The Supplement file contains the lists of genes that were associated with defects in G1 and G2 checkpoint responses to DNA damage in melanocyte and melanoma lines, using either significance analysis of microarrays (SAM) or the Bayesian approach described in Materials and Methods. The first page contains the gene names as given by Agilent. The second-fifth pages give the Agilent probe identification numbers and other identifiers for gene annotation. Pages 8 and 10 also include the gene ontology categories that were determined by the Expression Analysis Systematic Explorer (http://david.niaid.nih.gov/david/ease/htm) to be significantly enriched (<0.05) in the gene list.

Genes that discriminate effective and defective G1 and G2 checkpoint functions in melanomas

G1 checkpoint		G2 checkpoint	
SAM	**Bayesian**	**SAM**	**Bayesian**
AGL	ABR	FANCC	AC027607
ARCN1	AC007282	NM_001031617	AC108673
CD59	AC087588	PRX	AC140134
CDCA7	AC117456	THC1410663	ACSL3
CDKN1A	AC135893		AK000776
CKS1B	AF218008		ALMS1
DDB2	AL023656		APG12L
EFEMP2	ATOH8		ARV1
ENST00000312688	ATP6AP1		ASMTL
ENST00000317094	BBC3		BCAP29
ENST00000324418	BC009385		BE018697
ENST00000328779	BC020859		BTN2A2
ENST00000329179	BC038466		C10orf57
ENST00000330973	BCLAF1		C13orf1
ENST00000333058	C10orf4		C13orf9
FLJ10330	C11orf24		C14orf142
FLJ31153	C1orf41		C14orf168
FUSIP1	C6orf75		C14orf31
I_1842444	C6orf75		C16orf28
I_3252275	CARD9		C18orf25
ITGA3	CCNB1		C19orf13
MTVR1	CD59		C20orf149
RPL5	CDC2		C20orf55
SLC12A4	CDC7		C21orf63
THC1444796	CDCA7		CABLES2
TPTE	CDKN1A		CAPZA2
	CGI-94		COG1
	CKS1B		CTL2
	CORT		CTSC
	CSE-C		DATF1
	DCTN2		DDX55

DDB2
DDX18
DPP7
DYRK2
ECT2
EFEMP2
EML4
ENG
ENST00000249480
ENST00000312441
ENST00000312688
ENST00000313760
ENST00000314726
ENST00000315741
ENST00000317094
ENST00000318629
ENST00000328480
ENST00000333571
FAM49B
FBXW5
FGFR1
FIBP
FLJ10647
FLJ11259
FLJ12484
FLJ13448
FLJ13855
FLJ20850
FLJ21827
FLJ23233
FLJ35740
GABARAPL1
GAJ
GCSH
GMNN
HACE1
HDAC2
HRI
HSF2
HSPC133
I_1000644
I_1938997
I_1950158
I_3584237
IL6ST
ITGA3
KIAA0830
KIAA1005
LASS6
DKFZP434A1319
DKFZP566E144
DNCI1
EFNB1
EIF4EBP2
ENST00000297649
ENST00000299623
ENST00000313590
ENST00000314100
ENST00000321656
ENST00000323263
ENST00000325703
ENST00000328473
ENST00000328941
ENST00000329561
ENST00000330356
ENST00000330972
ENST00000331540
ENST00000332277
ENST00000332832
ENST00000333636
FAM32A
FBXO22
FCGR2A
FEM1C
FLJ21865
FLJ37953
FTHFSDC1
GLRX
GLS
GNG12
GRB2
GTF2H2
HAN11
HCFC2
HNRPA0
HOXB2
HSC20
HSPA4
I_1000003
I_1868291
I_3202278
I_958209
I_959101
I_963398
JM11
KIAA0433
KIAA0828
LIPE

LDHA
LIN9
LOC201191
LOC255374
LOC348262
LOC374395
LOC399818
LOC51035
LRP10
LYPDC1
MAN2B1
MAP3K10
MCFD2
MCOLN1
MDC1
MDM4
MED19
MGC17839
MGC21654
MGC34079
MGC40157
MGC4728
MRPL47
MRS2L
MTVR1
NAGK
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NM_001017408
NM_001023571
NM_001025160
NM_001029896
NM_001031734
NM_001033085
NM_001033582
NM_018908
NR_002225
NS5ATP13TP2
ORC3L
OTUB1
PEX3
PFDN5
PHF6
PPP1R16B
PRAF2
PRPF4B
PSAP
PSMD8
LOC146346
LOC200916
LOC284001
LOC348926
LOC51234
LOC54499
LOC90355
LOC96610
MAP3K14
MGC10067
MGC16279
MGC17943
MGC4093
MGC5509
MKNK2
MRPL18
MRPL45
MtFMT
NDUFB5
NM_001029857
NM_014951
NM_133458
NM_145111
NPAS2
NPM1
NUFIP1
OCIL
OGG1
PDXK
PHKA2
PMPCB
PPM1E
PRKAA1
PRX
PTPN11
RAM2
RIPK4
RNASEH1
RNMT
RSNL2
SCYE1
SENP3
SF3A3
SIAT8A
SIVA
SLC2A8
SMCR7
SMN2
SNAPC5

PTPN2
PXMP2
RAD50
RBKS
RFC4
RGS16
ROM1
RPA3
RRM2B
SAMD4
SFRS3
SIAT7F
SLC12A4
SLC35C1
SLC39A13
SLC6A8
SRPK1
SSNA1
TAF1B
TAF4
THC1444796
THC1448734
THC1467304
THC1486425
THC1503623
THC1538371
TMAP1
TncRNA
TNFRSF10B
TPTE
TTRAP
TXN
U60899
Ufm1
WAC
XM_371884
ZNF326
ZNF524

TESK1
THC1410663
THC1430719
THC1438380
THC1501849
THC1525200
THC1550605
TNFRSF6B
TRIM59
TU12B1-TY
UBE2H
UBE3C
UBQLN2
UCHL5
VIL2
VPS45A
XM_090998
XM_208658
XM_301800
ZNF265

