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Title	Things are getting hairy: Enterobacteria bacteriophage vB_PcaM_CBB
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Supplementary S2

Table S1 – Proteins in the genome of phage CBB that share homology (Detected using BLASTP).

Genes that share homology
CBB_47 (CBB_600) to CBB_50 (CBB_603)
CBB_147 to CBB_148 to CBB_149
CBB_160 to CBB_161
CBB_438 to CBB_439
CBB_480 to CBB_481 to CBB_482
CBB_536 to CBB_537
CBB_539 to CBB_540 to CBB_541 to CBB_543
CBB_549 to CBB_553
CBB_356 to CBB_10 (CBB_563)

Table S2 - Quasicore proteins of the T4 like phage identified within the CBB genome with sequence comparison to homologs in Enterobacter phage T4 and Vibrio phage KVP40 (reference strains of T4likeviruses and Schizot4likeviruses, respectively) using BLASTP.

Function	T4 like core protein	CBB homolog	Accession number of T4 protein	Identity	E-value	Accession number of KVP40	Identity	E-value
DNA replication, repair and recombination	gp49-Endonuclease VII	CBB_248	NP_049692.1	30	3.01E-06	NP_899379.1	32	1.00E-11
	gp30 - DNA ligase	CBB_100	NP_049813.1	30	1.00E-47	NP_899305.1	33	2.00E-63
	RNaseH	CBB_172	NP_049859.1	29	1.00E-13	NP_899249.1	24	1.00E-13
	gp52 - Type II DNA topoisomerase subunit	CBB_325	NP_049875.1	27	1.00E-33	NP_899529.1	30	4.00E-42
	Dda - short range DNA helicase	CBB_315	NP_049632.1	30	4.00E-30	NP_899402.1	28	1.18E+04
Auxiliary metabolism	NrdG - subunits of anaerobic ribonucleotide reductase complex	CBB_145	NP_049688.1	48	4.00E-51	NP_899263.1	43	3.00E-47
	Cd - dCMP deaminase	CBB_110	NP_049828.1	41	3.00E-38	NP_899367.1	39	1.00E-33
	Frd - Dihydrofolate reductase	CBB_313	NP_049850.1	30	2.00E-13	NP_899254.1	36	6.00E-18
	Td - thymidylate synthetase	CBB_223	NP_049848.1	43	4.00E-18	NP_899279.1	34	2.00E-57
	Tk - thymidine kinase	CBB_173	NP_049719.1	44	2.00E-51	NP_899436.1	46	3.00E-46
	gp1 - dNMP kinase	CBB_203	NP_049752.1	29	3.00E-04	NP_899338.1	67	0.59
	DenA- Endonuclease II	CBB_300	NP_049840.1	50	0.96	_	_	_

Conserved region of CBB portal vertex protein used to construct phylogenetic tree.

Sequence -

DMQPHQAMAYVERVKNDIHQRRIPSNKGGSTSLMDAAYNPLSILEDYFFPQTAEGRGSSVETLPGGDNLGQID DLRYFNNKLIRGLQIPASYLPMGPDDGGVALFGDGATQAMASELRFNNECMRYQRIISRIFDEEFKRYMIKNGY NISASSFEVTFNPPMNFAANRKAEMDAKLIQTYM

Table S3 – Phage portal vertex proteins used for phylogenetic study of CBB and the GAP32-like phage.

Phage	Portal vertex protein - Accession number
Enterobacteria_phage_IME08	YP_003734309.1
Escherichia_phage_slur07	YP_009197287.1
uncultured_Mediterranean_phage_uvMED	BAR36277.1
uncultured_Mediterranean_phage_uvMED(2)	BAR31405.1
uncultured_Mediterranean_phage_uvMED(3)	BAR29473.1

