

## Coordinates of the T4 genome

Gene	Strand	Start	Stop	Length (bp)	Length (aa)	Correlation Coeff.	pI	Mr
Start		1						
Pm	-	123						
Pm	-	377						
<i>rIIA</i>	-	2189	12	2178	725	0.99	6.131	82903
Pm	-	2263						
<i>rIIA.1</i>	-	2403	2200	204	67	0.89	7.156	8129
Pe (1.4-3.9)	-	2422						
60+	-	2802	2458	345	160	0.93	8.738	18600
60+	-	2990	2853	138				
60.1	-	3351	2971	381	126	0.96	9.364	14651
<i>mobA</i>	-	3767	3654	114	37	0.78	9.54	4192
Pe (3.6)	-	3847						
39	-	5328	3778	1551	516	0.96	7.103	57978
Pm	-	5349						
Term	-	5384						
39.1	-	5595	5398	198	65	0.79	7.997	7156
39.2	-	5839	5702	138	45	0.86	8.497	5107
<i>goF=comCa</i>	-	6267	5842	426	141	0.91	4.462	16682
<i>cef=mb</i>	-	6482	6267	216	71	0.95	5.203	8464
<i>motB</i>	-	7141	6653	489	162	0.98	9.205	18219
Pe (5.9-7.3)	-	7179						
<i>motB.1</i>	-	7650	7291	360	119	0.84	4.993	13804
<i>motB.2</i>	-	8161	7661	501	166	0.93	6.45	19736
Pe (8.1)	-	8182						
<i>dexA</i>	-	8908	8225	684	227	0.98	4.763	25966
<i>dexA.1</i>	-	9150	8908	243	80	0.90	5.31	9392
<i>dexA.2</i>	-	9388	9143	246	81	0.93	4.184	9518
<i>dda</i>	-	10729	9410	1320	439	0.99	7.982	49903
<i>dda.1</i>	-	11037	10726	312	103	0.84	9.776	12104
<i>srd</i>	-	11785	11039	747	248	0.89	9.999	29044
Pe (11.5)	-	11815						
<i>modA</i>	-	12510	11908	603	200	0.94	6.035	23350
<i>modB</i>	-	13130	12507	624	207	0.91	5.306	24244
Pe (12.8)	-	13150						
<i>modA.2</i>	-	13380	13198	183	60	0.83	4.11	7024
<i>modA.3</i>	-	13859	13389	471	156	0.94	6.628	18333
<i>modA.4</i>	-	14016	13852	165	54	0.91	5.852	6162
<i>srh</i>	-	14216	14013	204	67	0.66	6.7	8104
<i>mrh</i>	-	14676	14191	486	161	0.92	4.33	18494
<i>mrh.1</i>	-	15026	14685	342	113	0.77	3.649	12621
<i>mrh.2</i>	-	15232	15026	207	68	0.82	5.687	8257
Pe (15.0)	-	15252						
Term	-	15305						

