

## Supplementary Materials and methods and figures

### **SME-4 producing *Serratia marcescens* from Argentina belonging to the clade II of the *S. marcescens* phylogeny.**

Laura DABOS<sup>1,2‡</sup>, Rafael PATIÑO-NAVARRETE<sup>2‡</sup>, Marcela NASTRO<sup>3</sup>, Angela FAMIGLIETTI<sup>3</sup>,  
Philippe GLASER<sup>2,4</sup>, Carlos H. RODRIGUEZ<sup>3</sup>, Thierry NAAS<sup>1,2,5,6\*</sup>

#### **Supplementary material and methods.**

ProgressiveMauve and the Mauve distributed script stripSubsetLCBs<sup>1</sup> were used to extract all the regions with a minimum length of 500 bp shared by all the strains, generating a 2,877,168 bp core genome alignment. Recombinant variable positions were removed with Gubbins<sup>2</sup>, and a Maximum Likelihood phylogeny was inferred for the alignment of the 631,207 non-recombinant variable sites with RAxML using a General Time Reversible (GTR) model incorporating a gamma distribution rate among sites<sup>3</sup>. In parallel, a whole genome phylogeny was estimated by adding 321 *S. marcescens* genome sequences retrieved from public databases (Table S3) with kSNP3<sup>4</sup>, with a Kchooser estimated k-mer length of 21, and a fraction of core k-mers of 0.46, after the removal of two divergent strains fgi94 (GCF\_000330865) and CQMUS2 (GCF\_001557575). Phylogenetic clusters were defined with ClusterPicker<sup>5</sup> as described in Demzuck et al.<sup>5</sup>, initial and main support threshold of 0.9, a genetic distance threshold of 4.5, and a large cluster threshold of 20. All genomes were

annotated with Prokka<sup>7</sup>, the presence of carbapenemase genes was assessed with resfinder<sup>8</sup>. Graphic representations were generated with the genoplots<sup>9</sup> library in R v 3.4.4.

#### SUPPLEMENTARY REFERENCES

- S1. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. *PLoS One* 2010; 5: e111147.
- S2. Croucher NJ, Page AJ, Connor TR, et al. Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. *Nucleic Acids Res* 2015; 43: e15.
- S3. Stamatakis A. RAxML-VI-HPC: Maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* 2006; 22: 2688–90.
- S4. Gardner SN, Slezak T, Hall BG. kSNP3.0: SNP detection and phylogenetic analysis of genomes without genome alignment or reference genome. *Bioinformatics* 2015: btv271-.
- S5. Ragonnet-Cronin M, Hodcroft E, Hué S, et al. Automated analysis of phylogenetic clusters. *BMC Bioinformatics* 2013; 14: 317.
- S6. Demzuck W, Martin I, Peterson S, et al. Genomic epidemiology and molecular resistance mechanisms of azithromycin-resistant *Neisseria gonorrhoeae* in Canada from 1997 to 2014. *J Clin Microbiol* 2016; 44(1): 1-19.
- S7. Seemann T. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 2014; 30: 2068–9.
- S8. Zankari E, Hasman H, Cosentino S, et al. Identification of acquired antimicrobial resistance genes. *J Antimicrob Chemother* 2012; 67: 2640–4.
- S9. Guy L, Kultima JR, Andersson SG. genoPlotR: comparative gene and genome visualization in R. *Bioinformatics* 2010; 26: 2334–5.

## Supplementary Figure legends

Figure S1. Maximum likelihood tree obtained for all *S. marcescens* strains (Table S3) obtained with kSNP3, using the core SNPs. Branch tips represent the carbapenemase gene. In the columns are marked the name of the strains, for those used in the phylogeny represented in the Figure 2, and the assembly number for the remaining strains. Strains sequenced in this study are tagged by a green star on the right of its name, while the strains used for the figure 2 of the main text retrieved from the ncbi database are tagged with blue pentagons of the left. The colour of the strain name represents the Cluster of strains identified with ClusterPicker. Strains in black were not included in any cluster.

Figure S2. Comparison of the SmarGI1-1 and its genetic environment within the SME subclade. IS elements are only marked on the reference sequence for the island N12-00620 (KF615855). homologous regions are linked by brownish columns.

