

**Table S2.** Mapped transcription start sites (TSS)

Gene <sup>a</sup>	Score (bit) <sup>b</sup>	BRE/TATA box sequence	TSS <sup>c</sup>	Coord <sup>d</sup>	Dir <sup>e</sup>	Dist (nt) <sup>f</sup>	PE <sup>g</sup>	RACE <sup>h</sup>	Protein detected <sup>i</sup>	Div <sup>j</sup>
MJ0007	10.71	AAGATAAGATTTTTATG	ACTCTTTTAA <b>t</b> gAATT	8805	+	82	+	+	+	+
MJ0035	10.77	ATGGTAATCTTTTTATT	AAAAATATAT <b>C</b> gCCTT	37321	-	52	ND	+	+	+
MJ0068	12.25	AACAATAACTTTAAATA	CTAAGGTAAT <b>T</b> aATAA	65915	-	54	ND	+	+	+
MJ0084	12.06	TTAGAAAAAGATTTATA	TAGGTTTTAA <b>t</b> tAAAT	78718	+	28	ND	+	+	-
MJ0094	7.92	CTGGTAAAAAATAAAAA	AGATAGTTTT <b>T</b> aAGAA	89505	-	24	ND	+	+	-
MJ0113	14.65	ATAATAACGTTTATATA	AACTTAATCT <b>T</b> aATCT	111553	-	38	ND	+	+	+
MJ0136A	13.92	GCAGTAAGCATTTTATA	AATATTTAA <b>A</b> aCTAC	131332	+	135	+	+	+	+
MJ0136B	6.93	TAAAGAATATTTAAATA	TATAGTTTT <b>T</b> TgCAA	131355	+	112	+	+	+	+
MJ0161A	16.30	TCCCAAAAATTTATATA	TAAATCCTAT <b>T</b> aCCCA	165485	-	326	ND	+	+	+
MJ0161B	10.26	ATCATAATTATTATATG	ATATCTATTT <b>T</b> aTTAT	165200	-	41	ND	+	+	+
MJ0168	19.63	ACCGAAAAGTTTAAATA	CAGTATTTAT <b>T</b> gGAAA	171034	-	24	ND	+	+	+
MJ0176	18.83	ACCAAAAATTTTATATA	TATTTGTTTAT <b>a</b> CACT	178134	+	286	ND	+	+	+
MJ0199	14.52	TCCGATAATTATATATA	CTTAATCAAT <b>T</b> aTTAA	192346	+	36	ND	+	+	-
MJ0201	11.88	AAGATAAGTTATAAATA	TCTTAAACA <b>A</b> aCGGC	193495	-	12	-	+	-	+
MJ0202	8.94	TAAGAATTC TTAAATA	TAATCATATTT <b>a</b> TCgC	193488	+	88	-	+	+	+
MJ0205	13.72	AGCAAAAGATATTAATA	AAAATTTAA <b>A</b> gAGGG	198495	-	45	ND	+	+	-
MJ0217	6.25	AGCTGAAAAGTATAAAAG	AAAATATA <b>A</b> aAGGT	209106	-	159	ND	+	+	-
MJ0223	17.07	ATAAAAAATTTTATATA	AAAATATT <b>a</b> CAATAA	214490	-	19	ND	+	+	-
MJ0224A	8.82	TGCAAAAGATAAAATATA	TTCCCAT <b>A</b> ATTaTAAA	215116	-	47	ND	+	-	+
MJ0224B	10.36	AAAGATAAATATATATT	TAATTATA <b>A</b> AAaCCTA	215110	-	41	ND	+	-	+
MJ0237	8.99	CCCATTGGGTTTTTATA	TAAATAAGTT <b>T</b> aTTTG	227871	+	149	ND	+	+	+
MJ0252	8.84	ACATCAACTTTTTTATA	AAACTATA <b>a</b> CGCAAAA	238826	+	20	ND	+	+	+
MJ0269	16.17	CTCCAAAAC TTTTATATA	AATTGTT <b>A</b> ATgATTGA	255926	-	28	ND	+	+	-
MJ0299	15.97	AAAGTTAAATTTTATATA	TAAATATA <b>A</b> aTTAA	282956	-	41	ND	+	+	+
MJ0307	20.41	TTGGAAAAC TATTTTATA	AAATTT <b>T</b> TATTaTAAA	288310	-	30	ND	+	+	-
MJ0313	16.26	ATGCAAAAATTTT TATA	TAATTA <b>a</b> CATTaCTCC	293490	-	55	ND	+	+	+
MJ0318	16.18	ATGATAAGATATTAATA	AAACTATA <b>a</b> TTgTTAA	297462	-	25	+	+	+	+
MJ0319	11.73	AACAATAATTTTAAATA	AATATA <b>a</b> CAATtAAAA	297586	+	23	+	+	+	+
MJ0369	9.05	CCAAATAATTATATATG	AGTAT <b>T</b> CCCTTaCATG	336195	-	158	+	+	+	+
MJ0370A	15.81	ACCAATAGATTTT TATA	AATTGA <b>A</b> TAATaATAA	336157	+	154	+	+	+	+

