

Table S3
Box A, BoxB, POLR3D (RPC4), BDP1, and BRF1 scores on annotated tRNA genes and pseudogenes

Row number	tRNA gene	tRNA gene name in Genomic tRNA Database	anti-codon	tRNA gene position	Box A position	Box A score	Box B position	Box B score	POLR3D (RPC4) peak number	POLR3D (RPC4) peak score	% unique tag reads in POLR3	BDP1 peak number	BDP1 peak score	% unique tag reads in BDP1	BRF1 peak number	BRF1 peak score	% unique tag reads in BRF1
1	TRNAS23	chr17 7 tRNA ^{Ser} GCT+	GCT	chr17:8030909-8030990	7 [A] 60	5.30E-007	56 [B] 11	1.60E-008	POLR3D (RPC4) 2218	811.74	88.0	BDP1_733	48.34	60.0	BRF1_5553	198.92	77.6
2	TRNAL11	chr16 17 tRNA ^{Leu} CAG+	CAG	chr16:55891364-55891446	7 [A] 61	7.70E-005	57 [B] 11	1.60E-008	POLR3D (RPC4) 2182	715.14	78.6	BDP1_719	52.57	50.8	BRF1_5432	149.35	66.0
3	TRNAY4	chr2 2 tRNA ^{Tyr} GTA I+	GTA	chr2:27127154-27127242	7 [A] 67	6.50E-007	63 [B] 11	8.50E-008	POLR3D (RPC4) 400	596.04	93.8	BDP1_806	66.86	69.2	BRF1_726	159.02	61.9
4	TRNAT10	chr17 14 tRNA ^{Thr} CGT+	CGT	chr17:26901213-26901284	7 [A] 50	3.50E-005	46 [B] 11	4.80E-008	POLR3D (RPC4) 2253	555.87	97.6	BDP1_745	44.91	86.3	BRF1_5599	201.98	93.0
5	TRNAS16	chr6 62 tRNA ^{Ser} GCT+	GCT	chr6:28288794-28288875	7 [A] 60	5.30E-007	56 [B] 11	1.60E-008	POLR3D (RPC4) 1238	521.77	90.6	BDP1_1403	32.81	42.8	BRF1_2283	47.72	61.9
6	TRNAL28	chr6 74 tRNA ^{Leu} CAA I+	CAA	chr6:29016809-29016913	7 [A] 83	2.10E-005	79 [B] 11	1.60E-008	POLR3D (RPC4) 1282	487.69	90.8	BDP1_1415	38.90	73.8	BRF1_2303	49.42	84.9
7	TRNAL38	chr1 67 tRNA ^{Leu} CAG-	CAG	chr1:159766756-159766838	7 [A] 61	7.70E-005	57 [B] 11	1.60E-008	POLR3D (RPC4) 276	479.76	59.4	BDP1_169	22.61	22.4	BRF1_500	31.27	25.3
8	TRNAI13	chr2 5 tRNA ^{Ala} TAT I+	TAT	chr2:42891180-42891272	7 [A] 71	1.30E-005	67 [B] 11	2.30E-005	POLR3D (RPC4) 415	479.03	98.5	BDP1_813	122.65	61.6	BRF1_747	348.72	98.5
9	TRNAL25	chr6 100 tRNA ^{Leu} CAA I-	CAA	chr6:28971979-28972084	7 [A] 84	2.10E-005	80 [B] 11	1.60E-008	POLR3D (RPC4) 1281	473.64	92.1	BDP1_1414	33.89	83.3	BRF1_2302	72.52	89.1
10	TRNAI23	chr17 9 tRNA ^{Ala} AAT+	AAT	chr17:8031636-8031709	7 [A] 52	1.90E-006	48 [B] 11	8.50E-008	POLR3D (RPC4) 2220	471.55	77.9	BDP1_735	6.45	17.8	BRF1_5555	27.59	36.0
11	TRNAQ2	chr17 16 tRNA ^{Gln} TTG+	TTG	chr17:44624889-44624960	7 [A] 50	7.90E-007	46 [B] 11	2.20E-006	POLR3D (RPC4) 2281	465.55	84.0	BDP1_755	77.86	67.1	BRF1_5635	212.89	88.9
12	TRNAY6	chr8 4 tRNA ^{Tyr} GTA I+	GTA	chr8:67188156-67188248	7 [A] 71	5.50E-006	67 [B] 11	8.50E-008	POLR3D (RPC4) 1460	454.37	95.3	BDP1_1620	62.00	66.1	BRF1_2854	107.85	98.1
13	TRNAT6	chr16 15 tRNA ^{Thr} CGT+	CGT	chr16:14287251-14287322	7 [A] 50	3.50E-005	46 [B] 11	4.00E-007	POLR3D (RPC4) 2150	453.13	97.1	BDP1_707	52.09	70.5	BRF1_4203	286.02	95.0
14	TRNAQ22	chr6 131 tRNA ^{Gln} CTG-	CTG	chr6:27867114-27867185	7 [A] 50	8.10E-006	46 [B] 11	2.20E-006	POLR3D (RPC4) 1233	445.23	91.0	BDP1_1399	27.93	70.3	BRF1_2278	51.00	100.0
15	TRNAF10	chr19 14 tRNA ^{Phe} GAA-	GAA	chr19:1334361-1334433	7 [A] 51	9.20E-006	47 [B] 11	1.50E-007	POLR3D (RPC4) 2351	444.65	65.5	BDP1_781	192.00	60.9	BRF1_5813	670.15	97.5
16	TRNAS22	chr11 8 tRNA ^{Ser} GCT+	GCT	chr11:65872167-65872248	7 [A] 60	5.30E-007	56 [B] 11	1.60E-008	POLR3D (RPC4) 1858	444.31	92.7	BDP1_363	44.43	56.5	BRF1_4203	76.21	79.7
17	TRNAS18	chr15 10 tRNA ^{Ser} GCT-	GCT	chr15:38673315-38673396	7 [A] 60	5.30E-007	56 [B] 11	1.60E-008	POLR3D (RPC4) 2086	433.64	79.2	BDP1_670	22.52	51.6	BRF1_5145	61.68	52.1
18	TRNAR8	chr17 18 tRNA ^{Arg} CCT+	CCT	chr17:70541596-70541668	7 [A] 51	1.90E-006	47 [B] 11	4.70E-007	POLR3D (RPC4) 2291	430.94	84.7	BDP1_761	59.79	68.2	BRF1_5668	164.69	86.5
19	TRNAM14	chr17 20 tRNA^{Met} CAT-	CAT	chr17:78045886-78045957	7 [A] 50	3.00E-004	46 [B] 11	1.90E-005	POLR3D (RPC4) 2299	430.12	54.5	BDP1_765	52.56	60.0	BRF1_5705	168.63	91.9
20	TRNAL19	chr1 58 tRNA ^{Leu} CAA I+	CAA	chr1:247134677-247134782	7 [A] 84	2.10E-005	80 [B] 11	1.60E-008	POLR3D (RPC4) 384	422.49	97.3	BDP1_236	93.99	57.3	BRF1_667	165.96	96.2
21	TRNAS14	chr17 35 tRNA ^{Ser} AGA-	AGA	chr17:8070653-8070734	7 [A] 60	5.30E-007	56 [B] 11	6.80E-008	POLR3D (RPC4) 2231	420.68	70.3	BDP1_741	21.33	38.2	BRF1_5561	68.82	65.8
22	TRNAY5	chr5 15 tRNA ^{Val} AAC-	AAC	chr5:180548022-180548094	7 [A] 51	1.90E-005	47 [B] 11	6.90E-007	POLR3D (RPC4) 1088	418.98	46.0	BDP1_1332	40.47	44.7	BRF1_2153	112.81	88.4
23	TRNAL27	chr16 16 tRNA ^{Leu} AAG+	AAG	chr16:22215962-22216043	7 [A] 60	7.70E-005	56 [B] 11	1.60E-008	POLR3D (RPC4) 2157	414.90	70.4	BDP1_710	36.77	43.4	BRF1_5362	19.36	89.4
24	TRNAG18	chr17 10 tRNA ^{Gly} TCC+	TCC	chr17:8065591-8065662	7 [A] 50	1.90E-006	46 [B] 11	4.50E-009	POLR3D (RPC4) 2224	410.01	88.3	BDP1_737	27.39	66.6	BRF1_5557	120.20	84.0
25	TRNAR25	chr17 19 tRNA ^{Arg} TCG+	TCG	chr17:70542803-70542875	7 [A] 51	1.90E-006	47 [B] 11	1.60E-006	POLR3D (RPC4) 2293	409.57	91.3	BDP1_763	27.81	67.6	BRF1_5671	173.79	93.6
26	TRNAH2	chr15 8 tRNA ^{His} GTG-	GTG	chr15:43279903-43279974	7 [A] 50	2.90E-005	46 [B] 11	1.00E-007	POLR3D (RPC4) 2092	407.65	74.2	BDP1_674	20.00	80.0	BRF1_5159	118.44	87.8
27	TRNAS4	chr6 44 tRNA ^{Ser} AGA+	AGA	chr6:27554570-27554651	7 [A] 60	5.30E-007	56 [B] 11	6.80E-008	POLR3D (RPC4) 1194	405.23	72.5	No BDP1	N/A	N/A	BRF1_2254	33.55	45.2
28	TRNAA23	chr12 13 tRNA ^{Ala} TGC-	TGC	chr12:123972254-123972325	7 [A] 50	4.30E-007	46 [B] 11	3.20E-008	POLR3D (RPC4) 1934	398.89	82.3	BDP1_487	26.31	65.3	BRF1_4534	33.40	69.0
29	TRNAF11	chr11 13 tRNA ^{Phe} GAA-	GAA	chr11:59090429-59090501	7 [A] 51	9.20E-006	47 [B] 11	1.60E-007	POLR3D (RPC4) 1853	395.16	78.9	BDP1_358	20.10	40.6	No BRF1	N/A	N/A
30	TRNAR11	chr3 11 tRNA ^{Arg} ACG-	ACG	chr3:45705495-45705567	7 [A] 51	1.90E-006	47 [B] 11	2.00E-006	POLR3D (RPC4) 585	393.79	69.1	BDP1_986	36.76	32.6	BRF1_1115	116.64	87.8
31	TRNAT8	chr17 8 tRNA ^{Thr} AGT+	AGT	chr17:8031203-8031276	7 [A] 52	3.60E-006	48 [B] 11	4.50E-009	POLR3D (RPC4) 2219	393.20	81.7	BDP1_734	27.43	61.7	BRF1_5554	59.63	72.4
32	TRNAR21	chr14 7 tRNA ^{Arg} ACG+	ACG	chr14:22468750-22468822	7 [A] 51	1.90E-006	47 [B] 11	1.40E-006	POLR3D (RPC4) 2022	390.37	78.6	BDP1_650	23.92	56.6	BRF1_4808	73.74	74.3