Genes that are associated with G1 checkpoint function by Bayesian analysis

SUID	GeneSymbol	CLID	Accession	LLID	ChromosomeLocation	Cytoband
AGI_HUM1_OLIGO_A_23_P503182	ABR	Hs.159306	NM_021962	29	chr17:891700-891641	17p13.3
AGI_HUM1_OLIGO_A_23_P142878	ATOH8	Hs.135569	NM_032827	84913	chr2:85989408-85989467	2p11.2
AGI_HUM1_OLIGO_A_24_P74753	ATP6AP1	Hs.6551	NM_001183	537	chrX:152131734-152131969	Xq28
AGI_HUM1_OLIGO_A_24_P305312	BBC3	Hs.467020	NM_014417	27113	chr19:52416986-52416927	19q13.32
AGI_HUM1_OLIGO_A_24_P89512	BCLAF1	Hs.486542	NM_014739	9774	chr6:136560399-136560340	6q23.3
AGI_HUM1_OLIGO_A_24_P30141	C10orf4	Hs.303727	NM_145246	118924	chr10:95093466-95093407	10q23.33
AGI_HUM1_OLIGO_A_23_P12911	C11orf24	Hs.303025	NM_022338	53838	chr11:67804430-67804371	11q13.2
AGI_HUM1_OLIGO_A_23_P96872	C1orf41	Hs.525462	NM_016126	51668	chr1:53759520-53757325	1p32.3
AGI_HUM1_OLIGO_A_24_P89509	C6orf75	Hs.404186	NM_021820	60487	chr6:126313010-126313069	6q22.32
AGI_HUM1_OLIGO_A_24_P180830	CARD9	Hs.528581	NM_052813	64170	chr9:134615587-134615528	9q34.3
AGI_HUM1_OLIGO_A_23_P122197	CCNB1	Hs.23960	NM_031966	891	chr5:68487247-68489007	5q13.2
AGI_HUM1_OLIGO_A_32_P50275	CD59	Hs.278573	AK095453	966	chr11:33692213-33692272	11p13
AGI_HUM1_OLIGO_A_32_P87849	CDC2	Hs.334562	NM_033379	983		
AGI_HUM1_OLIGO_A_23_P148807	CDC7	Hs.533573	NM_003503	8317	chr1:91462848-91462907	1p22.2
AGI_HUM1_OLIGO_A_24_P171549	CDCA7	Hs.470654	AK075134	83879	chr2:174435437-174435496	2q31.1
AGI_HUM1_OLIGO_A_24_P89457	CDKN1A	Hs.370771	L47232	1026	chr6:36699033-36699092	6p21.31
AGI_HUM1_OLIGO_A_23_P11774	CGI-94	Hs.472038	NM_016037	51118	chr1:37902576-37902635	1p34.3
AGI_HUM1_OLIGO_A_23_P45917	CKS1B	Hs.374378	NM_001826	1163	chr1:152168319-152168378	1q22
AGI_HUM1_OLIGO_A_24_P246926	CORT	Hs.412311	NM_001302	1325	chr1:10221184-10221243	1p36.22
AGI_HUM1_OLIGO_A_23_P24616	CSE-C	Hs.10056	NM_170601	54414	chr11:124043869-124043810	11q24.2
AGI_HUM1_OLIGO_A_23_P76059	DCTN2	Hs.289123	AK096242	10540	chr12:56210315-56210256	12q13.3
AGI_HUM1_OLIGO_A_23_P52610	DDB2	Hs.446564	NM_000107	1643	chr11:47224932-47224991	11p11.2
AGI_HUM1_OLIGO_A_24_P165736	DDX18	Hs.363492	AK091227	8886	chr2:118683855-118683914	2q14.1
AGI_HUM1_OLIGO_A_23_P32975	DPP7	Hs.37916	BC016961	29952	chr9:135362411-135362393	9q34.3
AGI_HUM1_OLIGO_A_24_P942786	DYRK2	Hs.173135	AK024870	8445	chr12:66344810-66344869	12q15
AGI_HUM1_OLIGO_A_24_P366033	ECT2	Hs.518299	AK023267	1894	chr3:173841337-173841396	3q26.31
AGI_HUM1_OLIGO_A_23_P24414	EFEMP2	Hs.381870	AB030655	30008	chr11:65410842-65410783	11q13.1
AGI_HUM1_OLIGO_A_24_P273413	EML4	Hs.432438	AK001804	27436	chr2:42458223-42458282	2p21
AGI_HUM1_OLIGO_A_23_P83328	ENG	Hs.76753	NM_000118	2022	chr9:125955516-125954362	9q34.11
AGI_HUM1_OLIGO_A_23_P43255	FAM49B	Hs.492869	NM_016623	51571	chr8:130810442-130810383	8q24.21
AGI_HUM1_OLIGO_A_23_P112397	FBXW5	Hs.522507	NM_018998	54461	chr9:135192615-135192556	9q34.3
AGI_HUM1_OLIGO_A_24_P902338	FGFR1	Hs.264887	AI821117	2260	chr8:38323429-38323488	8p12
AGI_HUM1_OLIGO_A_23_P1615	FIBP	Hs.7768	NM_004214	9158	chr11:65430444-65429208	11q13.1
AGI_HUM1_OLIGO_A_23_P62831	FLJ10647	Hs.87016	NM_018166	55194	chr1:36215557-36215498	1p34.3
AGI_HUM1_OLIGO_A_24_P381455	FLJ11259	Hs.525634	BC018435	55332	chr12:100797541-100797600	12q23.2
