Supplementary table S1. Cell cycle genes

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
1	GSK3B	ENSG00000082701	2932	4617	BC012760	glycogen synthase kinase 3 beta	3q13.3
2	SKP2	ENSG00000145604	6502	10901	U33761	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase	5p13
3	ABL1	ENSG00000097007	25	76	M14752	ABL proto-oncogene 1, non-receptor tyrosine kinase	9q34.1
4	CCND2	ENSG00000118971	894	1583	AF518005	cyclin D2	12p13
5	CCND3	ENSG00000112576	896	1585		cyclin D3	6p21
6	CCNE1	ENSG00000105173	898	1589	M73812	cyclin E1	19q12
7	CCNE2	ENSG00000175305	9134	1590	AF091433	cyclin E2	8q22.1
8	CDC25A	ENSG00000164045	993	1725	M81933	cell division cycle 25A	3p21
9	CDK4	ENSG00000135446	1019	1773	M14505	cyclin-dependent kinase 4	12q13
10	CDK6	ENSG00000105810	1021	1777		cyclin-dependent kinase 6	7q21-q22
11	CDKN1A	ENSG00000124762	1026	1784	U03106	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	6p21.1
12	CDKN1B	ENSG00000111276	1027	1785	AF480891	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	12p13.1-p12
13	CDKN2A	ENSG00000147889	1029	1787	L27211	cyclin-dependent kinase inhibitor 2A	9p21
14	E2F1	ENSG00000101412	1869	3113		E2F transcription factor 1	20q11
15	E2F2	ENSG00000007968	1870	3114	L22846	E2F transcription factor 2	1p36
16	E2F3	ENSG00000112242	1871	3115	Y10479	E2F transcription factor 3	6p22
17	E2F4	ENSG00000205250	1874	3118	BC021050	E2F transcription factor 4, p107/p130-binding	16q22.1
18	E2F5	ENSG00000133740	1875	3119	X86097	E2F transcription factor 5, p130-binding	8q21.2
19	HDAC1	ENSG00000116478	3065	4852	D50405	histone deacetylase 1	1p34
20	HDAC2	ENSG00000196591	3066	4853	U31814	histone deacetylase 2	6q21
21	MCM6	ENSG00000076003	4175	6949		minichromosome maintenance complex component 6	2q14-q21
22	PTTG1	ENSG00000164611	9232	9690	AF062649	pituitary tumor-transforming 1	5q35.1
23	RB1	ENSG00000139687	5925	9884	M15400	retinoblastoma 1	13q14.2
24	RBL1	ENSG00000080839	5933	9893	L14812	retinoblastoma-like 1	20q11.23
25	SMAD3	ENSG00000166949	4088	6769	BC050743	SMAD family member 3	15q21-q22
26	SMAD4	ENSG00000141646	4089	6770	U44378	SMAD family member 4	18q21.1
27	TFDP1	ENSG00000198176	7027	11749	BC011685	transcription factor Dp-1	13q34
28	TGFB1	ENSG00000105329	7040	11766	X02812	transforming growth factor, beta 1	19q13.1
29	E2F6	ENSG00000169016	1876	3120	AF041381	E2F transcription factor 6	2p25.1
30	HDAC3	ENSG00000171720	8841	4854	AF059650	histone deacetylase 3	5q31.1-q31.2
31	HDAC4	ENSG00000068024	9759	14063	AB006626	histone deacetylase 4	2q37.3
32	HDAC5	ENSG00000108840	10014	14068	AF249731	histone deacetylase 5	17q21
33	HDAC6	ENSG00000094631	10013	14064	AF132609	histone deacetylase 6	Xp11.23
34	HDAC8	ENSG00000147099	55869	13315	AF230097	histone deacetylase 8	Xq13

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
35	UBE2F	ENSG00000184182	140739	12480	BC010549	ubiquitin-conjugating enzyme E2F (putative)	2q37.3
36	HSPA8	ENSG00000109971	3312	5241	Y00371	heat shock 70kDa protein 8	11q24.1
37	SORBS2	ENSG00000154556	8470	24098		sorbin and SH3 domain containing 2	4q35.1
38	NXF1	ENSG00000162231	10482	8071	AF112880	nuclear RNA export factor 1	11q12-q13
39	CDKN3	ENSG00000100526	1033	1791	U02681	cyclin-dependent kinase inhibitor 3	14q22
40	UBE2D3	ENSG00000109332	7323	12476	U39318	ubiquitin-conjugating enzyme E2D 3	4q24
41	ZNF248	ENSG00000198105	57209	13041	AJ491695	zinc finger protein 248	10p11.21
42	AFAP1	ENSG00000196526	60312	24017	AB209676	actin filament associated protein 1	4p16
43	MSL1	ENSG00000188895	339287	27905		male-specific lethal 1 homolog (Drosophila)	17q21.1
44	GSE1	ENSG00000131149	23199	28979	D80004	Gse1 coiled-coil protein	16q24.1
45	TSC22D1	ENSG00000102804	8848	16826	AJ222700	TSC22 domain family, member 1	13q14
46	LARP1	ENSG00000155506	23367	29531	AB018274	La ribonucleoprotein domain family, member 1	5q33.2
47	HIF1A	ENSG00000100644	3091	4910	U22431	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	14q23.2
48	DDX58	ENSG00000107201	23586	19102	AF038963	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	9p12
49	ANTXR1	ENSG00000169604	84168	21014	AF421380	anthrax toxin receptor 1	2p13.1
50	ETV4	ENSG00000175832	2118	3493	U18018	ets variant 4	17q21
51	IFIT2	ENSG00000119922	3433	5409	M14660	interferon-induced protein with tetratricopeptide repeats 2	10q23.31
52	SEPHS1	ENSG00000086475	22929	19685	BC000941	selenophosphate synthetase 1	10p14
53	DYNLL1	ENSG00000088986	8655	15476	U32944	dynein, light chain, LC8-type 1	12q24.23
54	SLC39A10	ENSG00000196950	57181	20861		solute carrier family 39 (zinc transporter), member 10	2q33.1
55	NCOA3	ENSG00000124151	8202	7670	AF012108	nuclear receptor coactivator 3	20q12
56	CNIH4	ENSG00000143771	29097	25013		cornichon family AMPA receptor auxiliary protein 4	1q42.12
57	DNAJB6	ENSG00000105993	10049	14888	AB014888	DnaJ (Hsp40) homolog, subfamily B, member 6	7q36.3
58	DKC1	ENSG00000130826	1736	2890	AJ224481	dyskeratosis congenita 1, dyskerin	Xq28
59	AOC2	ENSG00000131480	314	549	AF081363	amine oxidase, copper containing 2 (retina-specific)	17q21
60	XPR1	ENSG00000143324	9213	12827	AF099082	xenotropic and polytropic retrovirus receptor 1	1q25.1
61	RPL37	ENSG00000145592	6167	10347	L11567	ribosomal protein L37	5p13.1
62	OPN3	ENSG00000054277	23596	14007	AF140242	opsin 3	1q43
63	KMO	ENSG00000117009	8564	6381	AF056032	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	1q42-q44
64	TMED7	ENSG00000134970	51014	24253	AK074962	transmembrane emp24 protein transport domain containing 7	5q22.3
65	GRPEL1	ENSG00000109519	80273	19696	AF070525	GrpE-like 1, mitochondrial (E. coli)	4p16
66	ZCCHC14	ENSG00000140948	23174	24134	AB011151	zinc finger, CCHC domain containing 14	16q24.2
67	NR2F6	ENSG00000160113	2063	7977	X12794	nuclear receptor subfamily 2, group F, member 6	19p13.11

