

**Table 1.** Best 50 TRs found on *M. tuberculosis* H37Rv complete genome

start	end	length	repeat	score	ins	del	match	mism	A%	C%	G%	T%	word	nesting
374509	374720	30	7.1	620	0	0	182	30	11.8	21.7	37.7	28.8	aagctgcccgg...	
424010	424141	51	2.6	810	0	0	132	0	16.7	26.5	49.2	7.6	aacggcgcag...	
425450	425590	30	4.7	870	0	0	135	6	12.8	27.0	35.5	24.8	aagtcgcccga...	
426761	426868	30	3.6	580	0	0	103	5	15.7	23.1	40.7	20.4	aacaagcccgg...	
531461	531637	15	11.8	620	0	0	152	25	7.9	29.9	34.5	27.7	atgttgcgcg...	
569819	569976	56	2.8	980	0	0	157	1	14.6	40.5	40.5	4.4	aatccagctt...	
577284	577494	58	3.6	1530	0	0	211	0	23.2	23.7	42.2	10.9	aaggagtgtg...	
580575	580812	77	3.1	1610	0	0	238	0	18.5	26.1	42.4	13.0	accacccgct...	
631280	631425	12	12.2	700	0	0	130	16	17.8	49.3	29.5	3.4	accacgcccg...	*
631280	631434	36	4.3	830	0	0	146	9	19.4	49.0	28.4	3.2	aacgaccccg...	
960165	960321	53	3.0	1040	0	0	157	0	9.6	40.1	28.0	22.3	aatggcgcgg...	
964578	964861	24	11.0	830	2	2	237	17	7.4	27.5	53.2	12.0	aggtcggcgg...	
1262916	1263043	30	4.3	540	0	0	117	11	19.5	20.3	35.9	24.2	aagaagcccga...	
1263092	1263185	30	3.1	560	0	0	92	2	17.0	23.4	29.8	29.8	aatgcccagg...	
1305493	1305659	62	2.7	1010	0	0	166	1	12.0	31.7	44.3	12.0	aatctggcct...	
1451777	1451993	57	3.8	1600	0	0	217	0	10.6	24.0	51.2	14.3	aagcgcggcg...	
1630957	1631103	9	16.0	580	1	0	128	16	3.4	43.5	38.8	14.3	ccgcccgtg	
1773958	1774104	15	9.8	800	0	0	134	13	6.8	29.3	45.6	18.4	acgggcgctt...	
1895351	1895589	57	4.2	1820	0	0	239	0	12.1	26.4	47.3	14.2	acgatgcggg...	
1982018	1982223	75	2.7	1190	0	0	203	3	12.1	6.8	56.8	24.3	aagccggtga...	
1982885	1983323	78	5.6	3410	0	0	434	5	16.4	24.1	42.6	16.9	aacccgggca...	
2074434	2074631	56	3.5	1380	0	0	197	1	15.7	29.8	49.5	5.1	aagcgcggag...	
2163333	2163528	69	2.8	790	0	0	184	12	29.1	30.1	25.0	15.8	aaaccagggg...	
2163729	2164083	69	5.1	2820	0	0	354	1	32.1	33.0	22.0	13.0	aacggaatac...	
2165325	2165581	75	3.4	1700	0	0	254	3	28.8	35.4	23.0	12.8	aaacgggcct...	
2168952	2169166	78	2.8	770	0	0	200	15	23.7	33.5	26.5	16.3	aaacgcaccc...	
2347393	2347611	57	3.8	1580	0	0	218	1	14.2	44.3	29.2	12.3	aacaagtggc...	
2461324	2461502	57	3.1	1220	0	0	179	0	25.7	35.8	35.2	3.4	aatcaagca...	
2531891	2532207	53	6.0	2520	0	0	314	3	9.1	44.5	21.8	24.6	accggcgcga...	
2996001	2996165	51	3.2	1140	0	0	165	0	18.8	30.9	40.0	10.3	acctccgccc...	
