

No.	probeset_id	ratio	gene	gene full name	gene assignment	ENSEMBL ID	seqname	start	stop
1	10586448	0.131	2810417H13 Rik	RIKEN cDNA 2810417H13 gene	NM_026515	ENSMUST0000045802	chr9	65738130	65751358
2	10554445	0.147	Prc1	protein regulator of cytokinesis 1	NM_145150	ENSMUST0000047549	chr7	87439351	87461145
3	10462796	0.157	Kif11	kinesin family member 11	NM_010615	ENSMUST0000012587	chr19	37450893	37496349
4	10487480	0.159	Bub1	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	NM_001113179	NM_009772	chr2	127626857	127657596
5	10359890	0.165	Nuf2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	NM_023284	ENSMUST0000111368	chr1	171428065	171461595
6	10515836	0.17	Ccnb1	cyclin B1	NM_172301	ENSMUST0000072119	chr4	118614665	118615957
7	10390707	0.177	Top2a	topoisomerase (DNA) II alpha	NM_011623	ENSMUST0000068031	chr11	98854261	98885429
8	10487340	0.177	Ncaph	non-SMC condensin I	NM_144818	ENSMUST00	chr2	126929562	126959679

				complex, subunit H		000037712			
9	10462632	0.179	Kif20b	kinesin family member 20B	NM_183046	ENSMUST00 000087341	chr19	34996851	35050233
10	10562637	0.18	Ccnb1	cyclin B1	NM_172301	ENSMUST00 000072119	chr7	49361266	49362555
11	10411739	0.182	Ccnb1	cyclin B1	NM_172301	ENSMUST00 000072119	chr13	101548687	101556441
12	10385248	0.183	Hmmr	hyaluronan mediated motility receptor (RHAMM)	NM_013552	ENSMUST00 000020579	chr11	40514897	40546924
13	10576883	0.184	Shcbp1	Shc SH2- domain binding protein 1	NM_011369	ENSMUST00 000022945	chr8	4735976	4779554
14	10404061	0.184	Hist1h2bb	histone cluster 1, H2bb	NM_175664	ENSMUST00 000099703	chr13	23838603	23839393
15	10474984	0.186	Nusap1	nucleolar and spindle associated protein 1	NM_133851	NM_001042 652	chr2	119444034	119476980
16	10525591	0.187	Kntc1	kinetochore associated 1	NM_001042 421	ENSMUST00 000031366	chr5	124199735	124271602
17	10361375	0.188	Fbxo5	F-box protein 5	NM_025995	ENSMUST00 000019907	chr10	4541076	4547383

18	10594774	0.188	Ccnb2	cyclin B2	NM_007630	ENSMUST00 000034742	chr9	70255496	70269361
19	10568714	0.188	Mki67	antigen identified by monoclonal antibody Ki 67	NM_001081 117	BC053453	chr7	142881471	142907979
20	10601011	0.189	Kif4	kinesin family member 4	NM_008446	ENSMUST00 000048962	chrX	97821076	97922553
21	10394978	0.189	Rrm2	ribonucleotid e reductase M2	NM_009104	ENSMUST00 000020980	chr12	25393119	25398973
22	10500327	0.191	Hist2h3c2	histone cluster 2, H3c2	NM_054045	BC015270	chr3	96042039	96043050
23	10404069	0.191	Hist1h1a	histone cluster 1, H1a	NM_030609	ENSMUST00 000055770	chr13	23855537	23856283
24	10399391	0.192	Gen1	Gen homolog 1, endonucleas e (Drosophila)	NM_177331	ENSMUST00 000052581	chr12	11246547	11272593
25	10497122	0.193	Depdc1a	DEP domain containing 1a	NM_001172 092	NM_029523	chr3	159158409	159192540
26	10350838	0.193	2810417H13 Rik	RIKEN cDNA 2810417H13 gene	NM_026515	ENSMUST00 000045802	chr1	158723643	158723975

27	10451805	0.195	Sgol1	shugoshin-like 1 (<i>S. pombe</i>)	NM_028232	ENSMUST0000024736	chr17	53815385	53828637
28	10384373	0.195	Figl1	fidgetin-like 1	NM_001163359	NM_021891	chr11	11700291	11708935
29	10416037	0.198	Pbk	PDZ binding kinase	NM_023209	ENSMUST0000022612	chr14	66424676	66436659
30	10404063	0.198	Hist1h2ab	histone cluster 1, H2ab	NM_175660	BC117110	chr13	23842957	23843462
31	10515431	0.198	Kif2c	kinesin family member 2C	NM_134471	ENSMUST0000065896	chr4	116832266	116855189
32	10485963	0.199	Arhgap11a	Rho GTPase activating protein 11A	NM_181416	ENSMUST0000040215	chr2	113670173	113688818
33	10497520	0.199	Ect2	ect2 oncogene	NM_007900	NM_001177625	chr3	26996144	27052761
34	10497831	0.199	Ccna2	cyclin A2	NM_009828	ENSMUST0000029270	chr3	36463787	36470920
35	10483401	0.2	Spc25	SPC25, NDC80 kinetochore complex component, homolog (<i>S. cerevisiae</i>)	NM_025565	ENSMUST0000112319	chr2	69031952	69044214
36	10521731	0.2	Ncapg	non-SMC condensin I complex,	NM_019438	ENSMUST0000117396	chr5	46061272	46091191

				subunit G					
37	10563883	0.202	Depdc1a	DEP domain containing 1a	NM_001172092	NM_029523	chr7	65133346	65136664
38	10436106	0.202	C330027C09 Rik	RIKEN cDNA C330027C09 gene	NM_172616	ENSMUST0000117994	chr16	48994301	49019815
39	10557156	0.206	Plk1	polo-like kinase 1 (Drosophila)	NM_011121	ENSMUST0000033154	chr7	129302952	129313389
40	10458195	0.206	Cdc25c	cell division cycle 25 homolog C (S. pombe)	NM_009860	ENSMUST0000060710	chr18	34892647	34911162
41	10476989	0.207	Gins1	GIN5 complex subunit 1 (Psf1 homolog)	NM_027014	NM_001163476	chr2	150735337	150757014
42	10454709	0.209	Kif20a	kinesin family member 20A	NM_001166406	NM_009004	chr18	34784649	34792931
43	10578690	0.21	Neil3	nei like 3 (E. coli)	NM_146208	ENSMUST0000047768	chr8	54672221	54724350
44	10361110	0.21	Dtl	denticleless homolog (Drosophila)	NM_029766	ENSMUST0000027933	chr1	193361244	193399413
45	10504957	0.212	Smc2	structural maintenance of chromosome s 2	NM_008017	ENSMUST0000102915	chr4	52452121	52501132

