

**Supplement Data 1.**

GeneID	Anova.pValue	Stimulated Ave.	Control Ave.	Fold changes
IGFBP3	1.40E-08	5.144006496	2.377682045	6.80372321
GREM1	6.44E-10	7.000234478	4.482870056	5.725352109
RNA5SP392	0.002123534	6.047595732	3.727005206	4.995366491
CYR61	7.19E-07	5.077963665	2.824834686	4.767156473
THBS1	7.91E-07	5.166142886	2.929030571	4.714524645
STC2	1.32E-06	4.411791598	2.248362733	4.479783046
AC009469.1	4.33E-06	3.451380315	1.312315584	4.40476402
RP5-890E16.4	0.001130721	3.973857212	1.839089144	4.39166518
KRTAP2-3	0.000449872	3.753874984	1.711037113	4.120552724
B4GALT1	2.52E-07	4.963255958	2.944094758	4.053480491
CTGF	1.25E-05	7.620971335	5.616804005	4.011570996
MIR4647	0.01597002	5.246008355	3.273843518	3.923564283
AC015987.2	0.000113045	4.980079887	3.012509545	3.911088934
ELL2	1.35E-07	4.000802304	2.04776763	3.871881165
CTD-2033A16.1	3.12E-05	3.14154435	1.197407962	3.848073588
AC006483.1	0.021474196	5.985574932	4.062607521	3.792022201
CTD-2033D15.1	0.003115257	3.817440661	1.917959953	3.730788844
TXNRD1	1.25E-06	5.653994935	3.788408524	3.644160274
GAS6	5.46E-08	4.143507838	2.317588484	3.545328609
CCND1	3.36E-05	5.658070696	3.832383344	3.544758526
TGFB2	4.12E-05	4.022313275	2.211158235	3.509231298
ORAOV1	2.72E-06	4.430862772	2.660944673	3.410345957
RP11-789C17.5	0.000393793	2.826168894	1.087792458	3.336594664
RP11-73M18.8	0.000473126	2.599461965	0.871010112	3.313720342
P4HA2-AS1	0.002567517	5.910903504	4.188882926	3.298981249
KRT81	0.0016652	6.63408939	4.925015645	3.269508434
SLC2A1	3.02E-05	2.627331844	0.929839687	3.243366724
RP11-388M20.7	0.001300802	2.514968784	0.843889651	3.184527065
SDC1	0.000175332	3.586715047	1.931997278	3.14861589
LUM	0.002815078	4.537759476	2.884989937	3.144366837
DYX1C1-CCPG1	0.000191555	4.380009124	2.728449598	3.141730708
PAPPA-AS1	0.002756501	5.783915685	4.134607649	3.136831503
ANKRD1	0.002565501	3.521936988	1.880113072	3.120601022
SERPINE1	6.47E-05	8.117197446	6.476896564	3.117308384
RRAS2	6.45E-05	2.730662484	1.098956211	3.098792758
RP11-571M6.7	0.00230886	6.568195593	4.945970164	3.078495435
HADHA	0.000710342	4.427305269	2.865920727	2.951369479
MICA	0.000355224	2.538805046	1.015662946	2.874163434
RCAN1	0.000461962	3.381937212	1.858817199	2.874119432
MIR3652	0.026041118	4.67403717	3.154095088	2.867795364
RP11-1002K11.1	5.25E-05	2.187311881	0.672169708	2.858269941
UGCG	0.000282662	3.108521515	1.598706519	2.847735188
IGFBP5	0.000275342	6.792116764	5.301223513	2.810629428
CCDC80	7.90E-05	6.526948379	5.051101169	2.781469354
PRNP	0.001116001	5.46710365	3.99208134	2.779879429
RP5-1050D4.3	0.021541932	4.247807616	2.78297482	2.760314777
RP1-65P5.3	0.029524267	4.848228492	3.389381082	2.748886634
RP1-20B21.4	0.021209567	3.640807058	2.196484761	2.721349584
TGM2	0.00087961	5.278549808	3.850693993	2.690465515
AMIGO2	0.000961126	2.898817854	1.482444971	2.669136124
FHL1	0.000966669	4.42886761	3.016220044	2.662252789
ZMYM6NB	0.013396368	3.85740416	2.449188782	2.654086477

