

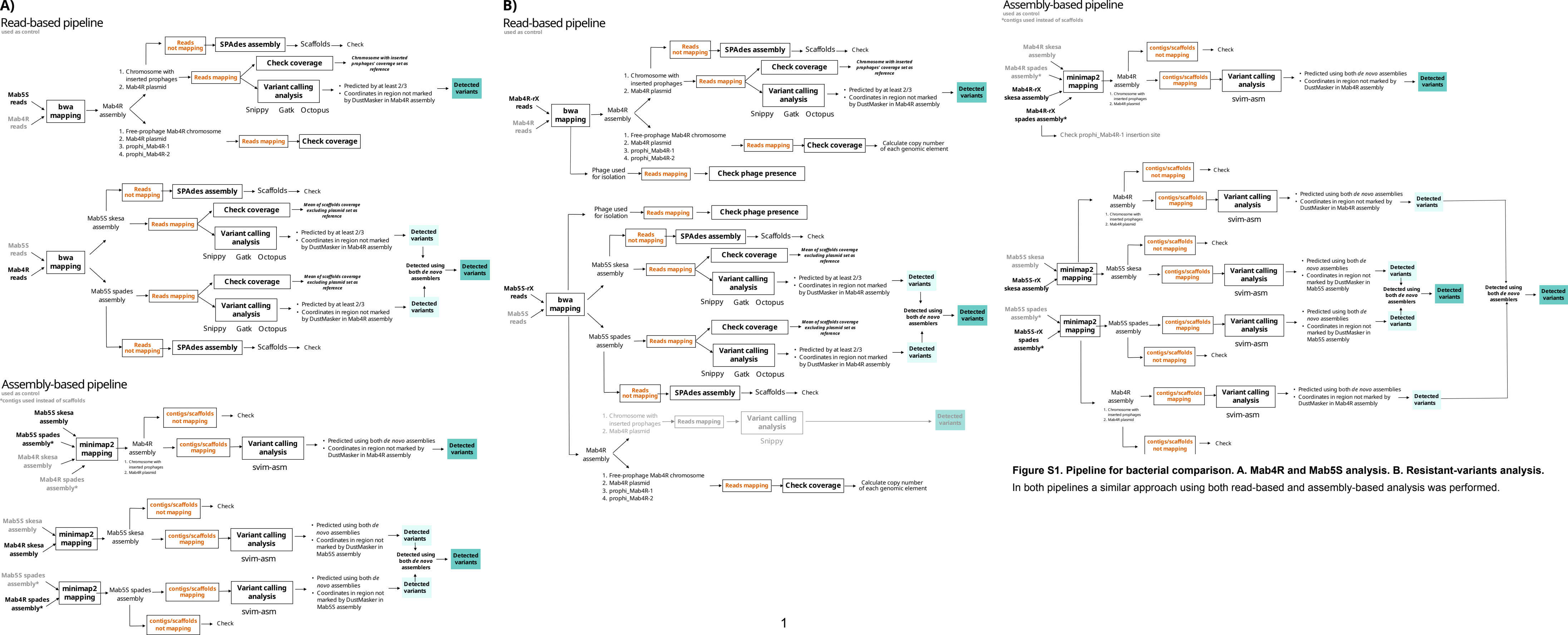


Table S1. Complete annotation of novel phages. Structural and functional annotation was performed with Pharokka followed by manual accuracy. Local phamilies ("phams") were defined with Phammseqs (--pangenome) and correspondence with Actinobacteria database was inferred with the custom pipeline Phage2Pham.

Phage	Start	Stop	Strand	Locus tag	Phrog	Description	Function	Local pham	Actinobacteria database pham (06 March 2026)
Falla	1	369	+	Falla_custom_2_geneCall	phrog_32197	NA	unknown function	pham_53	12063_genes
Falla	389	679	+	Falla_custom_3_geneCall				pham_119	284821_genes
Falla	682	951	+	Falla_custom_4_geneCall	phrog_28565	NA	unknown function	pham_11	11589_genes
Falla	992	1321	+	Falla_custom_5_geneCall	phrog_18656	NA	unknown function	pham_43	284803_genes
Falla	1472	1945	+	Falla_custom_6_geneCall	phrog_226	minor tail protein	tail	pham_56	285286_genes
Falla	1945	3609	+	Falla_custom_7_geneCall	phrog_9	terminase large subunit	head and packaging	pham_19	283330_genes
Falla	3606	5129	+	Falla_custom_8_geneCall	phrog_104	portal protein	head and packaging	pham_1	286710_genes
Falla	4993	5700	+	Falla_custom_9_geneCall	phrog_193	head maturation protease	head and packaging	pham_26	286176_genes
Falla	5960	6556	+	Falla_custom_10_geneCall	phrog_1793	head scaffolding protein	head and packaging	pham_47	241532_genes
Falla	6596	7585	+	Falla_custom_11_geneCall	phrog_10	major head protein	head and packaging	pham_29	286711_genes
Falla	7588	7878	+	Falla_custom_12_geneCall	phrog_35385	NA	unknown function	pham_31	89023_genes
Falla	7897	8373	+	Falla_custom_13_geneCall	phrog_1290	head-tail adaptor	connector	pham_34	267066_genes
Falla	8370	8744	+	Falla_custom_14_geneCall	phrog_763	head-tail adaptor	connector	pham_2	286739_genes
Falla	8741	9061	+	Falla_custom_15_geneCall	phrog_387	neck protein	connector	pham_49	276943_genes
Falla	9061	9495	+	Falla_custom_16_geneCall				pham_37	286777_genes
Falla	9492	10133	+	Falla_custom_17_geneCall	phrog_117	major tail protein	tail	pham_51	286730_genes
Falla	10156	10707	+	Falla_custom_18_geneCall	phrog_1550	QueC-like queuosine biosynthesis	moron_auxiliary_metabolic_gene_and_host_takeover	pham_52	8292_genes
Falla	10788	11180	+	Falla_custom_19_geneCall	phrog_32580	tail assembly chaperone	tail	pham_41	7674_genes
Falla	11234	11587	+	Falla_custom_20_geneCall	phrog_1326	tail assembly chaperone	tail	pham_44	274644_genes
Falla	11587	15036	+	Falla_custom_21_geneCall	phrog_971	endolysin	lysis	pham_39	285200_genes
Falla	15039	16151	+	Falla_custom_22_geneCall	phrog_106	minor tail protein	tail	pham_3	286712_genes
Falla	16153	18003	+	Falla_custom_23_geneCall	phrog_110	minor tail protein	tail	pham_4	286708_genes
Falla	18003	18446	+	Falla_custom_24_geneCall	phrog_1697	minor tail protein	tail	pham_50	7750_genes
Falla	18443	19543	+	Falla_custom_25_geneCall	phrog_1565	minor tail protein	tail	pham_5	281875_genes
Falla	19547	21865	+	Falla_custom_26_geneCall	phrog_746	minor tail protein	tail	pham_46	286853_genes
Falla	21875	22900	+	Falla_custom_27_geneCall	phrog_416	minor tail protein	tail	pham_6	286759_genes
Falla	22910	23272	+	Falla_custom_28_geneCall	phrog_240	head protein	head and packaging	pham_7	285116_genes
Falla	23287	24234	+	Falla_custom_29_geneCall	phrog_1512	endolysin	lysis	pham_57	280220_genes
Falla	24231	24449	+	Falla_custom_30_geneCall	phrog_6116	holin	lysis	pham_61	285603_genes
Falla	24446	24730	+	Falla_custom_31_geneCall	phrog_4511	NA	unknown function	pham_59	283586_genes

