTF2, PURA, PPM1K, TOMM22, GNAS, FOXC1, ORMDL3, JMJD1C, WASL, TBX18, SRCAP, PMP2A, C16ORF59, CLDN16, RAPIGAP, FOXM1, NFYC, PRKDC, NCAPH, GPM6A, SH3GLB2, PTK2B, HJURP, COMP, LACCI, BUB1, POU2F1, LARS, CD22, LIMD1, SNRNP70, AGO4, CD6, PCSK5, EHD4, ZBTB7B, PTPRC, TONSL, DTX3, ATP1A2, CDC25C, SMC3, CDC25A, ATRX, KRT72, RASSF6, AP2A1, PLN, THRAP3, ATP6V0A1, DSC2, MAPK8IP3, JAK1, ZC3H11A, BIK, MIST1BP1, UBXLN4, FAM126A	290	208	16881	3.64x10 ⁰	1.10x10 ⁻⁰¹	2.29x10 ⁻⁰²
GO:0008017~microtubule binding	13	3.571429	2.54x10 ⁻⁰⁴	CAPN6, KIF23, KIF14, KIFCI, KIF4A, KIF1A, CCDC88A, S100A8, PLK1, S100A9, SKA1, NME8, BCL2L1	290	85	16881	4.79x10 ⁰	7.86x10 ⁻⁰¹	2.27x10 ⁻⁰¹
GO:0004386~helicase activity	7	1.923077	3.37x10 ⁻⁰³	ATRX, FANCM, CHD9, DDX11, DDX3Y, SRCAP, EP400	290	80	16881	4.37x10 ⁰	9.96x10 ⁻⁰¹	5.45x10 ⁻⁰¹
GO:0003777~microtubule motor activity	6	1.648352	1.20x10 ⁻⁰²	KIF23, KIF14, KIFCI, KIF1A, KIF4A, SMC3	290	80	16881	4.37x10 ⁰	9.96x10 ⁻⁰¹	5.45x10 ⁻⁰¹

Table S1. Continued.

Term MF	Count	%	P-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini
GO:0004252~serine-type endopeptidase activity	11	3.021978	1.27x10 ⁻⁰²	IGHG1, IGHG2, IGHG3, IGLV3-19, IGHG4, IGLV1-44, F3, LTF, PCSK5, IGLC1, TMPRSS3	290	255	16881	2.51x10 ⁰	9.97x10 ⁻⁰¹	5.18x10 ⁻⁰¹
GO:0003682~chromatin binding	14	3.846154	1.76x10 ⁻⁰²	EGFR, APTX, WHSC1, SMC3, ATRX, TOP1, FANCM, CDC45, DDX11, TPR, POLQ, CDCA5, EP400, IFT74	290	391	16881	2.08x10 ⁰	1.00x10 ⁰	5.93x10 ⁻⁰¹
GO:0008253~5'-nucleotidase activity	3	0.824176	2.32x10 ⁻⁰²	NT5C1B-RDH14, NT5C1B, NT5DC2	290	14	16881	1.25x10 ⁰¹	1.00x10 ⁰	6.57x10 ⁻⁰¹
GO:0003677~DNA binding	40	10.98901	2.92x10 ⁻⁰²	KIF4A, HMGB3, ERCC6L2, FOXM1, THAP5, NFYC, SOX6, RORA, CALR, CDT1, FANCM, CHD9, TOP1, HSF1, DDX11, HJURP, DDX3Y, LTF, H2AFX, POLQ, TCF3, SPATA24, ZBTB7B, MKI67, APTX, ZBTB45, TAF6L, TET2, TTF2, QRICH1, ATRX, ZNF672, PRDM2, FOXC1, MIS18BP1, TBX18, SRCAP, GLYR1, EP400, ZIM3	290	1674	16881	1.39x10 ⁰	1.00x10 ⁰	7.08x10 ⁻⁰¹
GO:0003690~double-stranded DNA binding	5	1.373626	5.03x10 ⁻⁰²	EGFR, HMGB3, DDX11, APTX, PRKDC	290	81	16881	3.59x10 ⁰	1.00x10 ⁰	8.59x10 ⁻⁰¹
GO:0042393~histone binding	6	1.648352	5.87x10 ⁻⁰²	ATRX, UHRF1, HJURP, TONSL, HIST1H3B, H2AFX	290	122	16881	2.86x10 ⁰	1.00x10 ⁰	8.80x10 ⁻⁰¹
GO:0004674~protein serine/threonine kinase activity	12	3.296703	5.97x10 ⁻⁰²	MAP4K5, PLK1, NEK1, CDC42BPA, BUB1, MINK1, PRKDC, PRKACA, UHMK1, AKT3, CDK2, AKT2	290	376	16881	1.86x10 ⁰	1.00x10 ⁰	8.66x10 ⁻⁰¹
GO:0098641~cadherin binding involved in cell-cell adhesion	10	2.747253	6.24x10 ⁻⁰²	ARGLU1, COBLL1, EGFR, MYO6, SH3GLB2, WASEF2, HIST1H3B, RANGAPI, ANLN, EHD4	290	290	16881	2.01x10 ⁰	1.00x10 ⁰	8.59x10 ⁻⁰¹
GO:0035662~Toll-like receptor 4 binding	2	0.549451	6.67x10 ⁻⁰²	S100A8, S100A9	290	4	16881	2.91x10 ⁰	1.00x10 ⁰	8.60x10 ⁻⁰¹
GO:0051015~actin filament binding	6	1.648352	7.66x10 ⁻⁰²	EGFR, MYO6, MYO7A, ARPC4, MARCKS, TMOD1	290	132	16881	2.65x10 ⁰	1.00x10 ⁰	8.82x10 ⁻⁰¹
GO:0050544~arachidonic acid binding	2	0.549451	8.27x10 ⁻⁰²	S100A8, S100A9	290	5	16881	2.33x10 ⁰¹	1.00x10 ⁰	8.88x10 ⁻⁰¹
GO:0008026~ATP-dependent helicase activity	3	0.824176	8.77x10 ⁻⁰²	ERCC6L2, DDX11, TTF2	290	29	16881	6.02x10 ⁰	1.00x10 ⁰	8.89x10 ⁻⁰¹
GO:0004672~protein kinase activity	11	3.021978	9.02x10 ⁻⁰²	EGFR, MAP4K5, PLK1, NEK1, BUB1, ROR1, MINK1, PRKDC, AKT3, CDK2, AKT2	290	359	16881	1.78x10 ⁰	1.00x10 ⁰	8.84x10 ⁻⁰¹

BP, biological process, CC, cellular component; MF, molecular function; FDR, false discovery rate.