46	10520521	0.213	Cenpa	centromere protein A	NM_007681	ENSMUST0000031073	chr5	30969275	30977199
47	10408081	0.213	Hist1h1b	histone cluster 1, H1b	NM_020034	ENSMUST0000080511	chr13	21871752	21872423
48	10507112	0.216	Stil	Scf Tal1 interrupting locus	NM_009185		chr4	114672805	114715801
49	10450374	0.216	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	L78788	BC027314	chr17	35133669	35137691
50	10563780	0.216	E2f8	E2F transcription factor 8	NM_001013368	ENSMUST00000119223	chr7	56121799	56136966
51	10460738	0.218	Cdca5	cell division cycle associated 5	NM_026410	ENSMUST0000025704	chr19	6085097	6091775
52	10571870	0.218	Hmgb2	high mobility group box 2	NM_008252	ENSMUST0000067925	chr8	59990673	59993291
53	10474875	0.218	Casc5	cancer susceptibility candidate 5	NM_029617	ENSMUST0000028802	chr2	118872886	118929847
54	10346365	0.218	Sgol2	shugoshin-like 2 (S. pombe)	NM_199007	NM_001177867	chr1	58052910	58082741
55	10382998	0.218	Birc5	baculoviral IAP repeat-containing 5	NM_001012273	NM_009689	chr11	117710551	117717057
56	10353420	0.218	Mcm3	minichromos	NM_008563	ENSMUST00	chr1	20793054	20810341

				ome maintenance deficient 3 (S. cerevisiae)		000053266				
57	10480432	0.218	Mastl	microtubule associated serine threonine kinase-like	ENSMUST0000028119		chr2	22973585	23011436	
58	10360985	0.219	Cenpf	centromere protein F	NM_001081363	ENSMUST0000027900	chr1	191465528	191511965	
59	10400589	0.219	C79407	expressed sequence C79407	NM_172578	BC052175	chr12	66233719	66273585	
60	10541729	0.221	Cdca3	cell division cycle associated 3	NM_013538	ENSMUST0000024270	chr6	124768585	124783716	
61	10377405	0.221	Aurkb	aurora kinase B	NM_011496	ENSMUST0000021277	chr11	68859145	68865166	
62	10391811	0.222	Kif18b	kinesin family member 18B	NM_197959	ENSMUST0000021311	chr11	102766841	102786406	
63	10591781	0.222	Anln	anillin, actin binding protein	NM_028390	ENSMUST0000040912	chr9	22136456	22193667	
64	10474825	0.224	D2Ert750e	DNA segment, Chr 2, ERATO Doi 750, expressed	NM_026412	ENSMUST0000028803	chr2	118639739	118660375	

65	10510172	0.225	Hmgb2	high mobility group box 2	NM_008252	ENSMUST0000067925	chr4	145632869	145634248
66	10575733	0.225	Cenpn	centromere protein N	NM_028131	ENSMUST0000034205	chr8	119445640	119465404
67	10420877	0.225	Esco2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	NM_028039	ENSMUST0000022613	chr14	66437875	66452739
68	10474381	0.225	Kif18a	kinesin family member 18A	NM_139303	ENSMUST0000028527	chr2	109120895	109181906
69	10350392	0.225	Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	NM_009791	ENSMUST0000053364	chr1	141351350	141390667
70	10462866	0.227	Cep55	centrosomal protein 55	NM_001164362	NM_028760	chr19	38129530	38148911
71	10477187	0.228	Tpx2	TPX2, microtubule-associated protein homolog (Xenopus laevis)	NM_001141977	NM_028109	chr2	152673782	152720790
72	10518350	0.23	Hmgb2	high mobility group box 2	NM_008252	BC083108	chr4	146191520	146192064

73	10419323	0.232	Dlgap5	discs, large (Drosophila) homolog-associated protein 5	NM_144553	NM_001145949	chr14	48007454	48038082
74	10399087	0.232	Ncapg2	non-SMC condensin II complex, subunit G2	NM_133762	ENSMUST0000084828	chr12	117643875	117702005
75	10518352	0.233	Hmgb2	high mobility group box 2	NM_008252	ENSMUST0000067925	chr4	146460527	146461095
76	10438690	0.237	Rfc4	replication factor C (activator 1) 4	NM_145480	NM_013506	chr16	23114006	23127803
77	10573261	0.238	Asf1b	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	NM_024184	ENSMUST0000005607	chr8	86479561	86494094
78	10534974	0.241	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)	NM_008568	ENSMUST0000000505	chr5	138605817	138613090
79	10406968	0.241	Cenpk	centromere protein K	NM_021790	NM_181061	chr13	105018691	105041728
80	10453715	0.243	Rab18	RAB18, member RAS	BC056351	BC056351	chr18	7548985	7549588

				oncogene family					
81	10414315	0.243	Cdkn3	cyclin-dependent kinase inhibitor 3	NM_028222	ENSMUST0000067426	chr14	47380232	47391636
82	10490104	0.245	Aurka	aurora kinase A	NM_011497	ENSMUST0000028997	chr2	172181690	172196015
83	10594251	0.247	Kif23	kinesin family member 23	NM_024245	ENSMUST0000034815	chr9	61765289	61794564
84	10369815	0.247	Cdk1	cyclin-dependent kinase 1	NM_007659	ENSMUST0000020099	chr10	68799383	68815664
85	10538832	0.25	Mad2l1	MAD2 mitotic arrest deficient-like 1 (yeast)	NM_019499	ENSMUST0000101343	chr6	66485462	66491023
86	10420426	0.252	F630043A04 Rik	RIKEN cDNA F630043A04 gene	NM_198605	ENSMUST0000022536	chr14	58425398	58445000
87	10452709	0.252	Ndc80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	NM_023294	ENSMUST0000024851	chr17	71845442	71876197
88	10487577	0.252	Ckap2l	cytoskeleton associated protein 2-like	NM_181589	ENSMUST0000052708	chr2	129094617	129122900

89	10565570	0.253	4632434I11R ik	RIKEN cDNA 4632434I11 gene	NM_001080 995	ENSMUST00 000032877	chr7	100006035	100022715
90	10601705	0.253	Cenpi	centromere protein I	NM_145924	BC030328	chrX	130842694	130897178
91	10474769	0.253	Bub1b	budding uninhibited by benzimidazol es 1 homolog, beta (S. cerevisiae)	NM_009773	ENSMUST00 000038341	chr2	118423992	118467327
92	10486255	0.255	Oip5	Opa interacting protein 5	NM_001042 653	NM_133851	chr2	119435268	119444241
93	10571680	0.255	Mlf1ip	myeloid leukemia factor 1 interacting protein	NM_027973	NM_001001 184	chr8	47637409	47665361
94	10411728	0.255	Cenph	centromere protein H	NM_021886	ENSMUST00 000075550	chr13	101529641	101545854
95	10568150	0.255	Kif22	kinesin family member 22	NM_145588	ENSMUST00 000106320	chr7	134171245	134185934
96	10572906	0.257	Mcm5	minichromos ome maintenance deficient 5, cell division	NM_008566	ENSMUST00 000005545	chr8	77633427	77652338

				cycle 46 (S. cerevisiae)					
97	10479811	0.259	Mcm10	minichromosome maintenance deficient 10 (S. cerevisiae)	NM_027290	ENSMUST0000027980	chr2	4911770	4933837
98	10544106	0.262	Zc3hav1	zinc finger CCCH type, antiviral 1	ENSMUST0000114898	ENSMUST0000114898	chr6	38495309	38495809
99	10504470	0.262	Melk	maternal embryonic leucine zipper kinase	NM_010790	ENSMUST0000045607	chr4	44313789	44377547
100	10548086	0.264	Rad51ap1	RAD51 associated protein 1	NM_009013	ENSMUST0000112221	chr6	126873433	126889573
101	10540738	0.266	Fancd2	Fanconi anemia, complementation group D2	NM_001033244	ENSMUST0000036340	chr6	113481679	113547011
102	10587508	0.266	Ttk	Ttk protein kinase	NM_009445	NM_001110265	chr9	83728325	83765993
103	10446074	0.266	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	NM_010931	NM_001111079	chr17	56442527	56462909