<i>soc</i>	-	15573	15331	243	80	0.95	6.361	9117
Pl	-	15597						
Pl	-	16162						
<i>segF = 69</i>	-	16280	15606	675	224	0.78	10.148	26218
Pl	-	16359						
56	-	16785	16270	516	171	0.78	4.734	20425
<i>oriA</i>	-	16763						
Pm	-	16813						
<i>dam</i>	-	17625	16846	780	259	0.93	8.846	30420
61 = 58	-	18963	17935	1029	342	0.96	9.174	39782
Pm	-	19122						
61.1	-	19130	18966	165	54	0.92	5.333	5896
61.2	-	19758	19132	627	208	0.91	6.323	24334
<i>sp = rV</i>	-	20051	19758	294	97	0.93	4.769	10994
Pe (19.8)	-	20073						
61.4	-	20369	20112	258	85	0.75	9.828	10187
<i>dmd = 61.5</i>	-	20553	20371	183	60	0.75	5.138	7027
Pe (20.3)	-	20576						
41	-	22039	20612	1428	475	0.98	5.439	53602
Term	-	22347						
40	-	22393	22049	345	114	0.91	4.793	13291
<i>uvsX</i>	-	23561	22386	1176	391	0.98	5.310	43999
Pm	-	23752						
<i>segA</i>	-	24235	23570	666	221	0.92	9.933	25342
Pm	-	24460						
<i>-gt</i>	-	25455	24400	1056	351	0.97	9.079	40670
42	-	26219	25479	741	246	0.98	5.933	28492
Pm	-	26317						
<i>imm</i>	-	26624	26373	252	83	0.31	9.436	9343
<i>imm.1</i>	-	27013	26636	378	125	0.96	6.486	14074
Pe (26.4)	-	27044						
Term	-	27183						
43	-	29893	27197	2697	898	0.97	6.087	103622
Pm	-	29931						
Term	-	29967						
<i>regA</i>	-	30340	29972	369	122	0.77	8.939	14620
62	-	30905	30342	564	187	0.93	8.592	21364
44	-	31866	30907	960	319	0.98	7.016	35790
Term	-	31912						
45	-	32603	31917	687	228	0.98	4.759	24861
Pm	-	32626						
<i>rpbA</i>	-	33048	32659	390	129	0.98	7.283	14712
45.2	-	33246	33058	189	62	0.85	5.671	7477
Pm	-	33257						
46	-	34984	33302	1683	560	0.98	8.263	63588
Pm	-	35014						
46.1	-	35187	34981	207	68	0.73	4.068	8153

46.2	-	35431	35168	264	87	0.85	4.288	10268
Pe (35.3)	-	35662						
47	-	36447	35428	1020	339	0.98	4.981	39170
Pm	-	36576						
47.1	-	36584	36444	141	46	0.25	4.210	5321
Term	-	36622						
-gt	-	37826	36624	1203	400	0.94	6.358	46709
mobB	-	38679	37885	795	264	0.78	9.737	30367
Pm	-	38681						
Term	-	38731						
-gt.2	-	38922	38731	192	63	0.91	9.135	7322
-gt.3	-	39110	38907	204	67	0.91	9.609	7931
-gt.4	-	39396	39079	318	105	0.87	8.849	12445
-gt.5	-	39616	39398	217	72	0.95	4.22	8548
55	-	40157	39600	558	185	0.94	5.45	21537
Pm	-	40180						
55.1	-	40456	40193	264	87	0.79	4.114	9846
55.2	-	40785	40459	327	108	0.88	9.717	12727
Term	-	40836						
55.3	-	41038	40799	240	79	0.52	8.751	9153
55.4	-	41170	41039	132	43	0.52	8.575	5145
Pe (40.4)	-	41225						
55.5	-	41471	41178	294	97	0.75	9.821	11809
55.6	-	41646	41464	183	60	0.71	9.581	6962
Pe (41.0)	-	41670						
Term	-	41800						
nrdH	-	42113	41805	309	102	0.93	9.075	11720
55.8	-	42328	42116	213	70	0.80	9.26	7913
Pm	-	42805						
nrdG	-	42916	42446	471	156	0.78	8.312	18248
Pm	-	43023						
mobC	-	43538	42906	633	210	0.88	9.852	23978
nrdD+	-	44814	43535	1280	605	0.99	6.889	67964
I-TevII	-	45612	44836	777	258	0.98	9.808	30371
Pl	-	45625						
nrdD+	-	46385	45848	538				
Pm	-	46441						
49'	-	46699	46382	318	105			11888
49	-	46855	46382	474	157	0.79	8.618	18145
Pl	-	46879						
Term	-	46884						
pin	-	47382	46897	486	161	0.98	4.369	18817
Pe (46.7)	-	47416						
49.1	-	47521	47366	156	51	0.80	3.780	6163
49.2	-	47826	47506	321	106	0.89	4.352	12579
49.3	-	48131	47823	309	102	0.50	3.895	11938
nrdC	-	48391	48128	264	87	0.80	7.183	10050

