

Appendix 1.

Combinations of -35 and -10 consensus used to scan the 32 prokaryotic genomes

<i>n</i>	<i>a</i>	-35 consensus	-10 consensus
<i>Aquifex aeolicus</i> vf5	Others_AA	TTTAA	TAAAAAT
<i>Bacillus subtilis</i> 168	Firm_BS	TTGAA	TATAAT
<i>Borrelia burgdorferi</i> b31	Spiro_BB	TTTAA	TATAAT
<i>Brucella melitensis</i> 16m chr1	Proteo_BM	TTGAA	TATAAT
<i>Chlamydomphila pneumoniae</i> ar 39	Chla_CPn	TTTAA	TATAAT
<i>Clostridium perfringens</i> str13	Firm_CPe	TTTAA	TATAAT
<i>Deinococcus radiodurans</i> r1 chr1	Others_DR	TTGAC	TAAAAAT
<i>Escherichia coli</i> k12	Proteo_EC	TTGAC	TATAAT
<i>Haemophilus influenza</i> rd kw20	Proteo_HI	TTGAA	TAAAAAT
<i>Helicobacter pylori</i> j99	Proteo_HP	TTTAA	TAAAAAT
<i>Listeria innocua</i>	Firm_LI	TTGAA	TATAAT
<i>Listeria monocytogenes</i> strain EGD	Firm_LM	TTGAA	TATAAT
<i>Mycobacterium leprae</i> tn	Atb_ML	TTGAC	TAAAAAT
<i>Mycobacterium tuberculosis</i> h37rv	Atb_MT	TTGAC	TAAAAAT
<i>Mycoplasma genitalium</i> G37	Molli_MGe	TTGAA	TAAAAAT
<i>Mycoplasma pneumoniae</i> M129	Molli_MPn	TTTAA	TAAAAAT
<i>Neisseria meningitidis</i> mc58	Proteo_NM	TTGAA	TAAAAAT
<i>Oceanobacillus ihayensis</i> hte831	Firm_OI	TTGAA	TATAAT
<i>Pseudomonas aeruginosa</i> pa01	Proteo_PAe	TTGAA	TATAAT
<i>Rickettsia prowazekii</i> madrid e	Proteo_RPM	TTTAA	TATAAT
<i>Salmonella typhimurium</i> lt2	Proteo_ST	TTGAA	TATAAT
<i>Shewanella oneidensis</i> mr1	Proteo_SO	TTGAA	TAAAAAT
<i>Sinorhizobium meliloti</i> 1021	Proteo_SM	TTGAA	TATAAT
<i>Staphylococcus aureus</i> mw2	Firm_SA	TTTAA	TATAAT
<i>Streptococcus pneumoniae</i> r6	Firm_SPn	TTGAA	TATAAT
<i>Streptomyces coelicolor</i> a3 (2)	Atb_SC	TTGAC	TAAAAAT
<i>Thermoanaerobacter tengcongensis</i>	Firm_TT	TTGAA	TATAAT
<i>Thermotoga maritima</i>	Others_TM	TTGAA	TATAAT
<i>Treponema pallidum</i> nichols	Spiro_TPN	TTGAC	TATAAT
<i>Vibrio cholerae</i> n16961 chr1	Proteo_VC	TTGAA	TAAAAAT
<i>Xanthomonas campestris</i> atcc 33913	Proteo_XC	TTGAA	TATAAT
<i>Yersinia pestis</i>	Proteo_YP	TTGAA	TATAAT

Table 1.1 Combinations of -35 and -10 consensus used to analyse the 32 prokaryotic genomes. *n*: micro-organism name; *a*: abbreviation for micro-organism name (Atb: *Actinobacteria*, Chla: *Chlamydia*, Firm: *Firmicutes* (among which Molli.: *Mollicutes*), "Others" group, Proteo: *Proteobacteria*, Spiro: *Spirochaetales*).