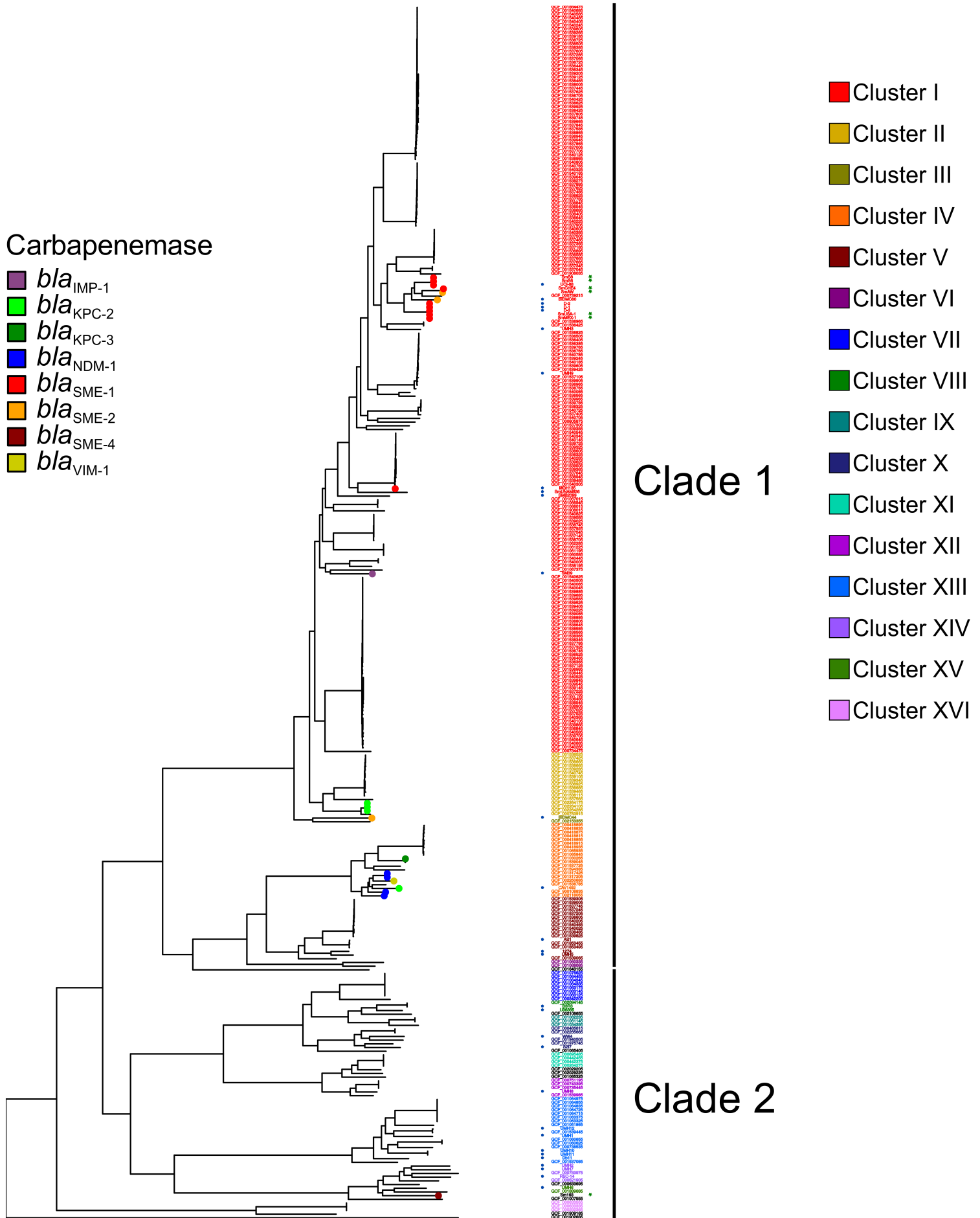


Fig. S1

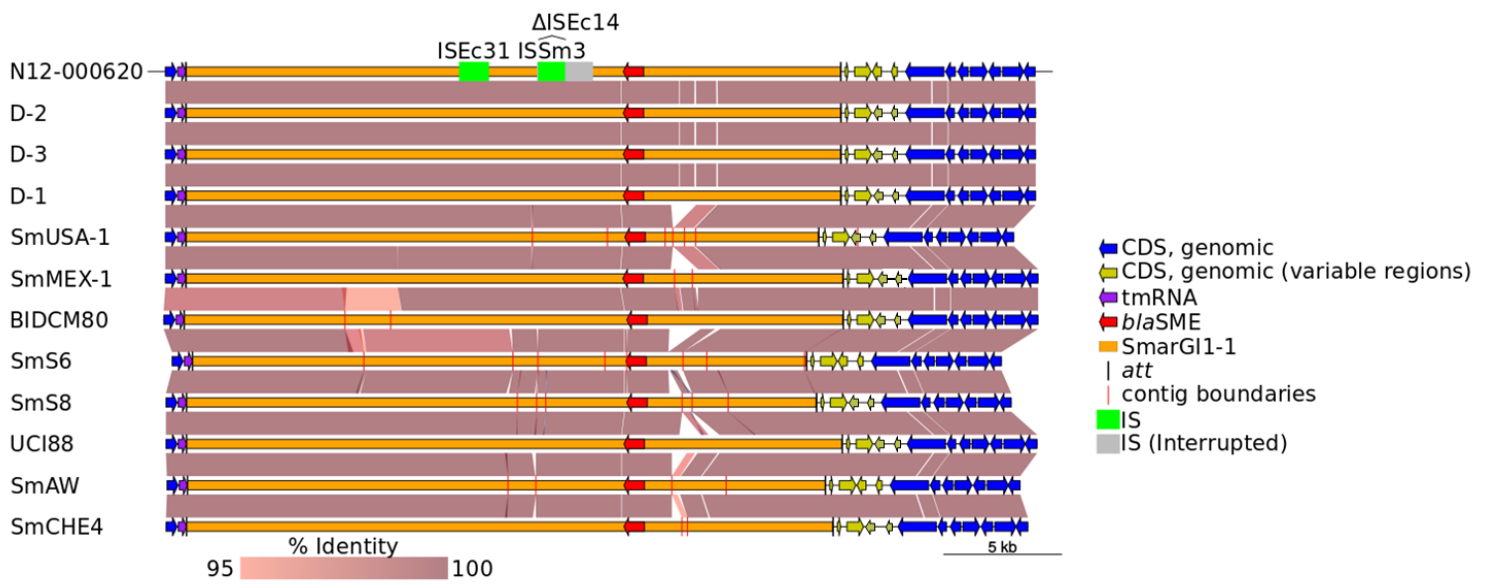


Fig. S2

**Table S1.** *S. marcescens* strains encoding or not *bla*<sub>SME</sub> genes identified, among the genomes of this study and found in public databases (last accessed February 2018), used for the whole genome phylogenetic analysis.

