

**Table S2.** Genes of lineage 3 with average  $dn/ds$  values ( $\omega$ )  $\geq 0.25$  and/or site-specific positive selection detected by CodeML (model M2a vs. model M1a). Genes are ordered according to  $\omega$ . Genes with  $\omega < 0.25$ , but with sites under positive selection are indicated by gray color. *virB* T4SS and *bep* genes are indicated by orange color. Orthologous genes present in genomes of other lineages are shown. Likelihood-ratio-test (LRT) results of the CodeML selection analysis are given for comparison of model M2a vs. M1a and model M8 vs. M7.

Gene	Product	Length (aa) <sup>a</sup>	Orthologs in other genomes <sup>3</sup>				$\omega$	PAML results <sup>b</sup>	
			<i>Brucella abortus</i>	<i>B. bacilliformis</i>	<i>B. schoenbuchensis</i>	<i>B. quintana</i>		M2a vs. M1a	M8 vs. M7
BARCL_1245	conserved protein of unknown function	91	BruAb1_1710	BARBAKC583_0136	BARSC_10259	BQ12030	16.73 $\pm$ 40.3	0.00	0.00
BARCL_0768	conserved exported protein of unknown function	77	no	no	BARSC_40129	BQ06010	16.69 $\pm$ 40.32	0.00	0.00
BARCL_0782	ATP-binding protein of ABC-transport system	245	BruAb2_0027	no	BARSC_40051	BQ06320	16.56 $\pm$ 40.39	1.28	3.00
BARCL_1321	conserved protein of unknown function	85	BruAb1_1804	no	BARSC_10329	BQ12930	0.82 $\pm$ 0.22	1.36	1.77
BARCL_0240	conserved exported protein of unknown function	49	no	BARBAKC583_0299	BARSC_20051	no	0.78 $\pm$ 0.22	5.92	5.96
BARCL_0077	VirB T4SS protein, VirB5	150	no	no	no	BQ10560 <sup>c</sup>	0.73 $\pm$ 0.09	11.02**	12.06**
BARCL_0647	VirB T4SS protein, VirB5	150	no	no	no	BQ10560 <sup>c</sup>	0.73 $\pm$ 0.09	11.02**	12.06**
BARCL_1163	conserved protein of unknown function	97	no	no	no	BQ11040	0.65 $\pm$ 0.34	2.11	2.27
BARCL_0505	glycine cleavage system T protein	373	BruAb2_0504	BARBAKC583_1096	BARSC_40500	BQ10130	0.64 $\pm$ 1.18	1.18	1.41
BARCL_0118	VirB T4SS effector protein, Bep (fragment)	223	no	no	no	BQ10650 <sup>c</sup>	0.62 $\pm$ 0.21	13.84**	14.52**
BARCL_0960	VirB T4SS effector protein, Bep	430	no	no	no	BQ10650 <sup>c</sup>	0.61 $\pm$ 0.18	11.42**	14.62**
BARCL_0491	protein of unknown function	120	no	no	BARSC_10073	no	0.6 $\pm$ 0.09	0.09	0.18
BARCL_0416	TonB protein	244	BruAb1_0622	BARBAKC583_0461	BARSC_20204	BQ04170	0.53 $\pm$ 0.17	0.37	0.53
BARCL_0125	Heme exporter protein CcmD	50	no	BARBAKC583_1287	BARSC_10492	BQ01050	0.5 $\pm$ 0.34	0.99	1.06
BARCL_0194	exported protein of unknown function	90	no	no	no	no	0.5 $\pm$ 0.16	14.42**	18.29**
BARCL_0632	VirB T4SS effector protein, Bep	528	no	no	no	BQ10650 <sup>c</sup>	0.5 $\pm$ 0.12	6.51*	11.62**
BARCL_1031	VirB T4SS effector protein, Bep	547	no	no	no	BQ10650 <sup>c</sup>	0.49 $\pm$ 0.06	16.29**	22.75**