MJ0370B	7.72	AGGGAATACTATATAAAA	ATTATTTGGTT <b>a</b> ATAG	336238	+	73	+	+	+	+
MJ0400	15.70	AACACAAATTTTAAATA	ATTTCTATATT <b>a</b> AAAC	361536	+	54	ND	+	+	+
MJ0405A	10.78	TTTGAACCCTTTATATA	AAATTGTTTAT <b>a</b> TAGA	365443	-	61	+	+	+	+
MJ0405B	13.06	CAAAAATTGTTTATATA	AAGTTAAAATT <b>a</b> TTGA	365418	-	36	+	+	+	+
MJ0406	9.37	CTAAAAATCTTTAAGTA	AATTTTAACTTT <b>t</b> AAAG	365430	+	128	-	+	+	+
MJ0428A	12.76	CACAAAATATTTTTATA	AATTATAAAATC <b>c</b> TTAA	385102	-	119	-	+	+	+
MJ0428B	6.83	TCCTTAAACTTTTTGTA	AGTTTTGGAGT <b>a</b> TATA	385063	-	80	-	+	+	+
MJ0429	7.39	TAGGTGAGTTATATATA	TAAGCAATAAAA <b>a</b> TaCA	385087	+	64	-	+	+	+
MJ0445A	14.82	ATCAACACATATATATA	AAGTAGATATT <b>a</b> CAAA	399406	-	226	ND	+	+	+
MJ0445B	7.82	AATCTAAGGTTTATTAA	CACTTTATATT <b>g</b> GACA	399347	-	167	ND	+	+	+
MJ0450	15.46	ACTATAAGATATAAATA	TAAAAATAATT <b>a</b> AGAA	403211	+	63	ND	+	+	+
MJ0507A	8.75	AAAAGTATTTATATATA	ATGGGGTTTTT <b>a</b> TATA	448306	-	38	ND	+	+	-
MJ0507B	12.39	TATATAAAGTATTTATA	ATATAATATCT <b>a</b> aGTT	448295	-	27	ND	+	+	-
MJ0510A	17.11	ACCGAAAATTTTATATA	ATCTTAGCAAT <b>a</b> TAAA	450696	-	140	ND	+	+	-
MJ0510B	12.06	TAAGTAAAATATTTATA	ATAATATGGAT <b>g</b> CTTT	450593	-	37	ND	+	+	-
MJ0533A	6.05	AATATTAATTATAAGAA	AAGATTACAAC <b>a</b> TTAA	469072	-	120	ND	+	+	+
MJ0533B	7.01	GATTACAACATTAAATA	AGTAATATATA <b>a</b> TAAA	469043	-	91	ND	+	+	+
MJ0533C	9.12	GGCGATAGTAATATATA	AATGTTAATTT <b>a</b> AGTA	469022	-	70	ND	+	+	+
MJ0547	9.05	ACCGAAGAGTATATATT	ACTTTAGTGTT <b>g</b> TAAA	484446	-	39	ND	+	+	-
MJ0555	9.36	AACATAAATCTAAAATA	ATACATTAACT <b>a</b> CTAT	490758	+	24	ND	+	+	+
MJ0561	12.72	TTAATTAACTTTAAATA	AAAAAAATATA <b>a</b> GGTT	495573	+	30	ND	+	+	+
MJ0622	15.46	AAGTTAAAGTATATATA	AAGTAAATTTT <b>g</b> TATA	552424	-	24	ND	+	+	+
MJ0660	14.23	ATCCATAAGTATTTATA	AGGTTGTTATT <b>g</b> AGCG	586407	-	42	ND	+	+	-
MJ0666A	2.18	CCACTAATTTCTTTATC	TTATATTTTCT <b>a</b> AACT	592655	-	45	-	+	-	+
MJ0666B	8.98	TCTATTAATTTTTTATA	ATATTTTCTTT <b>a</b> ATAT	592635	-	25	-	+	-	+
MJ0666C	12.47	TTTCTAAACTTTTATATA	TACTTCTCATT <b>g</b> GTGA	592619	-	9	-	+	-	+
MJ0667A	4.59	ATGAGAAGTAATATTAA	AAGTTTAgAAA <b>a</b> TATA	592661	+	41	+	+	+	+
MJ0667B	14.73	TAAAGAAAATATATAAA	AAAAATTTAAT <b>a</b> gATA	592676	+	26	+	+	+	+
MJ0673	12.91	ATAGTTAAGTTTTTATA	ATTCATTATTC <b>a</b> TAGA	599083	+	171	+	+	+	+
MJ0696	8.91	CCAAAAATAATAAATC	AATAATAACTT <b>a</b> TATG	622498	-	147	-	+	-	+
MJ0697A	0.64	CCATATATGCATATAAG	TATATTGCATT <b>a</b> GATT	622521	+	25	-	+	+	+
MJ0697B	10.60	ATAAGTTATTATTTATA	TATTATTTTTT <b>g</b> GTGA	622537	+	9	+	+	+	+
MJ0720	14.51	AACAAAACATTTTTTATG	TTATTAATATT <b>g</b> CTaT	654955	-	28	ND	+	+	+