<i>nrdC.1</i>	-	48635	48393	243	80	0.97	8.342	9444
<i>nrdC.2</i>	-	48936	48622	315	104	0.81	6.586	12159
<i>nrdC.3</i>	-	49859	48933	927	308	0.92	9.01	36297
<i>nrdC.4</i>	-	50915	49914	1002	333	0.95	7.63	38996
Pe (50.0)	-	50937						
<i>nrdC.5</i>	-	51995	50973	1023	340	0.92	9.327	39670
<i>nrdC.6</i>	-	52893	52066	828	275	0.96	9.20	31,725
<i>nrdC.7</i>	-	53302	52901	402	133	0.84	6.41	15309
<i>nrdC.8</i>	-	53885	53358	528	175	0.88	6.11	20758
Pe (54.0)	-	53907						
<i>nrdC.9</i>	-	54248	53946	303	100	0.75	9.68	11979
<i>nrdC.10</i>	-	55320	54343	978	325	0.93	4.85	36691
Pe (54.4)	-	55348						
Term	-	55432						
<i>nrdC.11</i>	-	56445	55435	1011	336	0.92	6.89	38899
<i>mobD</i>	-	57208	56429	780	259	0.79	9.957	30456
<i>mobD.1</i>	-	57828	57283	546	181	0.95	6.01	21179
<i>mobD.2</i>	-	57932	57828	105	34	-0.05	9.49	4205
Pe	-	57954						
<i>mobD.2a</i>	-	58165	58049	117	38	0.68	8.85	4516
<i>mobD.3</i>	-	58349	58155	195	64	0.91	4.95	7605
<i>mobD.4</i>	-	58534	58352	183	60	0.94	4.41	6858
<i>mobD.5</i>	-	58722	58534	189	62	0.82	4.061	7122
Pe (57.9)	-	58744						
Term	-	58813						
<i>rI.-1</i>	-	59205	58819	387	128	0.97	5.61	14649
<i>rI</i>	-	59495	59202	294	97	0.76	4.83	11125
<i>rI.1</i>	-	59720	59508	213	70	0.73	10.225	8273
Pl	-	59740						
<i>tk</i>	-	60344	59763	582	193	0.95	6.49	21624
<i>tk.1</i>	-	60534	60346	189	62	0.77	3.989	7238
<i>tk.2</i>	-	60716	60531	186	61	0.67	4.194	7134
<i>tk.3</i>	-	60925	60713	213	70	0.78	8.628	8507
Term	-	61369						
<i>tk.4</i>	-	61389	60922	468	155	0.94	6.124	17491
<i>vs</i>	-	61733	61386	348	115	0.67	8.744	13057
<i>vs.1</i>	-	62271	61726	546	181	0.95	9.798	20683
<i>regB</i>	-	62740	62279	462	153	0.85	8.444	17978
Pe (62.2)	-	62761						
<i>vs.3</i>	-	63078	62800	279	92	0.87	5.378	10904
<i>vs.4</i>	-	63344	63078	267	88	0.95	4.555	10211
<i>vs.5</i>	-	63557	63381	177	58	0.17	9.52	6,611
<i>vs.6</i>	-	63919	63557	363	120	0.93	5.902	13814
<i>vs.7</i>	-	64256	63927	330	109	0.75	9.031	12836
<i>vs.8</i>	-	64912	64253	660	219	0.87	9.21	25029
<i>denV</i>	-	65355	64939	417	138	0.94	9.393	16080
Pe (64.6)	-	65378						

