

	<i>R. bromii</i> L2-63 locus tag number after re-annotation	<i>R. bromii</i> L2-63 previous locus tag number	Synonym
Amy 1	L2-63_00433	RBR_04300	
Amy 2	L2-63_00496	RBR_04930	
Amy 3	L2-63_00613	RBR_06100	
Amy 4	L2-63_00682	RBR_06780	
Amy 5	L2-63_00780	RBR_07800	
Amy 6	L2-63_00862	RBR_08620	
Amy 7	L2-63_01126	RBR_11290	
Amy 8	L2-63_01910	RBR_19140	
Amy 9	L2-63_02041	RBR_20490	
Amy 10	L2-63_01094	RBR_10980	
Amy 11	L2-63_01356	RBR_13550	
Amy 12	L2-63_01357	RBR_13560	
Amy 13	L2-63_01115	RBR_11170	
Amy 14	L2-63_00370	RBR_03680	
Amy 15	L2-63_01911	RBR_19150	
Amy 16	L2-63_01654	Not detected	
Amy 17	L2-63_01441	Not detected	
Sca1	L2-63_00682	RBR_06780	Amy 4
Sca2	L2-63_01067	RBR_10710	
Sca3	L2-63_00731	RBR_07310	
Sca4	L2-63_00829	RBR_08290	
Sca5	L2-63_01064	Not detected	
Doc 1	L2-63_00285	RBR_02970	
Doc 2	L2-63_00287	RBR_02990	
Doc 3	L2-63_00546	RBR_05420	
Doc 4	L2-63_00576	RBR_05720	
Doc 5	L2-63_01402	RBR_14010	
Doc 6	L2-63_01443	RBR_14490	
Doc 7	L2-63_01793	RBR_17960	
Doc 8	L2-63_01861	RBR_18670	
Doc 9	L2-63_02145	RBR_21580	
Doc 10	L2-63_00682	RBR_06780	Amy 4
Doc 11	L2-63_02041	RBR_20490	Amy 9
Doc 12	L2-63_01094	RBR_10980	Amy 10
Doc 13	L2-63_01357	RBR_13560	Amy 12
Doc 14	L2-63_00436	RBR_04330	
Doc 15	L2-63_00485	RBR_04820	
Doc 16	L2-63_01616	RBR_16240	
Doc 17	L2-63_01862	RBR_18680	
Doc 18	L2-63_01881	RBR_18860	
Doc 19	L2-63_01944	RBR_19520	
Doc 20	L2-63_00125	RBR_01410	
Doc 21	L2-63_00158	RBR_01740	
Doc 22	L2-63_00434	RBR_04310	
Doc 23	L2-63_00717	RBR_07140	
Doc 24	L2-63_01374	RBR_13730	
Doc 25	L2-63_01451	RBR_14570	
Doc 26	L2-63_01574	RBR_15800	
Doc 27	L2-63_01654	Not detected	Amy 16

R. bromii L2-63 locus tag

Gene annotation

L2-63_00110	soi	1 Sporulation initiation inhibitor protein soI,soI,plasmid-partitioning protein RepA,Septum formation inhibitor-activating ATPase,plasmid partitioning protein RepA,CobQ/CobB/MinD/ParA nucleotide binding domain 117275:118102 reverse MW:30184
L2-63_00593	soi	2 Sporulation initiation inhibitor protein RepA,Septum formation inhibitor-activating ATPase,cell division ATPase MinD,CobQ/CobB/MinD/ParA nucleotide binding domain 636409:637176 reverse MW:27874
L2-63_01701	soi	3 Sporulation initiation inhibitor protein soI,plasmid-partitioning protein RepA,Septum formation inhibitor-activating ATPase,plasmid partitioning protein RepA,CobQ/CobB/MinD/ParA nucleotide binding domain 1791642:1792466 forward MW:29817
L2-63_01362	L2-63	01362 sporulation inhibitor KapQ,Inhibitor of the KlnA pathway to sporulation, predicted exonuclease,DNA polymerase II, alpha subunit, Gram-positive type,Exonuclease 1423530:1424420 forward MW:34040
L2-63_00972	siH	Stage I sporulation protein H,RNA polymerase factor sigma 70,RNA polymerase sigma-70 factor,Sigma 70, region 4 1035179:1035769 forward MW:21824
L2-63_01663	spo0A	Stage 0 sporulation protein G,chemotaxis-specific methyltransferase,Response regulator of citrate/malate metabolism,sporulation transcription factor Spo0A,Sporulation initiation factor Spo0A C terminal 1749036:1749806 forward MW:28974
L2-63_00354	nrk4	hypothetical protein,putative two-component response-regulatory protein, YnfT,Response regulator of the YnfK/Algh family,sporulation transcription factor Spo0A,Response regulator receiver domain 355792:356523 forward MW:28162
L2-63_00109	parB	1 Chromosome-partitioning protein parB,plasmid-partitioning protein RepB,ParB/RepB/Spo0I family partition protein,ParB-like nuclease domain 116374:117221 reverse MW:36513
L2-63_00592	parB	2 Probable chromosome-partitioning protein parB,plasmid-partitioning protein RepB,ParB/RepB/Spo0I family partition protein,ParB-like nuclease domain 635559:636407 reverse MW:31201
L2-63_01702	parB	3 Probable chromosome-partitioning protein parB,plasmid-partitioning protein,ParB/RepB/Spo0I family partition protein,ParB-like nuclease domain 1792423:1793364 forward MW:35407
L2-63_02000	parB	4 Probable chromosome-partitioning protein parB,plasmid-partitioning protein RepB,ParB/RepB/Spo0I family partition protein,ParB-like nuclease domain 2083908:2084753 reverse MW:32796
L2-63_02125	parB	5 Probable chromosome-partitioning protein parB,plasmid-partitioning protein RepB,ParB/RepB/Spo0I family partition protein,ParB-like nuclease domain 2188827:2189648 reverse MW:31711
L2-63_01542	sefP	Cell division protein sefP,Protein of unknown function (DUF552) 1620226:1620693 forward MW:17612
L2-63_01819	L2-63	01819 Septum formation initiator 1900610:1901056 reverse MW:17079
L2-63_01504	sigK	RNA polymerase sigma-35 factor precursor sporulation sigma factor SigK,RNA polymerase sigma- E factor,Sigma-70 region 2 1581366:1582067 reverse MW:26566
L2-63_00833	sigK	2 Stage II sporulation protein AC,sporulation sigma factor SigF,RNA polymerase sigma- F factor,Sigma-70, region 4 891831:892490 reverse MW:24772
L2-63_01505	L2-63	01505 sigma-E processing peptidase SpoIIIGA,Sporulation factor SpoIIIGA 1582078:1582881 reverse MW:29621
L2-63_00834	spoIIAB	Anti-sigma F factor,anti-sigma F factor,Signal transduction histidine kinase,anti-sigma F factor,Histidine kinase-, DNA gyrase B-, and Hsp90-like ATPase 892480:892920 reverse MW:15963