Synechococcus_phage_S-IOM18	YP_008126421.1
Synechococcus_phage_S-RIM2_R1_1999	YP_007675582.1
uncultured_Mediterranean_phage	ANS04762.1
Enterobacteria phage RB14	YP_002854503.1
Aeromonas_phage_25	YP_656382.1
Synechococcus_phage_metaG-MbCM1	YP_007001618.1
Enterobacteria_phage_RB16	YP_003858509.1
Aeromonas_phage_65	YP_004300925.1
Aeromonas_phage_Aeh1	NP_944108.1
Aeromonas_phage_PX29	YP_009011644.1
Enterobacteria_phage_JS10	YP_002922513.1
Aeromonas_phage_Aes508	YP_007010833.1
uncultured Mediterranean phage	ANS05306.1
Cyanophage_P-RSM6	YP_007675137.1
Escherichia_phage_ECML-134	YP_009102640.1
Prochlorococcus_phage_P-SSM3	YP_008129949.1
Shigella_phage_pSs-1	YP_009110988.1
Enterobacteria_phage_QL01	YP_009202903.1
Ralstonia_phage_RSP15	BAU39992.1
uncultured_Mediterranean_phage	ANS05306.1
uncultured_Mediterranean_phage(2)	ANS05306.1
uncultured_Mediterranean_phage_uvMED	BAR34134.1
Cyanophage_P-RSM1	YP_007877738.1
Cyanophage_Syn30	YP_007877943.1
Escherichia_phage_121Q	YP_009102185.1
Synechococcus_phage_S-CAM8	YP_008125640.1
Synechococcus_phage_S-RIM8_A.HR1	YP_007518198.1
Synechococcus_phage_syn9	YP_717798.1
Synechococcus_phage_S-CRM01	YP_004508471.1
Synechococcus_phage_S-RSM4	YP_003097343.1
Cyanophage_S-RIM50	AMO42907.1
Enterobacteria_phage_RB27	YP_009102372.1
Enterobacteria_phage_RB3	YP_009102372.1
Enterobacteria_phage_RB32	YP_803110.1
Escherichia_phage_vB_EcoM-UFV13	ANA50202.1
Salmonella_phage_STML-198	YP_009148150.1
Shigella_phage_SHFML-11	ANN86599.1
Aeromonas_phage_44RR2.8t	NP_932511.1
Cyanophage_P-TIM40	YP_009188207.1
Cyanophage_S-RIM32	AMO43137.1
Enterobacteria_phage_RB69	NP_861872.1
Enterobacteria_phage_vB_EcoM_VR20	YP_009207360.1
Enterobacteria_phage_vB_EcoM_VR5	YP_009205862.1
Enterobacteria_phage_vB_KleM-RaK2	YP_007007244.1
Escherichia_phage_APCEc01	YP_009225085.1

Escherichia_phage_PBECO_4	SCA80472.1
Escherichia_phage_vB_EcoM_JS09	YP_009030623.1
Aeromonas_phage_CC2	YP_007010339.1
Cronobacter_phage_vB_CsaM_GAP32	YP_006987350.1
Edwardsiella_phage_PEi20	YP_009190346.1
Enterobacteria_phage_Bp7	YP_007004276.1
Enterobacteria_phage_JSE	YP_002922232.1
Escherichia_phage_e11/2	YP_009030776.1
Escherichia_phage_UFV-AREG1	ANH50304.1
Escherichia_phage_vB_EcoM_PhAPEC2	YP_009056756.1
Pelagibacter_phage_HTVC008M	YP_007517949.1
Prochlorococcus_phage_P-HM1	YP_004322541.1
Prochlorococcus_phage_P-HM2	YP_004323487.1
Prochlorococcus_phage_P-RSM4	YP_004323264.1
Prochlorococcus_phage_P-SSM2	YP_214363.1
Prochlorococcus_phage_P-SSM4	YP_214665.1
Prochlorococcus_phage_P-SSM7	YP_004324951.1
Prochlorococcus_phage_Syn33	YP_004323727.1
Sinorhizobium_phage_phiM12	YP_009142980.1
Sinorhizobium_phage_phiN3	YP_009212309.1
Synechococcus_phage_S-PM2	YP_195138.1
Synechococcus_phage_S-ShM2	YP_004322786.1
Synechococcus_phage_S-SM1	YP_004323020.1
Synechococcus_phage_S-SSM5	YP_004324725.1
Synechococcus_phage_S-SSM7	YP_004324197.1
Vibrio_phage_KVP40	BAA77377.1
Vibrio_phage_nt-1	YP_008125180.1
Yersinia_phage_PST	YP_009153767.1
Prochlorococcus_phage_MED4-213	YP_007673752.1
Salmonella_phage_S16	YP_007501199.1
Salmonella_phage_vB_SnwM_CGG4-1	ANA49508.1
Synechococcus_phage_ACG-2014a	AIX28031.1
Synechococcus_phage_ACG-2014b	YP_009140680.1
Synechococcus_phage_ACG-2014d	AIX21202.1
Synechococcus_phage_ACG-2014e	YP_009134611.1
Synechococcus_phage_ACG-2014f	AIX42351.1
Synechococcus_phage_ACG-2014g	YP_009133666.1
Synechococcus_phage_ACG-2014h	YP_009008243.1
Synechococcus_phage_ACG-2014i	YP_009140894.1
Synechococcus_phage_ACG-2014j	YP_009134101.1
Synechococcus_phage_S-MbCM100	YP_009007965.1
Shigella_phage_Shfl2	YP_004415062.1
Escherichia_phage_HY03	AKJ72700.1
Vibrio_phage_VH7D	YP_009006286.1
uncultured_phage_MedDCM-OCT-S09-C7	ADD95604.1