<i>ipII</i>	-	65718	65416	303	100	0.94	9.349	11086
Pe (65.0)	-	65763						
<i>ipIII</i>	-	66415	65834	582	194	0.89	9.557	21689
Pe	-	66462						
<i>e</i>	-	66997	66503	495	164	0.97	9.599	18693
Pl	-	67005						
Pl	-	67018						
Pl	-	67234						
<i>nudE = e.1</i>	-	67490	67035	456	151	0.95	5.141	17025
<i>e.2</i>	-	67960	67652	309	102	0.96	6.485	12156
<i>e.3</i>	-	68319	67957	363	120	0.85	8.784	14156
<i>e.4</i>	-	68693	68301	393	130	0.60	9.647	15139
<i>e.5</i>	-	69270	68662	609	202	0.97	5.72	23816
Term	-	69306						
<i>e.6</i>	-	69905	69312	594	197	0.99	6.162	22045
Pe (69.9)	-	69931						
<i>e.7</i>	-	70303	69968	336	111	0.83	4.214	13070
Pe (69.4)	-	70323						
<i>e.8</i>	-	70623	70360	264	87	0.74	4.324	10199
Pe (69.8)	-	70660						
Term	-	70856						
<i>rnaC</i>	-	71046	70908	139				
<i>rnaD</i>	-	71171	71053	119				
<i>tRNAR</i>	-	71247	71173	75				
<i>segB</i>	-	71918	71253	666	221	0.96	9.320	26146
<i>tRNAI</i>	-	72033	71960	74				
<i>tRNAT</i>	-	72110	72035	76				
<i>tRNAS</i>	-	72204	72118	87				
<i>tRNAP</i>	-	72280	72203	78				
<i>tRNAG</i>	-	72364	72291	74				
<i>tRNAL</i>	-	72456	72369	88				
<i>tRNAE</i>	-	72530	72456	75				
Pm	-	72593						
Pl	-	72863						
<i>tRNA.2</i>	-	72915	72628	288	95	0.96	5.031	11285
<i>tRNA.3</i>	-	73328	72918	411	136	0.93	4.736	16035
<i>tRNA.4</i>	-	73514	73329	186	61	0.69	7.996	6558
Pe (72.6)	-	73536						
<i>ipI</i>	-	73878	73591	288	95	0.90	8.973	10177
Pe (73.0)	-	73903						
<i>57B</i>	-	74410	73952	459	152	0.83	5.089	17246
<i>57A</i>	-	74649	74407	243	80	0.97	4.248	8731
Pm	-	74877						
Pl	-	74999						
<i>1</i>	-	75374	74649	726	242	1.00	4.947	27332
Pm	-	75393						
<i>3</i>	-	75954	75424	531	176	0.93	4.267	19713

2 = 64	-	76885	76061	825	274	0.87	10.144	31613
4 = 50 = 65	-	77337	76885	453	150	0.77	9.793	17629
Pl	-	77358						
Pl	+	77362						
Pl	+	77381						
53	+	77385	77975	591	196	0.96	6.005	22968
Pl	+	77491						
5	+	77959	79686	1728	575	0.95	5.235	63121
<i>repEB</i>	-	78118	77981	138	45	0.35	5.19	5483
<i>repEA</i>	-	79237	79085	153	50	0.24	8.52	6130
Pe	-	79405						
5.1	+	79721	80215	495	164	0.86	4.593	18499
Pl	+	79799						
<i>segC</i>	+	80196	80618	423	140	0.90	9.74	15,945
5.3	+	80621	80791	171	56	0.75	9.960	6089
5.4	+	80779	81072	294	97	0.89	8.462	10221
6	+	81081	83063	1983	660	0.97	4.508	74436
7	+	83060	86158	3099	1032	0.96	4.953	119226
Pl	+	85812						
8	+	86151	87155	1005	334	0.91	4.453	38011
Term	+	87161						
Pl	+	87200						
9	+	87219	88085	867	288	0.91	4.929	31000
Pl	+	87885						
10	+	88085	89893	1809	602	0.94	4.275	66238
11	+	89893	90552	660	219	0.91	5.066	23708
12	+	90549	92132	1584	527	0.91	6.072	56220
<i>wac</i>	+	92129	93592	1464	487	0.95	4.445	51876
Term	+	93596						
13	+	93624	94553	930	309	0.92	4.917	34745
14	+	94555	95325	771	256	0.92	4.468	29575
Pl	+	95337						
15	+	95367	96185	819	272	0.94	4.772	31558
Pl	+	96153						
16	+	96194	96688	495	164	0.90	4.423	18388
17	+	96672	98504	1833	610	0.98	5.638	69764
Pl	+	96913						
17'A	+	96933	98504	1572	523		5.16	59245
17'B	+	96987	98504	1518	505		5.02	57108
17''	+	97254	98504	1251	416		4.67	46841
Pl	+	98513						
18	+	98536	100515	1980	659	0.95	4.795	71338
Pl	+	100564						
Pl	+	100623						
19	+	100632	101123	492	163	0.99	4.546	18462
Term	+	101131						
Pl	+	101184						