BARCL_0245	VirB T4SS effector protein, Bep	497	no	no	no	BQ10650 <sup>c</sup>	0.48 $\pm$ 0.11	10.19**	18.9**
BARCL_0481	putative flagellar motor protein	405	BruAb2_1079	BARBAKC583_1125	BARSC_10086	no	0.47 $\pm$ 0.08	0.02	0.15
BARCL_0075	VirB T4SS protein, VirB7	103	no	no	no	BQ10580 <sup>c</sup>	0.47 $\pm$ 0.09	0.43	0.8
BARCL_0645	VirB T4SS protein, VirB7	103	no	no	no	BQ10580 <sup>c</sup>	0.47 $\pm$ 0.09	0.43	0.8
BARCL_0690	conserved protein of unknown function	77	BruAb1_0849	BARBAKC583_0864	BARSC_40153	BQ07510	0.47 $\pm$ 0.21	6.46*	6.53*
BARCL_1342	protein of unknown function	556	no	no	no	no	0.46 $\pm$ 0.08	35.82**	55.96**
BARCL_0478	conserved protein of unknown function	242	no	BARBAKC583_1128	BARSC_10089	no	0.46 $\pm$ 0.08	0.00	0.02
BARCL_1207	DsbB domain protein	184	BruAb1_1630	BARBAKC583_0182	BARSC_10215	BQ11650	0.46 $\pm$ 0.09	3.33	4.32
BARCL_0640	VirB T4SS effector protein, Bep	539	no	no	no	BQ10650 <sup>c</sup>	0.45 $\pm$ 0.06	18.16**	23.35**
BARCL_0669	conserved protein of unknown function	77	no	no	no	BQ07720	0.44 $\pm$ 0.21	0.00	0.00
BARCL_1013	conserved protein of unknown function	158	no	no	no	BQ09010	0.43 $\pm$ 0.07	2.71	3.46
BARCL_1355	protein of unknown function	32	no	no	no	no	0.43 $\pm$ 0.35	0.00	0.00
BARCL_0639	VirB T4SS effector protein, Bep	625	no	no	no	BQ10650 <sup>c</sup>	0.43 $\pm$ 0.01	19.73**	23.36**
BARCL_1288	conserved protein of unknown function	225	BruAb1_1970	BARBAKC583_0098	BARSC_10295	BQ12360	0.43 $\pm$ 0.11	0.00	0.00
BARCL_1327	conserved protein of unknown function	387	BruAb1_1862	BARBAKC583_0063	BARSC_10335	BQ13000	0.42 $\pm$ 0.08	5.28	5.85
BARCL_1059	conserved protein of unknown function	141	BruAb1_0406	BARBAKC583_0375	BARSC_20121	BQ03120	0.42 $\pm$ 0.09	5.04	5.44
BARCL_0241	conserved protein of unknown function	131	BruAb2_0470	BARBAKC583_0300	BARSC_20052	BQ02980	0.42 $\pm$ 0.35	0.00	0.00

Gene	Product	Length (aa) <sup>d</sup>	Orthologs in other genomes <sup>a</sup>				$\omega$	PAML results <sup>b</sup>	
			<i>Brucella abortus</i>	<i>B. bacilliformis</i>	<i>B. schoenbuchensis</i>	<i>B. quintana</i>		M2a vs. M1a	M8 vs. M7
BARCL_0982	conserved protein of unknown function	464	no	no	no	no	0.42 ±0.1	59.2**	94.79**
BARCL_0631	VirB T4SS effector protein, Bep	538	no	no	no	BQ10650 <sup>c</sup>	0.42 ±0.06	15.09**	22.57**
BARCL_1351	conserved protein of unknown function	221	BruAb1_2010	no	no	no	0.42 ±0.13	0.00	-0.07
BARCL_0069	VirB T4SS effector protein, Bep	547	no	no	no	BQ10650 <sup>c</sup>	0.42 ±0.1	2.46	3.4
BARCL_0978	conserved protein of unknown function	40	BruAb1_1401	BARBAKC583_0931	BARSC_40323	BQ08690	0.41 ±0.37	0.92	1.20