MJ0746	16.23	ACCATTAATATTATATA	TATTTTATAAT <b>g</b> TAAAT	672878	-	31	+	+	+	-
MJ0765	15.95	TCAAAAATATATTTATA	AAGATTTTAAAT <b>g</b> TAAA	688516	-	62	ND	+	+	-
MJ0784	17.11	ATAGATAAATTTTATATA	ACAATAATATT <b>a</b> CCAA	706977	+	38	ND	+	+	-
MJ0800	13.27	GCACAAAGGAATATATA	ATGTTAGAATT <b>a</b> ATAA	723642	+	131	ND	+	+	-
MJ0822	15.20	ATCGTAAGATTTTATATA	AGGTATATACC <b>g</b> TCAA	744550	-	39	+	+	+	+
MJ0823	12.63	GTAGAAACTTTATAAAAA	TATAATGAATT <b>a</b> GAAA	744794	+	35	+	+	+	+
MJ0825	13.01	TCAGTTATGTTTATATA	AAATTATGAAA <b>g</b> ATTT	747343	-	56	+	+	+	+
MJ0826	17.29	ACGAAAAATTTTAAATA	CATAATTAATT <b>a</b> AGCA	747429	+	32	+	+	-	+
MJ0841A	9.18	CAGGCAAAGTTTTAAAA	TAAAATCCAAT <b>a</b> ATTT	768302	-	78	-	+	+	+
MJ0841B	5.78	GTTTTAAAATTAAAATA	AATAATTTTT <b>g</b> GTGAA	768294	-	70	-	+	+	+
MJ0842	5.38	AAAACCTGGATATATATA	TAAC TAATATC <b>g</b> AACC	768428	+	25	+	+	+	+
MJ0847	14.77	ATAGAAAACCTTATATA	AACTAAGTCTT <b>a</b> TGTA	773683	+	20	ND	+	+	-
MJ0864	5.05	GTTTCTAACTATATATA	TACCTTAATGT <b>g</b> AGGT	788088	-	11	+	+	+	+
MJ0865	4.26	ATACCTCATTATAAATA	TAATTTAAAG <b>g</b> AAAT	788198	+	67	+	+	+	+
MJ0882A	7.77	TTAAGAACTGTTTTATT	TATAATAAATT <b>a</b> ACTG	807717	+	61	ND	+	-	+
MJ0882B	3.43	ATTGTATTTTTTATAAT	AAGAATTT <b>g</b> TC <b>a</b> TAAA	807736	+	42	ND	+	-	+
MJ0891	10.05	CGCAAAAAGAATATATT	CAGTTTATAGT <b>g</b> AGGT	821616	+	89	+	+	+	+
MJ0923A	13.97	TTAAGAACTATTATATA	AAATATTAAT <b>a</b> GTAA	853279	+	88	-	+	-	+
MJ0923B	3.10	TGGTTAAATATTTAAATA	TATAGTCAGAA <b>g</b> GTAA	853303	+	64	-	+	-	+
MJ0923C	12.13	ATAGTAACACATTTATA	TAATAGAAAAT <b>a</b> TTTT	853316	+	51	-	+	-	+
MJ0923D	10.84	ATAGAAAATATTTTATA	TAAATAAGTCC <b>a</b> ATAG	853347	+	20	-	+	-	+
MJ0936	10.27	TAAAAAATTGTTATATA	TAGATAGTGTT <b>a</b> TAAA	865503	+	41	ND	+	+	-
MJ0952	9.08	ACAATAAGTTTTATTAA	TATCTCTTACT <b>a</b> TAGG	884415	-	118	+	+	+	+
MJ0953	13.82	ATAGTAAGAGATATATA	TAAAACCTTATT <b>g</b> TAAAG	884456	+	31	-	+	-	+
MJ0968	11.82	CACAATAATTCTTTATA	ATTTAATTA <b>a</b> T <b>g</b> GGGT	901986	+	9	ND	+	+	+
MJ0986	11.84	GCAAAAACTATATATATT	AAATAACTACC <b>a</b> ATAA	917748	-	182	-	+	-	+
MJ0987	13.94	AGGAAAAGATTTTATA	ATTTTACTATC <b>a</b> GCAA	917767	+	141	+	+	+	+
MJ0990	11.26	CAGATTAATTTTTTATA	ACCTACTTTT <b>a</b> TAAA	919937	-	23	+	+	+	+
MJ0991	14.60	AGAGGAAGCTATTTATA	AATTAAGTTTT <b>a</b> TTAG	920151	+	28	+	+	-	+
MJ0999	16.12	ACCGAAAGGTTTATATA	AACATATACAT <b>a</b> CCGA	928545	-	31	+	+	+	+
MJ1018	7.77	ACTATCACATATATATA	ATCATCTATCT <b>a</b> CTGC	949195	-	70	+	+	+	+
MJ1019A	8.04	ACCATAAATTATAAAAT	CTAAAAGCAGT <b>a</b> GATA	949196	+	62	-	+	+	+
MJ1019B	8.26	TCCAATCATATATATA	TAGGTATTTT <b>g</b> GTGAA	949249	+	9	+	+	+	+

