Figure S1. Top enriched KEGG pathways and GO annotations of the 15 hub genes. (A) Top enriched GO terms of hub genes classified into 'MF' 'CC' or 'BP' groups. (B) Top enriched KEGG pathways for 15 hub genes. MF, molecular function; BP, biological process; CC, cellular component; Fox O, forkhead box protein O; p53, cellular tumor antigen p53.

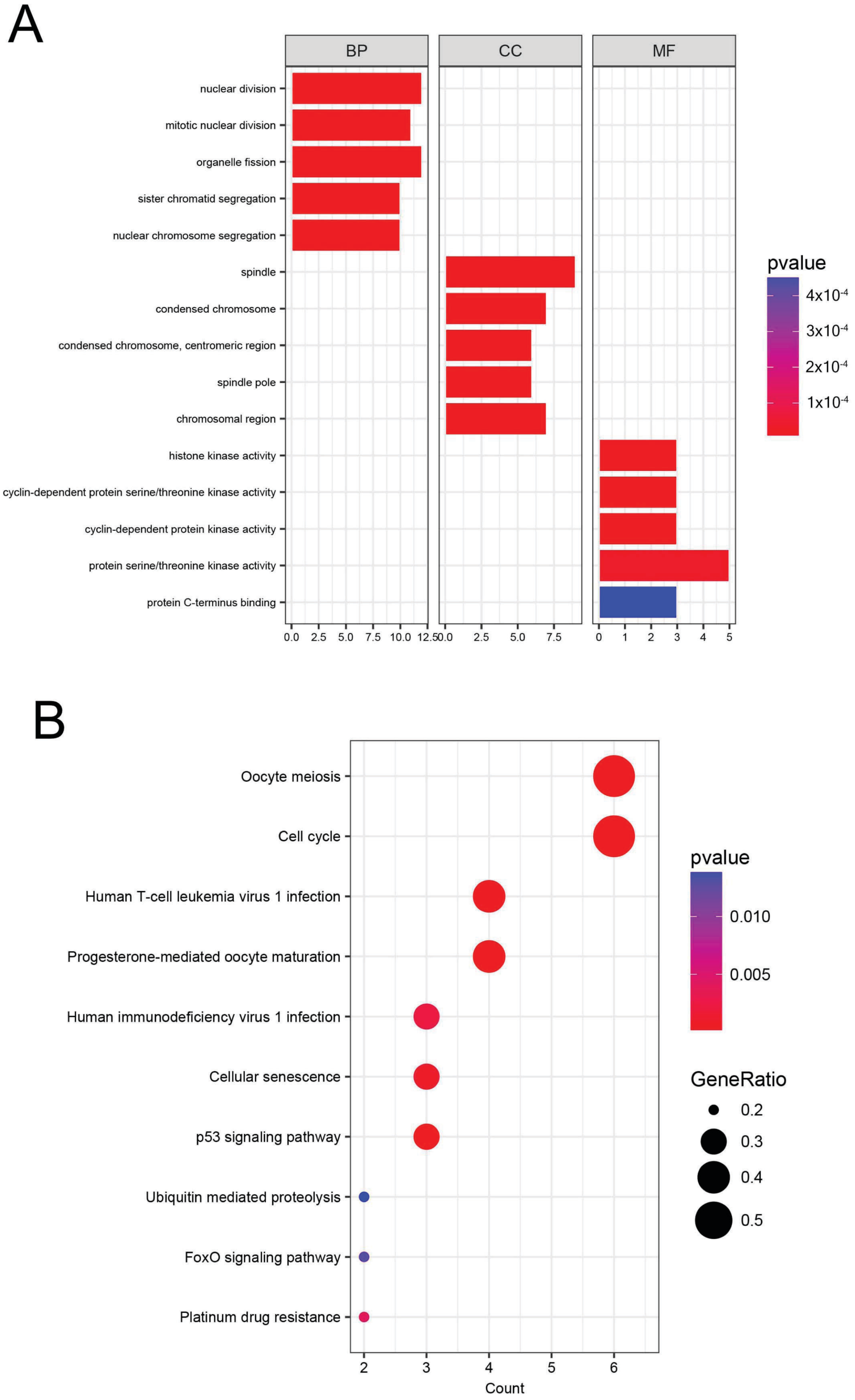

Table SI. All 322 consistently DEGs identified from the two datasets (GSE10810 and GSE65194).

Probes	Gene	GSE10810 (logFC)	GSE65194 (logFC)
37892_at	COL11A1	4.974342423	7.614150589
217428_s_at	COL10A1	4.773855519	5.941510835
204320_at	COL11A1	4.308199243	7.041689833
205941_s_at	COL10A1	4.179797824	7.185323901
202503_s_at	KIAA0101	3.656873558	6.300096327
201291_s_at	TOP2A	3.579629781	6.563078703
204351_at	S100P	3.528165339	6.620896592
223278_at	GJB2	3.463876610	5.270010001
227140_at	INHBA	3.451552990	4.112209403
229479_at	LINC01614[a]	3.320006011	4.030568064
209773_s_at	RRM2	3.288977815	6.845203487
201890_at	RRM2	3.261933149	5.506229608
229802_at	WISP1	3.255268910	4.380116263
201292_at	TOP2A	3.153355204	5.687091335
218039_at	NUSAP1	3.082037345	5.544430137
210387_at	HIST1H2BG /// HIST1H2BJ	3.019688558	5.082997094
204170_s_at	CKS2	2.948693231	4.803680413
219918_s_at	ASPM	2.840145269	5.297455226
219148_at	PBK	2.783093092	4.340917377
219978_s_at	NUSAP1	2.760984046	4.404392176
210511_s_at	INHBA	2.690719908	5.850674155
1555758_a_at	CDKN3	2.659767213	4.585694779
213909_at	LRRC15	2.655835957	4.021573661
210559_s_at	CDK1	2.649726223	5.229573252
222608_s_at	ANLN	2.621450473	4.523675580
218585_s_at	DTL	2.618825285	4.457637444
225846_at	ESRP1	2.607897703	2.423440498
203213_at	CDK1	2.577853776	4.467616589
209875_s_at	SPP1	2.572173330	4.718015129
204026_s_at	ZWINT	2.556868006	5.035521021
225655_at	UHRF1	2.551066706	4.008772296
209714_s_at	CDKN3	2.545705544	4.813957188
202954_at	UBE2C	2.502298374	5.494603001
209218_at	SQLE	2.498849680	4.625250079
202705_at	CCNB2	2.480149778	4.800353277
219121_s_at	ESRP1	2.477793376	5.784980529
204533_at	CXCL10	2.463180558	6.775683120
214710_s_at	CCNB1	2.448807881	5.151028526
209911_x_at	HIST1H2BD	2.433608005	3.722736165
201689_s_at	TPD52	2.381712030	4.599271901
223229_at	UBE2T	2.378439540	5.562611789
203953_s_at	CLDN3	2.376431419	4.277058138
210052_s_at	TPX2	2.373288114	5.197814569
201287_s_at	SDC1	2.358540629	3.089026718
207828_s_at	CENPF	2.354480040	5.182072102
202095_s_at	BIRC5	2.336609805	4.893001468
218883_s_at	CENPU	2.320651087	4.781702313
206102_at	GINS1	2.309766155	3.124930577
203755_at	BUB1B	2.306163565	4.039844004
218009_s_at	PRC1	2.276127707	5.680940136
203214_x_at	CDK1	2.262064590	4.970478235
203554_x_at	PTTG1	2.247389830	3.555885667
201688_s_at	TPD52	2.240743605	6.412326434
201690_s_at	TPD52	2.217144213	2.480276525
217755_at	HN1	2.209183178	3.663179120
203362_s_at	MAD2L1	2.194761694	4.686019754
203878_s_at	MMP11	2.181518957	5.662552219
208079_s_at	AURKA	2.161159717	4.254107948
1554408_a_at	TK1	2.150764231	4.166654569

Table SI. Continued.

Probes	Gene	GSE10810 (logFC)	GSE65194 (logFC)
204825_at	MELK	2.149856729	4.612823823
202870_s_at	CDC20	2.132407137	5.311440062
215779_s_at	HIST1H2BG /// HIST1H2BJ	2.130299619	3.779879678
214290_s_at	HIST2H2AA3 /// HIST2H2AA4	2.126507280	4.053592462
203744_at	HMGB3	2.119778937	2.523832383
202589_at	TYMS	2.107418588	4.062527017
222067_x_at	HIST1H2BD	2.082701983	3.181806807
203108_at	GPRC5A	2.075098264	4.886108396
1555778_a_at	POSTN	2.066881245	4.584360248
203876_s_at	MMP11	2.007240927	4.527117235
222043_at	CLU	-2.002360210	-3.421393152
209047_at	AQP1	-2.005078788	-3.021412614
204115_at	GNG11	-2.007884558	-2.625834639
205384_at	FXYD1	-2.022002451	-4.526599272
229310_at	KLHL29	-2.026718071	-3.556121626
218651_s_at	LARP6	-2.036982933	-2.149454961
209540_at	IGF1	-2.074562105	-4.706133092
227190_at	TMEM37	-2.085398112	-2.779583059
1556579_s_at	IGSF10	-2.088223909	-3.034559530
213029_at	NFIB	-2.088285607	-2.646606477
220276_at	RERGL	-2.090567689	-2.943609988
227148_at	PLEKHH2	-2.091278879	-2.871896401
232812_at	LOC401052	-2.092667067	-2.538597677
217546_at	MT1M	-2.094752204	-2.119095496
1558420_at	C14orf180	-2.103755684	-2.269644432
213924_at	GNAL	-2.109931985	-3.412009996
200696_s_at	GSN	-2.114826881	-2.181956111
202796_at	SYNPO	-2.115326499	-2.129939024
223430_at	SIK2	-2.120785837	-2.559206563
220061_at	ACSM5	-2.123346714	-3.447107252
203766_s_at	LMOD1	-2.128892294	-4.333272898
230360_at	GLDN	-2.150200793	-2.304156622
219091_s_at	MMRN2	-2.151356281	-2.205550194
213183_s_at	CDKN1C[a]	-2.155085916	-3.984231381
225720_at	SYNPO2	-2.159095975	-3.350998399
230670_at	IGSF10	-2.164693938	-2.251737180
225016_at	APCDD1	-2.165878759	-3.001146911
235570_at	RBMS3	-2.169284206	-3.893271123
213661_at	PAMR1	-2.172636137	-4.236560629
229127_at	JAM2	-2.200192592	-2.835944480
1558421_a_at	C14orf180	-2.205082867	-3.322302639
238009_at	SOX5	-2.206490422	-2.051109314
1560049_at	Transcribed locus[a]	-2.210569419	-3.307239101
227874_at	EMCN	-2.215879505	-2.923638758
230867_at	COL6A6	-2.224231302	-5.379551620
230595_at	PGM5-AS1	-2.242756708	-3.675895518
206481_s_at	LDB2	-2.245887178	-3.190397758
224964_s_at	GNG2	-2.252964674	-2.551552310
230463_at	CDNA FLJ36891 fis, clone BRACE2000368[a]	-2.255231676	-2.100203735
228770_at	GPR146	-2.256247188	-3.532710064
204273_at	EDNRB	-2.262439055	-3.496582832
228186_s_at	RSPO3	-2.267103767	-3.777335269
89977_at	ACSM5	-2.269116844	-2.622603929
243879_at	243879_at	-2.275011638	-2.308859983
229308_at	ANKRD29	-2.276228047	-3.006780343
219093_at	PID1	-2.277811699	-3.355643920
238062_at	GPIHBP1	-2.280898510	-4.521503163
203295_s_at	ATP1A2	-2.281590506	-2.143266911

Table SI. Continued.

Probes	Gene	GSE10810 (logFC)	GSE65194 (logFC)
220751_s_at	FAXDC2	-2.282030391	-3.206127356
228771_at	ADRBK2	-2.287375295	-2.692943875
229985_at	BTNL9	-2.305582620	-5.532799952
204570_at	COX7A1	-2.322033287	-3.660899221
238066_at	RBP7	-2.345337612	-4.813114448
213844_at	HOXA5	-2.348751405	-5.257729568
231773_at	ANGPTL1	-2.349733358	-2.783925287
211340_s_at	MCAM /// MIR6756	-2.351350553	-2.111733187
225571_at	LIFR	-2.351770387	-3.171263692
208335_s_at	ACKR1	-2.368155378	-4.652636844
209392_at	ENPP2	-2.377914700	-3.218217380
212701_at	TLN2	-2.386434196	-2.245128109
205619_s_at	MEOX1	-2.386944727	-3.300215057
236262_at	MMRN2	-2.399527407	-3.380475114
228501_at	GALNT15	-2.409225746	-2.043302554
238003_at	HEPACAM /// HEPN1	-2.409738608	-3.061120936
205208_at	ALDH1L1	-2.410742351	-2.157322745
202112_at	VWF	-2.412380520	-3.084231882
236359_at	SCN4B	-2.429149561	-4.821951844
32625_at	NPR1	-2.430244616	-4.318878980
226303_at	PGM5	-2.434124475	-3.382091862
218665_at	FZD4	-2.436835989	-2.574185438
1552616_a_at	ACACB	-2.436941905	-2.090919511
202746_at	ITM2A	-2.454627819	-3.410685980
225627_s_at	CACHD1	-2.456744829	-3.209532502
220868_s_at	SLC7A10	-2.457111545	-2.202331568
208186_s_at	LIPE	-2.457847252	-3.256467920
235368_at	ADAMTS5	-2.458996331	-3.836188249
204134_at	PDE2A	-2.478821615	-3.309883582
227762_at	ZBTB16[a]	-2.487917630	-4.598801533
204755_x_at	HLF	-2.509182595	-2.795268111
225575_at	LIFR	-2.512217829	-3.223513608
239523_at	TUSC5	-2.513331334	-4.805124557
209074_s_at	FAM107A	-2.526008181	-3.558223721
209087_x_at	MCAM	-2.538003851	-2.218638219
236038_at	RNF150	-2.538907954	-3.659086399
226322_at	TMTC1	-2.543077214	-3.938075211
213317_at	CLIC5	-2.558098203	-2.102045110
217047_s_at	FAM13A	-2.559989286	-2.144573396
228728_at	CPED1	-2.564811000	-3.095151961
242181_at	CDNA FLJ33489 fis, clone BRAMY2003585[a]	-2.567599977	-2.912753070
202920_at	ANK2	-2.567801925	-3.952200736
206955_at	AQP7 /// LOC100509620 /// LOC101930168	-2.570987785	-2.388774101
227006_at	PPP1R14A	-2.579312661	-4.691365475
204754_at	HLF	-2.579337475	-4.028007801
232313_at	TMEM132C	-2.589480507	-2.963168692
212097_at	CAV1	-2.601784381	-3.164337225
213348_at	CDKN1C	-2.607733865	-3.832289535
205883_at	ZBTB16	-2.610330524	-4.655759059
204753_s_at	HLF	-2.611045178	-2.809119047
1558828_s_at	MIR143HG	-2.619913251	-3.388882927
204955_at	SRPX	-2.623527381	-3.608737002
208609_s_at	TNXA /// TNXB	-2.624197988	-4.838112896
202973_x_at	FAM13A	-2.635543600	-2.145920688
223828_s_at	LGALS12	-2.678595360	-2.962115576
203435_s_at	MME	-2.679237652	-3.753758745
226625_at	TGFBR3	-2.680718639	-4.424851477

Table SI. Continued.

Probes	Gene	GSE10810 (logFC)	GSE65194 (logFC)
221928_at	ACACB	-2.684606017	-4.841202686
222351_at	PPP2R1B	-2.689374819	-2.971627825
227419_x_at	PLAC9	-2.690062017	-4.944166957
222083_at	GLYAT	-2.704775531	-2.249311452
204731_at	TGFBR3	-2.709240049	-4.903330506
203065_s_at	CAV1	-2.712575681	-2.674542256
205392_s_at	CCL14 /// CCL15-CCL14	-2.714057719	-4.816936452
1556427_s_at	LRRN4CL	-2.743425540	-4.571947596
203851_at	IGFBP6	-2.748982232	-4.002097700
235129_at	PPP1R1A	-2.752864876	-2.315320510
223316_at	CCDC3	-2.756428134	-2.822961778
219563_at	LINC00341 /// SYNE3	-2.791969387	-2.957273180
239398_at	KLHL31	-2.792499775	-2.145758536
211726_s_at	FMO2	-2.807905372	-4.417549871
212886_at	CCDC69	-2.824129494	-3.702042384
213247_at	SVEP1	-2.830549747	-2.722582673
229011_at	EMP1	-2.832137121	-2.253859061
209663_s_at	ITGA7	-2.839008082	-2.681996267
210517_s_at	AKAP12	-2.839060191	-2.966781284
228335_at	CLDN11	-2.839303370	-4.310450292
221748_s_at	TNS1	-2.870172700	-3.711485207
1553102_a_at	CCDC69	-2.884792929	-2.278092505
227530_at	AKAP12	-2.886505516	-3.679054807
243311_at	DEFB132	-2.901938132	-2.016854944
203434_s_at	MME	-2.916966495	-3.401438335
216331_at	ITGA7	-2.923689517	-3.965646664
206093_x_at	TNXA /// TNXB	-2.930429513	-7.011386802
210106_at	BLOC1S1-RDH5 /// RDH5	-2.945220316	-2.615273512
219689_at	SEMA3G	-2.947173228	-4.750160244
219935_at	ADAMTS5	-2.948787161	-4.886586216
229357_at	ADAMTS5	-2.956692146	-4.223573564
237154_at	LOC101930114	-2.961064865	-3.542087524
206262_at	ADH1C	-2.979419830	-3.310394632
202350_s_at	LOC100506558 /// MATN2	-2.986027169	-4.657379995
215918_s_at	SPTBN1	-2.996216462	-3.044536327
209894_at	LEPR /// LEPROT	-3.006392890	-3.985108007
226304_at	HSPB6	-3.008025622	-2.697256765
203881_s_at	DMD	-3.014213007	-3.482157633
216594_x_at	AKR1C1	-3.014936792	-3.382848273
228568_at	MYZAP	-3.015570001	-3.000834175
213486_at	COPG2IT1	-3.028938344	-4.277230763
230003_at	SLC16A7	-3.050245319	-3.477977213
225207_at	PDK4	-3.060328915	-4.561108902
208510_s_at	PPARG	-3.064310576	-2.931269626
237351_at	LOC284825	-3.097083907	-2.272274961
221747_at	TNS1	-3.099160664	-3.370137671
222513_s_at	SORBS1	-3.113802490	-2.978822380
232204_at	EBF1	-3.116423285	-2.827905238
212730_at	SYNM	-3.117618935	-4.465879026
223623_at	C2orf40	-3.118539164	-6.648498668
216333_x_at	TNXA /// TNXB	-3.135446045	-7.097391190
214456_x_at	SAA1 /// SAA2	-3.144872249	-4.127702032
1553243_at	ITIH5	-3.147392457	-3.604131283
211653_x_at	AKR1C2 /// LOC101930400	-3.150152707	-3.436010455
201540_at	FHL1	-3.161382126	-4.279881447
204389_at	MAOA	-3.167668137	-3.403891997
213451_x_at	TNXA /// TNXB	-3.195932647	-6.739511165
211696_x_at	HBB	-3.214007250	-4.043684132
243584_at	Transcribed locus[a]	-3.217046549	-2.560226874

Table SI. Continued.

Probes	Gene	GSE10810 (logFC)	GSE65194 (logFC)
204018_x_at	HBA1 /// HBA2	-3.221650355	-3.735137936
1554044_a_at	MRAP	-3.237977997	-2.735886333
206201_s_at	MEOX2	-3.249245689	-3.529974107
209220_at	GPC3	-3.262212225	-3.351272818
217414_x_at	HBA1 /// HBA2	-3.264181953	-4.022357154
213071_at	DPT	-3.266070856	-4.075799240
221795_at	NTRK2	-3.272585136	-5.512703757
214414_x_at	HBA1 /// HBA2	-3.273817762	-4.389416584
204151_x_at	AKR1C1	-3.298727719	-4.606898137
211745_x_at	HBA1 /// HBA2	-3.299939391	-4.081611317
1563182_at	ACVR1C	-3.311486525	-2.908677984
215695_s_at	GYG2	-3.322763374	-4.610059014
209458_x_at	HBA1 /// HBA2	-3.324388463	-4.196330636
219230_at	TMEM100	-3.330730071	-3.870583896
226018_at	MTURN	-3.342077466	-2.327864984
219064_at	ITIH5	-3.359137763	-5.413908652
217232_x_at	HBB	-3.368829995	-4.204253432
214063_s_at	TF	-3.370960230	-4.770999615
204894_s_at	AOC3	-3.382115562	-4.637223682
227646_at	EBF1	-3.392366666	-4.365730913
229487_at	EBF1	-3.409781685	-3.347936092
211699_x_at	HBA1 /// HBA2	-3.419376368	-3.906501281
208607_s_at	SAA1 /// SAA2 /// SAA2-SAA4	-3.422929113	-5.074691794
209686_at	S100B	-3.426783757	-4.734080185
233011_at	ANXA1	-3.440594642	-2.788065057
223727_at	KCNIP2	-3.440622407	-3.702146629
209116_x_at	HBB	-3.453556408	-4.158920068
43427_at	ACACB	-3.478526271	-6.138701502
228885_at	MAMDC2	-3.481568781	-3.569286688
204154_at	CDO1	-3.485514332	-3.603626411
209614_at	ADH1B	-3.495680583	-3.439067402
228854_at	Transcribed locus[a]	-3.501613004	-6.144374439
206209_s_at	CA4	-3.508801870	-4.523175570
209699_x_at	AKR1C2 /// LOC101930400	-3.520383149	-4.563661192
206488_s_at	CD36	-3.525327939	-5.160139443
222317_at	PDE3B	-3.540705987	-2.295386035
204388_s_at	MAOA	-3.553068387	-3.753130991
205498_at	GHR	-3.558989802	-4.266970904
205200_at	CLEC3B /// EXOSC7	-3.573197601	-5.468721077
227529_s_at	AKAP12	-3.589130195	-2.112703330
235849_at	SCARA5	-3.591373758	-6.281774905
205382_s_at	CFD	-3.604630501	-5.914991376
218934_s_at	HSPB7	-3.606294169	-2.823333249
203296_s_at	ATP1A2	-3.617931274	-5.028105164
228434_at	BTNL9	-3.627326240	-5.082740403
212741_at	MAOA	-3.636963950	-4.741116592
225420_at	GPAM	-3.639660491	-3.088257137
209616_s_at	CES1 /// LOC100653057	-3.641782869	-4.078328357
204997_at	GPD1	-3.644642644	-3.978049202
220065_at	TNMD	-3.655414730	-2.932995517
209555_s_at	CD36	-3.674727963	-5.179669067
239345_at	SLC19A3	-3.697846156	-2.187020487
49452_at	ACACB	-3.700464787	-6.863100007
229476_s_at	THRSP	-3.729851781	-4.815968225
244276_at	KLB	-3.732966653	-3.104339854
221295_at	CIDEA	-3.735226209	-3.239429215
203980_at	FABP4	-3.752179598	-7.571653296
213524_s_at	G0S2	-3.862675132	-4.739881759
222717_at	SDPR	-3.930055641	-4.913899484

Table SI. Continued.

