

Supplementary table 3

ID	Sample type	Isolation year	Farm/Province*	Allele**							Sequence type**	PubMLST ID
				<i>dnaA</i>	<i>ftsY</i>	<i>fusA</i>	<i>gyrB</i>	<i>recA</i>	<i>rpoB</i>	<i>uvrA</i>		
Au1	joint	2021	Ybbsitz	9	2	6	12	9	14	15	38	60
Au2	joint	2022	Weitersfeld	10	18	3	8	9	14	7	52	62
Au3	joint	2020	Thanstetten I	12	17	6	6	1	6	4	37	44
Au8	joint	2019	Leibnitz	15	10	9	8	17	9	14	35	89
Au18	joint	2022	Wettmannstätten	7	21	14	12	6	7	22	57	91
Bl 1	tonsil	2023	no data	10	14	6	8	9	21	4	74	97
Bl 5	tonsil	2023	no data	20	16	6	1	16	14	17	75	98
Bl 10	tonsil	2023	no data	17	11	15	8	9	14	11	81	99
Bl 14	tonsil	2023	no data	20	16	6	1	16	14	17	75	100
Bl 18	tonsil	2023	no data	15	5	6	12	9	22	7	76	101
Ge 1	joint	2020	Neustadt am Rübenberge	2	3	6	11	6	1	15	77	102
Ge 4	blood	2022	Donauwörth	10	14	6	12	9	14	15	78	103
Ge 12	blood	2020	Fürstenau	18	13	14	1	1	23	17	79	104
Ge 20	joint	2022	Beckum	21	13	4	1	1	9	7	80	105
Ge 24	joint	2019	Wennigsen	27	5	21	1	14	26	25	91	116
Hu 1	joint	2018	Bácsalmás	1	1	1	1	1	1	1	1	106
Hu 5	lung	2021	Pásztó	2	24	6	16	9	9	17	82	107
Hu 10	tonsil	2023	Kunszentmárton	2	25	13	12	9	14	15	83	108
Hu 15	tonsil	2023	Nyárád	18	3	13	12	9	14	17	84	109
Hu 21	joint	2023	Hajdúböszörmény	2	26	6	10	18	11	14	85	110
It 1	lung	2018	Bolzano	14	16	6	8	6	24	17	86	111
It 6	joint	2020	Pordenone III	11	27	6	11	17	25	10	87	112
It 9	joint	2022	Udine I	18	5	9	12	2	1	24	88	113
It 15	tonsils	2023	Mantova	25	15	13	12	9	14	1	89	114
It 20	tonsils	2023	Cremona II	26	28	9	8	9	9	1	90	115

*Province in case of the Italian isolates

**New allele types and sequence types are highlighted by red and bold numbers