

SVARAP: Sequence VARIability Analysis Program

An example of application: *rpoB* gene sequencing for identification of *Corynebacterium* species

Khamis, A., Raoult, D. & La Scola, B. (2004). *J Clin Microbiol* 42:3925-31.

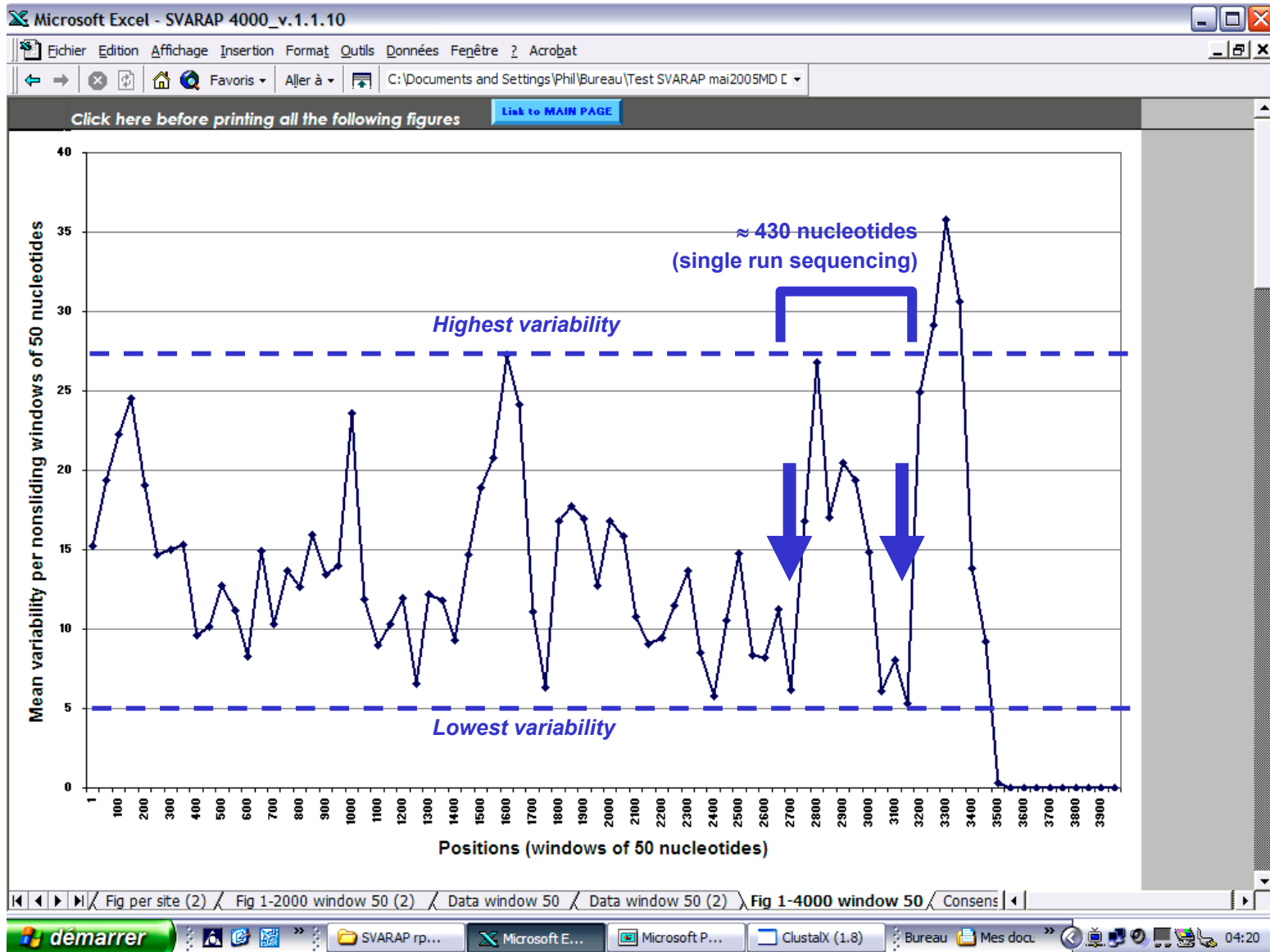
Clustal X alignment

The screenshot displays the ClustalX (1.8) interface. The main window shows a multiple sequence alignment of the *rpoB* gene. The alignment is color-coded by nucleotide: Adenine (A) in blue, Cytosine (C) in green, Guanine (G) in red, and Thymine (T) in yellow. The sequences are listed on the left, with accession numbers and strain identifiers (e.g., gi_46360981_gb). The alignment is shown in a grid format, with a ruler at the bottom indicating sequence positions from 700 to 790. A sequence quality plot is visible at the bottom of the alignment window.