L2-63_00835	spoIIAA	1 Stage II sporulation protein AA,Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor),anti-sigma F factor (antagonist of anti-sigma factor),anti-sigma F factor (antagonist of anti-sigma factor),STAS domain 892911:893229 reverse MW:11077
L2-63_01168	spoIIAA	2 Stage II sporulation protein AA,Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor),anti-sigma F factor (antagonist of anti-sigma factor),STAS domain 1241266:1241574 reverse MW:11133
L2-63_01395	L2-63	01395 stage II sporulation protein M 1459044:1459712 forward MW:24721
L2-63_01486	L2-63	01486 stage II sporulation protein R,Stage II sporulation protein R (spore II) 11 1533681:1554283 forward MW:23015
L2-63_00295	spoIIQ	Stage II sporulation protein Q,Membrane-bound metalloprotease,Peptidase family M23 296471:297199 forward MW:26396
L2-63_00381	spoIIQ	Stage II sporulation protein E,Stage II sporulation protein E (SpoIIe) 380299:382623 reverse MW:82850
L2-63_00388	rblU	Phosphoserine phosphatase rblU,Stage II sporulation protein E,Stage II sporulation protein E (SpoIIe) 393426:395069 reverse MW:61809
L2-63_00438	L2-63	00438 stage II sporulation protein P,Stage II sporulation protein P (SpoIIP) 445641:450638 forward MW:40615
L2-63_00209	sigK	1 Stage II sporulation protein AC,sporulation sigma factor SigG,RNA polymerase sigma- G factor,Sigma-70, region 4 228385:229167 forward MW:29578
L2-63_01805	L2-63	01805 stage III sporulation protein AG 1889807:1890256 reverse MW:16203
L2-63_01807	L2-63	01807 stage III sporulation protein AE,Stage III sporulation protein AE (spore III) 1891700:1891848 reverse MW:38770
L2-63_01808	L2-63	01808 stage III sporulation protein AD,Stage III sporulation protein AC/AD protein family 1891858:1892247 reverse MW:13366
L2-63_01809	L2-63	01809 stage III sporulation protein AC,Stage III sporulation protein AC/AD protein family 1892248:1892443 reverse MW:6989
L2-63_01810	L2-63	01810 stage III sporulation protein SpoAB,stage III sporulation protein AB,Stage III sporulation protein AB (spore III AB) 1892452:1892946 reverse MW:18375
L2-63_01804	L2-63	01804 SpoIIAB-like protein 1889250:1889793 reverse MW:19553
L2-63_01950	spoIIIE	Stage III sporulation protein E,DNA translocase FtsK,DNA segregation ATPase FtsK/SpoIIIE and related proteins,type VII secretion protein EssC,FtsK/SpoIIIE family 2032173:2034029 reverse MW:100193
L2-63_00486	spoIIID	14 kDa transcription factor sporulation transcriptional regulator SpoIIID,Stage III sporulation protein D 509822:510094 forward MW:10071
L2-63_01811	L2-63	01811 Uncharacterized protein conserved in bacteria,stage III sporulation protein AA 1892936:1893886 reverse MW:34345
L2-63_01925	sigK	RNA polymerase sigma-28 factor precursor sporulation sigma factor SigK,RNA polymerase sigma- K factor,Sigma-70 region 2 1353319:1354014 reverse MW:26172
L2-63_01857	spoIIV	Stage IV sporulation protein A,Stage IV sporulation protein A (spore IV) A1 1928504:1939982 reverse MW:55914
L2-63_01662	spoIIVB	SpoIIVB peptidase precursor,Predicted secreted protein containing a PDZ domain,stage IV sporulation protein B,SpoIIVB peptidase S55 1747865:1748887 forward MW:37314
L2-63_01939	L2-63	01939 sporulation protein YnfD,Putative stage IV sporulation protein YnfD 20219519:2020997 reverse MW:44472
L2-63_01941	L2-63	01941 Uncharacterized protein conserved in bacteria,sporulation integral membrane protein YnfL,Nucleoside recognition 2021053:2022123 forward MW:38307
L2-63_00575	L2-63	00575 stage V sporulation protein AE,SpoVA protein 620709:621062 forward MW:11671
L2-63_00785	L2-63	00785 stage V sporulation protein AC,SpoVA protein 857225:857680 reverse MW:15951
L2-63_00769	spoIIVAD	Stage V sporulation protein AD,Stage V sporulation protein AD,Stage V sporulation protein AD (SpoIIVAD) 833612:834622 reverse MW:35677
L2-63_00220	spoIIVT	Stage V sporulation protein T,Stage V sporulation protein T,SpoIIVT / AbrB like domain 237414:237956 forward MW:19830
L2-63_00283	spoIIVFA	Stage V sporulation protein FA,dipicolinate synthase subunit A,dipicolinic acid synthetase, A subunit 284892:285767 forward MW:31887
L2-63_01257	L2-63	01257 Spore coat associated protein IA (COI1A) 1223000:1223269 reverse MW:7358
L2-63_01256	L2-63	01256 CotB protein 122822:132308 reverse MW:10452
L2-63_01354	L2-63	01354 Muramidase-2 precursor,membrane-bound lytic murein transglycosylase D,Oxidation resistance protein,spore coat assembly protein Saf,LysM domain 1409244:1409549 reverse MW:11190
L2-63_00771	sigP	Processive diacylglycerol glucosyltransferase,diacylglycerol glucosyltransferase,Spore coat polysaccharide biosynthesis protein, predicted glycosyltransferase,undecaprenyl(diphospho-muramoyl)pentapeptide beta-N-acetylglucosaminyltransferase,Monogalactosylglycerol (MGDG) synthase 893615:893803 forward MW:42729
L2-63_01824	YnfP	Probable cell division protein ynfP,Stage V sporulation protein B,MatE 1903801:1905657 reverse MW:66913
L2-63_01012	fwW	2 Cell division protein fwW,cell wall shape-determining protein,stage V sporulation protein E,Cell cycle protein 1069360:1070616 forward MW:46915
