

Table 1: *Aquifex aelicus* novel ncRNAs, without rRNA operons, H2H, T2T, tRNAs; pred – predicted protein by BacProt without homology, hyp. prot – hypothetical protein, as – antisense, MI – of most interest, MIT – of most interest and tested within this work

ID	Location		Ori	GC	cDNA (+/-)	Annotation (old/BacProt)	Structure and Sequence					Remarks
	Start	Stop					RNALfold	Cons_P	Cons_t	RNAz_p	RNAz_t	
Putative Novel ncRNAs												
n1	8821	8885	-	0.509231	38/15	no/no	no	11	11	no	no	plasmid region, MI 300nt mogA antisense, 450nt
n2	15301	15474	+	-	0/0	no/no	-3.663	no	5	no	no	
n3	37620	37906	+	0.405575	20/14	no/no	-3.566	10	1	no	no	
n4	38976	39274	+	0.499554	39/30	no/no	no	7	6	no	no	
n5	66594	66673	+	0.575	15/0	no/no	no	9	9	no	no	MI
n6	66602	66673	-	0.584259	5/1	no/no	no	9	9	no	no	
n7	69101	69198	-	0.369728	809/545	no/no	-4.705	11	11	no	no	MI
n7	72296	72570	-	0.400848	4/1	aq_116/pred	-3.244	7	6	no	no	downstream of hyp. prot.
n8	82709	82790	+	0.413415	1/5	nusB/transcription	no	11	1	no	no	downstream of nusB
n9	82614	82916	-	0.414191	4/4	no/no	-3.933	11	10	no	no	200nt 300nt, MI
	92562	92661	+	0.417667	11/35	no/no	-3.422	11	1	no	no	
n10	92430	92716	-	0.382578	36/42	no/no	-3.422	11	2	no	no	rpm(as) phpA(as), >200nt, MI
	98085	98122	+	0.603509	6/0	no/no	no	no	11	no	no	
n11	108986	109116	+	0.403562	4/20	no/no	-3.155	11	8	0.560024	no	intergenic region hyp. prot. down- stream hyp. prot. down- stream downstream of CRISPR cluster
n12	138568	138832	+	0.539874	1/0	no/no	no	11	11	0.684197	no	
n13	177547	177600	+	0.288889	5/57	aspC4/GntR	no	11	6	no	no	hyp. prot. down- stream
n14	209886	209956	-	0.337559	0/24	aq_323/pred	-3.029	11	9	no	no	
n15	244481	244708	+	0.427485	12/22	aq_367/pred	-3.320	10	10	no	no	downstream of CRISPR cluster
	244517	244583	-	0.455721	1/3	no/no	no	10	10	no	no	
n16	261493	261555	+	0.408466	0/28	no/no	no	no	4	no	no	upstream of CRISPR cluster >200nt downstream of hyp. prot.
n17	263227	263275	+	0.515646	11/1	no/no	no	no	1	no	no	
	263219	263264	-	0.505797	4/3	no/no	no	no	1	no	no	
n18	263388	263570	-	0.367395	24/8	no/no	-3.715	no	1	no	no	downstream of hyp. prot.