Probes	Gene	GSE10810 (logFC)	GSE65194 (logFC)
1552509_a_at	CD300LG	-3.947713328	-5.713854067
218087_s_at	SORBS1	-3.953707256	-4.444915890
203549_s_at	LPL	-3.959101284	-5.702206589
239262_at	Transcribed locus[a]	-3.972403995	-4.792597953
210964_s_at	GYG2	-3.983526291	-3.386350064
228766_at	CD36	-3.989979254	-6.445012246
206742_at	FIGF /// PIR-FIGF	-4.065619017	-5.142647942
205478_at	PPP1R1A	-4.079040451	-4.322944467
206243_at	TIMP4	-4.115916422	-5.371772388
213706_at	GPD1	-4.163817187	-5.736438044
221796_at	NTRK2	-4.165863348	-5.115107252
219398_at	CIDEC	-4.185034441	-5.447944351
228409_at	PLIN4	-4.187134974	-6.150204056
219059_s_at	LYVE1	-4.191847970	-3.575457156
225424_at	GPAM	-4.206766942	-3.930299013
209763_at	CHRDL1	-4.208485528	-6.297795853
229778_at	SPX	-4.248922955	-2.566711179
204719_at	ABCA8	-4.279810110	-5.937530640
203548_s_at	LPL	-4.303123152	-4.860340966
229839_at	SCARA5	-4.391365693	-7.041536306
1552519_at	ACVR1C	-4.394341287	-4.386066809
219295_s_at	PCOLCE2	-4.513115299	-4.139449996
208383_s_at	PCK1	-4.580875770	-3.433355916
205913_at	PLIN1	-4.622433796	-6.460266315
209612_s_at	ADH1B	-4.673708458	-6.606583651
235978_at	FABP4	-4.742014503	-5.372201413
209613_s_at	ADH1B	-4.798081277	-6.763654096
207175_at	ADIPOQ	-4.893867509	-8.234528763
219140_s_at	RBP4	-4.981521322	-7.011996199
207092_at	LEP	-5.155413254	-6.893170505

[a] These probes and corresponding genes belong to lncRNA type.

Table SII. GO functional enrichment and KEGG pathway enrichment of the 322 commonly differentially expressed genes.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0001101	‘Response to acid chemical’	20/218	324/17381	$5.00\text{x}10^{-9}$	$1.61\text{x}10^{-5}$	$1.22\text{x}10^{-5}$	1036/1645/1646/2706/2934/358/3952/4915/5105/5166/54331/5468/55022/5950/7049/7298/8322/891/9370/948	20
BP	GO:0010876	‘Lipid localization’	21/218	380/17381	$1.43\text{x}10^{-8}$	$2.30\text{x}10^{-5}$	$1.75\text{x}10^{-5}$	10351/1066/1149/1191/130399/1645/301/32/338328/3624/3952/4023/5468/5950/6696/7069/80763/8322/857/9370/948	21
BP	GO:0140014	‘Mitotic nuclear division’	16/218	253/17381	$1.31\text{x}10^{-7}$	$1.26\text{x}10^{-4}$	$9.61\text{x}10^{-5}$	1028/1063/11065/11130/22974/332/3479/4085/51203/54443/6790/701/891/9055/9232/991	16
BP	GO:1901652	‘Response to peptide’	22/218	477/17381	$1.57\text{x}10^{-7}$	$1.26\text{x}10^{-4}$	$9.61\text{x}10^{-5}$	1036/10580/130399/23235/2690/2706/2791/286753/301/3479/3952/5105/5140/5166/54331/5468/55022/7049/7079/857/9370/948	22
BP	GO:0043434	‘Response to peptide hormone’	20/218	410/17381	$2.44\text{x}10^{-7}$	$1.57\text{x}10^{-4}$	$1.19\text{x}10^{-4}$	1036/10580/130399/23235/2690/2706/2791/286753/301/3952/5105/5140/5166/54331/5468/55022/7049/7079/857/9370	20
BP	GO:0006869	‘Lipid transport’	18/218	347/17381	$4.11\text{x}10^{-7}$	$2.20\text{x}10^{-4}$	$1.67\text{x}10^{-4}$	10351/1066/1191/1645/301/32/338328/3624/3952/5468/5950/6696/7069/80763/8322/857/9370/948	18
BP	GO:0000280	‘Nuclear division’	19/218	393/17381	$5.66\text{x}10^{-7}$	$2.60\text{x}10^{-4}$	$1.98\text{x}10^{-4}$	1028/1063/11065/11130/1164/22974/259266/332/3479/4085/51203/54443/6790/701/7153/891/9055/9232/991	19
BP	GO:0031145	‘Anaphase-promoting complex-dependent catabolic process’	9/218	80/17381	$6.98\text{x}10^{-7}$	$2.81\text{x}10^{-4}$	$2.14\text{x}10^{-4}$	11065/4085/6790/701/84417/891/9232/983/991	9
BP	GO:0070542	‘Response to fatty acid’	9/218	83/17381	$9.58\text{x}10^{-7}$	$3.42\text{x}10^{-4}$	$2.60\text{x}10^{-4}$	1646/5166/54331/5468/55022/7049/891/9370/948	9
BP	GO:0019915	‘Lipid storage’	8/218	63/17381	$1.15\text{x}10^{-6}$	$3.71\text{x}10^{-4}$	$2.82\text{x}10^{-4}$	1149/130399/32/3952/4023/5468/857/948	8
BP	GO:0051235	‘Maintenance of location’	16/218	302/17381	$1.40\text{x}10^{-6}$	$4.10\text{x}10^{-4}$	$3.12\text{x}10^{-4}$	1149/130399/161176/1756/259266/287/2934/32/3627/3952/4023/477/5468/83660/857/948	16
BP	GO:1901653	‘Cellular response to peptide’	17/218	345/17381	$1.76\text{x}10^{-6}$	$4.72\text{x}10^{-4}$	$3.59\text{x}10^{-4}$	10580/23235/2690/2706/2791/286753/3479/3952/5105/5140/5166/54331/5468/55022/857/9370/948	17
BP	GO:0048285	‘Organelle fission’	19/218	439/17381	$2.93\text{x}10^{-6}$	$6.71\text{x}10^{-4}$	$5.10\text{x}10^{-4}$	1028/1063/11065/11130/1164/22974/259266/332/3479/4085/51203/54443/6790/701/7153/891/9055/9232/991	19
BP	GO:0051783	‘Regulation of nuclear division’	12/218	181/17381	$3.10\text{x}10^{-6}$	$6.71\text{x}10^{-4}$	$5.10\text{x}10^{-4}$	1028/1063/11065/3479/4085/51203/54443/6790/701/891/9232/991	12

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0019216	'Regulation of lipid metabolic process'	17/218	360/17381	3.13x10^{-6}	6.71x10^{-4}	5.10x10^{-4}	10580/1149/301/32/3952/50486/5140/5166/5468/57678/6713/7069/83643/85329/857/9370/948	17
BP	GO:0031099	'Regeneration'	12/218	186/17381	4.11x10^{-6}	8.27x10^{-4}	6.29x10^{-4}	10631/2934/301/3479/4147/5468/6696/6790/7049/7298/891/983	12
BP	GO:0007088	'Regulation of mitotic nuclear division'	11/218	157/17381	4.74x10^{-6}	8.96x10^{-4}	6.81x10^{-4}	1028/1063/11065/3479/4085/51203/54443/6790/701/891/9232	11
BP	GO:0097305	'Response to alcohol'	12/218	190/17381	5.12x10^{-6}	9.15x10^{-4}	6.96x10^{-4}	1036/1365/2934/3624/3952/54331/5468/5950/7049/7298/9370/983	12
BP	GO:0071375	'Cellular response to peptide hormone stimulus'	15/218	303/17381	6.88x10^{-6}	1.07x10^{-3}	8.12x10^{-4}	10580/23235/2690/2706/2791/286753/3952/5105/5140/5166/54331/5468/55022/857/9370	15
BP	GO:0000819	'Sister chromatid segregation'	13/218	230/17381	6.97x10^{-6}	1.07x10^{-3}	8.12x10^{-4}	1063/11065/11130/332/4085/51203/701/7153/79682/891/9055/9232/991	13
BP	GO:0015850	'Organic hydroxy compound transport'	13/218	230/17381	6.97x10^{-6}	1.07x10^{-3}	8.12x10^{-4}	1066/1191/1645/358/364/3952/5468/5950/6696/857/9194/9370/948	13
BP	GO:0071229	'Cellular response to acid chemical'	12/218	197/17381	7.42x10^{-6}	1.08x10^{-3}	8.25x10^{-4}	1645/1646/358/3952/4915/5105/5166/54331/5468/55022/8322/891	12
BP	GO:0030301	'Cholesterol transport'	8/218	84/17381	1.04x10^{-5}	1.45x10^{-3}	1.10x10^{-3}	1066/1191/1645/3952/5468/857/9370/948	8
BP	GO:0000070	'Mitotic sister chromatid segregation'	10/218	142/17381	1.23x10^{-5}	1.65x10^{-3}	1.26x10^{-3}	1063/11065/11130/4085/51203/701/891/9055/9232/991	10
BP	GO:0010883	'Regulation of lipid storage'	6/218	42/17381	1.31x10^{-5}	1.68x10^{-3}	1.28x10^{-3}	1149/32/3952/4023/5468/948	6
BP	GO:0045981	'Positive regulation of nucleotide metabolic process'	10/218	145/17381	1.48x10^{-5}	1.76x10^{-3}	1.34x10^{-3}	2774/2819/3479/3627/4881/55022/56246/891/9590/983	10
BP	GO:1900544	'Positive regulation of purine nucleotide metabolic process'	10/218	145/17381	1.48x10^{-5}	1.76x10^{-3}	1.34x10^{-3}	2774/2819/3479/3627/4881/55022/56246/891/9590/983	10
BP	GO:0042787	'Protein ubiquitination involved in ubiquitin-dependent protein catabolic process'	12/218	214/17381	1.71x10^{-5}	1.96x10^{-3}	1.49x10^{-3}	11065/114818/1191/29128/401265/4085/6790/701/891/9232/983/991	12
BP	GO:0015918	'Sterol transport'	8/218	91/17381	1.87x10^{-5}	2.08x10^{-3}	1.58x10^{-3}	1066/1191/1645/3952/5468/857/9370/948	8
BP	GO:0071695	'Anatomical structure maturation'	10/218	150/17381	1.99x10^{-5}	2.13x10^{-3}	1.62x10^{-3}	1028/1910/30819/3202/342035/3479/3952/6790/7298/891	10
BP	GO:0010965	'Regulation of mitotic sister chromatid separation'	6/218	50/17381	3.64x10^{-5}	3.78x10^{-3}	2.88x10^{-3}	1063/11065/4085/701/891/9232	6
BP	GO:0046683	'Response to organophosphorus'	9/218	131/17381	4.10x10^{-5}	4.12x10^{-3}	3.13x10^{-3}	1036/1645/2819/358/5105/5138/6382/7298/9370	9
BP	GO:0051304	'Chromosome separation'	7/218	75/17381	4.27x10^{-5}	4.16x10^{-3}	3.17x10^{-3}	1063/11065/4085/701/7153/891/9232	7

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0051306	‘Mitotic sister chromatid separation’	6/218	52/17381	$4.57x10^{-5}$	$4.32x10^{-3}$	$3.29x10^{-3}$	1063/11065/4085/701/891/9232	6
BP	GO:0046890	‘Regulation of lipid biosynthetic process’	10/218	167/17381	$5.00x10^{-5}$	$4.50x10^{-3}$	$3.43x10^{-3}$	10580/301/32/3952/5166/57678/6713/7069/83643/9370	10
BP	GO:0070293	‘Renal absorption’	4/218	17/17381	$5.04x10^{-5}$	$4.50x10^{-3}$	$3.43x10^{-3}$	2934/3043/358/9370	4
BP	GO:1903580	‘Positive regulation of ATP metabolic process’	5/218	33/17381	$5.28x10^{-5}$	$4.59x10^{-3}$	$3.49x10^{-3}$	2819/3479/55022/891/983	5
BP	GO:0046323	‘Glucose import’	7/218	78/17381	$5.51x10^{-5}$	$4.66x10^{-3}$	$3.55x10^{-3}$	10580/2719/286753/3479/3952/55022/9370	7
BP	GO:1905818	‘Regulation of chromosome separation’	6/218	54/17381	$5.68x10^{-5}$	$4.68x10^{-3}$	$3.56x10^{-3}$	1063/11065/4085/701/891/9232	6
BP	GO:2000816	‘Negative regulation of mitotic sister chromatid separation’	5/218	34/17381	$6.13x10^{-5}$	$4.93x10^{-3}$	$3.75x10^{-3}$	1063/4085/701/891/9232	5
BP	GO:0071398	‘Cellular response to fatty acid’	6/218	55/17381	$6.31x10^{-5}$	$4.95x10^{-3}$	$3.76x10^{-3}$	1646/5166/54331/5468/55022/891	6
BP	GO:1905819	‘Negative regulation of chromosome separation’	5/218	35/17381	$7.08x10^{-5}$	$5.41x10^{-3}$	$4.12x10^{-3}$	1063/4085/701/891/9232	5
BP	GO:0016525	‘Negative regulation of angiogenesis’	8/218	110/17381	$7.37x10^{-5}$	$5.41x10^{-3}$	$4.12x10^{-3}$	3202/3627/4223/4881/5140/5468/64102/79812	8
BP	GO:0008217	‘Regulation of blood pressure’	10/218	175/17381	$7.41x10^{-5}$	$5.41x10^{-3}$	$4.12x10^{-3}$	10631/1910/3043/3952/4311/477/4881/5468/80763/9370	10
BP	GO:2000181	‘Negative regulation of blood vessel morphogenesis’	8/218	112/17381	$8.37x10^{-5}$	$5.98x10^{-3}$	$4.55x10^{-3}$	3202/3627/4223/4881/5140/5468/64102/79812	8
BP	GO:0045931	‘Positive regulation of mitotic cell cycle’	9/218	145/17381	$9.04x10^{-5}$	$6.16x10^{-3}$	$4.69x10^{-3}$	11065/301/3479/4085/51203/51514/6790/891/983	9
BP	GO:0001525	‘Angiogenesis’	17/218	469/17381	$9.23x10^{-5}$	$6.16x10^{-3}$	$4.69x10^{-3}$	126393/3202/358/3627/3952/3953/4162/4223/4881/5140/5168/5468/55273/64102/79812/84870/857	17
BP	GO:0033048	‘Negative regulation of mitotic sister chromatid segregation’	5/218	37/17381	$9.23x10^{-5}$	$6.16x10^{-3}$	$4.69x10^{-3}$	1063/4085/701/891/9232	5
BP	GO:0003014	‘Renal system process’	8/218	114/17381	$9.49x10^{-5}$	$6.16x10^{-3}$	$4.69x10^{-3}$	1910/2934/3043/358/4162/4881/80763/9370	8
BP	GO:0021700	‘Developmental maturation’	12/218	256/17381	$9.77x10^{-5}$	$6.16x10^{-3}$	$4.69x10^{-3}$	1028/1910/30819/3202/342035/3479/3952/5468/6790/7298/891/991	12
BP	GO:0044241	‘Lipid digestion’	4/218	20/17381	$9.96x10^{-5}$	$6.16x10^{-3}$	$4.69x10^{-3}$	1645/358/3952/948	4
BP	GO:0098813	‘Nuclear chromosome segregation’	13/218	297/17381	$1.00x10^{-4}$	$6.16x10^{-3}$	$4.69x10^{-3}$	1063/11065/11130/332/4085/51203/701/7153/79682/891/9055/9232/991	13
BP	GO:0032844	‘Regulation of homeostatic process’	17/218	473/17381	$1.02x10^{-4}$	$6.16x10^{-3}$	$4.69x10^{-3}$	1756/1910/2273/287/301/3202/3624/3627/3953/477/4881/5166/57678/6696/80763/857/948	17

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0033047	'Regulation of mitotic sister chro matid segregation'	6/218	60/17381	1.03x10^{-4}	6.16x10^{-3}	4.69x10^{-3}	1063/11065/4085/701/891/9232	6
BP	GO:0033046	'Negative regulation of sister Chromatid segregation'	5/218	39/17381	1.21x10^{-4}	6.90x10^{-3}	5.25x10^{-3}	1063/4085/701/891/9232	5
BP	GO:1900542	'Regulation of purine nucleotide Metabolic process'	12/218	262/17381	1.22x10^{-4}	6.90x10^{-3}	5.25x10^{-3}	1910/2774/2819/3479/3627/4881/5138/55022/56246/891/9590/983	12
BP	GO:0007517	'Muscle organ development'	15/218	389/17381	1.22x10^{-4}	6.90x10^{-3}	5.25x10^{-3}	1063/1301/1756/2273/3131/3479/3627/3679/4223/5950/6285/7049/857/891/983	15
BP	GO:0015909	'Long-chain fatty acid transport'	6/218	63/17381	1.36x10^{-4}	7.08x10^{-3}	5.38x10^{-3}	301/32/5468/7069/80763/948	6
BP	GO:0008643	'Carbohydrate transport'	9/218	153/17381	1.36x10^{-4}	7.08x10^{-3}	5.38x10^{-3}	10580/2719/286753/3479/358/364/3952/55022/9370	9
BP	GO:0051985	'Negative regulation of chromo some segregation'	5/218	40/17381	1.36x10^{-4}	7.08x10^{-3}	5.38x10^{-3}	1063/4085/701/891/9232	5
BP	GO:0006112	'Energy reserve metabolic process'	7/218	90/17381	1.37x10^{-4}	7.08x10^{-3}	5.38x10^{-3}	10580/3479/3952/3953/5502/55022/8908	7
BP	GO:1901342	'Regulation of vasculature development'	13/218	307/17381	1.40x10^{-4}	7.08x10^{-3}	5.38x10^{-3}	126393/3202/358/3627/3952/4223/4881/5140/5168/5468/55273/64102/79812	13
BP	GO:1901343	'Negative regulation of vasculature development'	8/218	121/17381	1.44x10^{-4}	7.08x10^{-3}	5.38x10^{-3}	3202/3627/4223/4881/5140/5468/64102/79812	8
BP	GO:0015908	'Fatty acid transport'	7/218	91/17381	1.47x10^{-4}	7.08x10^{-3}	5.38x10^{-3}	301/32/3952/5468/7069/80763/948	7
BP	GO:0033273	'Response to vitamin'	7/218	91/17381	1.47x10^{-4}	7.08x10^{-3}	5.38x10^{-3}	10631/2934/3627/3952/5468/6696/7298	7
BP	GO:2000060	'Positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process'	7/218	91/17381	1.47x10^{-4}	7.08x10^{-3}	5.38x10^{-3}	11065/1191/4085/701/891/983/991	7
BP	GO:0010884	'Positive regulation of lipid storage'	4/218	22/17381	1.47x10^{-4}	7.08x10^{-3}	5.38x10^{-3}	1149/32/4023/948	4
BP	GO:0006140	'Regulation of nucleotide metabolic process'	12/218	269/17381	1.56x10^{-4}	7.32x10^{-3}	5.57x10^{-3}	1910/2774/2819/3479/3627/4881/5138/55022/56246/891/9590/983	12
BP	GO:0015718	'Monocarboxylic acid transport'	9/218	156/17381	1.58x10^{-4}	7.32x10^{-3}	5.57x10^{-3}	1645/301/32/3952/5468/7069/80763/9194/948	9
BP	GO:0006006	'Glucose metabolic process'	10/218	192/17381	1.59x10^{-4}	7.32x10^{-3}	5.57x10^{-3}	10580/2819/32/3479/3952/3953/5105/5166/5950/9370	10
BP	GO:0046324	'Regulation of glucose import'	6/218	65/17381	1.62x10^{-4}	7.34x10^{-3}	5.58x10^{-3}	10580/2719/3479/3952/55022/9370	6
BP	GO:0006631	'Fatty acid metabolic process'	14/218	356/17381	1.68x10^{-4}	7.51x10^{-3}	5.72x10^{-3}	1066/1646/2690/301/32/3952/3991/4023/5166/5468/54988/57678/857/9370	14

