

Table S2. Primers designed for testing the possible contig unions and polymorphic repeats.

Contig	Position (5' - 3')	Primer	sequence	length (nt)	Tm (°C)*
1	949 - 928	leuC_R1	GAAGGCAGTAGACTTGTTTCTC	22	55.0
1	14021 - 14042	leuS_F1	CTAGCTATAACGTCCCTATTG	22	55.0
2	555 - 534	dnaN_R2	AAGGCAACAGTAAAAGCATTAT	22	55.1
2	13340 - 13361	mnmG_F2	CTGAAAACTAAACAAGCATCA	22	55.0
3	429 - 408	rsmH_R3	TATACATACGTTTCTGGGTCAC	22	54.3
3	4767 - 4786	clpX_F3	TCAGTACGACCACAAAATGA	20	55.2
4	590 - 571	trxA_R4	AAAGAGGGGAGTGTCTTAGG	20	55.0
4	6747 - 6767	pheS_F4	GCAGCTTATGAAGAAATAGCA	21	55.2
5	295 - 276	clpP_R5	CACGTATTAGCACAGCGTTA	20	55.2
5	4836 - 4857	glyQ_F5	GCTTTCCATATCTACCATCACT	22	55.0
6	768 - 747	lpdA_R6	CTTTAGATGGAACACAACCAAC	22	56.3
6	3567 - 3588	aroQ_F6	ATGCTAGTATGTGTGTGCCTG	22	55.3
7	333 - 312	der_R7	GCTCCAATGCCATATCTACTAT	22	55.2
7	12843 - 12864	secA_F7	CTCGTTGTATATTCTTTTAGCA	22	52.0
8	614 - 593	ssrA_R8	ACAAAAGCTAAAGAGAGGTTAG	22	52.0
8	9121 - 9142	infC_F8	TAAGATGCGTCAGTTAGTTAGC	22	54.3
9	339 - 318	prfA_R9	GCATATAGTAAAAGATGGTCTG	22	51.2
9	6362 - 6383	groL_F9	CTATGATGCAGCTAAGTCTCAA	22	55.1
9	6437 - 6456	groL_F9b	AGCTTTACAGTTTGCTGCTT	20	54.7
10	635 - 614	ilvI_R10	CTAAAACATGGGTTAGCTTAGG	22	55.1
10	6204 - 6223	dapB_F10	ATGGTGCCTTCGATAACTT	20	54.8
10	7566 - 7547	hisG_R10	ATGGCCTATATGAAGCAAAG	20	54.6
10	8612 - 8633	prmC_F10	TACCACTCCAGTTCCTAAGTC	22	55.2
11	274 - 251	prfB_R11	GTCTGTTACTATTAAGATTCAAGG	24	51.4
11	4765 - 4786	dapD_F11	AGTTGGTAAAAGAGTCCACATC	22	55.0
12	705 - 684	thrB_R12	ACCAAATATTAAGCCTCTGAA	22	55.0
12	8455 - 8474	P00109_F12	TACCAAGCTGTCCTTTTCTT	20	54.3
12	9424 - 9405	argF_R12	TTGGGTGAAAGCTATCAGTT	20	55.0
12	13964 - 13985	ileS_F12	TGTATGTAGATGATGGGTTAGC	22	54.4
13	1852 - 1873	gltX_F13	AGAGCTCCAAGTATGTTTGACT	22	54.9
14	752 - 731	hisS_R14	ATCTAGCTCTGGTTCTTTGAGA	22	55.1
14	16705 - 16725	cysGA_F14	CTGGTCCAGGAAATAAAGACT	21	55.1
15	812 - 791	iscU_R15	TGAGTTAGTACAAGGGAAAACC	22	55.2
15	11916 - 11936	thrC_F15	GACTCACTGCAAGACATGATT	21	55.3
16	589 - 568	argH_R16	ACCATGCTTTTCGATAGAGTTAC	22	55.3
16	1567 - 1588	argH_F16	GCTACAGAATTGGCAGACTACT	22	55.5
17	1212 - 1191	carB_R17	TTAGAGGAGGTCTAGCAGTTGT	22	55.1
17	5879 - 5900	dnaQ_F17	GATTATTTGTGTGATAGGTTCA	22	52.0
18	1216 - 1195	hisF_R18	AGTAAAGGGGTTGAAGTTAGGT	22	55.3
18	3184 - 3205	hisH_F18	GTCACAGCTAACTATGGAGTCA	22	54.6
19	952 - 931	aroB_R19	GTTATCCATCTGTCGTTTACCT	22	55.0
19	28434 - 28455	rlpK_F19	CGTTAACATATTGAAAGAGCTA	22	52.0
20	531 - 510	rrl_R20	AGCTAACCAATACTAATGAACC	22	52.2
20	13906 - 13927	metE_F20	TCTCTTTGGTTTCTGAAGTTCT	22	55.0
21	868 - 847	aspS_R21	ACCTTAGTAAGAAAGAACAGGA	22	51.9
21	10071 - 10092	lysS_F21	TACCAGCAGTTGCTATGTTAAG	22	55.1
22	396 - 375	pnp_R22	GTTTACAGTTAATGGGAAGAGC	22	54.9
22	4020 - 4041	tsaB_F22	GATAGGGTAGAGGCTTCTAAGG	22	55.6

*The melting temperature (Tm) indicated corresponds to that provided by Primer3Plus.