n19	266935	267001	+	0.50398	1/10	aq_391/pred	no	6	6	no	no	
n20	266912	267003	-	0.470652	11/4	no/no	no	6	6	no	no	downstream of nuoG
	269468	269542	-	0.516444	28/32	no/no	-4.144	6	6	no	no	
n21	292666	292714	+	0.568707	3/1	no/no	-4.086	no	9	no	no	MIT upstream of ahpC1
	292667	292715	-	0.568707	2/0	no/no	-4.086	no	9	no	no	
n22	298795	299037	+	0.426475	0/3	nuoG/pred	-4.415	10	5	no	no	downstream of oprC
	298870	298922	-	0.478616	0/1	no/no	-4.415	10	5	no	no	
n23	307432	307494	+	0.410053	1/1	no/no	no	no	8	no	no	MIT upstream of ahpC1
	307451	307678	-	0.441082	2/1	no/no	no	no	7	no	no	
n24	321624	321714	+	0.436264	20/23	no/no	-3.070	11	6	no	no	hyp. prot. (as), >300nt >300nt
	321590	321891	-	0.439404	24/46	no/no	-3.070	11	6	no	no	
n25	328934	328995	+	0.365054	582/250	no/no	no	9	9	no	no	downstream of xcpC
	328942	329005	-	0.331771	50/361	ahpC1/pred	no	9	9	no	no	
n26	339361	339604	+	0.447951	14/48	no/no	-3.524	11	11	no	no	hyp. prot. (as), >300nt >300nt
n27	344744	344949	+	0.368608	4/5	no/no	no	6	1	no	no	
n28	348000	348243	+	0.447951	14/48	no/no	-3.653	no	1	no	no	downstream of oprC
n29	348017	348286	-	0.42037	7/23	aq_512/pred	-3.653	no	2	no	no	
	348619	348810	+	0.375174	16/7	no/no	-4.626	no	2	no	no	
n30	348667	348760	-	0.460638	4/7	no/no	-4.626	no	2	no	no	downstream of rpoN hyp. prot.
	359456	359644	+	0.487125	57/26	no/no	-4.335	11	9	no	no	
n31	359544	359643	-	0.505	155/86	oprC/pred	-4.335	11	9	no	no	downstream of xcpC
	372923	373124	+	0.481848	59/17	no/no	-3.072	11	9	no	no	
n32	375019	375232	+	0.41838	23/16	no/no	-3.556	11	10	no	no	MI
n33	396954	397065	-	0.304762	76/84	no/no	no	11	1	no	no	
n34	409504	409662	+	0.414675	4/15	rpoN/pred	-3.069	10	6	no	no	downstream of rpoN hyp. prot.
	409394	409810	-	0.414868	56/708	aq_600/pred	-3.069	10	6	no	no	
n35	428282	428500	+	0.439269	82/87	no/no	-3.522	2	9	no	no	downstream of xcpC
	428442	428483	-	0.553968	12/49	xcpC/pred	-3.522	2	9	no	no	
n36	436095	436143	+	0.54898	1/0	no/no	-3.453	5	9	no	no	hyp. prot.?
	436082	436158	-	0.554978	3/3	no/no	-3.453	5	9	no	no	
n37	450543	450791	+	0.455957	7/0	no/no	-4.276	11	2	no	no	intergenic
n38	455174	455274	-	0.530363	10/2	no/no	no	10	8	no	no	
n39	509608	509676	+	0.535749	10/5	no/no	no	11	1	no	no	hyp. prot.?
n40	526085	526338	-	0.430184	24/9	aq_759/no	-3.440	11	2	no	no	
n41	533660	533952	-	0.413424	57/121	no/no	-4.754	11	11	no	no	intergenic
n42	547442	547773	+	0.454719	9/102	cycB1/no	-3.100	8	11	no	no	
n43	560089	560157	+	0.596618	31/3	no/no	-6.696	11	8	no	no	downstream of 5s RNA
	560076	560174	-	0.532997	16/33	acpS/no	-6.696	11	8	no	no	
n44	567788	567989	+	0.638449	845/65	no/no	-4.118	11	7	no	0.998998	hyp. prot. hyp. prot.
	567675	567915	-	0.526141	2237/899	murF/UDP...	-3.892	11	7	no	0.998998	
n45	585803	585896	+	0.414539	5/6	aq_848/no	no	6	11	no	no	hyp. prot. hyp. prot.
	585709	586070	-	0.398435	11/37	no/pred	no	6	11	no	no	

ID	Location			GC	cDNA (+/-)	Annotation (old/BacProt)	Structure and Sequence				Remarks	
	Start	Stop	Ori				RNALfold	Cons_P	Cons_t	RNAz_p		RNAz_t
n46	593338	593362	+	0.564	1/0	no/no	-3.034	no	1	no	no	
	593179	593437	-	0.429472	0/1	no/no	-3.034	11	11	no	no	
n47	613937	614182	+	0.445528	28/6	aq_888/no	-4.097	9	4	no	no	hyp. prot.