BARCL_0279	conserved protein of unknown function	218	no	BARBAKC583_1049	BARSC_40463	BQ09660	0.41 ±0.12	0.00	0.00
BARCL_1164	conserved protein of unknown function	139	BruAb1_1640	BARBAKC583_0248	BARSC_10151	BQ11050	0.41 ±0.07	3.14	3.26
BARCL_1170	conserved protein of unknown function	74	no	BARBAKC583_0239	BARSC_10161	no	0.4 ±0.25	0.33	0.63
BARCL_1173	conserved protein of unknown function	152	no	BARBAKC583_0234	BARSC_10165	BQ11080	0.4 ±0.08	2.39	2.47
BARCL_0957	Effector protein yopJ	249	no	no	no	BQ11580 <sup>c</sup>	0.4 ±0.07	5.23	5.99*
BARCL_0250	Effector protein yopJ	279	no	no	no	BQ11580 <sup>c</sup>	0.39 ±0.1	6.20*	8.93*
BARCL_0367	conserved protein of unknown function	164	BruAb1_0516	BARBAKC583_0416	BARSC_20162	BQ03740	0.38 ±0.34	0.00	0.20
BARCL_1270	ATP synthase epsilon chain	138	BruAb1_1778	BARBAKC583_0115	BARSC_10281	BQ12220	0.38 ±0.08	1.00	1.30
BARCL_0473	Inducible Bartonella autotransporter	673	no	BARBAKC583_1132 <sup>c</sup>	BARSC_10091 <sup>c</sup>	BQ10380 <sup>c</sup>	0.38 ±0.11	108.28**	128.21**
BARCL_1329	Antioxidant, AhpC/TSA family	143	BruAb1_1956	BARBAKC583_0053	BARSC_10347	BQ13100	0.37 ±0.22	-9.41	6.16
BARCL_0664	conserved protein of unknown function	210	no	BARBAKC583_0744	BARSC_40233	no	0.37 ±0.17	0.78	1.60
BARCL_1005	conserved protein of unknown function	134	BruAb1_1433	BARBAKC583_0954	BARSC_40346	BQ08930	0.37 ±0.08	0.83	0.83
BARCL_0054	conserved protein of unknown function	242	BruAb1_2088	BARBAKC583_1339	BARSC_10433	BQ00450	0.36 ±0.19	1.53	2.04
BARCL_0882	conserved protein of unknown function	249	BruAb1_1170	BARBAKC583_0582	BARSC_20329	BQ07020	0.36 ±0.1	0.00	0.00
BARCL_1123	Effector protein yopJ	339	no	no	no	BQ01158 <sup>c</sup>	0.35 ±0.13	6.19*	8.68*
BARCL_1011	conserved protein of unknown function	107	BruAb1_1447	no	no	no	0.35 ±0.34	9.59**	10.29**
BARCL_0115	FxsA cytoplasmic membrane protein	157	BruAb1_2048	BARBAKC583_1295	BARSC_10481	BQ00960	0.35 ±0.12	2.27	3.00
BARCL_0929	50S ribosomal protein L29	66	BruAb1_1230	BARBAKC583_0674	BARSC_40270	BQ08150	0.35 ±0.21	0.16	0.38
BARCL_0951	conserved protein of unknown function	225	BruAb1_0953	BARBAKC583_0651	BARSC_40294	BQ08380	0.35 ±0.29	3.82	3.79
BARCL_0446	conserved protein of unknown function	125	no	BARBAKC583_1158	BARSC_10119	no	0.34 ±0.15	0.00	0.09
BARCL_0480	putative flagellar motor protein	426	BruAb2_1080	BARBAKC583_1126	BARSC_10087	no	0.34 ±0.09	0.18	0.50
BARCL_1038	conserved protein of unknown function	144	BruAb1_0895	no	no	BQ04750	0.34 ±0.1	2.25	2.88
BARCL_0699	conserved protein of unknown function	85	BruAb1_1043	BARBAKC583_0854	BARSC_40141	BQ07410	0.34 ±0.07	0.01	0.26