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
68	FAM189B	ENSG00000160767	10712	1233	AF070550	family with sequence similarity 189, member B	1q21
69	FAM84B	ENSG00000168672	157638	24166	AJ417849	family with sequence similarity 84, member B	8q24.13
70	HSPA4	ENSG00000170606	3308	5237	AB023420	heat shock 70kDa protein 4	5q31.1
71	HIST2H2BE	ENSG00000184678	8349	4760	AY131979	histone cluster 2, H2be	1q21.2
72	SLC1A3	ENSG00000079215	6507	10941		solute carrier family 1 (glial high affinity glutamate transporter), member 3	5p13
73	RSRP1	ENSG00000117616	57035	25234		arginine/serine-rich protein 1	1p36.13-p35.1
74	HORMAD1	ENSG00000143452	84072	25245	AL136755	HORMA domain containing 1	1q21.2
75	XBP1	ENSG00000100219	7494	12801	M31627	X-box binding protein 1	22q12.1
76	SLBP	ENSG00000163950	7884	10904	Z71188	stem-loop binding protein	4p16.3
77	CDCA7	ENSG00000144354	83879	14628	BG354580	cell division cycle associated 7	2q31.1
78	UNG	ENSG00000076248	7374	12572	A64377	uracil-DNA glycosylase	12q23-q24.1
79	ZNF367	ENSG00000165244	195828	18320	AK091289	zinc finger protein 367	9q22
80	PLCXD1	ENSG00000182378	55344	23148	AK002185	phosphatidylinositol-specific phospholipase C, X domain containing 1	Xp22.33 and Yp11.32
81	ZRANB2	ENSG00000132485	9406	13058	AF065391	zinc finger, RAN-binding domain containing 2	1p31
82	NASP	ENSG00000132780	4678	7644	M97856	nuclear autoantigenic sperm protein (histone-binding)	1p34.1
83	INTS8	ENSG00000164941	55656	26048	AK091278	integrator complex subunit 8	8q22.1
84	DTL	ENSG00000143476	51514	30288	AF195765	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	1q32
85	TRMT2A	ENSG00000099899	27037	24974	BC017184	tRNA methyltransferase 2 homolog A (S. cerevisiae)	22q11.21
86	ALKBH7	ENSG00000125652	84266	21306	AY427650	alkB, alkylation repair homolog 7 (E. coli)	19p13.3
87	IVNS1ABP	ENSG00000116679	10625	16951	AB020657	influenza virus NS1A binding protein	1q25.1-q31.1
88	MAP2K6	ENSG00000108984	5608	6846	U39064	mitogen-activated protein kinase kinase 6	17q
89	ANAPC1	ENSG00000153107	64682	19988	AJ278357	anaphase promoting complex subunit 1	2q12.1
90	ANAPC11	ENSG00000141552	51529	14452	AF247565	anaphase promoting complex subunit 11	17q25.3
91	ANAPC13	ENSG00000129055	25847	24540	AF086169	anaphase promoting complex subunit 13	3q22.1
92	ANAPC2	ENSG00000176248	29882	19989	AB037827	anaphase promoting complex subunit 2	9q34.3
93	ANAPC4	ENSG00000053900	29945	19990	AF191338	anaphase promoting complex subunit 4	4p15.31
94	ANAPC7	ENSG00000196510	51434	17380	AF191340	anaphase promoting complex subunit 7	12q13.12
95	CDC26	ENSG00000176386	246184	17839	AF503918	cell division cycle 26	9q32
96	MYC	ENSG00000136997	4609	7553		v-myc avian myelocytomatosis viral oncogene homolog	8q24
97	RBL2	ENSG00000103479	5934	9894	X74594	retinoblastoma-like 2	16q12.2
98	SKP1	ENSG00000113558	6500	10899	U33760	S-phase kinase-associated protein 1	5q31
99	TGFB2	ENSG00000092969	7042	11768	M19154	transforming growth factor, beta 2	1q41

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
100	TGFB3	ENSG00000119699	7043	11769		transforming growth factor, beta 3	14q24
101	CDC6	ENSG00000094804	990	1744	U77949	cell division cycle 6	17q21.3
102	CDK2	ENSG00000123374	1017	1771	M68520	cyclin-dependent kinase 2	12q13
103	MCM2	ENSG00000073111	4171	6944	X67334	minichromosome maintenance complex component 2	3q21
104	MCM5	ENSG00000100297	4174	6948		minichromosome maintenance complex component 5	22q13.1-q13.2
105	ORC1	ENSG00000085840	4998	8487		origin recognition complex, subunit 1	1p32
106	PCNA	ENSG00000132646	5111	8729	J04718	proliferating cell nuclear antigen	20p13-p12.3
107	PKMYT1	ENSG00000127564	9088	29650	AK097642	protein kinase, membrane associated tyrosine/threonine 1	16p13.3
108	MBOAT1	ENSG00000172197	154141	21579	AK093994	membrane bound O-acyltransferase domain containing 1	6p22.3
109	SERPINB4	ENSG00000206073	6318	10570	X89015	serpin peptidase inhibitor, clade B (ovalbumin), member 4	18q21.33
110	CREBZF	ENSG00000137504	58487	24905	AF039942	CREB/ATF bZIP transcription factor	11q14.1
111	GMNN	ENSG00000112312	51053	17493	AF067855	geminin, DNA replication inhibitor	6p21.32
112	MSH2	ENSG00000095002	4436	7325	U03911	mutS homolog 2	2p21
113	WDR76	ENSG00000092470	79968	25773	AK023035	WD repeat domain 76	15q15.3
114	ATRIP		84126	33499	AF451323	ATR interacting protein	3p21.31
115	UBR5	ENSG00000104517	51366	16806	AF006010	ubiquitin protein ligase E3 component n-recognin 5	8q22
116	FAM111B	ENSG00000189057	374393	24200	BC062456	family with sequence similarity 111, member B	11q12.1
117	GINS2	ENSG00000131153	51659	24575	BC003186	GINS complex subunit 2 (Psf2 homolog)	16q24.1
118	ANKRD10	ENSG00000088448	55608	20265	AK000100	ankyrin repeat domain 10	13q33.3
119	DNAH11	ENSG00000105877	8701	2942	U83569	dynein, axonemal, heavy chain 11	7p21
120	ZNF414	ENSG00000133250	84330	20630	AK074191	zinc finger protein 414	19p13.2
121	ARGLU1	ENSG00000134884	55082	25482	BC071587	arginine and glutamate rich 1	13q33.3
122	CDCA7L	ENSG00000164649	55536	30777		cell division cycle associated 7-like	7p15.3
123	FAM214A	ENSG00000047346	56204	25609	AB037791	family with sequence similarity 214, member A	15q21.2-q21.3
124	POLD3	ENSG00000077514	10714	20932	D26018	polymerase (DNA-directed), delta 3, accessory subunit	11q14
125	RUNX1	ENSG00000159216	861	10471	X79549	runt-related transcription factor 1	21q22.3
126	CHAF1B	ENSG00000159259	8208	1911	U20980	chromatin assembly factor 1, subunit B (p60)	21q22.2
127	UBR7	ENSG00000012963	55148	20344	AK001345	ubiquitin protein ligase E3 component n-recognin 7 (putative)	14q32.12
128	RFC4	ENSG00000163918	5984	9972		replication factor C (activator 1) 4, 37kDa	3q27
129	FEN1	ENSG00000168496	2237	3650	L37374	flap structure-specific endonuclease 1	11q12
130	DONSON	ENSG00000159147	29980	2993	AF000002	downstream neighbor of SON	21q22.1
131	CLSPN	ENSG00000092853	63967	19715	AF297866	claspin	1p34.3
132	PAQR4	ENSG00000162073	124222	26386		progestin and adipoQ receptor family member IV	16p13
133	SLC25A29	ENSG00000197119	123096	20116	AK095532	solute carrier family 25 (mitochondrial carnitine/acylcarnitine carrier)	14q32.2