AGI_HUM1_OLIGO_A_23_P206077	FLJ12484	Hs.436102	NM_022767	64782	chr15:86904669-86904727	15q26.1
AGI_HUM1_OLIGO_A_23_P102037	FLJ13448	Hs.288945	NM_025147	80219	chr2:198541432-198541491	2q33.1
AGI_HUM1_OLIGO_A_24_P378506	FLJ13855	Hs.514297	NM_023079	65264	chr17:47480045-47480104	17q21.32
AGI_HUM1_OLIGO_A_23_P67589	FLJ20850	Hs.30783	NM_017967	55049	chr19:18563951-18564010	19p13.11
AGI_HUM1_OLIGO_A_23_P116207	FLJ21827	Hs.533738	NM_020153	56912	chr11:117954182-117953825	11q23.3
AGI_HUM1_OLIGO_A_23_P164638	FLJ23233	Hs.98593	NM_024691	79744	chr19:62697315-62697374	19q13.43
AGI_HUM1_OLIGO_A_32_P17577	FLJ35740	Hs.535962	AK058117	253650	chr9:38557353-38557294	9p13.1
AGI_HUM1_OLIGO_A_24_P4816	GABARAPL1	Hs.524250	NM_031412	23710	chr12:10265943-10266002	12p13.2
AGI_HUM1_OLIGO_A_23_P133123	GAJ	Hs.294088	NM_032117	84057	chr4:154913612-154913671	4q31.3
AGI_HUM1_OLIGO_A_32_P57702	GCSH	Hs.546256	NM_004483	2653		
AGI_HUM1_OLIGO_A_23_P19712	GMNN	Hs.234896	NM_015895	51053	chr6:24894087-24894146	6p22.2
AGI_HUM1_OLIGO_A_23_P250002	HACE1	Hs.434340	AB037741	57531	chr6:105221987-105221928	6q16.3
AGI_HUM1_OLIGO_A_23_P122304	HDAC2	Hs.3352	NM_001527	3066	chr6:114308443-114307765	6q21
AGI_HUM1_OLIGO_A_24_P123768	HRI	Hs.520205	AB037790	27102	chr7:5806795-5806736	7p22.1
AGI_HUM1_OLIGO_A_32_P9963	HSF2	Hs.158195	NM_004506	3298	chr6:122734475-122734534	6q22.31
AGI_HUM1_OLIGO_A_23_P142634	HSPC133	Hs.470553	NM_014168	29081	chr2:170874553-170871525	2q31.1
AGI_HUM1_OLIGO_A_24_P935033	IL6ST	Hs.532082	U58146	3572	chr5:55260652-55260584	5q11.2
AGI_HUM1_OLIGO_A_23_P55251	ITGA3	Hs.265829	NM_005501	3675	chr17:48642003-48642062	17q21.33
AGI_HUM1_OLIGO_A_23_P104624	KIAA0830	Hs.167115	AB020637	23052	chr11:94553745-94553804	11q21
AGI_HUM1_OLIGO_A_32_P123966	KIAA1005	Hs.298382	AB023222	23322	chr16:53414191-53414132	16q12.2
AGI_HUM1_OLIGO_A_32_P5480	LASS6	Hs.506829	AK024891	253782	chr2:169833547-169833606	2q24.3
AGI_HUM1_OLIGO_A_23_P47565	LDHA	Hs.2795	NM_005566	3939	chr11:18393098-18393157	11p15.1
AGI_HUM1_OLIGO_A_32_P233304	LIN9	Hs.120817	NM_173083	286826	chr1:223393638-223393579	1q42.12
AGI_HUM1_OLIGO_A_24_P185186	LOC201191	Hs.546517	NM_174920	201191	chr17:48665938-48665004	17q21.33
AGI_HUM1_OLIGO_A_24_P221198	LOC255374	Hs.257126	BC031288	255374	chr7:99337333-99337392	7q22.1
AGI_HUM1_OLIGO_A_24_P237878	LOC348262	Hs.514632	BC041068	348262	chr17_random:2179431-2179372	
AGI_HUM1_OLIGO_A_24_P86868	LOC399818	Hs.468488	AF318345	399818	chr10:126023341-126023282	10q26.13
AGI_HUM1_OLIGO_A_24_P258277	LOC51035	Hs.351296	NM_015853	51035	chr11:62220372-62219801	11q12.3
AGI_HUM1_OLIGO_A_24_P99216	LRP10	Hs.525232	NM_014045	26020	chr14:21336113-21336293	14q11.2
AGI_HUM1_OLIGO_A_32_P101031	LYPDC1	Hs.432395	AK075487	116372	chr2:133613259-133613200	2q21.2
AGI_HUM1_OLIGO_A_24_P370156	MAN2B1	Hs.356769	U68382	4125	chr19:12621201-12621018	19p13.2
AGI_HUM1_OLIGO_A_24_P284523	MAP3K10	Hs.466743	NM_002446	4294	chr19:45413243-45413302	19q13.2
AGI_HUM1_OLIGO_A_24_P103060	MCFD2	Hs.293689	NM_139279	90411	chr2:47104675-47104616	2p21
AGI_HUM1_OLIGO_A_23_P27571	MCOLN1	Hs.546413	NM_020533	57192	chr19:7499764-7499823	19p13.2
AGI_HUM1_OLIGO_A_23_P19455	MDC1	Hs.433653	D79992	9656	chr6:30773963-30773904	6p21.33
AGI_HUM1_OLIGO_A_24_P927377	MDM4	Hs.497492	BM893624	4194		
AGI_HUM1_OLIGO_A_23_P150510	MED19	Hs.43619	NM_153450	219541	chr11:57246727-57246668	11q12.1

