Supplementary materials for

`Unique genomic sequences in a novel *Mycobacterium avium* subsp. *hominissuis* lineage enabled fine scale transmission route tracing during pig movement'

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Supplementary Table 1. Information of MAH isolates in this study.

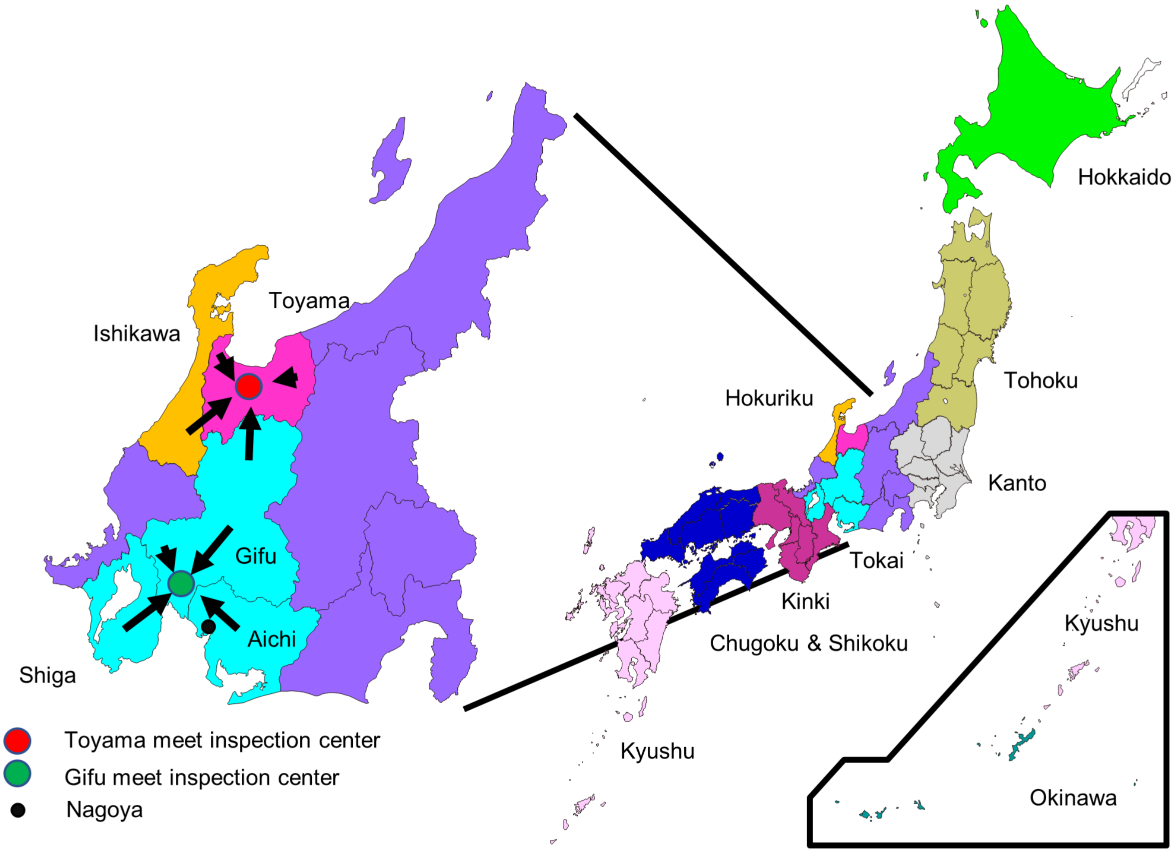
Isolate	Farm	Area	Sampling date	Sampling tissue	Reference
GM5	Gifu A	Tokai	15-Jul-2015	MEL	22
GM6	Gifu A	Tokai	15-Jul-2015	MEL	This study
GM10	Gifu A	Tokai	29-Jul-2015	MEL	22
GM11	Gifu A	Tokai	29-Jul-2015	MEL	This study
GM12	Shiga A	Tokai	05-Aug-2015	MEL	22
GM16	Aichi A	Tokai	01-Sep-2015	MEL	22
GM17	Aichi B	Tokai	01-Sep-2015	MEL	This study
GM21	Aichi B	Tokai	04-Sep-2015	MEL	22
GM23	Gifu A	Tokai	07-Sep-2015	MEL	This study
GM24	Gifu A	Tokai	07-Sep-2015	MEL	This study
GM25	Gifu A	Tokai	07-Sep-2015	MEL	This study
GM32	Gifu A	Tokai	05-Oct-2015	MEL	22
GM44	Gifu B	Tokai	24-Nov-2015	MEL	22
OCU467	Toyama A1	Hokuriku	25-Aug-1999	MEL	22
OCU468	Toyama A1	Hokuriku	01-Dec-1999	MEL	22
OCU469	Ishikawa B	Hokuriku	24-Dec-1999	MEL	22
OCU470	Toyama A1	Hokuriku	24-Dec-1999	MEL	22
OCU471	Ishikawa B	Hokuriku	28-Jan-2000	MEL	22
OCU472	Gifu B	Tokai	04-Feb-2000	MEL	22
OCU473	Ishikawa B	Hokuriku	08-Feb-2000	MEL	22
OCU474	Ishikawa B	Hokuriku	22-Dec-2000	MEL	22
OCU475	Toyama D	Hokuriku	05-Jan-2001	MEL	22
OCU476	Toyama D	Hokuriku	11-Jan-2001	MEL	22
OCU477	Toyama D	Hokuriku	11-Jan-2001	MEL	22
OCU478	Toyama A1	Hokuriku	18-Jan-2001	MEL	22
OCU479	Ishikawa B	Hokuriku	23-Jan-2001	MEL	22
OCU480	Ishikawa B	Hokuriku	26-Jan-2001	MEL	22
OCU481	Toyama D	Hokuriku	06-Feb-2001	MEL	22
OCU482	Ishikawa B	Hokuriku	09-Feb-2001	MEL	22
OCU483	Ishikawa B	Hokuriku	02-Dec-2004	MEL	22
OCU484	Toyama A2	Hokuriku	02-Dec-2004	MEL	22
OCU485	Toyama A3	Hokuriku	03-Dec-2004	MEL	22
OCU486	Toyama A1	Hokuriku	06-Dec-2004	MEL	22
Toy194	Toyama E	Hokuriku	26-Mar-2018	Liver	22
Toy195	Toyama E	Hokuriku	26-Mar-2018	MAL	22
gifu-1	Gifu C	Tokai	11-Mar-2016	MEL	This study
gifu-2	Gifu C	Tokai	11-Mar-2016	MEL	This study
gifu-6	Gifu C	Tokai	11-Mar-2016	MEL	This study
gifu-7	Gifu C	Tokai	11-Mar-2016	MEL	This study

gifu-8	Gifu C	Tokai	11-Mar-2016	MEL	This study
gifu-10	Gifu C	Tokai	11-Mar-2016	MEL	This study
gifu-11	Gifu C	Tokai	11-Mar-2016	MEL	This study
gifu-34	Gifu C	Tokai	22-Mar-2016	Feces (3 months old)	This study
gifu-41	Gifu C	Tokai	22-Mar-2016	Feces (4 months old)	This study
gifu-50	Gifu C	Tokai	22-Mar-2016	Feces (4 months old)	This study
gifu-51	Gifu C	Tokai	22-Mar-2016	Feces (4 months old)	This study
gifu-53	Gifu C	Tokai	22-Mar-2016	Feces (5 months old)	This study
gifu-67	Gifu C	Tokai	22-Mar-2016	Sawdust	This study
gifu-77	Gifu C	Tokai	22-Mar-2016	Soil	This study
gifu-92	Gifu C	Tokai	25-Mar-2016	MEL	This study

MEL: mesenteric lymph node.