33	TRNAS20	chr8 11 tRNA ^{Ser} AGA-	AGA	chr8:96351061-96351142	7 [A] 60	5.30E-007	56 [B] 11	6.80E-008	POLR3D (RPC4) 1658	388.45	69.2	BDP1_1644	48.33	37.0	BRF1_3008	88.68	86.6
34	TRNAY7	chr6 14 tRNA ^{Tyr} GTA I+	GTA	chr6:26677065-26677155	7 [A] 69	6.50E-007	65 [B] 11	4.80E-008	POLR3D (RPC4) 1139	387.51	98.3	BDP1_1371	34.96	76.4	BRF1_2226	103.35	98.0
35	TRNAA26	chr5 8 tRNA ^{Ala} TGC+	TGC	chr5:180566474-180566545	7 [A] 50	4.30E-007	46 [B] 11	3.20E-008	POLR3D (RPC4) 1092	385.91	82.0	BDP1_1335	50.69	55.3	BRF1_2157	148.01	89.0
36	TRNAY10	chr6 16 tRNA ^{Tyr} GTA I+	GTA	chr6:26685311-26685399	7 [A] 67	6.50E-007	63 [B] 11	4.80E-008	POLR3D (RPC4) 1143	385.72	98.1	BDP1_1373	37.18	63.8	BRF1_2228	46.08	97.8
37		chr6 169 tRNA^{Met} CAT-	CAT	chr6:26438508-26438579	7 [A] 50	3.00E-004	46 [B] 11	1.90E-005	POLR3D (RPC4) 1127	384.51	77.1	BDP1_1362	55.15	33.7	BRF1_2215	68.27	55.5
38	TRNAR20	chr17 21 tRNA ^{Arg} CCT-	CCT	chr17:70542121-70542193	7 [A] 51	1.90E-006	47 [B] 11	4.70E-007	POLR3D (RPC4) 2292	383.97	82.8	BDP1_762	41.76	57.7	BRF1_5670	191.40	89.8
39	TRNAR2	chr6 6 tRNA ^{Arg} ACG+	ACG	chr6:26436347-26436419	7 [A] 51	1.90E-006	47 [B] 11	1.40E-006	POLR3D (RPC4) 1126	379.01	80.2	No BDP1	N/A	N/A	BRF1_2214	16.04	38.2
40	TRNAK13	chr14 13 tRNA ^{Lys} CTT-	CTT	chr14:57776366-57776438	7 [A] 51	9.60E-007	47 [B] 11	3.50E-007	POLR3D (RPC4) 2045	378.26	77.4	BDP1_656	20.00	72.2	BRF1_4895	34.29	76.4
41	TRNAL7	chr16 27 tRNA ^{Leu} TAG-	TAG	chr16:22114533-22114614	7 [A] 60	2.10E-005	56 [B] 11	1.60E-008	POLR3D (RPC4) 2156	377.75	99.7	BDP1_709	55.00	90.7	BRF1_5360	116.00	100.0
42	TRNAA3	chr2 3 tRNA ^{Ala} AGC+	AGC	chr2:27127586-27127658	7 [A] 51	5.80E-005	47 [B] 11	5.10E-005	POLR3D (RPC4) 401	375.45	82.8	BDP1_807	63.23	48.3	BRF1_727	49.98	76.3
43	TRNAR27	chr7 3 tRNA ^{Arg} CCT+	CCT	chr7:138675986-138676058	7 [A] 51	1.90E-006	47 [B] 11	4.70E-007	POLR3D (RPC4) 1417	373.65	92.5	BDP1_1572	24.25	70.3	BRF1_2712	71.53	86.6
44	TRNAL1	chr14 20 tRNA ^{Leu} AAG+	AAG	chr14:20148131-20148212	7 [A] 60	7.70E-005	56 [B] 11	1.60E-008	POLR3D (RPC4) 2001	369.63	72.1	BDP1_643	23.69	51.4	BRF1_4793	70.08	58.9
45		chr17 23 tRNA ^{Arg} CCG-	CCG	chr17:63446475-63446547	7 [A] 51	1.90E-006	47 [B] 11	4.70E-007	POLR3D (RPC4) 2290	367.95	99.7	BDP1_759	44.00	95.4	BRF1_5659	166.00	100.0
46	TRNAG24	chr1 45 tRNA ^{Gly} TCC+	TCC	chr1:159767527-159767598	7 [A] 50	1.00E-005	46 [B] 11	4.50E-009	POLR3D (RPC4) 277	367.68	80.5	BDP1_170	17.45	32.3	BRF1_501	48.31	50.0

263	TRNAP16	chr16 3 tRNAPro TGG+	TGG	chr16:3148924-3148995	7 [A] 50	2.30E-005	46 [B] 11	1.90E-009	POLR3D (RPC4) 2131	120.46	11.8	No_BDP1	N/A	N/A	BRF1_5300	7.81	16.1
264	TRNAA19	chr6 104 tRNAAla TGC-	TGC	chr6:28892991-28893062	7 [A] 50	4.30E-007	46 [B] 11	1.10E-006	POLR3D (RPC4) 1275	118.47	71.0	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
265		chr6 21 tRNAmet CAT+	CAT	chr6:26809691-26809763	7 [A] 51	5.30E-005	47 [B] 11	6.20E-006	POLR3D (RPC4) 1147	117.78	94.3	No_BDP1	N/A	N/A	BRF1_2230	28.46	93.1
266	TRNAI2	chr6 29 tRNAIle TAT I+	TAT	chr6:27096104-27096197	7 [A] 72	1.30E-005	68 [B] 11	2.30E-005	POLR3D (RPC4) 1165	115.26	90.0	No_BDP1	N/A	N/A	BRF1_2235	45.02	91.6
267	TRNAU2	chr22 1 tRNASeC(e) TCA+	TCA	chr22:42877870-42877955	No Box A	N/A	60 [B] 11	3.20E-005	POLR3D (RPC4) 2487	113.17	48.0	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
268	TRNAK8	chr6 149 tRNAlys TTT-	TTT	chr6:27410748-27410820	7 [A] 51	9.60E-007	47 [B] 11	2.60E-007	POLR3D (RPC4) 1193	112.03	61.6	No_BDP1	N/A	N/A	BRF1_2253	4.77	14.2
269	TRNAL16	chr6 134 tRNALeu TAA-	TAA	chr6:27796877-27796959	7 [A] 61	5.30E-007	57 [B] 11	8.50E-008	POLR3D (RPC4) 1229	110.74	95.1	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
270	TRNAA27	chr6 67 tRNAAla AGC+	AGC	chr6:28786345-28786416	7 [A] 50	4.30E-007	46 [B] 11	6.80E-008	POLR3D (RPC4) 1257	109.71	81.8	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
271		chr6 61 tRNAmet CAT+	CAT	chr6:27853643-27853714	7 [A] 50	3.00E-004	46 [B] 11	3.00E-004	POLR3D (RPC4) 1232	108.88	62.7	No_BDP1	N/A	N/A	BRF1_2277	12.08	25.0
272	TRNAF7	chr6 109 tRNAphe GAA-	GAA	chr6:28866478-28866550	7 [A] 51	9.20E-006	47 [B] 11	1.50E-007	POLR3D (RPC4) 1270	106.29	46.9	No_BDP1	N/A	N/A	BRF1_2295	17.61	60.0
273	TRNAL10	chr6 155 tRNALeu TAA-	TAA	chr6:27306313-27306395	7 [A] 61	2.80E-007	57 [B] 11	3.50E-007	POLR3D (RPC4) 1178	103.70	95.2	No_BDP1	N/A	N/A	BRF1_2244	12.10	92.3
274	TRNAK24	chr16 30 tRNAlys CTT-	CTT	chr16:3170556-3170628	7 [A] 51	3.60E-006	47 [B] 11	4.00E-005	POLR3D (RPC4) 2135	103.18	85.2	No_BDP1	N/A	N/A	BRF1_5302	17.55	80.0
275	TRNAE2	chr1 5 tRNAglu TTC+	TTC	chr1:17071665-17071736	7 [A] 50	7.10E-006	46 [B] 11	4.50E-009	POLR3D (RPC4) 92	101.56	43.6	BDP1_49	14.44	28.5	BRF1_122	55.22	50.0
276		chr1 108 tRNAasn GTT-	GTT	chr1:146864938-146865011	7 [A] 52	1.30E-005	48 [B] 11	9.20E-006	POLR3D (RPC4) 172	100.53	6.3	BDP1_124	26.63	8.0	BRF1_405	81.79	25.8
277	TRNAR16	chr1 86 tRNAarg TCT-	TCT	chr1:157378025-157378098	7 [A] 52	5.80E-005	48 [B] 11	1.50E-007	POLR3D (RPC4) 200	100.20	99.0	BDP1_144	16.00	87.5	BRF1_448	31.00	100.0
278	TRNAP20	chr16 11 tRNAPro AGG+	AGG	chr16:3181990-3182061	7 [A] 50	2.30E-005	46 [B] 11	1.90E-009	POLR3D (RPC4) 2144	98.65	94.4	No_BDP1	N/A	N/A	BRF1_5309	27.73	77.4
279	TRNAA10	chr6 113 tRNAAla TGC-	TGC	chr6:28834120-28834191	7 [A] 50	4.30E-007	46 [B] 11	3.20E-008	POLR3D (RPC4) 1267	95.55	97.9	No_BDP1	N/A	N/A	BRF1_2294	23.00	100.0
280	TRNAE38P	chr2 12 Pseudo CTC+	CTC	chr2:150927523-150927595	7 [A] 51	1.80E-007	46 [B] 12	4.00E-007	POLR3D (RPC4) 518	95.49	57.3	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
281		chr5 2 tRNAval CAC+	CAG	chr5:180456676-180456748	7 [A] 51	2.70E-006	47 [B] 11	6.90E-007	POLR3D (RPC4) 1075	90.80	1.6	BDP1_1326	16.63	0.0	BRF1_2143	61.69	19.4
282	TRNAA28	chr6 68 tRNAAla AGC+	AGC	chr6:28795460-28795531	7 [A] 50	4.30E-007	46 [B] 11	3.80E-008	POLR3D (RPC4) 1258	89.58	63.8	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