AGI_HUM1_OLIGO_A_23_P329890	MGC17839	Hs.380228	NM_174926	219902	chr11:119738903-119738962	11q23.3
AGI_HUM1_OLIGO_A_23_P334218	MGC21654	Hs.492716	NM_145647	93594	chr8:124120749-124120808	8q24.13
AGI_HUM1_OLIGO_A_24_P373726	MGC34079	Hs.440722	BC025783	147687	chr19:63112512-63112453	19q13.43
AGI_HUM1_OLIGO_A_24_P339272	MGC40157	Hs.368934	NM_152350	125144	chr17:16543279-16543583	17p11.2
AGI_HUM1_OLIGO_A_23_P153256	MGC4728	Hs.230260	AK057209	374928	chr19:62710815-62710874	19q13.43
AGI_HUM1_OLIGO_A_23_P502425	MRPL47	Hs.283734	NM_020409	57129	chr3:180627615-180627556	3q26.33
AGI_HUM1_OLIGO_A_23_P111373	MRS2L	Hs.533291	NM_020662	57380	chr6:24532216-24532275	6p22.2
AGI_HUM1_OLIGO_A_24_P925586	MTVR1	Hs.25723	AF085877	23625	chr11:65112557-65112498	11q13.1
AGI_HUM1_OLIGO_A_23_P154208	NAGK	Hs.7036	NM_017567	55577	chr2:71274388-71275177	2p13.3
AGI_HUM1_OLIGO_A_24_P940763	NS5ATP13TP2	Hs.445081	AK021720	220323		
AGI_HUM1_OLIGO_A_23_P42045	ORC3L	Hs.410228	NM_181837	23595	chr6:88372512-88372571	6q15
AGI_HUM1_OLIGO_A_24_P52801	OTUB1	Hs.473788	AF161381	55611	chr11:63539433-63539700	11q13.1
AGI_HUM1_OLIGO_A_24_P794892	PEX3	Hs.7277	BF439431	8504	chr6:143783804-143783745	6q24.2
AGI_HUM1_OLIGO_A_24_P181120	PFDN5	Hs.288856	NM_002624	5204	chr12:51978186-51979363	12q13.13
AGI_HUM1_OLIGO_A_32_P229299	PHF6	Hs.356501	NM_032458	84295	chrX:132268337-132268396	Xq26.2
AGI_HUM1_OLIGO_A_32_P97763	PPP1R16B	Hs.45719	NM_015568	26051	chr20:38234443-38234502	20q11.23
AGI_HUM1_OLIGO_A_23_P96350	PRAF2	Hs.29595	NM_007213	11230	chrX:47955072-47955013	Xp11.23
AGI_HUM1_OLIGO_A_24_P941787	PRPF4B	Hs.159014	NM_003913	8899	chr6:4010126-4010185	6p25.2
AGI_HUM1_OLIGO_A_24_P309317	PSAP	Hs.523004	AK057878	5660	chr10:72923863-72923451	10q22.1
AGI_HUM1_OLIGO_A_23_P67466	PSMD8	Hs.78466	NM_002812	5714	chr19:43563453-43564629	19q13.2
AGI_HUM1_OLIGO_A_23_P309701	PTPN2	Hs.123352	NM_002828	5771	chr18:12784039-12783980	18p11.21
AGI_HUM1_OLIGO_A_24_P918065	PXMP2	Hs.430299	BC009836	5827	chr12:131520348-131520289	12q24.33
AGI_HUM1_OLIGO_A_24_P226198	RAD50	Hs.242635	NM_005732	10111	chr5:132055291-132055350	5q23.3
AGI_HUM1_OLIGO_A_23_P9523	RBKS	Hs.11916	NM_022128	64080	chr2:27979079-27979020	2p23.2
AGI_HUM1_OLIGO_A_23_P18196	RFC4	Hs.518475	NM_002916	5984	chr3:187829043-187828914	3q27.3
AGI_HUM1_OLIGO_A_23_P320578	RGS16	Hs.413297	NM_002928	6004	chr1:179807311-179807252	1q25.3
AGI_HUM1_OLIGO_A_23_P105002	ROM1	Hs.281564	NM_000327	6094	chr11:62157864-62157923	11q12.3
AGI_HUM1_OLIGO_A_23_P256455	RPA3	Hs.487540	NM_002947	6119	chr7:7421019-7420960	7p21.3
AGI_HUM1_OLIGO_A_23_P20225	RRM2B	Hs.512592	NM_015713	50484	chr8:103173817-103173758	8q22.3
AGI_HUM1_OLIGO_A_24_P383523	SAMD4	Hs.98259	NM_015589	23034	chr14:53245762-53245821	14q22.2
AGI_HUM1_OLIGO_A_32_P68516	SFRS3	Hs.405144	AL050041	6428	chr6:36616726-36616667	6p21.31
AGI_HUM1_OLIGO_A_23_P315892	SIAT7F	Hs.109672	NM_013443	30815	chr9:126024169-126024110	9q34.11
AGI_HUM1_OLIGO_A_23_P389391	SLC12A4	Hs.10094	NM_005072	6560	chr16:67754821-67754762	16q22.1
AGI_HUM1_OLIGO_A_23_P202720	SLC35C1	Hs.12211	NM_018389	55343	chr11:45798676-45798735	11p11.2
AGI_HUM1_OLIGO_A_23_P24345	SLC39A13	Hs.523664	NM_152264	91252	chr11:47402247-47402306	11p11.2
AGI_HUM1_OLIGO_A_24_P23400	SLC6A8	Hs.540696	U17986	6535	chrX:151427550-151427609	Xq28
AGI_HUM1_OLIGO_A_23_P19543	SRPK1	Hs.443861	NM_003137	6732	chr6:35847812-35847753	6p21.31
AGI_HUM1_OLIGO_A_24_P303915	SSNA1	Hs.530314	NM_003731	8636	chr9:135441577-135441636	9q34.3
AGI_HUM1_OLIGO_A_23_P165891	TAF1B	Hs.128275	NM_005680	9014	chr2:10081532-10081591	2p25.1
AGI_HUM1_OLIGO_A_23_P80062	TAF4	Hs.473243	NM_003185	6874	chr20:61235816-61235757	20q13.33
AGI_HUM1_OLIGO_A_32_P204691	TMAP1	Hs.250723	BC038747	439921	chr17:75266785-75266844	17q25.1
AGI_HUM1_OLIGO_A_24_P566916	TncRNA	Hs.523789	AK027191	283131	chr11:64968634-64968693	11q13.1
AGI_HUM1_OLIGO_A_24_P218265	TNFRSF10B	Hs.521456	NM_003842	8795	chr8:22899773-22899714	8p21.2
AGI_HUM1_OLIGO_A_32_P64966	TPTE	Hs.122986	NM_013315	7179	chr21:10010084-10007359	21p11.2
AGI_HUM1_OLIGO_A_23_P8311	TTRAP	Hs.403010	NM_016614	51567	chr6:24758372-24758313	6p22.2
AGI_HUM1_OLIGO_A_24_P175519	TXN	Hs.435136	NM_003329	7295	chr9:108392960-108386925	9q31.3
AGI_HUM1_OLIGO_A_24_P313109	Ufm1	Hs.524969	NM_016617	51569	chr13:36734027-36734086	13q13.3
AGI_HUM1_OLIGO_A_23_P201998	WAC	Hs.435610	NM_016628	51322	chr10:28913670-28913729	10p12.1
AGI_HUM1_OLIGO_A_24_P83437	ZNF326	Hs.306221	NM_181781	284695	chr1:89937780-89937839	1p22.2
AGI_HUM1_OLIGO_A_23_P376735	ZNF524	Hs.440291	NM_153219	147807	chr19:60806186-60806245	19q13.42