104	10352767	0.268	Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2	NM_010892	ENSMUST0000027931	chr1	193645412	193656928
105	10421029	0.268	Cdca2	cell division cycle associated 2	NM_175384	NM_001110162	chr14	68294678	68333898
106	10594426	0.27	Zwilch	Zwilch, kinetochore associated, homolog (Drosophila)	NM_026507	NM_145835	chr9	63984951	64020738
107	10493137	0.27	Iqgap3	IQ motif containing GTPase activating protein 3	NM_001033484	ENSMUST0000071812	chr3	87885973	87924970
108	10568731	0.272			---		chr7	143436704	143436871
109	10512065	0.274	Gm12387	predicted gene 12387	XR_032698		chr4	39842229	39843195
110	10496204	0.275	Cenpe	centromere protein E	NM_173762	ENSMUST0000062893	chr3	134875527	134936504
111	10528077	0.275	Dbf4	DBF4 homolog (S. cerevisiae)	NM_013726	ENSMUST0000002368	chr5	8396995	8422694
112	10524169	0.275	Pole	polymerase (DNA directed), epsilon	NM_011132	ENSMUST0000007296	chr5	110715364	110766474

113	10410560	0.275	Trip13	thyroid hormone receptor interactor 13	NM_027182	ENSMUST0000022053	chr13	74049906	74075215
114	10461723	0.277	Fam111a	family with sequence similarity 111, member A	BC038020	NM_026640	chr19	12648015	12664188
115	10533090	0.277	Rfc5	replication factor C (activator 1) 5	NM_028128	ENSMUST0000086461	chr5	117829154	117839042
116	10516246	0.279	Cdca8	cell division cycle associated 8	NM_026560	ENSMUST0000084296	chr4	124595708	124614147
117	10352048	0.279	Exo1	exonuclease 1	NM_012012	ENSMUST0000039725	chr1	177810929	177839424
118	10462973	0.279	Hells	helicase, lymphoid specific	NM_008234	ENSMUST0000025965	chr19	39005444	39042767
119	10577508	0.281	Ckap2	cytoskeleton associated protein 2	NM_001004140	ENSMUST0000046916	chr8	23278921	23296291
120	10450957	0.281	Cenpq	centromere protein Q	NM_031863	ENSMUST0000087114	chr17	41060004	41071500
121	10440794	0.283	2610039C10 Rik	RIKEN cDNA 2610039C10 gene	NM_025642	ENSMUST0000099554	chr16	90714919	90727628
122	10528915	0.283	Tyms	thymidylate synthase	NM_021288	NR_033402	chr5	30385367	30400135

123	10391461	0.283	Brca1	breast cancer 1	NM_009764	ENSMUST0000017290	chr11	101350078	101413179
124	10357436	0.285	Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog, <i>S. pombe</i>) (<i>S. cerevisiae</i>)	NM_008567	ENSMUST0000027601	chr1	130228167	130256241
125	10489078	0.287	Dsn1	DSN1, MIND kinetochore complex component, homolog (<i>S. cerevisiae</i>)	NM_025853	ENSMUST0000103129	chr2	156821001	156832811
126	10542079	0.287	Foxm1	forkhead box M1	NM_008021	BC065067	chr6	128312994	128335006
127	10371770	0.289	Gas2l3	growth arrest-specific 2 like 3	NM_001033331	NM_001079876	chr10	88874272	88906721
128	10590494	0.293	Kif15	kinesin family member 15	NM_010620	ENSMUST0000040717	chr9	122860182	122927851
129	10428672	0.293	Dscc1	defective in sister chromatid cohesion 1 homolog (<i>S. cerevisiae</i>)	NM_183089	ENSMUST0000023059	chr15	54907656	54922046

130	10368370	0.297	Gm8681	predicted gene 8681	XR_032130		chr10	25552961	25553502
131	10352709	0.299	Nsl1	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	NM_198654	ENSMUST0000078259	chr1	192886903	192908437
132	10409190	0.299	Cenpp	centromere protein P	NM_025495	ENSMUST0000021818	chr13	49559396	49748154
133	10474902	0.299	Rad51	RAD51 homolog (S. cerevisiae)	NM_011234	ENSMUST0000028795	chr2	118938553	118961809
134	10514466	0.299	Jun	Jun oncogene	NM_010591	ENSMUST0000107094	chr4	94715746	94718878
135	10437945	0.301	Mcm4	minichromosome maintenance deficient 4 homolog (S. cerevisiae)	NM_008565	ENSMUST0000023353	chr16	15623994	15637451
136	10492558	0.301	Smc4	structural maintenance of chromosomes 4	NM_133786	ENSMUST0000042901	chr3	68808894	68838551
137	10428763	0.301	Atad2	ATPase family, AAA domain containing 2	NM_027435	ENSMUST0000038194	chr15	57925601	57966637

138	10426669	0.301	Troap	trophinin associated protein	NM_030159	NM_001162506	chr15	98905409	98913838
139	10356461	0.301	Hjrp	Holliday junction recognition protein	NM_198652	BC057309	chr1	90155662	90174154
140	10432511	0.304	Racgap1	Rac GTPase-activating protein 1	NM_012025	ENSMUST0000023756	chr15	99450722	99482062
141	10396068	0.306	Ppil5	peptidylprolyl isomerase (cyclophilin) like 5	NM_001081406	ENSMUST00000110621	chr12	70269808	70279797
142	10379127	0.308	Spag5	sperm associated antigen 5	NM_017407	ENSMUST0000045026	chr11	78115099	78135959
143	10554325	0.308	5730590G19 Rik	RIKEN cDNA 5730590G19 gene	NM_029835	ENSMUST0000035977	chr7	86805082	86843246
144	10437040	0.31	Chaf1b	chromatin assembly factor 1, subunit B (p60)	NM_028083	ENSMUST0000023666	chr16	93884146	93906360
145	10367076	0.31	Prim1	DNA primase, p49 subunit	NM_008921	ENSMUST0000026461	chr10	127452228	127467086
146	10391339	0.312	Psmc3ip	proteasome (prosome, macropain) 26S subunit,	NM_008949	ENSMUST0000019447	chr11	100953471	100956717