L2-63_01010	fwI	Peptidoglycan synthase FwI precursor,peptidoglycan synthase FwI,Membrane carbonylpeptidase,penicillin binding protein,stage V sporulation protein D,Penicillin binding protein transpeptidase domain 1065978:1068248 forward MW:81515
L2-63_00437	gpr	Germination protease precursor,germination protease,GPR endopeptidase,germination protease 448572:449447 forward MW:31539
L2-63_01844	L2-63	01844 Bacillus/Clostridium GerA spore germination protein 1925442:1926896 reverse MW:53679
L2-63_01843	L2-63	01843 spore germination protein (amino acid permease) 1924375:1925443 reverse MW:39757
L2-63_01842	L2-63	01842 germination protein, GerG/C family 1923970:1924362 reverse MW:21502
L2-63_00389	sigK	Chemotaxis-specific amidase,Uncharacterized conserved protein,spore cortex-lytic enzyme,Putative peptidoglycan binding domain 395673:397265 reverse MW:56229
L2-63_01585	cwlC	Cell wall hydrolase CwlC,Cell wall hydrolases involved in spore germination,spore cortex-lytic enzyme,Cell Wall Hydrolase 1668618:1669055 reverse MW:16059
L2-63_00319	spmsA	Spore maturation protein A,Uncharacterized membrane protein,Nucleoside recognition 330363:330947 forward MW:20798
L2-63_00320	spmsB	Spore maturation protein B,hypothetical protein,Uncharacterized membrane protein 320976:321476 forward MW:19657
L2-63_00174	paIA	Protease synthase and sporulation negative regulatory protein PAI 1,ribosomal-protein-alanine acetyltransferase,Acetyltransferase (GNAT) family 188586:189110 forward MW:19857
L2-63_00444	yefM	hypothetical protein,hypothetical protein,putative sporulation protein YnfF,Domain of unknown function DUF 458034:458997 reverse MW:20110
L2-63_00863	xyfD	00863 Negative regulator of genetic competence, sporulation and motility 917748:918002 forward MW:20056
L2-63_00955	xyfD	Bifunctional xylose/deacetylase precursor,polysaccharide deacetylase family sporulation protein PdaB,Polysaccharide deacetylase 1018553:1019338 reverse MW:29076
L2-63_01073	yjfi	Uncharacterized spore protein yjfi,Uncharacterized conserved protein,sporulation protein YfjI,Sporulation protein YfjI (Spore YfjI) 1129826:1130245 forward MW:14853
L2-63_01507	L2-63	01507 Uncharacterized protein conserved in bacteria,sporulation protein, YnfM/C family,PRC-barrel domain 1584146:1584443 forward MW:10662
L2-63_01534	L2-63	01534 sporulation protein YnfB,Sporulation protein YnfB (Spore YnfB) 1609947:1610000 forward MW:24265
L2-63_01630	yhT	hypothetical protein,pheromone autoinducer 2 transporter,sporulation integral membrane protein YnfL,Domain of unknown function DUF20 1711378:1712697 reverse MW:49073
L2-63_01820	L2-63	01820 sporulation protein YnfP,YnfP family 1901459:1901731 reverse MW:5788
L2-63_01838	L2-63	01838 Putative sporulation transcription regulator WhaA,Uncharacterized protein conserved in bacteria,conserved hypothetical protein,Sporulation Regulator Wha C terminal domain 1919846:1920781 reverse MW:35064
L2-63_01940	L2-63	01940 sporulation protein YnfC,YnfP family 2020707:2020979 reverse MW:10041
L2-63_00312	L2-63	00312 sspC2 Ssp-3,small, acid-soluble spore proteins, alpha/beta type 312723:312920 reverse MW:7173

Key	Stages of sporulation	Function
	Sporulation initiation inhibitor	Regulation
	Stage I	Initiation of spore formation
	Stage II	Asymmetric cell division
	Stage III	Engulfment of forespore by mother cell
	Stage IV	Formation of cortex
	Stage V	Formation of coat
	Germination	Germination of spore
	Unknown sporulation genes	Genes not associated with any specific stage of sporulation

qseqid query (e.g., gene) sequence id	sseqid subject (e.g., reference genome) sequence id	pident percentage of identical matches	length alignment length	mismatch number of mismatches	gapopen number of gap openings	qstart start of alignment in query	qend end of alignment in query	sstart start of alignment in subject	send end of alignment in subject	evalue expect value	bitscore bit score
L2-63_00109	RBL236_01215	100	315	0	0	1	315	1	315	0	640
L2-63_00110	RBL236_01216	100	275	0	0	1	275	1	275	0	561
L2-63_00174	RBL236_01565	100	174	0	0	1	174	1	174	1.00E-128	360
L2-63_00209	RBL236_01600	100	260	0	0	1	260	1	260	0	525
L2-63_00220	RBL236_01740	100	180	0	0	1	180	1	180	6.00E-129	362
L2-63_00283	RBL236_01803	100	291	0	0	1	291	1	291	0	582
L2-63_00295	RBL236_01815	100	242	0	0	1	242	1	242	1.00E-179	496
L2-63_00312	RBL236_02214	100	65	0	0	1	65	1	65	1.00E-41	131
L2-63_00319	RBL236_02207	100	194	0	0	1	194	1	194	4.00E-139	389
L2-63_00320	RBL236_02206	100	166	0	0	1	166	1	166	1.00E-117	332
L2-63_00354	RBL236_02172	100	243	0	0	1	243	1	243	0	499
L2-63_00381	RBL236_02145	100	774	0	0	1	774	1	774	0	1576
L2-63_00388	RBL236_02138	100	547	0	0	1	547	1	547	0	1129
L2-63_00389	RBL236_02137	100	530	0	0	1	530	1	530	0	1074
L2-63_00437	RBL236_02089	100	291	0	0	1	291	1	291	0	578
L2-63_00438	RBL236_02088	100	365	0	0	1	365	1	365	0	749
L2-63_00444	RBL236_02082	100	187	0	0	1	187	1	187	2.00E-130	366
L2-63_00486	RBL236_00534	100	90	0	0	1	90	1	90	8.00E-60	179
L2-63_00575	RBL236_00250	100	117	0	0	1	117	1	117	1.00E-76	224