Falla	24730	24930	+	Falla_custom_32_geneCall	phrog_6071	NA	unknown function	pham_62	286233_genes
Falla	24930	25343	+	Falla_custom_33_geneCall	phrog_3798	NA	unknown function	pham_64	285314_genes
Falla	25439	26491	+	Falla_custom_34_geneCall	phrog_102	endolysin	lysis	pham_63	1116_genes
Falla	26605	26985	+	Falla_custom_35_geneCall	phrog_16498	NA	unknown function	pham_8	251412_genes
Falla	27128	27517	+	Falla_custom_36_geneCall	phrog_15118	HTH DNA binding protein	DNA_RNA_and_nucl eotide_metabolism	pham_12	1708_genes
Falla	27577	27744	+	Falla_custom_37_geneCall				pham_9	14683_genes
Falla	27748	28161	+	Falla_custom_38_geneCall	phrog_37790	NA	unknown function	pham_14	8427_genes
Falla	28218	28451	+	Falla_custom_39_geneCall				pham_68	12277_genes
Falla	28510	28794	-	Falla_custom_40_geneCall	phrog_93	endonuclease	DNA_RNA_and_nucl eotide_metabolism	pham_22	285203_genes
Falla	28784	29179	-	Falla_custom_41_geneCall	phrog_30353	NA	unknown function	pham_17	9892_genes
Falla	29172	29429	-	Falla_custom_42_geneCall	phrog_34418	NA	unknown function	pham_27	89309_genes
Falla	29172	29561	-	Falla_custom_43_geneCall	phrog_34418	NA	unknown function	pham_69	89290_genes
Falla	29580	30227	-	Falla_custom_44_geneCall	phrog_14876	DNA polymerase	DNA_RNA_and_nucl eotide_metabolism	pham_32	285259_genes
Falla	30214	31059	-	Falla_custom_45_geneCall	phrog_124	Sak4-like ssDNA annealing protein	DNA_RNA_and_nucl eotide_metabolism	pham_35	286859_genes
Falla	31056	32072	-	Falla_custom_46_geneCall	phrog_1218	exonuclease	DNA_RNA_and_nucl eotide_metabolism	pham_24	286740_genes
Falla	32062	34473	-	Falla_custom_47_geneCall	phrog_2573	DNA polymerase	DNA_RNA_and_nucl eotide_metabolism	pham_25	281841_genes
Falla	34382	34924	-	Falla_custom_48_geneCall	phrog_174	dCMP deaminase	DNA_RNA_and_nucl eotide_metabolism	pham_38	285536_genes
Falla	34921	35694	-	Falla_custom_49_geneCall	phrog_5131	thymidylate synthase	DNA_RNA_and_nucl eotide_metabolism	pham_13	1642_genes
Falla	35697	36590	-	Falla_custom_50_geneCall	phrog_13667	NA	unknown function	pham_40	1632_genes
Falla	36590	37048	-	Falla_custom_51_geneCall	phrog_12184	nucleotide pyrophosphohydrolase	other	pham_42	1711_genes
Falla	37045	37593	-	Falla_custom_52_geneCall	phrog_761	thymidylate kinase	other	pham_45	1637_genes
Falla	37594	39105	-	Falla_custom_53_geneCall	phrog_62	DNA helicase	DNA_RNA_and_nucl eotide_metabolism	pham_58	286782_genes
Falla	39270	39476	-	Falla_custom_54_geneCall	phrog_33511	NA	unknown function	pham_16	7751_genes
Falla	39473	39655	-	Falla_custom_55_geneCall	phrog_17534	NA	unknown function	pham_48	170739_genes
Falla	39659	40117	-	Falla_custom_56_geneCall	phrog_13148	NA	unknown function	pham_65	282141_genes
Falla	40151	42076	+	Falla_custom_57_geneCall	phrog_3123	NA	unknown function	pham_21	210763_genes
Falla	42316	43173	+	Falla_custom_58_geneCall	phrog_28441	NA	unknown function	pham_23	286230_genes
Falla	43170	43418	+	Falla_custom_59_geneCall	phrog_34004	NA	unknown function	pham_54	8662_genes
Falla	43411	43548	+	Falla_custom_60_geneCall	phrog_11565	NA	unknown function	pham_55	88679_genes
Falla	43536	43898	+	Falla_custom_61_geneCall	phrog_28269	NA	unknown function	pham_28	90316_genes
Falla	43895	44563	+	Falla_custom_62_geneCall	phrog_16564	NA	unknown function	pham_30	89135_genes
Falla	44364	44615	+	Falla_custom_63_geneCall	phrog_8685	NA	unknown function	pham_60	153408_genes
Falla	44619	44807	+	Falla_custom_64_geneCall	phrog_31858	NA	unknown function	pham_33	9791_genes
Falla	44804	45001	+	Falla_custom_65_geneCall				pham_66	9615_genes

Falla	44815	45309	+	Falla_custom_66_geneCall	phrog_658	NA	unknown function	pham_10	92679_genes
Falla	44998	45309	+	Falla_custom_67_geneCall	phrog_658	NA	unknown function	pham_36	279332_genes
Falla	45296	45766	+	Falla_custom_68_geneCall	phrog_1540	NA	unknown function	pham_123	89840_genes
Falla	45750	45995	+	Falla_custom_69_geneCall	phrog_14975	NA	unknown function	pham_15	284268_genes
Falla	45982	46287	+	Falla_custom_70_geneCall	phrog_36932	NA	unknown function	pham_18	10319_genes
Falla	46287	46586	+	Falla_custom_71_geneCall	phrog_333	HNH endonuclease	DNA_RNA_and_nucl eotide_metabolism	pham_20	282742_genes
Goset	1	360	+	Goset_custom_2_geneCall	phrog_32197	NA	unknown function	pham_53	12063_genes
Goset	360	629	+	Goset_custom_3_geneCall	phrog_28565	NA	unknown function	pham_11	11589_genes
Goset	670	993	+	Goset_custom_4_geneCall	phrog_18656	NA	unknown function	pham_43	284803_genes
Goset	1144	1617	+	Goset_custom_5_geneCall	phrog_226	minor tail protein	tail	pham_56	285286_genes
Goset	1617	3281	+	Goset_custom_6_geneCall	phrog_9	terminase large subunit	head and packaging	pham_19	283330_genes
Goset	3278	4801	+	Goset_custom_7_geneCall	phrog_104	portal protein	head and packaging	pham_1	286710_genes
Goset	4665	5372	+	Goset_custom_8_geneCall	phrog_193	head maturation protease	head and packaging	pham_26	286176_genes
Goset	5632	6228	+	Goset_custom_9_geneCall	phrog_1793	head scaffolding protein	head and packaging	pham_47	241532_genes
Goset	6268	7257	+	Goset_custom_10_geneCall	phrog_10	major head protein	head and packaging	pham_29	286711_genes
Goset	7260	7550	+	Goset_custom_11_geneCall	phrog_35385	NA	unknown function	pham_31	89023_genes
Goset	7569	8045	+	Goset_custom_12_geneCall	phrog_1290	head-tail adaptor	connector	pham_34	267066_genes
Goset	8042	8416	+	Goset_custom_13_geneCall	phrog_763	head-tail adaptor	connector	pham_2	286739_genes
Goset	8413	8733	+	Goset_custom_14_geneCall	phrog_387	neck protein	connector	pham_49	276943_genes
Goset	8733	9167	+	Goset_custom_15_geneCall				pham_37	286777_genes
Goset	9164	9805	+	Goset_custom_16_geneCall	phrog_117	major tail protein	tail	pham_51	286730_genes
Goset	9828	10379	+	Goset_custom_17_geneCall	phrog_1550	QueC-like queuosine biosynthesis	moron_auxiliary_met abolic_gene_and_hos t_takeover	pham_52	8292_genes
Goset	10460	10852	+	Goset_custom_18_geneCall	phrog_32580	tail assembly chaperone	tail	pham_41	7674_genes
Goset	10906	11259	+	Goset_custom_19_geneCall	phrog_1326	tail assembly chaperone	tail	pham_44	274644_genes
Goset	11259	14708	+	Goset_custom_20_geneCall	phrog_971	endolysin	lysis	pham_39	285200_genes
Goset	14711	15823	+	Goset_custom_21_geneCall	phrog_106	minor tail protein	tail	pham_3	286712_genes
Goset	15825	17675	+	Goset_custom_22_geneCall	phrog_110	minor tail protein	tail	pham_4	286708_genes
Goset	17675	18118	+	Goset_custom_23_geneCall	phrog_1697	minor tail protein	tail	pham_50	7750_genes
Goset	18115	19215	+	Goset_custom_24_geneCall	phrog_1565	minor tail protein	tail	pham_5	281875_genes
Goset	19219	21537	+	Goset_custom_25_geneCall	phrog_746	minor tail protein	tail	pham_46	286853_genes
Goset	21547	22572	+	Goset_custom_26_geneCall	phrog_416	minor tail protein	tail	pham_6	286759_genes
Goset	22582	22944	+	Goset_custom_27_geneCall	phrog_240	head protein	head and packaging	pham_7	285116_genes
Goset	22959	23906	+	Goset_custom_28_geneCall	phrog_1512	endolysin	lysis	pham_57	280220_genes
Goset	23903	24121	+	Goset_custom_29_geneCall	phrog_6116	holin	lysis	pham_61	285603_genes
Goset	24118	24402	+	Goset_custom_30_geneCall	phrog_4511	NA	unknown function	pham_59	283586_genes
Goset	24402	24602	+	Goset_custom_31_geneCall	phrog_6071	NA	unknown function	pham_62	286233_genes