				ATPase 3, interacting protein					
147	10467637	0.314	Arhgap19	Rho GTPase activating protein 19	NM_027667	NM_001163 495	chr19	41841078	41876524
148	10405185	0.316	Cks2	CDC28 protein kinase regulatory subunit 2	NM_025415	BC022647	chr13	51740694	51746023
149	10478160	0.316	Fam83d	family with sequence similarity 83, member D	BC068129	BC064129	chr2	158593776	158612373
150	10426016	0.319	Gtse1	G two S phase expressed protein 1	NM_013882	NM_001168 672	chr15	85690175	85707003
151	10521090	0.319	Tacc3	transforming , acidic coiled-coil containing protein 3	NM_001040 435	ENSMUST00 000074849	chr5	34000777	34021646
152	10547943	0.319	Ncapd2	non-SMC condensin I complex, subunit D2	NM_146171	ENSMUST00 000043848	chr6	125118025	125141613
153	10607747	0.321	Siah1b	seven in absentia 1B	NM_009173	ENSMUST00 000037928	chrX	160508635	160514072

154	10427166	0.321	Espl1	extra spindle poles-like 1 (S. cerevisiae)	NM_001014976	ENSMUST0000064924	chr15	102126724	102154788
155	10494428	0.321	Txnip	thioredoxin interacting protein	NM_001009935	NM_023719	chr3	96361880	96373525
156	10371591	0.321	4930547N16 Rik	RIKEN cDNA 4930547N16 gene	NM_029249	NM_029971	chr10	87554177	87609686
157	10548699	0.323	Gm8956	predicted gene 8956	XR_030853		chr6	133881605	133882427
158	10491805	0.325	Plk4	polo-like kinase 4 (Drosophila)	NM_011495	ENSMUST0000026858	chr3	40603963	40620805
159	10544501	0.325	Ezh2	enhancer of zeste homolog 2 (Drosophila)	NM_007971	NM_001146689	chr6	47480273	47545019
160	10353010	0.328	Mybl1	myeloblastos is oncogene-like 1	NM_008651	ENSMUST0000088658	chr1	9658912	9690290
161	10353004	0.328	Cks2	CDC28 protein kinase regulatory subunit 2	NM_025415	BC094919	chr1	8781724	8782300
162	10400649	0.33	Pole2	polymerase (DNA directed), epsilon 2	NM_011133	ENSMUST0000021359	chr12	70302760	70329177

				(p59 subunit)					
163	10606071	0.332	Ercc6l	excision repair cross-complementing rodent repair deficiency complementation group 6 - like	NM_146235	ENSMUST0000056904	chrX	99338296	99352372
164	10506118	0.332	Usp1	ubiquitin specific peptidase 1	NM_146144	ENSMUST0000030289	chr4	98590501	98602229
165	10390050	0.332	Eme1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	NM_177752	ENSMUST0000039949	chr11	94506314	94515068
166	10389606	0.332	Prr11	proline rich 11	NM_175563	ENSMUST0000051395	chr11	86902916	86922191
167	10403943	0.339	Hist1h2bm	histone cluster 1, H2bm	NM_178200	ENSMUST0000073900	chr13	21813967	21814347
168	10438378	0.339	Cdc45	cell division cycle 45 homolog (S. cerevisiae)	NM_009862	NM_001161623	chr16	18780545	18812065
169	10564978	0.339	Blm	Bloom syndrome homolog (human)	NM_007550	NM_001042527	chr7	87599977	87679996

170	10472916	0.342	Cdca7	cell division cycle associated 7	NM_025866	ENSMUST0000102691	chr2	72314265	72340390
171	10430825	0.344	Cenpm	centromere protein M	NM_025639	NM_178269	chr15	82064191	82075178
172	10368199	0.346	Myb	myeloblastos is oncogene	NM_010848	ENSMUST0000020158	chr10	20844736	20880790
173	10455813	0.346	Lmnb1	lamin B1	NM_010721	ENSMUST0000025486	chr18	56867518	56913078
174	10378053	0.346	Fam64a	family with sequence similarity 64, member A	NM_144526	ENSMUST0000021164	chr11	71856004	71860873
175	10582809	0.349	Tk1	thymidine kinase 1	NM_009387	ENSMUST0000026661	chr8	129000148	129000312
176	10515744	0.349	Cdc20	cell division cycle 20 homolog (S. cerevisiae)	NM_023223	ENSMUST0000006565	chr4	118105506	118109947
177	10495574	0.349	Sass6	spindle assembly 6 homolog (C. elegans)	NM_028349	NM_030016	chr3	116297926	116332065
178	10421877	0.351	Diap3	diaphanous homolog 3 (Drosophila)	NM_019670	ENSMUST0000022599	chr14	86949278	87541031
179	10355329	0.351	Bard1	BRCA1 associated RING domain 1	NM_007525	ENSMUST0000027393	chr1	71076939	71149492

180	10503416	0.351	Calb1	calbindin 1	NM_009788	ENSMUST00 000029876	chr4	15808411	15835211
181	10425945	0.351	Fbln1	fibulin 1	NM_010180	ENSMUST00 000057410	chr15	85036441	85116724
182	10546163	0.354	Mcm2	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	NM_008564	ENSMUST00 000058011	chr6	88833468	88848694
183	10374400	0.354	Fbxo48	F-box protein 48	NM_176982	ENSMUST00 000061327	chr11	16851413	16854775
184	10371578	0.356	Ascl1	achaete-scute complex homolog 1 (Drosophila)	NM_008553	ENSMUST00 000020243	chr10	86810957	86956405
185	10515257	0.356	Rad54l	RAD54 like (S. cerevisiae)	NM_009015	NM_001122 958	chr4	115769580	115796264
186	10588294	0.356	Topbp1	topoisomerase (DNA) II binding protein 1	NM_176979	ENSMUST00 000035164	chr9	103207545	103252762
187	10508151	0.356	Clspn	claspin homolog (Xenopus laevis)	NM_175554	ENSMUST00 000048391	chr4	126234211	126271147