	613956	614032	-	0.425541	2/3	no/no	-4.097	9	4	no	no	
n48	620055	620303	+	0.433467	24/70	nifU/pred	-3.130	11	9	no	no	
	620054	620211	-	0.437975	41/71	no/no	-3.130	11	9	no	no	MI
n49	622085	622449	+	0.421644	2/4	aq_900/shikimate	-3.502	11	11	no	no	upstream of aroE
n50	653826	654067	+	0.344904	29/13	no/no	-4.953	no	1	no	no	
n51	654477	654716	+	0.374028	7/82	aq_950/no	no	11	11	no	no	downstream of hyp. prot.
n52	663621	663719	+	0.517845	11/37	no/no	no	4	4	no	no	
n53	683853	683993	+	0.414657	31/48	no/no	no	11	11	no	no	
n54	692060	692111	+	0.467949	1/0	no/no	no	11	1	no	no	
	692018	692239	-	0.459459	1/4	no/no	no	11	1	no	no	
n55	713165	713342	+	0.466854	124/149	no/no	-3.393	11	11	no	no	
n56	714685	714852	-	0.374603	21/6	seld/pred	-3.050	7	7	no	no	upstream of seld
n57	739437	739680	+	0.473087	2/1	no/no	-3.638	11	9	no	no	MIT
	739499	739632	-	0.508955	4/2	no/no	-3.638	11	9	no	no	
n58	739705	739811	+	0.435202	41/144	no/no	-3.923	11	11	no	no	
n59	764473	764559	+	0.385824	2/0	no/no	no	no	2	no	no	
	764307	764563	-	0.354475	30/1	abcT3/pred	no	4	3	no	no	intergenic, upsream of abcT3
n60	805418	805489	+	0.348611	1/11	no/no	-4.006	no	1	no	no	
	805373	805483	-	0.348949	0/34	aq_1148/pred	-4.006	2	1	no	no	
n61	807371	807501	+	0.391603	32/73	no/no	no	no	1	no	no	
n62	822386	822796	+	0.430738	6/33	forG2/pred	no	10	7	no	no	
n63	827431	827698	+	0.424254	22/4	aq_1176/no	-3.218	5	5	no	no	hyp. prot.
	827533	827608	-	0.491667	2/2	no/no	no	5	5	no	no	
n64	843970	844156	-	0.408378	144/117	tRNA/no	-3.241	8	10	no	no	downstream of tRNA
n65	895418	895627	+	0.431746	4/1	no/no	no	7	8	no	no	
	895449	895522	-	0.512162	2/3	no/no	no	7	1	no	no	
n66	979905	979994	-	0.456667	0/5	no/no	-3.090	11	10	no	no	
n67	988611	988731	+	0.354821	26/644	aq_1391/pred	no	4	3	no	no	hyp. prot.
	988536	988766	-	0.367821	255/362	no/no	no	4	3	no	no	MI
n68	989704	989840	+	0.50073	476/756	aq_1392/auxin	-4.532	4	2	no	no	MIT, Aae-65 [?]
	989717	989811	-	0.556842	24/12	no/no	-4.296	4	1	no	no	
n69	1019731	1019833	-	0.521359	1/0	no/no	no	no	1	no	no	
n70	1046460	1046661	+	0.45396	3/0	no/no	-3.337	11	6	no	no	MI
n71	1081850	1081962	+	0.352802	4/105	pycA/pred	-3.173	7	7	no	no	intergenic
n72	1110143	1110381	+	0.488424	16/38	gltB/glutamate	no	11	11	no	no	intergenic, hyp. prot.
