S1 Table. Pairwise similarities between mycobacterial genomes. The matrix reflects the number of orthologous clusters having representation from any two given mycobacterial species. The maximum similarity in terms of having the maximum number of orthologous pairs between two genomes is marked in bold red and is represented row-wise.

	MYCTU	MYCS2	MYCUA	MYCA9	MYCTU	MYCA9	MYCLE	MYCKA	MYCVP	MYCMM
MYCTU	-	2507	2614	2245	2341	2590	1399	2991	2533	**2999**
MYCS2	2507	-	2673	3028	3312	3104	1318	3111	**3995**	3181
MYCUA	2614	2673	-	2340	2441	2759	1356	3094	2701	**3668**
MYCA9	2245	**3028**	2340	-	2488	2578	1262	2584	2864	2692
MYCTH	2341	**3312**	2441	2488	-	2879	1285	2822	3317	2839
MYCA1	2590	3104	2759	2578	2879	-	1341	**3294**	3089	3261
MYCLE	1399	1318	1356	1262	1285	1341	-	1398	1324	**1413**
MYCKA	2991	3111	3094	2584	2822	3294	1398	-	3166	**3808**
MYCVP	2533	**3995**	2701	2864	3317	3089	1324	3166	-	3213
MYCMM	2999	3181	3668	2692	2839	3261	1413	**3808**	3213	-

MYCTU: *M.tuberculosis*, MYCS2: *M. smegmatis*, MYCUA: *M. ulcerans*, MYCA9: *M. abscessus*, MYCTH: *M. thermoresistible*, MYCA1: *M. avium*, MYCLE: *M.leprae*, MYCKA: *M. kansasii*, MYCVP: *M. vanbaalenii*, MTCMM: *M. marinum.*