188	10406581	0.358	Dhfr	dihydrofolate reductase	NM_010049	NM_010829	chr13	93124738	93159008
189	10448506	0.358	Ccnf	cyclin F	NM_007634	ENSMUST0000073425	chr17	24359494	24388292
190	10515337	0.358	Nasp	nuclear autoantigenic sperm protein (histone-binding)	NM_016777	NM_001081475	chr4	116273657	116300546
191	10352267	0.361	Lin9	lin-9 homolog (C. elegans)	NM_001103182	NM_175186	chr1	182571095	182619494
192	10555695	0.361	Rrm1	ribonucleotide reductase M1	NM_009103	ENSMUST0000033283	chr7	109590331	109617441
193	10499639	0.363	Cks1b	CDC28 protein kinase 1b	NM_016904	ENSMUST0000029679	chr3	89219394	89222213
194	10592201	0.366	Chek1	checkpoint kinase 1 homolog (S. pombe)	NM_007691	ENSMUST0000034625	chr9	36516067	36534212
195	10535979	0.366	Rfc3	replication factor C (activator 1) 3	NM_027009	ENSMUST0000038131	chr5	152445400	152453754
196	10395612	0.369	G2e3	G2 M-phase specific E3 ubiquitin	NM_001015099		chr12	52449314	52476555

				ligase					
197	10404036	0.369	Hist1h2bg	histone cluster 1, H2bg	NM_178196	BC060304	chr13	23663265	23663891
198	10363575	0.371	Dna2	DNA replication helicase 2 homolog (yeast)	NM_177372	ENSMUST0000092462	chr10	62409792	62436925
199	10424779	0.371	Cks2	CDC28 protein kinase regulatory subunit 2	NM_025415	BC022647	chr15	75980710	75981317
200	10393431	0.371	Tk1	thymidine kinase 1	NM_009387	ENSMUST0000026661	chr11	117676839	117687267
201	10450519	0.371	Tcf19	transcription factor 19	NM_001163763	NM_025674	chr17	35649679	35653699
202	10361995	0.371	Fam54a	family with sequence similarity 54, member A	NM_027930	ENSMUST0000020167	chr10	20067630	20081125
203	10492469	0.374	Mlf1	myeloid leukemia factor 1	NM_001039543	NM_010801	chr3	67178019	67203925
204	10409031	0.376	Dek	DEK oncogene (DNA binding)	NM_025900	ENSMUST0000021807	chr13	47180151	47201535
205	10498620	0.376	Trim59	tripartite motif-containing	NM_025863	BC025430	chr3	68839210	68848589

				59					
206	10606436	0.376	Hmgn5	high-mobility group nucleosome binding domain 5	NM_016710	ENSMUST0000033597	chrX	106199873	106208698
207	10494407	0.379	Hist2h2bb	histone cluster 2, H2bb	NM_175666	BC019122	chr3	96073623	96082947
208	10474437	0.382	Ccdc34	coiled-coil domain containing 34	NM_026613	ENSMUST0000028580	chr2	109857996	109884805
209	10389134	0.384	Slfn9	schlafen 9	NM_172796	ENSMUST0000038211	chr11	82793805	82805332
210	10461391	0.384	Pcna	proliferating cell nuclear antigen	NM_011045	ENSMUST0000028817	chr19	9357740	9359001
211	10487930	0.384	Pcna	proliferating cell nuclear antigen	NM_011045	ENSMUST0000028817	chr2	132075022	132078916
212	10389395	0.384	Brip1	BRCA1 interacting protein C-terminal helicase 1	NM_178309	ENSMUST0000044423	chr11	85871638	86014695
213	10408225	0.387	Hist1h4c	histone cluster 1, H4c	NM_178208	NM_178208	chr13	23790007	23790321
214	10379363	0.387	Atad5	ATPase family, AAA	NM_001029856	ENSMUST00	chr11	79902914	79949293

				domain containing 5		000108239			
215	10406918	0.387			---		chr13	102167625	102234115
216	10359648	0.39	Scyl3	SCY1-like 3 (S. cerevisiae)	NM_028776	ENSMUST0000027876	chr1	165876481	165924912
217	10388234	0.39	Gsg2	germ cell-specific gene 2	NM_010353	ENSMUST0000052140	chr11	72948987	72951796
218	10503617	0.39	F730047E07 Rik	RIKEN cDNA F730047E07 gene	NM_199467	ENSMUST0000108222	chr4	24424055	24530096
219	10381548	0.39	BC030867	cDNA sequence BC030867	NM_153544	ENSMUST0000100392	chr11	102110196	102126497
220	10550102	0.392	Lig1	ligase I, DNA, ATP-dependent	NM_001083188	NM_010715	chr7	13862632	13896775
221	10350297	0.392	Kif14	kinesin family member 14	NM_001081258	ENSMUST0000047817	chr1	138362948	138424190
222	10498371	0.395	P2ry12	purinergic receptor P2Y, G-protein coupled 12	NM_027571	ENSMUST0000050360	chr3	59020191	59066747
223	10371888	0.395	Tmpo	thymopoietin	NM_001080129	NM_001080130	chr10	90611366	90644223
224	10478355	0.395	Mybl2	myeloblastosis oncogene-	NM_008652	ENSMUST0000018005	chr2	162880371	162910423

				like 2					
225	10368508	0.395	2610036L11 Rik	RIKEN cDNA 2610036L11 gene	NM_001109 747	ENSMUST00 000099985	chr10	29917006	29920298
226	10353733	0.398	Prim2	DNA primase, p58 subunit	NM_008922	ENSMUST00 000027312	chr1	33510656	33726625
227	10401852	0.398	4930534B04 Rik	RIKEN cDNA 4930534B04 gene	NM_181815	BC145501	chr12	92236932	92622818
228	10446027	0.398	Chaf1a	chromatin assembly factor 1, subunit A (p150)	NM_013733	ENSMUST00 000002914	chr17	56179839	56207450
229	10546834	0.398	Rad18	RAD18 homolog (<i>S. cerevisiae</i>)	NM_001167 730	NM_021385	chr6	112569879	112646664
230	10492582	0.398	Mir15b	microRNA 15b	NR_029529		chr3	68813678	68813775
231	10531579	0.398	Hmgb1	high mobility group box 1	NM_010439	BC094030	chr5	98504227	98504940
232	10591881	0.398	Hmgb1	high mobility group box 1	NM_010439	L38477	chr9	25032812	25033359
233	10495316	0.401	Psrc1	proline serine-rich coiled-coil 1	NM_019976		chr3	108186761	108191149
234	10503264	0.401	Ccne2	cyclin E2	NM_009830	NM_001159 595	chr4	11118501	11131926

235	10355327	0.401	Bard1	BRCA1 associated RING domain 1	NM_007525	ENSMUST0000074184	chr1	71074882	71075232
236	10495935	0.401	4930422G04 Rik	RIKEN cDNA 4930422G04 gene	NM_197997	ENSMUST0000043108	chr3	127258213	127284509
237	10508759	0.406	Rpa2	replication protein A2	NM_011284	ENSMUST0000102561	chr4	132324275	132334661
238	10576140	0.406	Cdt1	chromatin licensing and DNA replication factor 1	NM_026014	ENSMUST0000006760	chr8	125091915	125097454
239	10490815	0.406	Gm5841	predicted gene 5841	XR_031642		chr3	8327501	8329899
240	10372503	0.409	Lgr5	leucine rich repeat containing G protein coupled receptor 5	NM_010195	ENSMUST0000020350	chr10	114887370	115024836
241	10411782	0.409	Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	NM_001077495	NM_001024955	chr13	102450716	102538172
242	10408077	0.409	Hist1h2ak	histone cluster 1,	NM_178183	ENSMUST00	chr13	21845264	21845781