3007035	3007217	53	3.5	1300	0	0	183	0	6.0	42.6	29.5	21.9	actggcgcgg...	
3155880	3156086	54	3.8	1530	0	0	207	0	14.5	35.3	43.0	7.2	aagcgcgggg...	
3171465	3171623	54	2.9	1050	0	0	159	0	19.5	35.2	39.6	5.7	aagcgcggcg...	
3192196	3192350	53	2.9	1020	0	0	155	0	8.4	47.1	23.2	21.3	aacctctctc...	
3232648	3232863	56	3.9	1560	0	0	215	1	15.7	41.2	36.1	6.9	aagcgcggcg...	
3239468	3239785	79	4.6	1630	0	2	316	2	22.0	34.0	34.0	10.1	aaccagtgat...	
3336501	3336795	59	5.0	2280	0	0	293	2	12.5	33.9	42.4	11.2	aagcgcggcg...	
3343351	3343441	27	3.4	560	0	0	89	2	0.0	35.2	37.4	27.5	ccgccttctt...	
3594260	3594452	56	3.4	1210	0	0	189	4	15.5	47.7	23.3	13.5	aacgggcccga...	
3663724	3663991	63	4.1	1330	1	0	248	11	31.3	21.6	36.2	10.8	aacaatccgg...	
3663751	3663857	36	3.0	710	0	0	107	0	35.5	19.6	36.4	8.4	aacaatccgg...	*
3738610	3738900	9	32.0	590	1	1	238	47	3.4	44.7	36.8	15.1	ccgccgttg	
3820387	3820585	57	3.5	1120	1	0	193	4	16.6	30.7	42.2	10.6	aatcgctta...	
3928262	3928352	9	10.1	620	0	0	86	5	20.9	33.0	42.9	3.3	aacggcggc	
3943693	3944049	9	39.3	840	1	0	292	62	15.4	34.5	46.8	3.4	aacggcggc	
3944247	3944591	9	37.0	540	3	0	276	57	11.0	35.4	49.3	4.3	accggcggc	
3948444	3949270	9	88.9	860	7	0	648	152	15.0	36.2	45.1	3.7	accggcggc	
3949644	3949870	9	24.9	660	1	0	190	34	14.5	36.6	46.7	2.2	accggcggc	
4156796	4156964	59	2.9	1100	0	0	169	0	17.8	43.2	31.4	7.7	aacgcgggcg...	
4353277	4353428	51	3.0	810	0	0	147	5	23.7	55.3	15.1	5.9	aaaccacca...	

**Table 2.** Best 50 TRs found on *P. falciparum* chromosome 2

start	end	length	repeat	score	ins	del	match	mism	A%	C%	G%	T%	word	nesting
1	1153	21	55.0	6410	4	18	1081	54	39.2	41.5	4.9	14.5	aaaccctaaa...	
1	1153	7	167.9	6250	1	21	1083	69	39.2	41.5	4.9	14.5	aaaccct	*
1152	1826	14	48.2	2610	0	0	575	100	16.6	26.8	0.9	55.7	actcttactt...	*
1152	1854	42	17.1	3370	0	1	628	75	16.4	26.7	1.1	55.8	actcttactt...	
10514	12197	12	138.6	4660	6	0	1387	276	41.4	24.9	6.2	27.5	aacatgatta...	
13791	15789	21	95.3	3720	2	1	1605	392	31.1	19.7	12.4	36.9	aacttaggtc...	
15940	17287	21	64.3	3030	3	3	1107	238	29.4	20.6	12.2	37.8	aacataggtc...	
17592	21161	21	170.0	4880	5	3	2823	741	33.1	17.9	14.8	34.2	aacataggtc...	
91506	94675	39	81.3	26430	0	0	3048	122	20.2	17.2	15.0	47.7	aaaccagtat...	
94896	95457	57	9.9	4090	0	0	538	24	18.7	18.5	5.7	57.1	aatccttcag...	