L2-63_00592	RBL236_00267	100	282	0	0	1	282	1	282	0	560
L2-63_00593	RBL236_00268	100	255	0	0	1	255	1	255	0	520
L2-63_00769	RBL236_00442	100	336	0	0	1	336	1	336	0	696
L2-63_00771	RBL236_00444	100	380	0	0	1	380	1	380	0	781
L2-63_00785	RBL236_00458	100	151	0	0	1	151	1	151	6.00E-105	298
L2-63_00833	RBL236_01045	100	219	0	0	1	219	1	219	1.00E-160	445
L2-63_00834	RBL236_01046	100	146	0	0	1	146	1	146	3.00E-106	301
L2-63_00835	RBL236_01047	100	100	0	0	1	100	1	100	6.00E-69	203
L2-63_00863	RBL236_01075	100	184	0	0	1	184	1	184	2.00E-134	376
L2-63_00955	RBL236_00647	100	261	0	0	1	261	1	261	0	545
L2-63_00972	RBL236_00630	100	196	0	0	1	196	1	196	1.00E-142	398
L2-63_01010	RBL236_00592	100	756	0	0	1	756	1	756	0	1548
L2-63_01012	RBL236_00590	100	418	0	0	1	418	1	418	0	836
L2-63_01073	RBL236_00054	100	139	0	0	1	139	1	139	8.00E-97	277
L2-63_01168	RBL236_01925	100	102	0	0	1	102	1	102	9.00E-69	203
L2-63_01256	RBL236_00720	100	87	0	0	1	87	1	87	3.00E-60	180
L2-63_01257	RBL236_00721	100	66	0	0	1	66	1	66	1.00E-43	136
L2-63_01295	RBL236_00759	100	231	0	0	1	231	1	231	6.00E-170	470
L2-63_01354	RBL236_00818	100	101	0	0	1	101	1	101	5.00E-71	208
L2-63_01362	RBL236_00826	100	296	0	0	1	296	1	296	0	610
L2-63_01395	RBL236_02016	100	222	0	0	1	222	1	222	2.00E-158	440
L2-63_01486	RBL236_01482	100	200	0	0	1	200	1	200	8.00E-149	414
L2-63_01504	RBL236_01465	100	233	0	0	1	233	1	233	6.00E-171	473
L2-63_01505	RBL236_01464	100	267	0	0	1	267	1	267	0	522
L2-63_01507	RBL236_01462	100	95	0	0	1	95	1	95	1.00E-64	192
L2-63_01534	RBL236_01434	100	217	0	0	1	217	1	217	3.00E-158	439
L2-63_01542	RBL236_01426	100	155	0	0	1	155	1	155	8.00E-111	314
L2-63_01585	RBL236_01383	100	145	0	0	1	145	1	145	5.00E-107	303
L2-63_01630	RBL236_01338	100	439	0	0	1	439	1	439	0	879
L2-63_01662	RBL236_01308	100	340	0	0	1	340	1	340	0	694
L2-63_01663	RBL236_01307	100	256	0	0	1	256	1	256	0	526
L2-63_01701	RBL236_01269	100	274	0	0	1	274	1	274	0	561
L2-63_01702	RBL236_01268	100	313	0	0	1	313	1	313	0	640
L2-63_01804	RBL236_01615	100	180	0	0	1	180	1	180	2.00E-127	358
L2-63_01805	RBL236_01616	100	149	0	0	1	149	1	149	2.00E-102	292
L2-63_01807	RBL236_01618	100	372	0	0	1	372	1	372	0	717
L2-63_01808	RBL236_01619	100	129	0	0	1	129	1	129	2.00E-82	240
L2-63_01809	RBL236_01620	100	64	0	0	1	64	1	64	2.00E-37	120
L2-63_01810	RBL236_01621	100	164	0	0	1	164	1	164	3.00E-117	331
L2-63_01811	RBL236_01622	100	316	0	0	1	316	1	316	0	645
L2-63_01819	RBL236_01630	100	148	0	0	1	148	1	148	9.00E-100	285
L2-63_01820	RBL236_01631	100	90	0	0	1	90	1	90	2.00E-61	183
L2-63_01824	RBL236_01635	100	618	0	0	1	618	1	618	0	1241
L2-63_01838	RBL236_01649	100	311	0	0	1	311	1	311	0	642
L2-63_01842	RBL236_01653	100	196	0	0	1	196	1	196	4.00E-137	384
L2-63_01843	RBL236_01654	100	355	0	0	1	355	1	355	0	692
L2-63_01844	RBL236_01655	100	484	0	0	1	484	1	484	0	990
L2-63_01857	RBL236_01668	100	492	0	0	1	492	1	492	0	1004
L2-63_01939	RBL236_00668	100	392	0	0	1	392	1	392	0	800
L2-63_01940	RBL236_00669	100	90	0	0	1	90	1	90	2.00E-61	183
L2-63_01941	RBL236_00670	100	356	0	0	1	356	1	356	0	702
L2-63_01950	RBL236_00679	100	918	0	0	1	918	1	918	0	1869
L2-63_02000	RBL236_00192	100	281	0	0	1	281	1	281	0	583
L2-63_02125	RBL236_00069	100	273	0	0	1	273	1	273	0	556
L2-63_00109	RB5AMG_00413	60.86	304	114	2	5	308	4	302	1.00E-125	364
L2-63_00110	RB5AMG_01432	52.57	272	129	0	1	272	1	272	2.00E-105	310
L2-63_00174	RB5AMG_01839	98.27	173	3	0	1	173	1	173	4.00E-126	354
L2-63_00209	RB5AMG_01804	100	260	0	0	1	260	1	260	0	525
L2-63_00220	RB5AMG_00070	99.33	150	1	0	31	180	589	738	4.00E-100	306
L2-63_00283	RB5AMG_00088	98.97	291	3	0	1	291	1	291	0	576
L2-63_00295	RB5AMG_00100	99.17	242	2	0	1	242	1	242	1.00E-177	491
L2-63_00312	RB5AMG_00328	100	65	0	0	1	65	1	65	1.00E-41	131
L2-63_00319	RB5AMG_00335	100	194	0	0	1	194	1	194	4.00E-139	389
L2-63_00320	RB5AMG_00336	99.4	166	1	0	1	166	1	166	9.00E-116	327
L2-63_00354	RB5AMG_00443	98.77	243	3	0	1	243	1	243	2.00E-178	493
L2-63_00381	RB5AMG_00468	99.1	774	7	0	1	774	1	774	0	1561

L2-63_00388	RB5AMG_00476	98.17	547	10	0	1	547	1	547	0	1106
L2-63_00389	RB5AMG_00922	99.25	530	1	1	1	530	1	527	0	1061
L2-63_00437	RB5AMG_00988	99.66	291	1	0	1	291	1	291	0	576
L2-63_00438	RB5AMG_00987	98.63	365	5	0	1	365	1	365	0	741
L2-63_00444	RB5AMG_00981	98.4	187	3	0	1	187	1	187	8.00E-129	362
L2-63_00486	RB5AMG_02241	98.89	90	1	0	1	90	1	90	2.00E-58	176
L2-63_00575	RB5AMG_01771	100	117	0	0	1	117	1	117	1.00E-76	224
L2-63_00592	RB5AMG_01752	99.29	282	2	0	1	282	1	282	0	555
L2-63_00593	RB5AMG_01751	99.61	255	1	0	1	255	1	255	0	518
L2-63_00769	RB5AMG_01550	99.7	336	1	0	1	336	1	336	0	693
L2-63_00771	RB5AMG_01548	98.42	380	6	0	1	380	1	380	0	773
L2-63_00785	RB5AMG_01534	99.34	151	1	0	1	151	1	151	3.00E-104	296
L2-63_00833	RB5AMG_01486	99.54	219	1	0	1	219	1	219	4.00E-160	444
L2-63_00834	RB5AMG_01485	99.32	146	1	0	1	146	1	146	3.00E-105	299
L2-63_00835	RB5AMG_01484	100	100	0	0	1	100	1	100	6.00E-69	203
L2-63_00863	RB5AMG_01456	98.91	184	2	0	1	184	1	184	4.00E-133	373
L2-63_00955	RB5AMG_01304	100	261	0	0	1	261	1	261	0	545
L2-63_00972	RB5AMG_01287	98.98	196	2	0	1	196	1	196	1.00E-141	395