MAL: mandibular lymph node.

22: Komatsu *et al*., 2021 Gigabyte



Supplementary Figure 1. Location of each regions and prefectures in Japan. Pigs from Tokai area (southern Gifu, Shiga and Aichi Prefecture) are slaughtered in Gifu meat inspection center. Pigs from Hokuriku area (northern Gifu, Toyama and Ishikawa Prefecture) are slaughtered in Toyama meat inspection center.

Supplementary Table 2. VNTR profiles of 50 MAH isolates in this study.

Isolate	MATR and MIRU-VNTR profile																			location of farm
	MATR -1	MATR -2	MATR -3	MATR -4	MATR -5	MATR -6	MATR -7	MATR -8	MATR -9	MATR -11	MATR -12	MATR -13	MATR -14	MATR -15	MATR -16					
		MIRU-292	MIRU-X3						MIRU-10							MIRU -7	MIRU -25	MIRU -32	MIRU -47	
OCU467	2	2	3	2	3	3	2	2	2	0	3	2	3	2	0	1	2	9	2	Toyama
OCU468	1	2	4	2	3	3	3	3	2	5	3	2	4	4	3	1	2	9	2	Toyama
OCU469	2	0	3	3	3	3	4	5	2	3	3	2	3	2	3	1	3	9	2	Ishikawa
OCU470	1	2	4	2	3	3	3	3	2	5	3	2	4	4	3	1	3	9	2	Toyama
OCU471	2	2	2	1	3	3	4	1	1	4	3	2	3	3	3	1	2	9	2	Ishikawa
OCU472	1	2	4	2	3	3	3	3	2	5	3	2	4	4	3	1	2	9	2	Gifu
OCU473	2	2	3	2	3	3	3	4	2	3	3	2	5	4	3	1	3	9	2	Ishikawa
OCU474	2	2	2	1	3	3	4	1	1	0	3	2	3	4	2	1	2	9	2	Ishikawa
OCU475	1	2	4	2	3	3	3	3	2	5	3	2	4	4	3	1	2	9	2	Toyama
OCU476	1	2	4	2	3	3	3	3	2	5	3	2	4	4	3	1	2	9	2	Toyama
OCU477	2	3	2	1	1	3	4	1	1	4	3	2	2	4	2	1	2	7	2	Toyama
OCU478	2	2	3	2	3	3	2	2	2	3	3	2	3	2	2	1	2	7	2	Toyama
OCU479	1	2	4	2	3	3	3	2	2	5	3	2	4	4	2	1	2	7	2	Ishikawa
OCU480	2	2	2	1	3	3	4	1	1	4	3	2	3	4	2	1	3	9	2	Ishikawa
OCU481	1	2	3	2	3	3	3	2	1	5	3	2	3	2	2	1	2	9	2	Toyama
OCU482	1	2	3	2	3	3	3	2	1	5	3	2	0	2	2	1	2	9	2	Ishikawa
OCU483	2	1	4	1	2	1	4	1	2	4	3	2	2	2	0	1	2	9	2	Ishikawa
OCU484	2	3	4	2	3	3	4	4	2	2	3	2	2	2	3	1	3	9	2	Toyama
OCU485	2	2	3	2	3	3	2	2	2	3	3	2	2	2	3	1	3	9	2	Toyama
OCU486	2	1	2	1	1	3	4	1	1	4	3	2	2	4	3	1	2	9	2	Toyama
Toy-194	0	3	5	2	3	3	3	2	2	4	3	2	4	4	3	1	2	9	2	Toyama
Toy-195	2	3	5	2	3	3	4	2	2	2	3	2	2	4	3	1	2	9	2	Toyama
gifu-1	2	2	2	2	2	3	4	1	2	2	3	2	2	4	1	1	3	8	3	Gifu
gifu-2	2	2	5	2	3	1	4	1	2	2	3	2	2	2	2	1	2	8	2	Gifu
gifu-6	2	2	2	2	2	3	4	1	2	4	3	2	2	4	1	1	3	8	3	Gifu
gifu-7	2	2	2	2	3	1	4	1	1	4	3	2	2	4	1	1	4	8	3	Gifu
gifu-8	2	2	6	2	2	1	4	1	2	4	3	2	2	4	2	1	3	8	3	Gifu

gifu-10	2	2	2	2	2	3	4	1	2	4	3	2	2	4	1	1	3	8	3	Gifu
gifu-11	2	2	2	2	2	3	4	1	2	4	3	2	2	4	1	1	3	8	3	Gifu
gifu-34	2	2	2	2	3	1	4	1	1	4	3	2	2	4	1	1	2	8	3	Gifu
gifu-41	2	2	2	2	2	3	4	1	2	4	3	2	2	4	1	1	3	8	3	Gifu
gifu-50	1	2	4	2	3	3	3	3	2	5	3	2	4	4	2	1	2	8	2	Gifu
gifu-51	2	2	5	2	3	1	4	2	2	6	3	2	2	2	3	1	3	8	3	Gifu
gifu-53	2	2	2	2	3	1	4	1	1	4	3	2	2	4	1	1	4	8	3	Gifu
gifu-67	2	2	2	2	2	3	4	1	2	4	3	2	2	4	1	1	3	8	3	Gifu
gifu-77	2	2	2	1	2	1	4	1	1	4	3	2	2	2	1	1	4	8	3	Gifu
gifu-92	2	2	2	1	2	1	4	1	1	4	3	2	2	2	1	1	4	8	3	Gifu
GM5	2	0	3	3	2	3	4	4	2	2	3	2	2	2	3	1	4	8	3	Gifu
GM6	2	0	3	3	2	3	4	4	2	2	3	2	2	2	3	1	4	8	3	Gifu
GM10	2	4	3	1	2	2	1	3	4	3	3	2	2	1	2	1	1	8	3	Gifu
GM11	2	4	3	1	2	2	1	3	4	3	3	2	2	1	2	1	1	8	3	Gifu
GM12	2	4	3	1	2	2	1	3	4	3	3	2	2	1	2	1	1	8	3	Shiga
GM16	5	3	3	2	1	0	1	1	2	2	3	2	2	2	3	1	2	8	3	Aichi
GM17	1	3	3	2	3	1	3	2	5	2	2	2	1	2	2	1	2	8	3	Aichi
GM21	2	4	3	1	2	2	1	3	4	3	3	2	2	1	2	1	1	8	3	Aichi
GM23	2	4	3	1	2	2	1	3	4	3	3	2	2	1	2	1	1	8	3	Aichi
GM24	2	4	3	1	2	2	1	3	4	3	3	2	2	1	2	1	1	8	3	Gifu
GM25	2	4	3	1	2	2	1	3	4	3	3	2	2	1	2	1	1	8	3	Gifu
GM32	2	4	3	1	2	2	1	3	4	3	3	2	2	1	2	1	1	8	3	Gifu
GM44	2	3	4	2	3	3	3	2	5	4	3	2	1	2	2	1	2	8	2	Gifu

Supplementary Table 3. Information of MAH strains or isolates used for VNTR analysis in this study.