283	TRNAG14	chr1 2 tRNAgly CCC+	CCC	chr1:16926367-16926437	7 [A] 49	2.70E-006	45 [B] 11	6.10E-009	POLR3D (RPC4) 87	87.28	86.3	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
284	TRNAG2	chr16 34 tRNAgly CCC-	CCC	chr16:626737-626807	7 [A] 49	3.20E-005	45 [B] 11	4.50E-009	POLR3D (RPC4) 2123	87.06	22.0	BDP1_692	46.95	89.5	BRF1_5262	281.96	99.2
285	TRNAA36	chr6 94 tRNAAla AGC-	AGC	chr6:58250548-58250620	7 [A] 51	1.90E-005	47 [B] 11	1.10E-004	POLR3D (RPC4) 1304	86.70	75.9	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
286	TRNAS27	chr6 51 tRNAser TGA+	TGA	chr6:27621447-27621528	7 [A] 60	5.30E-007	56 [B] 11	6.80E-008	POLR3D (RPC4) 1205	85.70	50.9	No_BDP1	N/A	N/A	BRF1_2261	25.80	65.3
287	TRNAV25	chr1 90 tRNAval CAC-	CAC	chr1:147950712-147950785	7 [A] 52	2.70E-006	48 [B] 11	6.90E-007	POLR3D (RPC4) 186	82.67	69.3	BDP1_128	47.90	63.2	BRF1_410	70.81	87.6
288	TRNAD1	chr1 81 tRNAasp GTC-	GTC	chr1:159677239-159677310	7 [A] 50	8.10E-006	46 [B] 11	1.00E-007	POLR3D (RPC4) 212	81.92	4.7	BDP1_149	38.89	0.0	BRF1_461	134.22	0.0
289	TRNAR29	chr6 138 tRNAarg ACG-	ACG	chr6:27746323-27746395	7 [A] 51	1.90E-006	47 [B] 11	2.00E-006	POLR3D (RPC4) 1222	81.45	50.0	BDP1_1397	10.55	16.1	BRF1_2273	8.06	18.5
290	TRNAT5	chr6 151 tRNAthr CGT-	CGT	chr6:27379547-27379618	7 [A] 50	3.80E-004	46 [B] 11	1.10E-004	POLR3D (RPC4) 1190	80.54	100.0	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
291	TRNAG8	chr1 82 tRNAgly TCC-	TCC	chr1:159676585-159676656	7 [A] 50	1.00E-005	46 [B] 11	9.90E-007	POLR3D (RPC4) 211	80.13	39.3	No_BDP1	N/A	N/A	BRF1_459	90.39	53.5
292	TRNAC27	chr7 16 tRNACys GCA-	GCA	chr7:149019205-149019276	7 [A] 50	6.20E-006	46 [B] 11	6.80E-008	POLR3D (RPC4) 1438	76.50	40.6	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
293	TRNAV26	chr10 6 tRNAval TAC-	TAC	chr10:5935680-5935752	7 [A] 51	2.70E-006	47 [B] 11	1.90E-007	POLR3D (RPC4) 1760	76.00	100.0	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
294	TRNAA20	chr6 160 tRNAAla AGC-	AGC	chr6:26881750-26881822	7 [A] 51	2.30E-005	47 [B] 11	2.60E-004	POLR3D (RPC4) 1162	75.84	0.0	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
295		chr6 164 tRNAmet CAT-	CAT	chr6:26843553-26843625	7 [A] 51	1.90E-005	47 [B] 11	5.60E-006	POLR3D (RPC4) 1154	74.54	16.1	No_BDP1	N/A	N/A	BRF1_2231	33.13	13.7
296		chr1 135 tRNAasn GTT-	GTT	chr1:16719667-16719740	7 [A] 52	1.30E-005	48 [B] 11	9.20E-006	POLR3D (RPC4) 75	69.23	66.0	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
297	TRNAR17	chr6 156 tRNAarg ACG-	ACG	chr6:27289602-27289674	7 [A] 51	1.90E-006	47 [B] 11	2.00E-006	POLR3D (RPC4) 1176	68.32	22.8	BDP1_1378	16.23	23.5	BRF1_2241	20.99	40.5
298	TRNAG28	chr1 4 tRNAgly CCC+	CCC	chr1:17061003-17061073	7 [A] 49	1.20E-006	45 [B] 11	6.10E-009	POLR3D (RPC4) 90	67.99	15.2	No_BDP1	N/A	N/A	BRF1_121	22.18	29.6
299	TRNAT15	chr6 135 tRNAthr AGT-	AGT	chr6:27760453-27760526	7 [A] 52	1.90E-005	48 [B] 11	4.50E-009	POLR3D (RPC4) 1226	67.85	38.8	No_BDP1	N/A	N/A	BRF1_2274	11.89	29.6
300	TRNAV31	chr6 40 tRNAval TAC+	TAC	chr6:27366384-27366456	7 [A] 51	3.60E-006	47 [B] 11	4.70E-005	POLR3D (RPC4) 1186	67.00	100.0	No_BDP1	N/A	N/A	BRF1_2248	10.00	100.0
301	TRNAW2	chr6 170 tRNAtrp CCA-	CCA	chr6:26427309-26427380	7 [A] 50	1.40E-004	46 [B] 11	6.50E-005	POLR3D (RPC4) 1121	65.18	13.7	BDP1_1359	10.89	11.1	BRF1_2211	1.82	3.4
302		chr1 23 Pseudo CTG+	CTG	chr1:146292313-146292384	7 [A] 50	2.30E-004	46 [B] 11	2.20E-006	POLR3D (RPC4) 165	64.25	89.0	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
303	TRNAY8	chr6 15 tRNAtyr GTA I+	GTA	chr6:26683777-26683866	7 [A] 68	6.50E-007	64 [B] 11	4.80E-008	POLR3D (RPC4) 1142	63.86	93.8	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
304	TRNAC2	chr7 5 tRNACys GCA+	GCA	chr7:148638214-148638285	7 [A] 50	4.30E-007	46 [B] 11	2.20E-008	POLR3D (RPC4) 1427	60.75	45.5	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
305	TRNAK43P	chr6 118 Pseudo TTT-	TTT	chr6:28768966-28769039	7 [A] 52	9.60E-007	48 [B] 11	1.30E-006	POLR3D (RPC4) 1255	60.00	100.0	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
306		chr6 162 tRNAmet CAT-	CAT	chr6:26866529-26866601	7 [A] 51	1.90E-005	47 [B] 11	5.60E-006	POLR3D (RPC4) 1158	59.60	30.8	No_BDP1	N/A	N/A	BRF1_2233	23.47	76.0
307	TRNAT11	chr6 54 tRNAthr CGT+	CGT	chr6:27694114-27694187	7 [A] 52	3.60E-006	48 [B] 11	1.80E-006	POLR3D (RPC4) 1218	59.00	100.0	No_BDP1	N/A	N/A	BRF1_2269	11.00	100.0
308	TRNAK34	chr1 55 tRNAlys TTT+	TTT	chr1:203709894-203709966	7 [A] 51	2.90E-005	47 [B] 11	2.60E-007	POLR3D (RPC4) 300	58.76	69.3	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
309	TRNAG21	chr1 37 tRNAgly GCC+	GCC	chr1:159687091-159687161	7 [A] 49	1.20E-006	45 [B] 11	4.50E-009	POLR3D (RPC4) 235	58.65	0.0	BDP1_156	45.20	0.0	BRF1_471	11.28	0.6
310	TRNAG25	chr1 41 tRNAgly GCC+	GCC	chr1:159701882-159701952	7 [A] 49	1.20E-006	45 [B] 11	4.50E-009	POLR3D (RPC4) 262	57.73	0.0	BDP1_164	46.33	0.0	BRF1_489	89.77	0.0
311	TRNAA12	chr6 23 tRNAAla AGC+	AGC	chr6:26836235-26836307	7 [A] 51	2.30E-005	47 [B] 11	2.60E-004	POLR3D (RPC4) 1152	57.71	15.6	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
312	TRNAG23	chr1 39 tRNAgly GCC+	GCC	chr1:159694522-159694592	7 [A] 49	1.20E-006	45 [B] 11	4.50E-009	POLR3D (RPC4) 251	56.73	0.0	BDP1_160	46.33	0.0	BRF1_479	89.77	0.0
313	TRNAC28	chr7 15 tRNACys GCA+	GCA	chr7:149035693-149035764	7 [A] 50	6.20E-006	46 [B] 11	2.20E-008	POLR3D (RPC4) 1439	55.36	40.7	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
314	TRNAG15	chr1 35 tRNAgly GCC+	GCC	chr1:159679718-159679788	7 [A] 49	1.20E-006	45 [B] 11	4.50E-009	POLR3D (RPC4) 217	55.35	0.0	BDP1_151	13.15	0.7	BRF1_463	91.86	0.0
315	TRNAP12	chr16 6 tRNAPro CGG+	CGG	chr16:3162050-3162121	7 [A] 50	2.30E-005	46 [B] 11	1.90E-009	POLR3D (RPC4) 2133	54.86	36.9	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
316	TRNAS7	chr6 35 tRNAser CGA+	CGA	chr6:27285607-27285688	7 [A] 60	5.30E-007	56 [B] 11	8.50E-008	POLR3D (RPC4) 1174	54.17	51.3	No_BDP1	N/A	N/A	BRF1_2240	24.73	69.6

425		chr1 122 tRNAAsn GTT-	GTT	chr1:143200200-143200273	7 [A] 52	1.30E-005	48 [B] 11	1.90E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