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
134	DSCC1	ENSG00000136982	79075	24453		DNA replication and sister chromatid cohesion 1	8q24.12
135	RBBP8	ENSG00000101773	5932	9891	AF043431	retinoblastoma binding protein 8	18q11.2
136	ANAPC10	ENSG00000164162	10393	24077	AF132794	anaphase promoting complex subunit 10	4q31
137	CCND1	ENSG00000110092	595	1582	Z23022	cyclin D1	11q13
138	CDKN2D	ENSG00000129355	1032	1790		cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	19p13
139	CREBBP	ENSG00000005339	1387	2348	U85962	CREB binding protein	16p13.3
140	CUL1	ENSG00000055130	8454	2551	U58087	cullin 1	7q36.1
141	DBF4	ENSG00000006634	10926	17364	AF160876	DBF4 zinc finger	7q21.3
142	RBX1	ENSG00000100387	9978	9928	AF140598	ring-box 1, E3 ubiquitin protein ligase	22q13.2
143	SMAD2	ENSG00000175387	4087	6768	U65019	SMAD family member 2	18q21
144	ATM	ENSG00000149311	472	795	AB209133	ATM serine/threonine kinase	11q22-q23
145	ATR	ENSG00000175054	545	882	U76308	ATR serine/threonine kinase	3q23
146	CCNH	ENSG00000134480	902	1594	U12685	cyclin H	5q13.3-q14
147	CDC7	ENSG00000097046	8317	1745	AF015592	cell division cycle 7	1p22
148	EP300	ENSG00000100393	2033	3373	U01877	E1A binding protein p300	22q13.2
149	GADD45A	ENSG00000116717	1647	4095	M60974	growth arrest and DNA-damage-inducible, alpha	1p31.2
150	MCM3	ENSG00000112118	4172	6945	X62153	minichromosome maintenance complex component 3	6p12
151	MCM7	ENSG00000166508	4176	6950		minichromosome maintenance complex component 7	7q21.3-q22.1
152	MDM2	ENSG00000135679	4193	6973		MDM2 proto-oncogene, E3 ubiquitin protein ligase	12q13-q14
153	ORC2	ENSG00000115942	4999	8488		origin recognition complex, subunit 2	2q33
154	ORC3	ENSG00000135336	23595	8489	AF093535	origin recognition complex, subunit 3	6q
155	ORC4	ENSG00000115947	5000	8490	AF022108	origin recognition complex, subunit 4	2q22-q23
156	ORC5	ENSG00000164815	5001	8491		origin recognition complex, subunit 5	7q22.1
157	ORC6	ENSG00000091651	23594	17151	AF139658	origin recognition complex, subunit 6	16q12
158	PRKDC	ENSG00000253729	5591	9413		protein kinase, DNA-activated, catalytic polypeptide	8q11
159	TP53	ENSG00000141510	7157	11998	AF307851	tumor protein p53	17p13.1
160	ARF1	ENSG00000143761	375	652	M84326	ADP-ribosylation factor 1	1q42.13
161	MCM10	ENSG00000065328	55388	18043	AB042719	minichromosome maintenance complex component 10	10p13
162	MCM8	ENSG00000125885	84515	16147	AJ439063	minichromosome maintenance complex component 8	20p12.3
163	MCM9	ENSG00000111877	254394	21484	BC031658	minichromosome maintenance complex component 9	6q22.31
164	CDKN2AIP	ENSG00000168564	55602	24325	AK000043	CDKN2A interacting protein	4q35.1
165	HELLS	ENSG00000119969	3070	4861	AF155827	helicase, lymphoid-specific	10q24.2
166	TOPBP1	ENSG00000163781	11073	17008	AB019397	topoisomerase (DNA) II binding protein 1	3q22.1
167	HSPB8	ENSG00000152137	26353	30171	AF191017	heat shock 22kDa protein 8	12q24.23

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
168	ATAD2	ENSG00000156802	29028	30123	BC019909	ATPase family, AAA domain containing 2	8q24.13
169	WDR90	ENSG00000161996	197335	26960	AB067511	WD repeat domain 90	16p13.3
170	RFC2	ENSG00000049541	5982	9970		replication factor C (activator 1) 2, 40kDa	7q11.23
171	CENPU	ENSG00000151725	79682	21348	AK027121, AF516710	centromere protein U	4q35.1
172	LIPH	ENSG00000163898	200879	18483	AY093498	lipase, member H	3q27
173	ABCC5	ENSG00000114770	10057	56	AF104942	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	3q27
174	CENPQ	ENSG00000031691	55166	21347	AK001407	centromere protein Q	6p12.3
175	USP1	ENSG00000162607	7398	12607		ubiquitin specific peptidase 1	1p31.3
176	IER5	ENSG00000162783	51278	5393	BC000128	immediate early response 5	1q25.3
177	EFHC1	ENSG00000096093	114327	16406	AK001328	EF-hand domain (C-terminal) containing 1	6p12.3
178	RHPN1	ENSG00000158106	114822	19973	AB067516	rhophilin, Rho GTPase binding protein 1	8q24.3
179	RAD54L	ENSG00000085999	8438	9826	X97795	RAD54-like (S. cerevisiae)	1p32
180	ACTR2	ENSG00000138071	10097	169	AF006082	ARP2 actin-related protein 2 homolog (yeast)	2p14
181	E2F8	ENSG00000129173	79733	24727		E2F transcription factor 8	11p15
182	DHFRL1	ENSG00000178700	200895	27309	AL832912	dihydrofolate reductase-like 1	3q11.2
183	ASF1B	ENSG00000105011	55723	20996	AF279307	anti-silencing function 1B histone chaperone	19p13.12
184	CDH24	ENSG00000139880	64403	14265	AL137477	cadherin 24, type 2	14q11.2
185	MASTL	ENSG00000120539	84930	19042	BC009107	microtubule associated serine/threonine kinase-like	10p12.1
186	TCEB3	ENSG00000011007	6924	11620	L47345	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	1p36.1
187	EXO1	ENSG00000174371	9156	3511	AF042282	exonuclease 1	1q43
188	EZH2	ENSG00000106462	2146	3527		enhancer of zeste 2 polycomb repressive complex 2 subunit	7q35-q36
189	SH3GL2	ENSG00000107295	6456	10831	X99657	SH3-domain GRB2-like 2	9p22
190	C5orf42	ENSG00000197603	65250	25801		chromosome 5 open reading frame 42	5p13.2
191	BRCA1	ENSG00000012048	672	1100	U14680	breast cancer 1, early onset	17q21.31
192	HIST1H2AC	ENSG00000180573	8334	4733	Z80778	histone cluster 1, H2ac	6p22.1
193	ASIP	ENSG00000101440	434	745		agouti signaling protein	20q11.2-q12
194	RRM2	ENSG00000171848	6241	10452		ribonucleotide reductase M2	2p25-p24
195	HIST1H4C	ENSG00000197061	8364	4787	X60486	histone cluster 1, H4c	6p22.1
196	CHEK1	ENSG00000149554	1111	1925	AF016582, BC017575	checkpoint kinase 1	11q24.2
197	CDC45	ENSG00000093009	8318	1739	AF053074	cell division cycle 45	22q11.21
198	TFDP2	ENSG00000114126	7029	11751	U18422	transcription factor Dp-2 (E2F dimerization partner 2)	3q23
199	ZBTB17	ENSG00000116809	7709	12936	U20647	zinc finger and BTB domain containing 17	1p36.13