Strain	Assembly	Accession N°	<i>bla</i> <sub>SME</sub>	Accession N° of genomic island <sup>a</sup>	Size of genomic island (bp)	Origin <sup>b</sup>	Country
Sm163	GCA_003425745.1	NPKU00000000	<i>bla</i> <sub>SME-4</sub>	MH460878	28168	Human	Argentina
SmCHE4	GCA_003666905.1	NTFM00000000	<i>bla</i> <sub>SME-2</sub>	MH460880	27955	Human	Canada
SmMEX-1	GCA_003666885.1	NTFJ00000000	<i>bla</i> <sub>SME-1</sub>	MH460881	28421	Human	Mexico
SmS6	GCA_003666965.1	NTFO00000000	<i>bla</i> <sub>SME-1</sub>	MH460882	26549	Human	UK9
SmS8	GCA_003666945.1	NTFN00000000	<i>bla</i> <sub>SME-1</sub>	MH460883	27236	Human	UK9
SmAW	GCA_003666915.1	NTFL00000000	<i>bla</i> <sub>SME-2</sub>	MH460879	27577	Human	Switzerland
SmUSA-1	GCA_003666955.1	NTFK00000000	<i>bla</i> <sub>SME-1</sub>	MH460884	27360	Human	USA
MGH135	GCF_002152845	NZ_NGUD00000000.1	<i>bla</i> <sub>SME-1</sub>	BK010582	28351	Human,	USA
D-1	GCF_002104105	NZ_NBWX00000000.1	<i>bla</i> <sub>SME-1</sub>	BK010579	28318	Human	USA
D-2	GCF_002104115	NZ_NBWW00000000.1	<i>bla</i> <sub>SME-1</sub>	BK010580	28318	Human	USA
D-3	GCF_002104095	NZ_NBWV00000000	<i>bla</i> <sub>SME-1</sub>	BK010581	28318	Human	USA
UCI-88	GCF_001034405	LFBT00000000.1	<i>bla</i> <sub>SME-1</sub>	BK010583	28352	Human	USA
BIDMC44	GCF_000521925	JAPD00000000.1	<i>bla</i> <sub>SME-2</sub>	BK010577	28270	Human	USA
BIDMC80	GCF_000633715	JJNA00000000.1	<i>bla</i> <sub>SME-2</sub>	BK010578	28494	Human	USA
1274	GCA_002007925.2	CP019927.2	-			<i>Agave sisaliana</i>	Brazil
AS1	GCA_001932655.1	CP010584.1	-			<i>Anopheles stephensi</i>	China
B3R3	GCA_001417865.2	CP013046.2	-			<i>Zea mays</i>	China
CAV1492	GCA_001022215.1	CP011642.1	-			Human	USA
Db11	GCA_000513215.1	HG326223.1	-			Insect	Sweden
fgi94	GCA_000330865.1	CP003942.1	-			Fungus	Panama
RSC-14	GCA_001280365.1	CP012639.1	-			<i>Solanum nigrum</i>	South Korea
S217	GCA_002205475.1	CP021984.1	-			Environmental (soil)	India
SM39	GCA_000828775.1	AP013063.1	-			Human	Japan
SMB2099	GCA_900029885.1	HG738868.1	-			Human	Germany
SmUNAM836	GCA_001294565.1	CP012685.1	-			Human	Mexico
U36365	GCA_001672055.1	CP016032.1	-			Human	India
UMH1	GCA_002220615.1	CP018915.1	-			Human	USA
UMH10	GCA_002220695.1	CP018928.1	-			Human	USA
UMH11	GCA_002220575.1	CP018929.1	-			Human	USA
UMH12	GCA_002220595.1	CP018930.1	-			Human	USA
UMH2	GCA_002220515.1	CP018924.1	-			Human	USA
UMH3	GCA_002220655.1	CP018925.1	-	BK010584	11559	Human	USA
UMH5	GCA_002220635.1	CP018917.1	-			Human	USA
UMH6	GCA_002220675.1	CP018926.1	-			Human	USA

UMH7	GCA_002220715.1	CP018919.1	-		Human	USA
UMH8	GCA_002220535.1	CP018927.1	-		Human	USA
UMH9	GCA_002220555.1	CP018923.1	-	BK010585	Human	USA
WW4	GCA_000336425.1	CP003959.1	-		Environmental	Taiwan

---

<sup>b</sup> Organism were the bacterial isolate was recovered from.

**Table S2:** *S. marcescens* genomes found in public databases (last accessed November 2018), used for the whole genome phylogenetic analysis.

Assembly Accession #	Strain name	Carbapenemase	notes
GCF_000264275			
GCF_000292365			
GCF_000330865	fgi94		Complete genome; removed from kSNP analysis
GCF_000336425	WW4		Complete genome
GCF_000342205			
GCF_000418815			
GCF_000418835			
GCF_000418855			
GCF_000418875			
GCF_000418895			
GCF_000418915			
GCF_000418935			
GCF_000442375			
GCF_000442455			
GCF_000465615			
GCF_000513215	Db11		Complete genome
GCF_000521905			
GCF_000521925	BIDMC44	<i>bla<sub>SME-2</sub></i>	Complete genome
GCF_000633335			
GCF_000633555			
GCF_000633695			
GCF_000633715	BIDMC80	<i>bla<sub>SME-2</sub></i>	Complete genome
GCF_000695485			
GCF_000734475			
GCF_000735445			
GCF_000738535			
GCF_000739215			
GCF_000743395			
GCF_000751195			
GCF_000783915			
GCF_000783975			
GCF_000805875			
GCF_000828775	SM39	<i>bla<sub>IMP-1</sub></i>	Complete genome
GCF_001007555			
GCF_001022215	CAV1492	<i>bla<sub>KPC-2</sub></i>	Complete genome
GCF_001030265		<i>bla<sub>KPC-3</sub></i>	
GCF_001034395			
GCF_001034405	UCI-88	<i>bla<sub>SME-1</sub></i>	
GCF_001051865			
GCF_001060335			
GCF_001060585			
GCF_001060625			
GCF_001060655			
GCF_001061145			