L2-63_01010	RB5AMG_01251	98.68	756	10	0	1	756	1	756	0	1530
L2-63_01012	RB5AMG_01249	99.28	418	3	0	1	418	1	418	0	832
L2-63_01073	RB5AMG_01596	99.28	139	1	0	1	139	1	139	4.00E-96	275
L2-63_01168	RB5AMG_01064	98.02	101	2	0	1	101	1	101	1.00E-66	197
L2-63_01256	RB5AMG_01168	97.67	86	2	0	1	86	1	86	7.00E-59	176
L2-63_01257	RB5AMG_01169	98.48	66	1	0	1	66	1	66	8.00E-43	134
L2-63_01295	RB5AMG_00626	99.13	231	2	0	1	231	1	231	3.00E-169	468
L2-63_01354	RB5AMG_00569	98.02	101	2	0	1	101	1	101	7.00E-70	206
L2-63_01362	RB5AMG_00561	99.32	296	2	0	1	296	1	296	0	607
L2-63_01395	RB5AMG_00525	99.55	222	1	0	1	222	1	222	1.00E-157	438
L2-63_01486	RB5AMG_00206	100	200	0	0	1	200	1	200	8.00E-149	414
L2-63_01504	RB5AMG_00794	98.71	233	3	0	1	233	1	233	4.00E-169	468
L2-63_01505	RB5AMG_00795	99.25	267	2	0	1	267	1	267	0	516
L2-63_01507	RB5AMG_00797	100	95	0	0	1	95	1	95	1.00E-64	192
L2-63_01534	RB5AMG_00826	99.08	217	2	0	1	217	1	217	8.00E-157	436
L2-63_01542	RB5AMG_00834	100	155	0	0	1	155	1	155	8.00E-111	314
L2-63_01585	RB5AMG_00878	100	145	0	0	1	145	1	145	5.00E-107	303
L2-63_01630	RB5AMG_00155	99.09	439	4	0	1	439	1	439	0	870
L2-63_01662	RB5AMG_01655	97.65	340	8	0	1	340	1	340	0	677
L2-63_01663	RB5AMG_01656	100	256	0	0	1	256	1	256	0	526
L2-63_01701	RB5AMG_00414	57.66	274	116	0	1	274	1	274	3.00E-111	324
L2-63_01804	RB5AMG_00706	99.44	180	1	0	1	180	1	180	8.00E-126	354
L2-63_01805	RB5AMG_00705	97.99	149	3	0	1	149	1	149	3.00E-101	289
L2-63_01807	RB5AMG_00703	99.73	372	1	0	1	372	1	372	0	715
L2-63_01808	RB5AMG_00702	100	129	0	0	1	129	1	129	2.00E-82	240
L2-63_01809	RB5AMG_00701	100	64	0	0	1	64	1	64	2.00E-37	120
L2-63_01810	RB5AMG_00700	99.39	164	1	0	1	164	1	164	2.00E-116	328
L2-63_01811	RB5AMG_00699	98.42	316	5	0	1	316	1	316	0	639
L2-63_01819	RB5AMG_00691	100	148	0	0	1	148	1	148	9.00E-100	285
L2-63_01820	RB5AMG_00690	100	90	0	0	1	90	1	90	2.00E-61	183
L2-63_01824	RB5AMG_00686	99.84	618	1	0	1	618	1	618	0	1240
L2-63_01838	RB5AMG_00672	100	311	0	0	1	311	1	311	0	642
L2-63_01842	RB5AMG_00668	98.47	196	3	0	1	196	1	196	1.00E-134	377
L2-63_01843	RB5AMG_00667	98.59	355	5	0	1	355	1	355	0	684
L2-63_01844	RB5AMG_00666	99.17	484	4	0	1	484	1	484	0	985
L2-63_01857	RB5AMG_00651	99.19	492	4	0	1	492	1	492	0	994
L2-63_01939	RB5AMG_02145	98.47	392	6	0	1	392	1	392	0	791
L2-63_01940	RB5AMG_02146	100	90	0	0	1	90	1	90	2.00E-61	183
L2-63_01941	RB5AMG_02147	97.75	356	8	0	1	356	1	356	0	692
L2-63_01950	RB5AMG_02154	99.35	918	6	0	1	918	1	918	0	1858
L2-63_00209	RBATCC27255_01940	95.77	260	11	0	1	260	1	260	0	510
L2-63_00220	RBATCC27255_00711	98.89	180	2	0	1	180	1	180	8.00E-128	359
L2-63_00283	RBATCC27255_00276	97.94	291	6	0	1	291	1	291	0	573
L2-63_00295	RBATCC27255_00288	89.3	243	25	1	1	242	1	243	4.00E-154	431
L2-63_00319	RBATCC27255_00930	100	194	0	0	1	194	1	194	4.00E-139	389
L2-63_00320	RBATCC27255_00931	100	166	0	0	1	166	1	166	1.00E-117	332
L2-63_00354	RBATCC27255_00833	98.36	244	3	1	1	243	1	244	8.00E-177	488
L2-63_00381	RBATCC27255_01820	98.71	774	10	0	1	774	1	774	0	1553
L2-63_00388	RBATCC27255_01879	94.88	547	28	0	1	547	1	547	0	1051
L2-63_00389	RBATCC27255_00013	90.71	538	42	2	1	530	1	538	0	921
L2-63_00437	RBATCC27255_01877	97.25	291	8	0	1	291	1	291	0	566
L2-63_00438	RBATCC27255_01876	93.13	364	25	0	1	364	1	364	0	693
L2-63_00444	RBATCC27255_00268	97.86	187	4	0	1	187	1	187	1.00E-127	359
L2-63_00486	RBATCC27255_00018	96.67	90	3	0	1	90	1	90	4.00E-57	172
L2-63_00575	RBATCC27255_00264	94.02	117	7	0	1	117	1	117	7.00E-66	197
L2-63_00592	RBATCC27255_00140	98.58	282	4	0	1	282	1	282	0	552
L2-63_00593	RBATCC27255_00141	98.04	255	5	0	1	255	1	255	0	513
L2-63_00769	RBATCC27255_01887	96.43	336	12	0	1	336	1	336	0	678
L2-63_00771	RBATCC27255_01889	95.53	380	17	0	1	380	1	380	0	754
L2-63_00785	RBATCC27255_00613	93.38	151	10	0	1	151	1	151	4.00E-99	284
L2-63_00833	RBATCC27255_01851	96.8	219	7	0	1	219	1	219	8.00E-157	436
L2-63_00834	RBATCC27255_01850	91.1	146	13	0	1	146	1	146	5.00E-96	276
L2-63_00835	RBATCC27255_01849	98	100	2	0	1	100	1	100	2.00E-67	199
L2-63_00863	RBATCC27255_01811	95.11	184	9	0	1	184	1	184	3.00E-128	360
L2-63_00955	RBATCC27255_00979	100	261	0	0	1	261	1	261	0	545
L2-63_00972	RBATCC27255_00962	93.3	194	13	0	1	194	1	194	6.00E-131	368
L2-63_01010	RBATCC27255_00789	95.24	756	36	0	1	756	1	756	0	1399
L2-63_01012	RBATCC27255_00791	98.56	418	6	0	1	418	1	418	0	828
L2-63_01073	RBATCC27255_01953	95.68	139	6	0	1	139	1	139	1.00E-92	266
L2-63_01168	RBATCC27255_01426	100	102	0	0	1	102	1	102	9.00E-69	203
L2-63_01256	RBATCC27255_00511	97.67	86	2	0	1	86	1	86	1.00E-58	176

L2-63_01257	RBATCC27255_00510	100	66	0	0	1	66	1	66	1.00E-43	136
L2-63_01295	RBATCC27255_00917	98.27	231	4	0	1	231	1	231	2.00E-167	464
L2-63_01354	RBATCC27255_01015	99.01	101	1	0	1	101	1	101	2.00E-70	207
L2-63_01362	RBATCC27255_01007	98.65	296	4	0	1	296	1	296	0	605
L2-63_01395	RBATCC27255_00419	90.54	222	21	0	1	222	1	222	1.00E-142	400
L2-63_01486	RBATCC27255_01249	91.46	199	17	0	1	199	1	199	1.00E-138	388
L2-63_01504	RBATCC27255_00318	94.42	233	13	0	1	233	1	233	9.00E-162	449
L2-63_01505	RBATCC27255_00319	81.27	267	50	0	1	267	1	267	1.00E-155	437