426		chr1 123 tRNAAsn GTT-	GTT	chr1:143019971-143020044	7 [A] 52	1.30E-005	48 [B] 11	1.90E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
427	TRNAN34P	chr1 124 Pseudo GTT-	GTT	chr1:142455081-142455154	7 [A] 52	2.30E-005	48 [B] 11	1.30E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
428		chr1 125 Pseudo ???-	???	chr1:108297798-108297868	7 [A] 49	2.10E-005	45 [B] 11	5.60E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
429	TRNAK10	chr1 127 tRNALys CTT-	CTT	chr1:55196130-55196202	7 [A] 51	9.60E-007	47 [B] 11	1.70E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
430		chr1 128 Pseudo CTG-	CTG	chr1:17053487-17053558	7 [A] 50	2.20E-004	46 [B] 11	1.10E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
431	TRNAV13	chr1 129 tRNAVal CAC-	CAC	chr1:16879088-16879160	7 [A] 51	3.60E-006	47 [B] 11	9.40E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
432		chr1 12 tRNAAsn GTT+	GTT	chr1:143193197-143193270	7 [A] 52	1.90E-005	48 [B] 11	6.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
433	TRNAK5	chr11 2 tRNALys CTT+	CTT	chr11:51216476-51216548	7 [A] 51	1.20E-005	47 [B] 11	4.60E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
434		chr1 134 tRNAAsn GTT-	GTT	chr1:16731480-16731553	7 [A] 52	1.90E-005	48 [B] 11	1.70E-003	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
435		chr1 136 Pseudo ???-	???	chr1:7912926-7912995	7 [A] 48	1.20E-007	44 [B] 11	4.50E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
436		chr1 13 tRNAAsn GTT+	GTT	chr1:144097086-144097161	7 [A] 54	8.50E-004	50 [B] 11	1.00E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
437	TRNAR30P	chr1 14 Pseudo CCT+	CCT	chr1:144652936-144653006	7 [A] 49	1.80E-004	45 [B] 11	1.60E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
438	TRNAA45P	chr11 6 Pseudo TGC+	TGC	chr11:60520084-60520153	No Box A	N/A	44 [B] 11	1.10E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
439	TRNAR34P	chr11 7 Pseudo CCT+	CCT	chr11:63418343-63418411	7 [A] 47	6.40E-005	45 [B] 9	4.00E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
440	TRNAE29P	chr1 17 Pseudo TTC+	TTC	chr1:145016802-145016873	7 [A] 50	2.00E-004	46 [B] 11	4.70E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
441	TRNAR31P	chr1 18 Pseudo CCT+	CCT	chr1:145949915-145949985	7 [A] 49	1.80E-004	45 [B] 11	1.60E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
442	TRNAV35P	chr1 1 Pseudo CAC+	CAC	chr1:16924648-16924720	7 [A] 51	5.50E-006	47 [B] 11	9.40E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
443	TRNAN26	chr1 20 tRNAAsn ATT+	ATT	chr1:146185653-146185726	7 [A] 52	1.40E-004	48 [B] 11	3.90E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
444	TRNAE42P	chr12 14 Pseudo CTC-	CTC	chr12:112870928-112871000	7 [A] 51	6.40E-005	47 [B] 11	4.80E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
445	TRNAQ47P	chr12 15 Pseudo TTG-	TTG	chr12:96014822-96014895	7 [A] 52	7.40E-004	48 [B] 11	6.10E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
446	TRNAQ46P	chr12 16 Pseudo TTG-	TTG	chr12:48497457-48497531	9 [A] 51	4.80E-004	48 [B] 12	4.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
447	TRNAK12	chr12 1 tRNALys TTT+	TTT	chr12:27734573-27734645	7 [A] 51	5.80E-005	47 [B] 11	3.40E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
448		chr1 22 tRNAArg CTG+	CTG	chr1:146267561-146267632	7 [A] 50	1.90E-006	46 [B] 11	6.90E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
449	TRNAQ30	chr12 3 tRNAArg CTG+	CTG	chr12:73137449-73137521	7 [A] 51	1.90E-006	46 [B] 12	1.20E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
450		chr1 24 tRNAAsn GTT+	GTT	chr1:146344161-146344234	7 [A] 52	1.30E-005	48 [B] 11	1.90E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
451		chr1 27 Pseudo CTG+	CTG	chr1:147345988-147346059	7 [A] 50	1.00E-005	46 [B] 11	1.90E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
452	TRNAD15	chr12 7 tRNAAsp GTC+	GTC	chr12:121426877-121426947	7 [A] 49	8.10E-006	45 [B] 11	9.40E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
453	TRNAI29P	chr12 9 Pseudo AAT+	AAT	chr12:128282151-128282225	8 [A] 52	6.40E-004	49 [B] 11	1.60E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
454	TRNAE13	chr1 29 tRNAArg CTC+	CTC	chr1:147600896-147600964	7 [A] 47	3.10E-006	No Box B	N/A	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
455		chr1 30 tRNAAsn GTT+	GTT	chr1:147875233-147875306	7 [A] 52	1.30E-005	48 [B] 11	1.90E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
456	TRNAE8	chr1 31 tRNAArg TTC+	TTC	chr1:147986426-147986494	7 [A] 47	3.10E-006	No Box B	N/A	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
457	TRNAE39P	chr13 2 Pseudo CTC-	CTC	chr13:57356551-57356622	7 [A] 50	5.30E-007	46 [B] 11	2.10E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
458		chr1 33 Pseudo ???+	???	chr1:159657285-159657357	7 [A] 51	7.10E-006	47 [B] 11	6.10E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
459	TRNAE4	chr13 4 tRNAArg CTC-	CTC	chr13:40928061-40928132	7 [A] 50	2.90E-005	46 [B] 11	2.50E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
460	TRNAQ50P	chr13 6 Pseudo TTG-	TTG	chr13:35537747-35537818	7 [A] 50	1.20E-003	46 [B] 11	2.30E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
461		chr14 11 Pseudo CTA-	CTA	chr14:77770591-77770663	7 [A] 51	1.50E-005	47 [B] 11	1.60E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
462	TRNAE15	chr14 14 tRNAArg TTC-	TTC	chr14:31306567-31306637	6 [A] 50	4.10E-006	45 [B] 11	1.00E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
463	TRNAL40P	chr14 15 Pseudo TAG-	TAG	chr14:20215018-20215099	7 [A] 60	3.50E-005	56 [B] 11	8.80E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
464	TRNAY3	chr14 17 tRNAArg GTA I-	GTA	chr14:20197957-20198050	7 [A] 72	5.50E-006	68 [B] 11	1.00E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
465	TRNAG30	chr1 43 tRNAArg GCC+	GCC	chr1:159716980-159717050	7 [A] 49	1.20E-006	45 [B] 11	1.40E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