GCF_001061195			
GCF_001061225			
GCF_001062235			
GCF_001062285			
GCF_001063125			
GCF_001063145			
GCF_001063175			
GCF_001063325			
GCF_001063375			
GCF_001064335			
GCF_001064345			
GCF_001064455			
GCF_001064715			
GCF_001064725			
GCF_001064835			
GCF_001064855			
GCF_001064975			
GCF_001065325			
GCF_001065405			
GCF_001065845			
GCF_001065935			
GCF_001066015			
GCF_001066945			
GCF_001067015			
GCF_001067375			
GCF_001068085			
GCF_001076625			
GCF_001280365	RSC-14		Complete genome
GCF_001294565	SmUNAM836		Complete genome
GCF_001317205		<i>bla</i> <sub>NDM-1</sub>	
GCF_001317425		<i>bla</i> <sub>NDM-1</sub>	
GCF_001417865	B3R3		Complete genome
GCF_001536325			
GCF_001536345			
GCF_001536365			
GCF_001536385			
GCF_001536405			
GCF_001536425			
GCF_001536445			
GCF_001536465			
GCF_001536485			
GCF_001536505			
GCF_001536525			
GCF_001536545			
GCF_001536565			
GCF_001536585			
GCF_001536605			
GCF_001536625			
GCF_001536645			
GCF_001536665			

GCF\_001536685  
GCF\_001536705  
GCF\_001536725  
GCF\_001536745  
GCF\_001536765  
GCF\_001536845  
GCF\_001536895  
GCF\_001536945  
GCF\_001536965  
GCF\_001536985  
GCF\_001537005  
GCF\_001537025  
GCF\_001537045  
GCF\_001537065  
GCF\_001537085  
GCF\_001537105  
GCF\_001537125  
GCF\_001537145  
GCF\_001537165  
GCF\_001537185  
GCF\_001537205  
GCF\_001537225  
GCF\_001537245  
GCF\_001537285  
GCF\_001537305  
GCF\_001537325  
GCF\_001537345  
GCF\_001537365  
GCF\_001537405  
GCF\_001537425  
GCF\_001537445  
GCF\_001537465  
GCF\_001537485  
GCF\_001537505  
GCF\_001537525  
GCF\_001537545  
GCF\_001537565  
GCF\_001537585  
GCF\_001537605  
GCF\_001537625  
GCF\_001537645  
GCF\_001537665  
GCF\_001537685  
GCF\_001537705  
GCF\_001537725  
GCF\_001537745  
GCF\_001537765  
GCF\_001537785  
GCF\_001537805  
GCF\_001537825

GCF\_001537845  
GCF\_001537865  
GCF\_001537885  
GCF\_001537905  
GCF\_001537925  
GCF\_001538005  
GCF\_001538115  
GCF\_001538195  
GCF\_001538275  
GCF\_001538325  
GCF\_001538345  
GCF\_001538365  
GCF\_001538385  
GCF\_001538405  
GCF\_001538425  
GCF\_001538445  
GCF\_001538465  
GCF\_001538485  
GCF\_001538505  
GCF\_001538525  
GCF\_001538545  
GCF\_001538565  
GCF\_001538585  
GCF\_001538605  
GCF\_001538625  
GCF\_001538645  
GCF\_001538665  
GCF\_001538685  
GCF\_001538705  
GCF\_001538725  
GCF\_001538745  
GCF\_001538765  
GCF\_001538785  
GCF\_001538805  
GCF\_001538825  
GCF\_001538845  
GCF\_001538865  
GCF\_001538885  
GCF\_001538905  
GCF\_001538925  
GCF\_001538945  
GCF\_001538965  
GCF\_001538985  
GCF\_001539005  
GCF\_001539025  
GCF\_001539045  
GCF\_001539065  
GCF\_001539085  
GCF\_001539105  
GCF\_001539125