Nation	Region in Japan	No. of strains						Reference**
		human			Bathroom	Natural environment	Pig	
		HIV						
		negative	positive	unknown				
Japan	Hokkaido			31	3		5	13, 16
	Tohoku				3			13
	Kanto				15			13
	Chubu	97		94	4	7*	43*	4, 13, 14
	Kinki	93			60	22	70	13, 16
	Chugoku & Shikoku				8			13
	Kyushu						36	19
	Okinawa						19	4
	Unknown		28					4
Korea		77		98				14, 23
USA				32				14
Europe				37				14, 24
Russia		65	25					23

total: 972 strains or isolates

*: Isolates in this study

**: The numbers of references are the same as the manuscript and are as follows.

4: Adachi *et al*., 2016 J Med Microbiol

13: Arikawa *et al*., 2019 Infect Genet Evol

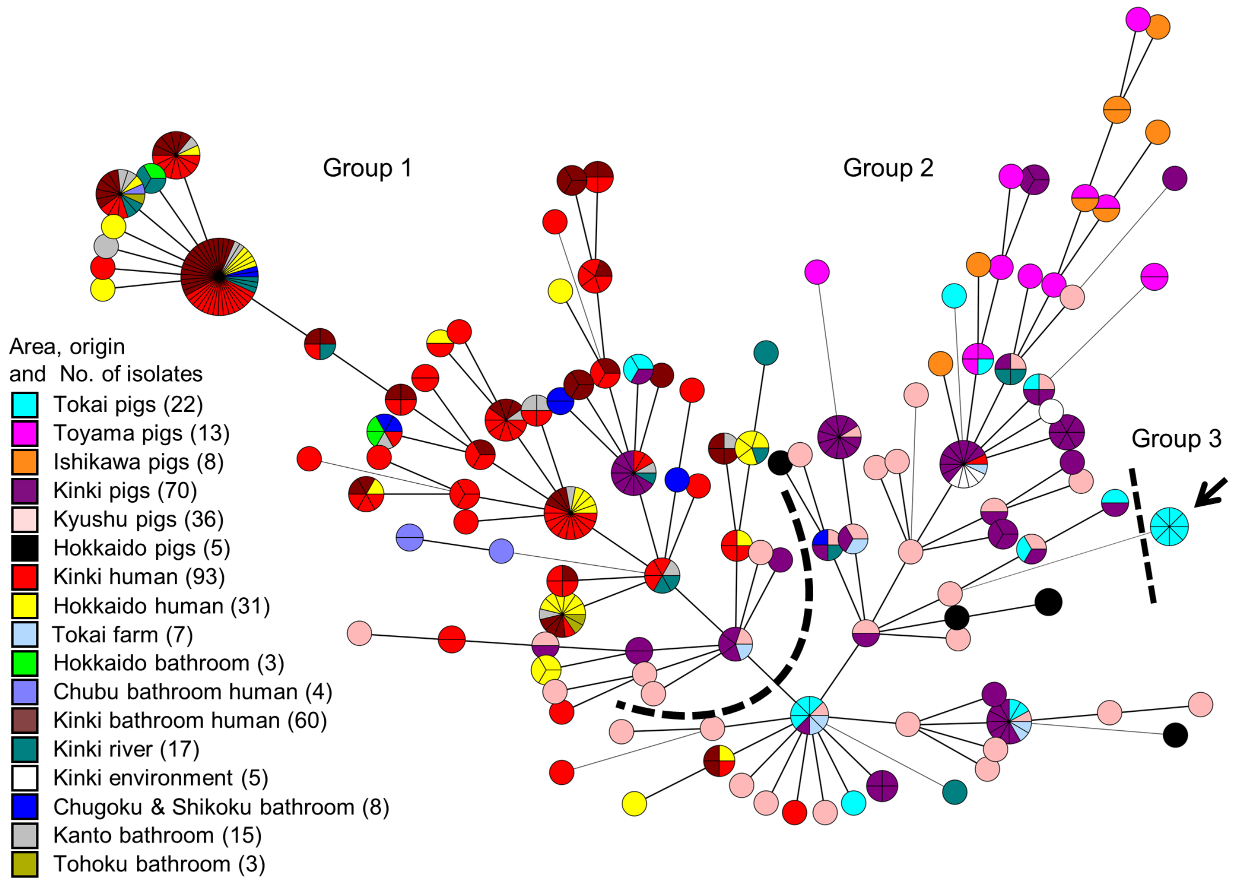
14: Ichikawa *et al*., 2015 Infect Genet Evol

16: Iwamoto *et al*., 2012 Infect Genet Evol

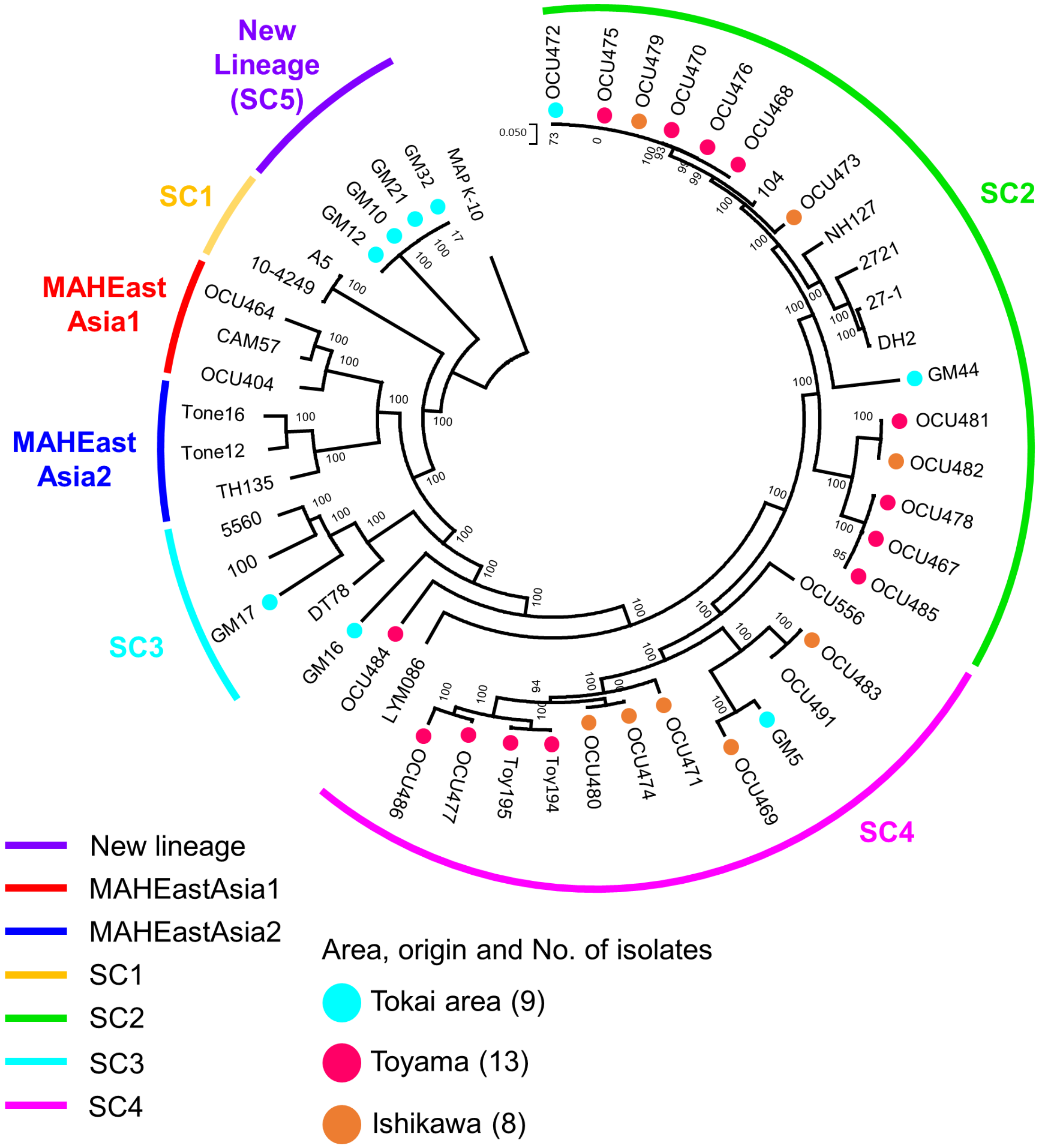
19: Subangkit *et al*., 2019 J vet med sci