466	TRNAD20P	chr1 44 Pseudo GTC+	GTC	chr1:159759559-159759630	7 [A] 50	2.30E-004	46 [B] 11	3.00E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
467	TRNAD13	chr1 46 tRNAAsp GTC+	GTC	chr1:159768539-159768610	No Box A	N/A	12 [B] 45	1.20E-003	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
468	TRNAD18	chr1 48 tRNAAsp GTC+	GTC	chr1:159841212-159841283	7 [A] 50	8.40E-005	46 [B] 11	3.00E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
469	TRNAA17	chr14 9 tRNAAla AGC+	AGC	chr14:88515195-88515267	7 [A] 51	1.50E-005	47 [B] 11	6.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
470	TRNAE16	chr1 49 tRNAArg TTC+	TTC	chr1:159849132-159849203	7 [A] 50	5.50E-006	46 [B] 11	1.60E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
471		chr1 50 tRNAAsn GTT+	GTT	chr1:159858089-159858162	7 [A] 52	2.50E-004	48 [B] 11	1.10E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
472	TRNAK36P	chr1 51 Pseudo CTT+	CTT	chr1:163832774-163832846	7 [A] 51	4.80E-005	47 [B] 11	1.70E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
473		chr1 53 Pseudo ???+	???	chr1:176944661-176944733	7 [A] 51	1.80E-003	47 [B] 11	3.40E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
474	TRNAY16P	chr15 5 Pseudo GTA-	GTA	chr15:90055306-90055378	7 [A] 51	9.20E-005	47 [B] 11	5.60E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
475	TRNAK42P	chr15 6 Pseudo CTT-	CTT	chr15:74461820-74461893	7 [A] 52	5.80E-005	48 [B] 11	2.10E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
476	TRNAP27P	chr1 57 Pseudo TGG+	TGG	chr1:236172485-236172556	7 [A] 50	2.60E-005	46 [B] 11	4.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
477	TRNAL45P	chr1 60 Pseudo TAA-	TAA	chr1:236173579-236173653	No Box A	N/A	49 [B] 11	1.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
478	TRNAR23	chr16 12 tRNAArg CCT+	CCT	chr16:3183919-3183991	7 [A] 51	9.20E-005	47 [B] 11	1.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A

479	TRNAQ31	chr16 14 tRNAGln TTG+	TTG	chr16:3359814-3359885	7 [A] 50	2.30E-006	46 [B] 11	1.40E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
480	TRNAG16	chr16 18 tRNAGly GCC+	GCC	chr16:69380098-69380168	7 [A] 49	1.20E-006	45 [B] 11	9.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
481	TRNAP23P	chr1 61 Pseudo TGG-	TGG	chr1:205244777-205244853	7 [A] 55	2.80E-004	51 [B] 11	6.10E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
482	TRNAQ28	chr16 21 tRNAGln CTG+	CTG	chr16:70282391-70282464	7 [A] 52	3.10E-006	No Box B	N/A	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
483	TRNAP26P	chr16 31 Pseudo TGG-	TGG	chr16:3160962-3161032	7 [A] 49	8.40E-005	45 [B] 11	1.60E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
484	TRNAP24P	chr16 33 Pseudo AGG-	AGG	chr16:3142610-3142681	7 [A] 50	2.30E-005	46 [B] 11	3.40E-005	No_POLR3D (RPC4)	N/A	N/A	BDP1_10982	5.74		No_BRF1	N/A	N/A
485	TRNAV30	chr1 63 tRNAVal AAC-	AAC	chr1:178450899-178450971	7 [A] 51	1.30E-004	47 [B] 11	6.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
486	TRNAE23	chr1 64 tRNAglu TTC-	TTC	chr1:170424162-170424230	5 [A] 49	1.80E-007	44 [B] 10	6.10E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
487	TRNAP5	chr16 4 tRNAPro AGG I+	AGG	chr16:3150387-3150481	7 [A] 73	7.70E-005	69 [B] 11	1.90E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
488	TRNAK15	chr16 5 tRNALys CTT+	CTT	chr16:3154940-3155012	7 [A] 51	5.50E-006	47 [B] 11	1.30E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
489		chr1 6 tRNAAsn GTT+	GTT	chr1:17074545-17074618	7 [A] 52	1.90E-005	48 [B] 11	2.30E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
490	TRNASUP3	chr17 11 tRNASup CTA+	CTA	chr17:15349410-15349483	15 [A] 44	2.30E-003	48 [B] 11	6.10E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
491	TRNAG26	chr17 13 tRNAGly CCC+	CCC	chr17:19704767-19704837	7 [A] 49	2.70E-006	45 [B] 11	4.80E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
492	TRNASUP1	chr17 17 tRNASup TTA+	TTA	chr17:56218375-56218445	7 [A] 49	1.20E-006	45 [B] 11	2.60E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
493		chr17 1 Pseudo ???+	???	chr17:7465182-7465250	No Box A	N/A	12 [B] 42	8.90E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
494		chr17 22 tRNAUndet ???-	???	chr17:63902552-63902626	7 [A] 53	7.70E-005	49 [B] 11	1.10E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
495	TRNAT22	chr17 24 tRNAThr AGT-	AGT	chr17:59957380-59957453	7 [A] 52	1.90E-005	49 [B] 10	1.30E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
496	TRNAU3	chr17 25 tRNASeC TCA-	TCA	chr17:35527079-35527152	8 [A] 51	1.40E-003	48 [B] 11	1.60E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
497	TRNAC1	chr17 30 tRNACys GCA-	GCA	chr17:34243501-34243572	7 [A] 50	2.70E-003	46 [B] 11	6.90E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
498	TRNAS30P	chr17 32 Pseudo TGA-	TGA	chr17:21952306-21952374	No Box A	N/A	43 [B] 11	9.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
499	TRNAQ41P	chr17 33 Pseudo TTG-	TTG	chr17:19447179-19447250	7 [A] 50	9.20E-005	46 [B] 11	4.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
500	TRNAE25	chr18 1 tRNAglu CTC+	CTC	chr18:41553749-41553820	7 [A] 50	1.90E-005	46 [B] 11	1.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
501	TRNAG33P	chr18 2 Pseudo TCC+	TCC	chr18:53496852-53496923	7 [A] 50	1.00E-005	46 [B] 11	8.30E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
502	TRNAG35P	chr18 3 Pseudo TCC+	TCC	chr18:53497175-53497246	7 [A] 50	1.00E-005	46 [B] 11	9.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
503	TRNAA16	chr1 87 tRNAAla AGC-	AGC	chr1:148284006-148284076	7 [A] 49	5.80E-005	45 [B] 11	1.60E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
504	TRNAP33P	chr1 88 Pseudo CCT-	CCT	chr1:147994895-147994965	7 [A] 49	1.90E-006	45 [B] 11	1.30E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
505	TRNAK35P	chr1 8 Pseudo CTT+	CTT	chr1:39742782-39742854	7 [A] 51	3.50E-004	47 [B] 11	4.00E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
506		chr19 11 Pseudo ???-	???	chr19:40803300-40803370	7 [A] 49	5.30E-007	45 [B] 11	3.40E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