MJ1035A	9.16	TATATAACTTAAATAAA	TATTTTTT <b>a</b> ATA <b>a</b> ACAA	967284	-	116	-	+	+	+
MJ1035B	11.30	GTAGTAAGATATTTATT	ATAATACTAAT <b>a</b> TCCC	967199	-	31	+	+	+	+
MJ1053	14.97	TACAAAACTTTAAATA	AAAATAGAT <b>a</b> T <b>a</b> AGGA	990383	-	35	+	+	+	+
MJ1054	14.64	AACGAAAATTATAAGTA	AATTAATTGTT <b>g</b> GAGG	990847	+	117	+	+	-	+
MJ1099	15.18	AACATTAAGTTTTTATA	TAATCATTTTT <b>g</b> AAAT	1040346	-	25	-	+	+	+
MJ1146A	15.04	TAAACAAATTATAAAAA	AAGTAATTATT <b>a</b> TTAA	1086364	-	33	+	+	+	+
MJ1146B	8.12	TTATAAAAAATATATATT	TATTATTAATC <b>c</b> TACA	1086357	-	26	+	+	+	+
MJ1158	14.68	TTAAAAAATAATATATA	TAAATTTTTT <b>a</b> TGTA	1097639	-	41	-	+	+	+
MJ1185	12.79	AACAAAATCTATAAAAT	AAATAAAAATT <b>a</b> ACAT	1125066	-	37	+	+	+	+
MJ1186	9.14	AATATAATATTTAAATA	CTTTACTTTTT <b>g</b> AAAA	1125163	+	28	-	+	-	+
MJ1225	12.75	AGGATAATCATTTTATA	ATATTAATATT <b>a</b> TGTG	1167042	+	58	+	+	+	+
MJ1228	14.47	ATAGTAATATTTATATA	TAGTTATTA <b>a</b> AGTTT	1171550	-	33	ND	+	+	-
MJ1246	11.39	AACGACACATATAAAAA	ATATAAATTTT <b>a</b> CGGT	1189802	-	30	ND	+	+	+
MJ1249	9.12	TTGAGAAGTTAAATATA	AAATCTAAAAC <b>a</b> ATAA	1191345	+	19	+	+	+	+
MJ1259	16.21	GCAAAAAACTATAAATA	TTGATATTAAT <b>a</b> ACTC	1201107	+	31	ND	+	+	-
MJ1260	13.38	ACCAAAAATTATTTAAA	CAATAATTATC <b>c</b> TGGC	1202056	+	227	ND	+	+	-
MJ1265	10.72	ATCAAAAAGCTTTAAAG	TAATAGTAATT <b>a</b> TATA	1210366	-	25	+	+	+	+
MJ1266	16.91	CTCGAAAATTTTAAATA	AAAATGAAATT <b>g</b> CCAT	1210494	+	73	+	+	+	+
MJ1311	4.04	AACCAAAAAGCTAAAAG	AAATATTAATT <b>t</b> GAAG	1256405	+	47	ND	+	+	+
MJ1333	11.75	GTGTTAAAATATTTATA	TAATGATATT <b>t</b> AAAAT	1282486	+	24	+	+	+	+
MJ1334	11.74	TCACCAAATTATTTATA	ACTATATAATT <b>g</b> TAAC	1284162	-	42	+	+	+	+
MJ1335	9.28	TATGTTACAATTATATA	TAGGTATAAAT <b>a</b> ATTT	1284195	+	140	-	+	-	+
MJ1338	15.40	ATAATAAAGTATTTATA	AAACTCTAAAT <b>g</b> CGTA	1286293	+	31	ND	+	+	-
MJ1403	13.57	ATCGTAAGATTTTATATA	ATATACTGCAT <b>a</b> AGTA	1365854	-	116	+	+	+	+
MJ1404	13.09	CTGTTAAACTTTTAAATA	TAATATCAATC <b>a</b> TCAA	1366077	+	29	+	+	+	+
MJ1486	8.70	ACAAAAAATATATTAA	AAAGCTAAAGT <b>a</b> TAGA	1458931	-	42	-	+	+	+
MJ1534	5.12	AATAGAAAACCTTAATTA	ATATAATAATT <b>g</b> TGT	1511775	+	31	+	+	+	+
MJ1543	6.20	ACCGAAAACCTTAAAT	CTAATAAAGGT <b>a</b> GCgA	1521373	+	39	ND	+	+	+
MJ1585	15.50	ATAGGAAATTATTAATA	TAACTATTTTT <b>g</b> TAGT	1559201	-	35	+	+	+	+
MJ1586	10.36	CCCACAATAAATATATG	AAAATAGTTAT <b>g</b> TGAG	1559214	+	39	+	+	+	+
MJ1592	11.77	ACTATAAATTTTTTATA	GTATAAAGATT <b>a</b> AAAA	1564540	+	57	ND	+	+	-
MJ1597A	15.03	CCAAAACTTTTTTATA	AAAACATTTT <b>G</b> aGTA	1568422	+	178	ND	+	+	+
MJ1597B	6.27	AAAGATATTTTTTAAAGTA	ATTTATTGTTT <b>c</b> TaTT	1568566	+	34	ND	+	+	+