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
200	BUB1	ENSG00000169679	699	1148	AF046078	BUB1 mitotic checkpoint serine/threonine kinase	2q13
201	BUB1B	ENSG00000156970	701	1149	AF107297	BUB1 mitotic checkpoint serine/threonine kinase B	15q15
202	BUB3	ENSG00000154473	9184	1151	AF053304	BUB3 mitotic checkpoint protein	10q24
203	CCNA2	ENSG00000145386	890	1578		cyclin A2	4q27
204	CDC25B	ENSG00000101224	994	1726		cell division cycle 25B	20p13
205	CDC25C	ENSG00000158402	995	1727	M34065	cell division cycle 25C	5q31
206	CDK1	ENSG00000170312	983	1722	BC014563	cyclin-dependent kinase 1	10q21.2
207	CDKN2C	ENSG00000123080	1031	1789	BC000598	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	1p32.3
208	ESPL1	ENSG00000135476	9700	16856	D79987	extra spindle pole bodies homolog 1 (S. cerevisiae)	12q13.13
209	FZR1	ENSG00000105325	51343	24824	AF083810	fizzy/cell division cycle 20 related 1 (Drosophila)	19p13.3
210	MAD2L1	ENSG00000164109	4085	6763	U65410	MAD2 mitotic arrest deficient-like 1 (yeast)	4q27
211	PLK1	ENSG00000166851	5347	9077		polo-like kinase 1	16p
212	TTK	ENSG00000112742	7272	12401		TTK protein kinase	6q14.1
213	YWHAB	ENSG00000166913	7529	12849	X57346	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta	20q13.1
214	YWHAE	ENSG00000108953	7531	12851	U54778	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon	17p13.3
215	YWHAG	ENSG00000170027	7532	12852	AF142498	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma	7q11.23
216	YWHAH	ENSG00000128245	7533	12853	X78138	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta	22q12.1-q13.1
217	YWHAQ	ENSG00000134308	10971	12854	AF070556	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta	2p25.2-p25.1
218	YWHAZ	ENSG00000164924	7534	12855	U28964	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	8q22.3
219	MPEG1	ENSG00000197629	219972	29619	AK097211	macrophage expressed 1	11q12.1
220	SREK1	ENSG00000153914	140890	17882	AF459094	splicing regulatory glutamine/lysine-rich protein 1	5q11.2-q12.1
221	H1F0	ENSG00000189060	3005	4714	X03473	H1 histone family, member 0	22q13.1
222	ANKRD36C	ENSG00000174501	400986	32946	AL832836	ankyrin repeat domain 36C	2q11.1
223	INSIG2	ENSG00000125629	51141	20452	AF527632	insulin induced gene 2	2q14.1
224	YEATS4	ENSG00000127337	8089	24859	AJ245746	YEATS domain containing 4	12q13-q15
225	UBE2T	ENSG00000077152	29089	25009	AF161499	ubiquitin-conjugating enzyme E2T	1q32.1
226	RAD51AP1	ENSG00000111247	10635	16956	AF006259	RAD51 associated protein 1	12p13.2-p13.1
227	CDCA5	ENSG00000146670	113130	14626	BG354578	cell division cycle associated 5	11q13.1
228	FANCI	ENSG00000140525	55215	25568	BC004277	Fanconi anemia, complementation group I	15q26.1
229	ZWINT	ENSG00000122952	11130	13195	AF067656	ZW10 interacting kinetochore protein	10q21-q22

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
230	RHOBTB3	ENSG00000164292	22836	18757	AB020685	Rho-related BTB domain containing 3	5q15
231	GOLGA8A	ENSG00000175265	23015	31972	BX648160	golgin A8 family, member A	15q14
232	NFE2L2	ENSG00000116044	4780	7782		nuclear factor, erythroid 2-like 2	2q31
233	ESCO2	ENSG00000171320	157570	27230	AF306679	establishment of sister chromatid cohesion N-acetyltransferase 2	8p21.1
234	CDKL5	ENSG00000008086	6792	11411	Y15057	cyclin-dependent kinase-like 5	Xp22
235	VPS25	ENSG00000131475	84313	28122	AB014763	vacuolar protein sorting 25 homolog (S. cerevisiae)	17q21.31
236	POLQ	ENSG00000051341	10721	9186	AF052573	polymerase (DNA directed), theta	3q13.3
237	H2AFX	ENSG00000188486	3014	4739	X14850	H2A histone family, member X	11q23.3
238	MSH5	ENSG00000204410	4439	7328	AF070071	mutS homolog 5	6p21.3
239	KLF6	ENSG00000067082	1316	2235	U51869	Kruppel-like factor 6	10p15
240	HRSP12	ENSG00000132541	10247	16897	BC008418	heat-responsive protein 12	8q22
241	DCTPP1	ENSG00000179958	79077	28777	BC001344	dCTP pyrophosphatase 1	16p11.2
242	GCLM	ENSG00000023909	2730	4312	L35546	glutamate-cysteine ligase, modifier subunit	1p21
243	HLA-DRA	ENSG00000204287	3122	4947		major histocompatibility complex, class II, DR alpha	6p21.3
244	MND1	ENSG00000121211	84057	24839	AY028916	meiotic nuclear divisions 1 homolog (S. cerevisiae)	4q31.3
245	PCBP1	ENSG00000169564	5093	8647		poly(rC) binding protein 1	2p13-p12
246	STIL	ENSG00000123473	6491	10879	M74558	SCL/TAL1 interrupting locus	1p32
247	NEIL3	ENSG00000109674	55247	24573	AB079071	nei endonuclease VIII-like 3 (E. coli)	4q34
248	FANCD2	ENSG00000144554	2177	3585	AF340183	Fanconi anemia, complementation group D2	3p25.3
249	SKA3	ENSG00000165480	221150	20262	AF361358	spindle and kinetochore associated complex subunit 3	13q11
250	PNRC2	ENSG00000189266	55629	23158	AF151042	proline-rich nuclear receptor coactivator 2	1p36.11
251	TUBB	ENSG00000196230	203068	20778	AB062393	tubulin, beta class I	6p21.33
252	TIMP1	ENSG00000102265	7076	11820		TIMP metallopeptidase inhibitor 1	Xp11.3-p11.23
253	NDC80	ENSG00000080986	10403	16909	AF017790	NDC80 kinetochore complex component	18p11.31
254	CENPL	ENSG00000120334	91687	17879	BC033154, BC019022, AK055606	centromere protein L	1q25.1
255	IRAK1	ENSG00000184216	3654	6112	L76191	interleukin-1 receptor-associated kinase 1	Xq28
256	HJURP	ENSG00000123485	55355	25444		Holliday junction recognition protein	2q37.1
257	STK17B	ENSG00000081320	9262	11396	AB011421	serine/threonine kinase 17b	2q33.1
258	STAT1	ENSG00000115415	6772	11362		signal transducer and activator of transcription 1, 91kDa	2q32.2-q32.3
259	CDCA2	ENSG00000184661	157313	14623	BG354575	cell division cycle associated 2	8p21.2
260	ARHGAP11A	ENSG00000198826	9824	15783	D87717	Rho GTPase activating protein 11A	15q13.3

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
261	KIFC1	ENSG00000237649	3833	6389	D14678	kinesin family member C1	6p21.32
262	CYP4V2	ENSG00000145476	285440	23198	AK022114	cytochrome P450, family 4, subfamily V, polypeptide 2	4q35.2
263	TUBB2A	ENSG00000137267	7280	12412	AY159127	tubulin, beta 2A class IIa	6p25.2
264	ARHGAP11B	ENSG00000187951	89839	15782	BC105788	Rho GTPase activating protein 11B	15q13.2
265	CKAP2L	ENSG00000169607	150468	26877	AL832036	cytoskeleton associated protein 2-like	2q13
266	MEPCE	ENSG00000146834	56257	20247	AF264752	methylphosphate capping enzyme	7q22.1
267	COQ6	ENSG00000119723	51004	20233	AF132944	coenzyme Q6 monooxygenase	14q24.1
268	TUBB4B	ENSG00000188229	10383	20771	BC019359	tubulin, beta 4B class IVb	9q34.3
269	WISP1	ENSG00000104415	8840	12769	AF100779	WNT1 inducible signaling pathway protein 1	8q24.22
270	IL6	ENSG00000136244	3569	6018	M18403	interleukin 6	7p21-p15
271	WSB1	ENSG00000109046	26118	19221	AF069313	WD repeat and SOCS box containing 1	17q11.2
272	HMGB2	ENSG00000164104	3148	5000		high mobility group box 2	4q31
273	MELK	ENSG00000165304	9833	16870	D79997	maternal embryonic leucine zipper kinase	9p13.1
274	GAS1	ENSG00000180447	2619	4165		growth arrest-specific 1	9q21.3-q22
275	AURKB	ENSG00000178999	9212	11390	AF004022	aurora kinase B	17p13.1
276	TUBA4A	ENSG00000127824	7277	12407	AK054731	tubulin, alpha 4a	2q36.1
277	RGS3	ENSG00000138835	5998	9999	AF006610	regulator of G-protein signaling 3	9q32
278	KIF11	ENSG00000138160	3832	6388	X85137	kinesin family member 11	10q24.1
279	SCYL1	ENSG00000142186	57410	14372	AF225424	SCY1-like 1 (S. cerevisiae)	11q11-q12
280	KIAA1524	ENSG00000163507	57650	29302	AB040957	KIAA1524	3q13.13
281	NNMT	ENSG00000166741	4837	7861	U08021	nicotinamide N-methyltransferase	11q23.1
282	LTBP3	ENSG00000168056	4054	6716	AF135960	latent transforming growth factor beta binding protein 3	11q12
283	MGAT2	ENSG00000168282	4247	7045	U15128	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	14q21
284	CASP3	ENSG00000164305	836	1504	BC016926	caspase 3, apoptosis-related cysteine peptidase	4q34
285	HP1BP3	ENSG00000127483	50809	24973	BC053327	heterochromatin protein 1, binding protein 3	1p36.12
286	TUBA3D	ENSG00000075886	113457	24071	K03460	tubulin, alpha 3d	2q21.1
287	UBE2C	ENSG00000175063	11065	15937	U73379	ubiquitin-conjugating enzyme E2C	20q13.12
288	ARL4A	ENSG00000122644	10124	695	U73960	ADP-ribosylation factor-like 4A	7p21.3
289	IQGAP3	ENSG00000183856	128239	20669	AY253300	IQ motif containing GTPase activating protein 3	1q21.3
290	FAM72A	ENSG00000196550	729533	24044	CR407567	family with sequence similarity 72, member A	1q32.1
291	FAM72B	ENSG00000188610	653820	24805	AL357493	family with sequence similarity 72, member B	1p12
292	PSRC1	ENSG00000134222	84722	24472		proline/serine-rich coiled-coil 1	1p13.3
293	TOP2A	ENSG00000131747	7153	11989		topoisomerase (DNA) II alpha 170kDa	17q21-q22