23: Iwamoto *et al*., 2014 Infect Genet Evol

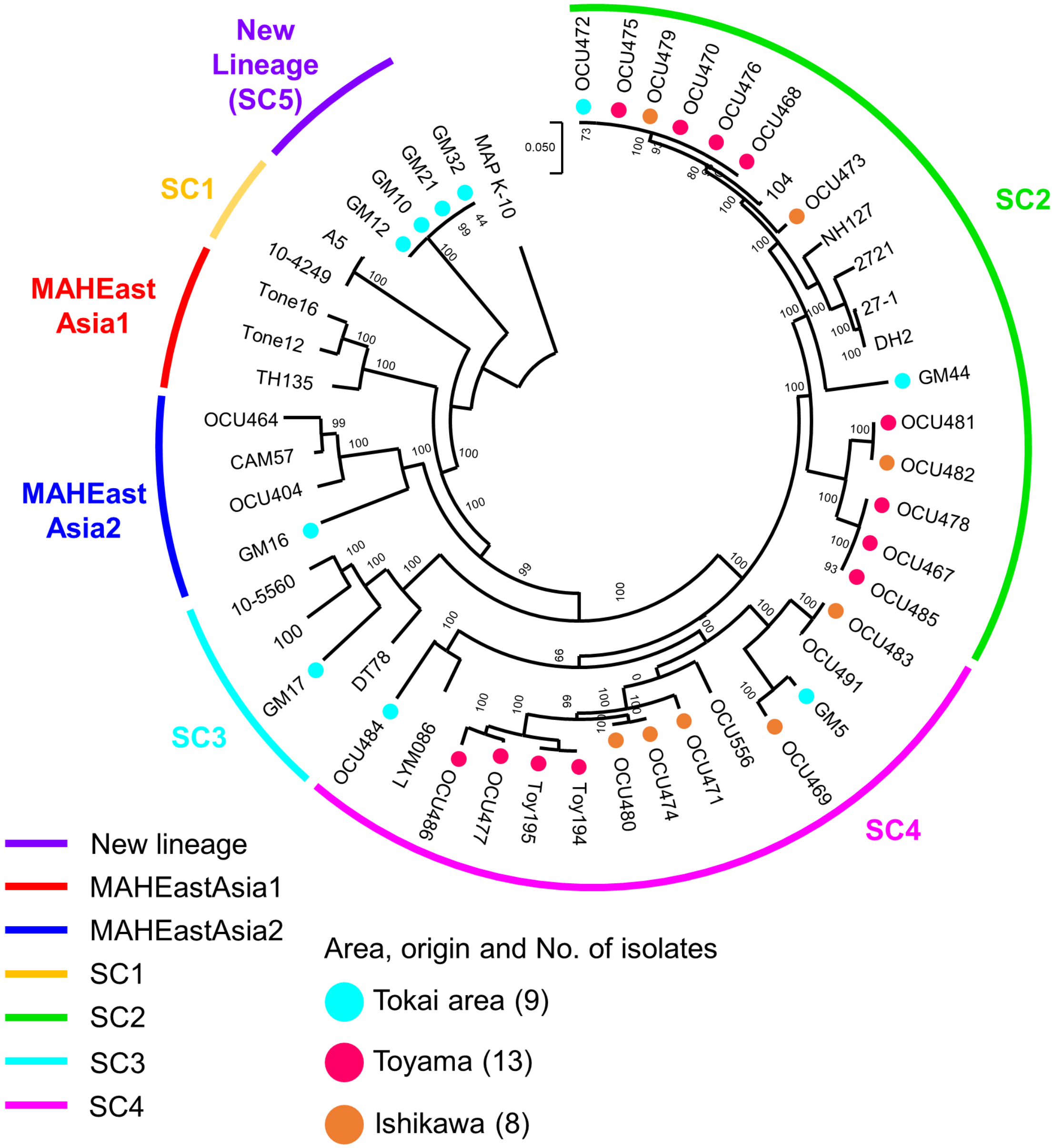
24: Starkova *et al*., 2013 Genetika



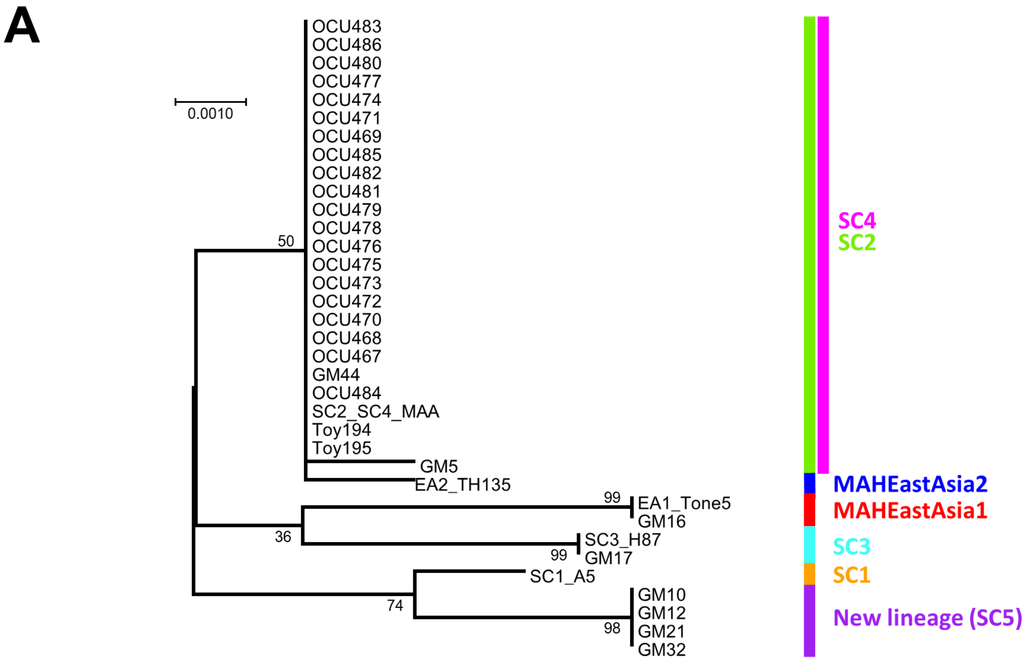
Supplementary Figure 2. Minimum spanning tree based on 7 loci Mycobacterial Interspersed Repetitive Unit VNTR genotyping of MAH isolates in Japan. Circles indicate different VNTR profiles. The size of each circle depended on the number of isolates sharing the same profiles. New lineages indicated by an arrow were clustered and consisted of isolates GM10, GM11, GM12, GM21, GM23, GM24, GM25, GM32.