				H2ak		000074752			
243	10498053	0.412	4930583H14 Rik	RIKEN cDNA 4930583H14 gene	NR_028121	NM_026358	chr3	51192334	51200462
244	10402073	0.412	2610021K21 Rik	RIKEN cDNA 2610021K21 gene	NM_030172	BC049109	chr12	100955741	101121652
245	10449999	0.412	Zfp101	zinc finger protein 101	NM_009542	ENSMUST00 000038834	chr17	33517637	33531544
246	10465861	0.415	Incenp	inner centromere protein	NM_016692	ENSMUST00 000025562	chr19	9946836	9973959
247	10514201	0.415	Haus6	HAUS augmin-like complex, subunit 6	NM_173400	ENSMUST00 000070607	chr4	86227188	86257926
248	10465912	0.415	Fen1	flap structure specific endonucleas e 1	NM_007999	ENSMUST00 000025651	chr19	10273628	10278433
249	10500543	0.418	Hmgb1	high mobility group box 1	NM_010439	BC094030	chr3	98383774	98384321
250	10355325	0.418	Bard1	BRCA1 associated RING domain 1	NM_007525	ENSMUST00 000097702	chr1	71074294	71074611
251	10349637	0.418	Fam72a	family with sequence similarity 72, member A	BC138225	NM_175382	chr1	133424480	133436449

252	10480087	0.418	Gm13310	karyopherin (importin) alpha 2 pseudogene	XR_032234		chr2	12004239	12005630
253	10591556	0.418	Spc24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	NM_026282	ENSMUST0000098942	chr9	21559886	21564733
254	10376459	0.42	Gm12260	histone cluster 1, H3 pseudogene	XM_905850		chr11	58775324	58775714
255	10582835	0.42	Hmgb1	high mobility group box 1	NM_010439	L38477	chr8	129505597	129506132
256	10489127	0.42	Rbl1	retinoblastoma-like 1 (p107)	NM_011249	NM_001139516	chr2	156971629	157030255
257	10385325	0.42	Pttg1	pituitary tumor-transforming gene 1	NM_013917	NM_001131054	chr11	43233764	43239753
258	10363743	0.42	Rtkn2	rhotekin 2	NM_001081346	ENSMUST0000105437	chr10	67442353	67521903
259	10373530	0.423	Cdk2	cyclin-dependent kinase 2	NM_183417	NM_016756	chr10	128134995	128142068
260	10600545	0.423	Hmgb1	high mobility	NM_010439	BC094030	chrX	74701925	74745544

				group box 1					
261	10372687	0.423	Nup107	nucleoporin 107	NM_134010	ENSMUST0000064848	chr10	117187677	117229761
262	10573451	0.423	Syce2	synaptonemal complex central element protein 2	NM_001168246	NM_027954	chr8	87396010	87411295
263	10472235	0.423	Dapl1	death associated protein-like 1	NM_029723	ENSMUST0000028369	chr2	59322714	59342940
264	10497483	0.426	Hmgb1	high mobility group box 1	NM_010439	BC110667	chr3	21979325	21979965
265	10476362	0.426	Mcm8	minichromosome maintenance deficient 8 (S. cerevisiae)	NM_025676	ENSMUST0000066559	chr2	132641930	132670005
266	10416736	0.426	6720463M24 Rik	RIKEN cDNA 6720463M24 gene	NM_175265	ENSMUST0000022656	chr14	99445596	99473759
267	10501402	0.426	Gpsm2	G-protein signalling modulator 2 (AGS3-like, C. elegans)	NM_029522	ENSMUST0000029482	chr3	108481556	108525061
268	10566142	0.429	Hmgb1	high mobility	NM_010439	BC094030	chr7	109668978	109669553

				group box 1					
269	10475362	0.429	Wdr76	WD repeat domain 76	NM_030234	ENSMUST0000110602	chr2	121332506	121370596
270	10478572	0.429	Ube2c	ubiquitin-conjugating enzyme E2C	NM_026785	NM_009394	chr2	164595429	164604320
271	10403945	0.429	Gm11275	predicted gene 11275	BC139425	NM_178210	chr13	21826931	21827706
272	10499366	0.429	Pmf1	polyamine-modulated factor 1	NM_025928	ENSMUST0000056370	chr3	88198060	88214256
273	10479765	0.429	Suv39h2	suppressor of variegation 3-9 homolog 2 (Drosophila)	NM_022724	NR_027509	chr2	3373092	3392236
274	10416655	0.432	Gm5465	predicted gene 5465	NM_001034882	ENSMUST0000100359	chr14	79851642	79854623
275	10496975	0.432	Slc44a5	solute carrier family 44, member 5	NM_001081263	ENSMUST0000089948	chr3	153636400	153934686
276	10572130	0.432	Lpl	lipoprotein lipase	NM_008509	ENSMUST0000015712	chr8	71404453	71431347
277	10488785	0.432	E2f1	E2F transcription factor 1	NM_007891	ENSMUST0000103145	chr2	154385374	154395588
278	10384145	0.435	H2afv	H2A histone family,	NM_029938	ENSMUST00	chr11	6328141	6339462

				member V		000060240			
279	10472782	0.435	Hat1	histone aminotransferase 1	NM_026115	ENSMUST0000112122	chr2	71227314	71279679
280	10372139	0.435	Nts	neurotensin	NM_024435	ENSMUST0000020040	chr10	101944390	101953069
281	10392413	0.435			---		chr11	108928298	108928404
282	10403834	0.438	Sfrp4	secreted frizzled-related protein 4	NM_016687	ENSMUST0000002883	chr13	19715041	19790804
283	10477986	0.438	Nnat	neuronatin	NM_010923	NM_180960	chr2	157385846	157388253
284	10354275	0.438	1700029F09 Rik	RIKEN cDNA 1700029F09 gene	BC119032	NM_029368	chr1	44143655	44159268
285	10408200	0.438	Hist1h4f	histone cluster 1, H4f	NM_175655		chr13	23643201	23643515
286	10381072	0.438	Cdc6	cell division cycle 6 homolog (S. cerevisiae)	NM_011799	NM_001025779	chr11	98769203	98785256
287	10499035	0.441	Mnd1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	NM_029797	NR_030680	chr3	83891855	83959635
288	10381526	0.441	Ppih	peptidyl prolyl isomerase H	NM_001110130	NM_028677	chr11	101985388	101985954
289	10366983	0.441	Tmem194		NM_001113	NM_173732	chr10	127114120	127138103

				transmembrane protein 194	211				
290	10605674	0.441	Pola1	polymerase (DNA directed), alpha 1	NM_008892	ENSMUST0000006856	chrX	90550106	90877494
291	10447702	0.441	Ppih	peptidyl prolyl isomerase H	NM_028677	NM_001110129	chr17	9614805	9615317
292	10509168	0.441	E2f2	E2F transcription factor 2	NM_177733	ENSMUST0000061721	chr4	135728309	135750643
293	10498386	0.444	Igsf10	immunoglobulin superfamily, member 10	NM_001162884	ENSMUST0000097075	chr3	59133093	59145254
294	10515884	0.444	Ppih	peptidyl prolyl isomerase H	NM_028677	NM_001110129	chr4	118972616	118993106
295	10554281	0.444	Fanci	Fanconi anemia, complementation group I	NM_145946	NM_017462	chr7	86537224	86595150
296	10495945	0.444	4930422G04 Rik	RIKEN cDNA 4930422G04 gene	NM_197997	ENSMUST0000043108	chr3	127286502	127320934
297	10586184	0.444	Tipin	timeless interacting protein	NM_025372	ENSMUST0000034964	chr9	64129414	64152601
298	10571696	0.444	Casp3	caspase 3	NM_009810	ENSMUST00	chr8	47702772	47724071