507	TRNAQ45P	chr19 12 Pseudo TTG-	TTG	chr19:9011356-9011428	7 [A] 51	3.60E-006	47 [B] 11	1.90E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
508	TRNAF17P	chr1 92 Pseudo GAA-	GAA	chr1:147939529-147939600	7 [A] 50	1.40E-004	46 [B] 11	4.50E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
509		chr1 93 tRNAAsn GTT-	GTT	chr1:147936681-147936754	7 [A] 52	2.30E-004	48 [B] 11	3.70E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
510	TRNAK7	chr19 3 tRNALys TTT+	TTT	chr19:19713207-19713277	6 [A] 50	4.80E-005	45 [B] 11	4.80E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
511		chr1 95 tRNAAsn GTT-	GTT	chr1:147882241-147882314	7 [A] 52	1.90E-005	48 [B] 11	9.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
512	TRNAR32P	chr1 96 Pseudo CCT-	CCT	chr1:147609705-147609775	7 [A] 49	1.90E-006	45 [B] 11	1.30E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
513	TRNAK30	chr19 6 tRNALys CTT-	CTT	chr19:57117208-57117280	7 [A] 51	9.60E-007	47 [B] 11	5.10E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
514	TRNAK32	chr19 7 tRNALys TTT-	TTT	chr19:54729745-54729817	7 [A] 51	9.60E-007	47 [B] 11	1.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
515	TRNAK38P	chr19 9 Pseudo TTT-	TTT	chr19:46439982-46440054	7 [A] 51	1.20E-005	47 [B] 11	5.60E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
516	TRNAS29P	chr20 2 Pseudo AGA+	AGA	chr20:29552364-29552435	7 [A] 50	7.00E-005	46 [B] 11	3.10E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
517	TRNAV33P	chr20 3 Pseudo CAC+	CAC	chr20:43384415-43384487	7 [A] 51	9.20E-005	47 [B] 11	2.00E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
518	TRNAL42P	chr20 4 Pseudo TAA-	TAA	chr20:55366835-55366909	No Box A	N/A	49 [B] 11	1.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
519	TRNAI30P	chr20 5 Pseudo AAT-	AAT	chr20:50651745-50651822	11 [A] 52	9.70E-004	52 [B] 11	1.40E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
520	TRNAL39	chr20 6 tRNALeu AAG-	AAG	chr20:48385749-48385830	7 [A] 60	7.70E-005	56 [B] 11	3.40E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
521	TRNAE43P	chr20 7 Pseudo CTC-	CTC	chr20:13918470-13918541	7 [A] 50	1.90E-005	46 [B] 11	6.10E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
522	TRNAS31P	chr2 10 Pseudo TGA+	TGA	chr2:131856612-131856681	No Box A	N/A	44 [B] 11	4.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
523	TRNAQ39P	chr2 11 Pseudo TTG+	TTG	chr2:131859603-131859674	7 [A] 50	4.80E-004	46 [B] 11	5.60E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
524	TRNASUP2	chr21 1 tRNASup TTA+	TTA	chr21:14848387-14848457	No Box A	N/A	45 [B] 11	6.10E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
525	TRNAV9	chr2 14 tRNA Tyr ATA I+	ATA	chr2:218818794-218818886	7 [A] 71	8.10E-006	67 [B] 11	4.00E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
526	TRNAQ44P	chr2 15 Pseudo CTG+	CTG	chr2:219199376-219199451	19 [A] 42	1.00E-003	50 [B] 11	6.10E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
527	TRNAK39P	chr2 16 Pseudo TTT-	TTT	chr2:223894559-223894631	7 [A] 51	4.30E-005	47 [B] 11	4.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
528	TRNAE40P	chr2 17 Pseudo TTC-	TTC	chr2:203937376-203937446	7 [A] 49	1.20E-006	45 [B] 11	6.10E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
529	TRNAE41P	chr2 18 Pseudo CTC-	CTC	chr2:159446417-159446488	7 [A] 50	2.90E-005	46 [B] 11	2.70E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
530	TRNAG32P	chr2 1 Pseudo CCC+	CCC	chr2:11609278-11609349	7 [A] 50	1.80E-007	46 [B] 11	4.50E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
531	TRNAS8	chr2 21 tRNA Ser TGA-	TGA	chr2:130749494-130749563	No Box A	N/A	44 [B] 11	4.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
532	TRNAQ36P	chr2 22 Pseudo TTG-	TTG	chr2:130746381-130746452	7 [A] 50	4.80E-004	46 [B] 11	5.60E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A

533	TRNAQ18	chr2 23 tRNA ^{Gln} TTG-	TTG	chr2:117498979-117499050	7 [A] 50	2.60E-005	46 [B] 11	4.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
534	TRNAE36P	chr2 24 Pseudo CTC-	CTC	chr2:95580921-95580992	7 [A] 50	1.20E-007	46 [B] 11	4.50E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
535	TRNAE31P	chr2 25 Pseudo CTC-	CTC	chr2:71126996-71127068	7 [A] 51	7.00E-005	47 [B] 11	2.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
536		chr2 26 Pseudo ???-	???	chr2:70517465-70517535	7 [A] 49	7.90E-007	45 [B] 11	3.40E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
537	TRNAQ34P	chr2 28 Pseudo TTG-	TTG	chr2:45790945-45791017	7 [A] 51	6.40E-005	47 [B] 11	1.60E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
538	TRNAL9	chr2 4 tRNA ^{Leu} AAG+	AAG	chr2:30131072-30131144	7 [A] 51	7.90E-007	47 [B] 11	1.50E-003	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
539	TRNAE10	chr2 6 tRNA ^{Glu} TTC+	TTC	chr2:74977554-74977622	5 [A] 49	1.80E-007	44 [B] 10	3.10E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
540	TRNAP25P	chr2 7 Pseudo AGG+	AGG	chr2:77749101-77749171	7 [A] 49	4.40E-004	45 [B] 11	1.50E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
541	TRNAP28P	chr2 8 Pseudo AGG+	AGG	chr2:87193084-87193155	7 [A] 50	4.40E-004	46 [B] 11	6.10E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
542	TRNAL46P	chr2 9 Pseudo TAA+	TAA	chr2:117497887-117497961	No Box A	N/A	49 [B] 11	1.30E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
543	TRNAE27P	chr3 10 Pseudo CTC-	CTC	chr3:105362214-105362285	No Box A	N/A	46 [B] 11	6.10E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
544	TRNAC31P	chr3 12 Pseudo GCA-	GCA	chr3:17716396-17716468	7 [A] 51	4.40E-004	47 [B] 11	7.50E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
545	TRNASUP4P	chr3 1 Pseudo CTA+	CTA	chr3:13808887-13808954	7 [A] 46	3.80E-004	42 [B] 11	4.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
546	TRNAD7	chr3 3 tRNA ^{Asp} GTC-	GTC	chr3:185848789-185848859	7 [A] 49	1.80E-004	45 [B] 11	2.00E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
