

**Next-generation systematics: An innovative approach to resolve the structure of
complex prokaryotic taxa**

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Supplementary Table 1. Details of strains and genomic features

S. no.	S-ID	Organism	Strain	Accession No.	size (Mb)	GC %	#Genes	RNA genes	Group	Species	Fraction
1	re10	Rhodococcus equi	103S	NC_014659	5.04	68.8	4740	64 A	A-1	A-1	0.73
2	re11	Rhodococcus equi	N1288	LRQY000000000	5.17	68.8	4942	56 A	A-1	A-1	0.70
3	re12	Rhodococcus equi	N1295	LRQZ000000000	5.31	68.7	5078	55 A	A-1	A-1	0.68
4	re13	Rhodococcus equi	N1301	LRRA000000000	5.65	68.5	5433	53 A	A-1	A-1	0.64
5	re14	Rhodococcus equi	ATCC 33707	NZ_CM001149	5.26	68.8	4986	68 A	A-1	A-1	0.69
6	re9	Rhodococcus equi	C7 ^T	APJC000000000	5.2	68.8	4978	55 A	A-1	A-1	0.69
7	ch56	Rhodococcus hoagii	DSM 20295 ^T	LRRF000000000	4.97	68.8	4705	54 A	A-1	A-1	0.73
8	rd55	Rhodococcus defluvii	Ca11 ^T	JPOC000000000	5.14	68.7	4740	56 A	A-2	A-2	0.73
9	r34	Rhodococcus sp.	BCP1	AVAE000000000	6.21	70.4	5889	58 B (B1)	B1-1	B1-1	0.34
10	r38	Rhodococcus sp.	EsD8	CAVJ000000000	6.63	70.1	6201	51 B (B1)	B1-1	B1-1	0.32
11	ra97	Rhodococcus aetherivorans	lcdP1	NZ_CP011341.1	5.92	70.6	5589	66 B (B1)	B1-1	B1-1	0.36
12	rrh31	Rhodococcus rhodochrous	ATCC 21198	AZHI000000000	6.48	70.2	6086	55 B (B1)	B1-1	B1-1	0.33
13	r42	Rhodococcus sp.	P14	AJFC000000000	5.68	70.4	5253	51 B (B1)	B1-2	B1-2	0.38
14	rrb102	Rhodococcus ruber	DSM 43338 ^T	LRRL000000000	5.3	70.7	4934	59 B (B1)	B1-2	B1-2	0.41
15	rrb103	Rhodococcus ruber	IEGM 231	CCSD010000000	5.99	70.2	5636	55 B (B1)	B1-2	B1-2	0.35
16	rrb104	Rhodococcus ruber	P25	LDUF010000000	5.73	70.5	5362	58 B (B1)	B1-2	B1-2	0.37
17	rrb32	Rhodococcus ruber	Chol-4	ANGC000000000	5.4	70.6	5029	67 B (B1)	B1-2	B1-2	0.40
18	rrb33	Rhodococcus ruber	BKS 20-38	AOEX000000000	6.13	69.7	5758	56 B (B1)	B1-3	B1-3	0.35
19	rph87	Rhodococcus phenolicus	DSM 44812 ^T	LRRH000000000	6.28	68.4	6000	58 B	B-4	B-4	0.33
20	r41	Rhodococcus sp.	R1101	AJVB000000000	4.66	67.9	4384	58 B (B2)	B2-5	B2-5	0.46
21	rg82	Rhodococcus gordoniae	DSM 44689 ^T	LPZN000000000	4.82	67.9	4519	59 B (B2)	B2-5	B2-5	0.44
22	rrh101	Rhodococcus rhodochrous	DSM 43241 ^T	LRRK000000000	5.18	68.2	4843	59 B (B2)	B2-6	B2-6	0.41
23	rrh29	Rhodococcus rhodochrous	BKS6-46	AGVW000000000	6.22	67.4	5612	59 B (B2)	B2-6	B2-6	0.36
24	r111	Rhodococcus sp.	Chr-9	JTIZ010000000	5.35	67.7	5169	56 B (B2)	B2-7	B2-7	0.39
25	r37	Rhodococcus sp.	R4	AFAQ000000000	8.86	69.5	8252	109 B (B2)	B2-7	B2-7	0.24
26	r93	Rhodococcus sp.	P52	JPJJ010000000	5.29	67.9	5061	57 B (B2)	B2-7	B2-7	0.40
27	rp25	Rhodococcus pyridinivorans	SB3094	NC_023150	5.23	68.0	4956	47 B (B2)	B2-7	B2-7	0.40
28	rp26	Rhodococcus pyridinivorans	AK37	AHBW000000000	5.25	67.9	5139	55 B (B2)	B2-7	B2-7	0.39
29	rp88	Rhodococcus pyridinivorans	DSM 44555 ^T	LRRIO000000000	5.18	67.9	4931	56 B (B2)	B2-7	B2-7	0.41

30	r43	Rhodococcus sp.	JVH1	AKKP00000000	9.18	67.0	8872	55 C	C-1	0.46
31	r44	Rhodococcus sp.	DK17	AJLQ00000000	9.11	67.1	8909	56 C	C-1	0.45
32	rj52	Rhodococcus jostii	RHA1	NC_008268	7.8	67.5	7474	62 C	C-1	0.54
33	ri20	Rhodococcus imtechensis	RKJ300 ^T	AJJH00000000	8.23	67.2	8331	54 C	C-2	0.48
34	ro24	Rhodococcus opacus	M213	AJYC00000000	9.2	67.0	8934	57 C	C-2	0.45
35	ro86	Rhodococcus opacus	DSM 43205^T	LRRG00000000	8.53	67.3	8267	53 C	C-2	0.49
36	rw47	Rhodococcus wratislaviensis	IFP 2016	ANIU00000000	9.7	66.9	9763	64 C	C-2	0.41
39	ro23	Rhodococcus opacus	PD630	AGVD00000000	9.16	67.0	8540	58 C	C-2	0.47
37	ro85	Rhodococcus opacus	R7	CPO08947.1	8.47	67.2	7859	60 C	C-3	0.51
38	rw96	Rhodococcus wratislaviensis	NBRC 100605 ^T	BAWF01000000	10.41	66.8	9785	57 C	C-3	0.41
40	ro22	Rhodococcus opacus	B4	NC_012522	7.91	67.9	7397	61 C	C-4	0.55
41	r105	Rhodococcus sp.	311R	CFHW01000000	6.35	62.6	6088	57 D	D-1	0.59
42	rey16	Rhodococcus erythropolis	SK121	ACNO00000000	6.79	62.5	6573	56 D	D-1	0.54
43	rey57	Rhodococcus erythropolis	JCM 6824	BBLL01000000	7.02	62.3	6816	54 D	D-1	0.52
44	rey58	Rhodococcus erythropolis	NRRL B-16532	JOILO1000000	6.94	62.4	6746	61 D	D-1	0.53
45	r60	Rhodococcus sp.	AJR001	LPZM00000000	7.26	62.4	7124	56 D	D-1	0.50
46	rey98	Rhodococcus erythropolis	CAS922i	LDPN01000000	7.21	62.3	7001	66 D	D-1	0.51
47	rq27	Rhodococcus qingshengii	BKS 20-40	AODN00000000	6.6	62.4	6431	55 D	D-1	0.55
48	rq89	Rhodococcus qingshengii	TUHH-12	JNCU01000000	7.43	61.7	8298	65 D	D-1	0.43
49	rq90	Rhodococcus qingshengii	JCM 15477^T	LRRJ00000000	7.26	62.4	7130	56 D	D-1	0.50
50	r107	Rhodococcus sp.	ARP2	LEKE01000000	6.3	62.4	6051	63 D	D-2	0.59
51	r40	Rhodococcus sp.	P27	AVCO00000000	6.26	62.4	6736	60 D	D-2	0.53
52	rey15	Rhodococcus erythropolis	PR4	NC_012490	6.52	62.3	6250	69 D	D-2	0.57
53	rey17	Rhodococcus erythropolis	CCM2595	NC_022115	6.28	62.5	5935	65 D	D-2	0.60
54	rey18	Rhodococcus erythropolis	XP	AGCF00000000	7.23	62.3	7123	67 D	D-2	0.50
55	rey19	Rhodococcus erythropolis	DN1	AUZK00000000	6.55	62.4	6545	56 D	D-2	0.54
56	rey59	Rhodococcus erythropolis	R138	ASKF01000000	6.77	62.3	6486	65 D	D-2	0.55
57	rey99	Rhodococcus erythropolis	BG43	NZ_CP011295.1	6.33	62.4	6011	72 D	D-2	0.59
58	ro84	Rhodococcus opacus	NRRL B-24011	JOIM01000000	6.38	62.4	6040	60 D	D-2	0.59
59	rrh30	Rhodococcus rhodochrous	ATCC 17895	ASJJ00000000	6.87	62.3	6617	53 D	D-2	0.54
60	r108	Rhodococcus sp.	AD45	JYOP01000000	6.79	61.7	6544	54 D	D-3	0.54
61	r113	Rhodococcus sp.	4J2A2	CEDU01000000	6.45	61.8	6211	55 D	D-3	0.57