Goset	24602	25012	+	Goset_custom_32_geneCall	phrog_3798	NA	unknown function	pham_64	285314_genes
Goset	25108	26160	+	Goset_custom_33_geneCall	phrog_102	endolysin	lysis	pham_63	1116_genes
Goset	26274	26654	+	Goset_custom_34_geneCall	phrog_16498	NA	unknown function	pham_8	251412_genes
Goset	26797	27186	+	Goset_custom_35_geneCall	phrog_15118	HTH DNA binding protein	DNA_RNA_and_nucl eotide_metabolism	pham_12	1708_genes
Goset	27246	27413	+	Goset_custom_36_geneCall				pham_9	14683_genes
Goset	27417	27830	+	Goset_custom_37_geneCall	phrog_37790	NA	unknown function	pham_14	8427_genes
Goset	27887	28120	+	Goset_custom_38_geneCall				pham_68	12277_genes
Goset	28179	28463	-	Goset_custom_39_geneCall	phrog_93	endonuclease	DNA_RNA_and_nucl eotide_metabolism	pham_22	285203_genes
Goset	28453	28848	-	Goset_custom_40_geneCall	phrog_30353	NA	unknown function	pham_17	9892_genes
Goset	28841	29098	-	Goset_custom_41_geneCall	phrog_34418	NA	unknown function	pham_27	89309_genes
Goset	28841	29230	-	Goset_custom_42_geneCall	phrog_34418	NA	unknown function	pham_69	89290_genes
Goset	29249	29893	-	Goset_custom_43_geneCall	phrog_14876	DNA polymerase	DNA_RNA_and_nucl eotide_metabolism	pham_32	285259_genes
Goset	29880	30725	-	Goset_custom_44_geneCall	phrog_124	Sak4-like ssDNA annealing protein	DNA_RNA_and_nucl eotide_metabolism	pham_35	286859_genes
Goset	30722	31738	-	Goset_custom_45_geneCall	phrog_1218	exonuclease	DNA_RNA_and_nucl eotide_metabolism	pham_24	286740_genes
Goset	31728	34139	-	Goset_custom_46_geneCall	phrog_2573	DNA polymerase	DNA_RNA_and_nucl eotide_metabolism	pham_25	281841_genes
Goset	34048	34590	-	Goset_custom_47_geneCall	phrog_174	dCMP deaminase	DNA_RNA_and_nucl eotide_metabolism	pham_38	285536_genes
Goset	34587	35357	-	Goset_custom_48_geneCall	phrog_5131	thymidylate synthase	DNA_RNA_and_nucl eotide_metabolism	pham_13	1642_genes
Goset	35360	36253	-	Goset_custom_49_geneCall	phrog_13667	NA	unknown function	pham_40	1632_genes
Goset	36253	36711	-	Goset_custom_50_geneCall	phrog_12184	nucleotide pyrophosphohydrolase	other	pham_42	1711_genes
Goset	36708	37256	-	Goset_custom_51_geneCall	phrog_761	thymidylate kinase	other	pham_45	1637_genes
Goset	37257	38768	-	Goset_custom_52_geneCall	phrog_62	DNA helicase	DNA_RNA_and_nucl eotide_metabolism	pham_58	286782_genes
Goset	38933	39139	-	Goset_custom_53_geneCall	phrog_33511	NA	unknown function	pham_16	7751_genes
Goset	39136	39318	-	Goset_custom_54_geneCall	phrog_17534	NA	unknown function	pham_48	170739_genes
Goset	39322	39780	-	Goset_custom_55_geneCall	phrog_13148	NA	unknown function	pham_65	282141_genes
Goset	39814	41739	+	Goset_custom_56_geneCall	phrog_3123	NA	unknown function	pham_21	210763_genes
Goset	41979	42836	+	Goset_custom_57_geneCall	phrog_28441	NA	unknown function	pham_23	286230_genes
Goset	42833	43081	+	Goset_custom_58_geneCall	phrog_34004	NA	unknown function	pham_54	8662_genes
Goset	43074	43211	+	Goset_custom_59_geneCall	phrog_11565	NA	unknown function	pham_55	88679_genes
Goset	43199	43561	+	Goset_custom_60_geneCall	phrog_28269	NA	unknown function	pham_28	90316_genes
Goset	43558	44226	+	Goset_custom_61_geneCall	phrog_16564	NA	unknown function	pham_30	89135_genes
Goset	44027	44278	+	Goset_custom_62_geneCall	phrog_8685	NA	unknown function	pham_60	153408_genes
Goset	44282	44470	+	Goset_custom_63_geneCall	phrog_31858	NA	unknown function	pham_33	9791_genes
Goset	44467	44664	+	Goset_custom_64_geneCall				pham_66	9615_genes
Goset	44478	44972	+	Goset_custom_65_geneCall	phrog_658	NA	unknown function	pham_10	92679_genes

Goset	44661	44972	+	Goset_custom_66_geneCall	phrog_658	NA	unknown function	pham_36	279332_genes
Goset	44959	45372	+	Goset_custom_67_geneCall	phrog_1540	NA	unknown function	pham_67	90643_genes
Goset	45359	45601	+	Goset_custom_68_geneCall	phrog_14975	NA	unknown function	pham_15	284268_genes
Goset	45588	45893	+	Goset_custom_69_geneCall	phrog_36932	NA	unknown function	pham_18	10319_genes
Goset	45883	46182	+	Goset_custom_70_geneCall	phrog_333	HNH endonuclease	DNA_RNA_and_nucl eotide_metabolism	pham_20	282742_genes
Goset	46179	46595	+	Goset_custom_71_geneCall	phrog_32690	NA	unknown function	pham_72	9567_genes
Goset	46592	46915	+	Goset_custom_72_geneCall	phrog_29561	NA	unknown function	pham_73	89601_genes
Goset	46706	46915	+	Goset_custom_73_geneCall	phrog_29561	NA	unknown function	pham_74	91590_genes
Goset	46912	47130	+	Goset_custom_74_geneCall				pham_70	23120_genes
Goset	47070	47306	+	Goset_custom_75_geneCall	phrog_17689	NA	unknown function	pham_71	90590_genes
Gegant	1	360	+	Gegant_custom_2_geneCall	phrog_32197	NA	unknown function	pham_53	12063_genes
Gegant	360	629	+	Gegant_custom_3_geneCall	phrog_28565	NA	unknown function	pham_11	11589_genes
Gegant	670	993	+	Gegant_custom_4_geneCall	phrog_18656	NA	unknown function	pham_43	284803_genes
Gegant	1144	1617	+	Gegant_custom_5_geneCall	phrog_226	minor tail protein	tail	pham_56	285286_genes
Gegant	1617	3281	+	Gegant_custom_6_geneCall	phrog_9	terminase large subunit	head and packaging	pham_19	283330_genes
Gegant	3278	4801	+	Gegant_custom_7_geneCall	phrog_104	portal protein	head and packaging	pham_1	286710_genes
Gegant	4665	5372	+	Gegant_custom_8_geneCall	phrog_193	head maturation protease	head and packaging	pham_26	286176_genes
Gegant	5632	6228	+	Gegant_custom_9_geneCall	phrog_1793	head scaffolding protein	head and packaging	pham_47	241532_genes
Gegant	6268	7257	+	Gegant_custom_10_geneCall	phrog_10	major head protein	head and packaging	pham_29	286711_genes
Gegant	7260	7550	+	Gegant_custom_11_geneCall	phrog_35385	NA	unknown function	pham_31	89023_genes
Gegant	7569	8045	+	Gegant_custom_12_geneCall	phrog_1290	head-tail adaptor	connector	pham_34	267066_genes
Gegant	8042	8416	+	Gegant_custom_13_geneCall	phrog_763	head-tail adaptor	connector	pham_2	286739_genes
Gegant	8413	8733	+	Gegant_custom_14_geneCall	phrog_387	neck protein	connector	pham_49	276943_genes
Gegant	8733	9167	+	Gegant_custom_15_geneCall				pham_37	286777_genes
Gegant	9164	9805	+	Gegant_custom_16_geneCall	phrog_117	major tail protein	tail	pham_51	286730_genes
Gegant	9828	10379	+	Gegant_custom_17_geneCall	phrog_1550	QueC-like queuosine biosynthesis	moron_auxiliary_met abolic_gene_and_hos t_takeover	pham_52	8292_genes
Gegant	10460	10852	+	Gegant_custom_18_geneCall	phrog_32580	tail assembly chaperone	tail	pham_41	7674_genes
Gegant	10906	11259	+	Gegant_custom_19_geneCall	phrog_1326	tail assembly chaperone	tail	pham_44	274644_genes
Gegant	11259	14708	+	Gegant_custom_20_geneCall	phrog_971	endolysin	lysis	pham_39	285200_genes
Gegant	14711	15823	+	Gegant_custom_21_geneCall	phrog_106	minor tail protein	tail	pham_3	286712_genes
Gegant	15825	17675	+	Gegant_custom_22_geneCall	phrog_110	minor tail protein	tail	pham_4	286708_genes
Gegant	17675	18118	+	Gegant_custom_23_geneCall	phrog_1697	minor tail protein	tail	pham_50	7750_genes
Gegant	18115	19215	+	Gegant_custom_24_geneCall	phrog_1565	minor tail protein	tail	pham_5	281875_genes
Gegant	19219	21537	+	Gegant_custom_25_geneCall	phrog_746	minor tail protein	tail	pham_46	286853_genes
Gegant	21547	22572	+	Gegant_custom_26_geneCall	phrog_416	minor tail protein	tail	pham_6	286759_genes
Gegant	22582	22944	+	Gegant_custom_27_geneCall	phrog_240	head protein	head and packaging	pham_7	285116_genes