95476	96669	66	18.1	7400	0	0	1097	97	20.0	18.9	11.9	49.2	aaatcagttt...	
122415	122731	12	26.4	1810	0	0	286	31	66.2	8.2	20.8	4.7	aaagaagatg...	*
122415	122734	24	13.3	2240	0	0	302	18	66.6	8.1	20.6	4.7	aaaaagacaa...	
123216	123455	36	6.7	1840	0	0	235	5	47.9	13.8	8.8	29.6	aaaaacaaat...	
131496	131886	48	8.1	2030	1	0	357	31	26.9	25.1	0.8	47.3	aaaaaaaaatt...	
145060	145386	33	9.9	1860	0	0	300	27	22.6	17.1	5.8	54.4	aacgtatttaa...	
169215	169434	27	8.1	1770	0	0	216	4	26.8	37.3	0.0	35.9	acatcctcat...	
183425	183649	18	12.5	1710	0	0	216	9	18.2	26.7	8.0	47.1	acatttgcat...	
202471	202685	21	10.2	1860	0	0	213	2	41.9	4.7	0.9	52.6	aatattatca...	
215427	215762	51	6.7	1710	0	2	314	22	25.3	22.6	3.3	48.8	aaaaatatttt...	
224939	225243	27	11.3	2020	0	0	286	19	29.5	7.9	8.9	53.8	acataattatg...	
265052	265318	18	14.8	2170	0	0	259	8	28.1	15.0	6.4	50.6	acactgttta...	
266304	266619	24	13.2	1720	0	0	286	30	25.0	20.3	8.5	46.2	actactgtgc...	*
266312	266663	60	5.9	1840	0	0	325	27	24.7	21.3	8.2	45.7	accacttgcc...	
338888	339396	60	8.5	3850	0	0	493	16	53.8	11.0	8.8	26.3	aaaataagtg...	
419342	419584	21	11.6	1700	0	0	230	13	28.0	10.3	18.1	43.6	actattatgt...	
494529	494894	22	16.8	2550	0	3	352	14	46.7	4.6	2.5	46.2	aaacataata...	
496764	496975	18	11.8	1740	0	0	207	5	32.1	11.8	11.3	44.8	atatgcatca...	
564077	564366	30	9.7	2000	0	0	275	15	31.4	8.6	5.2	54.8	atatgattat...	
580114	580664	15	36.7	3520	0	0	505	46	42.6	4.2	17.6	35.6	aataataata...	
584561	584939	24	15.8	1670	0	0	332	47	45.4	5.5	25.3	23.7	aaaaggtaaa...	
636849	637281	24	17.7	2930	3	0	407	17	28.6	12.7	9.5	49.2	acataatggta...	
643885	644202	18	17.7	1920	0	0	291	27	18.2	11.6	12.9	57.2	atgttcgtca...	
659026	659355	48	6.9	2740	0	0	328	2	65.2	2.1	20.0	12.7	aaaaaaaaacaa...	
662459	662712	24	10.6	2220	0	0	252	2	46.1	7.9	20.1	26.0	aaaaatagaa...	
697881	698238	15	23.9	1990	0	0	322	36	30.2	11.2	18.7	39.9	acaggtatga...	
727107	727368	18	14.6	1960	0	0	250	12	45.0	11.8	0.0	43.1	aataatatta...	
797665	798652	24	41.2	5920	0	0	895	93	36.1	12.6	25.5	25.8	aaattgtagc...	
806101	806376	18	15.3	1940	0	0	260	16	51.1	17.0	10.5	21.4	aaaaagtaaa...	
812113	812599	36	13.4	2370	3	0	438	43	47.4	4.7	9.7	38.2	aaaatgtttt...	
824205	824471	18	14.8	2210	0	0	260	7	12.0	15.0	9.7	63.3	attgtgttct...	
869891	870246	18	20.1	2240	0	2	334	22	17.7	11.0	7.9	63.5	atatttgatt...	