BARCL_1165	conserved protein of unknown function	228	BruAb1_1844	BARBAKC583_0247	no	BQ11000	0.34 ±0.08	4.53	5.07
BARCL_1200	conserved protein of unknown function	126	no	BARBAKC583_0193	BARSC_10208	BQ11450	0.33 ±0.15	1.08	1.44
BARCL_1199	conserved protein of unknown function	63	no	BARBAKC583_0195	BARSC_10207	BQ11430	0.33 ±0.15	0.00	0.00
BARCL_1225	conserved exported protein of unknown function	352	BruAb1_1693	BARBAKC583_0156	BARSC_10240	BQ11930	0.33 ±0.11	0.01	0.76
BARCL_0670	conserved protein of unknown function	813	no	BARBAKC583_0748	BARSC_40172	BQ07710	0.32 ±0.03	4.85	6.04*
BARCL_0198	Hemin binding protein	291	BruAb1_0115 <sup>c</sup>	BARBAKC583_1214 <sup>c</sup>	BARSC_40484 <sup>c</sup>	BQ02410 <sup>c</sup>	0.32 ±0.04	9.37**	17.43**
BARCL_0196	Hemin binding protein	277	BruAb1_0115 <sup>c</sup>	BARBAKC583_1214 <sup>c</sup>	BARSC_10559 <sup>c</sup>	BQ02410 <sup>c</sup>	0.32 ±0.08	8.84*	8.47*
BARCL_0016	conserved exported protein of unknown function	199	BruAb1_0152	BARBAKC583_1369	BARSC_10401	BQ00150	0.32 ±0.21	1.79	1.93
BARCL_1166	conserved protein of unknown function	297	no	no	BARSC_10157	BQ11020	0.32 ±0.1	3.22	4.86
BARCL_1020	conserved protein of unknown function	837	no	BARBAKC583_1109	no	BQ10280	0.32 ±0.13	0.00	14.52
BARCL_0475	Inducible Bartonella autotransporter	823	BruAb1_0895	BARBAKC583_1132 <sup>c</sup>	BARSC_10091 <sup>c</sup>	BQ10380 <sup>c</sup>	0.31 ±0.09	89.02**	105.99**
BARCL_0420	conserved protein of unknown function	175	BruAb1_0433	BARBAKC583_0391	BARSC_20137	BQ03450	0.31 ±0.07	0.00	0.00
BARCL_0103	3-phosphoshikimate 1-carboxyvinyltransferase	442	BruAb1_0025	BARBAKC583_1303	BARSC_10474	BQ00880	0.31 ±0.06	7.81*	9.68**
BARCL_0221	Protein slyX homolog	50	no	no	no	no	0.31 ±0.12	0.00	0.00
BARCL_0867	ABC transporter, permease protein	232	no	BARBAKC583_0597	BARSC_20344	BQ06870	0.3 ±0.1	2.19	2.56
BARCL_1177	conserved protein of unknown function	283	no	BARBAKC583_0229	BARSC_10169	BQ11120	0.3 ±0.07	0.88	2.30
BARCL_0327	conserved protein of unknown function	84	BruAb1_1516	BARBAKC583_0993	BARSC_40420	BQ03350	0.3 ±0.12	0.20	0.27
BARCL_0847	Lysophospholipase I2	293	BruAb1_0046	no	no	BQ05220	0.3 ±0.07	0.00	0.00
BARCL_1180	conserved protein of unknown function	87	no	BARBAKC583_0226	BARSC_10177	BQ11160	0.3 ±0.06	0.25	1.15
BARCL_0877	Phosphatidate cytidyltransferase	269	BruAb1_1163	BARBAKC583_0587	BARSC_20334	BQ06970	0.3 ±0.09	0.39	1.13
BARCL_0781	permease protein of ABC transporter	296	BruAb1_1771	no	BARSC_40052	BQ06310	0.3 ±0.42	2.31	3.25
BARCL_1274	ATP synthase delta subunit	194	BruAb1_1782	BARBAKC583_0111	BARSC_10285	BQ12260	0.3 ±0.04	2.17	3.83