Gegant	22959	23906	+	Gegant_custom_28_geneCall	phrog_1512	endolysin	lysis	pham_57	280220_genes
Gegant	23903	24124	+	Gegant_custom_29_geneCall	phrog_6116	holin	lysis	pham_61	285603_genes
Gegant	24121	24405	+	Gegant_custom_30_geneCall	phrog_4511	NA	unknown function	pham_59	283586_genes
Gegant	24405	24605	+	Gegant_custom_31_geneCall	phrog_6071	NA	unknown function	pham_62	286233_genes
Gegant	24608	25018	+	Gegant_custom_32_geneCall	phrog_3798	NA	unknown function	pham_64	285314_genes
Gegant	25114	26166	+	Gegant_custom_33_geneCall	phrog_102	endolysin	lysis	pham_63	1116_genes
Gegant	26280	26660	+	Gegant_custom_34_geneCall	phrog_16498	NA	unknown function	pham_8	251412_genes
Gegant	26803	27192	+	Gegant_custom_35_geneCall	phrog_15118	HTH DNA binding protein	DNA_RNA_and_nucl eotide_metabolism	pham_12	1708_genes
Gegant	27252	27419	+	Gegant_custom_36_geneCall				pham_9	14683_genes
Gegant	27423	27836	+	Gegant_custom_37_geneCall	phrog_37790	NA	unknown function	pham_14	8427_genes
Gegant	27893	28126	+	Gegant_custom_38_geneCall				pham_68	12277_genes
Gegant	28185	28469	-	Gegant_custom_39_geneCall	phrog_93	endonuclease	DNA_RNA_and_nucl eotide_metabolism	pham_22	285203_genes
Gegant	28459	28854	-	Gegant_custom_40_geneCall	phrog_30353	NA	unknown function	pham_17	9892_genes
Gegant	28847	29104	-	Gegant_custom_41_geneCall	phrog_34418	NA	unknown function	pham_27	89309_genes
Gegant	28847	29236	-	Gegant_custom_42_geneCall	phrog_34418	NA	unknown function	pham_69	89290_genes
Gegant	29255	29902	-	Gegant_custom_43_geneCall	phrog_14876	DNA polymerase	DNA_RNA_and_nucl eotide_metabolism	pham_32	285259_genes
Gegant	29889	30734	-	Gegant_custom_44_geneCall	phrog_124	Sak4-like ssDNA annealing protein	DNA_RNA_and_nucl eotide_metabolism	pham_35	286859_genes
Gegant	30731	31747	-	Gegant_custom_45_geneCall	phrog_1218	exonuclease	DNA_RNA_and_nucl eotide_metabolism	pham_24	286740_genes
Gegant	31737	34148	-	Gegant_custom_46_geneCall	phrog_2573	DNA polymerase	DNA_RNA_and_nucl eotide_metabolism	pham_25	281841_genes
Gegant	34057	34599	-	Gegant_custom_47_geneCall	phrog_174	dCMP deaminase	DNA_RNA_and_nucl eotide_metabolism	pham_38	285536_genes
Gegant	34596	35369	-	Gegant_custom_48_geneCall	phrog_5131	thymidylate synthase	DNA_RNA_and_nucl eotide_metabolism	pham_13	1642_genes
Gegant	35372	36265	-	Gegant_custom_49_geneCall	phrog_13667	NA	unknown function	pham_40	1632_genes
Gegant	36265	36723	-	Gegant_custom_50_geneCall	phrog_12184	nucleotide pyrophosphohydrolase	other	pham_42	1711_genes
Gegant	36720	37268	-	Gegant_custom_51_geneCall	phrog_761	thymidylate kinase	other	pham_45	1637_genes
Gegant	37269	38780	-	Gegant_custom_52_geneCall	phrog_62	DNA helicase	DNA_RNA_and_nucl eotide_metabolism	pham_58	286782_genes
Gegant	38945	39151	-	Gegant_custom_53_geneCall	phrog_33511	NA	unknown function	pham_16	7751_genes
Gegant	39148	39330	-	Gegant_custom_54_geneCall	phrog_17534	NA	unknown function	pham_48	170739_genes
Gegant	39334	39792	-	Gegant_custom_55_geneCall	phrog_13148	NA	unknown function	pham_65	282141_genes
Gegant	39826	41751	+	Gegant_custom_56_geneCall	phrog_3123	NA	unknown function	pham_21	210763_genes
Gegant	41991	42848	+	Gegant_custom_57_geneCall	phrog_28441	NA	unknown function	pham_23	286230_genes
Gegant	42845	43093	+	Gegant_custom_58_geneCall	phrog_34004	NA	unknown function	pham_54	8662_genes
Gegant	43086	43223	+	Gegant_custom_59_geneCall	phrog_11565	NA	unknown function	pham_55	88679_genes
Gegant	43211	43573	+	Gegant_custom_60_geneCall	phrog_28269	NA	unknown function	pham_28	90316_genes
Gegant	43570	44238	+	Gegant_custom_61_geneCall	phrog_16564	NA	unknown function	pham_30	89135_genes

Gegant	44039	44290	+	Gegant_custom_62_geneCall	phrog_8685	NA	unknown function	pham_60	153408_genes
Gegant	44294	44482	+	Gegant_custom_63_geneCall	phrog_31858	NA	unknown function	pham_33	9791_genes
Gegant	44479	44676	+	Gegant_custom_64_geneCall				pham_66	9615_genes
Gegant	44490	44984	+	Gegant_custom_65_geneCall	phrog_658	NA	unknown function	pham_10	92679_genes
Gegant	44673	44984	+	Gegant_custom_66_geneCall	phrog_658	NA	unknown function	pham_36	279332_genes
Gegant	44971	45387	+	Gegant_custom_67_geneCall	phrog_1540	NA	unknown function	pham_67	90643_genes
Gegant	45374	45616	+	Gegant_custom_68_geneCall	phrog_14975	NA	unknown function	pham_15	284268_genes
Gegant	45603	45908	+	Gegant_custom_69_geneCall	phrog_36932	NA	unknown function	pham_18	10319_genes
Gegant	45898	46197	+	Gegant_custom_70_geneCall	phrog_333	HNH endonuclease	DNA_RNA_and_nucl eotide_metabolism	pham_20	282742_genes
Gegant	46194	46610	+	Gegant_custom_71_geneCall	phrog_32690	NA	unknown function	pham_72	9567_genes
Gegant	46607	46930	+	Gegant_custom_72_geneCall	phrog_29561	NA	unknown function	pham_73	89601_genes
Gegant	46721	46930	+	Gegant_custom_73_geneCall	phrog_29561	NA	unknown function	pham_74	91590_genes
Gegant	46927	47145	+	Gegant_custom_74_geneCall				pham_70	23120_genes
Gegant	47085	47321	+	Gegant_custom_75_geneCall	phrog_17689	NA	unknown function	pham_71	90590_genes

Table S2. Genomic differences between Mab4R and Mab5S. For each change, detailed information is shown.

Genomic variation in Mab5S using Mab4R as reference						Annotation					
Genomic element	Coordinates	Strand	Type	Reference	Variant	Gene symbol and description	Mab4R locus	<i>M. abscessus</i> ATCC1977 locus	Position (nt)	Position (aa)	Effect
chromosome	966704	+	ins	G	GC	proP; MFS family permease, includes anhydromuropeptide permease AmpG	FPBODA_04755	MAB_0945	450/465	150/154	frameshift_variant c.449_450insC p.Tyr151fs
chromosome	1261022	-	snp	T	G	dsd1; D-serine deaminase, pyridoxal phosphate-dependent	FPBODA_06275	MAB_1253c	907/1083	303/360	missense_variant c.907A>C p.Met303Leu
chromosome	1578527		snp	T	C						
chromosome	1579352	+	snp	T	C	DNA/RNA non-specific endonuclease	FPBODA_07805	MAB_1555	573/2100	191/699	synonymous_variant
chromosome	1579355	+	snp	T	C	DNA/RNA non-specific endonuclease	FPBODA_07805	MAB_1555	576/2100	192/699	synonymous_variant
chromosome	1785762	+	del	GGGC	G	fAA1; Long-chain acyl-CoA synthetase (AMP-forming)	FPBODA_08830	MAB_1865	808/1758	270/585	conservative_inframe_deletion c.808_810delGGC p.Gly270del
chromosome	1801017	-	del	GC	G	AcrR; DNA-binding protein, AcrR family, includes nucleoid occlusion protein SlmA	FPBODA_08900	MAB_1881c	105/642	35/213	frameshift_variant c.105delG p.Gln36fs
chromosome	1987869	-	snp	A	G	nocobactin polyketide synthase NbtC	FPBODA_09860	MAB_2119c	1134/2955	378/984	synonymous_variant
chromosome	2094959		snp	A	G						
chromosome	2223692	+	snp	C	T	putative lipid transporter YdfJ, MMPL/SSD domain, RND superfamily	FPBODA_10785	MAB_2303	859/2994	287/997	synonymous_variant
chromosome	2249007	+	snp	C	T	FabG; NAD(P)-dependent dehydrogenase, short-chain alcohol dehydrogenase family	FPBODA_10895	MAB_2325	296/957	99/318	missense_variant c.296C>T p.Thr99Ile
chromosome	2607690	+	snp	A	G	Peptidoglycan/LPS O-acetylase OafA/YrhL, contains acyltransferase and SGNH-hydrolase domains	FPBODA_12740	MAB_2689	2064/2181	688/726	synonymous_variant
chromosome	3457119		ins	G	GA						
chromosome	3659705	+	snp	A	C	SdhB; Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	FPBODA_18055	MAB_3676	736/783	246/260	missense_variant c.736A>C p.Thr246Pro
chromosome	3941848	-	snp	C	T	Homeo-like domain protein	FPBODA_19590	MAB_0779	87/759	29/252	synonymous_variant
chromosome	3941899	-	snp	A	G	Homeo-like domain protein	FPBODA_19590	MAB_0779	36/759	12/252	synonymous_variant
chromosome	4128944	-	del	AG	A	Lys2b; Thioester reductase domain of alpha aminoacidate reductase Lys2 and NRPSs	FPBODA_20570	MAB_4098c	2987/3078	996/1025	frameshift_variant c.2987delC p.Pro996fs
chromosome	4426120	+	ins	C	CGCCACCTGTGG	YhhQ; queuosine precursor		MAB_4392			frameshift_variant-