Aeromonas_phage_phiAS4	YP_003969129.1
Aeromonas_phage_phiAS5	YP_003969303.1
Klebsiella phage vB_KpnM_KpV477	ANT40618.1
Klebsiella phage JD18	YP_009190743.1
Enterobacteria phage T4	NP_049782.1

Figure S1 - Maximum likelihood tree created from the alignment of the major capsid protein of 100 homologous sequences from different T4-like phages to that of major capsid protein of phage CBB found using a BLASTP search.

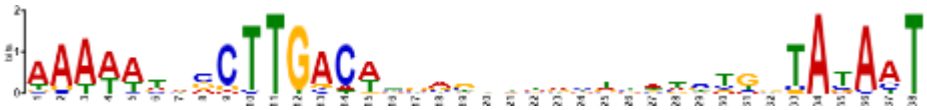


Table S4 – tRNA gene in the genome of phage CBB (Detected using tRNAscan –SE and ARAGORN).

Feature	Location	Function	Predection program
tRNA gene 1	268,792 bp - 268,878 bp	Ser, anticodon GCT	tRNAscan-SE
tRNA gene 1A	272,675 bp - 272,749 bp	tRNA-Trp(cca)	ARAGORN
tRNA gene 1B	275,819 bp - 275,892 bp	tRNA-Thr(tgt)	ARAGORN
tRNA gene 2	276,549 bp - 276,669 bp	Val, anticodon AAC (intron present 276,585 bp – 276,634 bp)	tRNAscan-SE
tRNA gene 3	280,358 bp - 280,440 bp	Leu, anticodon TAG	tRNAscan-SE
tRNA gene 4	288,346 bp – 288,417 bp	Arg, anticodon TCT	tRNAscan-SE
tRNA gene 5	289,995 bp - 290,067 bp	Sup, anticodon CTA or tRNA-Pyl(cta)	TRNAscan -SE ARAGORN
tRNA gene 6	290,284 bp – 290,367 bp	Leu, anticodon TAA	tRNAscan-SE
tRNA gene 7	290,373 bp – 290,482 bp	Val, anticodon GAC (intron present 290,373 bp – 290,482 bp)	tRNAscan-SE
tRNA gene 7A	290,748 bp - 290,824 bp	tRNA-Met(cat)	ARAGORN
tRNA gene 8	292,673 bp - 292,754 bp	Leu, anticodon TAA	tRNAscan-SE
tRNA gene 9	295,724 bp – 295,837 bp	Pseudo tRNA	tRNAscan-SE
tRNA gene 10	297,425 bp - 297,546 bp	Phe, anticodon GAA, (intron present 297,459 bp – 297,510 bp)	tRNAscan-SE
tRNA gene 11	299,090 bp - 299,176 bp	Leu, anticodon CAA	tRNAscan-SE
tRNA gene 12	302,062 bp – 302,132 bp	Glu, anticodon TTC	tRNAscan-SE