BARCL_1261	conserved protein of unknown function	95	no	no	BARSC_10278	BQ12190	0.3 ±0.13	0.00	0.00

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			<i>Brucella abortus</i>	<i>B. bacilliformis</i>	<i>B. schoenbuchensis</i>	<i>B. quintana</i>	M2a vs. M1a		M8 vs. M7		
BARCL_0197	Hemin binding protein	241	BruAb1_0115 <sup>c</sup>	BARBAK583_1214 <sup>c</sup>	BARSC_40297 <sup>c</sup>	BQ02410 <sup>c</sup>	0.29 ±0.04	35.92**	50.26**		
BARCL_0381	conserved protein of unknown function	172	BruAb1_0603	no	no	BQ03880	0.29 ±0.1	0.41	0.84		
BARCL_0292	conserved protein of unknown function	215	no	no	no	BQ09490	0.29 ±0.1	2.26	3.5		
BARCL_0559	conserved membrane protein of unknown function	363	BruAb1_0705	BARBAK583_0507	BARSC_20252	BQ04620	0.29 ±0.04	6.34*	7.89*		
BARCL_1065	mutator MutT protein	136	BruAb1_1915	BARBAK583_0364	BARSC_20107	BQ01900	0.28 ±0.19	3.35	4.25		
BARCL_0524	pantoate-β-alanine ligase	281	BruAb1_0355	BARBAK583_0476	BARSC_20219	BQ04310	0.28 ±0.09	0.00	0.00		
BARCL_1125	50S ribosomal protein L21	159	BruAb1_1829	BARBAK583_0309	BARSC_20058	BQ01320	0.28 ±0.06	1.80	3.18		
BARCL_0024	lysyl-tRNA synthetase	549	BruAb2_0442	BARBAK583_1360	BARSC_10409	BQ00220	0.28 ±0.44	2.84	4.69		
BARCL_1236	TolA protein	377	BruAb1_1683	BARBAK583_0145	BARSC_10253	BQ11830	0.28 ±0.05	0.20	0.78		
BARCL_1313	SurF1 family protein	255	BruAb1_0496	BARBAK583_0076	BARSC_10321	BQ12840	0.28 ±0.05	0.00	0.22		
BARCL_0171	Ribosomal-protein-alanine acetyltransferase	160	BruAb1_2125	BARBAK583_1242	BARSC_10535	BQ02150	0.28 ±0.13	2.03	2.25		
BARCL_0518	conserved membrane protein of unknown function	179	BruAb1_0675	BARBAK583_0470	BARSC_20213	BQ04250	0.28 ±0.03	6.16*	9.17*		
BARCL_1233	conserved protein of unknown function	152	BruAb1_1686	BARBAK583_0148	BARSC_10250	BQ11860	0.28 ±0.07	0.08	0.55		
BARCL_0949	conserved protein of unknown function	181	BruAb1_0955	BARBAK583_0653	BARSC_40292	BQ08360	0.27 ±0.07	0.00	0.00		
BARCL_0226	conserved protein of unknown function	473	no	BARBAK583_0286	BARSC_20039	BQ02810	0.27 ±0.06	0.00	0.51		
BARCL_0464	Flagellar hook-basal body complex protein flIE	112	BruAb2_0149	BARBAK583_1142	BARSC_10102	no	0.27 ±0.16	2.26	3.12		
BARCL_1107	Filament-A precursor	391	BruAb1_1817	BARBAK583_0323	BARSC_20069	BQ01520	0.27 ±0.04	0.62	2.17		
BARCL_0296	conserved protein of unknown function	128	BruAb1_1587	BARBAK583_1018	BARSC_40443	BQ09450	0.27 ±0.06	3.57	4.40		
BARCL_1082	glycerol-3-phosphate ABC transporter permease	283	BruAb2_0569	BARBAK583_0347	BARSC_20091	BQ01740	0.27 ±0.5	0.00	0.00		
BARCL_0468	conserved protein of unknown function	210	BruAb2_0153	BARBAK583_1138	BARSC_10098	no	0.27 ±0.07	1.35	2.53		