File C:\SeqrpoB\Coryneb.aln loaded.

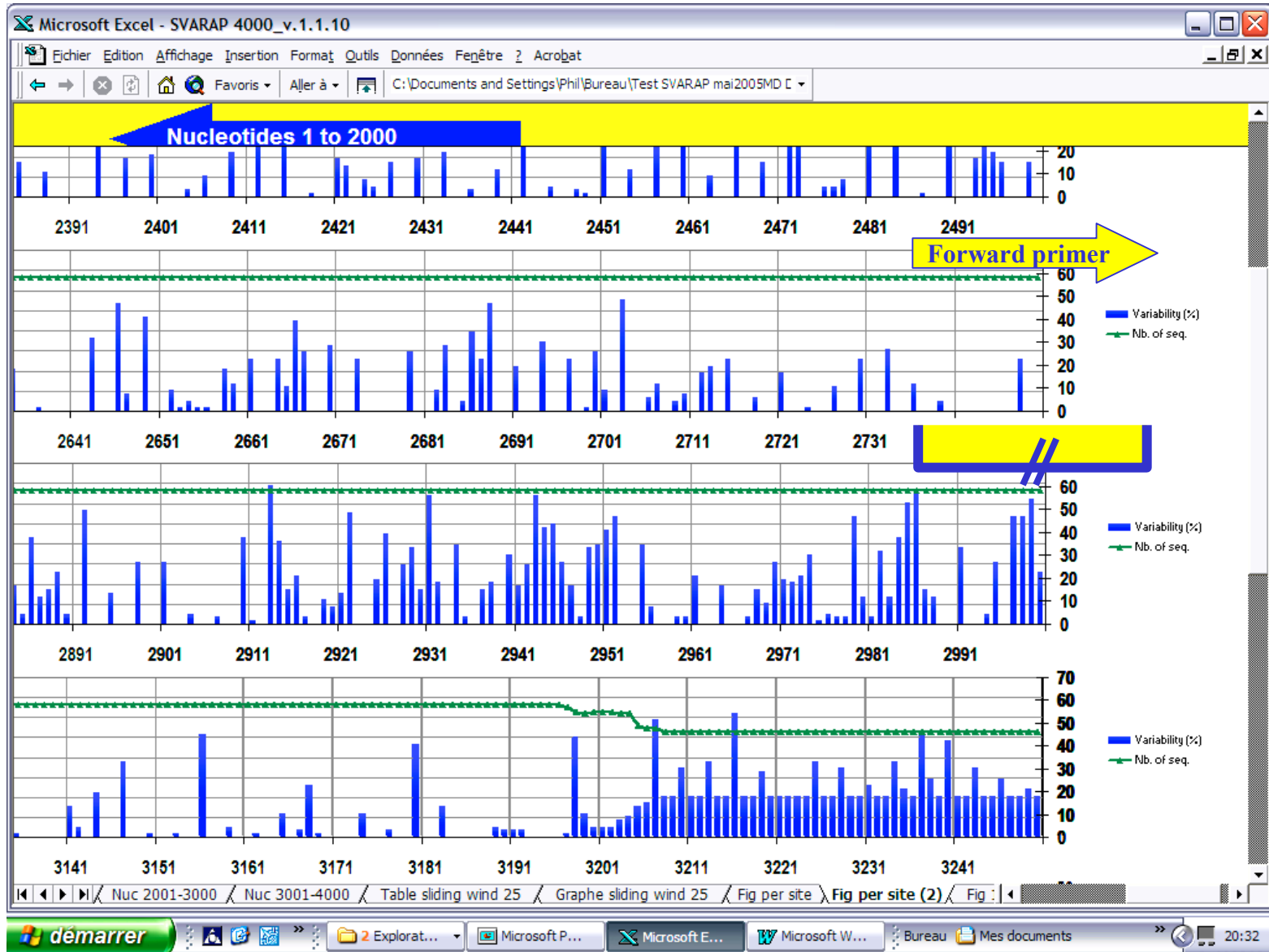
Corynebacterium species: variability in *rpoB*