GCF\_001539145  
GCF\_001539185  
GCF\_001539205  
GCF\_001539225  
GCF\_001539245  
GCF\_001539265  
GCF\_001539285  
GCF\_001539305  
GCF\_001539325  
GCF\_001539345  
GCF\_001539365  
GCF\_001539385  
GCF\_001539405  
GCF\_001539425  
GCF\_001539445  
GCF\_001539465  
GCF\_001539485  
GCF\_001539505  
GCF\_001539525  
GCF\_001539545  
GCF\_001539565  
GCF\_001539585  
GCF\_001539605  
GCF\_001539625  
GCF\_001539645  
GCF\_001539665  
GCF\_001539685  
GCF\_001539705  
GCF\_001539725  
GCF\_001539745  
GCF\_001539765  
GCF\_001539785  
GCF\_001539805  
GCF\_001539825  
GCF\_001539845  
GCF\_001539865  
GCF\_001539885  
GCF\_001539905  
GCF\_001539925  
GCF\_001539945  
GCF\_001539965  
GCF\_001539985  
GCF\_001540005  
GCF\_001540025  
GCF\_001540045  
GCF\_001540065  
GCF\_001540085  
GCF\_001540105  
GCF\_001540125  
GCF\_001540145

Complete genome

GCF_001540165		
GCF_001540185		
GCF_001540205		
GCF_001540225		
GCF_001540245		
GCF_001540265		
GCF_001540285		
GCF_001540305		
GCF_001540325		
GCF_001540345		
GCF_001540365		
GCF_001540385		
GCF_001540405		
GCF_001540425		
GCF_001540445		
GCF_001540465		
GCF_001540485		
GCF_001540505		
GCF_001540525		
GCF_001540545		
GCF_001540565		
GCF_001540585		
GCF_001540605		
GCF_001540625		
GCF_001540645		
GCF_001540665		
GCF_001540685		
GCF_001540705		
GCF_001540725		
GCF_001540745		
GCF_001540765		
GCF_001540785		
GCF_001540805		
GCF_001540825		
GCF_001557575		removed from kSNP analysis
GCF_001564475		
GCF_001594385		
GCF_001643155		
GCF_001672055	U36365	Complete genome
GCF_001853455		
GCF_001853495		
GCF_001889685		
GCF_001902635		
GCF_001908015		
GCF_001908035		
GCF_001909165		
GCF_001932655	AS1	Complete genome
GCF_001940505		
GCF_001975745		
GCF_002007925	1274	Complete genome

GCF_002029205		
GCF_002029225		
GCF_002094145		
GCF_002104095	D-3	<i>bla<sub>SME-1</sub></i>
GCF_002104105	D-1	<i>bla<sub>SME-1</sub></i>
GCF_002104115	D-2	<i>bla<sub>SME-1</sub></i>
GCF_002108655		
GCF_002118055		<i>bla<sub>NDM-1</sub></i>
GCF_002152845	MGH135	<i>bla<sub>SME-1</sub></i>
GCF_002153355		
GCF_002205475	S2I7	
GCF_002220515	UMH2	
GCF_002220535	UMH8	
GCF_002220555	UMH9	
GCF_002220575	UMH11	
GCF_002220595	UMH12	
GCF_002220615	UMH1	
GCF_002220635	UMH5	
GCF_002220655	UMH3	
GCF_002220675	UMH6	
GCF_002220695	UMH10	
GCF_002220715	UMH7	
GCF_002250685		<i>bla<sub>VIM-1</sub></i>
GCF_002264105		<i>bla<sub>KPC-2</sub></i>
GCF_002264175		<i>bla<sub>KPC-2</sub></i>
GCF_002264285		<i>bla<sub>KPC-2</sub></i>
GCF_002265665		
GCF_900029885	SMB2099	
GCF_900108835		<i>bla<sub>NDM-1</sub></i>
This study	Sm163	<i>bla<sub>SME-4</sub></i>
This study	SmCHE4	<i>bla<sub>SME-2</sub></i>
This study	SmAW	<i>bla<sub>SME-2</sub></i>
This study	SmMEX-1	<i>bla<sub>SME-1</sub></i>
This study	SmS6	<i>bla<sub>SME-1</sub></i>
This study	SmS8	<i>bla<sub>SME-1</sub></i>
This study	SmUSA-1	<i>bla<sub>SME-1</sub></i>

---