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0003012	'Muscle system process'	16/218	448/17381	$1.76x10^{-4}$	$7.75x10^{-3}$	$5.90x10^{-3}$	10580/126393/1756/1910/23336/25802/287/2934/30819/3479/3952/477/5348/6330/80763/857	16
BP	GO:0045765	'Regulation of angiogenesis'	12/218	273/17381	$1.78x10^{-4}$	$7.75x10^{-3}$	$5.90x10^{-3}$	126393/3202/358/3627/3952/4223/4881/5140/5168/5468/64102/79812	12
BP	GO:0032869	'Cellular response to insulin stimulus'	10/218	195/17381	$1.81x10^{-4}$	$7.75x10^{-3}$	$5.90x10^{-3}$	10580/23235/286753/3952/5105/5140/5166/5468/55022/9370	10
BP	GO:0015711	'Organic anion transport'	16/218	455/17381	$2.10x10^{-4}$	$8.87x10^{-3}$	$6.75x10^{-3}$	1645/301/3039/3043/32/358/3952/477/4915/5468/56301/7069/762/80763/9194/948	16
BP	GO:0042493	'Response to drug'	15/218	411/17381	$2.23x10^{-4}$	$9.29x10^{-3}$	$7.07x10^{-3}$	10351/1063/301/32/358/3624/4023/5138/5468/7079/7298/891/9370/94274/983	15
BP	GO:0006641	'Triglyceride metabolic process'	7/218	98/17381	$2.33x10^{-4}$	$9.50x10^{-3}$	$7.23x10^{-3}$	2167/3991/4023/5105/57678/7069/857	7
BP	GO:0010906	'Regulation of glucose metabolic process'	7/218	98/17381	$2.33x10^{-4}$	$9.50x10^{-3}$	$7.23x10^{-3}$	10580/32/3479/3952/3953/5166/9370	7
BP	GO:0030071	'Regulation of mitotic metaphase/anaphase transition'	5/218	45/17381	$2.41x10^{-4}$	$9.65x10^{-3}$	$7.35x10^{-3}$	1063/11065/4085/701/891	5
BP	GO:0051348	'Negative regulation of transferase activity'	14/218	369/17381	$2.43x10^{-4}$	$9.65x10^{-3}$	$7.35x10^{-3}$	1028/11065/131578/2167/4085/5468/5502/701/857/891/9052/9370/983/991	14
BP	GO:0048469	'Cell maturation'	9/218	166/17381	$2.52x10^{-4}$	$9.66x10^{-3}$	$7.35x10^{-3}$	1028/1910/30819/3202/342035/5468/6790/7298/891	9
BP	GO:1901990	'Regulation of mitotic cell cycle phase transition'	15/218	417/17381	$2.60x10^{-4}$	$9.66x10^{-3}$	$7.35x10^{-3}$	1028/1063/11065/2273/22974/301/4085/51514/54443/55022/6790/701/891/983/991	15
BP	GO:0045471	'Response to ethanol'	8/218	132/17381	$2.62x10^{-4}$	$9.66x10^{-3}$	$7.35x10^{-3}$	1036/1365/2934/3952/5950/7298/9370/983	8
BP	GO:0033045	'Regulation of sister chromatid segregation'	6/218	71/17381	$2.64x10^{-4}$	$9.66x10^{-3}$	$7.35x10^{-3}$	1063/11065/4085/701/891/9232	6
BP	GO:0051436	'Negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle'	6/218	71/17381	$2.64x10^{-4}$	$9.66x10^{-3}$	$7.35x10^{-3}$	11065/4085/701/891/983/991	6
BP	GO:0086001	'Cardiac muscle cell action potential'	6/218	71/17381	$2.64x10^{-4}$	$9.66x10^{-3}$	$7.35x10^{-3}$	1756/287/30819/477/6330/857	6
BP	GO:0086009	'Membrane repolarization'	5/218	46/17381	$2.67x10^{-4}$	$9.66x10^{-3}$	$7.35x10^{-3}$	287/30819/477/6330/857	5
BP	GO:1902099	'Regulation of metaphase/anaphase transition of cell cycle'	5/218	46/17381	$2.67x10^{-4}$	$9.66x10^{-3}$	$7.35x10^{-3}$	1063/11065/4085/701/891	5
BP	GO:0051439	'Regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle'	6/218	72/17381	$2.85x10^{-4}$	$1.02x10^{-2}$	$7.74x10^{-3}$	11065/4085/701/891/983/991	6

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0007091	‘Metaphase/anaphase transition of mitotic cell cycle’	5/218	47/17381	$2.96\text{x}10^{-4}$	$1.04\text{x}10^{-2}$	$7.88\text{x}10^{-3}$	1063/11065/4085/701/891	5
BP	GO:0045839	‘Negative regulation of mitotic nuclear division’	5/218	47/17381	$2.96\text{x}10^{-4}$	$1.04\text{x}10^{-2}$	$7.88\text{x}10^{-3}$	1063/4085/701/891/9232	5
BP	GO:0032868	‘Response to insulin’	11/218	248/17381	$3.07\text{x}10^{-4}$	$1.05\text{x}10^{-2}$	$8.00\text{x}10^{-3}$	10580/130399/23235/286753/3952/5105/5140/5166/5468/55022/9370	11
BP	GO:0060420	‘Regulation of heart growth’	6/218	73/17381	$3.07\text{x}10^{-4}$	$1.05\text{x}10^{-2}$	$8.00\text{x}10^{-3}$	32/3479/5950/7049/891/983	6
BP	GO:0032526	‘Response to retinoic acid’	7/218	103/17381	$3.17\text{x}10^{-4}$	$1.07\text{x}10^{-2}$	$8.17\text{x}10^{-3}$	2706/358/3952/5105/5468/5950/8322	7
BP	GO:0033762	‘Response to glucagon’	5/218	48/17381	$3.27\text{x}10^{-4}$	$1.07\text{x}10^{-2}$	$8.17\text{x}10^{-3}$	1036/2706/2791/5105/54331	5
BP	GO:0044784	‘Metaphase/anaphase transition of cell cycle’	5/218	48/17381	$3.27\text{x}10^{-4}$	$1.07\text{x}10^{-2}$	$8.17\text{x}10^{-3}$	1063/11065/4085/701/891	5
BP	GO:0060421	‘Positive regulation of heart’ growth	5/218	48/17381	$3.27\text{x}10^{-4}$	$1.07\text{x}10^{-2}$	$8.17\text{x}10^{-3}$	32/3479/7049/891/983	5
BP	GO:1905952	‘Regulation of lipid localization’	8/218	137/17381	$3.37\text{x}10^{-4}$	$1.09\text{x}10^{-2}$	$8.33\text{x}10^{-3}$	1149/32/3952/4023/5468/6696/9370/948	8
BP	GO:2000241	‘Regulation of reproductive process’	8/218	138/17381	$3.54\text{x}10^{-4}$	$1.13\text{x}10^{-2}$	$8.62\text{x}10^{-3}$	130399/1910/259266/3479/3624/6790/983/991	8
BP	GO:0010827	‘Regulation of glucose transport’	6/218	75/17381	$3.56\text{x}10^{-4}$	$1.13\text{x}10^{-2}$	$8.62\text{x}10^{-3}$	10580/2719/3479/3952/55022/9370	6
BP	GO:0010639	‘Negative regulation of organelle organization’	13/218	340/17381	$3.76\text{x}10^{-4}$	$1.17\text{x}10^{-2}$	$8.91\text{x}10^{-3}$	1063/1191/130271/25802/2934/3479/4085/55022/6711/701/7153/891/9232	13
BP	GO:2000058	‘Regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process’	7/218	106/17381	$3.78\text{x}10^{-4}$	$1.17\text{x}10^{-2}$	$8.91\text{x}10^{-3}$	11065/1191/4085/701/891/983/991	7
BP	GO:0051437	‘Positive regulation of ubiq uitin-protein ligase activity involved in regulation of mitotic cell cycle transition’	6/218	76/17381	$3.82\text{x}10^{-4}$	$1.17\text{x}10^{-2}$	$8.91\text{x}10^{-3}$	11065/4085/701/891/983/991	6
BP	GO:1905954	‘Positive regulation of lipid localization’	6/218	76/17381	$3.82\text{x}10^{-4}$	$1.17\text{x}10^{-2}$	$8.91\text{x}10^{-3}$	1149/32/4023/6696/9370/948	6
BP	GO:0010889	‘Regulation of sequestering of triglyceride’	3/218	12/17381	$3.94\text{x}10^{-4}$	$1.17\text{x}10^{-2}$	$8.91\text{x}10^{-3}$	1149/4023/5468	3
BP	GO:0019934	‘cGMP-mediated signaling’	3/218	12/17381	$3.94\text{x}10^{-4}$	$1.17\text{x}10^{-2}$	$8.91\text{x}10^{-3}$	1910/5138/948	3
BP	GO:2001241	‘Positive regulation of extrinsic apoptotic signaling pathway in absence of ligand’	3/218	12/17381	$3.94\text{x}10^{-4}$	$1.17\text{x}10^{-2}$	$8.91\text{x}10^{-3}$	3624/5519/8406	3
BP	GO:2001238	‘Positive regulation of extrinsic apoptotic signaling pathway’	5/218	50/17381	$3.97\text{x}10^{-4}$	$1.17\text{x}10^{-2}$	$8.91\text{x}10^{-3}$	3624/50486/5519/8406/857	5

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:1904667	'Negative regulation of ubiquitin protein ligase activity'	6/218	77/17381	$4.11\text{x}10^{-4}$	$1.20\text{x}10^{-2}$	$9.13\text{x}10^{-3}$	11065/4085/701/891/983/991	6
BP	GO:0019932	'Second-messenger-mediated signaling'	12/218	300/17381	$4.21\text{x}10^{-4}$	$1.22\text{x}10^{-2}$	$9.28\text{x}10^{-3}$	1756/1910/2774/287/3479/3627/477/5138/5140/54331/55273/948	12
BP	GO:0007059	'Chromosome segregation'	13/218	346/17381	$4.44\text{x}10^{-4}$	$1.27\text{x}10^{-2}$	$9.68\text{x}10^{-3}$	1063/11065/11130/332/4085/51203/701/7153/79682/891/9055/9232/991	13
BP	GO:0010743	'Regulation of macrophage derived foam cell differentiation'	4/218	29/17381	$4.47\text{x}10^{-4}$	$1.27\text{x}10^{-2}$	$9.68\text{x}10^{-3}$	4023/5468/9370/948	4
BP	GO:0045862	'Positive regulation of proteolysis'	14/218	393/17381	$4.59\text{x}10^{-4}$	$1.29\text{x}10^{-2}$	$9.84\text{x}10^{-3}$	11065/1191/130399/26577/2934/4085/5468/6790/701/7123/857/891/983/991	14
BP	GO:0016042	'Lipid catabolic process'	12/218	305/17381	$4.88\text{x}10^{-4}$	$1.36\text{x}10^{-2}$	$1.04\text{x}10^{-2}$	1149/2167/32/3952/3991/4023/5140/5168/5346/6696/85329/9370	12
BP	GO:0014074	'Response to purine-containing compound'	8/218	145/17381	$4.93\text{x}10^{-4}$	$1.37\text{x}10^{-2}$	$1.04\text{x}10^{-2}$	1036/2819/358/5105/5138/5468/6382/9370	8
BP	GO:0010885	'Regulation of cholesterol storage'	3/218	13/17381	$5.07\text{x}10^{-4}$	$1.37\text{x}10^{-2}$	$1.04\text{x}10^{-2}$	4023/5468/948	3
BP	GO:0007094	'Mitotic spindle assembly checkpoint'	4/218	30/17381	$5.11\text{x}10^{-4}$	$1.37\text{x}10^{-2}$	$1.04\text{x}10^{-2}$	1063/4085/701/891	4
BP	GO:0071173	'Spindle assembly checkpoint'	4/218	30/17381	$5.11\text{x}10^{-4}$	$1.37\text{x}10^{-2}$	$1.04\text{x}10^{-2}$	1063/4085/701/891	4
BP	GO:0071174	'Mitotic spindle checkpoint'	4/218	30/17381	$5.11\text{x}10^{-4}$	$1.37\text{x}10^{-2}$	$1.04\text{x}10^{-2}$	1063/4085/701/891	4
BP	GO:0046942	'Carboxylic acid transport'	12/218	307/17381	$5.17\text{x}10^{-4}$	$1.37\text{x}10^{-2}$	$1.05\text{x}10^{-2}$	1645/301/32/3952/477/4915/5468/56301/7069/80763/9194/948	12
BP	GO:0006936	'Muscle contraction'	13/218	352/17381	$5.22\text{x}10^{-4}$	$1.37\text{x}10^{-2}$	$1.05\text{x}10^{-2}$	10580/126393/1756/1910/23336/25802/287/30819/477/5348/6330/80763/857	13
BP	GO:1901987	'Regulation of cell cycle phase transition'	15/218	446/17381	$5.27\text{x}10^{-4}$	$1.38\text{x}10^{-2}$	$1.05\text{x}10^{-2}$	1028/1063/11065/2273/22974/301/4085/51514/54443/55022/6790/701/891/983/991	15
BP	GO:0006094	'Gluconeogenesis'	6/218	81/17381	$5.39\text{x}10^{-4}$	$1.39\text{x}10^{-2}$	$1.06\text{x}10^{-2}$	2819/3952/3953/5105/5950/9370	6
BP	GO:0051384	'Response to glucocorticoid'	8/218	147/17381	$5.40\text{x}10^{-4}$	$1.39\text{x}10^{-2}$	$1.06\text{x}10^{-2}$	1036/2706/301/358/6285/6382/7298/9370	8
BP	GO:1903052	'Positive regulation of proteolysis involved in cellular protein catabolic process'	9/218	185/17381	$5.57\text{x}10^{-4}$	$1.42\text{x}10^{-2}$	$1.08\text{x}10^{-2}$	11065/1191/4085/6790/701/857/891/983/991	9
BP	GO:0034694	'Response to prostaglandin'	4/218	31/17381	$5.81\text{x}10^{-4}$	$1.46\text{x}10^{-2}$	$1.11\text{x}10^{-2}$	1646/54331/5468/7049	4
BP	GO:0045841	'Negative regulation of mitotic metaphase/anaphase transition'	4/218	31/17381	$5.81\text{x}10^{-4}$	$1.46\text{x}10^{-2}$	$1.11\text{x}10^{-2}$	1063/4085/701/891	4
BP	GO:0019935	'Cyclic-nucleotide-mediated signaling'	7/218	114/17381	$5.87\text{x}10^{-4}$	$1.46\text{x}10^{-2}$	$1.11\text{x}10^{-2}$	1910/2774/3627/5138/5140/54331/948	7
BP	GO:0045732	'Positive regulation of protein catabolic process'	11/218	268/17381	$5.89\text{x}10^{-4}$	$1.46\text{x}10^{-2}$	$1.11\text{x}10^{-2}$	11065/1191/2719/4085/51514/6790/701/857/891/983/991	11

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0006639	‘Acylglycerol metabolic process’	7/218	115/17381	6.18×10^{-4}	1.51×10^{-2}	1.15×10^{-2}	2167/3991/4023/5105/57678/7069/857	7
BP	GO:0030299	‘Intestinal cholesterol absorption’	3/218	14/17381	6.40×10^{-4}	1.51×10^{-2}	1.15×10^{-2}	1645/3952/948	3
BP	GO:0098856	‘Intestinal lipid absorption’	3/218	14/17381	6.40×10^{-4}	1.51×10^{-2}	1.15×10^{-2}	1645/3952/948	3
BP	GO:0015849	‘Organic acid transport’	12/218	315/17381	6.49×10^{-4}	1.51×10^{-2}	1.15×10^{-2}	1645/301/32/3952/477/4915/5468/56301/7069/80763/9194/948	12
BP	GO:0006638	‘Neutral lipid metabolic process’	7/218	116/17381	6.51×10^{-4}	1.51×10^{-2}	1.15×10^{-2}	2167/3991/4023/5105/57678/7069/857	7
BP	GO:0055088	‘Lipid homeostasis’	7/218	116/17381	6.51×10^{-4}	1.51×10^{-2}	1.15×10^{-2}	1645/2167/338328/4023/5468/57678/857	7
BP	GO:0019319	‘Hexose biosynthetic process’	6/218	84/17381	6.55×10^{-4}	1.51×10^{-2}	1.15×10^{-2}	2819/3952/3953/5105/5950/9370	6
BP	GO:0051444	‘Negative regulation of ubiquitin-protein transferase activity’	6/218	84/17381	6.55×10^{-4}	1.51×10^{-2}	1.15×10^{-2}	11065/4085/701/891/983/991	6
BP	GO:1904668	‘Positive regulation of ubiquitin protein ligase activity’	6/218	84/17381	6.55×10^{-4}	1.51×10^{-2}	1.15×10^{-2}	11065/4085/701/891/983/991	6
BP	GO:1902100	‘Negative regulation of metaphase/anaphase transition of cell cycle’	4/218	32/17381	6.57×10^{-4}	1.51×10^{-2}	1.15×10^{-2}	1063/4085/701/891	4
BP	GO:0019217	‘Regulation of fatty acid metabolic process’	6/218	85/17381	6.97×10^{-4}	1.59×10^{-2}	1.21×10^{-2}	301/32/5166/5468/857/9370	6
BP	GO:0015758	‘Glucose transport’	7/218	118/17381	7.21×10^{-4}	1.63×10^{-2}	1.24×10^{-2}	10580/2719/286753/3479/3952/55022/9370	7
BP	GO:0019318	‘Hexose metabolic process’	10/218	233/17381	7.39×10^{-4}	1.66×10^{-2}	1.26×10^{-2}	10580/2819/32/3479/3952/3953/5105/5166/5950/9370	10
BP	GO:0006066	‘Alcohol metabolic process’	12/218	320/17381	7.45×10^{-4}	1.66×10^{-2}	1.27×10^{-2}	1066/125/126/32/3479/3952/3953/3991/5105/57678/5950/6713	12
BP	GO:0045598	‘Regulation of fat cell differentiation’	7/218	119/17381	7.58×10^{-4}	1.68×10^{-2}	1.28×10^{-2}	3952/4320/5468/7704/83643/85329/9370	7
BP	GO:0045926	‘Negative regulation of growth’	10/218	234/17381	7.64×10^{-4}	1.68×10^{-2}	1.28×10^{-2}	2273/2719/3624/4499/4881/5468/56920/5950/6696/948	10
BP	GO:0051784	‘Negative regulation of nuclear division’	5/218	58/17381	7.91×10^{-4}	1.70×10^{-2}	1.29×10^{-2}	1063/4085/701/891/9232	5
BP	GO:0010878	‘Cholesterol storage’	3/218	15/17381	7.92×10^{-4}	1.70×10^{-2}	1.29×10^{-2}	4023/5468/948	3
BP	GO:0030730	‘Sequestering of triglyceride’	3/218	15/17381	7.92×10^{-4}	1.70×10^{-2}	1.29×10^{-2}	1149/4023/5468	3
BP	GO:1990000	‘Amyloid fibril formation’	3/218	15/17381	7.92×10^{-4}	1.70×10^{-2}	1.29×10^{-2}	1191/2934/948	3
BP	GO:0016051	‘Carbohydrate biosynthetic process’	9/218	195/17381	8.12×10^{-4}	1.73×10^{-2}	1.31×10^{-2}	10580/2819/3479/3952/3953/5105/5950/8908/9370	9
BP	GO:0019432	‘Triglyceride biosynthetic process’	4/218	34/17381	8.31×10^{-4}	1.74×10^{-2}	1.32×10^{-2}	4023/5105/57678/7069	4
BP	GO:0031577	‘Spindle checkpoint’	4/218	34/17381	8.31×10^{-4}	1.74×10^{-2}	1.32×10^{-2}	1063/4085/701/891	4
BP	GO:0007051	‘Spindle organization’	8/218	157/17381	8.32×10^{-4}	1.74×10^{-2}	1.32×10^{-2}	22974/259266/26112/332/6790/891/9055/991	8

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0046622	'Positive regulation of organ growth'	5/218	59/17381	8.56x10^{-4}	1.78x10^{-2}	1.35x10^{-2}	32/3479/7049/891/983	5
BP	GO:0050663	'Cytokine secretion'	9/218	197/17381	8.72x10^{-4}	1.80x10^{-2}	1.37x10^{-2}	10631/1149/301/3952/4023/57678/6288/6711/948	9
BP	GO:1902850	'Microtubule cytoskeleton organization involved in mitosis'	7/218	122/17381	8.78x10^{-4}	1.80x10^{-2}	1.37x10^{-2}	22974/332/51203/6790/891/9055/991	7
BP	GO:0010675	'Regulation of cellular carbohydrate metabolic process'	7/218	123/17381	9.21x10^{-4}	1.83x10^{-2}	1.39x10^{-2}	10580/32/3479/3952/3953/5166/9370	7
BP	GO:0014823	'Response to activity'	5/218	60/17381	9.24x10^{-4}	1.83x10^{-2}	1.39x10^{-2}	10631/3952/5105/9370/983	5
BP	GO:0010742	'Macrophage derived foam cell differentiation'	4/218	35/17381	9.29x10^{-4}	1.83x10^{-2}	1.39x10^{-2}	4023/5468/9370/948	4
BP	GO:0030261	'Chromosome condensation'	4/218	35/17381	9.29x10^{-4}	1.83x10^{-2}	1.39x10^{-2}	51203/7153/891/983	4
BP	GO:0090077	'Foam cell differentiation'	4/218	35/17381	9.29x10^{-4}	1.83x10^{-2}	1.39x10^{-2}	4023/5468/9370/948	4
BP	GO:0098801	'Regulation of renal system process'	4/218	35/17381	9.29x10^{-4}	1.83x10^{-2}	1.39x10^{-2}	1910/4881/80763/9370	4
BP	GO:0046364	'Monosaccharide biosynthetic process'	6/218	90/17381	9.42x10^{-4}	1.85x10^{-2}	1.41x10^{-2}	2819/3952/3953/5105/5950/9370	6
BP	GO:0140115	'Export across plasma membrane'	3/218	16/17381	9.66x10^{-4}	1.86x10^{-2}	1.42x10^{-2}	30819/477/5348	3
BP	GO:2000811	'Negative regulation of anoikis'	3/218	16/17381	9.66x10^{-4}	1.86x10^{-2}	1.42x10^{-2}	4915/5166/857	3
BP	GO:0008645	'Hexose transport'	7/218	124/17381	9.66x10^{-4}	1.86x10^{-2}	1.42x10^{-2}	10580/2719/286753/3479/3952/55022/9370	7
BP	GO:0007093	'Mitotic cell cycle checkpoint'	8/218	161/17381	9.80x10^{-4}	1.88x10^{-2}	1.43x10^{-2}	1063/11130/4085/6790/701/7153/891/983	8
BP	GO:0008016	'Regulation of heart contraction'	10/218	242/17381	9.87x10^{-4}	1.88x10^{-2}	1.43x10^{-2}	1756/27129/287/30819/477/4881/5348/6330/80763/857	10
BP	GO:0001523	'Retinoid metabolic process'	6/218	91/17381	9.98x10^{-4}	1.89x10^{-2}	1.44x10^{-2}	1645/2719/338328/4023/5950/6382	6
BP	GO:0031960	'Response to corticosteroid'	8/218	162/17381	1.02x10^{-3}	1.92x10^{-2}	1.46x10^{-2}	1036/2706/301/358/6285/6382/7298/9370	8
BP	GO:0046460	'Neutral lipid biosynthetic process'	4/218	36/17381	1.04x10^{-3}	1.92x10^{-2}	1.46x10^{-2}	4023/5105/57678/7069	4
BP	GO:0046463	'Acylglycerol biosynthetic process'	4/218	36/17381	1.04x10^{-3}	1.92x10^{-2}	1.46x10^{-2}	4023/5105/57678/7069	4
BP	GO:1903364	'Positive regulation of cellular protein catabolic process'	9/218	202/17381	1.04x10^{-3}	1.92x10^{-2}	1.46x10^{-2}	11065/1191/4085/6790/701/857/891/983/991	9
BP	GO:1904666	'Regulation of ubiquitin protein ligase activity'	6/218	92/17381	1.06x10^{-3}	1.94x10^{-2}	1.47x10^{-2}	11065/4085/701/891/983/991	6
BP	GO:0015749	'Monosaccharide transport'	7/218	126/17381	1.06x10^{-3}	1.94x10^{-2}	1.47x10^{-2}	10580/2719/286753/3479/3952/55022/9370	7
BP	GO:0042246	'Tissue regeneration'	5/218	62/17381	1.07x10^{-3}	1.95x10^{-2}	1.48x10^{-2}	10631/2934/301/3479/891	5
BP	GO:0009187	'Cyclic nucleotide metabolic process'	9/218	203/17381	1.08x10^{-3}	1.95x10^{-2}	1.48x10^{-2}	1910/2774/358/3627/4881/5138/5140/56246/9590	9