	1110271	1110378	-	0.499691	67/14	no/no	no	11	9	no	no	
n73	1139519	1139750	+	0.4875	6/113	no/no	-3.504	4	9	no	no	MI
	1139514	1139759	-	0.487127	2/7	no/no	-3.504	4	9	no	no	
n74	1153547	1153769	+	0.646039	326/51	no/no	-5.035	6	11	no	0.999634	MIT
	1153499	1153856	-	0.650186	83/31	tmRNA/no	-5.035	6	11	no	0.999634	tmRNA
n75	1168995	1169068	+	0.624324	25/7	no/no	-3.842	3	1	no	no	
	1168974	1169071	-	0.55068	158/79	aq_1666/no	-3.842	3	3	no	no	MIT
n76	1191850	1192169	+	0.509479	259/228	rRNA/no	-4.629	5	9	no	0.999597	upstream of rRNA
n77	1217091	1217362	-	0.458456	3/1	no/no	-3.585	8	9	no	no	
n78	1219679	1219903	+	0.55437	382/1384	pheT/phenylalanyl-tRNA	-6.592	11	11	no	no	6S RNA
n79	1226365	1226540	+	0.394886	9/5	no/no	no	5	1	no	no	
	1226365	1226423	-	0.520339	2/5	no/no	no	5	1	no	no	
n80	1231909	1232006	+	0.378231	860/2339	no/no	-3.739	11	2	no	no	MI
	1231708	1231996	-	0.375894	191/93	no/no	-3.739	11	2	no	no	MI
n81	1256338	1256650	-	0.432481	9/7	fumB;tartrate/fumarate	-4.141	10	10	no	no	downstream of protein
n82	1272457	1272552	+	0.585417	17/6	no/no	-3.152	9	7	no	no	
n83	1288346	1288407	+	0.391935	84/10	no/no	-3.261	11	11	no	no	
n84	1302269	1302294	+	0.591026	1/0	no/no	-3.233	10	4	no	no	MI
n85	1303758	1303875	+	0.566384	5239/456	no/no	-4.150	11	11	no	0.708541	SRP RNA
	1303773	1303823	-	0.642484	15/5	no/no	-4.150	11	11	no	0.708541	
n86	1314643	1314907	+	0.334591	9/4	no/no	-3.718	5	1	no	no	
n87	1344102	1344198	+	0.490034	14/8	no/no	-3.253	8	9	no	no	
	1344014	1344214	-	0.418076	13/11	hflX/small	-3.253	11	11	no	no	hyp. prot.
n88	1348471	1348602	+	0.47803	14/10	no/no	-3.216	11	11	no	no	MI
	1348433	1348616	-	0.458152	7/10	no/no	-3.216	11	11	no	no	MI
n89	1352041	1352310	-	0.420247	1/0	fliP/flagellar	-3.821	11	11	no	no	intergenic
n90	1361752	1361840	-	0.407116	26/85	no/no	-3.447	11	11	no	no	
n91	1380117	1380156	+	0.5525	17/8	no/no	-3.347	10	1	no	no	
	1379991	1380161	-	0.391228	31/7	no/no	-3.955	10	6	no	no	
n92	1386353	1386453	+	0.536304	0/2	hisIE/phosphoribosyl-ATP	-3.551	11	7	no	no	intergenic
	1386359	1386479	-	0.533058	5/19	no/no	-3.551	11	7	no	no	

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	Start	Stop						Cons_P	Cons_t	RNAz_p	RNAz_t	
n93	1405450	1405526	-	0.355411	66/453	no/no	-3.623	5	8	no	no	
n94	1411631	1411894	-	0.496338	10/3	rpsB/30S	-3.295	11	11	no	no	intergenic, MI
n95	1423607	1423734	+	0.565365	4/2	tldD/peptidase	no	10	10	no	no	downstream of tldD, MI
	1423621	1423715	-	0.575789	8/1	no/no	no	10	10	no	no	MI
n96	1481418	1481667	+	0.4148	6/2	no/no	-3.362	11	7	no	no	
n97	1491296	1491381	+	0.362015	1/0	no/no	-4.597	11	11	no	no	
	1491199	1491559	-	0.402031	10/297	rfaG/glycosyl	-4.597	11	11	no	no	MI
n98	1540058	1540430	+	0.452279	7/8	coxB/pred	-4.959	5	5	0.697995	no	intergenic
n99	1541885	1542170	+	0.375524	24/17	no/no	-3.895	5	5	no	no	
	1541931	1542008	-	0.378633	2/4	no/no	-3.258	5	5	no	no	
Head to Head Transcripts (H2H)												
h2h1	1112811	1113061	+	0.449535	25/18	aq.1575/hypothetical	-3.144	11	11	no	no	upstream of hyp. prot.