tRNA gene 13	302,143 bp - 302,231 bp	tRNA-Tyr(gta)	ARAGORN
tRNA gene 14	302,564 bp - 302,654 bp	tRNA-Ser(tga)	ARAGORN
tRNA gene 15	302,662 bp - 302,780 bp	Ser, anticodon AGA (intron present 302,696 bp – 302,744 bp)	tRNAscan-SE
tRNA gene 16	304, 228 bp – 304,298 bp	Ile, anticodon GAT	tRNAscan-SE
tRNA gene 16A	307,123 bp - 307,195 bp	tRNA-Asn(gtt)	ARAGORN
tRNA gene 17	307,717 bp – 307,789 bp	Gln, anticodon TTG	tRNAscan-SE
tRNA gene 17A	308,195 bp - 308,267 bp	tRNA-Gly(tcc)	ARAGORN
tRNA gene 18	309,726 bp - 309,787 bp	Asp, anticodon GTC	tRNAscan-SE
tRNA gene 19	310, 643 bp – 310,718 bp	Arg, anticodon ACG	tRNAscan-SE
tRNA gene 20	311,782 bp – 311,853 bp	Pro, anticodon TGG	tRNAscan-SE
tRNA gene 21	311,859 bp - 311,931 bp	Pro, anticodon TGG	tRNAscan-SE
tRNA gene 22	312,275 bp – 312,348 bp	His, anticodon GTG	tRNAscan-SE
tRNA gene 23	312, 637 bp – 312,710 bp	Phe, anticodon GAA	tRNAscan-SE
tRNA gene 24	313,823 bp – 313,895 bp	Lys, anticodon TTT	tRNAscan-SE
tRNA gene 25	318,802 bp – 318,876 bp	Cys, anticodon GCA	tRNAscan-SE
tRNA gene 26	319,754 bp – 319,826 bp	Met, anticodon CAT	tRNAscan-SE
tRNA gene 26A	320,334 bp- 320,411 bp	tRNA-Met(cat)	ARAGORN
tRNA gene 27	320, 479 bp – 320,511 bp	Ala, anticondon TGC	tRNAscan-SE

Table S5 - Promoter 2 of Phage CBB found using MEME



Promoter	location	**Sequence**
Porf_36	13,365-13,402	AAAAATAGCTTGCATCACTCGTAATTATGAAGTATAAT
Porf_41	15,759-15,796	AAAAAGGAGTTGACAACAGTTGGCTCCTTTGCTATACT
Porf_44	17,515-17,552	AAAAATTCCCTTGCTTTCTTTCTTTCGTGTGGTATACT
Porf_83	39,070-39,107	AATACTGACTTGACACGAGGCAGCAAGAGTGTTACAAT
Porf_166	93,493-93,530	AAAAATAGCTTGATTTTGAGCTACATAATTGATATAAT
Porf_181	100,667`-100,704	ACAAATTGCTTGACATGGCAGTGAGTATCATATATCAT
Porf_189	106,894-106,931	GAATAAACCTTGACAGTACGATAAAAAAGTGCTACATT
Porf_360	262,781-262,818	AAATTTACCTTGACAAAATCAACTCCATCCCTGATAAT
Porf_395	281,079-281,116	AAAAATGACTTGGCAGGAGATTAATATTCCTGTACAAT
Porf_436	296,151-296,188	TAAAAATCCTTGACTTGCGTCGGTTGACCTGATAGAAT
Porf_491	319,303-319,340	CAAAACACCTTGACAGTGGCATCCTCTCATGGCAAAAT
Porf_497	323,285-323,322	AGATTTTGCTTGACAAGACGGCATTTTTTGTTTATAAT
Porf_503	326,287-326,324	AAATACCAGTTGACTCAACGTGGGTTAACTGGTATACT
Porf_510	329,125-329,162	AATTTGGCCTTGCAATCAGCGAACGCATGTGATATATT
Porf_524	336,865-336,902	AGAAAATCCTTGACTTGCTTCAGCAAGGCGAGTACACT
Porf_525	337,752-337,789	AAAAATACATTGACGTGGCACATTTTTTGTGCCATAAT
Porf_538	345,724-345,761	TATTTAGGCTTGACACGATGTTAAATCTTTGATATAAT
Porf_546	349,130-349,167	TAATTTGGCTTGACTTAGGCTTTCGAACTCCGTATAAT