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:1903522	'Regulation of blood circulation'	11/218	289/17381	1.09×10^{-3}	1.96×10^{-2}	1.49×10^{-2}	1756/27129/287/30819/3952/477/4881/5348/6330/80763/857	11
BP	GO:0044320	'Cellular response to leptin stimulus'	3/218	17/17381	1.16×10^{-3}	2.07×10^{-2}	1.57×10^{-2}	3952/3953/55022	3
BP	GO:0002576	'Platelet degranulation'	7/218	128/17381	1.16×10^{-3}	2.07×10^{-2}	1.57×10^{-2}	1191/1675/3479/7018/7123/7450/948	7
BP	GO:0051047	'Positive regulation of secretion'	13/218	386/17381	1.22×10^{-3}	2.15×10^{-2}	1.64×10^{-2}	10631/1910/3479/358/3624/3952/4023/4881/5950/6288/6382/6696/6711	13
BP	GO:0051983	'Regulation of chromosome segregation'	6/218	95/17381	1.25×10^{-3}	2.19×10^{-2}	1.67×10^{-2}	1063/11065/4085/701/891/9232	6
BP	GO:0044262	'Cellular carbohydrate metabolic process'	10/218	250/17381	1.26×10^{-3}	2.20×10^{-2}	1.68×10^{-2}	10580/32/3479/3952/3953/5105/5166/5502/8908/9370	10
BP	GO:0035265	'Organ growth'	8/218	168/17381	1.29×10^{-3}	2.24×10^{-2}	1.70×10^{-2}	32/3479/3952/3953/5950/7049/891/983	8
BP	GO:0051225	'Spindle assembly'	6/218	96/17381	1.32×10^{-3}	2.27×10^{-2}	1.72×10^{-2}	22974/259266/26112/332/6790/991	6
BP	GO:0051591	'Response to cAMP'	6/218	96/17381	1.32×10^{-3}	2.27×10^{-2}	1.72×10^{-2}	1036/2819/358/5105/6382/9370	6
BP	GO:0009612	'Response to mechanical stimulus'	9/218	210/17381	1.36×10^{-3}	2.31×10^{-2}	1.76×10^{-2}	10631/1301/1756/358/3627/477/5138/5468/891	9
BP	GO:0045444	'Fat cell differentiation'	9/218	210/17381	1.36×10^{-3}	2.31×10^{-2}	1.76×10^{-2}	2167/3952/4320/5468/56246/7704/83643/85329/9370	9
BP	GO:2000021	'Regulation of ion homeostasis'	9/218	210/17381	1.36×10^{-3}	2.31×10^{-2}	1.76×10^{-2}	1756/1910/2273/287/3627/477/4881/80763/857	9
BP	GO:0030835	'Negative regulation of actin filament depolymerization'	4/218	39/17381	1.40×10^{-3}	2.34×10^{-2}	1.78×10^{-2}	130271/25802/2934/6711	4
BP	GO:0050873	'Brown fat cell differentiation'	4/218	39/17381	1.40×10^{-3}	2.34×10^{-2}	1.78×10^{-2}	2167/3952/56246/9370	4
BP	GO:0071377	'Cellular response to glucagon stimulus'	4/218	39/17381	1.40×10^{-3}	2.34×10^{-2}	1.78×10^{-2}	2706/2791/5105/54331	4
BP	GO:1901615	'Organic hydroxy compound metabolic process'	15/218	492/17381	1.42×10^{-3}	2.34×10^{-2}	1.78×10^{-2}	1066/125/126/1645/32/3479/3952/3953/3991/4128/4881/5105/57678/5950/6713	15
BP	GO:0042063	'Gliogenesis'	10/218	254/17381	1.42×10^{-3}	2.34×10^{-2}	1.78×10^{-2}	1191/147495/2934/301/4147/4781/4915/5468/6285/983	10
BP	GO:0007062	'Sister chromatid cohesion'	7/218	133/17381	1.45×10^{-3}	2.38×10^{-2}	1.81×10^{-2}	1063/11130/332/4085/701/79682/991	7
BP	GO:0048545	'Response to steroid hormone'	13/218	394/17381	1.46×10^{-3}	2.38×10^{-2}	1.81×10^{-2}	1036/2706/301/358/477/5468/57678/6285/6382/6696/7298/857/9370	13
BP	GO:0016101	'Diterpenoid metabolic process'	6/218	98/17381	1.47×10^{-3}	2.38×10^{-2}	1.81×10^{-2}	1645/2719/338328/4023/5950/6382	6
BP	GO:1903050	'Regulation of proteolysis involved in cellular protein cata bolic process'	10/218	257/17381	1.55×10^{-3}	2.50×10^{-2}	1.90×10^{-2}	11065/1191/4085/55872/6790/701/857/891/983/991	10
BP	GO:0007584	'Response to nutrient'	8/218	173/17381	1.55×10^{-3}	2.50×10^{-2}	1.90×10^{-2}	10631/2934/3627/3952/5468/6696/7298/9370	8

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0008203	'Cholesterol metabolic process'	7/218	135/17381	1.58x10^{-3}	2.51x10^{-2}	1.91x10^{-2}	1066/32/3952/3953/3991/57678/6713	7
BP	GO:0048639	'Positive regulation of developmental growth'	8/218	174/17381	1.61x10^{-3}	2.51x10^{-2}	1.91x10^{-2}	2690/32/3479/3952/57678/7049/891/983	8
BP	GO:0007096	'Regulation of exit from mitosis'	3/218	19/17381	1.63x10^{-3}	2.51x10^{-2}	1.91x10^{-2}	1028/11065/54443	3
BP	GO:0008356	'Asymmetric cell division'	3/218	19/17381	1.63x10^{-3}	2.51x10^{-2}	1.91x10^{-2}	259266/6660/7704	3
BP	GO:0015669	'Gas transport'	3/218	19/17381	1.63x10^{-3}	2.51x10^{-2}	1.91x10^{-2}	3039/3043/358	3
BP	GO:0060419	'Heart growth'	6/218	100/17381	1.63x10^{-3}	2.51x10^{-2}	1.91x10^{-2}	32/3479/5950/7049/891/983	6
BP	GO:0055021	'Regulation of cardiac muscle tissue growth'	5/218	68/17381	1.63x10^{-3}	2.51x10^{-2}	1.91x10^{-2}	3479/5950/7049/891/983	5
BP	GO:0071300	'Cellular response to retinoic acid'	5/218	68/17381	1.63x10^{-3}	2.51x10^{-2}	1.91x10^{-2}	358/3952/5105/5468/8322	5
BP	GO:0042176	'Regulation of protein catabolic process'	13/218	399/17381	1.63x10^{-3}	2.51x10^{-2}	1.91x10^{-2}	11065/1191/2719/4085/51514/55872/6790/701/7079/857/891/983/991	13
BP	GO:0042551	'Neuron maturation'	4/218	41/17381	1.69x10^{-3}	2.59x10^{-2}	1.97x10^{-2}	1028/1910/30819/342035	4
BP	GO:0051899	'Membrane depolarization'	6/218	101/17381	1.71x10^{-3}	2.61x10^{-2}	1.98x10^{-2}	2273/287/477/6330/857/9370	6
BP	GO:0006109	'Regulation of carbohydrate metabolic process'	8/218	176/17381	1.73x10^{-3}	2.62x10^{-2}	2.00x10^{-2}	10580/2819/32/3479/3952/3953/5166/9370	8
BP	GO:0007052	'Mitotic spindle organization'	6/218	102/17381	1.80x10^{-3}	2.70x10^{-2}	2.06x10^{-2}	22974/332/6790/891/9055/991	6
BP	GO:0046620	'Regulation of organ growth'	6/218	102/17381	1.80x10^{-3}	2.70x10^{-2}	2.06x10^{-2}	32/3479/5950/7049/891/983	6
BP	GO:0031397	'Negative regulation of protein ubiquitination'	7/218	139/17381	1.87x10^{-3}	2.80x10^{-2}	2.13x10^{-2}	11065/4085/701/857/891/983/991	7
BP	GO:0010869	'Regulation of receptor biosynthetic process'	3/218	20/17381	1.90x10^{-3}	2.81x10^{-2}	2.14x10^{-2}	3202/5468/9370	3
BP	GO:0033158	'Regulation of protein import into nucleus, translocation'	3/218	20/17381	1.90x10^{-3}	2.81x10^{-2}	2.14x10^{-2}	3479/5138/983	3
BP	GO:0048638	'Regulation of developmental growth'	11/218	310/17381	1.91x10^{-3}	2.81x10^{-2}	2.14x10^{-2}	2690/32/3479/3952/56920/57678/5950/6696/7049/891/983	11
BP	GO:0000082	'G1/S transition of mitotic cell cycle'	10/218	265/17381	1.94x10^{-3}	2.85x10^{-2}	2.17x10^{-2}	1033/2273/301/3624/55022/6241/6790/7298/891/983	10
BP	GO:1902652	'Secondary alcohol metabolic process'	7/218	140/17381	1.95x10^{-3}	2.85x10^{-2}	2.17x10^{-2}	1066/32/3952/3953/3991/57678/6713	7
BP	GO:0051443	'Positive regulation of ubiquitin-protein transferase activity'	6/218	104/17381	1.99x10^{-3}	2.88x10^{-2}	2.19x10^{-2}	11065/4085/701/891/983/991	6
BP	GO:0015980	'Energy derivation by oxidation of organic compounds'	10/218	266/17381	2.00x10^{-3}	2.88x10^{-2}	2.19x10^{-2}	10580/2819/3479/3952/3953/5502/55022/8908/891/983	10
BP	GO:0009636	'Response to toxic substance'	9/218	222/17381	2.00x10^{-3}	2.88x10^{-2}	2.19x10^{-2}	10249/1066/3039/3043/6382/7298/891/948/983	9

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0046326	‘Positive regulation of glucose import’	4/218	43/17381	$2.03x10^{-3}$	$2.91x10^{-2}$	$2.21x10^{-2}$	10580/2719/3479/9370	4
BP	GO:0016202	‘Regulation of striated muscle tissue development’	7/218	142/17381	$2.11x10^{-3}$	$3.02x10^{-2}$	$2.30x10^{-2}$	1063/3479/5950/6285/7049/891/983	7
BP	GO:0051216	‘Cartilage development’	8/218	182/17381	$2.14x10^{-3}$	$3.03x10^{-2}$	$2.30x10^{-2}$	1300/1301/3202/3952/4781/6660/7298/7704	8
BP	GO:0000075	‘Cell cycle checkpoint’	9/218	225/17381	$2.19x10^{-3}$	$3.03x10^{-2}$	$2.30x10^{-2}$	1063/11130/4085/51514/6790/701/7153/891/983	9
BP	GO:0044321	‘Response to leptin’	3/218	21/17381	$2.19x10^{-3}$	$3.03x10^{-2}$	$2.30x10^{-2}$	3952/3953/55022	3
BP	GO:0061337	‘Cardiac conduction’	7/218	143/17381	$2.20x10^{-3}$	$3.03x10^{-2}$	$2.30x10^{-2}$	287/30819/477/4881/5348/6330/857	7
BP	GO:0015701	‘Bicarbonate transport’	4/218	44/17381	$2.21x10^{-3}$	$3.03x10^{-2}$	$2.30x10^{-2}$	3039/3043/358/762	4
BP	GO:0046850	‘Regulation of bone remodeling’	4/218	44/17381	$2.21x10^{-3}$	$3.03x10^{-2}$	$2.30x10^{-2}$	3952/3953/5166/6696	4
BP	GO:0055023	‘Positive regulation of cardiac muscle tissue growth’	4/218	44/17381	$2.21x10^{-3}$	$3.03x10^{-2}$	$2.30x10^{-2}$	3479/7049/891/983	4
BP	GO:0055078	‘Sodium ion homeostasis’	4/218	44/17381	$2.21x10^{-3}$	$3.03x10^{-2}$	$2.30x10^{-2}$	1910/477/4881/80763	4
BP	GO:0031398	‘Positive regulation of protein ubiquitination’	8/218	183/17381	$2.21x10^{-3}$	$3.03x10^{-2}$	$2.30x10^{-2}$	11065/1191/4085/701/857/891/983/991	8
BP	GO:0048511	‘Rhythmic process’	11/218	316/17381	$2.21x10^{-3}$	$3.03x10^{-2}$	$2.30x10^{-2}$	301/3131/3624/3952/4915/5468/7079/7153/7298/8322/9370	11
BP	GO:1901861	‘Regulation of muscle tissue development’	7/218	144/17381	$2.29x10^{-3}$	$3.11x10^{-2}$	$2.37x10^{-2}$	1063/3479/5950/6285/7049/891/983	7
BP	GO:0060047	‘Heart contraction’	10/218	272/17381	$2.35x10^{-3}$	$3.19x10^{-2}$	$2.42x10^{-2}$	1756/27129/287/30819/477/4881/5348/6330/80763/857	10
BP	GO:0034637	‘Cellular carbohydrate biosynthetic process’	5/218	74/17381	$2.37x10^{-3}$	$3.20x10^{-2}$	$2.43x10^{-2}$	10580/3479/3952/5105/8908	5
BP	GO:0030199	‘Collagen fibril organization’	4/218	45/17381	$2.40x10^{-3}$	$3.22x10^{-2}$	$2.45x10^{-2}$	1301/1805/4320/7146	4
BP	GO:0006721	‘Terpenoid metabolic process’	6/218	108/17381	$2.40x10^{-3}$	$3.22x10^{-2}$	$2.45x10^{-2}$	1645/2719/338328/4023/5950/6382	6
BP	GO:1901654	‘Response to ketone’	8/218	186/17381	$2.44x10^{-3}$	$3.22x10^{-2}$	$2.45x10^{-2}$	2706/358/54331/5468/6696/7049/7298/857	8
BP	GO:0005996	‘Monosaccharide metabolic process’	10/218	274/17381	$2.48x10^{-3}$	$3.22x10^{-2}$	$2.45x10^{-2}$	10580/2819/32/3479/3952/3953/5105/5166/5950/9370	10
BP	GO:0001570	‘Vasculogenesis’	5/218	75/17381	$2.51x10^{-3}$	$3.22x10^{-2}$	$2.45x10^{-2}$	4915/55273/7049/8322/857	5
BP	GO:0042632	‘Cholesterol homeostasis’	5/218	75/17381	$2.51x10^{-3}$	$3.22x10^{-2}$	$2.45x10^{-2}$	1645/2167/338328/4023/857	5
BP	GO:0055092	‘Sterol homeostasis’	5/218	75/17381	$2.51x10^{-3}$	$3.22x10^{-2}$	$2.45x10^{-2}$	1645/2167/338328/4023/857	5
BP	GO:1903779	‘Regulation of cardiac conduction’	5/218	75/17381	$2.51x10^{-3}$	$3.22x10^{-2}$	$2.45x10^{-2}$	287/477/4881/5348/857	5
BP	GO:0010881	‘Regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion’	3/218	22/17381	$2.51x10^{-3}$	$3.22x10^{-2}$	$2.45x10^{-2}$	1756/287/477	3

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0035812	'Renal sodium excretion'	3/218	22/17381	2.51x10^{-3}	3.22x10^{-2}	2.45x10^{-2}	1910/4881/80763	3
BP	GO:0035813	'Regulation of renal sodium excretion'	3/218	22/17381	2.51x10^{-3}	3.22x10^{-2}	2.45x10^{-2}	1910/4881/80763	3
BP	GO:0050995	'Negative regulation of lipid catabolic process'	3/218	22/17381	2.51x10^{-3}	3.22x10^{-2}	2.45x10^{-2}	1149/32/5140	3
BP	GO:0071379	'Cellular response to prostaglandin stimulus'	3/218	22/17381	2.51x10^{-3}	3.22x10^{-2}	2.45x10^{-2}	1646/54331/5468	3
BP	GO:0048634	'Regulation of muscle organ development'	7/218	147/17381	2.57x10^{-3}	3.27x10^{-2}	2.49x10^{-2}	1063/3479/5950/6285/7049/891/983	7
BP	GO:0003015	'Heart process'	10/218	276/17381	2.61x10^{-3}	3.31x10^{-2}	2.52x10^{-2}	1756/27129/287/30819/477/4881/5348/6330/80763/857	10
BP	GO:0042180	'Cellular ketone metabolic process'	9/218	231/17381	2.61x10^{-3}	3.31x10^{-2}	2.52x10^{-2}	1645/1646/2819/301/32/5166/5468/857/9370	9
BP	GO:0010828	'Positive regulation of glucose transport'	4/218	47/17381	2.82x10^{-3}	3.55x10^{-2}	2.70x10^{-2}	10580/2719/3479/9370	4
BP	GO:0086012	'Membrane depolarization during cardiac muscle cell action potential'	3/218	23/17381	2.86x10^{-3}	3.58x10^{-2}	2.73x10^{-2}	287/477/6330	3
BP	GO:2000209	'Regulation of anoikis'	3/218	23/17381	2.86x10^{-3}	3.58x10^{-2}	2.73x10^{-2}	4915/5166/857	3
BP	GO:1903321	'Negative regulation of protein modification by small protein conjugation or removal'	7/218	150/17381	2.87x10^{-3}	3.58x10^{-2}	2.73x10^{-2}	11065/4085/701/857/891/983/991	7
BP	GO:0031667	'Response to nutrient levels'	13/218	426/17381	2.89x10^{-3}	3.58x10^{-2}	2.73x10^{-2}	10631/130399/2934/32/3627/3952/5105/5166/5468/6696/7298/80763/9370	13
BP	GO:0060986	'Endocrine hormone secretion'	4/218	48/17381	3.04x10^{-3}	3.75x10^{-2}	2.85x10^{-2}	358/3624/3952/8322	4
BP	GO:2000649	'Regulation of sodium ion trans membrane transporter activity'	4/218	48/17381	3.04x10^{-3}	3.75x10^{-2}	2.85x10^{-2}	1756/477/5348/6330	4
BP	GO:0061448	'Connective tissue development'	9/218	237/17381	3.10x10^{-3}	3.80x10^{-2}	2.89x10^{-2}	1300/1301/3202/3952/4781/64102/6660/7298/7704	9
BP	GO:0044843	'Cell cycle G1/S phase transition'	10/218	284/17381	3.20x10^{-3}	3.91x10^{-2}	2.97x10^{-2}	1033/2273/301/3624/55022/6241/6790/7298/891/983	10
BP	GO:0016125	'Sterol metabolic process'	7/218	153/17381	3.21x10^{-3}	3.91x10^{-2}	2.97x10^{-2}	1066/32/3952/3953/3991/57678/6713	7
BP	GO:0032800	'Receptor biosynthetic process'	3/218	24/17381	3.24x10^{-3}	3.92x10^{-2}	2.98x10^{-2}	3202/5468/9370	3
BP	GO:0034695	'Response to prostaglandin E'	3/218	24/17381	3.24x10^{-3}	3.92x10^{-2}	2.98x10^{-2}	54331/5468/7049	3
BP	GO:0030834	'Regulation of actin filament depolymerization'	4/218	49/17381	3.28x10^{-3}	3.92x10^{-2}	2.99x10^{-2}	130271/25802/2934/6711	4
BP	GO:0071320	'Cellular response to cAMP'	4/218	49/17381	3.28x10^{-3}	3.92x10^{-2}	2.99x10^{-2}	2819/358/5105/9370	4