BARCL_0454	Flagellar motor switch protein flfY	170	BruAb2_1067	BARBAK583_1151	BARSC_10111	no	0.27 ±0.03	0.44	1.02		
BARCL_0397	Methyltransferase	162	no	no	BARSC_20184	BQ04020	0.26 ±0.06	0.00	0.16		
BARCL_1029	LysM/M23 peptidase domain protein	362	BruAb1_0900	BARBAK583_0521	BARSC_20269	BQ04790	0.26 ±0.04	0.28	1.27		
BARCL_0813	conserved protein of unknown function	126	BruAb1_1079	BARBAK583_0643	BARSC_20395	BQ05530	0.26 ±0.2	0.00	0.00		
BARCL_0063	conserved protein of unknown function	144	no	BARBAK583_1330	BARSC_10443	BQ00580	0.26 ±0.08	0.00	0.00		
BARCL_1062	ATP synthase B chain (modular protein)	210	BruAb1_0409	BARBAK583_0378	BARSC_20124	BQ03150	0.26 ±0.06	0.36	1.04		
BARCL_0618	conserved protein of unknown function	246	no	no	no	BQ10520 <sup>c</sup>	0.26 ±0.04	0.00	0.97		
BARCL_0651	conserved protein of unknown function	246	no	no	no	BQ10520 <sup>c</sup>	0.26 ±0.04	0.00	0.46		
BARCL_1326	conserved protein of unknown function	481	BruAb1_1861	BARBAK583_0064	BARSC_10334	BQ12990	0.26 ±0.05	2.91	4.32		
BARCL_1078	ABC transporter, periplasmic binding protein	300	no	BARBAK583_0350	BARSC_20094	BQ01770	0.26 ±0.08	3.07	5.27		
BARCL_1246	conserved protein of unknown function	121	BruAb1_1709	BARBAK583_0135	BARSC_10260	BQ12040	0.25 ±0.08	0.71	1.19		
BARCL_0390	Cytochrome c-type biogenesis protein ccmH	125	BruAb1_0629	BARBAK583_0433	BARSC_20179	BQ03960	0.25 ±0.04	0.00	0.00		
BARCL_0325	conserved protein of unknown function	350	BruAb1_1518	BARBAK583_0995	BARSC_40422	BQ03330	0.25 ±0.08	0.00	0.00		
BARCL_0892	Transcriptional regulator	128	BruAb1_1185	no	no	no	0.25 ±0.08	0.00	0.00		
BARCL_0449	conserved exported protein of unknown function	147	BruAb2_1064	BARBAK583_1155	BARSC_10115	no	0.25 ±0.07	3.02	3.88		
BARCL_1254	conserved protein of unknown function	506	BruAb1_1754	BARBAK583_0125	BARSC_10271	BQ12130	0.25 ±0.08	6.03*	8.46*		
BARCL_1171	putative phage protein	328	no	BARBAK583_0238	BARSC_10163	BQ11060	0.25 ±0.03	20.56**	23.36**		
BARCL_0059	heat shock protein GrpE	219	BruAb1_0167	BARBAK583_1334	BARSC_10438	BQ00500	0.25 ±0.16	9.59**	12.51**		
BARCL_0380	conserved protein of unknown function	162	BruAb1_0602	no	no	BQ03870	0.25 ±0.07	2.26	2.39		
BARCL_0145	conserved exported protein of unknown function	608	no	no	no	no	0.25 ±0.05	3.24	7.43		
BARCL_0735	conserved protein of unknown function	96	BruAb2_0644	BARBAK583_0797	BARSC_40109	BQ05830	0.25 ±0.16	5.73	5.83		
BARCL_0191	Formamidopyrimidine-DNA glycosylase	291	BruAb1_2156	BARBAK583_1221	BARSC_10554	BQ02370	0.25 ±0.17	1.54	1.94		
BARCL_1278	conserved protein of unknown function	190	BruAb1_1786	BARBAK583_0105	BARSC_10290	BQ12300	0.25 ±0.08	0.00	0.00		