						000093517			
299	10548600	0.444	Hmgb1l	high mobility group box 1-like	ENSMUST0000082150		chr6	131558311	131558910
300	10475610	0.444	Dut	deoxyuridine triphosphatase	NM_023595	NM_001159646	chr2	125072994	125084785
301	10419296	0.448	Wdhd1	WD repeat and HMG-box DNA binding protein 1	NM_172598	ENSMUST0000111792	chr14	47860619	47896488
302	10444911	0.448	Mdc1	mediator of DNA damage checkpoint 1	NM_001010833	ENSMUST0000082337	chr17	35981380	35996614
303	10570470	0.448	Hmgb1	high mobility group box 1	NM_010439	BC110667	chr8	14136310	14138876
304	10436442	0.448	Fam60a	family with sequence similarity 60, member A	NM_019643	ENSMUST0000054080	chr16	61377083	61379570
305	10437432	0.448	Nmral1	NmrA-like family domain containing 1	NM_026393	ENSMUST0000115851	chr16	4711317	4719112
306	10353341	0.448	Hmgb1	high mobility group box 1	NM_010439	L38477	chr1	19143391	19144047
307	10379989	0.448	Fam33a	family with sequence similarity 33,	NM_025377	ENSMUST0000020794	chr11	86922733	86938136

				member A					
308	10562084	0.448	Haus5	HAUS augmin-like complex, subunit 5	NM_027999	ENSMUST0000019697	chr7	31438733	31449992
309	10453252	0.448	Hmgb1	high mobility group box 1	NM_010439	L38477	chr17	82591215	82591949
310	10538338	0.448	Creb5	cAMP responsive element binding protein 5	NM_172728	ENSMUST0000047450	chr6	53237315	53646012
311	10561868	0.451	Wdr62	WD repeat domain 62	NM_146186	ENSMUST0000047189	chr7	31025157	31065415
312	10453867	0.451	Rbbp8	retinoblastoma binding protein 8	NM_001081223	ENSMUST0000115861	chr18	11791785	11901330
313	10429455	0.451	Hmgb1	high mobility group box 1	NM_010439	BC083067	chr15	73923563	73924894
314	10366277	0.451	E2f7	E2F transcription factor 7	NM_178609	ENSMUST0000073781	chr10	110182521	110224440
315	10465282	0.451	Pola2	polymerase (DNA directed), alpha 2	NM_008893	NM_001164057	chr19	5940546	5964197
316	10385426	0.451	Hmgb1	high mobility group box 1	NM_010439	BC111468	chr11	46056037	46057694

317	10462361	0.451	Hmgb1	high mobility group box 1	NM_010439	L38477	chr19	29234608	29235255
318	10565589	0.454	Hmgb1	high mobility group box 1	NM_010439	BC110667	chr7	103351511	103352046
319	10386949	0.454	Hmgb1	high mobility group box 1	NM_010439	L38477	chr11	63659787	63660320
320	10549497	0.454	Fam60a	family with sequence similarity 60, member A	NM_019643	ENSMUST0000054080	chr6	148869579	148894954
321	10573615	0.457	Orc6l	origin recognition complex, subunit 6-like (S. cerevisiae)	NM_019716	NM_001163791	chr8	87823690	87831970
322	10350590	0.457	Ska2l	spindle and kinetochore associated complex subunit 2-like	XM_890112		chr1	152396447	152396809
323	10453512	0.457	Kpna2	karyopherin (importin) alpha 2	NM_010655	D55720	chr17	90307792	90309769
324	10461930	0.457	D030056L22 Rik	RIKEN cDNA D030056L22 gene	BC020125	NM_177640	chr19	18787726	18792919
325	10592154	0.457	Hyls1	hydrolethalu	NM_029762	ENSMUST00	chr9	35368405	35377630

				s syndrome 1		000115110			
326	10569994	0.46	Hmgb1	high mobility group box 1	NM_010439	BC110667	chr8	4713207	4713716
327	10521690	0.46	Ppih	peptidyl prolyl isomerase H	NM_028677	NM_001110129	chr5	44304409	44305156
328	10498379	0.463	Igsf10	immunoglobulin superfamily, member 10	NM_001162884		chr3	59121847	59132793
329	10494322	0.463	Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	NM_023210	ENSMUST0000015893	chr3	95733214	95750899
330	10402750	0.463	Hmgb1	high mobility group box 1	NM_010439	L38477	chr12	113168702	113169248
331	10351047	0.467	Cenpl	centromere protein L	NM_027429	NM_001159930	chr1	163001072	163016457
332	10546088	0.467	H1fx	H1 histone family, member X	NM_198622	ENSMUST0000056403	chr6	87930415	87931476
333	10376444	0.467	Hist3h2ba	histone cluster 3, H2ba	NM_030082	ENSMUST0000078267	chr11	58762413	58763035
334	10355403	0.467	Fn1	fibronectin 1	NM_010233	ENSMUST0000055226	chr1	71632097	71699746

335	10552337	0.467	Hmg1l1	high-mobility group (nonhistone chromosomal) protein 1-like 1	NM_001111282	NM_010439	chr7	49276117	49277373
336	10498383	0.467	IgSF10	immunoglobulin superfamily, member 10	NM_001162884	ENSMUST0000097075	chr3	59131706	59135965
337	10360324	0.467	Gm2710	predicted gene 2710	XR_030924		chr1	174594102	174599908
338	10567412	0.47	Eri2	exoribonuclease 2	NM_027698	NM_016870	chr7	126915841	126937474
339	10408266	0.47	Hist1h2ba	histone cluster 1, H2ba	NM_175663	ENSMUST0000052776	chr13	24025641	24026025
340	10590648	0.47	Top2a	topoisomerase (DNA) II alpha	NM_011623	ENSMUST0000068031	chr9	3496414	3497471
341	10502029	0.47	Larp7	Larbinucleoprotein domain family, member 7	NM_138593	ENSMUST0000029588	chr3	127239632	127256267
342	10376950	0.47	Pmp22	peripheral myelin protein 22	NM_008885	ENSMUST0000018361	chr11	62945012	62973049