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
294	RHNO1	ENSG00000171792	83695	28206	AK021945	RAD9-HUS1-RAD1 interacting nuclear orphan 1	12p13.33
295	FAM83D	ENSG00000101447	81610	16122	AL023803	family with sequence similarity 83, member D	20q11.23
296	NCAPH	ENSG00000121152	23397	1112	BC024211	non-SMC condensin I complex, subunit H	2q11.2
297	KIF23	ENSG00000137807	9493	6392	X67155	kinesin family member 23	15q23
298	ZC3H3	ENSG00000014164	23144	28972	D63484	zinc finger CCCH-type containing 3	8q24.3
299	TUBA1A	ENSG00000167552	7846	20766	AF141347	tubulin, alpha 1a	12q13.12
300	MIS18BP1	ENSG00000129534	55320	20190	AB067490	MIS18 binding protein 1	14q21.1
301	CDCA8	ENSG00000134690	55143	14629	BG354581	cell division cycle associated 8	1p34.3
302	TUBD1	ENSG00000108423	51174	16811	AF201333	tubulin, delta 1	17q23.1
303	DNMT3B	ENSG00000088305	1789	2979		DNA (cytosine-5-)-methyltransferase 3 beta	20q11.2
304	CCNF	ENSG00000162063	899	1591	Z36714	cyclin F	16p13.3
305	NLRP2	ENSG00000022556	55655	22948	AK000517	NLR family, pyrin domain containing 2	19q13.42
306	SUCLG2	ENSG00000172340	8801	11450	AF058954	succinate-CoA ligase, GDP-forming, beta subunit	3p14.3
307	BRD8	ENSG00000112983	10902	19874	AF016270	bromodomain containing 8	5q31
308	BIRC3	ENSG00000023445	330	591	L49432	baculoviral IAP repeat containing 3	11q22
309	STAT5B	ENSG00000173757	6777	11367	BC065227	signal transducer and activator of transcription 5B	17q11.2
310	KLF9	ENSG00000119138	687	1123	BC069431	Kruppel-like factor 9	9q21.11
311	TRIP13	ENSG00000071539	9319	12307	L40384	thyroid hormone receptor interactor 13	5p15
312	HSPA2	ENSG00000126803	3306	5235	L26336, BC001752	heat shock 70kDa protein 2	14q23
313	PIF1	ENSG00000140451	80119	26220	AK026345	PIF1 5'-to-3' DNA helicase	15q22.1
314	SAP30	ENSG00000164105	8819	10532	AF055993	Sin3A-associated protein, 30kDa	4q34.1
315	ARHGEF39	ENSG00000137135	84904	25909	AK001187	Rho guanine nucleotide exchange factor (GEF) 39	9p13.3
316	CCDC107	ENSG00000159884	203260	28465	AK075523	coiled-coil domain containing 107	9q13.3
317	NUSAP1	ENSG00000137804	51203	18538	AF290612	nucleolar and spindle associated protein 1	15q14
318	CCNB1	ENSG00000134057	891	1579	U22364	cyclin B1	5q12
319	CCNB2	ENSG00000157456	9133	1580	AF002822	cyclin B2	15q21.3
320	CCNB3	ENSG00000147082	85417	18709	AJ314764	cyclin B3	Xp11
321	MAD1L1	ENSG00000002822	8379	6762	U33822	MAD1 mitotic arrest deficient-like 1 (yeast)	7p22
322	MAD2L2	ENSG00000116670	10459	6764	AF139365	MAD2 mitotic arrest deficient-like 2 (yeast)	1p36
323	GABPB1	ENSG00000104064	2553	4074	D13316	GA binding protein transcription factor, beta subunit 1	15q21.2
324	SHCBP1	ENSG00000171241	79801	29547	AK055931	SHC SH2-domain binding protein 1	16q11
325	CKS1B	ENSG00000173207	1163	19083	BC007751	CDC28 protein kinase regulatory subunit 1B	1q21.2
326	BTNL9	ENSG00000165810	153579	24176	AK057097	butyrophilin-like 9	5q35.3
327	KPNA2	ENSG00000182481	3838	6395	U09559	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	17q24.2

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
328	SMC4	ENSG00000113810	10051	14013	AF092564	structural maintenance of chromosomes 4	3q26.1
329	SGOL2	ENSG00000163535	151246	30812	AY094614	shugoshin-like 2 (S. pombe)	2q33.2
330	MKI67	ENSG00000148773	4288	7107	X65550	marker of proliferation Ki-67	10q26.2
331	PPP1R10	ENSG00000204569	5514	9284	Y13247	protein phosphatase 1, regulatory subunit 10	6p21.3
332	CKAP2	ENSG00000136108	26586	1990	AF177227	cytoskeleton associated protein 2	13q14
333	CNTROB	ENSG00000170037	116840	29616	AF331638	centrobin, centrosomal BRCA2 interacting protein	17p13.1
334	TTC38	ENSG00000075234	55020	26082		tetratricopeptide repeat domain 38	22q13
335	CDCA3	ENSG00000111665	83461	14624	BG354576	cell division cycle associated 3	12p13.31
336	RCAN1	ENSG00000159200	1827	3040		regulator of calcineurin 1	21q22.1-q22.2
337	CENPA	ENSG00000115163	1058	1851	U14518	centromere protein A	2p23.3
338	FOXM1	ENSG00000111206	2305	3818	Y12773	forkhead box M1	12p13
339	ATL2	ENSG00000119787	64225	24047		atlastin GTPase 2	2p22.3
340	BORA	ENSG00000136122	79866	24724	BC025367	bora, aurora kinase A activator	13q22.1
341	HINT3	ENSG00000111911	135114	18468	AK057688	histidine triad nucleotide binding protein 3	6q22.33
342	SPDL1	ENSG00000040275	54908	26010	BC012568	spindle apparatus coiled-coil protein 1	5q35.1
343	GAS2L3	ENSG00000139354	283431	27475	AK095594	growth arrest-specific 2 like 3	12q23.1
344	EIF5A2	ENSG00000163577	56648	3301	AF293386	eukaryotic translation initiation factor 5A2	3q26.2
345	CTNNA1	ENSG00000044115	1495	2509	D13866	catenin (cadherin-associated protein), alpha 1, 102kDa	5q31.2
346	TACC3	ENSG00000013810	10460	11524	AF093543	transforming, acidic coiled-coil containing protein 3	4p16.3
347	SGCD	ENSG00000170624	6444	10807	BX537948	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	5q33-q34
348	HN1	ENSG00000189159	51155	14569	AF086910	hematological and neurological expressed 1	17q25.1
349	RANGAP1	ENSG00000100401	5905	9854	X82260	Ran GTPase activating protein 1	22q13
350	KIF14	ENSG00000118193	9928	19181	D26361	kinesin family member 14	1q32.1
351	RRP1	ENSG00000160214	8568	18785	U79775	ribosomal RNA processing 1	21q22.3
352	KIF20B	ENSG00000138182	9585	7212	L16782	kinesin family member 20B	10q23.31
353	PBK	ENSG00000168078	55872	18282	AB027249	PDZ binding kinase	8p21.2
354	SRSF3	ENSG00000112081	6428	10785	L10838	serine/arginine-rich splicing factor 3	6p21
355	ASXL1	ENSG00000171456	171023	18318	AJ438952	additional sex combs like transcriptional regulator 1	20q11
356	BMP2	ENSG00000125845	650	1069		bone morphogenetic protein 2	20p12
357	CIT	ENSG00000122966	11113	1985	AB023166	citron rho-interacting serine/threonine kinase	12q24.23
358	CCNA1	ENSG00000133101	8900	1577	U66838	cyclin A1	13q12.3-q13
359	CHEK2	ENSG00000183765	11200	16627	AF086904	checkpoint kinase 2	22q12.1
360	WEE1	ENSG00000166483	7465	12761	X62048	WEE1 G2 checkpoint kinase	11p15.4
361	CDC23	ENSG00000094880	8697	1724	AF053977	cell division cycle 23	5q31