	1112815	1112907	-	0.43871	14/20	no/no	-3.144	11	11	no	no	
h2h2	1152396	1152684	+	0.327336	175/260	cap/pred	-3.384	6	2	no	no	
	1152431	1152502	-	0.356481	25/667	aq.1640/pred	-3.384	4	2	no	no	
h2h3	1506456	1506563	+	0.426852	35/44	glyS/glycine-tRNA	no	11	11	no	no	
	1506377	1506540	-	0.424593	31/44	aq.2140/no	no	11	11	no	no	
Tail to Tail Transcripts (T2T)												
t2t1	20900	21146	+	0.482321	11/16	aq.032/hypothetical	no	7	8	no	no	
	21003	21128	-	0.503968	8/1	aq.035/diguanylate	no	7	8	no	no	
t2t2	85245	85505	+	0.418135	13/66	cpx/pred	-3.857	11	8	no	no	
	85379	85439	+	0.425137	1/2	ribD1/riboflavin	-3.857	11	8	no	no	
t2t3	97265	97320	-	0.365476	0/1	apfA/pred	no	6	6	no	no	
	97259	97323	-	0.364103	0/12	aq.159/2-nitropropane	no	6	6	no	no	
t2t4	147335	147790	+	0.481725	16/74	fccB%27/pred	-3.589	11	11	no	no	
	147494	147652	-	0.472327	33/38	guaA/GMP	no	11	11	no	no	
t2t5	229888	230012	+	0.447733	29/41	ribA/bifunctional	-3.730	11	11	no	no	
	229900	230000	-	0.469967	10/24	leuS/leucyl-tRNA	-3.730	11	11	no	no	
t2t6	305555	305684	+	0.427436	3/14	aq.450/hypothetical	-4.479	11	11	no	no	
	305518	305774	-	0.4262	6/41	ilvB/acetolactate	-4.479	11	11	no	no	
t2t7	404444	404519	+	0.395175	45/173	aq.592/pred	no	11	11	no	no	
	404443	404520	-	0.394444	61/98	frdA/succinate	no	11	11	no	no	
t2t8	462957	463258	+	0.429801	3/36	atpA/F0F1	-3.306	11	11	no	no	
	463121	463208	-	0.415909	7/15	arsA1/pred	no	11	9	no	no	
t2t9	509162	509424	+	0.500634	236/121	hisH/imidazole	-3.197	11	11	no	no	
	509184	509430	-	0.518354	126/35	rpsG2/30S	no	11	11	no	no	
t2t10	608075	608182	+	0.521605	60/20	aq.880/no	-3.695	11	11	no	no	
	608075	608308	-	0.483333	22/12	aq.881/1-deoxy-D-xylulose-5-phosphate	-3.695	11	11	no	no	
t2t11	768269	768382	+	0.421053	5/9	abcT5/ABC	-4.487	11	9	no	no	
	768295	768365	-	0.54507	13/8	fabH/Beta-ketoacyl-acyl-carrier-protein	-4.487	11	9	no	no	
t2t12	907445	907578	+	0.373383	24/17	no/no	-3.692	11	11	no	no	
	907387	907759	-	0.401251	7/21	hspC/heat	-3.692	11	11	no	no	
t2t13	922776	922884	+	0.41682	19/40	omp/pred	-3.573	11	11	no	no	
	922811	922883	-	0.407306	4/24	cspC/cold-shock	-3.573	11	11	no	no	
t2t14	938900	938984	+	0.532941	95/41	aq.1323/4-diphosphocytidyl-2C-methyl-D-erythritol	no	11	8	no	no	
	938888	939157	-	0.486173	154/42	aq.1324/no	no	11	8	no	no	
t2t15	962368	962473	+	0.449686	4/21	aq.1354/hypothetical	no	8	9	no	no	
	962409	962483	-	0.432889	6/48	lipA/pred	no	8	9	no	no	
t2t16	1040664	1040710	+	0.404255	0/4	gcvT/no	-9.142	5	4	no	no	