62	rrh92	Rhodococcus rhodochrous	NRRL B-1306	JNWS01000000	6.78	61.7	6586	59 D	D-3	0.54
63	rf61	Rhodococcus fascians	A22b	JOKB01000000	5.91	64.3	5678	58 E (E1)	E1-1	0.45
64	r35	Rhodococcus sp.	114MFTsu3.1	ARTN00000000	5.55	64.7	5307	56 E (E1)	E1-2	0.48
65	r36	Rhodococcus sp.	29MFTsu3.1	ARND00000000	5.58	64.6	5352	56 E (E1)	E1-2	0.47
66	rf64	Rhodococcus fascians	A44a	JMEX01000000	5.95	64.5	5683	49 E (E1)	E1-2	0.45
67	rf65	Rhodococcus fascians	A73a	JMEW01000000	5.93	64.4	5639	55 E (E1)	E1-2	0.45
68	rf69	Rhodococcus fascians	02-815	JMFF01000000	6.24	64.3	5969	53 E (E1)	E1-2	0.42
69	rf70	Rhodococcus fascians	02-816c	JMFE01000000	6.08	64.5	5956	55 E (E1)	E1-2	0.43
70	rf75	Rhodococcus fascians	A76	JMEV01000000	6.03	64.6	5889	53 E (E2)	E2-3	0.43
71	r110	Rhodococcus sp.	BS-15	BAOX01000000	5.51	64.4	6162	43 E (E2)	E2-4	0.41
72	r114	Rhodococcus sp.	B7740	NZ_CP010797.1	5.34	64.9	5149	59 E (E2)	E2-5	0.49
73	rf72	Rhodococcus fascians	05-339-1	JMFC01000000	5.73	64.7	5561	51 E (E2)	E2-5	0.46
74	rf63	Rhodococcus fascians	04-516	JMFD01000000	5.82	64.2	5588	53 E (E2)	E2-6	0.45
75	rf73	Rhodococcus fascians	A21d2	JMFA01000000	5.98	64.1	5748	57 E (E2)	E2-6	0.44
76	rf74	Rhodococcus fascians	A25f	JMEZ01000000	5.87	64.1	5660	55 E (E2)	E2-6	0.45
77	rf81	Rhodococcus fascians	LMG 3625	JMEM01000000	5.94	64.1	5886	58 E (E2)	E2-6	0.43
78	r112	Rhodococcus sp.	PML 026	JZIS01000000	5.17	64.7	4965	60 E (E2)	E2-7	0.51
79	r39	Rhodococcus sp.	JG-3	AXVF00000000	5.27	64.6	5100	54 E (E2)	E2-7	0.50
80	rf100	Rhodococcus fascians	F7	LFDS01000000	5.25	64.7	5047	50 E (E2)	E2-7	0.50
81	rf62	Rhodococcus fascians	A3b	JMEY01000000	6.03	64.2	5846	55 E (E2)	E2-7	0.43
82	rf66	Rhodococcus fascians	A78	JMEU01000000	6	64.3	5783	53 E (E2)	E2-7	0.44
83	rf67	Rhodococcus fascians	GIC26	JMES01000000	5.34	64.5	5176	50 E (E2)	E2-7	0.49
84	rf68	Rhodococcus fascians	GIC36	JMER01000000	5.56	64.5	5392	52 E (E2)	E2-7	0.47
85	rf76	Rhodococcus fascians	D188	JMET01000000	5.44	64.6	5222	50 E (E2)	E2-7	0.48
86	rf77	Rhodococcus fascians	LMG 3602	JMEQ01000000	5.36	64.5	5227	53 E (E2)	E2-7	0.48
87	rf78	Rhodococcus fascians	LMG 3605	JMEP01000000	5.44	64.5	5215	52 E (E2)	E2-7	0.49
88	rf79	Rhodococcus fascians	LMG 3616	JMEO01000000	5.76	64.3	5567	52 E (E2)	E2-7	0.45
89	rf80	Rhodococcus fascians	LMG 3623 ^T	JMEN01000000	5.78	64.4	5519	52 E (E2)	E2-7	0.46
90	r45	Rhodococcus sp.	AW25M09	CAPS00000000	5.64	64.1	5522	50 E (E2)	E2-8	0.46
91	rc54	Rhodococcus corynebacteroides	DSM 20151^T	LPZL00000000	3.9	70.3	3607	50 F	F-1	0.75
92	rkr83	Rhodococcus kroppenstedtii	DSM 44908^T	LPZO00000000	3.91	70.1	3650	47 F	F-2	0.74
93	r94	Rhodococcus sp.	UNC23MFCrub1.1	JMLQ01000000	4.7	68.5	4440	55 F	F-3	0.61
94	r109	Rhodococcus sp.	MEB064	JXQS01000000	4.67	67.0	4415	52 F	F-4	0.62

95	r95	Rhodococcus sp.	UNC363MFTsu5.1	JMLO01000000	5.67	69.3	5300	57 G	G-1	0.61
96	r106	Rhodococcus sp.	RD6.2	CVQP01000000	5.57	68.4	5216	64 G	G-2	0.62
97	rt46	Rhodococcus triatomae	BKS 15-14	AODO00000000	5.83	69.0	5416	57 G	G-3	0.59
98	rk21	Rhodococcus kunmingensis	DSM 45001^T	LRRB00000000	5.62	66.2	5234	50 -	-	
99	rr28	Rhodococcus rhodnii	LMG 5362	APMY00000000	4.39	69.7	4251	54 -	-	
100	rr91	Rhodococcus rhodnii	NRRL B-16535 ^T	JOAA01000000	12.42	66.3	11568	79 -	-	
101	na53	Nocardia asteroides	NBRC 15531	BAFO02000000	6.96	69.9	6425	56 -	-	
102	nb6	Nocardia brasiliensis	ATCC 700358	NC_018681	9.44	68.1	8769	58 -	-	
103	nc7	Nocardia cyriacigeorgica	GUH2	NC_016887	6.19	68.4	5663	58 -	-	
104	nf8	Nocardia farcinica	IFM 10152	NC_006361	6.02	70.8	5738	62 -	-	
105	g3	Gordonia	KTR9	NC_018581	5.44	67.8	4985	54 -	-	
106	gb4	Gordonia bronchialis	DSM 43247	NC_013441	5.21	67.1	5038	53 -	-	
107	gp5	Gordonia polyisoprenivorans	VH2	NC_016906	5.67	67.0	5169	58 -	-	
108	sr48	Segniliparus rotundus	DSM 44985	NC_014168	3.16	66.8	3150	49 -	-	
109	srg49	Segniliparus rugosus	ATCC BAA-974	ACZI00000000	3.57	68.1	3535	49 -	-	
110	smn50	Smaragdicoccus niigatensis	DSM 44881	AQXZ00000000	5.32	64.3	5234	52 -	-	
111	tb51	Tomitella biformata	AHU 1821	BAVQ00000000	4.71	68.1	4389	56 -	-	
112	w115	Williamsia sp.	ARP1	JXYP00000000	4.75	68.6	4460	52 -	-	
113	w116	Williamsia sp.	D3	AYTE00000000	5.62	64.6	5632	51 -	-	
114	cd1	Corynebacterium diphtheriae	NCTC 03529	AJGI00000000	2.48	53.6	2490	56 -	-	
115	cd2	Corynebacterium diphtheriae	NCTC 05011	AJVH00000000	2.38	53.6	2341	51 -	-	

Notes:

1. The strains sequenced in this study are shown in red.
2. The subgroup information is provided in parenthesis in the column "Group".
3. The predicted species from the genomic analyses are coded with numbers following the group/subgroup designation.
4. The fraction of the genes in the core genome within the group is mentioned in the column "Fraction".

Supplementary Table 2A. Pairwise fragment BLAST similarity scores from the genomic sequences