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
362	CDK7	ENSG00000134058	1022	1778		cyclin-dependent kinase 7	5q12.1
363	GADD45B	ENSG00000099860	4616	4096	AF090950	growth arrest and DNA-damage-inducible, beta	19p13.3
364	GADD45G	ENSG00000130222	10912	4097	D83023	growth arrest and DNA-damage-inducible, gamma	9q22.1-q22.2
365	SFN	ENSG00000175793	2810	10773	BC023552	stratifin	1p36.11
366	SMC3	ENSG00000108055	9126	2468	AF020043	structural maintenance of chromosomes 3	10q25
367	WEE2	ENSG00000214102	494551	19684	AK131218	WEE1 homolog 2 (S. pombe)	7q32
368	CDC14A	ENSG00000079335	8556	1718	AF000367	cell division cycle 14A	1p21
369	CDC14B	ENSG00000081377	8555	1719	AF023158	cell division cycle 14B	9q22.3
370	CDC20	ENSG00000117399	991	1723	U05340	cell division cycle 20	1p34.1
371	CDC27	ENSG00000004897	996	1728	U00001	cell division cycle 27	17q21.32
372	MCM4	ENSG00000104738	4173	6947		minichromosome maintenance complex component 4	8q12-q13
373	PTTG2	ENSG00000250254	10744	9691	AF095288	pituitary tumor-transforming 2	4p14
374	RAD21	ENSG00000164754	5885	9811	BC050381	RAD21 homolog (S. pombe)	8q24.11
375	STAG1	ENSG00000118007	10274	11354	Z75330	stromal antigen 1	3q22.2-q22.3
376	CDH1	ENSG00000039068	999	1748	L08599	cadherin 1, type 1, E-cadherin (epithelial)	16q22.1
377	MEN1	ENSG00000133895	4221	7010	U93236	multiple endocrine neoplasia I	11q13
378	TBC1D8	ENSG00000204634	11138	17791	AB024057	TBC1 domain family, member 8 (with GRAM domain)	2q12.1
379	DNAJB1	ENSG00000132002	3337	5270	D49547	DnaJ (Hsp40) homolog, subfamily B, member 1	19p13.12
380	AKIRIN2	ENSG00000135334	55122	21407	BC000764	akirin 2	6q15
381	ANLN	ENSG00000011426	54443	14082	AF273437	anillin, actin binding protein	7p15-p14
382	NUP35	ENSG00000163002	129401	29797	AF514993	nucleoporin 35kDa	2q32
383	NDE1	ENSG00000072864	54820	17619	AF124431	nudE neurodevelopment protein 1	16p13.11
384	KIF2C	ENSG00000142945	11004	6393	U63743	kinesin family member 2C	1p34.1
385	GTSE1	ENSG00000075218	51512	13698	AF223408	G-2 and S-phase expressed 1	22q13.2-q13.3
386	G2E3	ENSG00000092140	55632	20338	AK000340	G2/M-phase specific E3 ubiquitin protein ligase	14q12
387	AURKA	ENSG00000087586	6790	11393	BC001280	aurora kinase A	20q13
388	DEPDC1B	ENSG00000035499	55789	24902	AF303178	DEP domain containing 1B	5q12
389	ADH4	ENSG00000198099	127	252	M15943	alcohol dehydrogenase 4 (class II), pi polypeptide	4q22
390	NUF2	ENSG00000143228	83540	14621	BG354574	NUF2, NDC80 kinetochore complex component	1q23.3
391	SPAG5	ENSG00000076382	10615	13452	AF063308	sperm associated antigen 5	17q11.2
392	CENPF	ENSG00000117724	1063	1857	U30872	centromere protein F, 350/400kDa	1q41
393	LMNA	ENSG00000160789	4000	6636	BC014507	lamin A/C	1q22
394	CEP55	ENSG00000138180	55165	1161	AK001402	centrosomal protein 55kDa	10q24.1
395	HMMR	ENSG00000072571	3161	5012	U29343	hyaluronan-mediated motility receptor (RHAMM)	5q34

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
396	DEPDC1	ENSG00000024526	55635	22949	AK000361	DEP domain containing 1	1p31.2
397	IDO1	ENSG00000131203	3620	6059	M34455	indoleamine 2,3-dioxygenase 1	8p12-p11
398	BIRC2	ENSG00000110330	329	590	L49431	baculoviral IAP repeat containing 2	11q22
399	PSMG3	ENSG00000157778	84262	22420	BC027171	proteasome (prosome, macropain) assembly chaperone 3	7p22.3
400	CENPE	ENSG00000138778	1062	1856	Z15005	centromere protein E, 312kDa	4q24-q25
401	AHI1	ENSG00000135541	54806	21575	AJ459824	Abelson helper integration site 1	6q23.2
402	TPX2	ENSG00000088325	22974	1249	AF098158	TPX2, microtubule-associated	20q11.2
403	IL7R	ENSG00000168685	3575	6024	M29696	interleukin 7 receptor	5p13
404	ARL6IP1	ENSG00000170540	23204	697	BC010281	ADP-ribosylation factor-like 6 interacting protein 1	16p12-p11.2
405	RAD51C	ENSG00000108384	5889	9820	AF029670	RAD51 paralog C	17q25.1
406	ZC3HC1	ENSG00000091732	51530	29913	AF151050	zinc finger, C3HC-type containing 1	7q32.2
407	FAM102B	ENSG00000162636	284611	27637	CR749397	family with sequence similarity 102, member B	1p13.3
408	HMGB3	ENSG00000029993	3149	5004	AF274572	high mobility group box 3	Xq28
409	MZT1	ENSG00000204899	440145	33830		mitotic spindle organizing protein 1	13q22.1
410	RAN	ENSG00000132341	5901	9846	M31469	RAN, member RAS oncogene family	12q24.33
411	CKAP5	ENSG00000175216	9793	28959		cytoskeleton associated protein 5	11p11.2
412	FAM64A	ENSG00000129195	54478	25483		family with sequence similarity 64, member A	17p13.2
413	SRD5A1	ENSG00000145545	6715	11284	M32313	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	5p15.31
414	PLEKHG4B	ENSG00000153404	153478	29399	BC008352	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B	5p15.33
415	HMG20B	ENSG00000064961	10362	5002	BC003505	high mobility group 20B	19p13.3
416	LRRC17	ENSG00000128606	10234	16895	U32907	leucine rich repeat containing 17	7q22.1
417	SMTN	ENSG00000183963	6525	11126	AY061972	smoothelin	22q12
418	ZNF521	ENSG00000198795	25925	24605	AK027354	zinc finger protein 521	18q11.2
419	CKS2	ENSG00000123975	1164	2000	X54942	CDC28 protein kinase regulatory subunit 2	9q22
420	MAPK13	ENSG00000156711	5603	6875	Y10488	mitogen-activated protein kinase 13	6p21
421	ECT2	ENSG00000114346	1894	3155	AA206473	epithelial cell transforming 2	3q26.1-q26.2
422	ERN2	ENSG00000134398	10595	16942	AA527544	endoplasmic reticulum to nucleus signaling 2	16p12.2
423	GPSM2	ENSG00000121957	29899	29501	AY136740	G-protein signaling modulator 2	1p13.3
424	KIF5B	ENSG00000170759	3799	6324	X65873	kinesin family member 5B	10p11.22
425	SEPN1	ENSG00000162430	57190	15999	AF166125	selenoprotein N, 1	1p36.13
426	NEK2	ENSG00000117650	4751	7745	U11050	NIMA-related kinase 2	1q32.3
427	HSPA1L	ENSG00000204390	3305	5234	D85730	heat shock 70kDa protein 1-like	6p21.3
428	FAM216A	ENSG00000204856	29902	30180	U79274	family with sequence similarity 216, member A	12q24.11