Supplementary Figure 3. Phylogenetic tree based on draft genome sequences generated by CSIphylogeny. Maximum likelihood tree was generated by CSI phylogeny version 1.4 (25) and was visualized via MEGA 7.0. The area and Prefecture of isolates in this study were indicated by the color dots. Lineage classification except for new lineage was based on Yano *et al* (21).



Supplementary Figure 4. Phylogenetic tree based on draft genome sequences generated by IQ-TREE. Maximum likelihood tree was generated by IQ-TREE (26) and visualized via MEGA 7.0. The Area and Prefecture of isolates in this study were indicated by the color dots. Lineage classification except for new lineage was based on Yano *et al* (21).

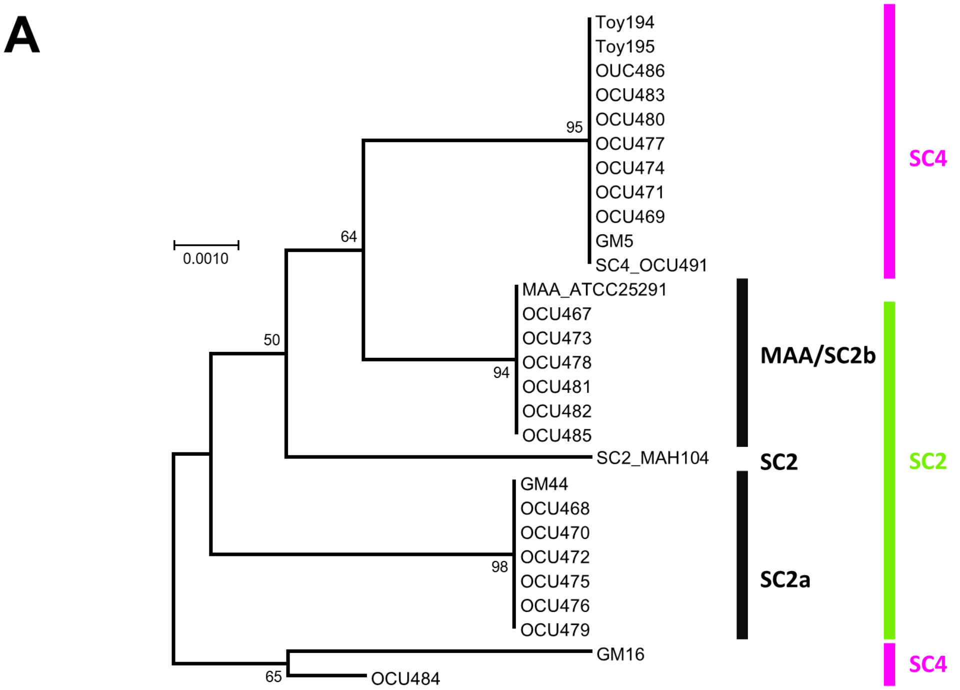


B

		SNP position	36	72	157	198	231	240	267	288	351	552	564	570	705	708	816	888	897	900	918	1077	1140	1239	1269	1317
Reference		EA1 (Tone5)	C	G	T	T	C	T	C	G	T	C	C	A	C	A	T	C	T	C	C	G	G	G	A	A
		EA2 (TH135)	C	G	T	T	C	C	C	A	C	C	G	G	C	A	T	C	C	G	G	G	G	G	G	G
		SC1 (A5)	C	T	T	C	T	C	G	G	C	C	G	G	C	A	T	C	C	G	C	C	C	A	A	G
		SC2/SC4/MAA	C	G	T	T	C	C	C	A	C	C	G	G	C	A	T	C	C	G	G	G	G	A	A	G
		SC3 (H87)	C	G	T	T	C	T	C	G	C	T	G	G	G	G	T	T	C	G	C	G	G	G	G	G
		MAS (ATCC49884)	C	G	T	T	C	C	C	A	C	C	G	G	C	A	C	C	C	G	G	G	G	A	A	G
		MAP (K10)	-	G	C	C	C	C	G	G	T	C	G	G	C	A	T	C	C	G	C	C	C	A	A	G
This study	New lineage (SC5)	GM10	T	G	T	C	C	C	G	G	T	C	G	G	C	A	T	C	T	C	C	C	C	A	A	G
		GM12	T	G	T	C	C	C	G	G	T	C	G	G	C	A	T	C	T	C	C	C	C	A	A	G
		GM21	T	G	T	C	C	C	G	G	T	C	G	G	C	A	T	C	T	C	C	C	C	A	A	G
		GM32	T	G	T	C	C	C	G	G	T	C	G	G	C	A	T	C	T	C	C	C	C	A	A	G
	SC2	GM44, OCU467 OCU468, OCU470 OCU472, OCU473 OCU475, OCU476 OCU478, OCU479 OCU481, OCU482 OCU485	C	G	T	T	C	C	C	A	C	C	G	G	C	A	T	C	C	G	G	G	G	A	A	G
	SC3	GM17	C	G	T	T	C	T	C	G	C	T	G	G	G	G	T	T	C	G	C	G	G	G	G	G
	SC4	GM5	C	G	T	T	C	C	C	A	C	C	C	A	C	A	T	C	C	G	G	G	G	A	A	G
		GM16	C	G	T	T	C	T	C	G	T	C	C	A	C	A	T	C	T	C	C	G	G	G	A	A
		OCU469, OCU471 OCU474, OCU477 OCU480, OCU483 OCU484, OCU486 Toy194, Toy195	C	G	T	T	C	C	C	A	C	C	G	G	C	A	T	C	C	G	G	G	G	A	A	G

Supplementary Figure 5. Allelic variants in *cinA* gene of pig MAH. A) Maximum likelihood tree generated by MEGA 7.0. Bootstrap values were calculated by 1,000 replications. The scale bar indicates genetic distance of each strain. Lineage classification except for new lineage was based on Yano *et al* (21). B) SNP cites in pig

MAH. New lineage shared the same SNP patterns, which were highlighted by gray. Some variations were detected in SC4. Reference SNP patterns were referred from Yano *et al* (21).