	rs16	rs16b	rs16c	rs16d	rs16e	rs16f	rs16g	rs16h	rs16i	rs16j	rs16k	rs16l	rs16m	rs16n	rs16o	rs16p	rs16q	rs16r	rs16s	rs16t	rs16u	rs16v	rs16w	rs16x	rs16y	rs16z	rs16aa	rs16ab	rs16ac	rs16ad	rs16ae	rs16af	rs16ag	rs16ah	rs16ai	rs16aj	rs16ak	rs16al	rs16am	rs16an	rs16ao	rs16ap	rs16aq	rs16ar	rs16as	rs16at	rs16au	rs16av	rs16aw	rs16ax	rs16ay	rs16az	rs16ba	rs16bb	rs16bc	rs16bd	rs16be	rs16bf	rs16bg	rs16bh	rs16bi	rs16bj	rs16bk	rs16bl	rs16bm	rs16bn	rs16bo	rs16bp	rs16bq	rs16br	rs16bs	rs16bt	rs16bu	rs16bv	rs16bw	rs16bx	rs16by	rs16bz	rs16ca	rs16cb	rs16cc	rs16cd	rs16ce	rs16cf	rs16cg	rs16ch	rs16ci	rs16cj	rs16ck	rs16cl	rs16cm	rs16cn	rs16co	rs16cp	rs16cq	rs16cr	rs16cs	rs16ct	rs16cu	rs16cv	rs16cw	rs16cx	rs16cy	rs16cz	rs16da	rs16db	rs16dc	rs16dd	rs16de	rs16df	rs16dg	rs16dh	rs16di	rs16dj	rs16dk	rs16dl	rs16dm	rs16dn	rs16do	rs16dp	rs16dq	rs16dr	rs16ds	rs16dt	rs16du	rs16dv	rs16dw	rs16dx	rs16dy	rs16dz	rs16ea	rs16eb	rs16ec	rs16ed	rs16ee	rs16ef	rs16eg	rs16eh	rs16ei	rs16ej	rs16ek	rs16el	rs16em	rs16en	rs16eo	rs16ep	rs16eq	rs16er	rs16es	rs16et	rs16eu	rs16ev	rs16ew	rs16ex	rs16ey	rs16ez	rs16fa	rs16fb	rs16fc	rs16fd	rs16fe	rs16ff	rs16fg	rs16fh	rs16fi	rs16fj	rs16fk	rs16fl	rs16fm	rs16fn	rs16fo	rs16fp	rs16fq	rs16fr	rs16fs	rs16ft	rs16fu	rs16fv	rs16fw	rs16fx	rs16fy	rs16fz	rs16ga	rs16gb	rs16gc	rs16gd	rs16ge	rs16gf	rs16gg	rs16gh	rs16gi	rs16gj	rs16gk	rs16gl	rs16gm	rs16gn	rs16go	rs16gp	rs16gq	rs16gr	rs16gs	rs16gt	rs16gu	rs16gv	rs16gw	rs16gx	rs16gy	rs16gz	rs16ha	rs16hb	rs16hc	rs16hd	rs16he	rs16hf	rs16hg	rs16hi	rs16hj	rs16hk	rs16hl	rs16hm	rs16hn	rs16ho	rs16hp	rs16hq	rs16hr	rs16hs	rs16ht	rs16hu	rs16hv	rs16hw	rs16hx	rs16hy	rs16hz	rs16ia	rs16ib	rs16ic	rs16id	rs16ie	rs16if	rs16ig	rs16ih	rs16ii	rs16ij	rs16ik	rs16il	rs16im	rs16in	rs16io	rs16ip	rs16iq	rs16ir	rs16is	rs16it	rs16iu	rs16iv	rs16iw	rs16ix	rs16iy	rs16iz	rs16ja	rs16jb	rs16jc	rs16jd	rs16je	rs16jf	rs16jg	rs16jh	rs16ji	rs16jj	rs16jk	rs16jl	rs16jm	rs16jn	rs16jo	rs16jp	rs16jq	rs16jr	rs16js	rs16jt	rs16ju	rs16jv	rs16jw	rs16jx	rs16jy	rs16jz	rs16ka	rs16kb	rs16kc	rs16kd	rs16ke	rs16kf	rs16kg	rs16kh	rs16ki	rs16kj	rs16kl	rs16km	rs16kn	rs16ko	rs16kp	rs16kq	rs16kr	rs16ks	rs16kt	rs16ku	rs16kv	rs16kw	rs16kx	rs16ky	rs16kz	rs16la	rs16lb	rs16lc	rs16ld	rs16le	rs16lf	rs16lg	rs16lh	rs16li	rs16lj	rs16lk	rs16ll	rs16lm	rs16ln	rs16lo	rs16lp	rs16lq	rs16lr	rs16ls	rs16lt	rs16lu	rs16lv	rs16lw	rs16lx	rs16ly	rs16lz	rs16ma	rs16mb	rs16mc	rs16md	rs16me	rs16mf	rs16mg	rs16mh	rs16mi	rs16mj	rs16mk	rs16ml	rs16mn	rs16mo	rs16mp	rs16mq	rs16mr	rs16ms	rs16mt	rs16mu	rs16mv	rs16mw	rs16mx	rs16my	rs16mz	rs16na	rs16nb	rs16nc	rs16nd	rs16ne	rs16nf	rs16ng	rs16nh	rs16ni	rs16nj	rs16nk	rs16nl	rs16nm	rs16nn	rs16no	rs16np	rs16nq	rs16nr	rs16ns	rs16nt	rs16nu	rs16nv	rs16nw	rs16nx	rs16ny	rs16nz	rs16oa	rs16ob	rs16oc	rs16od	rs16oe	rs16of	rs16og	rs16oh	rs16oi	rs16oj	rs16ok	rs16ol	rs16om	rs16on	rs16oo	rs16op	rs16oq	rs16or	rs16os	rs16ot	rs16ou	rs16ov	rs16ow	rs16ox	rs16oy	rs16oz	rs16pa	rs16pb	rs16pc	rs16pd	rs16pe	rs16pf	rs16pg	rs16ph	rs16pi	rs16pj	rs16pk	rs16pl	rs16pm	rs16pn	rs16po	rs16pp	rs16pq	rs16pr	rs16ps	rs16pt	rs16pu	rs16pv	rs16pw	rs16px	rs16py	rs16pz	rs16qa	rs16qb	rs16qc	rs16qd	rs16qe	rs16qf	rs16qg	rs16qh	rs16qi	rs16qj	rs16qk	rs16ql	rs16qm	rs16qn	rs16qo	rs16qp	rs16qq	rs16qr	rs16qs	rs16qt	rs16qu	rs16qv	rs16qw	rs16qx	rs16qy	rs16qz	rs16ra	rs16rb	rs16rc	rs16rd	rs16re	rs16rf	rs16rg	rs16rh	rs16ri	rs16rj	rs16rk	rs16rl	rs16rm	rs16rn	rs16ro	rs16rp	rs16rq	rs16rr	rs16rs	rs16rt	rs16ru	rs16rv	rs16rw	rs16rx	rs16ry	rs16rz	rs16sa	rs16sb	rs16sc	rs16sd	rs16se	rs16sf	rs16sg	rs16sh	rs16si	rs16sj	rs16sk	rs16sl	rs16sm	rs16sn	rs16so	rs16sp	rs16sq	rs16sr	rs16ss	rs16st	rs16su	rs16sv	rs16sw	rs16sx	rs16sy	rs16sz	rs16ta	rs16tb	rs16tc	rs16td	rs16te	rs16tf	rs16tg	rs16th	rs16ti	rs16tj	rs16tk	rs16tl	rs16tm	rs16tn	rs16to	rs16tp	rs16tq	rs16tr	rs16ts	rs16tt	rs16tu	rs16tv	rs16tw	rs16tx	rs16ty	rs16tz	rs16ua	rs16ub	rs16uc	rs16ud	rs16ue	rs16uf	rs16ug	rs16uh	rs16ui	rs16uj	rs16uk	rs16ul	rs16um	rs16un	rs16uo	rs16up	rs16uq	rs16ur	rs16us	rs16ut	rs16uu	rs16uv	rs16uw	rs16ux	rs16uy	rs16uz	rs16va	rs16vb	rs16vc	rs16vd	rs16ve	rs16vf	rs16vg	rs16vh	rs16vi	rs16vj	rs16vk	rs16vl	rs16vm	rs16vn	rs16vo	rs16vp	rs16vq	rs16vr	rs16vs	rs16vt	rs16vu	rs16vv	rs16vw	rs16vx	rs16vy	rs16vz	rs16wa	rs16wb	rs16wc	rs16wd	rs16we	rs16wf	rs16wg	rs16wh	rs16wi	rs16wj	rs16wk	rs16wl	rs16wm	rs16wn	rs16wo	rs16wp	rs16wq	rs16wr	rs16ws	rs16wt	rs16wu	rs16wv	rs16ww	rs16wx	rs16wy	rs16wz	rs16xa	rs16xb	rs16xc	rs16xd	rs16xe	rs16xf	rs16xg	rs16xh	rs16xi	rs16xj	rs16xk	rs16xl	rs16xm	rs16xn	rs16xo	rs16xp	rs16xq	rs16xr	rs16xs	rs16xt	rs16xu	rs16xv	rs16xw	rs16xx	rs16xy	rs16xz	rs16ya	rs16yb	rs16yc	rs16yd	rs16ye	rs16yf	rs16yg	rs16yh	rs16yi	rs16yj	rs16yk	rs16yl	rs16ym	rs16yn	rs16yo	rs16yp	rs16yq	rs16yr	rs16ys	rs16yt	rs16yu	rs16yv	rs16yw	rs16yx	rs16yy	rs16yz	rs16za	rs16zb	rs16zc	rs16zd	rs16ze	rs16zf	rs16zg	rs16zh	rs16zi	rs16zj	rs16zk	rs16zl	rs16zm	rs16zn	rs16zo	rs16zp	rs16zq	rs16zr	rs16zs	rs16zt	rs16zu	rs16zv	rs16zw	rs16zx	rs16zy	rs16zz
rs16	100	99.99	99.98	99.97	99.96	99.95	99.94	99.93	99.92	99.91	99.90	99.89	99.88	99.87	99.86	99.85	99.84	99.83	99.82	99.81	99.80	99.79	99.78	99.77	99.76	99.75	99.74	99.73	99.72	99.71	99.70	99.69	99.68	99.67	99.66	99.65	99.64	99.63	99.62	99.61	99.60	99.59	99.58	99.57	99.56	99.55	99.54	99.53	99.52	99.51	99.50	99.49	99.48	99.47	99.46	99.45	99.44	99.43	99.42	99.41	99.40	99.39	99.38	99.37	99.36	99.35	99.34	99.33	99.32	99.31	99.30	99.29	99.28	99.27	99.26	99.25	99.24	99.23	99.22	99.21	99.20	99.19	99.18	99.17	99.16	99.15	99.14	99.13	99.12	99.11	99.10	99.09	99.08	99.07	99.06	99.05	99.04	99.03	99.02	99.01	99.00	98.99	98.98	98.97	98.96	98.95	98.94	98.93	98.92	98.91	98.90	98.89	98.88	98.87	98.86	98.85	98.84	98.83	98.82	98.81	98.80	98.79	98.78	98.77	98.76	98.75	98.74	98.73	98.72	98.71	98.70	98.69	98.68	98.67	98.66	98.65	98.64	98.63	98.62	98.61	98.60	98.59	98.58	98.57	98.56	98.55	98.54	98.53	98.52	98.51	98.50	98.49	98.48	98.47	98.46	98.45	98.44	98.43	98.42	98.41	98.40	98.39	98.38	98.37	98.36	98.35	98.34	98.33	98.32	98.31	98.30	98.29	98.28	98.27	98.26	98.25	98.24	98.23	98.22	98.21	98.20	98.19	98.18	98.17	98.16	98.15	98.14	98.13	98.12	98.11	98.10	98.09	98.08	98.07	98.06	98.05	98.04	98.03	98.02	98.01	98.00	97.99	97.98	97.97	97.96	97.95	97.94	97.93	97.92	97.91	97.90	97.89	97.88	97.87	97.86	97.85	97.84	97.83	97.82	97.81	97.80	97.79	97.78	97.77	97.76	97.75	97.74	97.73	97.72	97.71	97.70	97.69	97.68	97.67	97.66	97.65	97.64	97.63	97.62	97.61	97.60	97.59	97.58	97.57	97.56	97.55	97.54	97.53	97.52	97.51	97.50	97.49	97.48	97.47	97.46	97.45	97.44	97.43	97.42	97.41	97.40	97.39	97.38	97.37	97.36	97.35	97.34	97.33	97.32	97.31	97.30	97.29	97.28	97.27	97.26	97.25	97.24	97.23	97.22	97.21	97.20	97.19	97.18	97.17	97.16	97.15	97.14	97.13	97.12	97.11	97.10	97.09	97.08	97.07	97.06	97.05	97.04	97.03	97.02	97.01	97.00	96.99	96.98	96.97	96.96	96.95	96.94	96.93	96.92	96.91	96.90	96.89	96.88	96.87	96.86	96.85	96.84	96.83	96.82	96.81	96.80	96.79	96.78	96.77	96.76	96.75	96.74	96.73	96.72	96.71	96.70	96.69	96.68	96.67	96.66	96.65	96.64	96.63	96.62	96.61	96.60	96.59	96.58	96.57	96.56	96.55	96.54	96.53	96.52	96.51	96.50	96.49	96.48	96.47	96.46	96.45	96.44	96.43	96.42	96.41	96.40	96.39	96.38	96.37	96.36	96.35	96.34	96.33	96.32	96.31	96.30	96.29	96.28	96.27	96.26	96.25	96.24	96.23	96.22	96.21	96.20	96.19	96.18	96.17	96.16	96.15	96.14	96.13	96.12	96.11	96.10	96.09	96.08	96.07	96.06	96.05	96.04	96.03	96.02	96.01	96.00	95.99	95.98	95.97	95.96	95.95	95.94	95.93	95.92	95.91	95.90	95.89	95.88	95.87	95.86	95.85	95.84	95.83	95.82	95.81	95.80	95.79	95.78	95.77	95.76	95.75	95.74	95.73	95.72	95.71	95.70	95.69	95.68	95.67	95.66	95.65	95.64	95.63	95.62	95.61	95.60	95.59	95.58	95.57	95.56	95.55	95.54	95.53	95.52	95.51	95.50	95.49	95.48	95.47	95.46	95.45	95.44	95.43	95.42	95.41	95.40	95.39	95.38	95.37	95.36	95.35	95.34	95.33	95.32	95.31	95.30	95.29	95.28	95.27	95.26	9																																																																																																																																																																																																																															

Supplementary table 2b. Pairwise AIC score from the genome sequences

e01	e02	e03	e04	e05	e06	e07	e08	e09	e10	e11	e12	e13	e14	e15	e16	e17	e18	e19	e20	e21	e22	e23	e24	e25	e26	e27	e28	e29	e30	e31	e32	e33	e34	e35	e36	e37	e38	e39	e40	e41	e42	e43	e44	e45	e46	e47	e48	e49	e50	e51	e52	e53	e54	e55	e56	e57	e58	e59	e60	e61	e62	e63	e64	e65	e66	e67	e68	e69	e70	e71	e72	e73	e74	e75	e76	e77	e78	e79	e80	e81	e82	e83	e84	e85	e86	e87	e88	e89	e90	e91	e92	e93	e94	e95	e96	e97	e98	e99	e100																																													
9856	9857	9858	9859	9860	9861	9862	9863	9864	9865	9866	9867	9868	9869	9870	9871	9872	9873	9874	9875	9876	9877	9878	9879	9880	9881	9882	9883	9884	9885	9886	9887	9888	9889	9890	9891	9892	9893	9894	9895	9896	9897	9898	9899	9900	9901	9902	9903	9904	9905	9906	9907	9908	9909	9910	9911	9912	9913	9914	9915	9916	9917	9918	9919	9920	9921	9922	9923	9924	9925	9926	9927	9928	9929	9930	9931	9932	9933	9934	9935	9936	9937	9938	9939	9940	9941	9942	9943	9944	9945	9946	9947	9948	9949	9950	9951	9952	9953	9954	9955	9956	9957	9958	9959	9960	9961	9962	9963	9964	9965	9966	9967	9968	9969	9970	9971	9972	9973	9974	9975	9976	9977	9978	9979	9980	9981	9982	9983	9984	9985	9986	9987	9988	9989	9990	9991	9992	9993	9994	9995	9996	9997	9998	9999	10000