20	+	101207	102781	1575	524	0.99	5.341	61037
Pl	+	102539						
67	+	102781	103023	243	80	0.77	3.662	9106
68	+	103023	103448	426	141	0.98	10.108	15874
Pl	+	103146						
21	+	103448	104086	639	212	0.95	4.725	23253
21'	+	103514	104086	573	190		5.134	20834
Pl	+	104095						
22	+	104117	104926	810	269	0.92	4.498	29906
Pl	+	104787						
Pl	+	104816						
23	+	104945	106510	1566	521	0.97	5.29	56023
Term	+	106537						
<i>segD</i>	-	107232	106561	672	223	0.99	9.740	25619
Pl	+	107301						
24	+	107323	108606	1284	427	0.92	4.618	46998
Term	+	108613						
Term	+	108668						
<i>rnlB = 24.1</i>	-	109640	108636	1005	334	0.99	5.666	37631
24.2	-	109928	109650	279	92	0.87	4.923	11003
24.3	-	110085	109915	171	56	0.85	10.22	6550
Term	-	110180						
<i>hoc</i>	-	111317	110187	1,131	376	0.93	4.626	40388
<i>inh</i>	-	112007	111327	681	226	0.97	4.304	25570
Pl	-	112029						
Pl	+	112034						
<i>segE</i>	+	112057	112674	618	205	0.92	4.559	22896
Pl	+	112588						
<i>uvsW</i>	+	112677	114440	1764	587	0.93	10.304	67526
Term	-	114472						
<i>uvsY.-2</i>	-	114663	114496	168	55	0.91	4.323	6062
Pl	-	114681						
<i>uvsY.-1</i>	-	114914	114690	225	74	0.74	4.939	8963
<i>uvsY</i>	-	115327	114914	414	137	0.88	8.53	15840
Pm	-	115371						
25	-	115802	115404	399	132	0.95	4.49	15096
26'	-	116089	115802	288	95		5.27	10856
Pl	-	116412						
26	-	116428	115802	627	208	0.86	5.748	23883
Pl	-	116436						
Pl	-	116444						
Pl	+	116467						
51	+	116479	117228	750	249	0.91	6.229	29340
27	+	117228	118403	1176	391	0.97	5.24	44462
28	+	118348	118881	534	177	0.94	5.75	20,122
29	+	118878	120650	1773	590	0.95	4.931	64416
48	+	120659	121753	1095	364	0.76	8.715	39738