GO analysis results

System	Gene Category	EASE scor	Gene Symbol
GO Biological Process	**mitotic cell cycle**	**2.53E-03**	**CCNB1; CDC2; CDKN1A; CKS1B; DCTN2; EML4; GMNN; ORC3L; RFC4; RPA3**
GO Biological Process	**cell cycle**	**3.48E-03**	**CCNB1; CDC2; CDKN1A; CKS1B; DCTN2; EML4; GAJ; GMNN; ORC3L; PSMD8; RAD50; RFC4; RPA3; SLC12A4**
GO Biological Process	**cell proliferation**	**4.38E-03**	**CCNB1; CDC2; CDKN1A; CKS1B; DCTN2; EML4; FLJ12484; GAJ; GMNN; MDM4; ORC3L; PSMD8; RAD50; RFC4; RPA3; SLC12A4; TXN**
GO Biological Process	**nuclear division**	**1.20E-02**	**CCNB1; CDC2; DCTN2; EML4; GAJ; RAD50**
GO Biological Process	**M phase**	**1.39E-02**	**CCNB1; CDC2; DCTN2; EML4; GAJ; RAD50**
GO Cellular Component	**vacuole**	**1.93E-02**	**CSE-C; DPP7; MAN2B1; PSAP; TXN**
GO Molecular Function	**protein kinase activity**	**2.40E-02**	**CDC2; CDKN1A; CKS1B; DYRK2; FGFR1; HRI; MAP3K10; PRPF4B; SRPK1**
GO Cellular Component	**replication fork**	**3.71E-02**	**ORC3L; RFC4; RPA3**
GO Molecular Function	**protein serine/threonine kinase activity**	**4.89E-02**	**CDC2; CKS1B; DYRK2; HRI; MAP3K10; PRPF4B; SRPK1**