Table S6 – Promoter 1 of Phage CBB found using MEME



Promoter	Location	Sequence
Porf_66	29,539-29,567	TGAAACAGAATAATTTTTTATGGTATAAT
Porf_113	54,897-54,925	TGAAACGTAAGGAATTTTTCTGCTATAAT
Porf_193	108,832-108,860	TGAAACAGCTTTAAAAATTATGGTATAGT
Porf_218	127,475-127,503	TGAAACGTACCAAAATTTTATGGTATAAT
Porf_235	145,858-145,886	TGGAACGACCTAAAAAAATGTGCTATAAT
Porf_244	168,994-169,022	TGGAACGTTTTTTAAAATTGTGGTATAAT
Porf_258	184,600-184,628	TGAAACGTATACATTTATTATGGTATAAT
Porf_262	187,472-187,500	TGAAACGAAAATAAAACGTATGATATAAT
Porf_265	191,483-191,511	TGAAACGGGTACATTTTTTATGATATAAT
Porf_272	195,587-195,615	TGAAACTGCACATAAAAATGTGGTATAAT
Porf_282	206,162-206,190	TGGAATGAGTTAAATTTTTGTGATATAAT
Porf_290	211,052-211,080	TGGAATGCATTAAAAAAATGTGGTATAAT
Porf_300	217,526-217,554	TGAAACAATAAAAAAACATGTGCTATAAT
Porf_307	224,015-224,043	TGAAACGCCAAAATAAAATATGGTATAAT
Porf_312	226,886-226,914	TGAAACAGCTTGGAATATTATGATATAAT
Porf_324	236,752-236,780	TGAAACAAAGAAACAAATTATGCTATAAT
Porf_329	243,482-243,510	TGAAATGGTAAAAAAAATTATGGTATAAT
Porf_418	289,731-289,759	TGAAACGGCGATAAAAACTGTGGTATAAT

Table S7- Promoter 3 of Phage CBB found using MEME based on analysis of 100bps upstream regions of structural genes



Promoter	Location	Sequence
Porf_112	54,769-54,782	ATAAATATTAATAT
Porf_165	93,137-93,150	ATGAATACCGCAAA
Porf_169	95,252-95,265	CTAAATACGGTATC
Porf_201	111,914-111,927	CTAAATATGATATA
Porf_204	133,744-113,757	ATAAATAACATTAT
Porf_205	116,515-116528	ATAAATACATTAAA
Porf_206	177,288-117,301	CTAAATATAATATA
Porf_210	120,228-120,241	ATAAATAAAATAAA
Porf_213	122,794-122,807	CTAAATTCATTAAA
Porf_224	132,558-132,571	ATAAATACTGGATA
Porf_226	137,986-137,999	ATAAATACTTGAAA
Porf_227	138,970-138,983	ATAAATATAAGAAA
Porf_228	140,195-140,208	ATAAATATTTGTAA
Porf_229	140,234-140,247	ATAAATAAGTAAAA
Porf_234	145,841-145,854	ATAAATACGGTATA
Porf_236	158,306-158,319	ATAAATAAAACAAA
Porf_237	161,845-161,858	ATAAATATTTCTAT
Porf_239	162,810-162,823	ATAAATACTTATAC
Porf_243	168,976-168,989	ATAAATACTTGATA
Porf_250	176,224-176,237	ATAAATAACTAATA
Porf_251	176,198-176211	ATAAATACGACTAT
Porf_256	182,056-182,069	ATAAATATCTTTAC
Porf_260	185,404-185,417	ATAAATATTTCTAT
Porf_271	195,498-195,511	ATAAATAACATTAA
Porf_276	199,519-199,532	ATAAATATATCTAT
Porf_289	210,031-210,044	ATAAATATTGTATA
Porf_298	216,496-216,509	CTAAATAAGGATAT
Porf_302	218,818-218,831	CTAAATAATTCTAT
Porf_320	231,630-231,643	ATAAATACTCAAAA
Porf_496	323,194-323,207	ATAAATACTTTATA
Porf_534	343,023-343,036	ATAAATAAATGAAA
Porf_537	345,717-345,730	CTAAATAATTAATA
Porf_551	353,119-353,132	CTAAATTTTACAAA
Porf_552	353,975-353,988	GTAAATACATAATA
Porf_553	354,727-354,740	GTAAATACAGGATA

Table S8- Terminators of Phage CBB detected using ARNold and confirmed using Mfold Quikfold