CDC16	0.001016973	3.162170185	1.758420567	2.645883644
TAF7	0.001575274	4.588243064	3.191637552	2.632813834
ENC1	0.001155021	4.450788636	3.064179737	2.614633799
PITPNA-AS1	0.014878921	3.299037215	1.924350109	2.59311665
TMEM47	0.000157409	2.275761804	0.922773694	2.554406467
RP11-1017G21.4	0.002557992	3.885109634	2.537727231	2.544500373
F3	0.006475169	4.748680607	3.421304006	2.509459393
DDAH1	0.005488604	4.361040994	3.052479988	2.476943577
NFE2L1	0.000344027	3.950987477	2.642464131	2.476878922
PCYOX1	0.001332257	3.078431006	1.772071221	2.473167214
GLS	0.000422507	3.52147102	2.2201712	2.464508267
TXNIP	0.003106099	2.66251602	1.37621497	2.439019091
P4HA2	0.003347905	3.606824124	2.343452869	2.400560432
DSP	0.001496188	2.647754082	1.385592424	2.398548577
ACTA2-AS1	0.012157947	6.279711656	5.023266795	2.389062939
ACTA2	0.012285911	6.297846711	5.045597476	2.382125191
PFKP	0.004232288	3.516949631	2.265649284	2.380558937
AC006369.2	0.006885491	3.138992761	1.90344982	2.35469947
GOLM1	0.002521099	3.580413074	2.357312997	2.334478135
TMEM30A	0.003056749	3.349712309	2.131755731	2.326170068
EDIL3	9.48E-05	6.249295604	5.03373478	2.322310413
SLC1A5	0.000807851	2.863216533	1.656500055	2.308117194
TGOLN2	0.001668862	4.065416115	2.874140267	2.283545994
PPIC	0.005427707	3.602940471	2.413660459	2.280389102
ATP1B3	0.007269476	5.215810738	4.02911928	2.276301186
PAPPA	0.004965198	4.314565499	3.151693952	2.239026413
LOX	0.004415408	3.003547832	1.865539316	2.20077021
ZMPSTE24	0.006973175	3.35160428	2.227224382	2.180078218
TGFBR2	0.005185435	2.850161232	1.745918625	2.149859841
PDCD1LG2	0.01147354	2.319146942	1.232375754	2.123981483
ACTC1	0.042531649	2.594563288	1.510088629	2.120603148
DNAJB4	0.016428768	3.513424665	2.429798293	2.119356626
PTPLA	0.033157268	3.972931337	2.890549364	2.117529361
PLOD1	0.012873598	3.965861819	2.89102084	2.10648987
ADM	0.026520773	2.193508663	1.124031315	2.098672933
CHAC1	0.019816998	2.324828464	1.266288941	2.08282196
RP11-161H23.5	0.006603151	7.972251241	6.918431504	2.076019129
GNS	0.004833002	4.446894421	3.397907825	2.069075939
C5orf30	0.019273401	4.365885577	3.32200825	2.061761317
REEP5	0.017333765	4.118876413	3.08946909	2.041185534
SMPD1	0.039584675	3.800818252	2.777860754	2.032080421
PSPH	0.012942148	2.310473124	1.290781889	2.027484991
RP5-977B1.11	0.007746063	7.80776102	6.801558328	2.008617267
CAP2	0.03175067	3.226264691	2.221144623	2.007110531
TUBA1C	0.007145594	5.670598299	4.66830632	2.003179883
COX5B	0.004812273	6.651420759	7.662900343	-2.015977567
TIMM8B	0.041632786	4.837812858	5.849518209	-2.016293069
EDF1	0.003571502	6.256239674	7.285157829	-2.040493557
SNRPC	0.042519905	5.142674195	6.177710551	-2.049165285
RP11-175B9.3	0.008022884	3.443159798	4.48112551	-2.053330291
ZFAS1	0.017893912	5.993744459	7.049818013	-2.079264876
AC016739.2	0.008394913	2.981349516	4.057359615	-2.108197604
CTD-2192J16.15	0.005792431	3.336689044	4.414165201	-2.11034103
PSMA7	0.00077989	6.775140492	7.859078737	-2.119814825
CTC-575D19.1	0.001214081	4.41636952	5.5064571	-2.128869596