925762	926041	22	12.7	2500	0	0	278	2	40.0	28.6	13.6	17.9	aagtcgcacc...	
927519	930156	21	125.8	3430	0	3	2078	560	35.9	14.3	17.9	32.0	aagacctatg...	
930523	934672	42	98.2	6290	7	1	3282	821	36.6	12.6	19.3	31.6	aaaagtaaga...	
930523	934672	21	197.4	6210	5	0	3283	862	36.6	12.6	19.3	31.6	aagacctaaag...	*
934750	936763	24	84.0	5570	6	2	1672	324	28.3	6.6	24.3	40.9	aatgatgtta...	
934760	936757	12	164.8	5460	7	0	1645	332	28.4	6.6	24.2	40.9	aatcatgtta...	*
946086	946547	56	8.8	1740	1	2	415	33	55.8	1.1	26.6	16.5	aaaagtaaga...	
946547	947091	7	78.1	4140	0	1	517	28	14.3	4.6	42.8	38.3	agggttt	

**Table 3.** Best 50 TRs found on *P. falciparum* chromosome 3

start	end	length	repeat	score	ins	del	match	mism	A%	C%	G%	T%	word	nesting
1	276	7	39.1	1550	2	2	256	16	38.8	42.8	4.3	14.1	aaaccct	
9200	10615	96	15.0	4100	8	4	1208	145	41.6	25.1	6.3	27.0	aacaacatca...	
9202	10607	12	116.9	3390	4	3	1156	238	41.6	25.1	6.3	27.0	aacatgatta...	*
9215	10615	36	39.5	4010	5	6	1183	179	41.5	25.1	6.4	27.0	aacaacatca...	*
16386	20340	21	188.5	7750	6	1	3182	767	31.9	20.2	12.6	35.3	aacttaggtc...	
20406	22960	21	121.6	4680	5	1	2052	498	31.0	20.0	13.1	36.0	aactaactta...	
23279	24068	21	37.6	1530	0	0	636	154	31.0	18.9	12.7	37.5	aacttaggtc...	
24182	26134	21	93.2	2210	4	1	1538	411	33.4	18.6	12.9	35.1	aacataggtc...	
27926	28273	21	16.7	1540	0	3	313	35	31.0	9.2	24.7	35.1	aaggtaaagta...	
29048	29916	21	41.5	2660	1	1	729	139	33.3	19.2	12.5	35.0	aactaactta...	
30010	30768	72	9.0	2710	5	0	613	37	37.0	14.1	19.5	29.4	aaagtaggtc...	
190811	191089	28	10.0	2230	0	0	272	7	48.7	13.3	1.8	36.2	aaatttatac...	
218379	218881	12	41.9	3310	0	0	463	40	12.5	9.1	32.0	46.3	atttgggttt...	
248556	249004	33	13.6	3240	0	0	426	23	52.1	3.8	14.9	29.2	aaaataaatg...	
320474	320705	18	12.9	1580	0	0	218	14	27.6	9.9	6.5	56.0	atattattcg...	
320474	320705	9	25.8	1550	0	0	215	17	27.6	9.9	6.5	56.0	atattatttc	*
327621	327869	15	16.6	1820	0	0	236	13	28.9	25.3	22.5	23.3	acattagctg...	
330117	330548	42	10.3	2980	0	0	409	23	29.9	17.8	10.0	42.6	accatcacca...	
334389	334611	24	9.3	1750	0	0	217	6	53.8	29.6	4.0	12.6	aaacaactca...	
344611	344819	18	11.6	1550	0	0	200	9	17.7	16.7	1.4	64.1	atatcatttt...	
345562	345759	24	8.2	1500	0	0	192	6	32.3	11.1	4.0	52.5	aaatattatt...	
390601	390893	18	16.3	1670	0	0	266	27	24.2	14.3	9.9	51.5	accgttcattg...	