Genomic variation in Mab5S using Mab4R as reference						Annotation					
Genomic element	Coordinates	Strand	Type	Reference	Variant	Gene symbol and description	Mab4R locus	<i>M. abscessus</i> ATCC1977 locus	Position (nt)	Position (aa)	Effect
chromosome	4765975	-	1980pb_ins	-	ATTGCGCGCTCTGGCCGCGGAGATGATCGCGT CGGCCTATGCCCGGGGACAAACCGAATCGGT GGTCGGGCGGGCCGCGAGCTCTACGGTCCA CGGGTCGAATCCCTATTGGGCGCAGGGTATT CGCTGCCGGTATAACCGGACGCAAGGCCATCT GGCCAGGGGACCCAGACCTGCCCATGACGGC GACCTTCATCGGGGATTTCGGCAAGGCACTCG CCGATCTCGGGCAACATCCCGCAGTTGTTGGC CAGGTCTTCCACGTCCCGTCCGACCCCCCAT CACCGGCAGGCAGTTCATCGAGTTGATCGCAA GTCAAGCCGGCACCGTCCCCAAAGTCGGAAAG GCTGACACCACCTATGGTCGCGCTCCTCAAGG TGGTGGCCCCGATCGTCCGCGAGGGCGCCGA GCTGCTGTATCAGTTGCAACAACTTCCTAGT GGACGACAGCAGGTTTCGCGCTCTACCGGCC GCACCGCGACTACTTGGCGGGCTGGCATTGAG CAGACCATCACCTGGTACCGAGCCGATCCAGA GCGGATCAAATACCGGCTACTCCCGGAAAAT CCCGGTAGAACCGCGTAGCGTAGATAGGAATG GCGGGAAACGAGGCGCCCAACTGGGATTTCTGT CGTCGCAACCGGTGCGCAGTGTGCCGGCGTC GCGTCAATGGTGGGCTACCGTGCGCGCGACAT TCCCGACGGAATCCATCTCGGTATGCCCTCAG CCACCTTGACATTATTGTCAGCCTCGATGACG GGGTCGAGAGCGCAGACTCCGCCGCCGCACT CGACGATGCCCGGCCCAATCCTTTGGTTCTCG GTGGGTTGCACACCCGTGCCCGCATATTCGG CAGCGTCTGGTCAGGCGGGGATACAGCTCG CGGTACATCCCCTGGCGTCCCGTGCCCTGTTT GGGGTGCCAGCGCAGAACTGCCGGTCAACCG ATTTCCAGGGACTCGAGATTCTGGGTGGTGCT GTGGCCGGCCTGCCGGAACGACCGCACGGC AACGTCGCTGGTCGGATGCGTTTCGATACCGTC GCGACCTACCTACGGAGTCGCGGAGGCAGC GCTCGGTGGCGCCCGTCCGCTCAGAGGTAGT GCAGGCCTGGCATCTGCTGGAGCGCAGTCAA GGACGAATTACTGTAAGCACCTTGGTTCCCG GGTAGGAATCAGCTCGCGCTATTTGACCACCC TGTTCCAGCGTGAGGTGCGGAGATCACCCAAG ACCGTGCGGATGCTGATGCGCTTCCAGCGGG CCACCAGTCTGCTCGCGCTATCGGCGCGACGC GGGCGTGTGACCTGGCGGGTATAGCCGCCG AAACCGGGTTACGCGATCAGGCGCATCTGACA CACGAGTTCGTGCGCTTACCGGCGTACCGCC ACGGACATGGCTGGCCGCGGAGTTCCGAAATA TACAAGACGGCGGACACTCGTTCGGATCAGAG TGTGAGCATGACTACCTTGACGCCCAGCGTGT GGCTGACCCCTTAAGGCCAAGGATGCCCGGCT CTCATCGAGTACTACGTCGACACCTTCGGCTTC CTGCTCGCGGCCCGCTACGGCGAGGGCGACC GGGTCGATCATGCCAGTTGAACTGGCCAGAA	transporter	FPBODA_23485	MAB_4714c	3435/3585	1146/1194	gene only predicted in Mab5S frameshift_variant p.Leu1146Val

Genomic variation in Mab5S using Mab4R as reference						Annotation					
Genomic element	Coordinates	Strand	Type	Reference	Variant	Gene symbol and description	Mab4R locus	<i>M. abscessus</i> ATCC1977 locus	Position (nt)	Position (aa)	Effect
					GGCACCGGCGGCATCATGTTGGGCAGCCACC GGCCCCGGCGGTGAATGGGCACTGGAGCCGGG AACCGCGGGCGCATACGTCGTGACCCGCGAC CCCGACGGCCTGTACCAGCGGATCGTTGCCAA GAAGGCCGACATTGTCCGGCCACTCGCCAAAA CCGACTACGGTGCCCACGAGTTCGCGGTTTCGC GATCCCGAAGGCAACCTGTGGTCGTTTGGCGA CTACACCGGCGAACC GGCGCCCGAGTAGCTC ACCTACACCAGGCCCAACAGCTGAATATCGCT GGCGTACTTGAGGATCAGCTCCTTGGTGACGT GCGGTATCTCACC GCTGTCTCCGACCTTCGCC TCGTGCACGGCGC						
		+				Zn-dependent glyoxalase%2C PhnB family	-	MAB_4713			Gene_locus_insertion
		+				AraC-type DNA-binding domain and AraC-containing proteins	-	MAB_4712			Gene_locus_insertion
		+				Nucleoside-diphosphate- sugar epimerase	-	MAB_4711			Gene_locus_insertion

Table S3. Copy number of genomic elements. Fold difference between the average number of sequence reads mapping the specific genomic feature relative to the reference (Mab4R chromosome, including prophages or Mab5S SKESA or SPAdes chromosomal scaffolds). For Mab5S and Mab5S-rX, the copy number was estimated independently for SKESA and SPAdes assemblies, and then the mean value was calculated.

	Reference coverage	Copy number		
		Mab4R plasmid	prophi_Mab4R-1	prophi_Mab4R-2
Mab4R-r1	136.99	3.72	6.12	0.96
Mab4R-r2	109.59	2.59	17.71	1.04
Mab4R-r3	158.29	2.41	31.63	0.92
Mab4R-r4	105.75	2.11	35.23	0.94
Mab4R-r5	236.11	2.81	1.97	1.08
Mab4R-r6	211.27	2.52	21.38	0.88
Mab4R-r7	198.48	2.81	2.43	1.16
Mab4R-r8	213.28	2.15	23.67	0.98
Mab4R-r9	150.72	3.19	15.41	1.02
Mab4R-r10	213.95	2.65	5.95	1.02
Mab4R-r11	131.13	2.14	22.01	0.92
Mab4R-r12	158.91	2.94	6.42	1.02
Mab4R-r13	233.23	2.53	12.2	0.91
Mab4R-r14	186.69	2.92	3.07	1.05
Mab4R-r15	173.99	2.09	26.97	0.97
Mab4R-r16	219.05	2.16	26.27	1.09
Mab4R-r17	203.87	2.74	23.7	0.88
Mab4R-r18	180.00	2.49	19.88	0.95
Mab5S-r1	106.86	1.94	0.98	1.01
Mab5S-r2	123.62	2.06	0.93	1.01
Mab5S-r3	107.78	1.91	0.97	1
Mab5S-r4	115.10	2.01	0.95	1.03
Mab5S-r5	82.78	1.99	0.9	1
Mab5S-r6 α	142.06	2.03	0.95	1.04
Mab5S-r6 β	91.68	1.95	0.9	1.02
Mab5S-r7	152.56	1.83	1.02	1.01
Mab5S-r8 α	118.30	1.97	0.96	1.05
Mab5S-r8 β	109.84	2	1.02	1.05
Mab5S-r9 α	95.54	2.02	0.93	1.04
Mab5S-r9 β	193.11	1.85	0.95	1.01
Mab4R	188.81	1.65	30.03	1.01
Mab5S	130.11	1.92	0.97	1.01

Table S4. Genomic alterations detected in Mab4R- and Mab5S-resistant variants. For each change, detailed information about the variation is shown. Due to the close relationship between the two isolates, the Mab4R genome was used as the reference for describing all changes.