RSPH9	0.014960344	1.407238947	2.503081477	-2.137378676
RPL10P3	0.006343236	2.043071802	3.148295427	-2.15132222
NDUFB11	0.02465188	3.219134811	4.340675122	-2.175791496
NDUFA12	0.006996685	5.697812021	6.833629855	-2.197430953
ATP5C1	0.006367844	4.373445145	5.518715603	-2.211875923
SNURF	0.002690037	3.797145995	4.956136358	-2.233011007
AC011737.2	0.002034895	5.310634238	6.473013995	-2.238263295
RP11-290D2.6	0.007718324	3.716853502	4.8863416	-2.249318718
MRPS15	0.018381576	1.998470196	3.171438668	-2.254751549
NDUFB2-AS1	0.001406701	5.100448545	6.281063353	-2.266733538
S100A13	0.007020315	2.332227417	3.515509219	-2.270927742
MRPS18A	0.024341671	1.854021574	3.04016329	-2.275433961
UQCRH	0.004540263	5.121884779	6.311945402	-2.281623306
RNF181	0.017500807	4.769673754	5.962560877	-2.286097798
RP11-259O2.3	0.021178	1.996575137	3.200275714	-2.3032972
ETFB	0.001187348	2.573658299	3.778482563	-2.30509189
PSMB3	0.01469637	5.686208991	6.895161711	-2.311697652
NDUFA11	0.001331855	4.494782148	5.706218807	-2.315681212
RP1-178F15.5	0.011577758	2.4015564	3.614660183	-2.318358674
RANBP1	0.00079101	2.269439938	3.487698894	-2.326657669
CKS2	0.031256716	2.812441892	4.050074643	-2.358112832
CHMP2A	0.003842377	3.606908841	4.849645233	-2.366469603
NSA2	0.003220401	3.795818763	5.04113976	-2.370712962
UBA52	0.000175076	4.965129183	6.212598221	-2.374245366
LAMTOR1	0.005166366	4.041332456	5.301464366	-2.395176396
APRT	0.014322956	3.880159219	5.142619562	-2.399045206
NHP2	0.009125865	4.776132344	6.051029579	-2.419815805
COX5A	0.007722317	4.666378501	5.952643461	-2.438958077
CTD-2090I13.1	4.1952E-08	2.831798177	4.123570186	-2.448285849
ZNF32-AS1	0.027886575	1.559346315	2.854441335	-2.453931572
MRPL9	0.006460824	2.270260224	3.569347978	-2.460732363
SNF8	0.000586854	2.191719413	3.503212231	-2.481982284
CTD-2410N18.5	0.00158137	3.497597678	4.809305366	-2.48235197
FUT5	0.00182388	4.690256415	6.003533336	-2.485053516
RP11-84A1.1	0.002402092	2.643102234	3.963311077	-2.497022538
AC024592.12	0.001938857	4.835155333	6.162458239	-2.509331209
NME1	0.001500138	4.069382586	5.397451274	-2.510663514
NDUFB4	0.000744867	4.953972555	6.284962446	-2.515752316
CTD-2616J11.9	0.026356594	5.606134168	6.947477118	-2.533870775
IGBP1	0.009108072	2.22867755	3.573239628	-2.539530989
RP11-203J24.9	0.001832162	3.273326671	4.618969569	-2.541434233
CTD-2616J11.11	0.009022456	2.684575751	4.034879268	-2.5496576
NACAP1	8.11136E-05	2.760348023	4.111335947	-2.550867433
POLR2G	0.012907732	2.797017803	4.152122239	-2.55815634
PSME2	0.000474571	4.566204243	5.934169047	-2.581062014
RP11-3P17.3	2.11265E-05	3.995960592	5.393134856	-2.633851969
POLR2J	0.002409043	4.445338914	5.851870807	-2.650991221
ATP5H	0.000120732	3.894359324	5.304166044	-2.657015639
RP11-51O6.1	3.8672E-07	5.725021532	7.142315338	-2.670840471
RP4-741O10.1	0.015224884	3.069482595	4.48853676	-2.674101387
COX7A2	0.000133478	6.316223368	7.736071434	-2.675573322
AC010761.8	7.12412E-09	6.547032629	7.979264302	-2.69863839
RP5-1052M9.1	0.006016996	5.134275164	6.575638757	-2.715774312
ATP5G1	0.000742619	4.459919932	5.909335214	-2.730973437
ITPA	0.00455006	2.347136464	3.816005505	-2.768048155