BARCL_1227	OpgC protein	373	BruAb1_1691	BARBAK583_0154	BARSC_10242	BQ11910	0.25 ±0.06	3.84	4.08		
BARCL_0565	conserved exported protein of unknown function	469	no	BARBAK583_0512	no	no	0.25 ±0.05	0.00	2.35		
BARCL_0605	conserved protein of unknown function	182	no	no	no	no	0.25 ±0.24	0.47	0.09		
BARCL_0566	conserved exported protein of unknown function	875	no	no	no	no	0.25 ±0.02	20.04**	40.96**		
BARCL_1373	Transmembrane protein	150	BruAb2_0497	no	no	BQ13370	0.25 ±0.05	0.70	1.34		
BARCLv2_0646	VirB T4SS protein, VirB6	329	no	no	no	BQ10570	0.23 ± 0.06	10.90**	14.51**		
BARCLv2_0076	VirB T4SS protein, VirB6	329	no	no	no	BQ10570	0.23 ± 0.05	11.23**	15.01**		
BARCLv2_1192	conserved protein of unknown function	277	no	BARBAK583_0204	no	BQ11320	0.23 ± 0.04	11.39**	11.22**		

Gene	Product	Length (aa) <sup>d</sup>	Orthologs in other genomes <sup>a</sup>				$\omega$	PAML results <sup>b</sup>	
			<i>Brucella abortus</i>	<i>B. bacilliformis</i>	<i>B. schoenbuchensis</i>	<i>B. quintana</i>		M2a vs. M1a	M8 vs. M7
BARCLv2_1175	conserved protein of unknown function	238	no	no	BARSCv2_10167	BQ11100	0.22 ± 0.05	6.66*	7.86*
BARCLv2_0757	lipoprotein A	233	no	BARBAKC583_0823	BARSCv2_40069	BQ06130	0.22 ± 0.03	20.99**	22.80**
BARCLv2_0548	conserved membrane protein of unknown function	192	no	BARBAKC583_0495	BARSCv2_20241	BQ04510	0.19 ± 0.11	6.76*	7.72*
BARCLv2_0042	conserved membrane protein of unknown function	237	BruAb1_0163	BARBAKC583_1350	BARSCv2_10420	no	0.19 ± 0.06	33.60**	36.01**
BARCLv2_0523	DNA repair protein RecO	231	BruAb1_0681	BARBAKC583_0475	BARSCv2_20218	BQ04300	0.17 ± 0.07	7.28*	7.52*
BARCLv2_1006	S-adenosyl-methyltransferase	332	BruAb1_1434	BARBAKC583_0955	BARSCv2_40347	BQ08940	0.17 ± 0.06	11.69**	14.05**
BARCLv2_0861	Ribose 5-phosphate isomerase	226	BruAb1_1015	BARBAKC583_0602	BARSCv2_20351	BQ06820	0.17 ± 0.09	13.79**	16.51**
BARCLv2_0562	metabolite transport protein	428	BruAb2_0524	no	BARSCv2_20257	BQ08640	0.16 ± 0.04	6.74*	8.27*
BARCLv2_0038	S-adenosyl-L-homocysteine hydrolase	459	BruAb1_2072	no	no	BQ00290	0.15 ± 0.09	6.86*	8.77*
BARCLv2_1344	conserved protein of unknown function	347	BruAb1_2032	BARBAKC583_0050	BARSCv2_10349	BQ13150	0.15 ± 0.03	9.25**	13.31**
BARCLv2_0176	DNA polymerase III gamma and tau subunit	604	BruAb1_0034	BARBAKC583_1238	BARSCv2_10539	BQ02200	0.14 ± 0.02	7.08*	10.63**
BARCLv2_0181	Uncharacterized ABC transporter ATP-binding protein yefJ	529	BruAb1_0006	no	BARSCv2_10544	no	0.13 ± 0.06	22.58**	27.27**
BARCLv2_1272	ATP synthase gamma chain	303	BruAb1_1780	BARBAKC583_0113	BARSCv2_10283	BQ12240	0.11 ± 0.03	7.21*	9.98**
BARCLv2_0732	Prolyl-tRNA synthetase	441	BruAb1_0836	BARBAKC583_0794	BARSCv2_40106	BQ05800	0.11 ± 0.03	6.24*	8.39*