Genes that are associated with G2 checkpoint function by Bayesian analysis

SUID	GeneSymbol	CLID	Accession	LLID	ChromosomeLocat	Cytoband
AGI_HUM1_OLIGO_A_24_P37319	ACSL3	Hs.471461	AB061712	2181	chr2:224001811-22	2q36.1
AGI_HUM1_OLIGO_A_23_P312179	ALMS1	Hs.184720	AB002326	7840	chr2:73802351-738	2p13.1
AGI_HUM1_OLIGO_A_23_P20970	APG12L	Hs.264482	BC011033	9140	chr5:115243648-11	5q22.3
AGI_HUM1_OLIGO_A_24_P144527	ARV1	Hs.275736	AK026629	64801	chr1:228159182-22	1q42.2
AGI_HUM1_OLIGO_A_23_P159539	ASMTL	Hs.533514	AK090498	8623	chrY:1167635-1167	Xp22.33
AGI_HUM1_OLIGO_A_23_P412526	BCAP29	Hs.303787	NM_018844	55973	chr7:106795072-10	7q22.3
AGI_HUM1_OLIGO_A_24_P346210	BTN2A2	Hs.373938	BC017497	10385	chr6:26498308-264	6p22.2
AGI_HUM1_OLIGO_A_23_P97853	C10orf57	Hs.169982	NM_025125	80195	chr10:81516617-81	10q22.3
AGI_HUM1_OLIGO_A_24_P116233	C13orf1	Hs.44235	AF055016	57213	chr13:48293707-48	13q14.2
AGI_HUM1_OLIGO_A_24_P860797	C13orf9	Hs.109520	AK094335	51028	chr2:71391562-713	2p13.3
AGI_HUM1_OLIGO_A_23_P99579	C14orf142	Hs.20142	NM_032490	84520	chr14:91660044-91	14q32.12
AGI_HUM1_OLIGO_A_23_P25913	C14orf168	Hs.525445	NM_031427	83544	chr14:72146251-72	14q24.3
AGI_HUM1_OLIGO_A_24_P330303	C14orf31	Hs.434914	NM_152330	122786	chr14:50186666-50	14q22.1
AGI_HUM1_OLIGO_A_23_P100141	C16orf28	Hs.161279	NM_023076	65259	chr16:1355346-135	16p13.3
AGI_HUM1_OLIGO_A_23_P412554	C18orf25	Hs.116486	NM_145055	147339	chr18:42095005-42	18q21.1
AGI_HUM1_OLIGO_A_32_P234722	C19orf13	Hs.407368	NM_015578	26065		
AGI_HUM1_OLIGO_A_23_P120364	C20orf149	Hs.79625	NM_024299	79144	chr20:62879788-62	20q13.33
AGI_HUM1_OLIGO_A_23_P386241	C20orf55	Hs.534072	NM_031424	83541	chr20:821839-8218	20p13
AGI_HUM1_OLIGO_A_23_P40433	C21orf63	Hs.208358	NM_058187	59271	chr21:32750413-32	21q22.11
AGI_HUM1_OLIGO_A_23_P307761	CABLES2	Hs.301040	BC003122	81928	chr20:61649348-61	20q13.33
AGI_HUM1_OLIGO_A_23_P307940	CAPZA2	Hs.446123	NM_006136	830	chr7:116112391-11	7q31.2
AGI_HUM1_OLIGO_A_23_P50020	COG1	Hs.283109	NM_018714	9382	chr17:71800463-71	17q25.1
AGI_HUM1_OLIGO_A_24_P10657	CTL2	Hs.515134	NM_020428	57153	chr19:10615558-10	19p13.2
AGI_HUM1_OLIGO_A_24_P115762	CTSC	Hs.128065	NM_148170	1075	chr11:87747550-87	11q14.2
AGI_HUM1_OLIGO_A_24_P944144	DATF1	Hs.517172	AB002331	11083	chr20:62245012-62	20q13.33
AGI_HUM1_OLIGO_A_23_P47839	DDX55	Hs.286173	AB046815	57696	chr12:122457722-1	12q24.31
AGI_HUM1_OLIGO_A_23_P14975	DKFZP434A1319	Hs.307084	NM_032140	84080	chr16:67473326-67	16q22.1
AGI_HUM1_OLIGO_A_24_P316364	DKFZP566E144	Hs.7527	BC003502	25996	chr11:113858220-1	11q23.2
AGI_HUM1_OLIGO_A_24_P221414	DNCI1	Hs.440364	NM_004411	1780	chr7:95338844-953	7q21.3
AGI_HUM1_OLIGO_A_24_P365807	EFNB1	Hs.144700	NM_004429	1947	chrX:66928624-669	Xq13.1
AGI_HUM1_OLIGO_A_24_P913374	EIF4EBP2	Hs.522995	AK001936	1979	chr10:71531037-71	10q22.1
AGI_HUM1_OLIGO_A_23_P50331	FAM32A	Hs.4766	NM_014077	26017	chr19:16162870-16	19p13.12
AGI_HUM1_OLIGO_A_24_P784846	FBXO22	Hs.458959	AK021906	26263	chr15:73937039-73	15q24.2
AGI_HUM1_OLIGO_A_23_P85716	FCGR2A	Hs.352642	NM_021642	2212	chr1:158756796-15	1q23.3
AGI_HUM1_OLIGO_A_23_P417237	FEM1C	Hs.47367	NM_020177	56929	chr5:114936731-11	5q22.3
AGI_HUM1_OLIGO_A_32_P213086	FLJ21865	Hs.29288	NM_022759	64772		
AGI_HUM1_OLIGO_A_24_P20139	FLJ37953	Hs.204619	AK095272	129450	chr2:201003224-20	2q33.1
AGI_HUM1_OLIGO_A_24_P235049	FTHFSDC1	Hs.268698	NM_015440	25902	chr6:151444631-15	6q25.1
AGI_HUM1_OLIGO_A_23_P69908	GLRX	Hs.28988	NM_002064	2745	chr5:95223935-952	5q15
AGI_HUM1_OLIGO_A_24_P294233	GLS	Hs.116448	NM_014905	2744	chr2:192032316-19	2q32.2
AGI_HUM1_OLIGO_A_23_P311732	GNG12	Hs.431101	NM_018841	55970	chr1:67539947-675	1p31.2
AGI_HUM1_OLIGO_A_24_P39654	GRB2	Hs.444356	NM_002086	2885	chr17:73925945-73	17q25.1
AGI_HUM1_OLIGO_A_24_P274640	GTF2H2	Hs.191356	NM_001515	2966	chr5:68988965-689	5q13.2
AGI_HUM1_OLIGO_A_24_P916141	HAN11	Hs.410596	AK025925	10238	chr17:62144552-62	17q23.3
AGI_HUM1_OLIGO_A_23_P25403	HCFC2	Hs.506558	NM_013320	29915	chr12:102999562-1	12q23.3
AGI_HUM1_OLIGO_A_24_P371670	HNRPA0	Hs.96996	NM_006805	10949	chr5:137165622-13	5q31.2
AGI_HUM1_OLIGO_A_24_P33077	HOXB2	Hs.514289	NM_002145	3212	chr17:47095623-47	17q21.32
AGI_HUM1_OLIGO_A_23_P40588	HSC20	Hs.182898	NM_172002	150274	chr22:27466507-27	22q12.1
AGI_HUM1_OLIGO_A_24_P377277	HSPA4	Hs.90093	X67643	3308	chr5:132511544-13	5q31.1
AGI_HUM1_OLIGO_A_24_P48983	JM11	Hs.522643	BC008769	90060	chrX:47951394-479	Xp11.23
AGI_HUM1_OLIGO_A_23_P213661	KIAA0433	Hs.212046	NM_015216	23262	chr5:102615015-10	5q21.1
AGI_HUM1_OLIGO_A_24_P72518	KIAA0828	Hs.195058	NM_015328	23382	chr7:128622911-12	7q32.1
AGI_HUM1_OLIGO_A_23_P38876	LIPE	Hs.95351	NM_005357	3991	chr19:47597658-47	19q13.2
AGI_HUM1_OLIGO_A_24_P475556	LOC146346	Hs.109731	AK057359	146346	chr16:74261081-74	16q22.3
AGI_HUM1_OLIGO_A_23_P143958	LOC200916	Hs.380933	AL110170	200916	chr3:171905176-17	3q26.2
AGI_HUM1_OLIGO_A_24_P940620	LOC284001	Hs.307972	BC040264	284001	chr17:80794406-80	17q25.3
AGI_HUM1_OLIGO_A_24_P649388	LOC348926	Hs.455099	BM561118	348926	chr21:32760422-32	21q22.11
AGI_HUM1_OLIGO_A_24_P100673	LOC51234	Hs.250905	NM_016454	51234	chr15:32238195-32	15q14
AGI_HUM1_OLIGO_A_24_P393811	LOC54499	Hs.93832	NM_019026	54499	chr1:162899844-16	1q24.1
AGI_HUM1_OLIGO_A_23_P122007	LOC90355	Hs.482976	NM_033211	90355	chr5:102690028-10	5q21.1
AGI_HUM1_OLIGO_A_24_P93316	LOC96610	Hs.449601	AK026408	96610	chr22:20998101-20	22q11.22
AGI_HUM1_OLIGO_A_23_P207319	MAP3K14	Hs.404183	NM_003954	9020	chr17:43816190-43	17q21.31
AGI_HUM1_OLIGO_A_32_P47566	MGC10067	Hs.190447	BC013425	134510	chr5:158683117-15	5q33.3
AGI_HUM1_OLIGO_A_23_P410613	MGC17943	Hs.257664	NM_152261	90488	chr12:105870000-1	12q23.3
AGI_HUM1_OLIGO_A_24_P96171	MGC4093	Hs.31895	NM_030578	80776	chr19:46552230-46	19q13.2
AGI_HUM1_OLIGO_A_32_P112655	MGC5509	Hs.303899	AK058000	79074	chr2:105572364-10	2q12.1
AGI_HUM1_OLIGO_A_23_P142310	MKNK2	Hs.515032	NM_017572	2872	chr19:1988572-198	19p13.3
AGI_HUM1_OLIGO_A_23_P8339	MRPL18	Hs.416998	NM_014161	29074	chr6:160128382-16	6q25.3
AGI_HUM1_OLIGO_A_23_P113623	MRPL45	Hs.462913	NM_032351	84311	chr17:36853876-36	17q12
AGI_HUM1_OLIGO_A_23_P117727	MtFMT	Hs.531615	NM_139242	123263	chr15:63014288-63	15q22.31
AGI_HUM1_OLIGO_A_24_P285831	NDUFB5	Hs.518424	NM_002492	4711	chr3:180654694-18	3q26.33
AGI_HUM1_OLIGO_A_23_P415984	NPAS2	Hs.156832	NM_002518	4862	chr2:101228706-10	2q11.2