RPL37P2	0.000707494	3.574227111	5.044536447	-2.770812977
ATP5O	4.33911E-05	5.1199926	6.600181515	-2.789852629
CTD-2090I13.3	3.03217E-07	4.934023142	6.419991678	-2.801051553
RP11-123M6.2	0.007990768	6.027355917	7.521889899	-2.817731184
AP000304.12	0.000236564	6.279752495	7.811302524	-2.890962767
PSMD8	0.000372258	3.525963704	5.05996071	-2.895870334
NACA2	9.28277E-06	2.687483463	4.22682786	-2.90662388
NDUFS6	0.00255821	3.737646323	5.287735063	-2.928351509
STOML2	0.005007779	2.543651336	4.108332225	-2.958120637
COX7B	0.00011143	3.584971781	5.151445488	-2.961798939
RBP1	0.002410823	1.774244167	3.358055662	-2.997607504
RPS15AP1	4.13788E-05	3.851330933	5.45110585	-3.030960219
TCEB2P1	2.07797E-05	6.706351764	8.323603285	-3.067900134
NDUFA8	0.001532161	3.192007206	4.815234917	-3.080634896
RP11-3P17.5	1.84733E-05	4.716083993	6.342398379	-3.087233032
PFDN5	4.89051E-07	5.182515112	6.83416841	-3.141934919
AC091133.1	0.001873838	2.448101922	4.108092891	-3.160145465
MRPL41	5.07576E-05	5.222985896	6.889333042	-3.174099044
GADD45GIP1	0.001289227	5.471123155	7.148048286	-3.197457385
RP11-480N24.3	0.003872501	4.365641255	6.044181113	-3.201038122
C16orf13	0.00103608	2.583830323	4.268263677	-3.2141413
EIF4EBP1	0.000859959	4.771217084	6.565542832	-3.468533333
ECI2	6.20306E-08	3.767191631	5.642243665	-3.668148469
RP11-234A1.1	3.66884E-07	3.076039032	5.036449196	-3.891726064
HIST1H4C	0.00152193	2.450099251	4.506482117	-4.159421433
C6orf201	5.57588E-07	1.608187422	3.778272294	-4.500498692
RPS11P5	2.8099E-08	4.176246146	6.361461944	-4.54794812
SCARNA22	1.83339E-05	2.618074587	5.437772497	-7.06014547