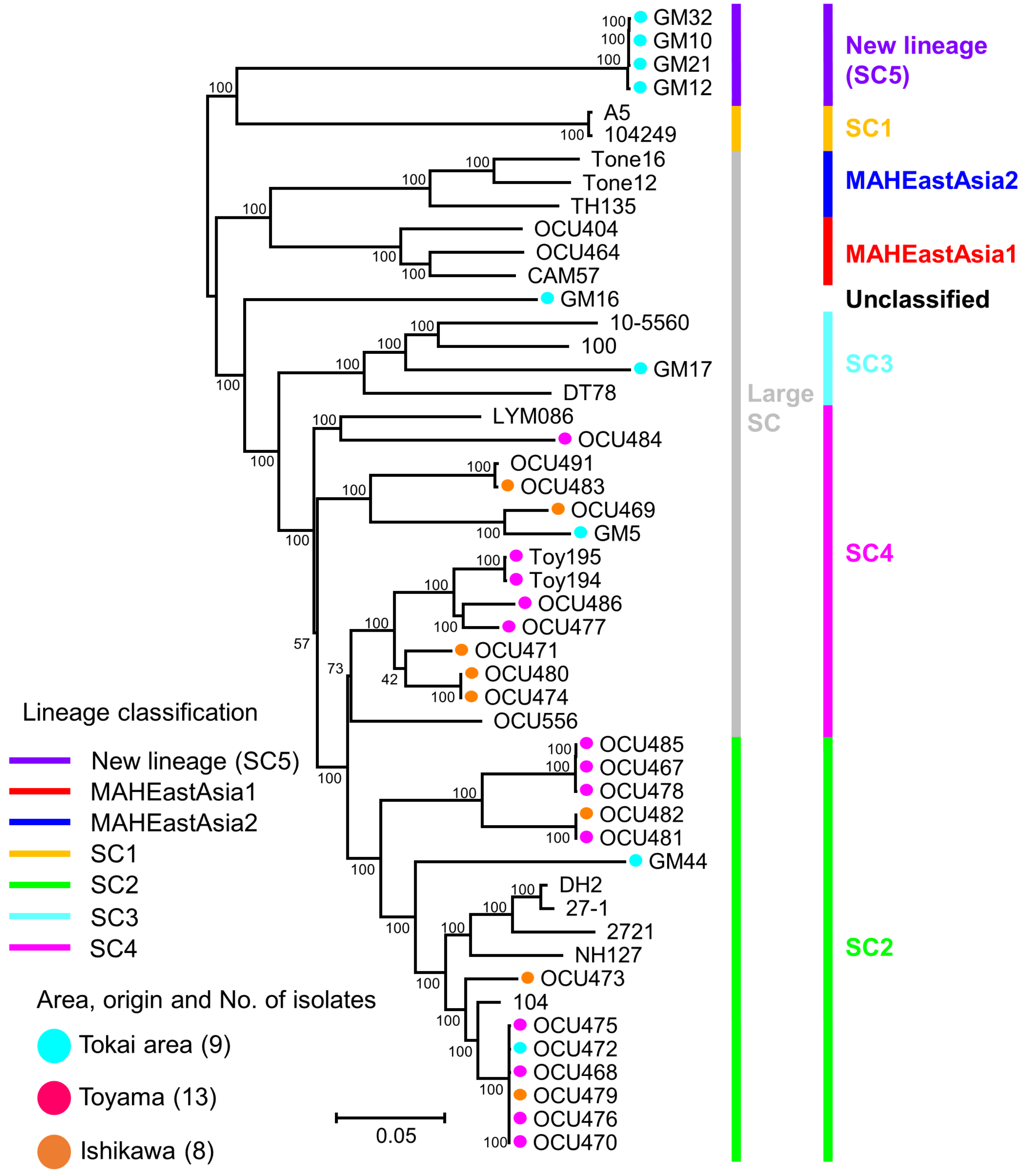


B

			SNP position	25	71	165	168	298	336	387	393	432	441	495	592	654	664	669	705	789	852	855	868
Reference			SC2 (Mah104)	C	T	T	C	A	G	G	G	C	C	G	C	C	T	A	C	A	A	C	G
			SC4 (OCU491)	C	C	C	T	G	G	G	A	C	C	C	C	C	T	A	C	G	C	C	G
			MAA (ATCC25291)	C	C	T	C	G	G	G	G	A	C	C	C	A	T	A	C	G	C	C	G
This study	New lineage (SC5)		GM10	C	C	C	T	G	C	G	A	C	C	C	C	A	T	A	C	G	C	C	G
			GM12	C	C	C	T	G	C	G	A	C	C	C	C	A	T	A	C	G	C	C	G
			GM21	C	C	C	T	G	C	G	A	C	C	C	C	A	T	A	C	G	C	C	G
			GM32	C	C	C	T	G	C	G	A	C	C	C	C	A	T	A	C	G	C	C	G
	SC2	SC2a	GM44, OCU468 OCU470, OCU472 OCU475, OCU476 OCU479	T	C	C	C	G	G	G	G	C	C	G	T	C	C	G	C	G	C	C	G
		SC2b	OCU467, OCU473 OCU478, OCU481 OCU482, OCU485	C	C	T	C	G	G	G	G	A	C	C	C	A	T	A	C	G	C	C	G
	SC3		GM17	C	T	T	C	G	G	G	G	C	C	C	C	C	T	A	T	G	C	C	G
	SC4		GM5, OCU469 OCU471, OCU474 OCU477, OCU480 OCU483, OCU486 Toy194, Toy195	C	C	C	T	G	G	G	A	C	C	C	C	C	T	A	C	G	C	C	G
			GM16	C	C	T	C	G	G	A	G	C	G	G	T	C	T	G	T	G	A	G	G
			OCU484	C	C	T	C	G	G	A	G	C	G	G	T	C	T	A	C	G	C	C	C

Supplementary Figure 6. Allelic variants in *sugA* gene of pig MAH. A) Maximum likelihood tree generated by MEGA 7.0. Bootstrap values were calculated by 1,000 replications. The scale bar indicates genetic distance of each strain. Lineage classification except for new lineage was based on Yano *et al* (21). B) SNP cites in pig

MAH. New lineage shared the same SNP patterns, which were highlighted by gray. Two type of SNP patterns were detected in SC2. Reference SNP patterns were referred from Yano *et al* (21).



Supplementary Figure 7. Lineage classification by fastBAPS. Lineage classification was predicted by fastBAPS (27). Bootstrap values were calculated by 1,000 replications. The scale bar indicates genetic distance of each strain. Lineage classification in the right side except for new lineage was based on Yano *et al* (21). Neighbor joining tree was generated by via MEGA 7.0 using alignment file obtained from CSI phylogeny version 1.4 (25).

Supplementary Table 4. Uniquely present or absent genes in new lineage (SC5).