	1040618	1040782	-	0.48303	82/12	npr/pred	-9.142	5	5	no	0.959026	
t2t17	1336433	1336708	+	0.455314	380/87	aq.1896/pred	no	11	11	no	no	
	1336544	1336642	-	0.509091	100/55	fold/methenyltetrahydrofolate	no	11	11	no	no	
t2t18	1375009	1375108	+	0.429	23/26	rhbB/ribonuclease	-3.950	11	11	no	no	
	1375010	1375325	-	0.425844	25/46	aq.1956/pred	-3.950	11	11	no	no	
t2t19	1436451	1436619	+	0.447535	27/38	hemX2/pred	-4.373	10	11	no	no	
	1436470	1436716	-	0.438597	79/73	aq.2044/pred	-4.373	10	11	no	no	
t2t20	1479248	1479345	+	0.443878	180/117	prmA/ribosomal	no	11	8	no	no	
	1479168	1479508	-	0.432845	12/62	acs%27/pred	-3.185	11	8	no	no	
t2t21	1514628	1514713	+	0.435271	10/3	aq.2146/pred	no	9	5	no	no	
	1514629	1514927	-	0.419064	15/58	pal/pred	-3.249	9	5	no	no	

ID	Location		Ori	GC	cDNA (+/-)	Annotation (old/BacProt)	Structure and Sequence				Remarks	
	Start	Stop					RNALfold	Cons_P	Cons_t	RNAz_p		RNAz_t
tRNAs (first id: aq_xxx (NCBI); second id from LOWE lab)												
263;1	168861	168974	+	0.60731	11/15	hemC;tRNA/no	-3.515	2	11	no	0.999385	
t02;2	168876	168975	-	0.648667	1/1	no/no	-3.515	2	11	no	0.999385	
	215831	216006	+	0.561932	32/12	dcuP;tRNA/pred	-3.204	11	11	no	no	
t03;3	215838	215901	-	0.644271	3/0	no/no	-3.204	8	3	no	no	
	217778	217911	+	0.621144	70/62	tRNA/no	-4.673	7	11	no	0.997945	transcribed with aq_t04
t04;4	217779	217960	-	0.599267	162/49	cysQ/pred	-4.673	7	11	no	0.997945	
	217802	217952	+	0.624283	84/30	tRNA/no	-4.673	7	11	no	0.997945	transcribed with aq_t03
t05;44	217780	217970	-	0.582548	642/203	cysQ/pred	-4.673	7	11	no	0.997945	
	296984	297066	+	0.583534	4/1	no/no	-3.087	11	9	no	0.997219	
t06;43	296967	297071	-	0.521587	13/2	tRNA/no	-3.087	11	9	no	0.997219	
	383154	383390	-	0.522644	9/2	recN;tRNA/pred	-3.532	11	10	no	0.994289	
t07;5	403079	403193	+	0.538841	9/3	aq_591;tRNA/pred	-3.179	11	8	no	no	
	403110	403226	-	0.4849	1/0	no/no	-3.179	11	2	no	no	
t08;42	443916	443998	+	0.595984	1/3	no/no	-5.009	2	11	no	no	
	443880	444010	-	0.509924	6/2	tRNA/no	-5.009	2	11	no	no	
t09;41	450374	450487	+	0.576901	64/35	topA/DNA	-3.854	11	11	no	0.999130	
	450323	450491	-	0.515385	68/20	tRNA/no	-3.854	11	11	no	0.999130	
t10;6	552596	552717	+	0.575956	78/36	mbhS3;tRNA/pred	no	11	11	no	no	
	552630	552691	-	0.689785	5/0	no/no	no	11	11	no	no	
t11;40	570914	571019	+	0.607233	37/7	no/no	-7.462	11	7	no	no	within rRNA operon
	570930	571148	-	0.598326	16/8	tRNA/no	-7.462	11	7	no	0.999894	