Supplementary Table 24. Pairwise AI similarity scores from 255 core genes

r00	r01	r02	r03	r04	r05	r06	r07	r08	r09	r10	r11	r12	r13	r14	r15	r16	r17	r18	r19	r20	r21	r22	r23	r24	r25	r26	r27	r28	r29	r30	r31	r32	r33	r34	r35	r36	r37	r38	r39	r40	r41	r42	r43	r44	r45	r46	r47	r48	r49	r50	r51	r52	r53	r54	r55	r56	r57	r58	r59	r60	r61	r62	r63	r64	r65	r66	r67	r68	r69	r70	r71	r72	r73	r74	r75	r76	r77	r78	r79	r80	r81	r82	r83	r84	r85	r86	r87	r88	r89	r90	r91	r92	r93	r94	r95	r96	r97	r98	r99	r100	r101	r102	r103	r104	r105	r106	r107	r108	r109	r110	r111	r112	r113	r114	r115	r116	r117	r118	r119	r120	r121	r122	r123	r124	r125	r126	r127	r128	r129	r130	r131	r132	r133	r134	r135	r136	r137	r138	r139	r140	r141	r142	r143	r144	r145	r146	r147	r148	r149	r150	r151	r152	r153	r154	r155	r156	r157	r158	r159	r160	r161	r162	r163	r164	r165	r166	r167	r168	r169	r170	r171	r172	r173	r174	r175	r176	r177	r178	r179	r180	r181	r182	r183	r184	r185	r186	r187	r188	r189	r190	r191	r192	r193	r194	r195	r196	r197	r198	r199	r200	r201	r202	r203	r204	r205	r206	r207	r208	r209	r210	r211	r212	r213	r214	r215	r216	r217	r218	r219	r220	r221	r222	r223	r224	r225	r226	r227	r228	r229	r230	r231	r232	r233	r234	r235	r236	r237	r238	r239	r240	r241	r242	r243	r244	r245	r246	r247	r248	r249	r250	r251	r252	r253	r254	r255	r256	r257	r258	r259	r260	r261	r262	r263	r264	r265	r266	r267	r268	r269	r270	r271	r272	r273	r274	r275	r276	r277	r278	r279	r280	r281	r282	r283	r284	r285	r286	r287	r288	r289	r290	r291	r292	r293	r294	r295	r296	r297	r298	r299	r300	r301	r302	r303	r304	r305	r306	r307	r308	r309	r310	r311	r312	r313	r314	r315	r316	r317	r318	r319	r320	r321	r322	r323	r324	r325	r326	r327	r328	r329	r330	r331	r332	r333	r334	r335	r336	r337	r338	r339	r340	r341	r342	r343	r344	r345	r346	r347	r348	r349	r350	r351	r352	r353	r354	r355	r356	r357	r358	r359	r360	r361	r362	r363	r364	r365	r366	r367	r368	r369	r370	r371	r372	r373	r374	r375	r376	r377	r378	r379	r380	r381	r382	r383	r384	r385	r386	r387	r388	r389	r390	r391	r392	r393	r394	r395	r396	r397	r398	r399	r400	r401	r402	r403	r404	r405	r406	r407	r408	r409	r410	r411	r412	r413	r414	r415	r416	r417	r418	r419	r420	r421	r422	r423	r424	r425	r426	r427	r428	r429	r430	r431	r432	r433	r434	r435	r436	r437	r438	r439	r440	r441	r442	r443	r444	r445	r446	r447	r448	r449	r450	r451	r452	r453	r454	r455	r456	r457	r458	r459	r460	r461	r462	r463	r464	r465	r466	r467	r468	r469	r470	r471	r472	r473	r474	r475	r476	r477	r478	r479	r480	r481	r482	r483	r484	r485	r486	r487	r488	r489	r490	r491	r492	r493	r494	r495	r496	r497	r498	r499	r500	r501	r502	r503	r504	r505	r506	r507	r508	r509	r510	r511	r512	r513	r514	r515	r516	r517	r518	r519	r520	r521	r522	r523	r524	r525	r526	r527	r528	r529	r530	r531	r532	r533	r534	r535	r536	r537	r538	r539	r540	r541	r542	r543	r544	r545	r546	r547	r548	r549	r550	r551	r552	r553	r554	r555	r556	r557	r558	r559	r560	r561	r562	r563	r564	r565	r566	r567	r568	r569	r570	r571	r572	r573	r574	r575	r576	r577	r578	r579	r580	r581	r582	r583	r584	r585	r586	r587	r588	r589	r590	r591	r592	r593	r594	r595	r596	r597	r598	r599	r600	r601	r602	r603	r604	r605	r606	r607	r608	r609	r610	r611	r612	r613	r614	r615	r616	r617	r618	r619	r620	r621	r622	r623	r624	r625	r626	r627	r628	r629	r630	r631	r632	r633	r634	r635	r636	r637	r638	r639	r640	r641	r642	r643	r644	r645	r646	r647	r648	r649	r650	r651	r652	r653	r654	r655	r656	r657	r658	r659	r660	r661	r662	r663	r664	r665	r666	r667	r668	r669	r670	r671	r672	r673	r674	r675	r676	r677	r678	r679	r680	r681	r682	r683	r684	r685	r686	r687	r688	r689	r690	r691	r692	r693	r694	r695	r696	r697	r698	r699	r700	r701	r702	r703	r704	r705	r706	r707	r708	r709	r710	r711	r712	r713	r714	r715	r716	r717	r718	r719	r720	r721	r722	r723	r724	r725	r726	r727	r728	r729	r730	r731	r732	r733	r734	r735	r736	r737	r738	r739	r740	r741	r742	r743	r744	r745	r746	r747	r748	r749	r750	r751	r752	r753	r754	r755	r756	r757	r758	r759	r760	r761	r762	r763	r764	r765	r766	r767	r768	r769	r770	r771	r772	r773	r774	r775	r776	r777	r778	r779	r780	r781	r782	r783	r784	r785	r786	r787	r788	r789	r790	r791	r792	r793	r794	r795	r796	r797	r798	r799	r800	r801	r802	r803	r804	r805	r806	r807	r808	r809	r810	r811	r812	r813	r814	r815	r816	r817	r818	r819	r820	r821	r822	r823	r824	r825	r826	r827	r828	r829	r830	r831	r832	r833	r834	r835	r836	r837	r838	r839	r840	r841	r842	r843	r844	r845	r846	r847	r848	r849	r850	r851	r852	r853	r854	r855	r856	r857	r858	r859	r860	r861	r862	r863	r864	r865	r866	r867	r868	r869	r870	r871	r872	r873	r874	r875	r876	r877	r878	r879	r880	r881	r882	r883	r884	r885	r886	r887	r888	r889	r890	r891	r892	r893	r894	r895	r896	r897	r898	r899	r900	r901	r902	r903	r904	r905	r906	r907	r908	r909	r910	r911	r912	r913	r914	r915	r916	r917	r918	r919	r920	r921	r922	r923	r924	r925	r926	r927	r928	r929	r930	r931	r932	r933	r934	r935	r936	r937	r938	r939	r940	r941	r942	r943	r944	r945	r946	r947	r948	r949	r950	r951	r952	r953	r954	r955	r956	r957	r958	r959	r960	r961	r962	r963	r964	r965	r966	r967	r968	r969	r970	r971	r972	r973	r974	r975	r976	r977	r978	r979	r980	r981	r982	r983	r984	r985	r986	r987	r988	r989	r990	r991	r992	r993	r994	r995	r996	r997	r998	r999	r1000
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Supplementary Table 3. GGDC analyses within each phylogenetic group

Group A						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
NC_014659	LRRF00000000	93.1	1.71	93.1 - 93.1	0.0087	96.73
NC_014659	APJC00000000	91.5	1.40055	91.5 - 91.5	0.0105	96.26
NC_014659	LRQY00000000	93.1	1.71	93.1 - 93.1	0.0087	96.73
NC_014659	LRQZ00000000	90.8	2.02	90.8 - 90.8	0.0112	96.07
NC_014659	LARRA00000000	93.1	1.7	93.1 - 93.2	0.0087	96.74
NC_014659	NZ_CM001149	92	1.2636	92 - 92%	0.01	96.42
NC_014659	JPOC00000000	27	3.020253	27 - 27%	0.1603	0.03
Group B1-1						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
NZ_CP011341.1	LRRLO00000000	44.6	2.56	44.6 - 44.6	0.0852	7.67
NZ_CP011341.1	LPZN00000000	21.4	2.34	21.4 - 21.4	0.2055	0
NZ_CP011341.1	LRRK00000000	21.6	2.35	21.6 - 21.7	0.2027	0
NZ_CP011341.1	LRRIO00000000	21.5	2.34	21.5 - 21.5	0.2041	0
NZ_CP011341.1	AVAE00000000	92.2	2.575147	92.1 - 92.2	0.0098	96.47
NZ_CP011341.1	AZHI00000000	92.9	2.791065	92.9 - 92.9	0.0089	96.68
NZ_CP011341.1	CAVJ00000000	94.5	2.854621	94.5 - 94.5	0.0072	97.08
NZ_CP011341.1	AJVB00000000	22	2.920821	22 - 22%	0.1994	0
NZ_CP011341.1	AGVW00000000	21.6	2.966245	21.6 - 21.6	0.2032	0
NZ_CP011341.1	AFAQ00000000	21.4	2.888954	21.4 - 21.4	0.2051	0
NZ_CP011341.1	AHBW00000000	21.6	2.966435	21.6 - 21.6	0.2031	0
NZ_CP011341.1	JPJJ01000000	21.5	2.961796	21.5 - 21.5	0.2045	0
NZ_CP011341.1	JTIZ01000000	21.5	2.957577	21.5 - 21.5	0.2045	0
NZ_CP011341.1	NC_023150	21.5	2.97309	21.5 - 21.5	0.2042	0
NZ_CP011341.1	LRRH00000000	22.7	2.37	22.7 - 22.7	0.1932	0
NZ_CP011341.1	AJFC00000000	45	3.333403	45 - 45%	0.0844	8.16
NZ_CP011341.1	CCSD01000000	44.8	3.306344	44.7 - 44.8	0.0849	7.83
NZ_CP011341.1	LDUF01000000	44.8	3.327868	44.8 - 44.8	0.0848	7.89
NZ_CP011341.1	ANGC00000000	44.7	3.339426	44.7 - 44.7	0.0852	7.68
NZ_CP011341.1	AOEX00000000	43.5	3.256966	43.5 - 43.5	0.0886	6.05
Group B1-2						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
LRRLO00000000	AVAE00000000	44.1	2.55	44.1 - 44.1	0.0869	6.83
LRRLO00000000	AFAQ00000000	21.5	2.34	21.5 - 21.5	0.2046	0
LRRLO00000000	CAVJ00000000	44.9	2.56	44.9 - 44.9	0.0844	8.11
LRRLO00000000	AJVB00000000	22	2.35	22 - 22%	0.1993	0
LRRLO00000000	AJFC00000000	93	1.73	93 - 93%	0.0089	96.69
LRRLO00000000	JPJJ01000000	21.6	2.35	21.6 - 21.6	0.2028	0
LRRLO00000000	JTIZ01000000	21.6	2.35	21.6 - 21.6	0.203	0
LRRLO00000000	NZ_CP011341.1	44.6	2.56	44.6 - 44.6	0.0852	7.67
LRRLO00000000	LPZN00000000	21.4	2.34	21.4 - 21.4	0.2056	0
LRRLO00000000	NC_023150	21.6	2.35	21.6 - 21.6	0.2028	0
LRRLO00000000	AHBW00000000	21.8	2.35	21.8 - 21.8	0.2015	0
LRRLO00000000	LRRIO00000000	21.5	2.34	21.5 - 21.5	0.2037	0
LRRLO00000000	LRRH00000000	22.6	2.36	22.6 - 22.6	0.1936	0