Terminator	Coordinates	Sequence	ΔG kcal/mol

Torf8	3,939-3,974	GGGGGAACATGAAAGTTCCCCTgTTTTTTTCCTTGA	-13.8
Torf18	7,952 - 7,980	GGGGAACATTGTTCCCCTTTTTAAGTGAG	-10.9
Torf26	10,171 - 10,208	AGTACTGGTGAAATATCCAGTACTgTTTTTATGTACAG	-11.4
Torf39	15,175 - 15,205	AGGTTGACTTCGGTCGGCCTtTTTTGTTATACTT	-11.8
Torf47	19,234 - 19,268	GGGCAACCAAATAACGGTTGCCCTTTTTTGTATTC	-15.3
Torf52	22,047 - 22, 081	GCCGCTGTCATAATGACGGCGGCTTACTTTATGGG	-18
Torf67	30,374 - 30,401	GGGGCTTAATTGCCCCTTTTCTATAGGA	-11.1
Torf70	32,322 - 32, 354	GGACGGTACAGTGTATCGTCCTTTTTTAATTGA	-12.2
Torf80	38,447 - 38,475	GCCCCGAAATTCGGGGCTTTCTTTTTAAA	-13.4
Torf87	41,945 - 41,972	GGGATACTTCGGTATCCCTTCTTTTTTAAT	-14
Torf106	51,742- 51,774	AGGCCACTTAGTTGTGGCCTTTTTCTTTTAAGG	-12.6
Torf111	54,040 - 54,067	GGAGCCATATGGCTCCTTTTTTATTTTA	-11.9
Torf113	56,086 - 56, 116	GGAGTACTTCGGTACTCCaTTTTAAGTAAGA	-14.4
Torf123	63,856 - 63, 887	GGGGATACTTAGGTATCCCCTTTTTAATTGGA	-14.3
Torf124	64,214 - 64,242	GGCCACGCAATGTGGCCTTTTTTATTGGA	-11
Torf146	76-523 - 76,553	AGCACCTGCAAGGGTGCTTTTTTTGTTTATA	-10
Torf149	84,839 - 84, 869	AGCGGTCACTTGACCGCTTTTTTCTTTTGTG	-11.6
Torf152	86,569 - 86,596	GGGAGTGTTAGCTCCCTTTTACATTTCA	-10
Torf163	92,758 - 92, 787	CCCGTCATAAATGGCGGGTTTTCTATTAAA	-10.4
Torf165	93,533 - 93,565	AGGAAATCGTGAGATTTCCTTTTTTCGTTTGGA	-12.3
Torf173	97,558 - 97,590	TGGGCTGATATAATCAGTCCATATTTTTATGGG	-11
Torf183	104,263 - 104, 292	GCCTCACTCCGGTGGGGCTTTTTCATTTAA	-12
Torf188	106,936 - 106, 971	GGACAGGCAGCGATGCTCTGTCCTTTTTTATTTTAA	-13.8
Torf197	110,637 - 110, 666	GGGCATCTTAGGATGCCCTTTTTTCAATTG	-13
Torf202	113,016 - 113,052	GGAAGAATCTTAATAGGGTTCTTCCTTTTTTCGTTTA	-13.2
Torf204	116,418 - 116,485	GGAGCCATATGGCTCCTTTTTTGTTTTC	-11.9
Torf205	117,258 - 117, 289	GCCCTGGACTTGTCTAGGGCTTTTTTATTGCT	-14.7
Torf215	124,614 - 124, 647	AGCACTGAAAACTCAGTGCTtTTCTTTTTATCAA	-10.9
Torf216	126, 042 - 126, 072	AGGGGCATTATGCCCCTtTTGTTTTATGAGG	-11.2
Torf224	130,573 - 130,603 (complement)	AGGGAGCTTTTGCTCCCTTTCTTTTTACACC	-12.6
Torf223	130,586 - 130, 616	AGGGAGCAAAAGCTCCCTTTTTTTGTTATTG	-12.1
Torf225	132,578 - 132, 611	AGGTCAACTTATGTTGGCCTtTTGTTTTTTGTAG	-10.6
Torf228	138, 985 - 139, 017 (complement)	AGGGAGATACTTATCTCCCTTTTTTCATTGTGA	-11.2
Torf236	148, 214 - 148, 255 (complement)	GGGAGCCATATGGCTCCCTTTTTCTTTATTT	-15.2
Torf235	148,227 - 148, 256	GGGAGCCATATGGCTCCCTTTTTTGTTATA	-15.2
Torf237	158,318 - 158, 348 (complement)	GGGCATCTTCGGATGCCCTTTATTCTTGCAT	-16
Torf246	173, 110 - 173, 140	AGGAGCCATTAGGCTCCTTTTTTTATGATAT	12.1
Torf247	173, 095 - 173, 128 (complement)	AAGGAGCCTAATGGCTCCTTtTTGTTTATAGGTC	13.5
Torf257	184, 538 - 184, 566	GGACGCTTTATGCGTCCTTTTCGCATTTC	-11.3