<i>n</i>	<i>a</i>	<i>at</i>	<i>g</i>	<i>CI</i>		<i>CII</i>		$p1_{CI} \times p2_{CI}$ (%)	$p1_{CII} \times p2_{CII}$ (%)
				<i>upsp_{CI}</i>	<i>p2_{CI}</i> (%)	<i>upsp_{CII}</i>	<i>p2_{CII}</i> (%)		
<i>Aquifex aeolicus vf5</i>	Others_AA	57.62	1522	19	8.9	73	21.9	1.3	4.8
<i>Bacillus subtilis 168</i>	Firm_BS	59.27	3979	115	14.5	416	34.0	2.9	10.5
<i>Borrelia burgdorferi b31</i>	Spiro_BB	73.07	850	25	58.1	40	81.6	2.9	4.7
<i>Brucella melitensis 16m</i>	Proteo_BM	45.56	2059	0	0	4	4.3	0	0.2
<i>Chlamydomphila pneumoniae ar 39</i>	Chla_CPn	62.55	1069	6	26.1	14	46.7	0.6	1.3
<i>Clostridium perfringens str13</i>	Firm_CPe	74.93	2532	511	64.1	730	87.4	20.2	28.8
<i>Deinococcus radiodurans r1</i>	Others_DR	34.01	2521	0	0	1	0.5	0	0.0
<i>Escherichia coli k12</i>	Proteo_EC	52.34	4173	3	3.1	22	8.7	0.1	0.5
<i>Haemophilus influenzae rd ku20</i>	Proteo_HI	64.22	1673	8	25.8	20	54.1	0.5	1.2
<i>Helicobacter pylori j99</i>	Proteo_HP	62.95	1478	7	22.6	17	50.0	0.5	1.2
<i>Listeria innocua</i>	Firm_LI	64.25	2962	145	20.3	501	53.0	4.9	16.9
<i>Listeria monocytogenes strain EGD</i>	Firm_LM	63.97	2837	147	20.8	488	52.7	5.2	17.2
<i>Mycobacterium leprae tn</i>	Atb_ML	49.55	2670	0	0	1	0.8	0	0.0
<i>Mycobacterium tuberculosis h37rv</i>	Atb_MT	35.47	3909	0	0	2	0.7	0	0.1
<i>Mycoplasma genitalium G37</i>	Molli_MGe	69.54	441	1	25.0	1	25.0	0.2	0.2
<i>Mycoplasma pneumoniae M129</i>	Molli_MPn	61.74	644	2	11.1	10	38.5	0.3	1.6
<i>Neisseria meningitidis mc58</i>	Proteo_NM	51.90	1954	3	6.0	13	14.1	0.2	0.7
<i>Oceanobacillus ihyensis hte831</i>	Firm_OI	66.41	3398	217	24.6	576	54.9	6.4	17.0
<i>Pseudomonas aeruginosa pa01</i>	Proteo_PAe	35.28	5565	0	0	6	1.7	0	0.1
<i>Rickettsia prowazekii madrid e</i>	Proteo_RPM	73.16	796	2	33.3	6	100	0.3	0.8
<i>Salmonella typhimurium lt2</i>	Proteo_ST	51.22	4334	10	8.6	40	11.7	0.2	0.9
<i>Shewanella oneidensis mr1</i>	Proteo_SO	56.69	4501	10	8.5	38	22.8	0.2	0.8
<i>Sinorhizobium meliloti 1021</i>	Proteo_SM	39.50	3272	0	0	6	1.6	0	0.2
<i>Staphylococcus aureus mw2</i>	Firm_SA	69.77	2610	225	40.2	431	69.3	8.6	16.5
<i>Streptococcus pneumoniae r6</i>	Firm_SPn	62.39	1861	59	27.7	120	42.1	3.2	6.5
<i>Streptomyces coelicolor a3 (2)</i>	Atb_SC	29.15	4665	0	0	0	0	0	0
<i>Thermoanaerobacter tengcongensis</i>	Firm_TT	63.83	2588	150	25.8	407	56.9	5.8	15.7
<i>Thermotoga maritima</i>	Others_TM	54.59	1790	31	10.2	120	17.0	1.7	6.7
<i>Treponema pallidum nichols</i>	Spiro_TPN	47.00	980	1	2.4	8	6.4	0.1	0.8
<i>Vibrio cholerae n16961</i>	Proteo_VC	54.80	2618	2	6.7	5	6.9	0.1	0.2
<i>Xanthomonas campestris atcc 33913</i>	Proteo_XC	35.55	4120	0	0	0	0	0	0
<i>Yersinia pestis</i>	Proteo_YP	55.36	4090	3	5.8	20	14.7	0.1	0.5

Table 2.2 Frequencies of genes with a putative $\sigma 70$ promoter harbouring an UP element, under two constraint sets, in 32 prokaryotic genomes. *n*: micro-organism name; *a*: abbreviation for micro-organism name (see Table 2.1); *at*: average percentage of nucleotides T and A over the 350 bp-long region upstream of start codon, computed over the total number *g* of genes in the genome; *upsp_{CI}*: number of genes with an UP element harboured in the Strong Promoter region, identified under constraint set *CI*; *upsp_{CII}*: *idem*, under the more relaxed constraint set *CII* (see text, Section "Genome analysis upon request" for the definition of *CI* and *CII* constraints); $p2_{CI} = 100 \times upsp_{CI}/sp_{CI}$, $p2_{CII} = 100 \times upsp_{CII}/sp_{CII}$, with *sp_{CI}* (resp. *sp_{CII}*) the number of genes harbouring a Strong Promoter under constraints *CI* (resp. *CII*). The percentages indicated in the two rightmost columns are respectively $p1_{CI} \times p2_{CI} = upsp_{CI}/g$ and $p1_{CII} \times p2_{CII} = upsp_{CII}/g$, that is the ratio of the number of genes identified with an UP element in their putative strong promoter, to the number *g* of genes encoding proteins in the genome considered.