547	TRNAH8	chr3 4 tRNA ^{His} GTG-	GTG	chr3:149799253-149799324	7 [A] 50	1.20E-003	46 [B] 11	1.80E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
548	TRNAL33	chr3 5 tRNA ^{Leu} AAG-	AAG	chr3:149703918-149703999	7 [A] 60	1.50E-005	56 [B] 11	3.40E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
549	TRNAE9	chr3 8 tRNA ^{Glu} CTC-	CTC	chr3:126895867-126895938	7 [A] 50	2.00E-004	46 [B] 11	5.10E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
550	TRNAQ42P	chr3 9 Pseudo TTG-	TTG	chr3:108103568-108103639	7 [A] 50	5.90E-004	46 [B] 11	3.80E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
551	TRNAQ54P	chr4 1 Pseudo TTG+	TTG	chr4:156603338-156603409	7 [A] 50	4.80E-004	46 [B] 11	7.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
552	TRNAL31	chr4 2 tRNA ^{Leu} TAA-	TAA	chr4:156604428-156604502	No Box A	N/A	49 [B] 11	1.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
553	TRNAQ7	chr4 4 tRNA ^{Gln} TTG-	TTG	chr4:40603500-40603572	7 [A] 51	2.90E-005	47 [B] 11	1.80E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
554	TRNASUP5P	chr4 5 Pseudo TTA-	TTA	chr4:7376739-7376810	7 [A] 50	2.30E-006	46 [B] 11	4.00E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
555	TRNAC32P	chr5 1 Pseudo ACA I+	ACA	chr5:151968789-151968964	7 [A] 154	4.30E-007	150 [B] 11	5.20E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
555		chr5 20 tRNA ^{Leu} CAG-	CAG	chr5:159324619-159324696	7 [A] 56	1.70E-005	52 [B] 11	2.30E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
557	TRNAQ53P	chr5 21 Pseudo CTG-	CTG	chr5:151228267-151228338	7 [A] 50	1.90E-005	46 [B] 11	6.10E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
558	TRNAD3	chr5 22 tRNA ^{Asp} GTC-	GTC	chr5:141754172-141754243	7 [A] 50	4.40E-004	46 [B] 11	2.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
559	TRNAQ33P	chr5 23 Pseudo TTG-	TTG	chr5:77354532-77354604	7 [A] 51	5.50E-004	47 [B] 11	6.10E-009	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
560	TRNAK2	chr5 24 tRNA ^{Lys} CTT-	CTT	chr5:26234296-26234368	7 [A] 51	2.20E-004	47 [B] 11	1.30E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
561	TRNAF9	chr6 103 tRNA ^{Phe} GAA-	GAA	chr6:28899072-28899145	7 [A] 52	9.20E-006	48 [B] 11	1.60E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
562	TRNAA44P	chr6 111 Pseudo AGC-	AGC	chr6:28854523-28854594	7 [A] 50	8.50E-004	46 [B] 11	1.30E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
563	TRNAF4	chr6 112 tRNA ^{Phe} GAA-	GAA	chr6:28839353-28839426	7 [A] 52	9.20E-006	48 [B] 11	5.60E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
564	TRNAF13P	chr6 116 Pseudo GAA-	GAA	chr6:28802834-28802906	7 [A] 51	2.30E-004	47 [B] 11	3.70E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
565	TRNAA46P	chr6 122 Pseudo TGC-	TGC	chr6:28709838-28709909	7 [A] 50	1.20E-006	46 [B] 11	4.60E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
566	TRNAL12	chr6 126 tRNA ^{Leu} AAG-	AAG	chr6:28554379-28554460	7 [A] 60	2.10E-005	56 [B] 11	7.70E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
567	TRNAV28	chr6 133 tRNA ^{Val} CAC-	CAC	chr6:27804306-27804378	7 [A] 51	2.70E-006	47 [B] 11	1.90E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
568	TRNAA21	chr6 159 tRNA ^{Ala} AGC-	AGC	chr6:26903985-26904057	7 [A] 51	1.50E-005	47 [B] 11	6.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
569	TRNAA6	chr6 18 tRNA ^{Ala} AGC+	AGC	chr6:26781569-26781641	7 [A] 51	1.50E-005	47 [B] 11	7.00E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
570	TRNAA7	chr6 19 tRNA ^{Ala} AGC+	AGC	chr6:26790694-26790766	7 [A] 51	1.50E-005	47 [B] 11	6.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
571		chr6 26 tRNA ^{Undet} ???+	???	chr6:26860609-26860682	7 [A] 52	4.30E-005	48 [B] 11	3.20E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
572	TRNAV15	chr6 32 tRNA ^{Val} CAC+	CAC	chr6:27226001-27226073	7 [A] 51	1.70E-004	47 [B] 11	3.10E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
573	TRNAI28P	chr6 39 Pseudo AAT+	AAT	chr6:27359843-27359916	7 [A] 52	1.40E-004	48 [B] 11	2.10E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
574	TRNAF3	chr6 56 tRNA ^{Phe} GAA+	GAA	chr6:27740524-27740599	7 [A] 54	1.70E-005	50 [B] 11	1.30E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
575	TRNAV27	chr6 58 tRNA ^{Val} CAC+	CAC	chr6:27758467-27758540	7 [A] 52	6.50E-007	48 [B] 11	1.30E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
576	TRNAI21	chr6 63 tRNA ^{Ala} TAT I+	TAT	chr6:28613346-28613439	7 [A] 72	1.30E-005	68 [B] 11	2.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
577	TRNAQ25	chr6 79 tRNA ^{Gln} TTG+	TTG	chr6:37395973-37396045	8 [A] 50	1.50E-007	47 [B] 11	2.60E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
578	TRNAL18	chr6 81 tRNA ^{Leu} TAA+	TAA	chr6:69971099-69971181	7 [A] 61	2.80E-007	57 [B] 11	6.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
579	TRNAC29	chr6 82 tRNA ^{Gly} GCC+	GCC	chr6:142620469-142620539	7 [A] 49	5.80E-005	45 [B] 11	1.60E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
580	TRNAQ32	chr6 84 tRNA ^{Gln} TTG+	TTG	chr6:145545552-145545623	7 [A] 50	7.90E-007	46 [B] 11	2.00E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
581	TRNAE33P	chr6 85 Pseudo TTC-	TTC	chr6:163130004-163130072	4 [A] 50	1.80E-007	43 [B] 11	7.50E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
582	TRNAV37P	chr6 86 Pseudo TAC-	TAC	chr6:156910738-156910812	No Box A	N/A	49 [B] 11	4.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
583	TRNAF15P	chr6 88 Pseudo GAA-	GAA	chr6:79724729-79724801	7 [A] 51	3.90E-005	47 [B] 11	8.70E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
584	TRNAA43	chr6 89 tRNA ^{Ala} AGC-	AGC	chr6:58304582-58304654	7 [A] 51	2.10E-005	47 [B] 11	6.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
585	TRNAA42	chr6 90 tRNA ^{Ala} AGC-	AGC	chr6:58295403-58295475	7 [A] 51	2.60E-005	47 [B] 11	6.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
586	TRNAA41	chr6 91 tRNA ^{Ala} AGC-	AGC	chr6:58290638-58290710	7 [A] 51	1.50E-005	47 [B] 11	6.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A