Change	Genomic variation in Mab4S						Annotation						
	Genomic element	Coordinates	Strand	Type	Reference	Variant	Gene symbol	Description	Mab4R locus	<i>M. abscessus</i> ATCC1977 locus	Position (nt)	Position (aa)	Effect
C1	chromosome	941538	-	ins	A	AC	menE	O-succinylbenzoic acid-CoA ligase MenE or related acyl-CoA synthetase (AMP-forming)	FPBODA_04705	MAB_0935c	1606/1752	536/583	frameshift_variant c.1606dupG p.Val536fs
C2	chromosome	943131	-	ins	G	GT	menE	O-succinylbenzoic acid-CoA ligase MenE or related acyl-CoA synthetase (AMP-forming)	FPBODA_04705	MAB_0935c	13/1752	5/583	frameshift_variant c.13dupA p.Thr5fs
C3	chromosome	947868	-	snp	C	T	papA3	Acyltransferase papA3	FPBODA_04720	MAB_0938c	1019/1461	340/486	stop_gained c.1019G>A p.Trp340*
C4	chromosome	948162	-	ins	A	AC	papA3	Acyltransferase papA3	FPBODA_04720	MAB_0938c	724/1461	242/486	frameshift_variant c.724dupG p.Val242fs
C5	chromosome	950031	+	snp	A	G	fabD	ACP malonyltransferase S-	FPBODA_04725	MAB_0939	884/11094	295/3697	missense_variant c.884A>G p.Gln295Arg
C6	chromosome	950229-950387	+	del	AGGCGGCC GCGGGTAT CGCGGGTG TCATCAAG GTCATCCT GTCGCTCG AGAACGAG CTGTTGCC GCAGCACCC GCAATTTTC AGAACCCG TCGCCGCA CATTCCCT GGGACAGG CTTCCGGT GGAGGTCG TCAGGGAG GCCCCGCC GTGGGGCC GCAATG	A	fabD	ACP malonyltransferase S-	FPBODA_04725	MAB_0939	1081/11094	361-413/3697	inframe_deletion_EAAAGIAG VIKIVLSLENELLPQHRNFQN PSPHIPWDRPLVEVREAR PWGRN
C7	chromosome	950495	+	ins	G	GC	fabD	ACP malonyltransferase S-	FPBODA_04725	MAB_0939	1354/11094	452/3697	frameshift_variant c.1353dupC p.Ala452fs
C8	chromosome	951318	+	del	TG	T	fabD	ACP malonyltransferase S-	FPBODA_04725	MAB_0939	2173/11094	725/3697	frameshift_variant c.2173delG p.Ala725fs
C9	chromosome	951610	+	ins	C	CA	fabD	ACP malonyltransferase S-	FPBODA_04725	MAB_0939	2465/11094	822/3697	frameshift_variant c.2464dupA p.Thr822fs
C10	chromosome	952016	+	snp	C	T	fabD	ACP malonyltransferase S-	FPBODA_04725	MAB_0939	2869/11094	957/3697	stop_gained c.2869C>T p.Gln957*
C11	chromosome	954906	+	ins	C	CG	fabD	ACP malonyltransferase S-	FPBODA_04725	MAB_0939	5765/11094	1922/3697	frameshift_variant c.5764dupG p.Ala1922fs
C12	chromosome	956905	+	ins	C	CG	fabD	ACP malonyltransferase S-	FPBODA_04725	MAB_0939	7763/11094	2588/3697	frameshift_variant

Change	Genomic variation in Mab4S						Annotation						
	Genomic element	Coordinates	Strand	Type	Reference	Variant	Gene symbol	Description	Mab4R locus	<i>M. abscessus</i> ATCC1977 locus	Position (nt)	Position (aa)	Effect
								malonyltransferase					c.7762dupG p.Asp2588fs
C13	chromosome	957222	+	complex	TC	GGG	fabD	ACP malonyltransferase	FPBODA_04725	MAB_0939	8075/11094	2692/3697	frameshift_variant&missense_variant c.8075_8076delTCinsGGG p.Val2692fs
C14	chromosome	1059195	-	snp	C	T	ykoV	Ku protein	FPBODA_05225	MAB_1032c	547/771	183/256	missense_variant c.547G>A p.Gly183Arg
C15	chromosome	1704715	-	del	GC	G	fur	Fe2+ or Zn2+ uptake regulation protein Fur/Zur	FPBODA_08430	MAB_1678c	24/459	8/152	frameshift_variant c.24delG p.Pro9fs
C16	chromosome	1704715	-	ins	G	GC	fur	Fe2+ or Zn2+ uptake regulation protein Fur/Zur	FPBODA_08430	MAB_1678c	24/459	8/152	frameshift_variant c.24dupG p.Pro9fs
C17	chromosome	1746157	-	snp	A	G	ugpE	ABC-type glycerol-3-phosphate transport system, permease component	FPBODA_08625	MAB_1716c	155/816	52/271	missense_variant c.155T>C p.Leu52Ser
C18	chromosome	2439523-2439742	+	del				Iron-containing redox enzyme family protein	FPBODA_11845	MAB_2508	785-1008/1008	262-335/335	partial_deletion_frameshift_variant p.Pro263Gln
C19	chromosome	2439743-2464384	-	del				Iron-binding zinc finger CDGSH type domain-containing protein	FPBODA_11850	MAB_2509c			complete_deletion
			-	del			hemK	Methylase of polypeptide chain release factors	FPBODA_11855	MAB_2510c			complete_deletion
			+	del			fliA	DNA-directed RNA polymerase specialized sigma subunit	FPBODA_11860	MAB_2511			complete_deletion
			-	del				hypothetical protein	FPBODA_11865				complete_deletion
			+	del			spolIAA	Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor)	FPBODA_11870	MAB_2512			complete_deletion
			-	del			rsbW	Anti-sigma factor RsbW	FPBODA_11875	MAB_2513c			complete_deletion
			-	del				hypothetical protein	FPBODA_11880	MAB_2514c			complete_deletion
			-	del				hypothetical protein	FPBODA_11895	MAB_2514c			complete_deletion
			-	del				BON domain-containing protein	FPBODA_11900	MAB_2515c			complete_deletion
			-	del			fet4	Low affinity Fe/Cu permease	FPBODA_11905	MAB_2516c			complete_deletion
			-	del			fet4	Low affinity Fe/Cu permease	FPBODA_11910	MAB_2517c			complete_deletion
			+	del			csbD	CsbD family protein	FPBODA_11915	MAB_2518			complete_deletion
			-	del			usfY	protein UsfY	FPBODA_11920	MAB_2519c			complete_deletion
			-	del				NADPH-dependent FMN reductase-like domain-containing protein	FPBODA_11925	MAB_2520c			complete_deletion
			-	del				Transmembrane	FPBODA_11930	MAB_2521c			complete_deletion

Change	Genomic variation in Mab4S						Annotation						
	Genomic element	Coordinates	Strand	Type	Reference	Variant	Gene symbol	Description	Mab4R locus	<i>M. abscessus</i> ATCC1977 locus	Position (nt)	Position (aa)	Effect
								protein					
			-	del				Metallothionein	FPBODA_11935	MAB_2522c			complete_deletion
			-	del			amiR	Two-component response regulator, AmiR/NasT family, consists of REC and RNA-binding antiterminator (ANTAR) domains	FPBODA_11940	MAB_2523c			complete_deletion
			+	del			ldcC	Arginine/lysine/ornithine decarboxylase	FPBODA_11945	MAB_2524			complete_deletion
			-	del			phoU	Phosphate uptake regulator PhoU	FPBODA_11950	MAB_2525c			complete_deletion
			-	del				DUF2383 domain-containing protein	FPBODA_11955	MAB_2526c			complete_deletion
			+	del				Protein PS1	FPBODA_11960	MAB_2527			complete_deletion
			-	del				Rho termination factor N-terminal domain-containing protein	FPBODA_11965	MAB_2528c			complete_deletion
			-	del				PAS domain S-box/diguanylate cyclase (GGDEF) domain-containing protein	FPBODA_11970	MAB_2529c			complete_deletion
			-	del			katE	Catalase	FPBODA_11975	MAB_2530c			complete_deletion
			-	del				Sodium:proton antiporter	FPBODA_11980	MAB_2531c			complete_deletion
			+	del				Haemophore haem-binding domain-containing protein	FPBODA_11985	MAB_2533			complete_deletion
			-	del			amiR	Two-component response regulator, AmiR/NasT family, consists of REC and RNA-binding antiterminator (ANTAR) domains	FPBODA_11990	MAB_2534c			complete_deletion
			+	del			proY	L-asparagine transporter or related permease	FPBODA_11995	MAB_2535			complete_deletion
			+	del				hypothetical protein	FPBODA_12000				complete_deletion
			-	del			ilvB	thiamine pyrophosphate-requiring protein	FPBODA_12005	MAB_2537c			complete_deletion
			-	del			dAP2	Dipeptidyl aminopeptidase/acylaminoacyl peptidase	FPBODA_12010	MAB_2538c			complete_deletion
C20	chromosome	2464385-2466046	-	del			menE	O-succinylbenzoic acid-CoA ligase MenE or related acyl-CoA	FPBODA_12015	MAB_2539c			complete_deletion