AGI_HUM1_OLIGO_A_32_P49423	NPM1	Hs.519452	NM_002520	4869	chr5:170813246-17	5q35.1
AGI_HUM1_OLIGO_A_24_P270376	NUFIP1	Hs.525006	BC017745	26747	chr13:43315659-43	13q14.12
AGI_HUM1_OLIGO_A_24_P241183	OCIL	Hs.268326	NM_013269	29121	chr12:9724817-972	12p13.31
AGI_HUM1_OLIGO_A_24_P414183	OGG1	Hs.380271	NM_016819	4968	chr3:9774021-977	3p25.3
AGI_HUM1_OLIGO_A_24_P65949	PDXK	Hs.284491	BC021550	8566	chr21:44013499-44	21q22.3
AGI_HUM1_OLIGO_A_23_P159671	PHKA2	Hs.54941	NM_000292	5256	chrX:18272745-18	Xp22.13
AGI_HUM1_OLIGO_A_23_P134464	PMPCB	Hs.184211	NM_004279	9512	chr7:102513216-10	7q22.1
AGI_HUM1_OLIGO_A_32_P73796	PPM1E	Hs.245044	NM_014906	22843	chr17:57536431-57	17q23.2
AGI_HUM1_OLIGO_A_23_P110725	PRKAA1	Hs.43322	NM_006251	5562	chr5:40808534-408	5p13.1
AGI_HUM1_OLIGO_A_24_P390909	PRX	Hs.205457	AF321192	57716	chr19:45596552-45	19q13.2
AGI_HUM1_OLIGO_A_32_P61757	PTPN11	Hs.506852	BC030949	5781	chr12:111359534-1	12q24.13
AGI_HUM1_OLIGO_A_24_P125871	RIPK4	Hs.517310	NM_020639	54101	chr21:42045288-42	21q22.3
AGI_HUM1_OLIGO_A_24_P937582	RNASEH1	Hs.502765	AK027610	246243	chr2:3154680-315	2p25.3
AGI_HUM1_OLIGO_A_24_P48408	RNMT	Hs.8086	NM_003799	8731	chr18:13754222-13	18p11.21
AGI_HUM1_OLIGO_A_23_P417363	RSNL2	Hs.122927	AK057267	79745	chr2:29371946-29	2p23.2
AGI_HUM1_OLIGO_A_24_P354523	SCYE1	Hs.480465	NM_004757	9255	chr4:107728818-10	4q24
AGI_HUM1_OLIGO_A_24_P926972	SENP3	Hs.513926	AK000923	26168	chr17:7669688-76	17p13.1
AGI_HUM1_OLIGO_A_32_P63913	SF3A3	Hs.77897	BC002395	10946	chr1:37847039-37	1p34.3
AGI_HUM1_OLIGO_A_23_P87684	SIAT8A	Hs.408614	X77922	6489		
AGI_HUM1_OLIGO_A_32_P15389	SIVA	Hs.112058	NM_021709	10572		
AGI_HUM1_OLIGO_A_24_P64182	SLC2A8	Hs.179522	NM_014580	29988	chr9:125545507-12	9q33.3
AGI_HUM1_OLIGO_A_23_P501372	SMCR7	Hs.534534	NM_139162	125170	chr17:18369454-18	17p11.2
AGI_HUM1_OLIGO_A_23_P58466	SMN2	Hs.202179	NM_000344	6607	chr5:69077604-69	5q13.2
AGI_HUM1_OLIGO_A_23_P383977	SNAPC5	Hs.30174	NM_006049	10302	chr15:64503507-64	15q22.31
AGI_HUM1_OLIGO_A_24_P341882	TESK1	Hs.79358	NM_006285	7016	chr9:35599401-35	9p13.3
AGI_HUM1_OLIGO_A_23_P378526	TNFRSF6B	Hs.434878	NM_016434	8771	chr20:63053756-63	20q13.33
AGI_HUM1_OLIGO_A_23_P407718	TRIM59	Hs.212957	NM_173084	286827	chr3:161476786-16	3q25.33
AGI_HUM1_OLIGO_A_32_P76720	TU12B1-TY	Hs.48428	NM_016575	51559	chr12:102669370-1	12q23.3
AGI_HUM1_OLIGO_A_24_P316619	UBE2H	Hs.344165	U25433	7328	chr7:129090155-12	7q32.2
AGI_HUM1_OLIGO_A_24_P265135	UBE3C	Hs.118351	BC014029	9690	chr7:156417464-15	7q36.3
AGI_HUM1_OLIGO_A_23_P114164	UBQLN2	Hs.522668	NM_013444	29978	chrX:55559844-55	Xp11.21
AGI_HUM1_OLIGO_A_24_P188325	UCHL5	Hs.145469	BC025369	51377	chr1:190278571-19	1q31.2
AGI_HUM1_OLIGO_A_24_P51375	VIL2	Hs.487027	AF351612	7430	chr6:159130012-15	3q11.2
AGI_HUM1_OLIGO_A_24_P362394	VPS45A	Hs.443750	NM_007259	11311	chr1:147271493-14	1q21.2
AGI_HUM1_OLIGO_A_24_P242299	ZNF265	Hs.194718	NM_005455	9406	chr1:70899188-70	1p31.1