**Supplement Data 2.**

NAME	Reaction	SIZE	ES	NES	FDR q-value
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	Stim.	129	0.58	2.45	<0.001
NABA_MATRISOME	Stim.	178	0.55	2.40	<0.001
NABA_ECM_REGULATORS	Stim.	49	0.65	2.34	<0.001
NABA_MATRISOME_ASSOCIATED	Stim.	119	0.55	2.28	<0.001
HALLMARK_UV_RESPONSE_DN	Stim.	83	0.53	2.09	<0.001
GO_CELL_ADHESION_MOLECULE_BINDING	Stim.	68	0.62	2.41	<0.001
GO_LYSOSOMAL_LUMEN	Stim.	36	0.70	2.38	<0.001
GO_CELL_SURFACE	Stim.	199	0.51	2.27	0.002
GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	Stim.	103	0.56	2.27	0.001
GO_ENDOPLASMIC_RETICULUM_PART	Stim.	479	0.48	2.26	0.001
GO_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	Stim.	161	0.53	2.25	0.001
GO_LOCOMOTION	Stim.	313	0.49	2.25	0.001
GO_INTEGRIN_BINDING	Stim.	44	0.64	2.23	0.001
GO_INTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	Stim.	257	0.49	2.22	0.001
GO_REGULATION_OF_CELL_ADHESION	Stim.	195	0.50	2.21	<0.001
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_HEXOSYL_GROUPS	Stim.	69	0.57	2.21	<0.001
GO_GOLGI_APPARATUS_PART	Stim.	379	0.47	2.21	<0.001
GO_ENDOPLASMIC_RETICULUM_LUMEN	Stim.	78	0.56	2.20	<0.001
GO_UDP_GLYCOSYLTRANSFERASE_ACTIVITY	Stim.	39	0.64	2.20	<0.001
GO_NUCLEAR_OUTER_MEMBRANE_ENDOPLASMIC_RETICULUM_MEMBRANE_NETWORK	Stim.	422	0.47	2.19	<0.001
GO_VACUOLAR_LUMEN	Stim.	42	0.63	2.19	<0.001
GO_GLYCOSYLATION	Stim.	92	0.54	2.18	<0.001
GO_SECRETORY_GRANULE	Stim.	90	0.54	2.18	<0.001
GO_GOLGI_MEMBRANE	Stim.	322	0.47	2.17	<0.001
GO_REGULATION_OF_CELLULAR_COMPONENT_MOVEMENT	Stim.	262	0.47	2.17	<0.001
HALLMARK_OXIDATIVE_PHOSPHORYLATION	Con.	176	-0.50	-2.60	<0.001
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIF5_AND_SUBSEQUENT_BINDING_TO_43S	Con.	55	-0.71	-3.09	<0.001
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	Con.	47	-0.79	-3.13	<0.001
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	Con.	95	-0.68	-3.14	<0.001
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	Con.	62	-0.74	-3.25	<0.001
REACTOME_METABOLISM_OF_RNA	Con.	216	-0.62	-3.26	<0.001
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS	Con.	75	-0.76	-3.41	<0.001
REACTOME_METABOLISM_OF_MRNA	Con.	193	-0.66	-3.47	<0.001
REACTOME_TRANSLATION	Con.	146	-0.70	-3.51	<0.001
REACTOME_INFLUENZA_LIFE_CYCLE	Con.	118	-0.77	-3.74	<0.001
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	Con.	111	-0.80	-3.88	<0.001
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	Con.	104	-0.82	-3.88	<0.001
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	Con.	106	-0.82	-3.89	<0.001
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	Con.	102	-0.85	-4.07	<0.001