54	+	121753	122715	963	320	0.87	5.383	34981
Term	+	122720						
alt.-3	-	123032	122742	291	96	0.93	4.58	10704
Pe	-	123057						
alt.-2	-	123268	123065	204	67	0.70	9.81	7382
alt.-1	-	123450	123265	186	61	0.95	5.71	6622
alt	-	125502	123454	2049	682	0.95	6.158	75819
Pl	-	125525						
Term	-	125558						
alt.1	-	125748	125560	189	62	0.89	4.371	7153
30	-	127208	125745	1464	487	0.98	6.315	55299
Pm	-	127234						
30.1	-	127474	127205	270	89	0.82	8.00	10833
30.2	-	128310	127474	837	278	0.94	6.241	32433
Pm	-	128355						
30.3'	-	128629	128402	228	75	-0.17	10.4	8945
30.3	-	128765	128307	459	152	0.85	8.849	17088
30.4	-	128964	128758	207	68	0.95	4.535	8064
30.5	-	129158	128961	198	65	0.82	5.091	7252
30.6	-	129445	129158	288	95	0.88	7.19	10814
30.7	-	129852	129487	366	121	0.82	7.305	14131
Pe (128.2)	-	129883						
30.8	-	130253	129921	333	110	0.94	6.612	12893
Pe (128.6)	-	130274						
Term	-	130358						
Term	-	130402						
30.9	-	130540	130364	177	58	0.92	11.44	6519
rIII	-	131033	130785	249	82	0.90	8.479	9325
Pl	-	131167						
31	-	131516	131181	336	111	0.89	5.315	12079
Pm	-	131540						
31.1	-	131881	131573	309	102	0.84	9.113	11520
31.2	-	132118	131882	237	78	0.71	9.806	9397
cd	-	132699	132118	582	193	0.90	7.833	21200
cd.1	-	133034	132696	339	112	0.84	8.138	12814
cd.2	-	133261	133031	231	76	0.69	4.823	10131
Pe (131.7)	-	133295						
Term	-	133376						
cd.3	-	133609	133334	276	91	0.88	4.82	10131
cd.4	-	133812	133612	201	66	0.83	4.19	7918
cd.5	-	134032	133805	228	75	0.81	8.521	8738
pseT	-	134907	134002	906	301	0.96	8.671	34622
pseT.1	-	135135	134908	228	75	0.74	8.455	8833
pseT.2	-	135431	135132	300	99	0.75	8.577	11645
pseT.3	-	135781	135428	354	117	0.90	8.947	13136
alc	-	136275	135772	504	167	0.94	7.23	18962
Pe (134.4)	-	136300						

Pl	+	136889						
<i>rnlA = 63</i>	-	137464	136340	1125	374	0.96	4.885	43514
<i>denA</i>	-	137951	137517	435	144	0.94	9.442	16744
Term	-	137950						
<i>nrdB+</i>	-	138457	137955	503	388	0.92	4.924	45357
<i>I-TevIII</i>	-	138886	138593	294	97	0.78	9.011	11331
Pl	-	138933						
Pm	-	138939						
<i>nrdB+</i>	-	139719	139056	664				
Pm	-	139878						
<i>nrdB.1</i>	-	139967	139716	252	83	0.83	9.874	9409
Term	-	140384						
<i>mobE</i>	-	140416	139991	426	141	0.94	10.102	16448
<i>nrdA</i>	-	142680	140416	2265	754	0.98	6.117	85982
Pm	-	142725						
<i>nrdA.1</i>	-	142997	142671	327	108	0.70	9.035	12362
<i>nrdA.2</i>	-	143214	142951	264	87	0.96	5.233	10065
<i>td+</i>	-	143546	143235	312	286	0.89	8.617	33077
<i>I-TevI</i>	-	144431	143694	738	245	0.83	9.625	28175
Pl	-	144449						
<i>td+</i>	-	145112	144564	549				
Pm	-	145142						
<i>frd</i>	-	145690	145109	582	193	0.98	6.35	21714
<i>frd.1</i>	-	146004	145762	243	80	0.75	4.843	9471
Term	-	146051						
<i>frd.2</i>	-	146529	146143	387	128	0.73	4.281	14742
<i>frd.3</i>	-	146802	146575	228	75	0.85	3.699	8820
Pe (144.6)	-	146839	146833					
Term	-	146925						
32	-	147853	146948	906	301	0.96	4.681	33509
Pl	-	147998						
Pm	-	148057						
<i>segG = 32.1</i>	-	148541	147909	633	210	0.95	7.194	24564
59	-	149196	148543	654	217	0.89	9.387	26000
33	-	149531	149193	339	112	0.93	4.38	12831
<i>dsbA</i>	-	149778	149509	270	89	0.96	4.969	10379
Pm	-	149873						
<i>rnh</i>	-	150704	149787	918	305	0.97	8.535	35562
Pe (148.6)	-	150727						
Pl	+	150780						
34	+	150809	154678	3870	1289	0.94	5.206	140416
Pm	-	153011						
35	+	154687	155805	1119	372	0.84	4.96	40123
Term	+	155811						
Pl	+	155850						
36	+	155868	156533	666	221	0.92	8.072	23343
Pl	+	156369						