LRRLO0000000	ANGC000000000	94.8	1.43	94.8 - 94.8	0.0068	97.16
LRRLO0000000	AOEX000000000	60.3	2.82	60.3 - 60.3	0.0511	53.34
LRRLO0000000	CCSD010000000	92.2	1.84	92.2 - 92.2	0.0097	96.48
LRRLO0000000	LDUF010000000	92.9	1.74	92.9 - 92.9	0.009	96.68
LRRLO0000000	AGVW000000000	21.7	2.35	21.7 - 21.7	0.2026	0
LRRLO0000000	AZHI000000000	44.1	2.55	44.1 - 44.1	0.0869	6.84
LRRLO0000000	LRRK000000000	21.7	2.35	21.7 - 21.7	0.2026	0
Group B1-3						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
AOEX000000000	AVAE000000000	42.7	[40.1 - 45.2]	42.7 - 42.7	0.091	5.07
AOEX000000000	AFAQ000000000	21.3	[19.1 - 23.7]	21.3 - 21.3	0.2059	0
AOEX000000000	CAVJ000000000	43.3	[40.8 - 45.9]	43.3 - 43.3	0.089	5.84
AOEX000000000	AJVB000000000	21.8	[19.6 - 24.3]	21.8 - 21.9	0.2008	0
AOEX000000000	AJFC000000000	60.6	[57.8 - 63.4]	60.6 - 60.6	0.0505	54.46
AOEX000000000	JPJJ010000000	21.6	[19.3 - 24.0]	21.6 - 21.6	0.2035	0
AOEX000000000	JTIZ010000000	21.4	[19.1 - 23.8]	21.4 - 21.4	0.2054	0
AOEX000000000	NZ_CP011341.1	43.5	[41 - 46%]	43.5 - 43.5	0.0886	6.05
AOEX000000000	LPZN000000000	21.4	[19.1 - 23.8]	21.4 - 21.4	0.2052	0
AOEX000000000	NC_023150	21.2	[19 - 23.6%]	21.2 - 21.2	0.2071	0
AOEX000000000	AHBW000000000	21.4	[19.1 - 23.8]	21.4 - 21.4	0.2052	0
AOEX000000000	LRRIO000000000	21.4	[19.1 - 23.8]	21.4 - 21.4	0.2052	0
AOEX000000000	LRRH000000000	22.2	[20 - 24.7%]	22.2 - 22.2	0.1973	0
AOEX000000000	ANGC000000000	59.6	[56.8 - 62.4]	59.6 - 59.6	0.0523	51.08
AOEX000000000	LRRLO000000000	60.3	[57.5 - 63.1]	60.3 - 60.3	0.0511	53.34
AOEX000000000	CCSD010000000	60	[57.2 - 62.8]	60 - 60%	0.0516	52.39
AOEX000000000	LDUF010000000	60.5	[57.6 - 63.2]	60.5 - 60.5	0.0508	53.87
AOEX000000000	AGVW000000000	21.5	[19.2 - 23.9]	21.4 - 21.5	0.2046	0
AOEX000000000	AZHI000000000	42.9	[40.4 - 45.5]	42.9 - 42.9	0.0902	5.37
AOEX000000000	LRRK000000000	21.4	[19.2 - 23.9]	21.4 - 21.4	0.2049	0
Group B-4						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
LRRH000000000	AVAE000000000	22.9	2.37	22.9 - 22.9	0.1915	0
LRRH000000000	AFAQ000000000	22	2.35	22 - 22%	0.1996	0
LRRH000000000	CAVJ000000000	22.9	2.37	22.9 - 22.9	0.1915	0
LRRH000000000	AJVB000000000	22.6	2.36	22.5 - 22.6	0.1943	0
LRRH000000000	AJFC000000000	22.7	2.37	22.7 - 22.7	0.1928	0
LRRH000000000	JPJJ010000000	22.2	2.36	22.2 - 22.2	0.1978	0
LRRH000000000	JTIZ010000000	22.2	2.36	22.2 - 22.2	0.1976	0
LRRH000000000	NZ_CP011341.1	22.7	2.37	22.7 - 22.7	0.1932	0
LRRH000000000	LPZN000000000	22	2.35	22 - 22%	0.1993	0
LRRH000000000	NC_023150	21.9	2.35	21.9 - 21.9	0.2007	0
LRRH000000000	AHBW000000000	22	2.35	22 - 22%	0.1995	0
LRRH000000000	LRRIO000000000	21.9	2.35	21.9 - 21.9	0.1999	0
LRRH000000000	ANGC000000000	22.7	2.37	22.7 - 22.7	0.1933	0
LRRH000000000	AOEX000000000	22.2	2.36	22.2 - 22.2	0.1973	0
LRRH000000000	LRRLO000000000	22.6	2.36	22.6 - 22.6	0.1936	0
LRRH000000000	CCSD010000000	22.6	2.37	22.6 - 22.7	0.1934	0
LRRH000000000	LDUF010000000	22.6	2.36	22.6 - 22.6	0.1939	0

LRRH00000000	AGVW00000000	22.4	2.36	22.4 - 22.4	0.1959	0
LRRH00000000	AZHI00000000	23	2.37	23 - 23%	0.1903	0
LRRH00000000	LRRK00000000	22	2.35	22 - 22%	0.1993	0
Group B2-5						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
LPZN00000000	AVAE00000000	21.8	2.35	21.8 - 21.8	0.201	0
LPZN00000000	AFAQ00000000	41.9	2.53	41.9 - 41.9	0.0932	4.3
LPZN00000000	CAVJ00000000	21.8	2.35	21.8 - 21.8	0.2008	0
LPZN00000000	AJVB00000000	85.7	2.49	85.7 - 85.7	0.0168	94.07
LPZN00000000	AJFC00000000	21.6	2.34	21.6 - 21.6	0.2033	0
LPZN00000000	JPJJ01000000	42.5	2.53	42.5 - 42.5	0.0914	4.91
LPZN00000000	JTIZ01000000	42	2.53	41.9 - 42%	0.0931	4.33
LPZN00000000	NZ_CP011341.1	21.4	2.34	21.4 - 21.4	0.2055	0
LPZN00000000	NC_023150	42.2	2.53	42.2 - 42.2	0.0923	4.62
LPZN00000000	AHBW00000000	43	2.54	43 - 43%	0.09	5.44
LPZN00000000	LRRIO00000000	43	2.54	43 - 43%	0.0899	5.5
LPZN00000000	LRRH00000000	22	2.35	22 - 22%	0.1993	0
LPZN00000000	ANGC00000000	21.6	2.34	21.6 - 21.6	0.2033	0
LPZN00000000	AOEX00000000	21.4	2.34	21.4 - 21.4	0.2052	0
LPZN00000000	LRRLO00000000	21.4	2.34	21.4 - 21.4	0.2056	0
LPZN00000000	CCSD01000000	21.6	2.34	21.6 - 21.6	0.2035	0
LPZN00000000	LDUF01000000	21.7	2.35	21.7 - 21.7	0.2019	0
LPZN00000000	AGVW00000000	41.8	2.52	41.8 - 41.8	0.0936	4.19
LPZN00000000	AZHI00000000	21.8	2.35	21.8 - 21.8	0.2016	0
LPZN00000000	LRRK00000000	41.7	2.52	41.7 - 41.7	0.0938	4.12
Group B2-6a						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
LRRK00000000	AVAE00000000	21.8	2.35	21.8 - 21.8	0.2013	0
LRRK00000000	AFAQ00000000	57.1	2.76	57.1 - 57.1	0.0568	42.4
LRRK00000000	CAVJ00000000	21.8	2.35	21.8 - 21.8	0.2009	0
LRRK00000000	AJVB00000000	41.6	2.52	41.6 - 41.6	0.0944	3.95
LRRK00000000	AJFC00000000	21.8	2.35	21.8 - 21.8	0.2009	0
LRRK00000000	JPJJ01000000	59.3	2.8	59.3 - 59.3	0.0528	50.04
LRRK00000000	JTIZ01000000	59.1	2.79	59.1 - 59.1	0.0532	49.24
LRRK00000000	NZ_CP011341.1	21.6	2.35	21.6 - 21.7	0.2027	0
LRRK00000000	LPZN00000000	41.7	2.52	41.7 - 41.7	0.0938	4.12
LRRK00000000	NC_023150	59.2	2.8	59.2 - 59.2	0.0531	49.54
LRRK00000000	AHBW00000000	58.9	2.79	58.9 - 58.9	0.0535	48.76
LRRK00000000	LRRIO00000000	58.7	2.79	58.7 - 58.7	0.0539	47.89
LRRK00000000	LRRH00000000	22	2.35	22 - 22%	0.1993	0
LRRK00000000	ANGC00000000	21.6	2.35	21.6 - 21.6	0.2027	0
LRRK00000000	AOEX00000000	21.4	2.34	21.4 - 21.4	0.2049	0
LRRK00000000	LRRLO00000000	21.7	2.35	21.7 - 21.7	0.2026	0
LRRK00000000	CCSD01000000	21.6	2.35	21.6 - 21.6	0.2029	0
LRRK00000000	LDUF01000000	21.5	2.34	21.5 - 21.5	0.2043	0
LRRK00000000	AGVW00000000	62.5	2.85	62.5 - 62.6	0.0473	60.44
LRRK00000000	AZHI00000000	21.8	2.35	21.8 - 21.8	0.2013	0