t12;39	571019	571085	+	0.606965	2/0	no/no	-7.462	11	7	no	0.999894	within rRNA operon
	570959	571148	-	0.59386	2/19	tRNA/no	-7.462	11	7	no	0.999894	
t13;38	601690	601811	+	0.56612	6/1	no/no	-3.034	11	10	no	0.998506	
	601690	601811	-	0.56612	8/2	nadC;tRNA/nicotinate- nucleotide	-3.034	11	10	no	0.998506	
t14;37	619930	619946	+	0.772549	1/0	no/no	-3.113	11	8	no	no	
	619821	619991	-	0.558674	3/0	ispB;tRNA/polyprenyl	-3.113	11	11	no	no	
t15;36	643550	643738	+	0.495944	744/303	aq_931/no	-4.039	11	11	no	no	
	643505	643698	-	0.537457	308/173	tRNA/no	-4.039	11	11	no	no	
t16;7	727357	727468	+	0.622917	11/1	gcsH1;tRNA/no	-4.425	5	5	0.999349	0.998875	
	727370	727441	-	0.676389	3/0	no/no	-4.425	5	5	0.999349	0.998875	
t17;35	730596	730676	+	0.670782	9/2	no/no	-4.148	11	8	no	0.996849	
	730557	730693	-	0.507056	19/1	tRNA/no	-4.148	11	8	no	0.996849	
t18;34	844008	844270	+	0.449176	1425/1063	forG1/pyruvate/- ketoisovalerate	-3.764	8	10	no	0.845674	
	844106	844260	-	0.471828	397/155	tRNA/no	-3.509	8	10	no	0.845674	
t19;33	861845	861983	+	0.515108	10/7	no/no	-4.838	8	2	no	no	
	861740	861988	-	0.441767	14/3	aq_1223/pred	-4.838	8	2	no	no	
t20;32	898193	898392	+	0.5545	511/252	hvsT/pred	-4.099	9	11	no	0.995791	
	898256	898394	-	0.594005	475/127	tRNA/no	-4.099	9	11	no	0.995791	
1340;3	955423	955496	+	0.668018	6/1	no/no	-4.411	11	10	0.996839	0.861024	
	955407	955510	-	0.609615	55/33	tig;tRNA/pred	-4.411	11	10	0.996839	0.861024	
t22;8	970375	970467	+	0.615771	60/30	tRNA/no	-3.089	11	7	no	no	
	970372	970474	-	0.582848	278/77	no/no	-3.089	11	7	no	no	
t23;9	971982	972102	+	0.565014	125/88	aq_1365;tRNA/car- bohydrate	-4.591	11	7	no	no	
	972001	972121	-	0.593939	1227/283	thiE1/no	-4.591	11	7	no	no	
t24;10	1050467	1050560	+	0.579433	4/5	tRNA/no	-3.069	10	11	no	0.998451	
	1050489	1050567	-	0.579325	9/1	no/no	-3.069	10	11	no	0.998451	
t25;30	1147682	1147847	+	0.521687	7/4	no/no	-3.953	11	11	0.995770	0.913677	
	1147755	1147847	-	0.598566	4/3	tRNA/no	-3.953	11	11	0.995770	0.913677	
t26;29	1174258	1174391	+	0.511194	119/121	hsiV/ATP- dependent	-4.465	11	11	no	0.992841	
	1174304	1174399	-	0.585069	50/19	tRNA/no	-4.465	11	11	no	0.992841	
t27;11	1193706	1193895	+	0.593158	4/18	tRNA/no	-7.648	5	8	no	0.999142	
	1193769	1193835	-	0.605473	6/1	no/no	-7.648	5	8	no	0.999142	
t28;12	1193706	1193924	+	0.597565	16/8	tRNA/no	-7.648	5	8	no	0.999142	
	1193835	1193940	-	0.608491	37/7	no/no	-7.648	5	8	no	0.999142	