MJ1619	12.94	CACTTAACCCATAAATA	AAATATTATTT <b>a</b> GGAT	1594518	-	29	ND	+	+	+
MJ1636	9.36	AACGGAAAATATTTTAA	AAATATCTATA <b>a</b> TTGA	1617181	+	54	ND	+	+	-
MJ0722*	8.17	TTAATAATATTAATATA	TATAGTTCaTT <b>g</b> CAAA	656690	-	138	+	ND	-	+
MJ0723*	13.07	TCCAAAATTTTTATATA	TATAGTTCaTT <b>g</b> CAAA	656604	+	147	+	ND	-	+
MJ0740*	9.34	GTGATTAATGATATATA	AGATAAATAAT <b>g</b> ACAA	668883	-	27	+	ND	+	-
MJ0210	NA	NA	processing site	NA	NA	NA	-	-	+	+
MJ0387	NA	NA	processing site	NA	NA	NA	ND	-	+	-
MJ0499	NA	NA	processing site	NA	NA	NA	ND	-	+	+
MJ0006	NA	NA	NA	NA	NA	NA	-	-	+	+
MJ0135	NA	NA	NA	NA	NA	NA	-	-	-	+
MJ0150	NA	NA	NA	NA	NA	NA	ND	-	+	+
MJ0209	NA	NA	NA	NA	NA	NA	-	-	+	+
MJ0537	NA	NA	NA	NA	NA	NA	ND	-	+	-
MJ0672	NA	NA	NA	NA	NA	NA	-	-	-	+
MJ0676	NA	NA	NA	NA	NA	NA	ND	-	+	-
MJ0721	NA	NA	NA	NA	NA	NA	ND	-	+	+
MJ0732	NA	NA	NA	NA	NA	NA	ND	-	+	-
MJ0890	NA	NA	NA	NA	NA	NA	-	-	-	+
MJ0922	NA	NA	NA	NA	NA	NA	-	-	-	+
MJ1000	NA	NA	NA	NA	NA	NA	-	-	+	+
MJ1036	NA	NA	NA	NA	NA	NA	-	-	-	+
MJ1100	NA	NA	NA	NA	NA	NA	-	-	+	+
MJ1147	NA	NA	NA	NA	NA	NA	-	-	-	+
MJ1157	NA	NA	NA	NA	NA	NA	-	-	-	+
MJ1197	NA	NA	NA	NA	NA	NA	-	-	+	+
MJ1224	NA	NA	NA	NA	NA	NA	-	-	-	+
MJ1248	NA	NA	NA	NA	NA	NA	-	-	-	+
MJ1332	NA	NA	NA	NA	NA	NA	-	-	+	+
MJ1423	NA	NA	NA	NA	NA	NA	-	-	+	+
MJ1424	NA	NA	NA	NA	NA	NA	-	-	+	+
MJ1533	NA	NA	NA	NA	NA	NA	-	-	+	+
MJ1555	NA	NA	NA	NA	NA	NA	ND	-	+	-
MJ1656	NA	NA	NA	NA	NA	NA	ND	-	+	-