Group B2-6b						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
AGVW00000000	LPZN00000000	41.8	2.52	41.8 - 41.8	0.0936	4.19
AGVW00000000	LRR100000000	59.9	2.81	59.9 - 59.9	0.0517	52.1
AGVW00000000	LRRH00000000	22.4	2.36	22.4 - 22.4	0.1959	0
AGVW00000000	LRRLO0000000	21.7	2.35	21.7 - 21.7	0.2026	0
AGVW00000000	LRRK00000000	62.5	2.85	62.5 - 62.6	0.0473	60.44
AGVW00000000	AVAE00000000	21.7	2.950495	21.7 - 21.7	0.2018	0
AGVW00000000	CAVJ000000000	21.7	2.942169	21.7 - 21.7	0.2018	0
AGVW00000000	NZ_CP011341.1	21.6	2.966245	21.6 - 21.6	0.2032	0
AGVW00000000	AZHI000000000	21.7	2.943735	21.7 - 21.7	0.202	0
AGVW00000000	AJFC000000000	21.8	2.935339	21.8 - 21.8	0.2013	0
AGVW00000000	CCSD01000000	21.7	2.942023	21.7 - 21.7	0.2021	0
AGVW00000000	LDUF01000000	21.7	2.951113	21.7 - 21.7	0.2026	0
AGVW00000000	ANGC000000000	21.7	2.949395	21.7 - 21.7	0.2021	0
AGVW00000000	AOEX000000000	21.5	2.942441	21.4 - 21.5	0.2046	0
AGVW00000000	AJVB000000000	42	3.102589	42 - 42%	0.0931	4.34
AGVW00000000	JTIZ01000000	59.3	3.199612	59.3 - 59.3	0.0529	49.9
AGVW00000000	AFAQ000000000	58.7	3.005453	58.7 - 58.7	0.0539	47.91
AGVW00000000	JPJJ01000000	61.2	3.219722	61.2 - 61.2	0.0495	56.38
AGVW00000000	NC_023150	60.8	3.294971	60.8 - 60.8	0.0503	54.86
AGVW00000000	AHBW000000000	60.2	3.224831	60.2 - 60.2	0.0513	52.88
Group B2-7						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
LRR100000000	AVAE000000000	22	2.35	22 - 22%	0.199	0
LRR100000000	AFAQ000000000	84.2	2.59	84.1 - 84.2	0.0186	93.29
LRR100000000	CAVJ000000000	22.1	2.35	22.1 - 22.1	0.1983	0
LRR100000000	AJVB000000000	42.8	2.54	42.8 - 42.8	0.0905	5.25
LRR100000000	AJFC000000000	21.8	2.35	21.8 - 21.8	0.2017	0
LRR100000000	JPJJ01000000	86.9	2.41	86.8 - 86.9	0.0156	94.59
LRR100000000	JTIZ01000000	87.4	2.36	87.4 - 87.4	0.015	94.82
LRR100000000	NZ_CP011341.1	21.5	2.34	21.5 - 21.5	0.2041	0
LRR100000000	LPZN000000000	43	2.54	43 - 43%	0.0899	5.5
LRR100000000	NC_023150	86.4	2.44	86.4 - 86.4	0.0161	94.38
LRR100000000	AHBW000000000	87.8	2.32	87.8 - 87.8	0.0145	94.99
LRR100000000	LRRH000000000	21.9	2.35	21.9 - 21.9	0.1999	0
LRR100000000	ANGC000000000	21.7	2.35	21.7 - 21.7	0.2025	0
LRR100000000	AOEX000000000	21.4	2.34	21.4 - 21.4	0.2052	0
LRR100000000	LRRLO0000000	21.5	2.34	21.5 - 21.5	0.2037	0
LRR100000000	CCSD01000000	21.7	2.35	21.7 - 21.7	0.2018	0
LRR100000000	LDUF01000000	21.8	2.35	21.8 - 21.8	0.2016	0
LRR100000000	AGVW000000000	59.9	2.81	59.9 - 59.9	0.0517	52.1
LRR100000000	AZHI000000000	22	2.35	22 - 22%	0.1992	0
LRR100000000	LRRK000000000	58.7	2.79	58.7 - 58.7	0.0539	47.89
Group C-1						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
NC_008268	LRRG000000000	60.3	2.82	60.3 - 60.3	0.0511	53.41
NC_008268	AKKP000000000	90.3	3.284781	90.3 - 90.3	0.0118	95.89

NC_008268	AJLQ00000000	93.9	2.847251	93.9 - 94%	0.0078	96.95
NC_008268	NC_008268	100	Inf	100 - 100%	0	98.3
NC_008268	AJJH00000000	60.4	3.143948	60.4 - 60.4%	0.0509	53.65
NC_008268	AJYC00000000	59.8	3.227206	59.8 - 59.8%	0.0519	51.78
NC_008268	ANIU00000000	60.1	3.16812	60.1 - 60.1%	0.0514	52.82
NC_008268	CP008947.1	58.7	3.333428	58.7 - 58.7%	0.0538	48.09
NC_008268	BAWF01000000	58.5	3.135921	58.5 - 58.5%	0.0543	47.12
NC_008268	AGVD00000000	60	3.280012	60 - 60%	0.0515	52.48
NC_008268	NC_012522	42	3.123612	42 - 42%	0.0929	4.42
Group C-2						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
LRRG00000000	AKKP00000000	60.1	2.81	60.1 - 60.1%	0.0515	52.57
LRRG00000000	AJLQ00000000	59.5	2.8	59.4 - 59.5%	0.0526	50.5
LRRG00000000	AJJH00000000	81.2	2.74	81.2 - 81.2%	0.0219	91.47
LRRG00000000	NC_008268	60.3	2.82	60.3 - 60.3%	0.0511	53.41
LRRG00000000	NC_012522	42.8	2.53	42.8 - 42.8%	0.0907	5.18
LRRG00000000	AGVD00000000	70.6	2.93	70.6 - 70.6%	0.0352	79.46
LRRG00000000	AJYC00000000	85.2	2.53	85.2 - 85.2%	0.0174	93.83
LRRG00000000	CP008947.1	59.2	2.8	59.2 - 59.2%	0.053	49.6
LRRG00000000	ANIU00000000	97.1	0.96	97.1 - 97.1%	0.0042	97.67
LRRG00000000	BAWF01000000	58.2	2.78	58.2 - 58.2%	0.0549	46.13
Group C-3						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
BAWF01000000	AKKP00000000	58.2	2.78	58.2 - 58.2%	0.0548	46.17
BAWF01000000	AJLQ00000000	57.1	2.76	57.1 - 57.1%	0.0569	42.26
BAWF01000000	AJJH00000000	57.4	2.76	57.4 - 57.4%	0.0563	43.39
BAWF01000000	NC_008268	58.5	2.78	58.5 - 58.5%	0.0543	47.12
BAWF01000000	NC_012522	43.5	2.54	43.5 - 43.5%	0.0884	6.12
BAWF01000000	AGVD00000000	58.5	2.78	58.5 - 58.6%	0.0542	47.41
BAWF01000000	AJYC00000000	57.8	2.77	57.8 - 57.8%	0.0555	44.83
BAWF01000000	CP008947.1	91.6	1.92	91.6 - 91.6%	0.0104	96.31
BAWF01000000	LRRG00000000	58.2	2.78	58.2 - 58.2%	0.0549	46.13
BAWF01000000	ANIU00000000	57.5	2.76	57.5 - 57.5%	0.0562	43.65
Group C-4						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
AGVD00000000	AKKP00000000	59.8	2.81	59.8 - 59.8%	0.052	51.64
AGVD00000000	AJLQ00000000	59.2	2.8	59.2 - 59.2%	0.053	49.77
AGVD00000000	AJJH00000000	69.2	2.92	69.2 - 69.2%	0.0373	76.75
AGVD00000000	NC_008268	60	2.81	60 - 60%	0.0515	52.48
AGVD00000000	NC_012522	43.2	2.54	43.2 - 43.2%	0.0894	5.71
AGVD00000000	AJYC00000000	69.8	2.92	69.8 - 69.8%	0.0363	78.03
AGVD00000000	CP008947.1	59.1	2.8	59.1 - 59.2%	0.0531	49.47
AGVD00000000	LRRG00000000	70.6	2.93	70.6 - 70.6%	0.0352	79.46
AGVD00000000	ANIU00000000	70	2.92	70 - 70%	0.0362	78.27
AGVD00000000	BAWF01000000	58.5	2.78	58.5 - 58.6%	0.0542	47.41
Group C-5						

NC_022115	AGCF00000000	88.3	2.889517	88.3 - 88.3	0.014	95.18
NC_022115	AUZK00000000	87.6	2.25441	87.6 - 87.6	0.0147	94.92
NC_022115	ASKF01000000	89.1	2.133519	89.1 - 89.1	0.0131	95.48
NC_022115	NZ_CP011295.1	89	1.339991	89 - 89%	0.0132	95.45
NC_022115	JOIM01000000	100	0.089949	99.9 - 99.9	0.0003	98.26
NC_022115	ASJJ00000000	100	1.05517	99.6 - 99.6	0.0008	98.19
NC_022115	JYOP01000000	24.1	[21.8 - 26.5	24.1 - 24.1	0.1815	0.01
NC_022115	CEDU01000000	24	[21.7 - 26.5	24 - 24%	0.1819	0
NC_022115	JNWS01000000	24.1	[21.8 - 26.5	24.1 - 24.1	0.1814	0.01
Group D-3						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
JNWS01000000	JYOP01000000	88.8	2.862449	88.8 - 88.8	0.0134	95.37
JNWS01000000	CEDU01000000	83.4	2.723753	83.4 - 83.4	0.0194	92.85
Group E1-1						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
JOKB01000000	ARTN00000000	56.8	3.348659	56.8 - 56.8	0.0575	41.15
JOKB01000000	ARND00000000	-9999			-9999	
JOKB01000000	JMEX01000000	57	3.327823	57 - 57.1%	0.0569	42.17
JOKB01000000	JMEW01000000	59.3	3.348787	59.3 - 59.3	0.0528	50.12
JOKB01000000	JMFF01000000	57.3	3.348982	57.3 - 57.3	0.0565	43.01
JOKB01000000	JMFE01000000	57.5	3.332635	57.5 - 57.5	0.0562	43.62
JOKB01000000	JMEV01000000	22	2.899647	22 - 22%	0.1992	0
JOKB01000000	BAOX01000000	21.3	2.821507	21.3 - 21.3	0.2064	0
JOKB01000000	NZ_CP010797.1	20.2	2.875993	20.2 - 20.2	0.2175	0
JOKB01000000	JMFC01000000	22.5	2.907818	22.5 - 22.5	0.1946	0
JOKB01000000	JMFD01000000	20.6	2.840616	20.6 - 20.6	0.2134	0
JOKB01000000	JMFA01000000	21.3	2.868488	21.3 - 21.3	0.2062	0
JOKB01000000	JMEZ01000000	20.9	2.863237	20.9 - 20.9	0.2103	0
JOKB01000000	JMEM01000000	22.1	2.878388	22.1 - 22.1	0.1987	0
JOKB01000000	JZIS01000000	20.6	2.865046	20.6 - 20.6	0.213	0
JOKB01000000	AXVF00000000	20.6	2.878426	20.6 - 20.6	0.2132	0
JOKB01000000	LFDS01000000	20.4	2.869638	20.4 - 20.4	0.2153	0
JOKB01000000	JMEY01000000	23	2.894318	23 - 23%	0.1906	0
JOKB01000000	JMEU01000000	22.9	2.910638	22.9 - 22.9	0.1915	0
JOKB01000000	JMES01000000	20.5	2.859485	20.5 - 20.5	0.2144	0
JOKB01000000	JMER01000000	20.6	2.857774	20.6 - 20.6	0.2129	0
JOKB01000000	JMET01000000	22.5	2.901807	22.5 - 22.5	0.195	0
JOKB01000000	JMEQ01000000	20.7	2.865869	20.7 - 20.7	0.2124	0
JOKB01000000	JMEP01000000	22.5	2.901084	22.5 - 22.5	0.1945	0
JOKB01000000	JMEO01000000	23.1	2.899508	23.1 - 23.1	0.1894	0
JOKB01000000	JMEN01000000	22.6	2.898779	22.6 - 22.6	0.1942	0
JOKB01000000	CAPS00000000	21.6	2.830852	21.6 - 21.6	0.2032	0
Group E1-2						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
ARTN00000000	JOKB01000000	56.8	3.348659	56.8 - 56.8	0.0575	41.15
ARTN00000000	ARND00000000	-9999			-9999	
ARTN00000000	JMEX01000000	91.6	2.838378	91.6 - 91.6	0.0103	96.31