t29;13	1196950	1197202	+	0.570883	462/139	rRNA;tRNA/no	-4.020	9	11	no	0.998404	transcribed with 5S RNA
t30;28	1197104	1197201	-	0.537415	443/211	aq_1695a/pred	-4.020	9	11	no	0.998404	
	1231188	1231304	+	0.587749	11/5	no/no	-4.541	11	9	no	0.998319	
t31;27	1231159	1231324	-	0.521687	144/37	murE;tRNA/UDP- N-acetylmuramyl- tripeptide	-4.541	11	11	no	0.998319	
	1242810	1242918	+	0.531804	203/82	no/no	-4.295	11	2	no	no	
t32;26	1242824	1242994	-	0.588694	81/63	tRNA/no	-4.295	11	8	no	0.970277	
	1242899	1243017	+	0.557423	102/76	no/no	-4.295	11	8	no	0.970277	
t33;14	1242824	1243017	-	0.575773	93/40	tRNA/no	-4.295	11	8	no	0.970277	
	1245125	1245372	+	0.475941	5/0	rpsT/no	-5.274	11	10	no	no	
t34;15	1245141	1245168	-	0.608333	2/0	no/no	-5.274	11	1	no	no	
	1356464	1356743	+	0.6375	23/5	tRNA/no	-5.429	11	10	0.999604	0.999175	
t35;16	1356461	1356575	-	0.603188	61/15	no/no	-5.429	11	9	0.999604	0.999175	
	1356515	1356744	+	0.656087	90/24	tRNA/no	-5.429	11	10	0.999604	0.999175	
	1356560	1356774	-	0.611163	86/23	no/no	-4.557	11	11	0.999604	0.999175	

ID	Location			GC	cDNA (+/-)	Annotation (old/BacProt)	Structure and Sequence					Remarks
	Start	Stop	Ori				RNALfold	Cons_P	Cons_t	RNAz_p	RNAz_t	
t36;17	1356515	1356748	+	0.653276	88/34	tRNA/no	-5.429	11	10	0.999604	0.999175	
	1356574	1356774	-	0.613267	64/23	no/no	-4.557	11	11	0.999604	0.999175	
t37;18	1356751	1356875	+	0.528533	15/8	tRNA/no	-4.557	11	11	no	0.997874	
	1356770	1356874	-	0.566984	93/33	no/no	-4.036	11	11	no	0.997874	
t38;19	1358311	1358461	+	0.484768	24/20	secE;tRNA/no	-4.137	10	11	0.998811	0.998895	
	1358323	1358422	-	0.572	76/26	no/no	-4.137	10	11	0.998811	0.998895	
t39;25	1375982	1376086	+	0.580635	27/8	no/no	no	no	7	no	no	
	1375993	1376087	-	0.609825	40/19	tRNA/no	no	no	7	no	no	
t40;24	1452919	1452999	+	0.597119	35/39	no/no	-3.347	11	7	no	0.997397	
	1452935	1452978	-	0.671212	9/0	tRNA/no	-3.347	11	4	no	0.997397	
t41;23	1453025	1453145	+	0.578512	61/18	no/no	-3.792	11	8	no	0.955503	
	1453025	1453147	-	0.574255	169/26	tRNA/no	-3.792	11	8	no	0.955503	
t42;22	1515319	1515429	+	0.517117	11/39	no/no	-5.597	4	5	no	no	transcribed with aq_t43
t43;21	1515286	1515521	-	0.521045	32/19	tRNA/no	-5.597	4	10	no	0.963569	transcribed with aq_t42
	1515405	1515520	+	0.616092	94/26	no/no	-5.597	4	10	no	0.963569	
t44;20	1515286	1515521	-	0.521045	32/19	tRNA/no	-5.597	4	10	no	0.963569	MIT
	1531016	1531131	+	0.583333	1141/437	ihfB/no	-4.333	7	9	no	0.995079	
	1531004	1531130	-	0.56168	335/136	tRNA/no	-4.333	7	9	no	0.995079	