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
429	INPP5K	ENSG00000132376	51763	33882		inositol polyphosphate-5-phosphatase K	17p13.3
430	GCSAM	ENSG00000174500	257144	20253	BC030506	germinal center-associated, signaling and motility	3q13.13
431	DLGAP5	ENSG00000126787	9787	16864	D13633	discs, large (Drosophila) homolog-associated protein 5	14q22.3
432	CEP70	ENSG00000114107	80321	29972	AF202146	centrosomal protein 70kDa	3q22.3
433	LBR	ENSG00000143815	3930	6518	L25931	lamin B receptor	1q42.1
434	BIRC5	ENSG00000089685	332	593	U75285	baculoviral IAP repeat containing 5	17q25.3
435	KBTBD2	ENSG00000170852	25948	21751	AB040922	kelch repeat and BTB (POZ) domain containing 2	7p14.3
436	OLR1	ENSG00000173391	4973	8133	D89050	oxidized low density lipoprotein (lectin-like) receptor 1	12p13.1-p12.3
437	HBG2	ENSG00000196565	3048	4832	BC029387	hemoglobin, gamma G	11p15.5
438	SLC17A2	ENSG00000112337	10246	10930	U90544	solute carrier family 17, member 2	6p22.2
439	PWP1	ENSG00000136045	11137	17015	BC000067	PWP1 homolog (S. cerevisiae)	12q23.3
440	BTBD3	ENSG00000132640	22903	15854	AB023169	BTB (POZ) domain containing 3	20p12.2
441	USB1	ENSG00000103005	79650	25792	AK023216	U6 snRNA biogenesis 1	16q13
442	FOPNL	ENSG00000133393	123811	26435	AL832498	FGFR1OP N-terminal like	16p13.11
443	SFPQ	ENSG00000116560	6421	10774	X70944	splicing factor proline/glutamine-rich	1p34.3
444	PRC1	ENSG00000198901	9055	9341	AF044588	protein regulator of cytokinesis 1	15q26.1
445	KNSTRN	ENSG00000128944	90417	30767	AK027408	kinetochore-localized astrin/SPAG5 binding protein	15q15.1
446	UBE2S	ENSG00000108106	27338	17895	BC004236	ubiquitin-conjugating enzyme E2S	19q13.43
447	PCF11	ENSG00000165494	51585	30097	AB020631	PCF11 cleavage and polyadenylation factor subunit	11q13
448	PLAG1	ENSG00000181690	5324	9045	U65002	pleiomorphic adenoma gene 1	8q12
449	SAPCD2	ENSG00000186193	89958	28055	BC024299	suppressor APC domain containing 2	9q34.3
450	XPO4	ENSG00000132953	64328	17796	AB051508	exportin 4	13q11
451	PRR11	ENSG00000068489	55771	25619		proline rich 11	17q23.2
452	VANGL1	ENSG00000173218	81839	15512	AB075805	VANGL planar cell polarity protein 1	1p13.1
453	ZPBP	ENSG00000042813	11055	15662	D17570	zona pellucida binding protein	7p14.3
454	TROAP	ENSG00000135451	10024	12327	U04810	trophinin associated protein	12q13.12
455	GAS6	ENSG00000183087	2621	4168		growth arrest-specific 6	13q34
456	LRIF1	ENSG00000121931	55791	30299	AY190122	ligand dependent nuclear receptor interacting factor 1	1p13.3
457	ANAPC5	ENSG00000089053	51433	15713	AF191339	anaphase promoting complex subunit 5	12q24.31
458	CDC16	ENSG00000130177	8881	1720	U18291	cell division cycle 16	13q34
459	CDKN1C	ENSG00000129757	1028	1786	D64137	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	11p15.5
460	CDKN2B	ENSG00000147883	1030	1788	AB060808	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	9p21
461	SMC1A	ENSG00000072501	8243	11111	S78271	structural maintenance of chromosomes 1A	Xp11.22-p11.21

Supplementary table S1. Cell cycle genes (continued)

	HGNC symbol	Ensembl ID	Entrez ID	HGNC.ID	Accession Numbers	Approved Name	Chr. location
462	SMC1B	ENSG00000077935	27127	11112	AJ504806	structural maintenance of chromosomes 1B	22q13
463	STAG2	ENSG00000101972	10735	11355	Z75331	stromal antigen 2	Xq25

Supplementary table S2.

Cross-table of concordance between Ki67 immunohistochemical staining and gene expression signature classifications in Cohorts 1 and 2

		Number of patients grouped by Ki67 status in Cohorts 1 and 2							
		Cohort 1 (n=379)				Cohort 2 (n=209)			
Characteristics		Ki67 < 16 (n=184)	Ki67 ≥ 16 (n=195)	nC	nD	Ki67 < 16 (n=140)	Ki67 ≥ 16 (n=69)	nC	nD
		n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)
Gene expression signatures									
GGI									
	Grade 1	120 (65)	14 (7)	301 (79)	78 (21)	119 (85)	20 (29)	168 (80)	41 (20)
	Grade 3	64 (35)	181 (93)			21 (15)	49 (71)		
70-Gene									
	Good	142 (77)	32 (16)	305 (80)	74 (19)	102 (73)	8 (12)	163 (78)	46 (22)
	Poor	42 (23)	163 (84)			38 (27)	61 (88)		
Recurrence score									
	Low	71 (39)	5 (3)	296 (78)	83 (22)	70 (50)	8 (12)	166 (79)	43 (21)
	Intermediate	35 (19)	10 (5)			35 (25)	5 (7)		
	High	78 (42)	180 (92)			35 (25)	56 (81)		
Cell Cycle score									
	Low	70 (38)	3 (1)	326 (86)	53 (14)	103 (74)	11 (16)	187 (89)	22 (11)
	Intermediate	64 (35)	16 (8)			26 (19)	22 (32)		
	High	50 (27)	176 (91)			11 (8)	36 (52)		
PAM50									
	Luminal A	111 (60)	15 (7)	307 (81)	72 (19)	54 (39)	3 (4)	150 (72)	59 (28)
	Luminal B	24 (13)	54 (28)			27 (19)	18 (27)		
	HER2-enriched	12 (6)	41 (21)			18 (13)	30 (43)		
	Basal-Like	14 (8)	78 (40)			8 (6)	15 (22)		
	Normal-Like	23 (12)	7 (4)			33 (24)	3 (4)		

GGI = Genomic grade index, nC = Number of concordant cases, nD = Number of discordant cases
Numbers in red = Cases in which Ki67 and gene expression signatures are not in agreement.

Supplementary table S3.

