

Table S2. Genes at recombination hot regions.

Position corresponds to genome coordinate of strain TH135.

Rank	position	D_i	bootstrap	H_i	TH135 Genbank locus_tag (gene name): product name	remarks
49	131567	377.2909	94	3.06902	MAH_0127: mammalian cell entry protein	role in survival in macrophage
57	131586	376.363	94	3.04148	MAH_0127: mammalian cell entry protein	
62	132561	375.7288	97	3.02266	MAH_0128: mammalian cell entry protein	
41	132744	378.2581	97	3.09772	MAH_0128: mammalian cell entry protein	
38	132747	378.3197	98	3.09955	MAH_0128: mammalian cell entry protein	
60	132759	376.0313	95	3.03164	MAH_0128: mammalian cell entry protein	
47	132775	377.4877	99	3.07486	MAH_0128: mammalian cell entry protein	
43	132777	377.9421	95	3.08834	MAH_0128: mammalian cell entry protein	
1	132936	389.9274	100	3.44402	MAH_0128: mammalian cell entry protein	
2	132945	389.1011	100	3.4195	MAH_0128: mammalian cell entry protein	
19	133068	381.5691	100	3.19598	MAH_0128: mammalian cell entry protein	
30	133081	379.8247	96	3.14421	MAH_0128: mammalian cell entry protein	
32	133087	379.3166	98	3.12913	MAH_0128: mammalian cell entry protein	
56	133120	376.4254	94	3.04333	MAH_0128: mammalian cell entry protein	
61	600736	375.7849	93	3.02432	MAH_0590: hypothetical protein	downstream of otsA
59	600739	376.1985	87	3.0366	MAH_0590: hypothetical protein	
46	600777	377.6563	91	3.07986	MAH_0590: hypothetical protein	
51	600787	376.9647	95	3.05934	MAH_0590: hypothetical protein	
58	600790	376.206	90	3.03682	MAH_0590: hypothetical protein	
7	600867	384.9519	98	3.29637	MAH_0590: hypothetical protein	
4	600869	385.6619	100	3.31744	MAH_0590: hypothetical protein	
5	600893	385.28	97	3.30611	MAH_0590: hypothetical protein	
6	600909	385.0687	97	3.29984	MAH_0590: hypothetical protein	
3	600939	385.7922	100	3.3213	MAH_0591 (otsA): UDP-forming alpha, alpha-trehalose-phosphate synthase	role in glycolipid and capsule synthesis
18	601011	382.1693	99	3.21379	MAH_0591 (otsA): UDP-forming alpha, alpha-trehalose-phosphate synthase	
24	601050	381.0178	97	3.17962	MAH_0591 (otsA): UDP-forming alpha, alpha-trehalose-phosphate synthase	
63	601335	375.4343	92	3.01392	MAH_0591 (otsA): UDP-forming alpha, alpha-trehalose-phosphate synthase	
34	1035948	379.1258	95	3.12347	MAH_1028 (mfd): transcription-repair coupling factor	role in nucleotide excision repair. disfold inactive RNA polymerase molecules stalled at DNA lesions
36	1035960	378.4501	98	3.10342	MAH_1028 (mfd): transcription-repair coupling factor	
42	1035981	378.2255	95	3.09675	MAH_1028 (mfd): transcription-repair coupling factor	
45	1036041	377.746	93	3.08252	MAH_1028 (mfd): transcription-repair coupling factor	
44	1036050	377.7845	94	3.08367	MAH_1028 (mfd): transcription-repair coupling factor	
48	1036059	377.2935	95	3.0691	MAH_1028 (mfd): transcription-repair coupling factor	
50	1036156	376.9918	94	3.06014	MAH_1028 (mfd): transcription-repair coupling factor	
54	1036188	376.6015	92	3.04856	MAH_1028 (mfd): transcription-repair coupling factor	
55	1036203	376.4761	95	3.04484	MAH_1028 (mfd): transcription-repair coupling factor	
65	1036284	375.1459	96	3.00536	MAH_1028 (mfd): transcription-repair coupling factor	
66	1036296	374.9779	96	3.00038	MAH_1028 (mfd): transcription-repair coupling factor	
53	1036632	376.6021	96	3.04858	MAH_1028 (mfd): transcription-repair coupling factor	
31	1036674	379.7094	98	3.14079	MAH_1028 (mfd): transcription-repair coupling factor	
12	1036827	384.0225	98	3.26879	MAH_1028 (mfd): transcription-repair coupling factor	
13	1036830	384.0188	96	3.26868	MAH_1028 (mfd): transcription-repair coupling factor	
14	1036878	383.9736	95	3.26734	MAH_1028 (mfd): transcription-repair coupling factor	
23	1036971	381.105	95	3.18221	MAH_1028 (mfd): transcription-repair coupling factor	
35	1037073	378.5029	96	3.10499	MAH_1028 (mfd): transcription-repair coupling factor	
33	1037079	379.1512	98	3.12422	MAH_1028 (mfd): transcription-repair coupling factor	
20	1037106	381.321	94	3.18862	MAH_1028 (mfd): transcription-repair coupling factor	
21	1037118	381.2282	96	3.18586	MAH_1028 (mfd): transcription-repair coupling factor	
26	1037151	380.8534	97	3.17474	MAH_1028 (mfd): transcription-repair coupling factor	
28	1037208	380.3949	98	3.16113	MAH_1028 (mfd): transcription-repair coupling factor	
37	1037231	378.405	99	3.10208	MAH_1028 (mfd): transcription-repair coupling factor	
64	1037269	375.2491	95	3.00842	MAH_1028 (mfd): transcription-repair coupling factor	
39	3934637	378.3096	97	3.09925	MAH_3653 (rsbP): response regulator receiver modulated serine phospho two component signal transduction system. Serine phosphatase for anti-anti sigma	
25	3934653	380.862	97	3.17499	MAH_3653 (rsbP): response regulator receiver modulated serine phosphatase	
22	3934662	381.1592	97	3.18382	MAH_3653 (rsbP): response regulator receiver modulated serine phosphatase	
17	3934767	382.3262	98	3.21845	MAH_3653 (rsbP): response regulator receiver modulated serine phosphatase	
16	3934839	383.2928	98	3.24713	MAH_3653 (rsbP): response regulator receiver modulated serine phosphatase	
9	3935006	384.775	96	3.29112	MAH_3654 (fadE25): acyl-CoA dehydrogenase	nonsynonymous substitutions were not found, upstream of rsbP
8	3935018	384.9079	100	3.29506	MAH_3654 (fadE25): acyl-CoA dehydrogenase	
10	3935055	384.5809	96	3.28536	MAH_3654 (fadE25): acyl-CoA dehydrogenase	
11	3935074	384.2398	94	3.27524	MAH_3654 (fadE25): acyl-CoA dehydrogenase	
15	3935123	383.533	95	3.25426	MAH_3654 (fadE25): acyl-CoA dehydrogenase	
27	3935231	380.4358	98	3.16235	MAH_3654 (fadE25): acyl-CoA dehydrogenase	
40	3935369	378.2853	95	3.09853	MAH_3654 (fadE25): acyl-CoA dehydrogenase	
52	3935651	376.9396	95	3.05859	MAH_3654 (fadE25): acyl-CoA dehydrogenase	
29	3935717	380.0256	96	3.15017	MAH_3654 (fadE25): acyl-CoA dehydrogenase	