587		chr6 92 tRNAMet CAT-	CAT	chr6:58276451-58276523	7 [A] 51	7.00E-005	47 [B] 11	6.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
588	TRNAA35	chr6 95 tRNAAla AGC-	AGC	chr6:58249836-58249908	7 [A] 51	1.90E-005	47 [B] 11	1.30E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
589	TRNAC21	chr7 11 tRNACys GCA+	GCA	chr7:148925979-148926050	7 [A] 50	6.20E-006	46 [B] 11	3.40E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
590	TRNAS28	chr7 12 tRNA Ser AGA+	AGA	chr7:148936400-148936471	7 [A] 50	8.10E-006	46 [B] 11	2.20E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
591	TRNAC25	chr7 17 tRNACys GCA-	GCA	chr7:148974979-148975050	7 [A] 50	8.10E-006	46 [B] 11	2.20E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
592	TRNAC22	chr7 18 tRNACys GCA-	GCA	chr7:148941089-148941160	7 [A] 50	6.20E-006	46 [B] 11	2.70E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
593	TRNAC19	chr7 20 tRNACys GCA-	GCA	chr7:148917097-148917168	7 [A] 50	6.20E-006	46 [B] 11	2.20E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
594	TRNAY17P	chr7 24 Pseudo GTA-	GTA	chr7:148684678-148684753	7 [A] 54	4.30E-007	46 [B] 15	1.70E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
595	TRNAC4	chr7 25 tRNACys GCA-	GCA	chr7:148683699-148683770	7 [A] 50	6.20E-006	46 [B] 11	3.40E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
596	TRNAQ48P	chr7 26 Pseudo TTG-	TTG	chr7:57257922-57257993	7 [A] 50	4.80E-004	46 [B] 11	1.40E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
597	TRNAQ52P	chr7 4 Pseudo TTG+	TTG	chr7:141149826-141149897	7 [A] 50	1.50E-005	46 [B] 11	4.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
598	TRNAC11	chr7 7 tRNACys GCA+	GCA	chr7:148874564-148874635	7 [A] 50	6.20E-006	46 [B] 11	3.80E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
599	TRNAC13	chr7 8 tRNACys GCA+	GCA	chr7:148884735-148884806	7 [A] 50	6.20E-006	46 [B] 11	3.40E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
600	TRNAY11	chr7 9 tRNATyr GTA+	GTA	chr7:148886066-148886138	7 [A] 51	1.80E-004	47 [B] 11	2.20E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
601	TRNAY5	chr8 12 tRNATyr GTA I-	GTA	chr8:66772086-66772173	7 [A] 66	5.50E-006	62 [B] 11	5.60E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
602	TRNAL41P	chr8 13 Pseudo TAA-	TAA	chr8:47859203-47859277	12 [A] 48	2.10E-003	49 [B] 11	2.80E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
603	TRNAQ43P	chr8 14 Pseudo TTG-	TTG	chr8:32992188-32992259	7 [A] 50	2.10E-005	46 [B] 11	1.90E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
604	TRNAE28P	chr8 1 Pseudo CTC+	CTC	chr8:11830789-11830860	7 [A] 50	1.20E-007	46 [B] 11	3.10E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
605	TRNAE17	chr8 2 Pseudo TTT+	TTT	chr8:18164483-18164552	5 [A] 50	1.20E-005	44 [B] 11	2.60E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
606	TRNAE35P	chr8 3 tRNAGlu CTC+	CTC	chr8:59667352-59667422	6 [A] 50	5.50E-004	45 [B] 11	1.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
607		chr8 7 Pseudo CTC+	CTC	chr8:70234894-70234968	6 [A] 54	4.70E-006	46 [B] 14	6.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
608		chr8 8 tRNAUndet ???+	???	chr8:99222638-99222706	No Box A	N/A	43 [B] 11	1.60E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
609	TRNAF14P	chr8 9 Pseudo GAA-	GAA	chr8:124339906-124339978	7 [A] 51	3.90E-005	47 [B] 11	1.00E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
610	TRNAM10	chr9 1 tRNAMet CAT+	CAT	chr9:19393996-19394070	7 [A] 53	1.30E-004	49 [B] 11	5.60E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
611	TRNAR6	chr9 2 tRNAArg TCG+	TCG	chr9:112000624-112000696	7 [A] 51	1.90E-006	47 [B] 11	1.50E-004	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
612	TRNAW8	chr9 3 tRNATrp CCA I+	CCA	chr9:114656810-114656908	9 [A] 75	5.90E-004	73 [B] 11	3.80E-008	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
613	TRNAQ6	chr9 5 tRNAGln CTG-	CTG	chr9:125695343-125695415	6 [A] 52	3.20E-005	47 [B] 11	5.60E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
614	TRNAD2	chr9 6 tRNAAsp GTC-	GTC	chr9:76707810-76707881	7 [A] 50	2.20E-004	46 [B] 11	1.00E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
615	TRNAQ9	chr9 8 tRNAGln TTG-	TTG	chr9:5085085-5085156	7 [A] 50	1.50E-005	46 [B] 11	1.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
616	TRNAQ40P	chrX 1 Pseudo TTG+	TTG	chrX:55223391-55223462	7 [A] 50	4.80E-004	46 [B] 11	4.20E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
617	TRNAL37	chrX 2 tRNALeu TAA-	TAA	chrX:55224480-55224554	No Box A	N/A	49 [B] 11	1.50E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
618	TRNAE37P	chrX 3 Pseudo CTC-	CTC	chrX:51322852-51322923	7 [A] 50	5.90E-004	46 [B] 11	6.00E-005	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
619		chrX 5 tRNAIle GAT-	GAT	chrX:3843271-3843344	7 [A] 52	2.80E-007	48 [B] 11	6.90E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
620		chrX 6 tRNAIle GAT-	GAT	chrX:3804842-3804915	7 [A] 52	2.80E-007	48 [B] 11	6.90E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
621		chrX 7 tRNAIle GAT-	GAT	chrX:3766418-3766491	7 [A] 52	2.80E-007	48 [B] 11	6.90E-006	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A
622	TRNAQ35P	chrY 1 Pseudo TTG-	TTG	chrY:8300140-8300214	9 [A] 51	2.60E-005	48 [B] 12	6.00E-007	No_POLR3D (RPC4)	N/A	N/A	No_BDP1	N/A	N/A	No_BRF1	N/A	N/A

Table S3. Annotated tRNA genes and pseudogenes classified by decreasing POLR3D (RPC4) peak scores. A light blue label in the first column indicates genes in group 1 (POLR3D (RPC4) peak scores >269), light green genes in group 2 (POLR3D (RPC4) peak scores >165 to 269), pink genes in group 3 (POLR3D (RPC4) peak scores >0 to 165), and orange genes in group 4 (no POLR3D (RPC4) peak). The genes labeled turquoise in the third column correspond to initiator tRNAMet genes. The cells in yellow indicate predicted pseudogenes which are likely to be expressed (see text). Box A and Box B position columns indicate the number of nucleotides before (starting at TSS) and after the A and B boxes, respectively.