Torf261	187,504 - 187, 543	GGCATCCTAGCGGAGAGTTAGGATGCTTTTTTTATACATG	-17.1
Torf262	187,863 - 187, 892	TGCCCCAGGATTGGGGCGTTTTGTTTTAAG	-11.6
Torf265	192,281 - 192, 313	AGGGAGCGTAATGCTCCCTcTTTTTATTTGGAT	-11.7
Torf269	194, 180 - 194, 209	GGAGAACATATGTTCTCCTTTTTCTTTTTT	-10.7
Torf270	174, 166 - 194, 198 (complement)	AGGAGAACATATGTTCTCCTTTTTTTATTACTC	-11.2
Torf277	202, 130 - 202, 164	TTGGGGCAACGGATTTGCCCCGATTTCATTTCATG	-13.7
Torf279	203, 777 - 203, 808	AGGACGCTTATTGCGTCCTTTTTGTTTTTTAG	-11.8
Torf303	221, 845 - 221, 873	TCCCGTCTATGACGGGATTTTTTATCAGG	-10.4
Torf305	223,790 - 223, 816	GGAGGCTTTGCCTCCTTTTTCATGGAT	-10
Torf310	225,406 - 225, 434 (complement)	GGGAGCTTACGCTCCCTTTTTTATGCATT	-11.5
Torf323	236,722 - 236, 757	TAACGACGCTCCAGAGCGTCGTTATTTTTTTGAAAC	-15
Torf325	240,252 - 240,279	GGACGCATAAAGCGTCCTTTATTTTTAAT	-10.8
Torf330	244,250 - 244, 279	GCCCTGCATTGTCAGGGCTTTCTTTTTGTC	-10.5
Torf333	246,154 - 246, 182	AGGGGAGTAATCCCCTTTTCCGTTTAGTA	-11
Torf338	249,187 - 249, 219	TGGGGAATGAAAGTTCCCCGcTTTTTAATTTAA	-13.5
Torf340	251, 689 - 251, 720	AGCTCCCAACACTTGGGGGCTTTTTTCATATG	-12.1
Torf344	254, 455 - 254, 489	AGCTGGCCTTAGTTGGTCAGCTTTTTTAAGTAAGA	-13.2
Torf364	265, 682 - 265, 712	CCCTGTACTAAGTACAGGGTTTTTAATTGAG	-11.4
Torf446	300, 688 - 300, 723	TGCCGCCAACATTGTTGGCGGTAcTTTTAAGTTAGA	-15.4
Torf448	301, 467 - 301, 490	GGGCGAAAGCCCTTTTTTAATTGA	-10.8
Torf468	311, 288 - 311, 323	GGGATTTTCCGTAAGGGAAATCCCTTTTTTCGTTTA	-17.8
Torf488	318, 141 - 318, 173	AGGGAGCGGATTGCTCCCTgTTTTATAATGCAT	-12.3
Torf494	321, 450 - 321, 478	GGCAGCCATTGGCTGCCTTTTTTCGTTTA	-13.1
Torf495	322, 016 - 322, 046	GGCACTCATAAAGAGTGCCTTTTGTTTTACG	-12.6
Torf496	322,001 - 322, 035 (complement)	AGGCACTCTTTATGAGTGCCTtTTTTTCTTGTATA	-13.6
Torf500	325, 314 - 325, 350	TTCGGGGATTAACTATCCCCGAAacTTTTAATGGTGA	-14.6
Torf515	333, 025 - 333, 050	GGGTTGACTTCGGTCAGCCCTTTATTTTAATT	-16.8
Torf518	334,640 - 334, 671	GGGTTGACTTCGGTCAGCCCTTTTTTGTATAA	-16.8
Torf520	335, 395 - 335, 426	GGGTTGACTTCGGTCAGCCCTTTTTGCTATAC	-16.8
Torf525	338, 856 - 338, 888	TGCCAAACATCGTGTTTGGCATTTTTTATTAAA	-11.2
Torf542	348,061 - 348, 089	ACTCCCTACGGGGAGTTTTTTATTGAGGC	-11.6
Torf546	349, 505 - 349, 535	CCGCCAGCATTGTTGGCGGTTTTTTAATTGC	-12.5
Torf547	350, 176 - 350, 206	AAGCCCCAAAAGGGGCTTTTTTAATTTGTGA	-11.8
Torf548	350,166 - 350, 191	GCCCCAAAAGGGGCTTTTTTAATTTG	-10.4
Torf553	353, 992 - 354, 024 (complement)	AGCTCAACTTAGGTTGGGCTTTTTCTGTTTTTG	-10.1