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:1903362	‘Regulation of cellular protein catabolic process’	10/218	285/17381	$3.28x10^{-3}$	$3.92x10^{-2}$	$2.99x10^{-2}$	11065/1191/4085/55872/6790/701/857/891/983/991	10
BP	GO:0031100	‘Animal organ regeneration’	5/218	80/17381	$3.33x10^{-3}$	$3.95x10^{-2}$	$3.00x10^{-2}$	5468/6790/7049/7298/983	5
BP	GO:0051651	‘Maintenance of location in cell’	5/218	80/17381	$3.33x10^{-3}$	$3.95x10^{-2}$	$3.00x10^{-2}$	161176/259266/2934/83660/857	5
BP	GO:0002064	‘Epithelial cell development’	8/218	196/17381	$3.37x10^{-3}$	$3.98x10^{-2}$	$3.03x10^{-2}$	1365/3202/5138/53405/6382/64102/7298/9370	8
BP	GO:0030198	‘Extracellular matrix’ organization	11/218	335/17381	$3.46x10^{-3}$	$4.07x10^{-2}$	$3.10x10^{-2}$	10631/11096/1300/1301/1805/3679/4320/58494/6696/7146/7450	11
BP	GO:0045840	‘Positive regulation of mitotic nuclear division’	4/218	50/17381	$3.53x10^{-3}$	$4.12x10^{-2}$	$3.14x10^{-2}$	11065/3479/51203/6790	4
BP	GO:0009165	‘Nucleotide biosynthetic process’	11/218	336/17381	$3.54x10^{-3}$	$4.12x10^{-2}$	$3.14x10^{-2}$	1910/2774/358/4881/5138/55022/56246/6241/7083/7298/9590	11
BP	GO:0043062	‘Extracellular structure organization’	11/218	336/17381	$3.54x10^{-3}$	$4.12x10^{-2}$	$3.14x10^{-2}$	10631/11096/1300/1301/1805/3679/4320/58494/6696/7146/7450	11
BP	GO:0043161	‘Proteasome-mediated ubiquitin-dependent protein catabolic process’	12/218	387/17381	$3.65x10^{-3}$	$4.21x10^{-2}$	$3.20x10^{-2}$	11065/1191/4085/55872/6790/701/84417/857/891/9232/983/991	12
BP	GO:0044062	‘Regulation of excretion’	3/218	25/17381	$3.65x10^{-3}$	$4.21x10^{-2}$	$3.20x10^{-2}$	1910/4881/80763	3
BP	GO:0032409	‘Regulation of transporter activity’	9/218	243/17381	$3.65x10^{-3}$	$4.21x10^{-2}$	$3.20x10^{-2}$	1756/2273/287/30819/477/5348/5468/6330/857	9
BP	GO:0033002	‘Muscle cell proliferation’	8/218	199/17381	$3.69x10^{-3}$	$4.23x10^{-2}$	$3.22x10^{-2}$	3479/4881/5468/5950/7049/891/9370/983	8
BP	GO:0043255	‘Regulation of carbohydrate biosynthetic process’	5/218	82/17381	$3.70x10^{-3}$	$4.23x10^{-2}$	$3.22x10^{-2}$	10580/3479/3952/3953/9370	5
BP	GO:0071103	‘DNA conformation change’	10/218	290/17381	$3.71x10^{-3}$	$4.23x10^{-2}$	$3.22x10^{-2}$	301/3017/3149/51203/7153/79682/8339/891/983/9837	10
BP	GO:1901293	‘Nucleoside phosphate biosynthetic process’	11/218	339/17381	$3.78x10^{-3}$	$4.28x10^{-2}$	$3.26x10^{-2}$	1910/2774/358/4881/5138/55022/56246/6241/7083/7298/9590	11
BP	GO:0001960	‘Negative regulation of cytokine-mediated signaling pathway’	4/218	51/17381	$3.79x10^{-3}$	$4.28x10^{-2}$	$3.26x10^{-2}$	5468/83643/857/9370	4
BP	GO:0050994	‘Regulation of lipid catabolic process’	4/218	51/17381	$3.79x10^{-3}$	$4.28x10^{-2}$	$3.26x10^{-2}$	1149/32/5140/85329	4
BP	GO:1903322	‘Positive regulation of protein modification by small protein conjugation or removal’	8/218	200/17381	$3.81x10^{-3}$	$4.28x10^{-2}$	$3.26x10^{-2}$	11065/1191/4085/701/857/891/983/991	8
BP	GO:0050886	‘Endocrine process’	5/218	83/17381	$3.90x10^{-3}$	$4.37x10^{-2}$	$3.32x10^{-2}$	358/3624/3952/4311/8322	5
BP	GO:1900371	‘Regulation of purine nucleotide biosynthetic process’	7/218	159/17381	$3.97x10^{-3}$	$4.43x10^{-2}$	$3.37x10^{-2}$	1910/2774/4881/5138/55022/56246/9590	7

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene Ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0030042	'Actin filament depolymerization'	4/218	52/17381	4.07x10^{-3}	4.53x10^{-2}	3.45x10^{-2}	130271/25802/2934/6711	4
BP	GO:0042044	'Fluid transport'	3/218	26/17381	4.09x10^{-3}	4.53x10^{-2}	3.45x10^{-2}	1910/358/364	3
BP	GO:0030808	'Regulation of nucleotide biosyn thetic process'	7/218	160/17381	4.10x10^{-3}	4.53x10^{-2}	3.45x10^{-2}	1910/2774/4881/5138/55022/56246/9590	7
BP	GO:0048871	'Multicellular organismal homeostasis'	11/218	343/17381	4.13x10^{-3}	4.55x10^{-2}	3.46x10^{-2}	1149/1910/32/358/3953/5166/5950/6696/7018/9079/948	11
BP	GO:0000086	'G2/M transition of mitotic' cell cycle	9/218	248/17381	4.17x10^{-3}	4.58x10^{-2}	3.49x10^{-2}	1063/2273/22974/51514/6790/891/9133/983/9833	9
BP	GO:0009896	'Positive regulation of catabolic process'	13/218	447/17381	4.33x10^{-3}	4.74x10^{-2}	3.60x10^{-2}	11065/1191/2719/2819/3479/4085/51514/6790/701/857/891/983/991	13
BP	GO:0060043	'Regulation of cardiac muscle cell proliferation'	4/218	53/17381	4.36x10^{-3}	4.75x10^{-2}	3.62x10^{-2}	5950/7049/891/983	4
BP	GO:0003018	'Vascular process in circulatory system'	7/218	162/17381	4.39x10^{-3}	4.75x10^{-2}	3.62x10^{-2}	1910/3043/3952/477/4881/5138/857	7
BP	GO:0046058	'cAMP metabolic process'	7/218	162/17381	4.39x10^{-3}	4.75x10^{-2}	3.62x10^{-2}	1910/2774/3627/5138/5140/56246/9590	7
BP	GO:1901655	'Cellular response to ketone'	5/218	86/17381	4.54x10^{-3}	4.88x10^{-2}	3.72x10^{-2}	2706/358/54331/5468/6696	5
BP	GO:0052652	'Cyclic purine nucleotide metabolic process'	7/218	163/17381	4.54x10^{-3}	4.88x10^{-2}	3.72x10^{-2}	1910/2774/358/4881/5138/56246/9590	7
BP	GO:0010882	'Regulation of cardiac muscle contraction by calcium ion signaling'	3/218	27/17381	4.56x10^{-3}	4.89x10^{-2}	3.72x10^{-2}	1756/287/477	3
CC	GO:0005811	'Lipid droplet'	8/227	72/18511	2.76x10-06	4.29x10^{-4}	3.12x10^{-4}	1149/2167/3991/50486/5346/63924/729359/857	8
CC	GO:0005578	'Proteinaceous extracellular matrix'	17/227	365/18511	2.84x10-06	4.29x10^{-4}	3.12x10^{-4}	10631/11096/1300/1301/131873/1805/256691/2719/342035/4147/4320/7049/7079/7146/7450/79812/8840	17
CC	GO:0005911	'Cell-cell junction'	16/227	423/18511	7.10x10-05	5.57x10^{-3}	4.06x10^{-3}	10580/11346/1365/220296/2706/287/301/364/477/5010/5239/5348/58494/6330/8322/83660	16
CC	GO:0043034	'Costamere'	4/227	19/18511	7.39x10-05	5.57x10^{-3}	4.06x10^{-3}	1756/23336/287/5239	4
CC	GO:0000779	'Condensed chromosome, centromeric region'	8/227	116/18511	9.22x10-05	5.57x10^{-3}	4.06x10^{-3}	1063/11130/332/4085/6790/701/79682/891	8
CC	GO:0042383	'Sarcolemma'	8/227	122/18511	1.31x10^{-4}	6.60x10^{-3}	4.81x10^{-3}	1756/23336/287/301/358/477/5239/5348	8
CC	GO:0005819	'Spindle'	13/227	318/18511	1.60x10^{-4}	6.89x10^{-3}	5.02x10^{-3}	1063/22974/259266/26112/332/4085/51203/6790/701/891/9055/983/991	13
CC	GO:0044449	'Contractile fiber part'	10/227	209/18511	2.66x10^{-4}	9.29x10^{-3}	6.76x10^{-3}	100820829/11346/171024/1756/23336/25802/287/5239/6711/7079	10

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
CC	GO:0000777	'Condensed chromosome kinetochore'	7/227	103/18511	2.78x10^{-4}	9.29x10^{-3}	6.76x10^{-3}	1063/11130/332/4085/701/79682/891	7
CC	GO:0030016	'Myofibril'	10/227	213/18511	3.09x10^{-4}	9.29x10^{-3}	6.76x10^{-3}	100820829/11346/171024/1756/23336/25802/287/5239/6711/7079	10
CC	GO:0014704	'Intercalated disc'	5/227	50/18511	3.59x10^{-4}	9.29x10^{-3}	6.76x10^{-3}	287/477/5239/5348/6330	5
CC	GO:0000940	'Condensed chromosome outer kinetochore'	3/227	12/18511	3.69x10^{-4}	9.29x10^{-3}	6.76x10^{-3}	1063/701/891	3
CC	GO:0043292	'Contractile fiber'	10/227	224/18511	4.60x10^{-4}	1.07x10^{-2}	7.79x10^{-3}	100820829/11346/171024/1756/23336/25802/287/5239/6711/7079	10
CC	GO:0000922	'Spindle pole'	8/227	150/18511	5.35x10^{-4}	1.15x10^{-2}	8.41x10^{-3}	1063/22974/259266/4085/6790/891/9055/991	8
CC	GO:0030017	'Sarcomere'	9/227	192/18511	6.22x10^{-4}	1.25x10^{-2}	9.13x10^{-3}	100820829/11346/171024/1756/25802/287/5239/6711/7079	9
CC	GO:0030864	'Cortical actin cytoskeleton'	5/227	59/18511	7.75x10^{-4}	1.46x10^{-2}	1.07x10^{-2}	100820829/130271/2934/54443/6711	5
CC	GO:0005938	'Cell cortex'	10/227	247/18511	9.78x10^{-4}	1.74x10^{-2}	1.27x10^{-2}	100820829/1300/130271/2934/53405/54443/6711/857/9590/9833	10
CC	GO:0000776	'Kinetochore'	7/227	133/18511	1.28x10^{-3}	1.89x10^{-2}	1.38x10^{-2}	1063/11130/332/4085/701/79682/891	7
CC	GO:0034358	'Plasma lipoprotein particle'	4/227	39/18511	1.29x10^{-3}	1.89x10^{-2}	1.38x10^{-2}	1191/338328/4023/6288	4
CC	GO:1990777	'Lipoprotein particle'	4/227	39/18511	1.29x10^{-3}	1.89x10^{-2}	1.38x10^{-2}	1191/338328/4023/6288	4
CC	GO:0000793	'Condensed chromosome'	9/227	216/18511	1.43x10^{-3}	1.89x10^{-2}	1.38x10^{-2}	1063/11130/332/4085/6790/701/7153/79682/891	9
CC	GO:0030055	'Cell-substrate junction'	13/227	402/18511	1.44x10^{-3}	1.89x10^{-2}	1.38x10^{-2}	10580/171024/1756/2273/2934/301/4162/4311/5239/7145/83660/857/9590	13
CC	GO:0044291	'Cell-cell contact zone'	5/227	68/18511	1.48x10^{-3}	1.89x10^{-2}	1.38x10^{-2}	287/477/5239/5348/6330	5
CC	GO:0071682	'Endocytic vesicle lumen'	3/227	19/18511	1.53x10^{-3}	1.89x10^{-2}	1.38x10^{-2}	3039/3043/6288	3
CC	GO:0032994	'Protein-lipid complex'	4/227	41/18511	1.56x10^{-3}	1.89x10^{-2}	1.38x10^{-2}	1191/338328/4023/6288	4
CC	GO:0005680	'Anaphase-promoting complex'	3/227	21/18511	2.06x10^{-3}	2.39x10^{-2}	1.74x10^{-2}	11065/701/991	3
CC	GO:0043235	'Receptor complex'	11/227	325/18511	2.32x10^{-3}	2.54x10^{-2}	1.85x10^{-2}	10580/130399/2690/3679/3953/3977/4881/4915/7018/7049/948	11
CC	GO:0000780	'Condensed nuclear chromosome, centromeric region'	3/227	22/18511	2.36x10^{-3}	2.54x10^{-2}	1.85x10^{-2}	6790/701/891	3
CC	GO:0000775	'Chromosome, centromeric region'	8/227	191/18511	2.52x10^{-3}	2.61x10^{-2}	1.90x10^{-2}	1063/11130/332/4085/6790/701/79682/891	8
CC	GO:0098552	'Side of membrane'	14/227	482/18511	2.59x10^{-3}	2.61x10^{-2}	1.90x10^{-2}	100820829/2774/2791/301/338328/3627/4162/5239/54331/6382/7018/7049/762/948	14
CC	GO:0098797	'Plasma membrane protein complex'	9/227	241/18511	3.00x10^{-3}	2.85x10^{-2}	2.08x10^{-2}	1756/2706/2774/2791/3479/3679/5239/54331/7049	9

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
CC	GO:0060205	'Cytoplasmic vesicle lumen'	11/227	338/18511	$3.14x10^{-3}$	$2.85x10^{-2}$	$2.08x10^{-2}$	1191/1675/2934/3039/3043/3479/6286/6288/7018/7123/7450	11
CC	GO:0072686	'Mitotic spindle'	5/227	81/18511	$3.19x10^{-3}$	$2.85x10^{-2}$	$2.08x10^{-2}$	22974/259266/4085/6790/983	5
CC	GO:0031983	'Vesicle lumen'	11/227	339/18511	$3.21x10^{-3}$	$2.85x10^{-2}$	$2.08x10^{-2}$	1191/1675/2934/3039/3043/3479/6286/6288/7018/7123/7450	11
CC	GO:0030018	'Z disc'	6/227	119/18511	$3.50x10^{-3}$	$2.91x10^{-2}$	$2.12x10^{-2}$	100820829/11346/171024/1756/287/5239	6
CC	GO:0005925	'Focal adhesion'	12/227	394/18511	$3.54x10^{-3}$	$2.91x10^{-2}$	$2.12x10^{-2}$	10580/171024/2273/2934/301/4162/4311/5239/7145/83660/857/9590	12
CC	GO:0030496	'Midbody'	7/227	160/18511	$3.64x10^{-3}$	$2.91x10^{-2}$	$2.12x10^{-2}$	1063/259266/26112/332/6790/9055/983	7
CC	GO:0005924	'Cell-substrate adherens junction'	12/227	397/18511	$3.76x10^{-3}$	$2.91x10^{-2}$	$2.12x10^{-2}$	10580/171024/2273/2934/301/4162/4311/5239/7145/83660/857/9590	12
CC	GO:0005876	'Spindle microtubule'	4/227	52/18511	$3.76x10^{-3}$	$2.91x10^{-2}$	$2.12x10^{-2}$	51203/6790/9055/983	4
CC	GO:0030863	'Cortical cytoskeleton'	5/227	85/18511	$3.93x10^{-3}$	$2.97x10^{-2}$	$2.16x10^{-2}$	100820829/130271/2934/54443/6711	5
CC	GO:0045121	'Membrane raft'	10/227	301/18511	$4.14x10^{-3}$	$2.98x10^{-2}$	$2.17x10^{-2}$	10580/1756/1910/287/3991/477/5348/5519/857/948	10
CC	GO:0098857	'Membrane microdomain'	10/227	302/18511	$4.23x10^{-3}$	$2.98x10^{-2}$	$2.17x10^{-2}$	10580/1756/1910/287/3991/477/5348/5519/857/948	10
CC	GO:0034364	'High-density lipoprotein particle'	3/227	27/18511	$4.28x10^{-3}$	$2.98x10^{-2}$	$2.17x10^{-2}$	1191/338328/6288	3
CC	GO:0015629	'Actin cytoskeleton'	13/227	457/18511	$4.35x10^{-3}$	$2.98x10^{-2}$	$2.17x10^{-2}$	100820829/10580/11346/130271/171024/25802/27129/2934/5239/53405/54443/6711/83660	13
CC	GO:0005581	'Collagen trimer'	5/227	88/18511	$4.56x10^{-3}$	$3.06x10^{-2}$	$2.23x10^{-2}$	1300/1301/131873/342035/9370	5
CC	GO:0099568	'Cytoplasmic region'	10/227	309/18511	$4.96x10^{-3}$	$3.22x10^{-2}$	$2.35x10^{-2}$	100820829/1300/130271/2934/53405/54443/6711/857/9590/9833	10
CC	GO:0031091	'Platelet alpha granule'	5/227	90/18511	$5.01x10^{-3}$	$3.22x10^{-2}$	$2.35x10^{-2}$	1191/1675/3479/7450/948	5
CC	GO:0016328	'Lateral plasma membrane'	4/227	57/18511	$5.23x10^{-3}$	$3.29x10^{-2}$	$2.40x10^{-2}$	1365/1756/2706/301	4
CC	GO:0031674	'I band'	6/227	132/18511	$5.79x10^{-3}$	$3.57x10^{-2}$	$2.60x10^{-2}$	100820829/11346/171024/1756/287/5239	6
CC	GO:0009897	'External side of plasma membrane'	9/227	270/18511	$6.26x10^{-3}$	$3.62x10^{-2}$	$2.64x10^{-2}$	301/338328/3627/4162/6382/7018/7049/762/948	9
CC	GO:0031461	'Cullin-RING ubiquitin ligase complex'	7/227	177/18511	$6.29x10^{-3}$	$3.62x10^{-2}$	$2.64x10^{-2}$	11065/114818/1164/401265/51514/701/991	7
CC	GO:0070938	'Contractile ring'	2/227	10/18511	$6.31x10^{-3}$	$3.62x10^{-2}$	$2.64x10^{-2}$	54443/9055	2
CC	GO:0051233	'Spindle midzone'	3/227	31/18511	$6.35x10^{-3}$	$3.62x10^{-2}$	$2.64x10^{-2}$	26112/6790/701	3
CC	GO:0098589	'Membrane region'	11/227	378/18511	$7.16x10^{-3}$	$4.01x10^{-2}$	$2.92x10^{-2}$	10580/1756/1910/287/3991/477/5348/5519/7018/857/948	11
CC	GO:1902911	'Protein kinase complex'	5/227	99/18511	$7.47x10^{-3}$	$4.06x10^{-2}$	$2.95x10^{-2}$	10580/1164/130399/891/983	5

Table SII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
CC	GO:0000778	'Condensed nuclear chromosome kinetochore'	2/227	11/18511	$7.66\text{x}10^{-3}$	$4.06\text{x}10^{-2}$	$2.95\text{x}10^{-2}$	701/891	2
CC	GO:0005890	'Sodium:potassium-exchanging ATPase complex'	2/227	11/18511	$7.66\text{x}10^{-3}$	$4.06\text{x}10^{-2}$	$2.95\text{x}10^{-2}$	477/5348	2
CC	GO:0005833	'Hemoglobin complex'	2/227	12/18511	$9.11\text{x}10^{-3}$	$4.73\text{x}10^{-2}$	$3.44\text{x}10^{-2}$	3039/3043	2
CC	GO:0031093	'Platelet alpha granule lumen'	4/227	67/18511	$9.24\text{x}10^{-3}$	$4.73\text{x}10^{-2}$	$3.44\text{x}10^{-2}$	1191/1675/3479/7450	4
CC	GO:0005834	'Heterotrimeric G-protein complex'	3/227	36/18511	$9.65\text{x}10^{-3}$	$4.78\text{x}10^{-2}$	$3.48\text{x}10^{-2}$	2774/2791/54331	3
CC	GO:1905360	'GTPase complex'	3/227	36/18511	$9.65\text{x}10^{-3}$	$4.78\text{x}10^{-2}$	$3.48\text{x}10^{-2}$	2774/2791/54331	3
CC	GO:0016324	'Apical plasma membrane'	9/227	292/18511	$1.02\text{x}10^{-2}$	$4.96\text{x}10^{-2}$	$3.61\text{x}10^{-2}$	146894/287/301/338328/358/5348/7018/762/948	9
MF	GO:0008201	'Heparin binding'	10/206	160/17354	$2.17\text{x}10^{-5}$	$5.41\text{x}10^{-3}$	$4.77\text{x}10^{-3}$	10631/11096/26577/3627/4023/6288/7049/7123/84870/8840	10
MF	GO:1901681	'Sulfur compound binding'	12/206	232/17354	$2.20\text{x}10^{-5}$	$5.41\text{x}10^{-3}$	$4.77\text{x}10^{-3}$	10631/11096/26577/2719/32/3627/4023/6288/7049/7123/84870/8840	12
MF	GO:0005539	'Glycosaminoglycan binding'	11/206	213/17354	$4.93\text{x}10^{-5}$	$6.34\text{x}10^{-3}$	$5.59\text{x}10^{-3}$	10631/10894/11096/26577/3627/4023/6288/7049/7123/84870/8840	11
MF	GO:0033218	'Amide binding'	13/206	294/17354	$5.17\text{x}10^{-5}$	$6.34\text{x}10^{-3}$	$5.59\text{x}10^{-3}$	1191/1910/2690/30819/32/3624/4311/4881/5468/7298/8322/9452/948	13
MF	GO:0019838	'Growth factor binding'	8/206	130/17354	$1.62\text{x}10^{-4}$	$1.59\text{x}10^{-2}$	$1.40\text{x}10^{-2}$	130399/152831/3489/3977/4915/7049/8840/948	8
MF	GO:0042277	'Peptide binding'	11/206	260/17354	$2.86\text{x}10^{-4}$	$2.29\text{x}10^{-2}$	$2.02\text{x}10^{-2}$	1191/1910/2690/30819/3624/4311/4881/5468/8322/9452/948	11
MF	GO:0031406	'Carboxylic acid binding'	9/206	184/17354	$3.59\text{x}10^{-4}$	$2.29\text{x}10^{-2}$	$2.02\text{x}10^{-2}$	10894/1645/1646/2167/32/5105/5468/7298/9370	9
MF	GO:0043177	'Organic acid binding'	9/206	185/17354	$3.73\text{x}10^{-4}$	$2.29\text{x}10^{-2}$	$2.02\text{x}10^{-2}$	10894/1645/1646/2167/32/5105/5468/7298/9370	9
MF	GO:0033293	'Monocarboxylic acid binding'	5/206	58/17354	$6.17\text{x}10^{-4}$	$3.02\text{x}10^{-2}$	$2.66\text{x}10^{-2}$	1645/1646/2167/32/5468	5
MF	GO:0016709	'Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen'	4/206	34/17354	$6.77\text{x}10^{-4}$	$3.02\text{x}10^{-2}$	$2.66\text{x}10^{-2}$	1645/1646/2327/6713	4
MF	GO:0017046	'Peptide hormone binding'	4/206	34/17354	$6.77\text{x}10^{-4}$	$3.02\text{x}10^{-2}$	$2.66\text{x}10^{-2}$	1910/2690/3624/4881	4
MF	GO:0035173	'Histone kinase activity'	3/206	17/17354	$9.91\text{x}10^{-4}$	$3.93\text{x}10^{-2}$	$3.46\text{x}10^{-2}$	6790/891/983	3
MF	GO:0042562	'Hormone binding'	5/206	65/17354	$1.04\text{x}10^{-3}$	$3.93\text{x}10^{-2}$	$3.46\text{x}10^{-2}$	1910/2690/3624/477/4881	5

Table SII. Continued.