JMEV01000000	JMEP01000000	29.2	3.061572	29.2 - 29.2%	0.1465	0.08
JMEV01000000	JMEO01000000	29.1	3.03946	29.1 - 29.1%	0.1474	0.07
JMEV01000000	JMEN01000000	29	3.035506	29 - 29%	0.1477	0.07
JMEV01000000	CAPS00000000	30.7	3.018599	30.7 - 30.7%	0.1381	0.14
Group E2-4						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
BAOX01000000	JOKB01000000	21.3	2.821507	21.3 - 21.3%	0.2064	0
BAOX01000000	ARTN00000000	20.9	2.826377	20.9 - 21%	0.2097	0
BAOX01000000	ARND00000000	-9999			-9999	
BAOX01000000	JMEX01000000	21.2	2.825755	21.2 - 21.3%	0.2066	0
BAOX01000000	JMEW01000000	21.3	2.817231	21.3 - 21.3%	0.2058	0
BAOX01000000	JMFF01000000	21	2.815155	21 - 21%	0.2092	0
BAOX01000000	JMFE01000000	21.4	2.825742	21.4 - 21.4%	0.2054	0
BAOX01000000	JMEV01000000	46.5	3.124931	46.5 - 46.5%	0.0803	10.83
BAOX01000000	NZ_CP010797.1	45	3.200654	45 - 45%	0.0844	8.17
BAOX01000000	JMFC01000000	45	3.157344	45 - 45%	0.0842	8.25
BAOX01000000	JMFD01000000	31.8	3.033918	31.8 - 31.8%	0.1327	0.22
BAOX01000000	JMFA01000000	32.1	3.027924	32.1 - 32.1%	0.1315	0.24
BAOX01000000	JMEZ01000000	31.9	3.02665	31.9 - 31.9%	0.132	0.23
BAOX01000000	JMEM01000000	31.9	3.02298	31.9 - 31.9%	0.1321	0.23
BAOX01000000	JZIS01000000	28.7	3.010007	28.7 - 28.7%	0.1496	0.06
BAOX01000000	AXVF00000000	28.5	3.006439	28.5 - 28.5%	0.1505	0.06
BAOX01000000	LFDS01000000	28.4	3.008569	28.4 - 28.4%	0.1511	0.05
BAOX01000000	JMEY01000000	28	3.006953	28 - 28%	0.1539	0.04
BAOX01000000	JMEU01000000	28	3.005871	28 - 28%	0.1538	0.04
BAOX01000000	JMES01000000	28.7	3.007533	28.7 - 28.7%	0.1497	0.06
BAOX01000000	JMER01000000	28.6	3.00579	28.6 - 28.6%	0.15	0.06
BAOX01000000	JMET01000000	28.1	3.005423	28.1 - 28.1%	0.1529	0.05
BAOX01000000	JMEQ01000000	28.2	3.005574	28.2 - 28.2%	0.1526	0.05
BAOX01000000	JMEP01000000	28.1	3.005423	28.1 - 28.1%	0.153	0.05
BAOX01000000	JMEO01000000	28.1	3.005776	28.1 - 28.1%	0.1529	0.05
BAOX01000000	JMEN01000000	28	3.00574	28 - 28%	0.1539	0.04
BAOX01000000	CAPS00000000	31.1	3.007535	31.1 - 31.1%	0.1361	0.17
Group E2-5						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
NZ_CP010797.1	JOKB01000000	20.2	2.875993	20.2 - 20.2%	0.2175	0
NZ_CP010797.1	ARTN00000000	20.1	2.903683	20.1 - 20.1%	0.2183	0
NZ_CP010797.1	ARND00000000	-9999			-9999	
NZ_CP010797.1	JMEX01000000	20.2	2.892591	20.2 - 20.2%	0.2179	0
NZ_CP010797.1	JMEW01000000	20.3	2.886779	20.3 - 20.3%	0.2168	0
NZ_CP010797.1	JMFF01000000	20.2	2.886077	20.1 - 20.2%	0.2181	0
NZ_CP010797.1	JMFE01000000	20.2	2.885661	20.2 - 20.2%	0.2173	0
NZ_CP010797.1	JMEV01000000	42.4	3.220153	42.4 - 42.4%	0.0917	4.82
NZ_CP010797.1	BAOX01000000	45	3.200654	45 - 45%	0.0844	8.17
NZ_CP010797.1	JMFC01000000	87.2	2.909668	87.2 - 87.2%	0.0152	94.75
NZ_CP010797.1	JMFD01000000	31.6	3.177853	31.6 - 31.6%	0.1339	0.2
NZ_CP010797.1	JMFA01000000	31.5	3.121973	31.4 - 31.5%	0.1345	0.19
NZ_CP010797.1	JMEZ01000000	31.5	3.148921	31.5 - 31.5%	0.1343	0.19

NZ_CP010797.1	JMEM01000000	31.4	3.133552	31.4 - 31.4	0.1346	0.19
NZ_CP010797.1	JZIS01000000	27.5	3.077759	27.5 - 27.5	0.157	0.03
NZ_CP010797.1	AXVF00000000	27.4	3.062715	27.4 - 27.4	0.1576	0.03
NZ_CP010797.1	LFDS01000000	27.4	3.083969	27.4 - 27.4	0.1576	0.03
NZ_CP010797.1	JMEY01000000	27.4	3.026672	27.4 - 27.4	0.1576	0.03
NZ_CP010797.1	JMEU01000000	27.2	3.027126	27.2 - 27.2	0.1591	0.03
NZ_CP010797.1	JMES01000000	27.3	3.041463	27.3 - 27.3	0.1579	0.03
NZ_CP010797.1	JMER01000000	27.3	3.032581	27.3 - 27.3	0.158	0.03
NZ_CP010797.1	JMET01000000	27.4	3.057615	27.4 - 27.4	0.1573	0.03
NZ_CP010797.1	JMEQ01000000	27.3	3.057156	27.3 - 27.3	0.1582	0.03
NZ_CP010797.1	JMEP01000000	27.4	3.056768	27.4 - 27.4	0.1575	0.03
NZ_CP010797.1	JMEO01000000	27.2	3.031559	27.2 - 27.2	0.1586	0.03
NZ_CP010797.1	JMEN01000000	27.3	3.030267	27.3 - 27.3	0.1584	0.03
NZ_CP010797.1	CAPS00000000	29.6	3.022032	29.6 - 29.7	0.1441	0.09
Group E2-6						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
JMFD01000000	JOKB01000000	20.6	2.840616	20.6 - 20.6	0.2134	0
JMFD01000000	ARTN00000000	20.4	2.854134	20.4 - 20.4	0.2157	0
JMFD01000000	ARND00000000	-9999			-9999	
JMFD01000000	JMEX01000000	20.5	2.848266	20.5 - 20.5	0.2142	0
JMFD01000000	JMEW01000000	20.6	2.849756	20.6 - 20.6	0.2134	0
JMFD01000000	JMFF01000000	20.4	2.845946	20.4 - 20.4	0.2149	0
JMFD01000000	JMFE01000000	20.6	2.854172	20.6 - 20.6	0.2138	0
JMFD01000000	JMEV01000000	32.9	3.084305	32.9 - 32.9	0.1274	0.32
JMFD01000000	BAOX01000000	31.8	3.033918	31.8 - 31.8	0.1327	0.22
JMFD01000000	NZ_CP010797.1	31.6	3.177853	31.6 - 31.6	0.1339	0.2
JMFD01000000	JMFC01000000	31.5	3.132992	31.5 - 31.5	0.1342	0.19
JMFD01000000	JMFD01000000	100	0.002646	100 - 100%	0	98.3
JMFD01000000	JMFA01000000	87	3.114755	87 - 87%	0.0154	94.64
JMFD01000000	JMEZ01000000	69.6	3.294275	69.6 - 69.6	0.0367	77.55
JMFD01000000	JMEM01000000	68	3.345255	68 - 68%	0.039	74.38
JMFD01000000	JZIS01000000	28.1	3.056643	28.1 - 28.1	0.1534	0.04
JMFD01000000	AXVF00000000	28.1	3.050903	28.1 - 28.1	0.1531	0.05
JMFD01000000	LFDS01000000	28.3	3.081406	28.3 - 28.3	0.1522	0.05
JMFD01000000	JMEY01000000	28.5	3.041157	28.5 - 28.5	0.1507	0.05
JMFD01000000	JMEU01000000	28.1	3.032277	28.1 - 28.1	0.1533	0.04
JMFD01000000	JMES01000000	28.2	3.045261	28.2 - 28.2	0.1525	0.05
JMFD01000000	JMER01000000	28.1	3.034748	28.1 - 28.1	0.1531	0.05
JMFD01000000	JMET01000000	28.2	3.045535	28.2 - 28.2	0.1527	0.05
JMFD01000000	JMEQ01000000	28	3.043152	28 - 28%	0.1535	0.04
JMFD01000000	JMEP01000000	28.2	3.044245	28.2 - 28.2	0.1527	0.05
JMFD01000000	JMEO01000000	28	3.029697	28 - 28%	0.1538	0.04
JMFD01000000	JMEN01000000	28	3.027513	28 - 28%	0.1535	0.04
JMFD01000000	CAPS00000000	30.9	3.022337	30.9 - 30.9	0.1375	0.15
Group E2-7						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
JMEN01000000	JOKB01000000	22.6	2.898779	22.6 - 22.6	0.1942	0
JMEN01000000	JMEY01000000	80.8	3.204293	80.8 - 80.8	0.0225	91.16