Change	Genomic variation in Mab4S						Annotation						
	Genomic element	Coordinates	Strand	Type	Reference	Variant	Gene symbol	Description	Mab4R locus	<i>M. abscessus</i> ATCC1977 locus	Position (nt)	Position (aa)	Effect
								synthetase (AMP-forming)					
C21	chromosome	2465073-2466046	-	del			menE	O-succinylbenzoic acid-CoA ligase MenE or related acyl-CoA synthetase (AMP-forming)	FPBODA_12015	MAB_2539c	1-985/1647	1-328/548	partial_deletion
C22	chromosome	2466047-2467023	-	del			yqjQ	Short-chain dehydrogenase	FPBODA_12020	MAB_2540c			complete_deletion
C23	chromosome	2467024-2467718	-	del			acrR	DNA-binding protein, AcrR family, includes nucleoid occlusion protein SlmA	FPBODA_12025	MAB_2541c			complete_deletion
C24	chromosome	2467610-2467718	-	del			acrR	DNA-binding protein, AcrR family, includes nucleoid occlusion protein SlmA	FPBODA_12025	MAB_2541c	422-609/609	141-202/202	partial_deletion
C25	chromosome	2467719-2468326 ; 2471147-2478960	+	del				Putative pyridoxine/pyridoxamine 5'-phosphate oxidase	FPBODA_12030	MAB_2542			complete_deletion
			+	del			yticJ	putative amidohydrolase YtcJ	FPBODA_12050	MAB_2546			complete_deletion
			-	del				Cupin type-2 domain-containing protein	FPBODA_12055	MAB_2547c			complete_deletion
			-	del			ubiG	2-polyprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinol methylase	FPBODA_12060	MAB_2548c			complete_deletion
			+	del				hypothetical protein	FPBODA_12065	MAB_2549			complete_deletion
			-	del			desA1	Putative acyl-[acyl-carrier-protein] desaturase desA1	FPBODA_12070	MAB_2550c			complete_deletion
			+	del			ASdes	ASdes TB sRNA	FPBODA_12075				complete_deletion
			+	del				Polyketide cyclase / dehydrase and lipid transport	FPBODA_12080	MAB_2551			complete_deletion
			-	del			oafA	Peptidoglycan/LPS O-acetylase OafA/YrhL, contains acyltransferase and SGNH-hydrolase domains	FPBODA_12085	MAB_2552c			complete_deletion
			+	del				Integral membrane protein	FPBODA_12090	MAB_2553			complete_deletion
C26	chromosome	2468327-2468514	-	del			acrR	DNA-binding protein, AcrR family, includes nucleoid occlusion protein SlmA	FPBODA_12035	MAB_2543c	1-110/681	1-37/226	partial_deletion
		2470130-2471146	-	del			nit2	Omega-amidase YafV/Nit2, hydrolyzes	FPBODA_12045	MAB_2545c	1-889/984	1-326/327	partial_deletion

Change	Genomic variation in Mab4S						Annotation						
	Genomic element	Coordinates	Strand	Type	Reference	Variant	Gene symbol	Description	Mab4R locus	<i>M. abscessus</i> ATCC1977 locus	Position (nt)	Position (aa)	Effect
								alpha-ketoglutaramate					
C27	chromosome	2468327-2468934	-	del			acrR	DNA-binding protein, AcrR family, includes nucleoid occlusion protein SlmA	FPBODA_12035	MAB_2543c			complete_deletion
		2470035-2471146	-	del			nit2	Omega-amidase YafV/Nit2, hydrolyzes alpha-ketoglutaramate	FPBODA_12045	MAB_2545c			complete_deletion
C28	chromosome	2468935-2470034	-	del			aguA	Agmatine/peptidylarginine deiminase	FPBODA_12040	MAB_2544c			complete_deletion
C29	chromosome	2478960-2490935	+	del				hypothetical protein	FPBODA_12095	MAB_2554			complete_deletion
			+	del			celA1	Cellulase/cellobiase CelA1	FPBODA_12100	MAB_2555			complete_deletion
			-	del				MPT63-like domain-containing protein	FPBODA_12105	MAB_2556c			complete_deletion
			-	del			pncA	Nicotinamidase-related amidase	FPBODA_12110	MAB_2557c			complete_deletion
			+	del			ybdK	Gamma-glutamyl:cysteine ligase YbdK, ATP-grasp superfamily	FPBODA_12115	MAB_2558			complete_deletion
			-	del			fkpA	FKBP-type peptidyl-prolyl cis-trans isomerase	FPBODA_12120	MAB_2559c			complete_deletion
			+	del				LGFP repeat	FPBODA_12125	MAB_2560			complete_deletion
			-	del			pepCK	phosphoenolpyruvate carboxykinase (GTP)	FPBODA_12130	MAB_2561c			complete_deletion
			-	del			arsR	DNA-binding transcriptional regulator, ArsR family	FPBODA_12135	MAB_2562c			complete_deletion
			+	del				DUF5313 domain-containing protein	FPBODA_12140	MAB_2563			complete_deletion
			+	del			cynT	Carbonic anhydrase	FPBODA_12145	MAB_2564			complete_deletion
			-	del			arsR	Rv2640c family ArsR-like transcriptional regulator	FPBODA_12150	MAB_2565c			complete_deletion
			+	del				ArsI/CadI family heavy metal resistance metalloenzyme	FPBODA_12155	MAB_2566			complete_deletion
			+	del			arsB	ACR3 family arsenite efflux transporter	FPBODA_12160	MAB_2567			complete_deletion
			+	del			wzb	Protein-tyrosine-phosphatase	FPBODA_12165	MAB_2568			complete_deletion
			-	del			fetB	ABC-type iron transport system FetAB, permease component	FPBODA_12170	MAB_2569c			complete_deletion
C30	chromosome	2490936-2492552	-	del				Membrane transport protein MMPL domain-containing protein	FPBODA_12175	MAB_0478*	1601-2970/2970	534-989/989	partial_deletion

Change	Genomic variation in Mab4S						Annotation						
	Genomic element	Coordinates	Strand	Type	Reference	Variant	Gene symbol	Description	Mab4R locus	<i>M. abscessus</i> ATCC1977 locus	Position (nt)	Position (aa)	Effect
C31	chromosome	2490936-2494130	-	del				Membrane transport protein MMPL domain-containing protein	FPBODA_12175	MAB_0478*			complete_deletion
C32	chromosome	2494131-2500892	-	del			mmpS4	Membrane protein mmpS4	FPBODA_12180	MAB_2572c			complete_deletion
			-	del			ubiH	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	FPBODA_12185	MAB_2573c			complete_deletion
			-	del			menE	O-succinylbenzoic acid-CoA ligase MenE or related acyl-CoA synthetase (AMP-forming)	FPBODA_12190	MAB_2574c			complete_deletion
			-	del			ycgM	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	FPBODA_12195	MAB_2575c			complete_deletion
			-	del				2,3-dihydroxybiphenyl-1,2-dioxygenase	FPBODA_12200	MAB_2576c			complete_deletion
			+	del			acrR	DNA-binding protein, AcrR family, includes nucleoid occlusion protein SlmA	FPBODA_12205	MAB_2577			complete_deletion
C33	chromosome	2500893-2501235	-	del			yaeQ	Uncharacterized conserved protein YaeQ, suppresses RfaH defect	FPBODA_12210	MAB_2578c	210-552/552	70-183/183	partial_deletion
C34	chromosome	2819738	-	ins	C	CGGT	yjhB	ADP-ribose pyrophosphatase YjhB, NUDIX family	FPBODA_13770	MAB_2893c	831/1023	277/340	conservative_inframe_insertion c.829_831dupACC p.Thr277dup
C35	chromosome	3060146	-	del	AC	A	nrmA	nanoRNase/pAp phosphatase, hydrolyzes c-di-AMP and oligoRNAs	FPBODA_15005	MAB_3129c	704/996	235/331	frameshift_variant c.704delG p.Gly235fs
C36	chromosome	3060533	-	complex	TCGGCG	GGGTC	nrmA	nanoRNase/pAp phosphatase, hydrolyzes c-di-AMP and oligoRNAs	FPBODA_15005	MAB_3129c	318/996	105/331	frameshift_variant&missense_variant c.313_318delCGCCGGAinsGACC p.Arg105fs
C37	chromosome	3060795	-	ins	C	GCCCT GCTGG CCTTC GCCAG CAGGG CCACG GCACC GTCC	nrmA	nanoRNase/pAp phosphatase, hydrolyzes c-di-AMP and oligoRNAs	FPBODA_15005	MAB_3129c	51/996	17/331	inframe_insertion_GRCRGPAGEGQQG
C38	chromosome	3223057	-	del	TGCCTTCTTGACCGGA	T	hupB	DNA-binding protein HupB	FPBODA_15820	MAB_3292c	422/624	136/207	disruptive_inframe_deletion c.408_422delTCCGGTCAAG AAGGC p.Pro137_Ala141del