B, KEGG pathway enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
N/A	hsa03320	'PPAR signaling pathway'	10/111	74/7440	1.17×10^{-7}	2.21×10^{-5}	2.04×10^{-5}	10580/2167/364/4023/5105/5346/5468/729359/9370/948	10
N/A	hsa04152	'AMPK signaling pathway'	10/111	120/7440	1.07×10^{-5}	1.01×10^{-3}	9.29×10^{-4}	32/3479/3952/3953/3991/5105/5468/5519/9370/948	10
N/A	hsa04114	'Oocyte meiosis'	9/111	124/7440	8.97×10^{-5}	5.62×10^{-3}	5.20×10^{-3}	3479/4085/5519/6790/891/9133/9232/983/991	9
N/A	hsa04923	'Regulation of lipolysis in adipocytes'	6/111	54/7440	1.39×10^{-4}	6.53×10^{-3}	6.03×10^{-3}	2167/364/3991/4881/5140/5346	6
N/A	hsa04964	'Proximal tubule bicarbonate reclamation'	4/111	23/7440	3.34×10^{-4}	1.26×10^{-2}	1.16×10^{-2}	358/477/5105/762	4
N/A	hsa04110	'Cell cycle'	8/111	124/7440	5.00×10^{-4}	1.44×10^{-2}	1.33×10^{-2}	1028/4085/701/891/9133/9232/983/991	8
N/A	hsa04920	'Adipocytokine signaling pathway'	6/111	69/7440	5.38×10^{-4}	1.44×10^{-2}	1.33×10^{-2}	32/3952/3953/5105/9370/948	6
N/A	hsa04914	'Progesterone-mediated oocyte maturation'	7/111	99/7440	6.55×10^{-4}	1.54×10^{-2}	1.42×10^{-2}	3479/4085/5140/6790/891/9133/983	7
N/A	hsa05144	'Malaria'	5/111	49/7440	7.63×10^{-4}	1.59×10^{-2}	1.47×10^{-2}	2532/3039/3043/6382/948	5
N/A	hsa04512	'ECM-receptor interaction'	6/111	82/7440	1.34×10^{-3}	2.53×10^{-2}	2.33×10^{-2}	131873/3679/6382/6696/7450/948	6
N/A	hsa00360	'Phenylalanine metabolism'	3/111	17/7440	1.89×10^{-3}	3.00×10^{-2}	2.77×10^{-2}	10249/4128/8639	3
N/A	hsa00350	'Tyrosine metabolism'	4/111	36/7440	1.91×10^{-3}	3.00×10^{-2}	2.77×10^{-2}	125/126/4128/8639	4

GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; BP, biological process; CC, cellular component; MF, molecular function; N/A, not available; PPAR, peroxisome proliferator-activated receptor; AMPK, 5' adenosine monophosphate-activated protein kinase; ECM, extracellular matrix; cAMP, cyclic adenosine 3',5'-monophosphate; RING, ring finger protein; NAD(P)H, nicotinamide-adenine dinucleotide phosphate.

Table SIII. GO functional enrichment and KEGG pathway enrichment of the 15 hub genes.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0000280	‘Nuclear division’	12/15	393/17381	$6.47x10^{-18}$	$1.66x10^{-15}$	$5.87x10^{-16}$	1063/11065/11130/22974/332/6790/701/7153/891/9055/9232/991	12
BP	GO:0140014	‘Mitotic nuclear division’	11/15	253/17381	$6.49x10^{-18}$	$1.66x10^{-15}$	$5.87x10^{-16}$	1063/11065/11130/22974/332/6790/701/891/9055/9232/991	11
BP	GO:0048285	‘Organelle fission’	12/15	439/17381	$2.47x10^{-17}$	$4.21x10^{-15}$	$1.49x10^{-15}$	1063/11065/11130/22974/332/6790/701/7153/891/9055/9232/991	12
BP	GO:0000819	‘Sister chromatid segregation’	10/15	230/17381	$3.84x10^{-16}$	$4.90x10^{-14}$	$1.74x10^{-14}$	1063/11065/11130/332/701/7153/891/9055/9232/991	10
BP	GO:0098813	‘Nuclear chromosome segregation’	10/15	297/17381	$5.08x10^{-15}$	$5.19x10^{-13}$	$1.84x10^{-13}$	1063/11065/11130/332/701/7153/891/9055/9232/991	10
BP	GO:0007059	‘Chromosome segregation’	10/15	346/17381	$2.36x10^{-14}$	$2.01x10^{-12}$	$7.13x10^{-13}$	1063/11065/11130/332/701/7153/891/9055/9232/991	10
BP	GO:0000070	‘Mitotic sister chromatid segregation’	8/15	142/17381	$9.97x10^{-14}$	$7.28x10^{-12}$	$2.58x10^{-12}$	1063/11065/11130/701/891/9055/9232/991	8
BP	GO:0031145	‘Anaphase-promoting complex-dependent catabolic process’	7/15	80/17381	$2.09x10^{-13}$	$1.34x10^{-11}$	$4.73x10^{-12}$	11065/6790/701/891/9232/983/991	7
BP	GO:0051304	‘Chromosome separation’	6/15	75/17381	$2.55x10^{-11}$	$1.45x10^{-9}$	$5.14x10^{-10}$	1063/11065/701/7153/891/9232	6
BP	GO:0007093	‘Mitotic cell cycle checkpoint’	7/15	161/17381	$3.10x10^{-11}$	$1.59x10^{-9}$	$5.62x10^{-10}$	1063/11130/6790/701/7153/891/983	7
BP	GO:0045930	‘Negative regulation of mitotic cell cycle’	8/15	305/17381	$4.75x10^{-11}$	$2.20x10^{-9}$	$7.81x10^{-10}$	1063/11130/6790/701/7153/891/9232/983	8
BP	GO:0051783	‘Regulation of nuclear division’	7/15	181/17381	$7.09x10^{-11}$	$3.02x10^{-9}$	$1.07x10^{-9}$	1063/11065/6790/701/891/9232/991	7
BP	GO:0007052	‘Mitotic spindle organization’	6/15	102/17381	$1.69x10^{-10}$	$6.63x10^{-9}$	$2.35x10^{-9}$	22974/332/6790/891/9055/991	6
BP	GO:0042787	‘Protein ubiquitination involved in ubiquitin-dependent protein catabolic process’	7/15	214/17381	$2.30x10^{-10}$	$8.40x10^{-9}$	$2.98x10^{-9}$	11065/6790/701/891/9232/983/991	7
BP	GO:0000075	‘Cell cycle checkpoint’	7/15	225/17381	$3.27x10^{-10}$	$1.11x10^{-8}$	$3.95x10^{-9}$	1063/11130/6790/701/7153/891/983	7
BP	GO:0010965	‘Regulation of mitotic sister chromatid separation’	5/15	50/17381	$4.71x10^{-10}$	$1.51x10^{-8}$	$5.33x10^{-9}$	1063/11065/701/891/9232	5

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:1902850	‘Microtubule cytoskeleton organization involved in mitosis’	6/15	122/17381	5.02×10^{-10}	1.51×10^{-8}	5.35×10^{-9}	22974/332/6790/891/9055/991	6
BP	GO:1901990	‘Regulation of mitotic cell transition’	8/15	417/17381	5.70×10^{-10}	1.55×10^{-8}	5.50×10^{-9}	1063/11065/22974/6790/701/891/983/991	8
BP	GO:0051306	‘Mitotic sister chromatid separation’	5/15	52/17381	5.78×10^{-10}	1.55×10^{-8}	5.50×10^{-9}	1063/11065/701/891/9232	5
BP	GO:1905818	‘Regulation of chromosome separation’	5/15	54/17381	7.02×10^{-10}	1.79×10^{-8}	6.36×10^{-9}	1063/11065/701/891/9232	5
BP	GO:1901987	‘Regulation of cell cycle phase transition’	8/15	446/17381	9.71×10^{-10}	2.36×10^{-8}	8.37×10^{-9}	1063/11065/22974/6790/701/891/983/991	8
BP	GO:0033047	‘Regulation of mitotic sister chromatid segregation’	5/15	60/17381	1.21×10^{-9}	2.81×10^{-8}	9.95×10^{-9}	1063/11065/701/891/9232	5
BP	GO:0007051	‘Spindle organization’	6/15	157/17381	2.31×10^{-9}	4.92×10^{-8}	1.74×10^{-8}	22974/332/6790/891/9055/991	6
BP	GO:0007088	‘Regulation of mitotic nuclear division’	6/15	157/17381	2.31×10^{-9}	4.92×10^{-8}	1.74×10^{-8}	1063/11065/6790/701/891/9232	6
BP	GO:0033045	‘Regulation of sister chromatid segregation’	5/15	71/17381	2.87×10^{-9}	5.64×10^{-8}	2.00×10^{-8}	1063/11065/701/891/9232	5
BP	GO:0051436	‘Negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle’	5/15	71/17381	2.87×10^{-9}	5.64×10^{-8}	2.00×10^{-8}	11065/701/891/983/991	5
BP	GO:0051439	‘Regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle’	5/15	72/17381	3.08×10^{-9}	5.83×10^{-8}	2.07×10^{-8}	11065/701/891/983/991	5
BP	GO:0051437	‘Positive regulation of ubiquitin-protein protein ligase activity involved in regulation of mitotic cell cycle transition’	5/15	76/17381	4.06×10^{-9}	7.41×10^{-8}	2.62×10^{-8}	11065/701/891/983/991	5
BP	GO:1904667	‘Negative regulation of ubiquitin protein ligase activity’	5/15	77/17381	4.34×10^{-9}	7.64×10^{-8}	2.71×10^{-8}	11065/701/891/983/991	5
BP	GO:1903052	‘Positive regulation of proteolysis involved in cellular protein catabolic process’	6/15	185/17381	6.20×10^{-9}	1.06×10^{-7}	3.74×10^{-8}	11065/6790/701/891/983/991	6
BP	GO:0051444	‘Negative regulation of ubiquitin-protein transferase activity’	5/15	84/17381	6.76×10^{-9}	1.08×10^{-7}	3.82×10^{-8}	11065/701/891/983/991	5
BP	GO:1904668	‘Positive regulation of ubiquitin protein ligase activity’	5/15	84/17381	6.76×10^{-9}	1.08×10^{-7}	3.82×10^{-8}	11065/701/891/983/991	5
BP	GO:2000060	‘Positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process’	5/15	91/17381	1.01×10^{-8}	1.57×10^{-7}	5.55×10^{-8}	11065/701/891/983/991	5

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:1903364	‘Positive regulation of cellular protein catabolic process’	6/15	202/17381	1.05x10^{-8}	1.57x10^{-7}	5.55x10^{-8}	11065/6790/701/891/983/991	6
BP	GO:1904666	‘Regulation of ubiquitin protein ligase activity’	5/15	92/17381	1.07x10^{-8}	1.57x10^{-7}	5.55x10^{-8}	11065/701/891/983/991	5
BP	GO:0051983	‘Regulation of chromosome segregation’	5/15	95/17381	1.26x10^{-8}	1.79x10^{-7}	6.34x10^{-8}	1063/11065/701/891/9232	5
BP	GO:0043161	‘Proteasome-mediated ubiquitin-dependent protein catabolic process’	7/15	387/17381	1.42x10^{-8}	1.96x10^{-7}	6.94x10^{-8}	11065/6790/701/891/9232/983/991	7
BP	GO:2000816	‘Negative regulation of mitotic sister chromatid separation’	4/15	34/17381	1.64x10^{-8}	2.21x10^{-7}	7.81x10^{-8}	1063/701/891/9232	4
BP	GO:1905819	‘Negative regulation of chromosome separation’	4/15	35/17381	1.85x10^{-8}	2.43x10^{-7}	8.59x10^{-8}	1063/701/891/9232	4
BP	GO:0051443	‘Positive regulation of ubiquitin-protein transferase activity’	5/15	104/17381	1.99x10^{-8}	2.55x10^{-7}	9.02x10^{-8}	11065/701/891/983/991	5
BP	GO:2000058	‘Regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process’	5/15	106/17381	2.19x10^{-8}	2.73x10^{-7}	9.69x10^{-8}	11065/701/891/983/991	5
BP	GO:0033048	‘Negative regulation of mitotic sister chromatid segregation’	4/15	37/17381	2.33x10^{-8}	2.84x10^{-7}	1.01x10^{-7}	1063/701/891/9232	4
BP	GO:0033046	‘Negative regulation of sister chromatid segregation’	4/15	39/17381	2.90x10^{-8}	3.45x10^{-7}	1.22x10^{-7}	1063/701/891/9232	4
BP	GO:0051321	‘Meiotic cell cycle’	6/15	241/17381	3.01x10^{-8}	3.50x10^{-7}	1.24x10^{-7}	6790/701/7153/9232/983/991	6
BP	GO:0051985	‘Negative regulation of chromosome segregation’	4/15	40/17381	3.22x10^{-8}	3.64x10^{-7}	1.29x10^{-7}	1063/701/891/9232	4
BP	GO:0010498	‘Proteasomal protein catabolic process’	7/15	437/17381	3.27x10^{-8}	3.64x10^{-7}	1.29x10^{-7}	11065/6790/701/891/9232/983/991	7
BP	GO:0000086	‘G2/M transition of mitotic cell cycle’	6/15	248/17381	3.57x10^{-8}	3.88x10^{-7}	1.38x10^{-7}	1063/22974/6790/891/9133/983	6
BP	GO:0044839	‘Cell cycle G2/M phase transition’	6/15	257/17381	4.41x10^{-8}	4.60x10^{-7}	1.63x10^{-7}	1063/22974/6790/891/9133/983	6
BP	GO:1903050	‘Regulation of proteolysis involved in cellular protein catabolic process’	6/15	257/17381	4.41x10^{-8}	4.60x10^{-7}	1.63x10^{-7}	11065/6790/701/891/983/991	6
BP	GO:0051438	‘Regulation of ubiquitin-protein transferase activity’	5/15	124/17381	4.83x10^{-8}	4.84x10^{-7}	1.72x10^{-7}	11065/701/891/983/991	5
BP	GO:2001251	‘Negative regulation of chromosome organization’	5/15	124/17381	4.83x10^{-8}	4.84x10^{-7}	1.72x10^{-7}	1063/701/7153/891/9232	5
BP	GO:0030071	‘Regulation of mitotic metaphase/anaphase transition’	4/15	45/17381	5.24x10^{-8}	5.15x10^{-7}	1.82x10^{-7}	1063/11065/701/891	4

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0000226	‘Microtubule cytoskeleton organization’	7/15	472/17381	5.55x10^{-8}	5.33x10^{-7}	1.89x10^{-7}	22974/332/6790/891/9055/983/991	7
BP	GO:0045732	‘Positive regulation of protein catabolic process’	6/15	268/17381	5.66x10^{-8}	5.33x10^{-7}	1.89x10^{-7}	11065/6790/701/891/983/991	6
BP	GO:1902099	‘Regulation of metaphase/anaphase transition of cell cycle’	4/15	46/17381	5.74x10^{-8}	5.33x10^{-7}	1.89x10^{-7}	1063/11065/701/891	4
BP	GO:0007091	‘Metaphase/anaphase transition of mitotic cell cycle’	4/15	47/17381	6.27x10^{-8}	5.62x10^{-7}	1.99x10^{-7}	1063/11065/701/891	4
BP	GO:0045839	‘Negative regulation of mitotic nuclear division’	4/15	47/17381	6.27x10-8	5.62x10^{-7}	1.99x10^{-7}	1063/701/891/9232	4
BP	GO:0044784	‘Metaphase/anaphase transition of cell cycle’	4/15	48/17381	6.83x10^{-8}	5.95x10^{-7}	2.11x10^{-7}	1063/11065/701/891	4
BP	GO:0007062	‘Sister chromatid cohesion’	5/15	133/17381	6.87x10^{-8}	5.95x10^{-7}	2.11x10^{-7}	1063/11130/332/701/991	5
BP	GO:1903362	‘Regulation of cellular protein catabolic process’	6/15	285/17381	8.15x10^{-8}	6.94x10^{-7}	2.46x10^{-7}	11065/6790/701/891/983/991	6
BP	GO:0031397	‘Negative regulation of protein ubiquitination’	5/15	139/17381	8.57x10^{-8}	7.18x10^{-7}	2.54x10^{-7}	11065/701/891/983/991	5
BP	GO:0033044	‘Regulation of chromosome organization’	6/15	301/17381	1.13x10^{-7}	9.28x10^{-7}	3.29x10^{-7}	1063/11065/701/7153/891/9232	6
BP	GO:1903321	‘Negative regulation of protein modification by small protein conjugation or removal’	5/15	150/17381	1.25x10^{-7}	1.02x10^{-6}	3.60x10^{-7}	11065/701/891/983/991	5
BP	GO:0051784	‘Negative regulation of nuclear division’	4/15	58/17381	1.48x10^{-7}	1.18x10^{-6}	4.19x10^{-7}	1063/701/891/9232	4
BP	GO:0010948	‘Negative regulation of cell cycle process’	6/15	328/17381	1.87x10^{-7}	1.47x10^{-6}	5.21x10^{-7}	1063/6790/701/891/9232/983	6
BP	GO:0140013	‘Meiotic nuclear division’	5/15	171/17381	2.41x10^{-7}	1.87x10^{-6}	6.61x10^{-7}	6790/701/7153/9232/991	5
BP	GO:0031398	‘Positive regulation of protein ubiquitination’	5/15	183/17381	3.38x10^{-7}	2.54x10^{-6}	8.99x10^{-7}	11065/701/891/983/991	5
BP	GO:1903046	‘Meiotic cell cycle process’	5/15	183/17381	3.38x10^{-7}	2.54x10^{-6}	8.99x10^{-7}	6790/701/7153/9232/991	5
BP	GO:0010389	‘Regulation of G2/M transition of mitotic cell cycle’	5/15	194/17381	4.51x10^{-7}	3.34x10^{-6}	1.18x10^{-6}	1063/22974/6790/891/983	5
BP	GO:1903322	‘Positive regulation of protein modification by small protein conjugation or removal’	5/15	200/17381	5.25x10^{-7}	3.83x10^{-6}	1.36x10^{-6}	11065/701/891/983/991	5
BP	GO:0045862	‘Positive regulation of proteolysis’	6/15	393/17381	5.42x10^{-7}	3.90x10^{-6}	1.38x10^{-6}	11065/6790/701/891/983/991	6
BP	GO:0031331	‘Positive regulation of cellular catabolic process’	6/15	396/17381	5.66x10^{-7}	4.02x10^{-6}	1.42x10^{-6}	11065/6790/701/891/983/991	6