L2-63_01507	RBATCC27255_00321	93.68	95	6	0	1	95	1	95	1.00E-51	159
L2-63_01534	RBATCC27255_01678	98.62	217	3	0	1	217	1	217	3.00E-156	434
L2-63_01542	RBATCC27255_01686	99.35	155	1	0	1	155	1	155	4.00E-110	312
L2-63_01585	RBATCC27255_00370	100	145	0	0	1	145	1	145	5.00E-107	303
L2-63_01630	RBATCC27255_00334	93.93	428	26	0	12	439	12	439	0	760
L2-63_01662	RBATCC27255_00445	95.88	340	14	0	1	340	1	340	0	670
L2-63_01663	RBATCC27255_00446	96.88	256	8	0	1	256	1	256	0	516
L2-63_01804	RBATCC27255_01654	98.89	180	2	0	1	180	1	180	4.00E-125	352
L2-63_01805	RBATCC27255_01653	97.32	149	4	0	1	149	1	149	9.00E-100	285
L2-63_01807	RBATCC27255_01651	98.66	372	5	0	1	372	1	372	0	706
L2-63_01808	RBATCC27255_01650	99.22	129	1	0	1	129	1	129	2.00E-82	239
L2-63_01809	RBATCC27255_01649	100	64	0	0	1	64	1	64	2.00E-37	120
L2-63_01810	RBATCC27255_01648	98.78	164	2	0	1	164	1	164	5.00E-116	328
L2-63_01811	RBATCC27255_01647	98.42	316	5	0	1	316	1	316	0	639
L2-63_01819	RBATCC27255_01638	88.71	124	14	0	25	148	1	124	2.00E-73	217
L2-63_01820	RBATCC27255_01636	94.44	90	5	0	1	90	1	90	1.00E-57	173
L2-63_01824	RBATCC27255_01632	97.57	618	15	0	1	618	1	618	0	1219
L2-63_01838	RBATCC27255_01615	94.86	311	16	0	1	311	1	311	0	614
L2-63_01842	RBATCC27255_01611	87.11	194	25	0	1	194	1	194	4.00E-116	330
L2-63_01843	RBATCC27255_01610	95.21	355	17	0	1	355	1	355	0	665
L2-63_01844	RBATCC27255_01609	96.07	484	19	0	1	484	1	484	0	957
L2-63_01857	RBATCC27255_01596	95.73	492	21	0	1	492	1	492	0	969
L2-63_01939	RBATCC27255_01142	92.6	392	29	0	1	392	1	392	0	751
L2-63_01940	RBATCC27255_01143	96.67	90	3	0	1	90	1	90	7.00E-60	179
L2-63_01941	RBATCC27255_01144	93.22	354	24	0	3	356	1	354	0	662
L2-63_01950	RBATCC27255_01151	96.51	918	32	0	1	918	1	918	0	1815
L2-63_00174	2595398400	24.29	140	97	3	32	171	7	137	1.00E-06	43.9
L2-63_00209	2595399457	93.85	260	16	0	1	260	1	260	1.00E-176	489
L2-63_00220	2595399501	84.44	180	28	0	1	180	1	180	1.00E-112	321
L2-63_00283	2595398729	68.73	291	91	0	1	291	1	291	7.00E-148	419
L2-63_00295	2595398956	56.97	251	99	4	1	242	1	251	6.00E-94	278
L2-63_00312	2595400464	98.46	65	1	0	1	65	1	65	2.00E-41	130
L2-63_00319	2595399509	75.92	191	46	0	1	191	1	191	6.00E-108	310
L2-63_00320	2595399510	72.73	165	45	0	1	165	1	165	3.00E-85	250
L2-63_00381	2595399462	67.62	772	248	2	1	772	1	770	0	1090
L2-63_00388	2595399148	23.15	337	222	14	106	435	73	379	5.00E-05	43.9
L2-63_00389	2595399706	59.89	531	186	7	1	530	1	505	0	558
L2-63_00437	2595399393	79.73	291	59	0	1	291	1	291	3.00E-168	471
L2-63_00438	2595399392	59.73	365	136	3	8	363	4	366	9.00E-160	455
L2-63_00444	2595399920	74.29	175	45	0	13	187	13	187	5.00E-90	263
L2-63_00486	2595398834	81.11	90	17	0	1	90	1	90	3.00E-49	152
L2-63_00575	2595400172	82.91	117	20	0	1	117	1	117	2.00E-64	193
L2-63_00592	2595398421	80.3	269	53	0	14	282	14	282	4.00E-158	444
L2-63_00593	2595398422	85.83	254	36	0	1	254	1	254	1.00E-164	458
L2-63_00769	2595399459	73.21	336	90	0	1	336	1	336	3.00E-170	479
L2-63_00771	2595399461	66.84	374	123	1	1	373	1	374	0	523
L2-63_00785	2595398783	76.82	151	35	0	1	151	1	151	4.00E-77	228
L2-63_00833	2595399524	76.04	217	52	0	2	218	3	219	1.00E-123	352
L2-63_00834	2595399525	81.75	137	25	0	5	141	5	141	5.00E-81	237
L2-63_00835	2595399526	77	100	23	0	1	100	7	106	6.00E-53	162
L2-63_00863	2595398441	42.39	184	105	1	1	183	1	184	9.00E-52	166
L2-63_00955	2595399157	78.12	256	56	0	1	256	1	256	1.00E-157	441
L2-63_00972	2595398017	60.44	182	72	0	8	189	8	189	7.00E-79	236
L2-63_01010	2595399249	73.13	748	199	2	10	756	11	757	0	1151
L2-63_01012	2595399251	79	419	87	1	1	418	1	419	0	664
L2-63_01073	2595400105	79.43	141	26	1	1	138	1	141	1.00E-66	201
L2-63_01256	2595398202	68.29	82	26	0	4	85	1	82	2.00E-39	127
L2-63_01257	2595398201	55.74	61	27	0	6	66	1	61	5.00E-21	78.6
L2-63_01295	2595398702	86.22	225	31	0	7	231	1	225	2.00E-142	400
L2-63_01354	2595400301	61.39	101	39	0	1	101	1	101	9.00E-44	139
L2-63_01362	2595398229	50.86	291	139	1	1	291	1	287	2.00E-105	311
L2-63_01395	2595397949	58.3	223	92	1	1	222	1	223	2.00E-85	254
L2-63_01486	2595399310	58.42	190	79	0	8	197	3	192	1.00E-82	246
L2-63_01504	2595400087	88.89	216	24	0	18	233	15	230	3.00E-138	390
L2-63_01505	2595400086	57.46	228	97	0	37	264	1	228	1.00E-93	278
L2-63_01507	2595398181	72.34	94	26	0	1	94	1	94	1.00E-46	146
L2-63_01534	2595398261	57.14	217	89	2	1	213	1	217	3.00E-87	259
L2-63_01542	2595398253	79.35	155	31	1	1	154	1	155	8.00E-82	240
L2-63_01630	2595399725	63.85	426	154	0	1	426	1	426	0	544
L2-63_01662	2595399596	59.23	336	134	2	1	335	5	338	4.00E-130	378
L2-63_01663	2595399595	79.22	255	53	0	1	255	1	255	6.00E-149	419
L2-63_01804	2595399285	67.4	181	58	1	1	180	1	181	5.00E-84	248
L2-63_01805	2595399284	72.97	148	40	0	2	149	3	150	2.00E-65	198
L2-63_01807	2595399282	59.52	373	150	1	1	372	1	373	1.00E-152	437
L2-63_01808	2595399281	69.84	126	38	0	1	126	1	126	1.00E-54	169
L2-63_01809	2595399280	92.19	64	5	0	1	64	1	64	2.00E-34	112
L2-63_01810	2595399279	47.77	157	80	1	10	164	1	157	4.00E-45	147
L2-63_01811	2595399278	60.86	304	119	0	9	312	9	312	2.00E-139	399
L2-63_01819	2595400262	70.09	107	31	1	43	148	2	108	2.00E-47	150