Clinico-pathological characteristics of patient subgroups in cohort 1

Variables	All (n=379)		ER+/LN-(n=104)		ER+/LN+(n=167)		ER-(n=103)	
	#	%	#	%	#	%	#	%
ER								
Positive	276	73	104	100	167	100	0	0
Negative	103	27	0	0	0	0	103	100
PR								
Positive	233	61	90	87	134	80	4	4
Negative	146	39	14	13	33	20	99	96
HER2								
Positive	79	21	10	10	32	19	37	36
Negative	300	79	94	90	135	81	66	64
Elston-Ellis grade								
I	34	9	17	17	16	10	0	0
II	172	46	54	52	86	52	28	27
III	170	45	32	31	63	38	75	73
Missing cases = 3								
Nodal status								
Positive	221	59	0	0	167	100	54	52
Negative	153	41	104	100	0	0	49	48
Missing cases = 5								
Tumor Size								
< 20mm	167	44	59	57	66	40	37	36
≥ 20mm	209	56	44	43	100	60	65	64
Missing cases = 3								
Age at menopause								
< 50	65	37	18	35	26	37	19	39
≥ 50	110	63	33	65	45	63	30	61
Missing cases = 204								
Systematic adjuvant								
None	2	1	1	1	0	0	1	1
Chemotherapy	269	38	38	22	133	32	98	87
Endocrine therapy	269	38	98	58	158	38	8	7
Both	163	23	33	19	124	30	6	5
Ki67*								
< 16	184	49	65	62	96	57	18	17
≥ 16	195	51	39	38	71	43	85	83
IHC subgroups**								
Luminal A-like	152	40	61	59	86	51	0	0
Luminal B-like	82	22	33	32	49	29	0	0
Her2 positive	79	21	10	9	32	19	37	36
Triple negative	66	17	0	0	0	0	66	64
GGI								
Grade 1	134	35	51	49	68	41	11	11
Grade 3	245	65	53	51	99	59	92	89
70-Gene								
Good	174	46	68	65	94	56	7	7
Poor	205	54	36	35	73	44	96	93
CCS								
Low	73	19	30	29	35	21	6	6
Intermediate	80	21	23	22	44	26	10	10
High	226	60	51	49	88	53	87	84
RS								
Low	76	20	41	39	34	20	0	0
Intermediate	45	12	14	13	27	16	1	1
High	258	68	49	47	106	63	102	99
PAM50								
Luminal A	126	33	54	52	66	40	2	2
Luminal B	78	21	27	26	50	30	1	1
Her2-enriched	53	14	3	3	23	14	27	26
Basal-like	92	24	12	12	11	6	69	67
Normal-like	30	8	8	7	17	10	4	4

= Number of patients, % = Percentage, ER = estrogen receptor alpha, PR = progesterone receptor, RS = Recurrence score, CCS = Cell cycle score, * = Ki67 cut-off (median value), ** = Luminal A (ER+, PR+/PR-, HER-, Ki67 low), Luminal A (ER+, PR+/PR-, HER-, Ki67 High), Her2 like(HER2+), Basal like (ER-, PR-, HER2-)

Supplementary table S4.

Change in C-index when adding gene expression signatures to Ki67/IHC for All, ER+/LN-, ER+/LN-, ER- patients in Cohorts 1 and 2.

Models	All		ER+ / LN-		ER+ / LN+		ER-	
	Cohort 1 (n=379)	Cohort 2 (n=209)	Cohort 1 (n=104)	Cohort 2 (n=115)	Cohort 1 (n=167)	Cohort 2 (n=65)	Cohort 1 (n=103)	Cohort 2 (n=24)
	C-Index		C-Index		C-Index		C-Index	
Univariate								
Ki67	0.57	0.59	0.58	0.58	0.59	0.54	0.52	0.57
IHC	0.61	0.59	0.59	0.56	0.60	0.54	0.59	0.55
GGI	0.57	0.61	0.59	0.59	0.61	0.56	0.54	0.68
70-Gene	0.57	0.61	0.51	0.55	0.61	0.60	0.50	0.55
RS	0.60	0.61	0.63	0.60	0.62	0.57	0.51	0.52
CCS	0.57	0.62	0.57	0.57	0.62	0.62	0.54	0.71
PAM50	0.63	0.64	0.61	0.66	0.65	0.62	0.59	0.54
	C-Index		C-Index		C-Index		C-Index	
Ki67 + G.Sigs								
Ki67 + GGI	0.59	0.62	0.61	0.60	0.62	0.57	0.56	0.70
Ki67 + 70-Gene	0.59	0.62	0.59	0.59	0.63	0.61	0.50	0.58
Ki67 + RS	0.61	0.62	0.63	0.64	0.63	0.57	0.52	0.57
Ki67 + CCS	0.59	0.63	0.60	0.59	0.63	0.63	0.55	0.72
Ki67 + PAM50	0.63	0.64	0.66	0.66	0.66	0.62	0.59	0.56
IHC + G.Sigs								
IHC + GGI	0.63	0.63	0.61	0.58	0.64	0.57	0.60	0.70
IHC + 70-Gene	0.62	0.62	0.60	0.58	0.64	0.61	0.59	0.60
IHC + RS	0.64	0.62	0.64	0.64	0.64	0.57	0.59	0.58
IHC + CCS	0.62	0.63	0.60	0.56	0.64	0.63	0.60	0.73
IHC + PAM50	0.64	0.64	0.65	0.68	0.67	0.62	0.61	0.60

C-Index = Concordance index, ER = Estrogen receptor, LN = Lymph node metastasis, GGI = Genomic grade index, RS = Recurrence score, CCS = Cell cycle score, G.sigs = Gene expression signatures, IHC = Immunohistochemical markers

Supplementary Table S5.
Clinico-pathological characteristics of patient subgroups in cohort 2

Variables	All (n=209)		ER+/LN- (n=115)		ER+/LN+ (n=65)		ER- (n=24)	
	#	%	#	%	#	%	#	%
ER								
Positive	185	89	115	100	65	100	0	0
Negative	24	11	0	0	0	0	24	100
PR								
Positive	175	84	106	92	56	86	8	33
Negative	34	16	9	8	9	14	16	67
HER2								
Positive	40	19	16	14	10	15	13	54
Negative	169	81	99	86	55	85	11	46
Elston-Ellis grade								
I	56	27	45	39	8	12	2	8
II	111	54	60	53	40	63	8	34
III	40	19	9	8	16	25	14	58
Missing cases = 2								
Nodal status								
Positive	74	36	0	0	65	100	9	39
Negative	129	64	115	100	0	0	14	61
Missing cases = 6								
Tumor Size								
< 20mm	90	43	66	57	16	24	7	29
≥ 20mm	119	57	49	43	49	76	17	71
Age								
< 50	39	19	20	17	15	23	4	17
≥ 50	170	81	95	83	50	77	20	83
Systematic adjuvant therapy								
None	113	54	99	86	1	1	12	50
Chemotherapy	19	9	1	1	15	23	3	12
Endocrine therapy	72	35	15	13	45	69	9	38
Both	4	2	0	0	4	7	0	0
Missing cases = 6								
Ki67								
< 16	140	67	91	79	37	56	9	38
≥ 16	69	33	24	21	28	44	15	62
IHC subtypes**								
Luminal A-like	121	58	86	75	33	51	0	0
Luminal B-like	37	18	13	11	22	34	0	0
Her2 positive	40	19	16	14	10	15	13	54
Triple negative	11	5	0	0	0	0	11	46
Missing cases = 6								
GGI								
Grade 1	139	67	91	79	38	58	7	29
Grade 3	70	33	24	21	27	42	17	71
70-Gene								
Good	110	53	79	69	26	40	2	8
Poor	99	47	36	31	39	60	22	92
CCS								
Low	114	55	77	67	30	46	5	21
Intermediate	48	23	20	17	20	31	7	29
High	47	22	18	16	15	23	12	50
RS								
Low	78	37	58	50	18	28	0	0
Intermediate	40	19	25	22	14	21	1	4
High	91	44	32	28	33	51	23	96
PAM50								
Luminal A	57	27	40	35	15	24	1	4
Luminal B	45	22	25	22	17	26	0	0
Her2-enriched	48	23	15	13	17	26	16	67
Basal-like	23	11	8	7	8	12	7	29
Normal-like	36	17	27	23	8	12	0	0

= Number of patients, % = Percentage, ER = estrogen receptor alpha, PR = progesterone receptor, RS = Recurrence score, CCS = Cell cycle score, ** = Luminal A (ER+, PR+/PR-, HER-, Ki67 low), Luminal A (ER+, PR+/PR-, HER-, Ki67 High), Her2 like (HER2+), Basal like (ER-, PR-, HER2-)