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:1902749	‘Regulation of cell cycle G2/M phase transition’	5/15	204/17381	$5.79\mathrm{x}10^{-7}$	$4.05\mathrm{x}10^{-6}$	$1.44\mathrm{x}10^{-6}$	1063/22974/6790/891/983	5
BP	GO:0042176	‘Regulation of protein catabolic process’	6/15	399/17381	$5.92\mathrm{x}10^{-7}$	$4.09\mathrm{x}10^{-6}$	$1.45\mathrm{x}10^{-6}$	11065/6790/701/891/983/991	6
BP	GO:1901991	‘Negative regulation of mitotic cell cycle phase transition’	5/15	224/17381	$9.19\mathrm{x}10^{-7}$	$6.26\mathrm{x}10^{-6}$	$2.22\mathrm{x}10^{-6}$	1063/6790/701/891/983	5
BP	GO:0051225	‘Spindle assembly’	4/15	96/17381	$1.14\mathrm{x}10^{-6}$	$7.63\mathrm{x}10^{-6}$	$2.70\mathrm{x}10^{-6}$	22974/332/6790/991	4
BP	GO:0009896	‘Positive regulation of catabolic process’	6/15	447/17381	$1.15\mathrm{x}10^{-6}$	$7.63\mathrm{x}10^{-6}$	$2.70\mathrm{x}10^{-6}$	11065/6790/701/891/983/991	6
BP	GO:1901988	‘Negative regulation of cell cycle phase transition’	5/15	235/17381	$1.16\mathrm{x}10^{-6}$	$7.63\mathrm{x}10^{-6}$	$2.70\mathrm{x}10^{-6}$	1063/6790/701/891/983	5
BP	GO:0044774	‘Mitotic DNA integrity checkpoint’	4/15	109/17381	$1.89\mathrm{x}10^{-6}$	$1.23\mathrm{x}10^{-5}$	$4.34\mathrm{x}10^{-6}$	6790/7153/891/983	4
BP	GO:0007094	‘Mitotic spindle assembly checkpoint’	3/15	30/17381	$2.08\mathrm{x}10^{-6}$	$1.29\mathrm{x}10^{-5}$	$4.59\mathrm{x}10^{-6}$	1063/701/891	3
BP	GO:0071173	‘Spindle assembly checkpoint’	3/15	30/17381	$2.08\mathrm{x}10^{-6}$	$1.29\mathrm{x}10^{-5}$	$4.59\mathrm{x}10^{-6}$	1063/701/891	3
BP	GO:0071174	‘Mitotic spindle checkpoint’	3/15	30/17381	$2.08\mathrm{x}10^{-6}$	$1.29\mathrm{x}10^{-5}$	$4.59\mathrm{x}10^{-6}$	1063/701/891	3
BP	GO:0031396	‘Regulation of protein ubiquitination’	5/15	265/17381	$2.10\mathrm{x}10^{-6}$	$1.29\mathrm{x}10^{-5}$	$4.59\mathrm{x}10^{-6}$	11065/701/891/983/991	5
BP	GO:0045841	‘Negative regulation of mitotic metaphase/anaphase transition’	3/15	31/17381	$2.30\mathrm{x}10^{-6}$	$1.40\mathrm{x}10^{-5}$	$4.97\mathrm{x}10^{-6}$	1063/701/891	3
BP	GO:1902100	‘Negative regulation of metaphase/ anaphase transition of cell cycle’	3/15	32/17381	$2.54\mathrm{x}10^{-6}$	$1.53\mathrm{x}10^{-5}$	$5.41\mathrm{x}10^{-6}$	1063/701/891	3
BP	GO:0031577	‘Spindle checkpoint’	3/15	34/17381	$3.06\mathrm{x}10^{-6}$	$1.82\mathrm{x}10^{-5}$	$6.45\mathrm{x}10^{-6}$	1063/701/891	3
BP	GO:1903320	‘Regulation of protein modification by small protein conjugation or removal’	5/15	291/17381	$3.33\mathrm{x}10^{-6}$	$1.94\mathrm{x}10^{-5}$	$6.89\mathrm{x}10^{-6}$	11065/701/891/983/991	5
BP	GO:0030261	‘Chromosome condensation’	3/15	35/17381	$3.35\mathrm{x}10^{-6}$	$1.94\mathrm{x}10^{-5}$	$6.89\mathrm{x}10^{-6}$	7153/891/983	3
BP	GO:0016572	‘Histone phosphorylation’	3/15	37/17381	$3.97\mathrm{x}10^{-6}$	$2.28\mathrm{x}10^{-5}$	$8.08\mathrm{x}10^{-6}$	6790/891/983	3
BP	GO:0045931	‘Positive regulation of mitotic cell cycle’	4/15	145/17381	$5.91\mathrm{x}10^{-6}$	$3.35\mathrm{x}10^{-5}$	$1.19\mathrm{x}10^{-5}$	11065/6790/891/983	4
BP	GO:0007077	‘Mitotic nuclear envelope disassembly’	3/15	44/17381	$6.74\mathrm{x}10^{-6}$	$3.79\mathrm{x}10^{-5}$	$1.34\mathrm{x}10^{-5}$	891/9133/983	3
BP	GO:0010639	‘Negative regulation of organelle organization’	5/15	340/17381	$7.11\mathrm{x}10^{-6}$	$3.95\mathrm{x}10^{-5}$	$1.40\mathrm{x}10^{-5}$	1063/701/7153/891/9232	5
BP	GO:0030397	‘Membrane disassembly’	3/15	48/17381	$8.79\mathrm{x}10^{-6}$	$4.78\mathrm{x}10^{-5}$	$1.69\mathrm{x}10^{-5}$	891/9133/983	3
BP	GO:0051081	‘Nuclear envelope disassembly’	3/15	48/17381	$8.79\mathrm{x}10^{-6}$	$4.78\mathrm{x}10^{-5}$	$1.69\mathrm{x}10^{-5}$	891/9133/983	3
BP	GO:0031570	‘DNA integrity checkpoint’	4/15	164/17381	$9.62\mathrm{x}10^{-6}$	$5.17\mathrm{x}10^{-5}$	$1.83\mathrm{x}10^{-5}$	6790/7153/891/983	4
BP	GO:0051348	‘Negative regulation of transferase activity’	5/15	369/17381	$1.06\mathrm{x}10^{-5}$	$5.63\mathrm{x}10^{-5}$	$2.00\mathrm{x}10^{-5}$	11065/701/891/983/991	5
BP	GO:0090307	‘Mitotic spindle assembly’	3/15	59/17381	$1.64\mathrm{x}10^{-5}$	$8.65\mathrm{x}10^{-5}$	$3.07\mathrm{x}10^{-5}$	22974/332/991	3
BP	GO:0006977	‘DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest’	3/15	62/17381	$1.91\mathrm{x}10^{-5}$	$9.95\mathrm{x}10^{-5}$	$3.52\mathrm{x}10^{-5}$	6790/891/983	3

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0072431	'Signal transduction involved in mitotic G1 DNA damage checkpoint'	3/15	63/17381	2.00x10^{-5}	0.000102292	3.62x10^{-5}	6790/891/983	3
BP	GO:1902400	'Intracellular signal transduction involved in G1 DNA damage checkpoint'	3/15	63/17381	2.00x10^{-5}	0.000102292	3.62x10^{-5}	6790/891/983	3
BP	GO:0072413	'Signal transduction involved in mitotic cell cycle checkpoint'	3/15	65/17381	2.20x10^{-5}	0.000109125	3.87x10^{-5}	6790/891/983	3
BP	GO:1902402	'Signal transduction involved in mitotic DNA damage checkpoint'	3/15	65/17381	2.20x10^{-5}	0.000109125	3.87x10^{-5}	6790/891/983	3
BP	GO:1902403	'Signal transduction involved in mitotic DNA integrity checkpoint'	3/15	65/17381	2.20x10-5	0.000109125	3.87x10^{-5}	6790/891/983	3
BP	GO:0072401	'Signal transduction involved in DNA integrity checkpoint'	3/15	67/17381	2.41x10-5	0.000117279	4.16x10^{-5}	6790/891/983	3
BP	GO:0072422	'Signal transduction involved in DNA damage checkpoint'	3/15	67/17381	2.41x10-5	0.000117279	4.16x10^{-5}	6790/891/983	3
BP	GO:0072395	'Signal transduction involved in cell cycle checkpoint'	3/15	68/17381	2.52x10-5	0.000121472	4.30x10^{-5}	6790/891/983	3
BP	GO:0031571	'Mitotic G1 DNA damage checkpoint'	3/15	71/17381	2.87x10^{-5}	0.000135756	4.81x10^{-5}	6790/891/983	3
BP	GO:0044819	'Mitotic G1/S transition checkpoint'	3/15	71/17381	2.87x10^{-5}	0.000135756	4.81x10^{-5}	6790/891/983	3
BP	GO:0044783	'G1 DNA damage checkpoint'	3/15	72/17381	2.99x10^{-5}	0.000140287	4.97x10^{-5}	6790/891/983	3
BP	GO:0035404	'Histone-serine phosphorylation'	2/15	12/17381	4.57x10^{-5}	0.00021017	7.45x10^{-5}	6790/891	2
BP	GO:0055015	'Ventricular cardiac muscle cell development'	2/15	12/17381	4.57x10^{-5}	0.00021017	7.45x10^{-5}	891/983	2
BP	GO:0006998	'Nuclear envelope organization'	3/15	86/17381	5.10x10^{-5}	0.000231247	8.19x10^{-5}	891/9133/983	3
BP	GO:0007050	'Cell cycle arrest'	4/15	251/17381	5.11x10^{-5}	0.000231247	8.19x10^{-5}	1033/6790/891/983	4
BP	GO:0045132	'Meiotic chromosome segregation'	3/15	88/17381	5.46x10^{-5}	0.000242635	8.60x10^{-5}	701/7153/9232	3
BP	GO:0071158	'Positive regulation of cell cycle arrest'	3/15	88/17381	5.46x10^{-5}	0.000242635	8.60x10^{-5}	6790/891/983	3
BP	GO:0000082	'G1/S transition of mitotic cell cycle'	4/15	265/17381	6.32x10^{-5}	0.000278251	9.86x10^{-5}	1033/6790/891/983	4
BP	GO:0072331	'Signal transduction by p53 class mediator'	4/15	270/17381	6.79x10^{-5}	0.000296659	0.000105109	22974/6790/891/983	4
BP	GO:0090068	'Positive regulation of cell cycle process'	4/15	274/17381	7.19x10^{-5}	0.000311433	0.000110344	11065/6790/891/983	4
BP	GO:0044843	'Cell cycle G1/S phase transition'	4/15	284/17381	8.26x10^{-5}	0.000354889	0.000125741	1033/6790/891/983	4
BP	GO:0044773	'Mitotic DNA damage checkpoint'	3/15	102/17381	8.48x10^{-5}	0.000361192	0.000127974	6790/891/983	3
BP	GO:0055012	'Ventricular cardiac muscle cell differentiation'	2/15	17/17381	9.38x10^{-5}	0.000396296	0.000140412	891/983	2
BP	GO:0030330	'DNA damage response, signal transduction by p53 class mediator'	3/15	109/17381	0.000103332	0.000432808	0.000153348	6790/891/983	3
BP	GO:0002082	'Regulation of oxidative phosphorylation'	2/15	18/17381	0.000105517	0.000434039	0.000153785	891/983	2

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0034501	‘Protein localization to kinetochore’	2/15	18/17381	0.000105517	0.000434039	0.000153785	701/983	2
BP	GO:2000134	‘Negative regulation of G1/S transition of mitotic cell cycle’	3/15	110/17381	0.000106174	0.000434039	0.000153785	6790/891/983	3
BP	GO:0007127	‘Meiosis I’	3/15	113/17381	0.000115006	0.000462739	0.000163953	6790/7153/9232	3
BP	GO:0071156	‘Regulation of cell cycle arrest’	3/15	113/17381	0.000115006	0.000462739	0.000163953	6790/891/983	3
BP	GO:1902807	‘Negative regulation of cell cycle G1/S phase transition’	3/15	117/17381	0.000127509	0.000509039	0.000180358	6790/891/983	3
BP	GO:0071459	‘Protein localization to chromosome, centromeric region’	2/15	21/17381	0.00014461	0.000572836	0.000202962	701/983	2
BP	GO:0042770	‘Signal transduction in response to DNA damage’	3/15	123/17381	0.000147876	0.000581266	0.000205948	6790/891/983	3
BP	GO:0043457	‘Regulation of cellular respiration’	2/15	24/17381	0.000189775	0.000740267	0.000262284	891/983	2
BP	GO:2000241	‘Regulation of reproductive process’	3/15	138/17381	0.000207781	0.000804365	0.000284995	6790/983/991	3
BP	GO:0001556	‘Oocyte maturation’	2/15	26/17381	0.000223244	0.000857728	0.000303902	6790/891	2
BP	GO:0016202	‘Regulation of striated muscle tissue development’	3/15	142/17381	0.000226049	0.000862021	0.000305423	1063/891/983	3
BP	GO:1901861	‘Regulation of muscle tissue development’	3/15	144/17381	0.00023556	0.00089164	0.000315917	1063/891/983	3
BP	GO:0045787	‘Positive regulation of cell cycle’	4/15	374/17381	0.000238609	0.000896538	0.000317653	11065/6790/891/983	4
BP	GO:0006997	‘Nucleus organization’	3/15	145/17381	0.000240412	0.00089672	0.000317717	891/9133/983	3
BP	GO:0048634	‘Regulation of muscle organ development’	3/15	147/17381	0.00025031	0.000926871	0.0003284	1063/891/983	3
BP	GO:0000077	‘DNA damage checkpoint’	3/15	155/17381	0.000292537	0.001075441	0.00038104	6790/891/983	3
BP	GO:2000045	‘Regulation of G1/S transition of mitotic cell cycle’	3/15	162/17381	0.000333058	0.001215663	0.000430722	6790/891/983	3
BP	GO:1903580	‘Positive regulation of ATP metabolic process’	2/15	33/17381	0.000361422	0.001309836	0.000464089	891/983	2
BP	GO:0060045	‘Positive regulation of cardiac muscle cell proliferation’	2/15	35/17381	0.000406879	0.001464191	0.000518778	891/983	2
BP	GO:1902806	‘Regulation of cell cycle G1/S phase transition’	3/15	181/17381	0.000460873	0.001646895	0.000583512	6790/891/983	3
BP	GO:0031099	‘Regeneration’	3/15	186/17381	0.00049906	0.001770968	0.000627472	6790/891/983	3
BP	GO:0051445	‘Regulation of meiotic cell cycle’	2/15	44/17381	0.000644008	0.002254027	0.000798625	983/991	2
BP	GO:0055023	‘Positive regulation of cardiac muscle tissue growth’	2/15	44/17381	0.000644008	0.002254027	0.000798625	891/983	2
BP	GO:0048599	‘Oocyte development’	2/15	45/17381	0.000673626	0.002341651	0.000829671	6790/891	2
BP	GO:0006323	‘DNA packaging’	3/15	208/17381	0.00069118	0.002386438	0.00084554	7153/891/983	3

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0009994	'Oocyte differentiation'	2/15	48/17381	0.000766378	0.002610795	0.000925032	6790/891	2
BP	GO:0060421	'Positive regulation of heart growth'	2/15	48/17381	0.000766378	0.002610795	0.000925032	891/983	2
BP	GO:0045840	'Positive regulation of mitotic nuclear division'	2/15	50/17381	0.000831452	0.002813723	0.000996931	11065/6790	2
BP	GO:0060043	'Regulation of cardiac muscle cell proliferation'	2/15	53/17381	0.000933902	0.00313963	0.001112404	891/983	2
BP	GO:0051310	'Metaphase plate congression'	2/15	55/17381	0.001005416	0.003357957	0.001189759	1063/891	2
BP	GO:0055025	'Positive regulation of cardiac muscle tissue development'	2/15	57/17381	0.001079492	0.003581949	0.001269122	891/983	2
BP	GO:0046622	'Positive regulation of organ growth'	2/15	59/17381	0.001156122	0.003811472	0.001350444	891/983	2
BP	GO:0051785	'Positive regulation of nuclear division'	2/15	61/17381	0.001235298	0.004046394	0.00143368	11065/6790	2
BP	GO:0021700	'Developmental maturation'	3/15	256/17381	0.001260314	0.004102042	0.001453396	6790/891/991	3
BP	GO:0060038	'Cardiac muscle cell proliferation'	2/15	63/17381	0.001317014	0.004259456	0.00150917	891/983	2
BP	GO:0055021	'Regulation of cardiac muscle tissue growth'	2/15	68/17381	0.001532357	0.004924745	0.001744888	891/983	2
BP	GO:1901992	'Positive regulation of mitotic cell cycle phase transition'	2/15	70/17381	0.001622896	0.005183124	0.001836435	11065/983	2
BP	GO:0055013	'Cardiac muscle cell development'	2/15	71/17381	0.001669105	0.005297593	0.001876993	891/983	2
BP	GO:0060420	'Regulation of heart growth'	2/15	73/17381	0.001763396	0.005562317	0.001970787	891/983	2
BP	GO:0018105	'Peptidyl-serine phosphorylation'	3/15	289/17381	0.00178481	0.005595325	0.001982482	6790/891/983	3
BP	GO:0071103	'DNA conformation change'	3/15	290/17381	0.00180253	0.005610089	0.001987713	7153/891/983	3
BP	GO:0014855	'Striated muscle cell proliferation'	2/15	74/17381	0.001811477	0.005610089	0.001987713	891/983	2
BP	GO:0034502	'Protein localization to chromosome'	2/15	75/17381	0.00186018	0.005691927	0.002016709	701/983	2
BP	GO:0051303	'Establishment of chromosome localization'	2/15	75/17381	0.00186018	0.005691927	0.002016709	1063/891	2
BP	GO:0050000	'Chromosome localization'	2/15	76/17381	0.001909503	0.005808073	0.002057861	1063/891	2
BP	GO:0055006	'Cardiac cell development'	2/15	77/17381	0.001959447	0.005924719	0.00209919	891/983	2
BP	GO:0031100	'Animal organ regeneration'	2/15	80/17381	0.00211299	0.006351399	0.002250367	6790/983	2
BP	GO:0018209	'Peptidyl-serine modification'	3/15	308/17381	0.002140635	0.006396079	0.002266198	6790/891/983	3
BP	GO:0045844	'Positive regulation of striated muscle tissue development'	2/15	81/17381	0.002165405	0.006396079	0.002266198	891/983	2
BP	GO:0048636	'Positive regulation of muscle organ development'	2/15	81/17381	0.002165405	0.006396079	0.002266198	891/983	2
BP	GO:1901863	'Positive regulation of muscle tissue development'	2/15	82/17381	0.002218435	0.006515058	0.002308353	891/983	2
BP	GO:0048477	'Oogenesis'	2/15	83/17381	0.002272079	0.00663447	0.002350662	6790/891	2

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0000079	'Regulation of cyclin-dependent protein serine/threonine kinase activity'	2/15	84/17381	0.002326337	0.006678416	0.002366232	1033/891	2
BP	GO:0042775	'Mitochondrial ATP synthesis coupled electron transport'	2/15	84/17381	0.002326337	0.006678416	0.002366232	891/983	2
BP	GO:1901989	'Positive regulation of cell cycle phase transition'	2/15	84/17381	0.002326337	0.006678416	0.002366232	11065/983	2
BP	GO:0042773	'ATP synthesis coupled electron transport'	2/15	85/17381	0.002381207	0.006797747	0.002408513	891/983	2
BP	GO:1904029	'Regulation of cyclin-dependent protein kinase activity'	2/15	88/17381	0.002549482	0.007237697	0.002564392	1033/891	2
BP	GO:0055024	'Regulation of cardiac muscle tissue development'	2/15	90/17381	0.002664711	0.007523023	0.002665486	891/983	2
BP	GO:1903578	'Regulation of ATP metabolic process'	2/15	91/17381	0.002723236	0.007646008	0.00270906	891/983	2
BP	GO:0010972	'Negative regulation of G2/M transition of mitotic cell cycle'	2/15	92/17381	0.002782366	0.00776934	0.002752758	6790/983	2
BP	GO:0016925	'Protein sumoylation'	2/15	94/17381	0.002902441	0.00797391	0.00282524	332/7153	2
BP	GO:0055017	'Cardiac muscle tissue growth'	2/15	94/17381	0.002902441	0.00797391	0.00282524	891/983	2
BP	GO:1902750	'Negative regulation of cell cycle G2/M phase transition'	2/15	94/17381	0.002902441	0.00797391	0.00282524	6790/983	2
BP	GO:0060419	'Heart growth'	2/15	100/17381	0.003277106	0.008955086	0.00317288	891/983	2
BP	GO:0022904	'Respiratory electron transport chain'	2/15	102/17381	0.003406782	0.00921093	0.003263529	891/983	2
BP	GO:0046620	'Regulation of organ growth'	2/15	102/17381	0.003406782	0.00921093	0.003263529	891/983	2
BP	GO:0014706	'Striated muscle tissue development'	3/15	369/17381	0.003571922	0.009606591	0.003403716	1063/891/983	3
BP	GO:0006119	'Oxidative phosphorylation'	2/15	105/17381	0.003605761	0.009646826	0.003417971	891/983	2
BP	GO:0060537	'Muscle tissue development'	3/15	387/17381	0.00408372	0.010868651	0.003850876	1063/891/983	3
BP	GO:0007517	'Muscle organ development'	3/15	389/17381	0.004143216	0.010969862	0.003886737	1063/891/983	3
BP	GO:0010256	'Endomembrane system organization'	3/15	396/17381	0.004355649	0.011472868	0.004064957	891/9133/983	3
BP	GO:0055007	'Cardiac muscle cell differentiation'	2/15	116/17381	0.004380789	0.011479913	0.004067453	891/983	2
BP	GO:0007098	'Centrosome cycle'	2/15	118/17381	0.004529311	0.01180856	0.004183896	6790/983	2
BP	GO:0042493	'Response to drug'	3/15	411/17381	0.004833094	0.012536605	0.00444185	1063/891/983	3
BP	GO:0043467	'Regulation of generation of precursor metabolites and energy'	2/15	124/17381	0.00498878	0.012875083	0.004561776	891/983	2
BP	GO:0031023	'Microtubule organizing center organization'	2/15	127/17381	0.00522629	0.013420273	0.004754943	6790/983	2
BP	GO:0007292	'Female gamete generation'	2/15	129/17381	0.005387494	0.013765046	0.0048771	6790/891	2
BP	GO:0016570	'Histone modification'	3/15	444/17381	0.005992804	0.015235438	0.005398075	6790/891/983	3
BP	GO:0000910	'Cytokinesis'	2/15	137/17381	0.006055055	0.015317491	0.005427147	6790/9055	2