Change	Genomic variation in Mab4S						Annotation						
	Genomic element	Coordinates	Strand	Type	Reference	Variant	Gene symbol	Description	Mab4R locus	<i>M. abscessus</i> ATCC1977 locus	Position (nt)	Position (aa)	Effect
C39	chromosome	3369368	-	snp	C	T	codB	Purine-cytosine permease or related protein	FPBODA_16550	MAB_3432c	276/1326	92/441	synonymous_variant c.276G>A p.Leu92Leu
C40	chromosome	3457119		ins	G	GA	Non coding region; affecting proph_Mab4R-1 position 424 (5pb before immunity repressor)						
C41	chromosome	3457168		snp	G	T	Non coding region; affecting proph_Mab4R-1 position 384 (54pb before immunity repressor)						
C42	chromosome	4507790	-	snp	T	G	rfaB	Glycosyltransferase involved in cell wall biosynthesis	FPBODA_22370	MAB_4480c	458/1182	153/393	missense_variant c.458A>C p.Gln153Pro
C43	chromosome	4528489	+	ins	G	GC	trmB	tRNA (guanosine(46)-N7)-methyltransferase TrmB	FPBODA_22470	MAB_4506	296/816	99/271	frameshift_variant c.295dupC p.Leu99fs
C44	chromosome	4855205-4855358	-	del	ACGGCGGC AATCAGCC GATAAAGC TCGGCATC ACCATAGA AACGCAAC GCCAACGC CGACAACG TATCCCCC GCAACCAC CGTGATC TCGTGACA TCGGGAAT GACCAGCC GCTGCCCC ACACCAAC GGCTCCAG GATCGGAA ATCCCGCT GG	A	xkdP	Cytoplasmic potassium-binding protein Kbp/XkdP/YgaU, contains LysM domain	FPBODA_23950	MAB_4806c	252/1350	85/449	frameshift_variant p.Ser85fs
C45	plasmid	2622		del	AT	A	Non coding region; affecting Mab4R plasmid (between hypothetical protein and transcriptional regulator)						

*Similarity below the threshold: 98% Query Cover 87.04% Identity (with MAB_2650 94% Query Cover 47,69% Identity)

Table S5. Evidence of the described genomic alterations. For each variant and change, supporting information, including variant callers identifying the variation and coverage, provided by Snippy, is shown. If Snippy does not detect a change, Gatk coverage is provided instead.

	Change	Confidence		
		Softwares detecting change	Coverage	Confirmed by conventional PCR?
Mab4R-r1	C2	Snippy_Gatk_Octopus	GT:24 G:0	-
Mab4R-r2	C2	Snippy_Gatk_Octopus	GT:15 G:0	-
	C44	Svim_asm	-	-
Mab4R-r3	C2	Snippy_Gatk_Octopus	GT:25 G:0	-
Mab4R-r4	C8	Snippy_Gatk_Octopus	T:48 TG:0	-
Mab4R-r5	C2	Snippy_Gatk_Octopus	GT:59 G:0	-
	C40	Snippy_Gatk_Octopus	GA:303 G:14	-
Mab4R-r6	C11	Snippy_Gatk_Octopus	CG:171 C:0	-
	C40	Snippy_Gatk_Octopus	GA:1313 G:19	-
Mab4R-r7	C11	Snippy_Gatk_Octopus	CG:116 C:0	-
	C40	Gatk_Octopus	G:77 GA:447	-
Mab4R-r8	C5	Snippy_Gatk_Octopus	G:88 A:0	-
	C40	Snippy_Gatk_Octopus	GA:1254 G:0	-
Mab4R-r9	C1	Snippy_Gatk_Octopus	AC:117 A:0	-
Mab4R-r10	C4	Snippy_Gatk_Octopus	AC:196 A:0	-
	C40	Gatk_Octopus	G:42 GA:890	-
Mab4R-r11	C34	Snippy_Gatk_Octopus	CGGT:68 C:1	-
	C40	Snippy_Gatk	GA:3108 G:4	-
	C6	Svim_asm	-	-
Mab4R-r12	C7	Snippy_Gatk_Octopus	GC:138 G:0	-
	C39	Snippy_Gatk_Octopus	T:157 C:0	-
Mab4R-r13	C8	Snippy_Gatk_Octopus	T:186 TG:0	-
	C40	Snippy_Gatk_Octopus	GA:838 G:0	-
Mab4R-r14	C11	Snippy_Gatk_Octopus	CG:156 C:0	-
	C40	Snippy_Gatk_Octopus	GA:290 G:0	-
Mab4R-r15	C12	Snippy_Gatk_Octopus	CG:79 C:0	-
	C34	Snippy_Gatk_Octopus	CGGT:108 C:0	-
Mab4R-r16	C11	Snippy_Gatk_Octopus	CG:88 C:2	-
	C40	Snippy_Gatk_Octopus	GA:5751 G:58	-
	C41	Gatk_Octopus	G: 205 T:1818	-
Mab4R-r17	C9	Snippy_Gatk_Octopus	CA:130 C:0	-
Mab4R-r18	C2	Snippy_Gatk_Octopus	GT:29 G:0	-

	Change	Confidence		
		Softwares detecting change	Coverage	Confirmed by conventional PCR?
Mab5S-r1	C3	Snippy_Gatk_Octopus	A:95 G:0	-
Mab5S-r2	C10	Snippy_Gatk_Octopus	A:98 G:0	-
	C14	Snippy_Gatk_Octopus	T:100 C:1	-
Mab5S-r3	C35	Snippy_Gatk_Octopus	T:84 TG:0	-
Mab5S-r4	C15	Snippy_Gatk_Octopus	G:123 GC:0	Yes
Mab5S-r5	C16	Snippy_Gatk_Octopus	GC:87 G:3	Yes
Mab5S-r6 α	C42	Snippy_Gatk_Octopus	C:110 A:0	-
	C13	Snippy_Gatk_Octopus	CCC:105 GA:0	-
Mab5S-r6 β	C15	Snippy_Gatk_Octopus	G:86 GC:0	Yes
	C38	Snippy_Gatk_Octopus	C:25 CCAAGAAGGCTCCGGT:0	-
	C42	Snippy_Gatk_Octopus	C:71 A:0	-
	C43	Snippy_Gatk_Octopus	AG:79 A:0	-
Mab5S-r7	C21	Svim_asm	-	-
	C22	Svim_asm	-	-
	C23	Svim_asm	-	-
	C25	Svim_asm	-	Yes
	C26	Svim_asm	-	-
	C29	Svim_asm	-	-
	C30	Svim_asm	-	-
	C45	Snippy_Gatk_Octopus	A:214 AT:0	-
Mab5S-r8 α	C17	Snippy_Gatk_Octopus	G:130 A:0	-
	C18	Svim_asm	-	-
	C19	Svim_asm	-	-
	C20	Svim_asm	-	-
	C22	Svim_asm	-	-
	C23	Svim_asm	-	-
	C25	Svim_asm	-	Yes
	C27	Svim_asm	-	-
	C28	Svim_asm	-	-
	C45	Snippy_Gatk_Octopus	A:256 AT:0	-
Mab5S-r8 β	C17	Snippy_Gatk_Octopus	G:123 A:0	-
	C36	Snippy_Gatk_Octopus	GACCC:74 CGCCGA:0	-
	C18	Svim_asm	-	-
	C19	Svim_asm	-	-
	C20	Svim_asm	-	-
	C20	Svim_asm	-	-

	Change	Confidence		
		Softwares detecting change	Coverage	Confirmed by conventional PCR?
	C22	Svim_asm	-	-
	C23	Svim_asm	-	-
	C25	Svim_asm	-	Yes
	C27	Svim_asm	-	-
	C28	Svim_asm	-	-
Mab5S-r9 α	C37	Gatk_Octopus	G:2 GGACGGTGCCGTGGCCCTGCTGGCGAAGG CCAGCAGGGC:66	-
	C24	Svim_asm	-	Yes
	C25	Svim_asm	-	Yes
	C27	Svim_asm	-	-
	C28	Svim_asm	-	-
	C29	Svim_asm	-	-
	C31	Svim_asm	-	-
	C32	Svim_asm	-	-
	C33	Svim_asm	-	-
	C24	Svim_asm	-	Yes
Mab5S-r9 β	C25	Svim_asm	-	Yes
	C27	Svim_asm	-	-
	C28	Svim_asm	-	-
	C29	Svim_asm	-	-
	C31	Svim_asm	-	-
	C32	Svim_asm	-	-
	C33	Svim_asm	-	-
	C33	Svim_asm	-	-