L2-63_01820	2595400260	77.78	90	20	0	1	90	1	90	3.00E-47	147
L2-63_01824	2595398673	61.83	613	217	4	6	617	2	598	0	760

L2-63_01838	2595398659	74.19	310	80	0	1	310	1	310	1.00E-173	486
L2-63_01842	2595398655	33.51	194	125	2	1	191	1	193	3.00E-36	126
L2-63_01843	2595398654	30.51	354	239	2	1	352	1	349	2.00E-49	171
L2-63_01844	2595398653	71.64	483	137	0	1	483	4	486	0	709
L2-63_01857	2595398642	79.88	492	99	0	1	492	1	492	0	840
L2-63_01939	2595398762	49.23	392	199	0	1	392	1	392	9.00E-138	401
L2-63_01940	2595398761	63.33	90	31	1	3	90	2	91	1.00E-32	110
L2-63_01941	2595398760	51.81	359	166	2	1	356	1	355	4.00E-124	363
L2-63_01950	2595398753	78.67	661	119	6	266	918	344	990	0	1032
L2-63_02000	2595398708	62.95	278	88	3	1	278	1	263	2.00E-117	340
L2-63_02125	2595400026	49.82	273	134	2	2	272	9	280	7.00E-91	273
L2-63_02125	2595399002	69.18	279	72	5	2	273	5	276	2.00E-132	379
L2-63_00109	L2-63_00109	100	315	0	0	1	315	1	315	0	640
L2-63_00110	L2-63_00110	100	275	0	0	1	275	1	275	0	561
L2-63_00174	L2-63_00174	100	174	0	0	1	174	1	174	1.00E-128	360
L2-63_00209	L2-63_00209	100	260	0	0	1	260	1	260	0	525
L2-63_00220	L2-63_00220	100	180	0	0	1	180	1	180	6.00E-129	362
L2-63_00283	L2-63_00283	100	291	0	0	1	291	1	291	0	582
L2-63_00295	L2-63_00295	100	242	0	0	1	242	1	242	1.00E-179	496
L2-63_00312	L2-63_00312	100	65	0	0	1	65	1	65	1.00E-41	131
L2-63_00319	L2-63_00319	100	194	0	0	1	194	1	194	4.00E-139	389
L2-63_00320	L2-63_00320	100	166	0	0	1	166	1	166	1.00E-117	332
L2-63_00354	L2-63_00354	100	243	0	0	1	243	1	243	0	499
L2-63_00381	L2-63_00381	100	774	0	0	1	774	1	774	0	1576
L2-63_00388	L2-63_00388	100	547	0	0	1	547	1	547	0	1129
L2-63_00389	L2-63_00389	100	530	0	0	1	530	1	530	0	1074
L2-63_00437	L2-63_00437	100	291	0	0	1	291	1	291	0	578
L2-63_00438	L2-63_00438	100	365	0	0	1	365	1	365	0	749
L2-63_00444	L2-63_00444	100	187	0	0	1	187	1	187	2.00E-130	366
L2-63_00486	L2-63_00486	100	90	0	0	1	90	1	90	8.00E-60	179
L2-63_00575	L2-63_00575	100	117	0	0	1	117	1	117	9.00E-77	224
L2-63_00592	L2-63_00592	100	282	0	0	1	282	1	282	0	560
L2-63_00593	L2-63_00593	100	255	0	0	1	255	1	255	0	520
L2-63_00769	L2-63_00769	100	336	0	0	1	336	1	336	0	696
L2-63_00771	L2-63_00771	100	380	0	0	1	380	1	380	0	781
L2-63_00785	L2-63_00785	100	151	0	0	1	151	1	151	6.00E-105	298
L2-63_00833	L2-63_00833	100	219	0	0	1	219	1	219	1.00E-160	445
L2-63_00834	L2-63_00834	100	146	0	0	1	146	1	146	3.00E-106	301
L2-63_00835	L2-63_00835	100	100	0	0	1	100	1	100	5.00E-69	203
L2-63_00863	L2-63_00863	100	184	0	0	1	184	1	184	1.00E-134	376
L2-63_00955	L2-63_00955	100	261	0	0	1	261	1	261	0	545
L2-63_00972	L2-63_00972	100	196	0	0	1	196	1	196	1.00E-142	398
L2-63_01010	L2-63_01010	100	756	0	0	1	756	1	756	0	1548
L2-63_01012	L2-63_01012	100	418	0	0	1	418	1	418	0	836
L2-63_01073	L2-63_01073	100	139	0	0	1	139	1	139	8.00E-97	277
L2-63_01168	L2-63_01168	100	102	0	0	1	102	1	102	8.00E-69	203
L2-63_01256	L2-63_01256	100	87	0	0	1	87	1	87	3.00E-60	180
L2-63_01257	L2-63_01257	100	66	0	0	1	66	1	66	1.00E-43	136
L2-63_01295	L2-63_01295	100	231	0	0	1	231	1	231	6.00E-170	470
L2-63_01354	L2-63_01354	100	101	0	0	1	101	1	101	5.00E-71	208
L2-63_01362	L2-63_01362	100	296	0	0	1	296	1	296	0	610
L2-63_01395	L2-63_01395	100	222	0	0	1	222	1	222	2.00E-158	440
L2-63_01486	L2-63_01486	100	200	0	0	1	200	1	200	8.00E-149	414
L2-63_01504	L2-63_01504	100	233	0	0	1	233	1	233	6.00E-171	473
L2-63_01505	L2-63_01505	100	267	0	0	1	267	1	267	0	522
L2-63_01507	L2-63_01507	100	95	0	0	1	95	1	95	1.00E-64	192
L2-63_01534	L2-63_01534	100	217	0	0	1	217	1	217	3.00E-158	439
L2-63_01542	L2-63_01542	100	155	0	0	1	155	1	155	8.00E-111	314
L2-63_01585	L2-63_01585	100	145	0	0	1	145	1	145	5.00E-107	303
L2-63_01630	L2-63_01630	100	439	0	0	1	439	1	439	0	879
L2-63_01662	L2-63_01662	100	340	0	0	1	340	1	340	0	694
L2-63_01663	L2-63_01663	100	256	0	0	1	256	1	256	0	526
L2-63_01701	L2-63_01701	100	274	0	0	1	274	1	274	0	561
L2-63_01702	L2-63_01702	100	313	0	0	1	313	1	313	0	640
L2-63_01804	L2-63_01804	100	180	0	0	1	180	1	180	2.00E-127	358
L2-63_01805	L2-63_01805	100	149	0	0	1	149	1	149	2.00E-102	292
L2-63_01807	L2-63_01807	100	372	0	0	1	372	1	372	0	717
L2-63_01808	L2-63_01808	100	129	0	0	1	129	1	129	1.00E-82	240
L2-63_01809	L2-63_01809	100	64	0	0	1	64	1	64	2.00E-37	120
L2-63_01810	L2-63_01810	100	164	0	0	1	164	1	164	3.00E-117	331
L2-63_01811	L2-63_01811	100	316	0	0	1	316	1	316	0	645
L2-63_01819	L2-63_01819	100	148	0	0	1	148	1	148	8.00E-100	285
L2-63_01820	L2-63_01820	100	90	0	0	1	90	1	90	2.00E-61	183
L2-63_01824	L2-63_01824	100	618	0	0	1	618	1	618	0	1241
L2-63_01838	L2-63_01838	100	311	0	0	1	311	1	311	0	642
L2-63_01842	L2-63_01842	100	196	0	0	1	196	1	196	4.00E-137	384
L2-63_01843	L2-63_01843	100	355	0	0	1	355	1	355	0	692
L2-63_01844	L2-63_01844	100	484	0	0	1	484	1	484	0	990
L2-63_01857	L2-63_01857	100	492	0	0	1	492	1	492	0	1004
L2-63_01939	L2-63_01939	100	392	0	0	1	392	1	392	0	800
L2-63_01940	L2-63_01940	100	90	0	0	1	90	1	90	2.00E-61	183
L2-63_01941	L2-63_01941	100	356	0	0	1	356	1	356	0	702
L2-63_01950	L2-63_01950	100	918	0	0	1	918	1	918	0	1869
L2-63_02000	L2-63_02000	100	281	0	0	1	281	1	281	0	583
L2-63_02125	L2-63_02125	100	273	0	0	1	273	1	273	0	556