GO analysis results

System	Gene Category	EASE score	Gene Symbol
GO Biological	**regulation of protein biosynthesis**	**1.10E-02**	**EIF4EBP2; MKNK2; PRKAA1**
GO Molecular	**hydrolase activity**	**2.53E-02**	**C13ORF9; CTSC; DKFZP566E144; FLJ21865; GLS; GNG12; KIAA0433; KIAA0828; LIPE; MGC10067;OGG1; PMPCB; PPM1E; PTPN11; RNASEH1; SENP3; UCHL5**
GO Biological	**regulation of biosynthesis**	**2.63E-02**	**EIF4EBP2; MKNK2; PRKAA1**
GO Molecular	**catalytic activity**	**3.26E-02**	**ARV1; ASMTL; C13ORF9; CTSC; DKFZP434A1319; DKFZP566E144; FBXO22; FLJ21865; GLRX; GLS; GNG12; KIAA0433; KIAA0828; LIPE; MAP3K14; MGC10067; MGC4093; MKNK2; MTFMT; NDUFB5; OGG1; PDXK; PHKA2; PMPCB; PPM1E; PRKAA1; PTPN11; RNASEH1; RNMT; SENP3; SIAT8A; TESK1; TNFRSF6B; UCHL5**
GO Cellular C	**mitochondrion**	**3.80E-02**	**C13ORF9; DKFZP566E144; GLS; MRPL18; MRPL45; MTFMT; NDUFB5; OGG1; PMPCB; RNASEH1**
GO Biological	**RNA metabolism**	**4.55E-02**	**HNRPA0; NUFIP1; RNASEH1; RNMT; SCYE1; SF3A3; ZNF265**
GO Molecular	**RNA binding**	**4.63E-02**	**HNRPA0; NPM1; NUFIP1; RNASEH1; RNMT; SCYE1; SF3A3; ZNF265**

Genes that are associated with G1 checkpoint function by SAM analysis

SUID	GeneSymbol	CLID	Accession	LLID	ChromosomeLocation	Cytoband
AGI_HUM1_OLIGO_A_23_P200298	AGL	Hs.904	NM_000028	178	chr1:99852152-99852211	1p21.2
AGI_HUM1_OLIGO_A_24_P201531	ARCN1	Hs.33642	NM_001655	372	chr11:118010634-118010693	11q23.3
AGI_HUM1_OLIGO_A_32_P50275	CD59	Hs.278573	AK095453	966	chr11:33692213-33692272	11p13
AGI_HUM1_OLIGO_A_24_P171549	CDCA7	Hs.470654	AK075134	83879	chr2:174435437-174435496	2q31.1
AGI_HUM1_OLIGO_A_24_P89457	CDKN1A	Hs.370771	L47232	1026	chr6:36699033-36699092	6p21.31
AGI_HUM1_OLIGO_A_23_P45917	CKS1B	Hs.374378	NM_001826	1163	chr1:152168319-152168378	1q22
AGI_HUM1_OLIGO_A_23_P52610	DDB2	Hs.446564	NM_000107	1643	chr11:47224932-47224991	11p11.2
AGI_HUM1_OLIGO_A_23_P24414	EFEMP2	Hs.381870	AB030655	30008	chr11:65410842-65410783	11q13.1
AGI_HUM1_OLIGO_A_24_P222844	FLJ10330	Hs.342307	NM_018061	55119	chr1:108589168-108589227	1p13.3
AGI_HUM1_OLIGO_A_24_P193509	FLJ31153	Hs.514179	BC022321	123811	chr16:15940120-15933885	16p13.11
AGI_HUM1_OLIGO_A_32_P45493	FUSIP1	Hs.3530	NM_006625	10772	chr1_random:1393456-1393397	
AGI_HUM1_OLIGO_A_23_P55251	ITGA3	Hs.265829	NM_005501	3675	chr17:48642003-48642062	17q21.33
AGI_HUM1_OLIGO_A_24_P925586	MTVR1	Hs.25723	AF085877	23625	chr11:65112557-65112498	11q13.1
AGI_HUM1_OLIGO_A_23_P12140	RPL5	Hs.532359	NM_000969	6125	chr1:92770931-92770990	1p22.1
AGI_HUM1_OLIGO_A_23_P389391	SLC12A4	Hs.10094	NM_005072	6560	chr16:67754821-67754762	16q22.1
AGI_HUM1_OLIGO_A_32_P64966	TPTE	Hs.122986	NM_013315	7179	chr21:10010084-10007359	21p11.2

Genes that are associated with G2 checkpoint function by SAM analysis

SUID	GeneSymb	CLID	Accession	LLID	ChromosomeLocation
AGI_HUM1_OLIGO_A_23_P32021	FANCC	Hs.494529	NM_000136	2176	chr9:93202990-93202931
AGI_HUM1_OLIGO_A_24_P390909	PRX	Hs.205457	AF321192	57716	chr19:45596552-45596493