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0045981	'Positive regulation of nucleotide metabolic process'	2/15	145/17381	0.006758665	0.016929794	0.005998403	891/983	2
BP	GO:1900544	'Positive regulation of purine nucleotide metabolic process'	2/15	145/17381	0.006758665	0.016929794	0.005998403	891/983	2
BP	GO:0035051	'Cardiocyte differentiation'	2/15	146/17381	0.006849128	0.017072705	0.006049038	891/983	2
BP	GO:0071695	'Anatomical structure maturation'	2/15	150/17381	0.007216523	0.017901181	0.006342575	6790/891	2
BP	GO:0055002	'Striated muscle cell development'	2/15	154/17381	0.007592744	0.018653327	0.006609069	891/983	2
BP	GO:0070507	'Regulation of microtubule cytoskeleton organization'	2/15	154/17381	0.007592744	0.018653327	0.006609069	22974/6790	2
BP	GO:0071900	'Regulation of protein serine/threonine kinase activity'	3/15	495/17381	0.008092353	0.019785609	0.007010248	1033/891/983	3
BP	GO:0071281	'Cellular response to iron ion'	1/15	10/17381	0.008598893	0.020824807	0.007378446	891	1
BP	GO:1990001	'Inhibition of cysteine-type endopeptidase activity involved in apoptotic process'	1/15	10/17381	0.008598893	0.020824807	0.007378446	332	1
BP	GO:0048469	'Cell maturation'	2/15	166/17381	0.008773794	0.021148154	0.007493012	6790/891	2
BP	GO:0035265	'Organ growth'	2/15	168/17381	0.008978201	0.021539253	0.007631582	891/983	2
BP	GO:0055001	'Muscle cell development'	2/15	169/17381	0.009081209	0.02168457	0.007683069	891/983	2
BP	GO:0022900	'Electron transport chain'	2/15	170/17381	0.009184752	0.021829806	0.007734528	891/983	2
BP	GO:0045333	'Cellular respiration'	2/15	172/17381	0.009393439	0.021861957	0.00774592	891/983	2
BP	GO:0007135	'Meiosis II'	1/15	11/17381	0.009454976	0.021861957	0.00774592	701	1
BP	GO:0039692	'Single stranded viral RNA replication via double stranded DNA intermediate'	1/15	11/17381	0.009454976	0.021861957	0.00774592	7153	1
BP	GO:0060281	'Regulation of oocyte development'	1/15	11/17381	0.009454976	0.021861957	0.00774592	6790	1
BP	GO:0070601	'Centromeric sister chromatid cohesion'	1/15	11/17381	0.009454976	0.021861957	0.00774592	701	1
BP	GO:1905879	'Regulation of oogenesis'	1/15	11/17381	0.009454976	0.021861957	0.00774592	6790	1
BP	GO:0043902	'Positive regulation of multi-organism process'	2/15	174/17381	0.009604254	0.022007955	0.007797648	6790/7153	2
BP	GO:0048639	'Positive regulation of developmental growth'	2/15	174/17381	0.009604254	0.022007955	0.007797648	891/983	2
BP	GO:1901796	'Regulation of signal transduction by p53 class mediator'	2/15	176/17381	0.009817192	0.022395469	0.007934948	22974/6790	2
BP	GO:0000022	'Mitotic spindle elongation'	1/15	12/17381	0.010310369	0.023209684	0.008223433	9055	1
BP	GO:0051988	'Regulation of attachment of spindle microtubules to kinetochore'	1/15	12/17381	0.010310369	0.023209684	0.008223433	891	1
BP	GO:0090128	'Regulation of synapse maturation'	1/15	12/17381	0.010310369	0.023209684	0.008223433	991	1
BP	GO:0032886	'Regulation of microtubule-based process'	2/15	182/17381	0.010468669	0.023462675	0.008313071	22974/6790	2

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0006367	‘Transcription initiation from RNA polymerase II promoter’	2/15	185/17381	0.010801488	0.024102884	0.008539903	891/983	2
BP	GO:0000212	‘Meiotic spindle organization’	1/15	13/17381	0.011165072	0.024278093	0.008601982	6790	1
BP	GO:0033127	‘Regulation of histone phosphorylation’	1/15	13/17381	0.011165072	0.024278093	0.008601982	891	1
BP	GO:0033160	‘Positive regulation of protein import into nucleus, translocation’	1/15	13/17381	0.011165072	0.024278093	0.008601982	983	1
BP	GO:0051231	‘Spindle elongation’	1/15	13/17381	0.011165072	0.024278093	0.008601982	9055	1
BP	GO:0090266	‘Regulation of mitotic cell cycle spindle assembly checkpoint’	1/15	13/17381	0.011165072	0.024278093	0.008601982	891	1
BP	GO:1903504	‘Regulation of mitotic spindle checkpoint’	1/15	13/17381	0.011165072	0.024278093	0.008601982	891	1
BP	GO:0000712	‘Resolution of meiotic recombination intermediates’	1/15	14/17381	0.012019087	0.025590639	0.00906703	7153	1
BP	GO:0048313	‘Golgi inheritance’	1/15	14/17381	0.012019087	0.025590639	0.00906703	983	1
BP	GO:0051382	‘Kinetochore assembly’	1/15	14/17381	0.012019087	0.025590639	0.00906703	1063	1
BP	GO:0097340	‘Inhibition of cysteine-type endopeptidase activity’	1/15	14/17381	0.012019087	0.025590639	0.00906703	332	1
BP	GO:0097341	‘Zymogen inhibition’	1/15	14/17381	0.012019087	0.025590639	0.00906703	332	1
BP	GO:0033002	‘Muscle cell proliferation’	2/15	199/17381	0.012416276	0.026326627	0.009327798	891/983	2
BP	GO:0048308	‘Organelle inheritance’	1/15	15/17381	0.012872413	0.027069148	0.009590881	983	1
BP	GO:0090231	‘Regulation of spindle checkpoint’	1/15	15/17381	0.012872413	0.027069148	0.009590881	891	1
BP	GO:0007100	‘Mitotic centrosome separation’	1/15	16/17381	0.013725051	0.028743856	0.010184248	6790	1
BP	GO:0048738	‘Cardiac muscle tissue development’	2/15	215/17381	0.014383811	0.03000052	0.010629497	891/983	2
BP	GO:0051299	‘Centrosome separation’	1/15	17/17381	0.014577002	0.030279869	0.010728474	6790	1
BP	GO:0009636	‘Response to toxic substance’	2/15	222/17381	0.015284717	0.031621419	0.011203799	891/983	2
BP	GO:0051307	‘Meiotic chromosome separation’	1/15	18/17381	0.015428265	0.031662022	0.011218185	7153	1
BP	GO:0051383	‘Kinetochore organization’	1/15	18/17381	0.015428265	0.031662022	0.011218185	1063	1
BP	GO:0007095	‘Mitotic G2 DNA damage checkpoint’	1/15	19/17381	0.016278843	0.033009876	0.011695743	983	1
BP	GO:0007096	‘Regulation of exit from mitosis’	1/15	19/17381	0.016278843	0.033009876	0.011695743	11065	1
BP	GO:0060074	‘Synapse maturation’	1/15	19/17381	0.016278843	0.033009876	0.011695743	991	1
BP	GO:0033158	‘Regulation of protein import into nucleus, translocation’	1/15	20/17381	0.017128734	0.034595981	0.012257717	983	1
BP	GO:0007281	‘Germ cell development’	2/15	241/17381	0.017850247	0.035885655	0.012714662	6790/891	2
BP	GO:0010971	‘Positive regulation of G2/M transition of mitotic cell cycle’	1/15	21/17381	0.017977941	0.035885655	0.012714662	983	1
BP	GO:0031440	‘Regulation of mRNA 3’-end processing’	1/15	21/17381	0.017977941	0.035885655	0.012714662	891	1
BP	GO:0006352	‘DNA-templated transcription, initiation’	2/15	243/17381	0.018130364	0.036049089	0.012772568	891/983	2
BP	GO:1903429	‘Regulation of cell maturation’	1/15	22/17381	0.018826462	0.03728807	0.013211552	6790	1

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0010951	‘Negative regulation of endopeptidase activity’	2/15	250/17381	0.019125624	0.03773434	0.01336967	332/9232	2
BP	GO:0007064	‘Mitotic sister chromatid cohesion’	1/15	23/17381	0.019674299	0.038667564	0.013700322	991	1
BP	GO:0045927	‘Positive regulation of growth’	2/15	257/17381	0.020143781	0.03943859	0.013973504	891/983	2
BP	GO:0006266	‘DNA ligation’	1/15	24/17381	0.020521452	0.039571555	0.014020615	7153	1
BP	GO:0039694	‘Viral RNA genome replication’	1/15	24/17381	0.020521452	0.039571555	0.014020615	7153	1
BP	GO:0051642	‘Centrosome localization’	1/15	24/17381	0.020521452	0.039571555	0.014020615	6790	1
BP	GO:0051984	‘Positive regulation of chromosome segregation’	1/15	24/17381	0.020521452	0.039571555	0.014020615	891	1
BP	GO:1900542	‘Regulation of purine nucleotide metabolic process’	2/15	262/17381	0.020884902	0.040120996	0.014215288	891/983	2
BP	GO:0010466	‘Negative regulation of peptidase activity’	2/15	263/17381	0.021034503	0.040257045	0.014263491	332/9232	2
BP	GO:0021591	‘Ventricular system development’	1/15	25/17381	0.021367922	0.040365324	0.014301855	1063	1
BP	GO:0061842	‘Microtubule organizing center localization’	1/15	25/17381	0.021367922	0.040365324	0.014301855	6790	1
BP	GO:1902751	‘Positive regulation of cell cycle G2/M phase transition’	1/15	25/17381	0.021367922	0.040365324	0.014301855	983	1
BP	GO:0015980	‘Energy derivation by oxidation of organic compounds’	2/15	266/17381	0.021486043	0.040365324	0.014301855	891/983	2
BP	GO:0046034	‘ATP metabolic process’	2/15	266/17381	0.021486043	0.040365324	0.014301855	891/983	2
BP	GO:0006140	‘Regulation of nucleotide metabolic process’	2/15	269/17381	0.021941675	0.041070315	0.014551641	891/983	2
BP	GO:0051146	‘Striated muscle cell differentiation’	2/15	270/17381	0.022094458	0.041205357	0.014599488	891/983	2
BP	GO:0046688	‘Response to copper ion’	1/15	26/17381	0.022213709	0.04127711	0.014624911	983	1
BP	GO:0050685	‘Positive regulation of mRNA processing’	1/15	27/17381	0.023058814	0.042538101	0.015071693	891	1
BP	GO:0071539	‘Protein localization to centrosome’	1/15	27/17381	0.023058814	0.042538101	0.015071693	6790	1
BP	GO:0007143	‘Female meiotic nuclear division’	1/15	28/17381	0.023903237	0.043468164	0.015401224	6790	1
BP	GO:0044818	‘Mitotic G2/M transition checkpoint’	1/15	28/17381	0.023903237	0.043468164	0.015401224	983	1
BP	GO:0070979	‘Protein K11-linked ubiquitination’	1/15	28/17381	0.023903237	0.043468164	0.015401224	11065	1
BP	GO:1905508	‘Protein localization to microtubule organizing center’	1/15	28/17381	0.023903237	0.043468164	0.015401224	6790	1
BP	GO:0030262	‘Apoptotic nuclear changes’	1/15	29/17381	0.024746979	0.04484293	0.015888318	7153	1
BP	GO:0016579	‘Protein deubiquitination’	2/15	291/17381	0.025405986	0.045874414	0.016253783	983/991	2
BP	GO:0040020	‘Regulation of meiotic nuclear division’	1/15	30/17381	0.02559004	0.046044051	0.016313888	991	1
BP	GO:0009205	‘Purine ribonucleoside triphosphate metabolic process’	2/15	296/17381	0.026223002	0.046899191	0.016616873	891/983	2

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
BP	GO:0006921	'Cellular component disassembly involved in execution phase of apoptosis'	1/15	31/17381	0.026432421	0.046899191	0.016616873	7153	1
BP	GO:0008608	'Attachment of spindle microtubules to kinetochore'	1/15	31/17381	0.026432421	0.046899191	0.016616873	891	1
BP	GO:0010458	'Exit from mitosis'	1/15	31/17381	0.026432421	0.046899191	0.016616873	11065	1
BP	GO:0009199	'Ribonucleoside triphosphate metabolic process'	2/15	301/17381	0.027050804	0.047830314	0.016946779	891/983	2
BP	GO:0009144	'Purine nucleoside triphosphate metabolic process'	2/15	303/17381	0.027384923	0.048254124	0.017096939	891/983	2
BP	GO:0070646	'Protein modification by small protein removal'	2/15	306/17381	0.027889297	0.048973988	0.017351995	983/991	2
BP	GO:1901976	'Regulation of cell cycle checkpoint'	1/15	33/17381	0.028115144	0.049201501	0.017432605	891	1
BP	GO:0009167	'Purine ribonucleoside monophosphate metabolic process'	2/15	310/17381	0.028567725	0.049485799	0.017533335	891/983	2
BP	GO:0048638	'Regulation of developmental growth'	2/15	310/17381	0.028567725	0.049485799	0.017533335	891/983	2
BP	GO:0009126	'Purine nucleoside monophosphate metabolic process'	2/15	311/17381	0.028738386	0.049485799	0.017533335	891/983	2
BP	GO:0010039	'Response to iron ion'	1/15	34/17381	0.028955487	0.049485799	0.017533335	891	1
BP	GO:0014037	'Schwann cell differentiation'	1/15	34/17381	0.028955487	0.049485799	0.017533335	983	1
BP	GO:0045070	'Positive regulation of viral genome replication'	1/15	34/17381	0.028955487	0.049485799	0.017533335	7153	1
BP	GO:0045737	'Positive regulation of cyclin-dependent protein serine/threonine kinase activity'	1/15	34/17381	0.028955487	0.049485799	0.017533335	891	1
BP	GO:0019058	'Viral life cycle'	2/15	313/17381	0.029080968	0.049534583	0.017550619	7153/983	2
BP	GO:0001701	'In utero embryonic development'	2/15	315/17381	0.029425225	0.049954452	0.017699383	891/9133	2
CC	GO:0005819	'Spindle'	9/15	318/18511	$5.32\text{x}10^{-13}$	$2.66\text{x}10^{-11}$	$6.72\text{x}10^{-12}$	1063/22974/332/6790/701/891/9055/983/991	9
CC	GO:0000793	'Condensed chromosome'	7/15	216/18511	$1.59\text{x}10^{-10}$	$3.97\text{x}10^{-9}$	$1.00\text{x}10^{-9}$	1063/11130/332/6790/701/7153/891	7
CC	GO:0000779	'Condensed chromosome, centromeric region'	6/15	116/18511	$2.54\text{x}10^{-10}$	$4.23\text{x}10^{-9}$	$1.07\text{x}10^{-9}$	1063/11130/332/6790/701/891	6
CC	GO:0000922	'Spindle pole'	6/15	150/18511	$1.21\text{x}10^{-9}$	$1.51\text{x}10^{-8}$	$3.81\text{x}10^{-9}$	1063/22974/6790/891/9055/991	6
CC	GO:0098687	'Chromosomal region'	7/15	352/18511	$4.78\text{x}10^{-9}$	$4.31\text{x}10^{-8}$	$1.09\text{x}10^{-8}$	1063/11130/332/6790/701/891/983	7
CC	GO:0000775	'Chromosome, centromeric region'	6/15	191/18511	$5.17\text{x}10^{-9}$	$4.31\text{x}10^{-8}$	$1.09\text{x}10^{-8}$	1063/11130/332/6790/701/891	6

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
CC	GO:0000777	'Condensed chromosome kinetochore'	5/15	103/18511	1.39x10^{-8}	9.92x10^{-8}	2.51x10^{-8}	1063/11130/332/701/891	5
CC	GO:0000776	'Kinetochore'	5/15	133/18511	5.03x10^{-8}	3.15x10^{-7}	7.95x10^{-8}	1063/11130/332/701/891	5
CC	GO:0000940	'Condensed chromosome outer kinetochore'	3/15	12/18511	9.43x10^{-8}	5.24x10^{-7}	1.32x10^{-7}	1063/701/891	3
CC	GO:0030496	'Midbody'	5/15	160/18511	1.27x10^{-7}	6.34x10^{-7}	1.60x10^{-7}	1063/332/6790/9055/983	5
CC	GO:0005680	'Anaphase-promoting complex'	3/15	21/18511	5.68x10^{-7}	2.58x10^{-6}	6.52x10^{-7}	11065/701/991	3
CC	GO:0000780	'Condensed nuclear chromosome, centromeric region'	3/15	22/18511	6.57x10^{-7}	2.74x10^{-6}	6.91x10^{-7}	6790/701/891	3
CC	GO:0005813	'Centrosome'	6/15	469/18511	1.06x10^{-6}	4.06x10^{-6}	1.03x10^{-6}	1063/6790/891/9133/983/991	6
CC	GO:0000152	'Nuclear ubiquitin ligase complex'	3/15	40/18511	4.18x10^{-6}	1.49x10^{-5}	3.77x10^{-6}	11065/701/991	3
CC	GO:0005876	'Spindle microtubule'	3/15	52/18511	9.29x10^{-6}	3.10x10^{-5}	7.82x10^{-6}	6790/9055/983	3
CC	GO:0005874	'Microtubule'	5/15	393/18511	1.06x10^{-5}	3.31x10^{-5}	8.36x10^{-6}	22974/332/6790/9055/983	5
CC	GO:0000778	'Condensed nuclear chromosome kinetochore'	2/15	11/18511	3.36x10^{-5}	9.82x10^{-5}	2.48x10^{-5}	701/891	2
CC	GO:0072686	'Mitotic spindle'	3/15	81/18511	3.54x10^{-5}	9.82x10^{-5}	2.48x10^{-5}	22974/6790/983	3
CC	GO:0000794	'Condensed nuclear chromosome'	3/15	95/18511	5.70x10^{-5}	0.000149934	3.79x10^{-5}	6790/701/891	3
CC	GO:0045120	'Pronucleus'	2/15	15/18511	6.40x10^{-5}	0.000159907	4.04x10^{-5}	1063/6790	2
CC	GO:0051233	'Spindle midzone'	2/15	31/18511	0.00028115	0.000669406	0.000169113	6790/701	2
CC	GO:0031461	'Cullin-RING ubiquitin ligase complex'	3/15	177/18511	0.000359358	0.000816723	0.00020633	11065/701/991	3
CC	GO:0000307	'Cyclin-dependent protein kinase holoenzyme complex'	2/15	41/18511	0.000493477	0.001072776	0.000271017	891/983	2
CC	GO:0000151	'Ubiquitin ligase complex'	3/15	297/18511	0.001612375	0.003359115	0.000848618	11065/701/991	3
CC	GO:1902554	'Serine/threonine protein kinase complex'	2/15	85/18511	0.002104658	0.004209317	0.001063406	891/983	2
CC	GO:1902911	'Protein kinase complex'	2/15	99/18511	0.0028412	0.005463846	0.00138034	891/983	2
CC	GO:0005814	'Centriole'	2/15	124/18511	0.004414613	0.00817521	0.002065316	6790/7153	2
CC	GO:0005875	'Microtubule associated complex'	2/15	148/18511	0.006226953	0.01111956	0.002809152	332/6790	2
CC	GO:0044450	'Microtubule organizing center part'	2/15	166/18511	0.007773886	0.013025422	0.003290633	6790/7153	2
CC	GO:0070938	'Contractile ring'	1/15	10/18511	0.008075761	0.013025422	0.003290633	9055	1
CC	GO:0097539	'Ciliary transition fiber'	1/15	10/18511	0.008075761	0.013025422	0.003290633	1063	1
CC	GO:0033267	'Axon part'	2/15	181/18511	0.0091824	0.014347499	0.003624631	22974/6790	2
CC	GO:0031616	'Spindle pole centrosome'	1/15	12/18511	0.009683592	0.014672109	0.003706638	6790	1
CC	GO:0043073	'Germ cell nucleus'	1/15	19/18511	0.015291863	0.022488033	0.005681187	6790	1
CC	GO:0061695	'Transferase complex, transferring phosphorus-containing groups'	2/15	263/18511	0.018691956	0.026702794	0.006745969	891/983	2
CC	GO:0097431	'Mitotic spindle pole'	1/15	25/18511	0.020075344	0.027882423	0.00704398	6790	1
MF	GO:0035173	'Histone kinase activity'	3/15	17/17354	3.53x10^{-7}	2.43x10^{-5}	1.41x10^{-05}	6790/891/983	3

Table SIII. Continued.

A, GO functional enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
MF	GO:0004693	'Cyclin-dependent protein serine/ threonine kinase activity'	3/15	30/17354	$2.09x10^{-6}$	$5.32x10^{-5}$	$3.09x10^{-05}$	891/9133/983	3
MF	GO:0097472	'Cyclin-dependent protein kinase activity'	3/15	31/17354	$2.31x10^{-6}$	$5.32x10^{-5}$	$3.09x10^{-05}$	891/9133/983	3
MF	GO:0004674	'Protein serine/threonine kinase activity'	5/15	450/17354	$2.78x10^{-5}$	0.000479058	0.000277715	6790/701/891/9133/983	5
MF	GO:0008022	'Protein C-terminus binding'	3/15	180/17354	0.000455524	0.006286233	0.003644193	1063/7153/991	3
MF	GO:0004869	'Cysteine-type endopeptidase inhibitor activity'	2/15	58/17354	0.001120919	0.012890571	0.007472795	332/9232	2
MF	GO:0044389	'Ubiquitin-like protein ligase binding'	3/15	313/17354	0.002251022	0.022188648	0.012862984	11065/6790/891	3
MF	GO:0042826	'Histone deacetylase binding'	2/15	108/17354	0.003821624	0.032961508	0.019108121	7153/991	2

B, KEGG pathway enrichment

Ontology	ID	Description	Gene ratio	BgRatio	P-value	P.adjust	q-value	Gene ID	Count
MF	GO:0042826	'Histone deacetylase binding'	2/15	108/17354	0.003821624	0.032961508	0.019108121	7153/991	2
N/A	hsa04110	'Cell cycle'	6/10	124/7440	$3.78x10^{-9}$	$3.59x10^{-8}$	$1.39x10^{-08}$	701/891/9133/9232/983/991	6
N/A	hsa04114	'Oocyte meiosis'	6/10	124/7440	$3.78x10^{-9}$	$3.59x10^{-8}$	$1.39x10^{-08}$	6790/891/9133/9232/983/991	6
N/A	hsa04914	'Progesterone-mediated oocyte maturation'	4/10	99/7440	$5.83x10^{-6}$	$3.69x10^{-5}$	$1.43x10^{-05}$	6790/891/9133/983	4
N/A	hsa04115	'p53 signaling pathway'	3/10	72/7440	$9.93x10^{-5}$	0.000471862	0.000182994	891/9133/983	3
N/A	hsa05166	'Human T-cell leukemia virus 1 infection'	4/10	255/7440	0.000240453	0.000913722	0.000354352	701/9133/9232/991	4
N/A	hsa04218	'Cellular senescence'	3/10	160/7440	0.001048181	0.003319238	0.001287239	891/9133/983	3
N/A	hsa05170	'Human immunodeficiency virus 1 infection'	3/10	212/7440	0.002360359	0.006406689	0.002484589	891/9133/983	3
N/A	hsa01524	'Platinum drug resistance'	2/10	73/7440	0.004061202	0.009645356	0.003740581	332/7153	2
N/A	hsa04068	'FoxO signaling pathway'	2/10	132/7440	0.012807013	0.026124999	0.010131579	891/9133	2
N/A	hsa04120	'Ubiquitin mediated proteolysis'	2/10	137/7440	0.01375	0.026124999	0.010131579	11065/991	2
N/A	hsa05203	'Viral carcinogenesis'	2/10	201/7440	0.028333822	0.048940238	0.018979594	983/991	2