CD630_31200	2595398499	50.77	65	32	0	2	66	5	69	2.00E-13	63.9
CD630_31200	RBATCC27255_01718	52	125	57	2	1	122	1	125	1.00E-38	128
CD630_34940	2595400260	39.76	83	49	1	2	84	9	90	1.00E-14	63.2
CD630_34940	L2-63_01820	41.46	82	47	1	3	84	10	90	6.00E-16	66.6
CD630_34940	RBL236_01631	41.46	82	47	1	3	84	10	90	6.00E-16	66.6
CD630_34940	RB5AMG_00690	41.46	82	47	1	3	84	10	90	6.00E-16	66.6
CD630_34940	RBATCC27255_01636	41.46	82	47	1	3	84	10	90	9.00E-16	66.2
CD630_34990	RB5AMG_00070	38.67	150	90	2	31	179	589	737	1.00E-27	108
CD630_34990	2595399501	48.33	180	91	2	1	179	1	179	2.00E-50	162
CD630_34990	L2-63_00220	48.89	180	90	2	1	179	1	179	5.00E-53	168
CD630_34990	RBL236_01740	48.89	180	90	2	1	179	1	179	6.00E-53	168
CD630_34990	RBATCC27255_00711	48.89	180	90	2	1	179	1	179	6.00E-53	168
CD630_35410	RB5AMG_00336	31.71	164	112	0	9	172	1	164	6.00E-32	113
CD630_35410	L2-63_00320	32.48	157	106	0	9	165	1	157	1.00E-31	112
CD630_35410	RBL236_02206	32.48	157	106	0	9	165	1	157	1.00E-31	112
CD630_35410	RBATCC27255_00931	32.48	157	106	0	9	165	1	157	1.00E-31	112
CD630_35410	2595399510	33.54	164	109	0	9	172	1	164	2.00E-33	117
CD630_35420	L2-63_00319	37.43	187	116	1	7	192	5	191	2.00E-43	144
CD630_35420	RBL236_02207	37.43	187	116	1	7	192	5	191	3.00E-43	144
CD630_35420	RBATCC27255_00930	37.43	187	116	1	7	192	5	191	3.00E-43	144
CD630_35420	RB5AMG_00335	37.43	187	116	1	7	192	5	191	3.00E-43	144
CD630_35420	2595399509	41.88	191	110	1	3	192	1	191	3.00E-48	157
CD630_35640	L2-63_01486	37.75	204	112	3	10	213	8	196	2.00E-43	145
CD630_35640	RBL236_01482	37.75	204	112	3	10	213	8	196	2.00E-43	145
CD630_35640	RB5AMG_00206	37.75	204	112	3	10	213	8	196	2.00E-43	145
CD630_35640	2595399510	38.76	178	97	2	42	219	32	197	1.00E-42	144
CD630_35640	RBATCC27255_01249	39.08	174	90	3	3	213	37	196	3.00E-40	137
CD630_35670	RBATCC27255_01595	19.04	478	354	15	20	483	22	480	3.00E-07	51.2
CD630_35670	L2-63_01858	19.46	478	352	15	20	483	22	480	3.00E-09	57.4
CD630_35670	RBL236_01669	19.46	478	352	15	20	483	22	480	3.00E-09	57.4
CD630_35670	RB5AMG_00650	19.79	470	344	15	28	483	30	480	9.00E-10	58.9
CD630_35670	2595400301	30.43	46	32	0	463	508	3	48	0.078	31.6
CD630_35670	2595400301	39.02	41	25	0	466	506	58	98	0.002	36.2
CD630_35690	2595399797	26.19	42	31	0	191	232	267	308	9.6	25.8
CD630_35690	RBATCC27255_00247	31.25	64	40	2	51	111	62	124	7.3	26.6
CD630_35690	RB5AMG_01957	31.25	64	40	2	51	111	62	124	7.7	26.2
CD630_35690	L2-63_00974	56.25	16	7	0	147	162	7	22	8.3	23.9
CD630_36730	L2-63_00594	41.38	261	149	3	3	261	17	275	8.00E-64	202
CD630_36730	RBL236_00269	41.38	261	149	3	3	261	17	275	8.00E-64	202
CD630_36730	RB5AMG_01750	41.38	261	149	3	3	261	17	275	9.00E-64	202
CD630_36730	RBATCC27255_00142	41.98	262	146	3	3	261	17	275	2.00E-65	207
CD630_36730	2595398423	46.12	258	133	3	6	260	13	267	4.00E-70	219
sp O31674 YKVI_BACSU	2595400104	36.36	33	17	1	309	341	127	155	3	27.3
sp O31674 YKVI_BACSU	L2-63_01499	40.3	67	37	3	17	80	121	187	0.016	35
sp O31674 YKVI_BACSU	RBL236_01470	40.3	67	37	3	17	80	121	187	0.016	35
sp O31674 YKVI_BACSU	RB5AMG_00788	40.3	67	37	3	17	80	121	187	0.016	34.7
sp O31674 YKVI_BACSU	RBATCC27255_00313	40.3	67	37	3	17	80	121	187	0.02	34.7
sp O34765 YLBV_BACSU	RBATCC27255_01144	21.35	356	237	6	2	356	4	317	2.00E-15	75.1
sp O34765 YLBV_BACSU	2595398760	21.59	389	246	8	16	400	20	353	5.00E-17	80.1
sp O34765 YLBV_BACSU	L2-63_01941	21.9	347	226	9	11	356	17	319	1.00E-15	75.9
sp O34765 YLBV_BACSU	RBL236_00670	21.9	347	226	9	11	356	17	319	1.00E-15	75.9
sp O34765 YLBV_BACSU	RB5AMG_02147	21.9	347	226	7	11	356	17	319	4.00E-15	74.3
sp P26937 SP4FB_BACSU	L2-63_01645	22.5	120	88	2	40	158	3	118	0.003	35.8
sp P26937 SP4FB_BACSU	RBL236_01323	22.5	120	88	2	40	158	3	118	0.003	35.8
sp P26937 SP4FB_BACSU	RB5AMG_00140	22.5	120	88	2	40	158	3	118	0.003	35.8
sp P26937 SP4FB_BACSU	L2-63_01069	25.53	94	56	3	70	149	86	179	0.026	33.5
sp P26937 SP4FB_BACSU	2595400221	28.87	142	98	2	17	158	16	154	3.00E-10	57
sp P37478 WALR_BACSU	L2-63_01735	41.13	231	132	2	1	227	1	231	2.00E-56	181
sp P37478 WALR_BACSU	RBL236_00915	41.13	231	132	2	1	227	1	231	3.00E-56	181
sp P37478 WALR_BACSU	L2-63_00649	43.3	224	123	2	4	227	3	222	6.00E-56	179
sp P37478 WALR_BACSU	RBL236_00323	43.3	224	123	2	4	227	3	222	6.00E-56	179
sp P37478 WALR_BACSU	RBATCC27255_00119	43.3	224	123	2	4	227	3	222	6.00E-56	179
sp P50850 YLYX_BACSU	2595399157	38.86	193	117	1	121	312	46	238	7.00E-46	157
sp P50850 YLYX_BACSU	L2-63_00955	38.86	193	117	1	121	312	46	238	1.00E-45	156
sp P50850 YLYX_BACSU	RBL236_00647	38.86	193	117	1	121	312	46	238	1.00E-45	156
sp P50850 YLYX_BACSU	RBATCC27255_00979	38.86	193	117	1	121	312	46	238	1.00E-45	156
sp P50850 YLYX_BACSU	RB5AMG_01304	38.86	193	117	1	121	312	46	238	1.00E-45	156
sp Q45581 YBBH_BACSU	2595399270	19.53	215	169	2	1	211	1	215	8.00E-04	38.5
sp Q45581 YBBH_BACSU	RB5AMG_00951	26.47	102	73	1	179	280	339	438	0.003	37
sp Q45581 YBBH_BACSU	L2-63_00475	26.47	102	73	1	179	280	339	438	0.003	37
sp Q45581 YBBH_BACSU	RB5AMG_01148	33.75	80	52	1	176	254	168	168	7.00E-04	38.5
sp Q45581 YBBH_BACSU	2595398802	34.25	73	46	1	179	251	339	409	3.00E-04	40.4