<sup>a</sup>Suffix A, B, C, or D was used when more than one promoter was identified for a gene; \*, TSS previously determined (1).

<sup>b</sup>Promoter score calculated as the sum of the scores of all the promoter elements (BRE, TATA box, PPE, and Inr) and a spacer penalty score applied for suboptimal spacing between the TATA box and the TSS.

<sup>c</sup>Lower case bold, major start site; lower case but not bold, alternative start site; NA, not available.

<sup>d</sup>Coordinate of the major TSS in the chromosome of *M. jannaschii* (NCBI accession no. NC\_000909.1).

<sup>e</sup>Direction of transcription: +, transcription toward a larger genomic coordinate; -, transcription toward a smaller genomic coordinate.

<sup>f</sup>Distance from the major TSS to the start of the nearest downstream gene (translation start locations from David E. Graham, University of Texas).

<sup>g</sup>Primer extension: +, TSS mapped; -, experiment done but TSS not observed; ND, experiment not done.

<sup>h</sup>Rapid amplification of 5' cDNA ends: +, TSS mapped; -, experiment done but TSS not observed; ND, experiment not done.

<sup>i</sup>+, protein product detected by proteomics (2); -, protein product not detected.

<sup>j</sup>+, divergent gene; -, not divergent gene.

## REFERENCES

1. Ouhammouch, M., Dewhurst, R.E., Hausner, W., Thomm, M. and Geiduschek, E.P. (2003) Activation of archaeal transcription by recruitment of the TATA-binding protein. *Proc. Natl. Acad. Sci. USA*, **100**, 5097-5102.
2. Zhu, W., Reich, C.I., Olsen, G.J., Giometti, C.S. and Yates, J.R., 3rd. (2004) Shotgun proteomics of *Methanococcus jannaschii* and insights into methanogenesis. *J. Proteome Res.*, **3**, 538-548.