395394	396037	12	53.7	5200	0	0	616	28	34.3	21.4	16.8	27.5	aatcaactgag...	
413015	413228	21	10.2	1690	0	0	208	6	36.0	18.7	2.3	43.0	aatatatatc...	
431462	431891	21	20.5	2170	0	0	382	48	41.9	10.9	27.9	19.3	aaagtgtag...	
435250	435882	15	42.4	3500	5	8	594	18	50.1	0.0	28.1	21.8	aaagaaggat...	*
435268	435882	72	9.1	4240	2	3	606	3	49.9	0.0	28.1	22.0	aaagaaggat...	
435286	435882	42	15.4	3510	3	6	579	9	49.7	0.0	28.1	22.1	aaagaaggat...	*
436865	437342	15	31.9	4230	0	0	468	10	44.6	0.0	28.9	26.6	aaatgtggag...	
535108	535382	24	11.5	1790	0	0	257	18	30.9	10.2	4.4	54.5	aaatcatttg...	
584019	584264	4	61.5	1580	0	0	225	21	42.7	0.0	26.4	30.9	aatg	
594915	595306	33	12.7	2440	1	6	387	4	58.7	0.0	0.0	41.3	aaaaataaat...	
615452	615672	24	9.2	1530	0	0	210	11	27.1	36.7	18.6	17.6	aacacctgga...	
706464	706657	26	7.5	1600	0	0	192	2	59.3	0.0	6.2	34.5	aaataaatat...	
713900	714163	51	5.2	1850	0	0	257	7	36.0	13.6	7.6	42.8	aaagataaatt...	
730253	730639	24	16.1	3230	0	0	377	10	57.4	2.6	20.7	19.4	aaaagaaaat...	
752025	752222	21	9.4	1530	0	0	192	6	40.4	36.9	3.0	19.7	aaaatattcg...	
753893	754137	36	6.8	1930	0	0	241	4	16.3	30.2	6.1	47.3	aatcatttgt...	
896487	896726	12	20.0	2160	0	0	237	3	34.6	0.0	15.4	50.0	atatatgtat...	
905677	905935	12	21.6	2070	0	0	249	10	34.0	8.5	7.3	50.2	actattatta...	
943085	943357	18	15.2	1910	0	0	257	16	42.1	12.8	3.3	41.8	aaaaattatt...	
954471	954805	36	9.3	2830	0	0	331	4	36.1	14.9	0.0	49.0	acattatata...	
956423	956697	12	22.9	1710	0	0	252	23	6.9	15.3	21.5	56.4	cgttctgttt...	
958369	958625	36	7.1	1970	0	0	251	6	31.1	16.7	5.4	46.7	accatatgta...	
958376	958629	18	14.1	1800	0	0	240	14	31.1	16.1	5.5	47.2	accatatgta...	*
1040360	1042928	21	122.5	2630	2	4	2013	554	35.1	14.1	18.7	32.1	aagacctatg...	
1040468	1041744	21	60.8	2880	1	0	1037	239	35.4	12.5	20.5	31.6	aaagtaagac...	
1045737	1046857	21	53.3	2290	2	1	910	209	37.8	12.4	18.9	30.9	aaaccttaag...	
1047846	1049576	12	143.5	5360	3	1	1440	279	28.5	5.2	25.1	41.2	agtagtcatg...	
1059507	1059922	56	7.7	2260	1	2	390	12	56.0	0.0	27.9	16.1	aaaagtaaga...	

**Legends of Tables 1, 2 and 3:**

- start, end                    start, end of the TR
- length                      length of the consensus word
- repeat                      number of repetitions
- score                        total score of the alignment between the TR and the model TR
- ins, del, match, mism     number of insertions, deletions, matches and mismatches (of the alignment between the TR and the model TR)
- A%, C%, G%, T%            percentage of bases in the TR
- consensus                  consensus word (only the first 10 bases)
- nesting                      flag that indicates a probably nested expansion