JMEN01000000	JMFD01000000	28	3.027513	28 - 28%	0.1535	0.04
JMEN01000000	JMEX01000000	23.1	2.906309	23.1 - 23.1%	0.1896	0
JMEN01000000	JMEW01000000	22.5	2.893871	22.5 - 22.5%	0.1946	0
JMEN01000000	JMEU01000000	80.5	2.969147	80.5 - 80.5%	0.0227	90.98
JMEN01000000	JMES01000000	78.2	3.267375	78.2 - 78.2%	0.0255	89.1
JMEN01000000	JMER01000000	79.3	3.320445	79.3 - 79.3%	0.0242	90.03
JMEN01000000	JMFF01000000	22.2	2.889654	22.2 - 22.2%	0.1977	0
JMEN01000000	JMFE01000000	22.6	2.898558	22.6 - 22.6%	0.1937	0
JMEN01000000	JMFC01000000	28.2	3.04425	28.2 - 28.2%	0.1523	0.05
JMEN01000000	JMFA01000000	28.8	3.051789	28.8 - 28.8%	0.1488	0.06
JMEN01000000	JMEZ01000000	28.5	3.02761	28.5 - 28.5%	0.1508	0.05
JMEN01000000	JMEV01000000	29	3.035506	29 - 29%	0.1477	0.07
JMEN01000000	JMET01000000	80.7	2.688965	80.7 - 80.7%	0.0225	91.12
JMEN01000000	JMEQ01000000	81.4	3.111312	81.4 - 81.4%	0.0218	91.58
JMEN01000000	JMEP01000000	80.7	2.692911	80.7 - 80.7%	0.0225	91.13
JMEN01000000	JMEO01000000	82.4	2.724175	82.4 - 82.4%	0.0206	92.26
JMEN01000000	JMEM01000000	29.4	3.048811	29.4 - 29.4%	0.1453	0.08
JMEN01000000	LFDS01000000	79.1	3.080221	79.1 - 79.1%	0.0244	89.9
JMEN01000000	ARTN00000000	20.3	2.869777	20.3 - 20.4%	0.216	0
JMEN01000000	ARND00000000	-9999			-9999	
JMEN01000000	AXVF00000000	80.8	2.862236	80.8 - 80.8%	0.0224	91.17
JMEN01000000	CAPS00000000	26.9	3.01071	26.9 - 26.9%	0.1606	0.03
JMEN01000000	BAOX01000000	28	3.00574	28 - 28%	0.1539	0.04
JMEN01000000	JZIS01000000	80.1	3.123756	80.1 - 80.1%	0.0233	90.65
JMEN01000000	NZ_CP010797.1	27.3	3.030267	27.3 - 27.3%	0.1584	0.03
Group E2-8						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
CAPS00000000	JOKB01000000	21.6	2.830852	21.6 - 21.6%	0.2032	0
CAPS00000000	ARTN00000000	20.6	2.828702	20.6 - 20.6%	0.2136	0
CAPS00000000	ARND00000000	-9999			-9999	
CAPS00000000	JMEX01000000	21.5	2.839691	21.5 - 21.5%	0.2038	0
CAPS00000000	JMEW01000000	21.5	2.840446	21.5 - 21.5%	0.2042	0
CAPS00000000	JMFF01000000	21.1	2.835341	21.1 - 21.1%	0.2083	0
CAPS00000000	JMFE01000000	21.6	2.84452	21.6 - 21.6%	0.2032	0
CAPS00000000	JMEV01000000	30.7	3.018599	30.7 - 30.7%	0.1381	0.14
CAPS00000000	BAOX01000000	31.1	3.007535	31.1 - 31.1%	0.1361	0.17
CAPS00000000	NZ_CP010797.1	29.6	3.022032	29.6 - 29.7%	0.1441	0.09
CAPS00000000	JMFC01000000	29.7	3.015213	29.7 - 29.7%	0.1437	0.09
CAPS00000000	JMFD01000000	30.9	3.022337	30.9 - 30.9%	0.1375	0.15
CAPS00000000	JMFA01000000	30.9	3.024549	30.9 - 30.9%	0.1374	0.15
CAPS00000000	JMEZ01000000	30.8	3.015266	30.8 - 30.8%	0.1379	0.15
CAPS00000000	JMEM01000000	30.8	3.01487	30.8 - 30.8%	0.1377	0.15
CAPS00000000	JZIS01000000	27.1	3.015674	27.1 - 27.1%	0.1597	0.03
CAPS00000000	AXVF00000000	26.9	3.013666	26.9 - 26.9%	0.1605	0.03
CAPS00000000	LFDS01000000	26.9	3.01572	26.9 - 26.9%	0.1609	0.02
CAPS00000000	JMEY01000000	26.8	3.005878	26.8 - 26.8%	0.1615	0.02
CAPS00000000	JMEU01000000	26.8	3.007005	26.8 - 26.8%	0.1616	0.02
CAPS00000000	JMES01000000	26.9	3.011975	26.9 - 26.9%	0.1606	0.03
CAPS00000000	JMER01000000	27.1	3.012532	27.1 - 27.1%	0.1593	0.03

CAPS00000000	JMET01000000	26.9	3.013386	26.9 - 26.9	0.161	0.02
CAPS00000000	JMEQ01000000	26.6	3.009438	26.6 - 26.6	0.1626	0.02
CAPS00000000	JMEP01000000	26.9	3.012704	26.9 - 26.9	0.1609	0.02
CAPS00000000	JMEO01000000	26.9	3.009852	26.9 - 26.9	0.1606	0.03
CAPS00000000	JMEN01000000	26.9	3.01071	26.9 - 26.9	0.1606	0.03
Group F-1						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
LPZL00000000	JMLQ01000000	21.3	2.34	21.3 - 21.3	0.2064	0
LPZL00000000	JXQS01000000	20.6	2.32	20.6 - 20.6	0.2134	0
LPZL00000000	LPZO00000000	43.7	2.54	43.7 - 43.7	0.088	6.32
Group G-3						
Query genome	Reference genome	DDH	Model C.I.	Bootstrap	Distance	Prob. DDH >= 70%
AODO00000000	JMLO01000000	21.2	2.921555	21.2 - 21.2	0.2073	0
AODO00000000	CVQP01000000	27.7	3.020569	27.7 - 27.7	0.1556	0.04

Supplementary Table 4. A list of group A specific genes

Locus tag	Function	Protein Sequence	Nucleotide sequence
ch56_peg917	hypothetical protein	MRIRHLIAAVPVALLVLTGCS DG GSDSPKDKNDAGETTITAEAG ADAQETAVSVMCAQVVAYLDA TQQQAESTGQPFDRDAKGA EFL DMLKANGGTVVAAYNQAVA AGEPTLDPATATWEDVPAEARE LIEQSVQSGISGSC	atgcgattcgacatctgatcgcccgctccccgtcgccctgctggtcctcaccggctgcagtgcg gtggcgactcggaccgaaggacaccaagaacgacgcggcgagaccaccatcacggccgagg ccggcgccgacgccaggagaccgggtctcggtgatgtgcgcgaggtggtggcctacctgac gcgacgcagcagcaggccgagagcaccgggcagccgttcgaccgggatgcgaagggcgccgag ttctcgacatgctgaaggcgaacggcggcaccgtggtggcggcgtaaccagcaggcgggtg cggccggtgagccgacgctcgatccggcgaccgacgctgggaggacgtgccggccgaggcccg tgagctcatcgagcagtcggtgacgtccgggatctccggcagctgctga
ch56_peg2696	hypothetical protein	MIDDADITAHLTDEVRALPYPGR WSNPPFAGDGA AVIARDGDLTE LRVDRRAGRVDWVDLQTGAGQ MLAPSLRVLGALAAAYATALRDT RGAGDRALRRIERTFLDSVRTVS ADLAADGTFWATAAEELGDGVL GGDDLPEPLTVVPAGGSTV VIA MPMLRLHRLADEGLT LSYRS AVSYVTLSDDLDTLANTARPGA QASGPARVLVVDGQSPLTADAL AFPALRTLILVEPATLPEHLAAAA AALAVVTVGPREFARIADLLAH HAV	atgatcgacgacgccgacatcacggcgcacctgaccgacgaggtgcgggcgctcccctatccggg gcggtggtcgaatcctcgttcgcggtgacggcgcggggtgatcgcccgacggcgacctga cggagttgcgctcgaccggcgggccggtcgcgtcgactgggtggatctgcagaccggagccggg cagatgctcgaccgctcgtcgcgctcctcgggcgctcgcggcggcgtacgcgacagcattacg ggacaccgaggagccggcgaccgcgctgctgcatcgagcggacgttctcgtattccgtcc gcacgggtgcccgatctggccgacggcaggttctggccaccgggcggaggaaactcggc gacggtgtgctcggcgggtgacgacctcccgaccgctcaccgtggtaccggcgggagggtcgac cgtcgtcatcgatgccgatgctcggctgcaccggcgctcggcagcagggactcacctgtc cgactaccgctccggtgtctacgtgacgtgtccgacgacctcgacaccacactggcgaaca cagcccggcgggtgcacaggcgtcgggaccggccgggtgctcgtcgtcgacgggcagagccc gctcaccgacgacccctgcctttccggcgtcggacgctgatcctcgtcagccccccact gccggagcatctcgccgacggccggcctcgggtggtgacctcggcccccggaaccgt tcggcgatcgccgatctcctcgccaccacgcagctgta

Locus tag	Function	Protein Sequence	Nucleotide sequence
ch56_peg2789	hypothetical protein	MAGGRKRHVAGAAAAGALAVA GTFGAAPAAATVTGQG DVRTF GNSILVTMLNIDSTTDAPTRCAT VVFDTAGR PVITDLQE IYDGG LG IWWTTMP TETLHLA GQYTGSA DYRV TTECRDDDGVVRLADTVV TLPEGELVGNPPRYSELFPGF	atggccggaggacggaaacggcacgtcgcgggggcccgcggcgggtgactcgcggtggccg ggacattcgggtgcagcgcggccgcggcgacggtgaccgggcagggcgacgtcgcacctcgg caactcgatcctcgtgacgatgctgaacatgactccaccaccgacgcaccgacgcggtgcgca ccgtcgtcttcgacaccgccggccgaccggtgatcaccgatctgcaggagatctacgacggtggac tcggcatctggtggaccacgatcccaccgagacactccatctcgcggggcagtacacgggcagc gccgattaccgctcaccaccgagtgccgggacgacgacggtgtcgtgcgactggccgacaccgt cgtcacctgccgagggcgaaactcgtcgggaaccgccccgggtactcggaaactgttcgggccgtt ctag
ch56_peg2885	hypothetical protein	LDRRFHDRFLHVFGRRLIGHVFS SSPRARPSVCLSNVTRPRGGDG CVLVPRARDCLVSLHVLHVSRYH CRIARCLAGWRRSTAHAPDRSR PERLLIQRASRDRDLY	ttggaccgacgcttcacgatcggttcctgcacgttttcgggcggcgcttgatcgccacgtatttc ctcgagccccgggcgctccatccgtctgtctgaatgtgacggccgcgccccggcgatgg ttgtgtactgtacctcgggcacgagattgtctgctcctcactccacagtgtccgttatc actgcagaatcgcgcggtgcctggctggatggcggcgatccacggcgatgcgcctgacctca cggccccgagcgcctgctcatccagcgtgcctcacgtgacagggattacctgtactga
ch56_peg4192	hypothetical protein	MNRQTIEHRGWVVA AAAATAV ASGLLGA AVAGGDDQAESNPAT LTTEEGTDS PEDPSGLEQTNSF GYIPEHETTLETDPIGPEGGIED DPFELGGGRIDPAVVVPADA TLTPAG	atgaatcgacagacgatcgagcaccgcggtgggtggtcgcggcagcggccccacggccgtcg catcgggactgctcggggccgctcgcgggagcgacgaccaggccgagtcgaatcccggcac gctcaccaccgaggaggaaggaccgactcgcggaggaccgagcgggtctcgagcagaccaat tccttcggctacatccccgagcacgagacaccctcgagaccgatcccatcggaccggagggtgg cggcatcaggacgacccgttcgaaactcggcggcgccatcgacccggccgtcgtcgtcccgg tgcccgcagacgcgaccctcaccacccggccggttga