Table 4. Characteristics of the 20 lineage-defining large sequence polymorphisms (LSPs) found in *M. tuberculosis*

RD	Start	Stop	Size, bp	Affected ORF(s)	Forward (F) and reverse (R) PCR Primers (5'-3')	AT	Expected PCR product size, bp		Comment	Ref.
							H37Rv	deleted		1
105	79567	83034	3,467	Rv0071-Rv0074	F: GGAGTCGTTGAGGGTGTTCATCAGCTCAGTC R: CGCCAAGGCCGCATAGTCACGGTCG	64	4252	785		1
115	453364	455971	2,607	Rv0376c-Rv0378	F: TTCGGGGGCCAGGTCGTTGAT R: CCGCGGGAATGCCTGCTGTTAT	64	3442	835		1
122	669793	670964	1,171	Rv0576	F: GCCGGCACCGCTAATCGCTACTT R: TTCTCTTGGGCATGATCATCCTTTCGTTA	64	1456	285		1
142	1332182	1335033	2,851	Rv1189-Rv1192	F: TCCGCGACGACGAACAACGAC R: TCACTTCCATTTCCAGCGGCAACT	64	3634	783		1
150	1896862	1899349	2,487	Rv1671-Rv1674c	F: TGTGGCGTGGCTCGGCAAATAG R: CGGGACGGCAAACGGGTGAT	64	3266	779		1
174	2237049	2240699	3,650	Rv1992c-Rv1997	F: GGTGCCCTCCCGCAGAACTGTG R: AGCGCGATCGCAGCGGTGAA	64	4524	874		1
181	2535429	2536140	711	Rv2262c-Rv2263	F: CGCAACGGCCGCGGTGAACTCT R: CGGGCGGCTGCGGGAACCTT	62	1712	1001		1
182	2545194	2551674	6,480	Rv2270-Rv2280	F: TGTTATACGCCCTGTCGGCGGTCACCAT R: GCGCATCCCGCCGGCGTTGGTT	64	7292	812		1
183	2585853	2588770	2,917	Rv2313c-Rv2315c	F: CCGAACCGCCCGCATCAAG R: ACGACGGCCGAAACCACAGGAA	64	3965	1048		1
193	2704306	2704807	501	Rv2406c-	F: CCGACTACGCCTGGCGCTAAACC	64	1308	807		1

RD	**Start**	**Stop**	**Size, bp**	**Affected ORF(s)**	**Forward (F) and reverse (R) PCR Primers (5'-3')**	**AT**	**Expected PCR product size, bp**		**Comment**	**Ref.**
				Rv2407	R: GTAGGGGCCACCCGGATTGTCAC					
207	3120521	3127920	7,399	Rv2814c-Rv2820c	F: GACGAGTTCGCGCTCAAAATGT R: CCCCGGCGAGGAACAGAA	64	8,577	1,178		1
219	3448504	3451396	2,892	Rv3083-Rv3085	F: GCGTCGGTGCCCAGTTGC R: GCGACGGCGGTTTTGATGC	64	3,609	717		1
239	4092077	4092919	842	Rv3651	F: GGCCAACATCGACCACCTACCC R: ATCCTCGCTACCGGCACCTCAT	64	1,730	888		1
702	216795	218516	1,722	Rv0186	F: TTCCGAGGACCCGTTGTTGAGTGC R: GGGCGGGTTGGGTTGCTGGTC	64	2,088	718	217874-217522 rearranged sequence	2
711	1501713	1503655	1,943	Rv1333-Rv1336	F: GGCCGCCCTGCTCAAGAACCT R: CCTAGGCCGGCGACGAAGTG	64	2,884	941		2
724	2265112	2266239	1,128	Rv2018-Rv2019	F: CCATGCGATTTGACTTCCGATTGA R: ATATACCGTGCCGCGACTTGCTCT	64	1,288	≈1,650	insertion of IS*6110*	2
726	3904958	3906706	1,749	Rv3485c-Rv3487c	F: GCCCGGGCGGATGCTGTT R: CGGCGGCGCGTTTGTCA	64	2,062	313		This study
750	1710767	1711556	790	Rv1519-Rv1520	F: GTCGGCGGTCTGCTTCGTTCC R: CCTGTCGGCCGGGTGTCTTTC	64	1,533	743		This study
761	1502787	1503881	1,094	Rv1334-Rv1336	F: GCCGGCGTGCTCAATGCTCAG R: CCTAGGCCGGCGACGAAGTGC	60	1,389	295		This study

RD	Start	Stop	Size, bp	Affected ORF(s)	Forward (F) and reverse (R) PCR Primers (5'-3')	AT	Expected PCR product size, bp		Comment	Ref.
*pks*15/1 7bp del.	na	na	7	Rv2946c-Rv2947c	F: CTGGGTTGGCCTGCACGTGGGCCATAA R: GCCCCCGCAGAGGCGCCGGTT	62	143	143		3

RD, region of difference; AT, annealing temperature; na, not applicable.

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