BARCLv2_0692	phosphoribosylformylglycinamide synthase I	222	BruAb1_0853	BARBAKC583_0861	BARSCv2_40150	BQ07490	0.10 ± 0.02	9.52**	11.51**
BARCLv2_0542	DNA repair protein	461	BruAb1_0471	BARBAKC583_0489	BARSCv2_20235	BQ04450	0.10 ± 0.03	12.67**	18.86**
BARCLv2_0923	30S ribosomal protein S8	132	BruAb1_1224	BARBAKC583_0712	BARSCv2_40264	BQ08090	0.10 ± 0.09	6.23*	8.56*
BARCLv2_0242	glutamate-cysteine ligase	457	BruAb2_0469	BARBAKC583_0301	BARSCv2_20053	BQ02990	0.10 ± 0.03	9.01*	13.83**
BARCLv2_0743	peptide chain release factor RF-2	317	BruAb1_0927	BARBAKC583_0804	BARSCv2_40117	BQ05900	0.10 ± 0.03	8.38*	10.04**
BARCLv2_1271	ATP synthase beta chain	530	BruAb1_1779	BARBAKC583_0114	BARSCv2_10282	BQ12230	0.09 ± 0.02	8.47*	8.92*
BARCLv2_0362	conserved membrane protein of unknown function	957	BruAb1_0503	BARBAKC583_0410	BARSCv2_20156	BQ03650	0.09 ± 0.01	6.35*	8.42*
BARCLv2_0924	30S ribosomal protein S14	100	BruAb1_1225	BARBAKC583_0711	BARSCv2_40265	BQ08100	0.09 ± 0.07	11.89**	12.52*
BARCLv2_0329	sensor histidine kinase	445	BruAb1_1513	BARBAKC583_0990	BARSCv2_40418	BQ03380	0.08 ± 0.05	8.09*	9.76**
BARCLv2_0136	cytochrome o ubiquinol oxidase subunit I	672	BruAb1_0490	BARBAKC583_1274	BARSCv2_10503	BQ01160	0.08 ± 0.01	7.58*	10.68**
BARCLv2_0477	flagellar M-ring protein	554	BruAb2_1083	BARBAKC583_1129	BARSCv2_10090	no	0.08 ± 0.01	6.03*	11.35**
BARCLv2_0096	Iron transport protein, inner membrane component	287	no	BARBAKC583_1309	BARSCv2_10466	BQ00810	0.08 ± 0.01	22.06**	26.61**
BARCLv2_0165	transcriptional regulator	137	BruAb1_2132	BARBAKC583_1248	BARSCv2_10529	BQ02090	0.08 ± 0.04	6.79*	7.01*
BARCLv2_0611	gid-family protein	455	BruAb1_0906	BARBAKC583_0551	BARSCv2_20300	no	0.07 ± 0.01	6.35*	7.95*
BARCLv2_0747	DNA repair protein RadC	261	BruAb1_1284	BARBAKC583_0830	BARSCv2_40060	BQ06240	0.07 ± 0.01	14.09**	16.76**
BARCLv2_1073	ribonucleoside-diphosphate reductase 2 alpha chain	708	BruAb2_0865	BARBAKC583_0356	BARSCv2_20099	BQ01820	0.04 ± 0.01	6.44*	8.71*

<sup>a</sup>for ortholog assignment the “Phylo Profile Synteny” tool of MaGe [58] was used (parameters: Bidirectional Blast Hit, 30 % identities, 0.6 for minLrap and maxLrap), automated ortholog assignments were manually curated.

<sup>b</sup>LRT statistics for model M2a vs. model M1a and model M8 vs. model M7, values indicating significant positive selection are depicted by asterisks (\*: p <0.05, \*\*: p <0.01).

<sup>c</sup>more than one orthologous gene is present in the corresponding genome, no clear ortholog assignment possible.

<sup>d</sup>aa means analyzed gene length in amino acids.