37	+	156542	159622	3081	1026	0.87	8.537	109226
Term	+	159628						
38	+	159649	160200	552	183	0.88	6.633	22311
Pl	+	160209						
<i>t</i>	+	160221	160877	657	218	0.94	7.921	25178
Term	+	160924						
<i>asiA</i>	-	161150	160878	273	90	0.95	5.395	10590
Pe (158.7)	-	161175						
<i>asiA.1</i>	-	161315	161163	153	50	0.89	4.51	5935
<i>arn</i>	-	161590	161312	279	92	0.81	4.351	10903
<i>arn.1</i>	-	161805	161674	132	43	0.54	8.334	5173
<i>arn.2</i>	-	162172	161876	297	98	0.59	5.243	12402
<i>arn.3</i>	-	162630	162172	459	152	0.90	5.078	17837
<i>arn.4</i>	-	162833	162627	207	68	0.99	9.24	12802
<i>motA</i>	-	163602	162967	636	211	0.96	8.772	23577
Pe (161.1)	-	163637						
Term	-	163724						
<i>motA.1</i>	-	163879	163730	150	49	0.49	10.036	4842
52	-	165204	163876	1329	442	0.99	8.799	50582
52.1	-	165349	165209	141	46	0.42	8.649	5098
Term	-	165332						
<i>ac</i>	-	165497	165342	156	51	0.51	3.916	5472
<i>stp</i>	-	165585	165505	81	26	-0.14	10.28	3,184
<i>ndd</i>	-	166040	165585	456	151	0.85	9.524	16935
<i>ndd.1</i>	-	166316	166101	216	71	0.86	4.111	8143
<i>ndd.2</i>	-	166435	166325	111	36	0.09	5.818	4354
<i>ndd.2a</i>	-	166554	166432	123	40	0.73	7.14	4303
<i>ndd.3</i>	-	166628	166548	81	26	-0.49	8.25	3019
<i>ndd.4</i>	-	166764	166636	129	42	0.11	8.622	4954
Pe (164.2)	-	166771						
<i>ndd.5</i>	-	166913	166815	99	32	0.81	7.082	3687
<i>ndd.6</i>	-	166996	166910	87	28	-0.05	8.014	3406
Pe (164.5)	-	167050						
<i>denB</i>	-	167660	167103	558	185	0.91	7.232	21162
Term	-	167736						
<i>denB.1</i>	-	167937	167743	195	64	0.52	8.134	7452
<i>rIIB</i>	-	168903	167965	939	312	0.96	6.24	35544
End			168903					

### Legend for Table 1

Genes are listed sequentially as they appear in the GenBank file (accession number AF158101), clockwise on the circular map (by convention) starting with the first base 5' of *rIIB*. Recently renamed genes, or those with multiple names, are labeled with =. Intron-containing or translational bypass genes (i.e., *nrdB*<sup>+</sup>, *60*<sup>+</sup>) are noted with a + for each reading frame. Genes marked with a prime (') are overlapping with, or internal to, the designated gene. Transcription

signals listed are Pe, Pm and Pl for early, middle and late promoters, respectively, and Ter for terminator. Pe entries in parentheses are promoter designations used in earlier literature.

The coding strand is noted as either the GenBank deposited (+) sequence or the complement (-).

Start and stop coordinates denote the first base of the coding region (usually the A of the initiator ATG) and the last base of the stop codon. Promoter coordinates given are either the mapped or predicted transcript start sites (the "+1" position), and terminator coordinates are the first 5' base of the hairpin.

The length (bp) entry includes the stop codon of each coding sequence. Only the mature protein length (aa) is given for those proteins that arise from spliced or bypassed genes.

The correlation coefficient given for each gene is the probability of an ORF being a T4 gene based on the codon usage in characterized T4 genes. The program was written by Gary Stormo and is available at the web site: <http://www.lecb.ncifcrf.gov/~toms/delila/frame.html>

pI and Mr are calculated values.