343	10403948	0.47	Hist1h2be	histone cluster 1, H2be	NM_001177653	NM_178194	chr13	21845983	21846421
344	10518526	0.473	Angptl7	angiopoietin-like 7	NM_001039554	ENSMUST0000030840	chr4	147869292	147874571
345	10404024	0.473	Hist1h4h	histone cluster 1, H4h	NM_153173	BC087952	chr13	23622919	23623388
346	10446441	0.473	Ddx11	DEAD H (Asp-Glu-Ala-Asp)	NM_001003919		chr17	66472860	66501508
347	10583952	0.476	Ncapd3	non-SMC condensin II complex, subunit D3	NM_178113	ENSMUST0000073127	chr9	26837760	26902900
348	10556297	0.476	Adm	adrenomedullin	NM_009627	ENSMUST0000033054	chr7	117771175	117773334
349	10467420	0.476	Pdlim1	PDZ and LIM domain 1 (elfin)	NM_016861	ENSMUST0000068439	chr19	40295663	40346023
350	10408210	0.476	Hist1h2bc	histone cluster 1, H2bc	NM_023422	NM_001110555	chr13	23665679	23666059
351	10408113	0.476	Hist1h4i	histone cluster 1, H4i	NM_175656	BC092144	chr13	22132505	22133221
352	10596958	0.476			---		chr9	108641084	108641189
353	10360745	0.48	Lbr	lamin B receptor	NM_133815	ENSMUST0000005003	chr1	183745447	183772492

354	10587778	0.48			---		chr9	90246833	90247009
355	10362581	0.48	Tube1	epsilon-tubulin 1	NM_028006	ENSMUST0000019991	chr10	38853829	38870864
356	10528790	0.48	Xrcc2	X-ray repair complementing defective repair in Chinese hamster cells 2	NM_020570	ENSMUST0000030773	chr5	25195630	25211615
357	10508721	0.48	Snora44	small nucleolar RNA, HACA box 44	AF357394		chr4	131865856	131865984
358	10435581	0.48	Polq	polymerase (DNA directed), theta	NM_029977	NM_001159369	chr16	37010793	37095483
359	10497503	0.48	Kpna2	karyopherin (importin) alpha 2	NM_010655	D55720	chr3	25109938	25111527
360	10497325	0.483	Hmgb1	high mobility group box 1	NM_010439	L38477	chr3	13669613	13670145
361	10431915	0.483	Slc38a4	solute carrier family 38, member 4	NM_027052	ENSMUST0000023101	chr15	96825254	96886387
362	10571214	0.483	Rnf122	ring finger protein 122	NM_175136	ENSMUST0000046941	chr8	32222318	32242227

363	10492679	0.483	4930579G24 Rik	RIKEN cDNA 4930579G24 gene	NM_029482	ENSMUST00 000029388	chr3	79433020	79436742
364	10392284	0.486	Kpna2	karyopherin (importin) alpha 2	NM_010655	D55720	chr11	106849943	106860839
365	10408212	0.486	Hist1h2be	histone cluster 1, H2be	NM_001177 653	NM_178194	chr13	23675610	23714427
366	10591773	0.486	Hmgn2	high mobility group nucleosomal binding domain 2	NM_016957	BC090836	chr9	22124391	22125902
367	10455439	0.486	Hmgb1	high mobility group box 1	NM_010439	BC094030	chr18	44221252	44221789
368	10507653	0.486			---		chr4	119193595	119193971
369	10548735	0.486	Dusp16	dual specificity phosphatase 16	NM_130447	NM_001048 054	chr6	134665486	134742646
370	10383731	0.486	Smtn	smoothelin	NM_001159 284	NM_013870	chr11	3417526	3439295
371	10401948	0.486			---		chr12	96617055	96617161
372	10408687	0.486	Hmgb1	high mobility group box 1	NM_010439	BC094030	chr13	36650420	36650934
373	10403978	0.486	Gm11277	predicted gene 11277	NM_001110 555	NM_001097	chr13	22127756	22128136

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374	10606619	0.49	Sytl4	synaptotagm in-like 4	NM_013757	ENSMUST00 000033608	chrX	130470922	130516351
375	10582501	0.49	Fanca	Fanconi anemia, complement ation group A	NM_016925	ENSMUST00 000035495	chr8	125792200	125842476
376	10517141	0.49	Hmgn2	high mobility group nucleosomal binding domain 2	NM_016957	BC090836	chr4	133520654	133523906
377	10408085	0.493	Hist1h2an	histone cluster 1, H2an	NM_178184	NM_001177 544	chr13	21878695	21879087
378	10371307	0.493	Nfyb	nuclear transcription factor-Y beta	NM_010914	ENSMUST00 000105309	chr10	82211445	82226886
379	10579659	0.493	Hmgn2	high mobility group nucleosomal binding domain 2	NM_016957	BC090836	chr8	74827954	74829162
380	10591369	0.493	Dnmt1	DNA methyltransf erase (cytosine-5) 1	NM_010066	ENSMUST00 000004202	chr9	20711653	20764332

381	10451547	0.493	Gm16494	predicted gene 16494	XM_001480078		chr17	47153645	47153905
382	10438091	0.493	2610318N02 Rik	RIKEN cDNA 2610318N02 gene	BC039993	ENSMUST0000093336	chr16	17113491	17125199
383	10444927	0.493	Nrm	nurim (nuclear envelope membrane protein)	NM_134122	ENSMUST0000074259	chr17	35998263	36002347
384	10407081	0.493	Depdc1b	DEP domain containing 1B	NM_178683	ENSMUST0000051594	chr13	109106531	109197976
385	10542038	0.497	Hmgb1	high mobility group box 1	NM_010439	BC094030	chr6	127361146	127418425
386	10604735	0.497	Rbmx	RNA binding motif protein, X chromosome	NM_011252	NM_001166623	chrX	54639535	54646199
387	10574378	0.497	Gins3	GIN5 complex subunit 3 (Psf3 homolog)	NM_030198	ENSMUST0000034094	chr8	98157459	98168959
388	10410092	0.497	Zfp367	zinc finger protein 367	NM_175494	ENSMUST0000059817	chr13	64234365	64254507
389	10399254	0.497	Cenpo	centromere protein O	NM_134046	NM_138305	chr12	4211672	4234294
390	10424413	0.497	Hmgb1	high mobility group box 1	NM_010439	BC111468	chr15	63463246	63463909

391	10508996	0.497	2610002D18 Rik	RIKEN cDNA 2610002D18 gene	BC138271	NM_001081 099	chr4	134067017	134079679
392	10531707	0.497	Lin54	lin-54 homolog (C. elegans)	NM_001115 010	NM_172714	chr5	100871060	100929658
393	10553857	0.497	Hmgb1	high mobility group box 1	NM_010439	L38477	chr7	70750905	70751437
394	10408197	0.497	Hist1h2bh	histone cluster 1, H2bh	NM_178197	ENSMUST00 000078156	chr13	23634791	23635228

Supplemental table 1: Genes that are downregulated (<0.5 fold ratio) by Sunitinib treatment of MPC 4/30 cells.