Absent/ Present*	Annotated protein	Genes on the genomic island (GI) / phage (Ph)				BLAST search result				
		GM10	GM12	GM21	GM32	Strain	Coverage	Identity	E-value	Accession
Absent gene (6)	hypothetical protein	-	-	-	-					
	Serine/threonine-protein kinase PknL	-	-	-	-					
	hypothetical protein	-	-	-	-					
	hypothetical protein	-	-	-	-					
	hypothetical protein	-	-	-	-					
	hypothetical protein	-	-	-	-					
Present gene (97)	hypothetical protein	-	-	-	-	MAH strain OCU464[a]	99%	100%	0.00E+00	CP009360
	hypothetical protein	-	-	-	-	MAH strain 101115[a]	99%	100%	2.00E-94	CP040255
	hypothetical protein	-	-	-	-	*Chloropicon primus* strain CCMP1205	2%	88.37%	0.031	CP031034
	IS*481* family transposase IS*Mav5*	GI	GI	GI	GI	MAH strain mc2 2500[a]	100%	99.02%	0.00E+00	CP036220
	hypothetical protein	-	-	GI	GI	*M. canettii* CIPT 140010059	100%	76.70%	7.00E-127	HE572590
	hypothetical protein	-	-	-	-	*M. colombiense* CECT 3035	83%	87.17%	3.00E-56	CP020821
	hypothetical protein	GI	GI	GI	GI	*M. sp.* KMS	100%	84.36%	0.00E+00	CP000518
	hypothetical protein	GI	-	-	GI	*M. sp.* KMS	98%	74.24%	5.00E-42	CP000518
	hypothetical protein	GI	GI	GI	GI	*M. sp.* KMS	75%	82.45%	0.00E+00	CP000518
	hypothetical protein	GI	GI	GI	GI	*M. branderi* JCM 12687	97%	83.72%	0.00E+00	AP022606
	hypothetical protein	GI	GI	GI	GI	Mycobacterium phage Dori	75%	67.58%	9.00E-54	NC_023703
	Tyrosine recombinase XerC	GI	GI	GI	GI	*M. chimaera* strain AUSMDU00007395	98%	68.74%	4.00E-146	CP045963
	Serine recombinase PinR	GI	GI	GI	GI	*Rhodococcus biphenylivorans* strain TG9	67%	69.21%	6.00E-39	CP022208
	hypothetical protein	GI	GI	GI	GI	*M. chimaera* strain AUSMDU00007395	96%	83.67%	5.00E-66	CP045963
	hypothetical protein	GI	GI	GI	GI	*Mycolicibacterium alvei* JCM 12272	25%	71.26%	2.00E-71	AP022565

hypothetical protein	GI	GI	GI	GI	PREDICTED: *Monopterus albus*	13%	93.75%	0.65	XM_020592160
hypothetical protein	GI	GI	GI	GI	*Hordeum vulgare* subsp. *vulgare*	7%	81.36%	0.017	AK376348
hypothetical protein	GI	GI	GI	GI	*M. marinum* M	79%	71.65%	1.00E-17	CP000854
hypothetical protein	GI	GI	GI	GI	*M. intracellulare* ATCC 13950	94%	73.97%	0.00E+00	CP003322
hypothetical protein	GI	GI	GI	GI	*Streptomyces sp.* RTd22	9%	100%	0.002	CP015726
hypothetical protein	GI	GI	GI	GI	*M. marinum* strain 1218R	75%	84.69%	3.00E-20	CP025779
hypothetical protein	GI	-	GI	GI	MAH strain MAC109[a]	100%	98.00%	1.00E-64	CP029332
IS*481* family transposase IS*3514*	GI	GI	GI	GI	Mycolicibacterium helvum JCM 30396	100%	79.17%	0.00E+00	AP022596
hypothetical protein	GI	GI	GI	GI	*M. shottsii* JCM 12657	17%	76.40%	2.00E-06	AP022572
Tyrosine recombinase XerC	GI	GI	GI	GI	*M. saskatchewanense* JCM 13016	99%	74.67%	1.00E-117	AP022573
hypothetical protein	GI	GI	GI	GI	*M. conspicuum* JCM 14738	50%	74.44%	4.00E-11	AP022613
hypothetical protein	GI	GI	GI	GI	*Rathayibacter sp.* VKM Ac-2804	23%	73.73%	2.00E-08	CP047420
hypothetical protein	GI	GI	GI	GI	*Rhodobacteraceae bacterium* SH-1	30%	84.62%	1.1	CP027665
Putative prophage phiRv2 integrase	GI	GI	GI	GI	*M. sp.* JS623	96%	74.40%	0.00E+00	CP003078
hypothetical protein	-	-	-	-	MAA strain DSM 44156	95%	80.62%	0.00E+00	CP046507
hypothetical protein	-	-	-	-	*Gordonia alkanivorans* strain YC-RL2	38%	66.40%	8.00E-04	CP027114
hypothetical protein	-	-	-	-	*Mycolicibacter hiberniae* JCM 13571	85%	67.13%	3.00E-28	AP022609
hypothetical protein	-	-	-	-	*Mycolicibacterium doricum* JCM 12405	78%	74.63%	3.00E-53	AP022605
hypothetical protein	-	-	-	-	*Mycolicibacter hiberniae* JCM 13571	23%	72.03%	1.00E-09	AP022609
hypothetical protein	-	-	-	-	*Mycolicibacter hiberniae* JCM 13571	43%	91.45%	3.00E-37	AP022609
hypothetical protein	-	-	-	-	MAP strain MAPK_JJ1/13	100%	100.00%	0.00E+00	CP033909
hypothetical protein	-	-	-	-	MAP strain DSM 44135	100%	100.00%	0.00E+00	CP053068
hypothetical protein	GI	GI	-	GI	MAH JP-H-1[a]	100%	96.19%	0.00E+00	AP020326
hypothetical protein	-	-	-	-	MAP strain Telford[a]	100%	99.42%	1.00E-78	CP033688