REACTOME_PEPTIDE_CHAIN_ELONGATION	Con.	87	-0.90	-4.13	<0.001
GO_CYTOSOLIC_RIBOSOME	Con.	100	-0.86	-4.11	<0.001
GO_RIBOSOMAL_SUBUNIT	Con.	149	-0.79	-3.99	<0.001
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	Con.	167	-0.77	-3.92	<0.001
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	Con.	101	-0.82	-3.86	<0.001
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	Con.	110	-0.79	-3.81	<0.001
GO_MULTI_ORGANISM_METABOLIC_PROCESS	Con.	107	-0.78	-3.75	<0.001
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	Con.	113	-0.77	-3.72	<0.001
GO_CYTOSOLIC_PART	Con.	147	-0.72	-3.71	<0.001
GO_RIBOSOME	Con.	196	-0.70	-3.71	<0.001
GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	Con.	57	-0.88	-3.70	<0.001
GO_PROTEIN_TARGETING_TO_MEMBRANE	Con.	115	-0.75	-3.69	<0.001
GO_TRANSLATIONAL_INITIATION	Con.	133	-0.74	-3.68	<0.001
GO_LARGE_RIBOSOMAL_SUBUNIT	Con.	87	-0.80	-3.62	<0.001
GO_RRNA_METABOLIC_PROCESS	Con.	182	-0.67	-3.51	<0.001
GO_SMALL_RIBOSOMAL_SUBUNIT	Con.	62	-0.79	-3.41	<0.001
GO_RNA_CATABOLIC_PROCESS	Con.	170	-0.67	-3.39	<0.001
GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	Con.	38	-0.88	-3.36	<0.001
GO_RIBOSOME_BIOGENESIS	Con.	216	-0.61	-3.22	<0.001
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	Con.	90	-0.69	-3.19	<0.001
GO_OXIDATIVE_PHOSPHORYLATION	Con.	73	-0.69	-3.12	<0.001

\* ES= Enrichment Score

\*NES= Normalized Enrichment Score

**Supplement Data 3.**

Target Genes		Sequence	Product (bp)
hGREM1	F	ATGACATTCAGAACCAGCAA	268
	R	TAGGCACAGTAAGAAGAACAGATA	
hIGFBP3	F	AAGTTGACTACGAGTCTCAG	83
	R	ACGGCAGGGACCATATTC	
hIGFBP5	F	GGTTTGCCTCAACGAAAAGA	105
	R	GAGTAGGTCTCCTCGGCCAT	
hSTC2	F	ATGCTACCTCAAGCACGACC	185
	R	TCTGCTCACACTGAACC	
hCTGF	F	GTGCACCGCCAAAGATGGT	66
	R	AAGGACTCTCCGCTGCGGTA	
hPAPPA	F	GTCATCTTTGCCTGGAAGGGAGAA	129
	R	AGGGCTGTTCAACATCAGGATGAC	
hTHBS1	F	ACATGCCACGGCCAACAAA	101
	R	AGTGGCCCAGGTAGTTGCACTT	
hGAPDH	F	GTCTCCTCTGACTTCAACAGCG	131
	R	ACCACCCTGTTGCTGTAGCCAA	

**Supplement Data 4.**

Gene Symbol	Gene Description
NDC80	NDC80 homolog, kinetochore complex component ( <i>S. cerevisiae</i> )
AURKB	aurora kinase B
BIRC5	baculoviral IAP repeat containing 5
CDCA8	cell division cycle associated 8
CDC20	cell division cycle 20 homolog ( <i>S. cerevisiae</i> )
CKAP5	cytoskeleton associated protein 5
CENPN	centromere protein N
ZWINT	ZW10 interactor
SGOL2	shugoshin-like 2 ( <i>S. pombe</i> )
SPC25	SPC25, NDC80 kinetochore complex component, homolog ( <i>S. cerevisiae</i> )
CENPM	centromere protein M
KIF23	kinesin family member 23
AURKA	aurora kinase A
CCNB1	cyclin B1
CCNB2	cyclin B2
CKS1B	CDC28 protein kinase regulatory subunit 1B
PTTG1	pituitary tumor-transforming 1
UBE2C	ubiquitin-conjugating enzyme E2C
RRM2	ribonucleotide reductase M2
HIST1H4C	histone cluster 1, H4c
SMC4	structural maintenance of chromosomes 4
SMC2	structural maintenance of chromosomes 2
NCAPG	non-SMC condensin I complex, subunit G
TPX2	TPX2, microtubule-associated, homolog ( <i>Xenopus laevis</i> )
CLSPN	claspin
CENPE	centromere protein E, 312kDa
PRC1	protein regulator of cytokinesis 1
DLGAP5	discs, large ( <i>Drosophila</i> ) homolog-associated protein 5
CENPF	centromere protein F, 350/400kDa (mitosin)