hypothetical protein	-	-	-	-	MAH strain 101115	100%	90.58%	0.00E+00	CP040255
Sulfate-binding protein	-	-	-	-	*M. colombiense* CECT 3035	99%	88.60%	0.00E+00	CP020821
putative sulfate transporter	-	-	-	-	*M. colombiense* CECT 3035	100%	89.45%	0.00E+00	CP020821
hypothetical protein	GI	-	-	GI	*Rhodococcus sp*. YL-1	4%	93.94%	0.053	CP017299
hypothetical protein	-	GI	-	GI	MAH strain OCU901s_S2_2s[a]	100%	99.37%%	2.00E-155	CP018014
hypothetical protein	GI	GI	GI	GI	*M. marinum* E11	74%	75.42%	6.00E-12	HG917972
hypothetical protein	GI	GI	GI	GI	MAA strain DSM 44156	73%	72.95%	3.00E-167	CP046507
Transcriptional regulator WhiB	GI	GI	GI	GI	*M. sp.* DSM 104308 isolate 901379	48%	76.00%	2.00E-15	LR130759
hypothetical protein	GI	GI	GI	GI	*Streptomyces cinereoruber* strain ATCC 19740	7%	94.12%	0.009	CP023693
hypothetical protein	GI	GI	GI	GI	*Sorangium cellulosum* So0157-2	5%	85.71%	0.002	CP003969
hypothetical protein	GI	GI	GI	GI	*Arthrobacter sp.* AQ5-05	13%	96.43%	0.59	CP046105
hypothetical protein	GI	GI	GI	GI	*M. sp.* DSM 104308 isolate 901379	29%	78.79%	4.00E-04	LR130759
hypothetical protein	GI	GI	GI	GI	MAA strain DSM 44156	64%	71.12%	4.00E-19	CP046507
hypothetical protein	GI	GI	GI	GI	*M. mantenii* JCM 18113	76%	68.65%	4.00E-56	AP022590
Putative 8-oxo-dGTP diphosphatase 3	GI	GI	GI	GI	*M. branderi* JCM 12687	83%	75.88%	6.00E-82	AP022606
hypothetical protein	GI	GI	GI	GI	*M. canettii* CIPT 140070010	99%	74.96%	2.00E-108	FO203509
hypothetical protein	GI	GI	GI	GI	*M. canettii* CIPT 140070010	71%	75.00%	2.00E-11	FO203509
hypothetical protein	GI	GI	GI	GI	*M. canettii* CIPT 140070010	81%	70.29%	1.00E-32	FO203509
hypothetical protein	GI	GI	GI	GI	*M. avium* strain RCAD0278	77%	90.48%	3.00E-48	CP016396
hypothetical protein	GI	GI	GI	GI	*M. mantenii* JCM 18113	89%	73.43%	9.00E-25	AP022590
hypothetical protein	GI	GI	GI	GI	MAH strain MAH11	60%	75.00%	8.00E-12	CP035744
hypothetical protein	GI	GI	GI	GI	MAA strain DSM 44156	52%	79.81%	5.00E-43	CP046507
hypothetical protein	GI	GI	GI	GI	*Burkholderia cenocepacia* strain FDAARGOS_734	9%	93.75%	0.080	CP054817
hypothetical protein	-	-	-	-	MAH strain MAH11[a]	100%	100%	0.000	CP035744

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hypothetical protein	-	-	-	-	MAH strain 101115	95%	91.77%	0.00E+00	CP040255
hypothetical protein	-	-	-	-	*M. indicus* pranii MTCC 9506	78%	84.44%	1.00E-31	CP002275
HTH-type transcriptional regulator MmpR5	-	-	-	-	MAH strain OCU901s_S2_2s[a]	100%	98.78%	0.00E+00	CP018014
hypothetical protein	-	-	-	-	MAP strain DSM 44135	100%	94.72%	0.00E+00	CP053068
hypothetical protein	GI	-	GI	-	MAA strain DSM 44156[a]	97%	95.69%	0.00E+00	CP046507
hypothetical protein	-	-	-	-	MAP strain DSM 44135[a]	99%	99.87%	0.00E+00	CP053068
hypothetical protein	-	-	-	-	*Mycobacteroides abscessus* strain 199	70%	67.25%	2.00E-26	CP029076
hypothetical protein	-	-	-	-	*M. canettii* CIPT 140070017	72%	66.59%	3.00E-52	FO203510
hypothetical protein	GI/Ph	Ph	-	GI	MAP strain DSM 44135	90%	83.81%	1.00E-75	CP053068
hypothetical protein	GI/Ph	Ph	Ph	GI/Ph	MAP strain DSM 44135	92%	82.86%	1.00E-62	CP053068
hypothetical protein	GI/Ph	Ph	Ph	GI/Ph	MAP strain DSM 44135	100%	94.60%	0.00E+00	CP053068
Tyrosine recombinase XerC	GI/Ph	Ph	Ph	GI/Ph	MAH strain MAC109	93%	84.51%	0.00E+00	CP029332
Tyrosine recombinase XerC	GI/Ph	Ph	Ph	GI	*M. saskatchewanense* JCM 13016	78%	70.50%	3.00E-102	AP022573
hypothetical protein	GI/Ph	Ph	Ph	GI/Ph	*Sphingomonas panacis* strain DCY99	23%	79.71%	0.002	CP014168
F420H(2)-dependent biliverdin reductase	GI	GI	GI	GI	MAH JP-H-1[a]	98%	98.04%	2.00E-39	AP020326
hypothetical protein	-	-	-	-	MAA strain DSM 44135[a]	100%	99.33%	2.00E-67	CP046507
Tyrosine recombinase XerC	-	-	-	-	*Mycolicibacterium sarraceniae* JCM 30395	99%	78.02%	0.00E+00	AP022595
hypothetical protein	-	-	-	-	*Burkholderia sp.* MSMB0266	13%	81.54%	0.009	CP013417
hypothetical protein	-	-	-	-	MAP strain Telford	100%	99.31%	0.00E+00	CP033688
hypothetical protein	-	-	-	-	MAP strain DSM 44135	100%	99.66%	0.00E+00	CP053068
hypothetical protein	GI	-	GI	GI	MAP strain DSM 44135	100%	95.46%	0.00E+00	CP053068
hypothetical protein	GI	-	GI	GI	MAP strain DSM 44135	100%	98.62%	0.00E+00	CP053068
hypothetical protein	GI	-	GI	GI	MAP strain DSM 44135	100%	98.83%	0.00E+00	CP053068
hypothetical protein	GI	-	GI	GI	MAP strain DSM 44135	100%	95.08%	3.00E-74	CP053068

hypothetical protein	GI	-	GI	GI	*M. xenopi* JCM 15661T	66%	91.05%	0.00E+00	AP022314
hypothetical protein	-	-	GI	-	MAH strain MAH11[a]	99%	100%	3.00E-120	CP035744
hypothetical protein	-	-	GI	-	MAP strain DSM 44135	100%	99.06%	3.00E-100	CP053068
hypothetical protein	-	-	GI	-	MAA strain DSM 44135[a]	100%	97.38%	2.00E-180	CP053068
hypothetical protein	-	-	-	-	MAH TH135[a]	100%	95.24%	8.00E-88	AP012555
hypothetical protein	-	-	-	-	MAP strain DSM 44135	100%	99.33%	2.00E-67	CP053068
hypothetical protein	-	-	-	-	MAP strain DSM 44135	100%	98.51%	0.00E+00	CP053068
Methyl-branched lipid omega-hydroxylase	-	-	-	-	MAP strain DSM 44135	100%	98.95%	0.00E+00	CP053068
hypothetical protein	-	-	-	-	MAP strain DSM 44135	100%	98.85%	0.00E+00	CP053068
hypothetical protein	GI	GI	-	GI	MAH TH135[a]	100%	99.11%	0.00E+00	AP012555

[a]: The genes which had more than 95% coverage and similarity with MAH strain via BLAST analysis.

Supplementary Table 5. Geographic and host features of MAH lineages.

Lineage		Geographical origin	Host or niche	Notable feature of the chromosome
EastAsia	EA1*	Japan, Korea	Human adult, bathroom	Highly mosaic
	EA2*	Japan, Korea	Human adult, bathroom	Relatively few imports, inversion
SC1		USA	Little information	Little information
SC2/4	SC2*	Germany, Belgium, the Netherlands, Russia, USA, Japan (pig)	Human adult and child, soil, dust, pig	Relatively few imports
	SC4*		Animals, soil, dust, human adult and child	Close relative of SC2, highly mosaic
SC3		USA, Germany, Japan (pig)	Animals, water, soil, human	Highly mosaic
SC5		Japan (pig)	Pig	Close

*: Lineage East Asia and SC2/4 was divided into two lineages respectively in the past study (21).

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