« One shot » visualization of nucleotide variability (nonsliding window of 50 nucleotides)



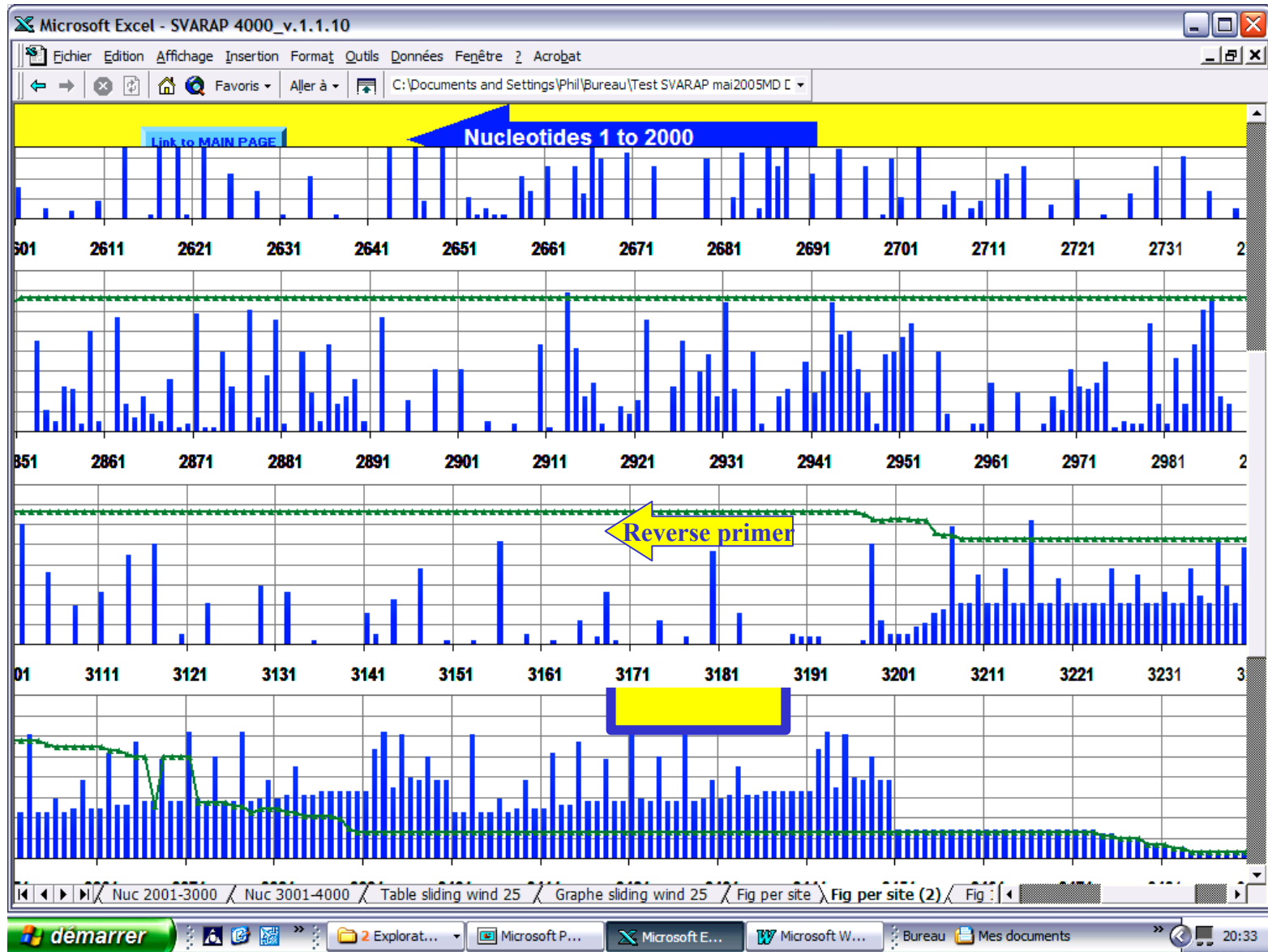
Corynebacterium species: variability in *rpoB*

« One shot » vizualisation of nucleotide site-by-site variability (nuc. 2001-4000 of the alignment)



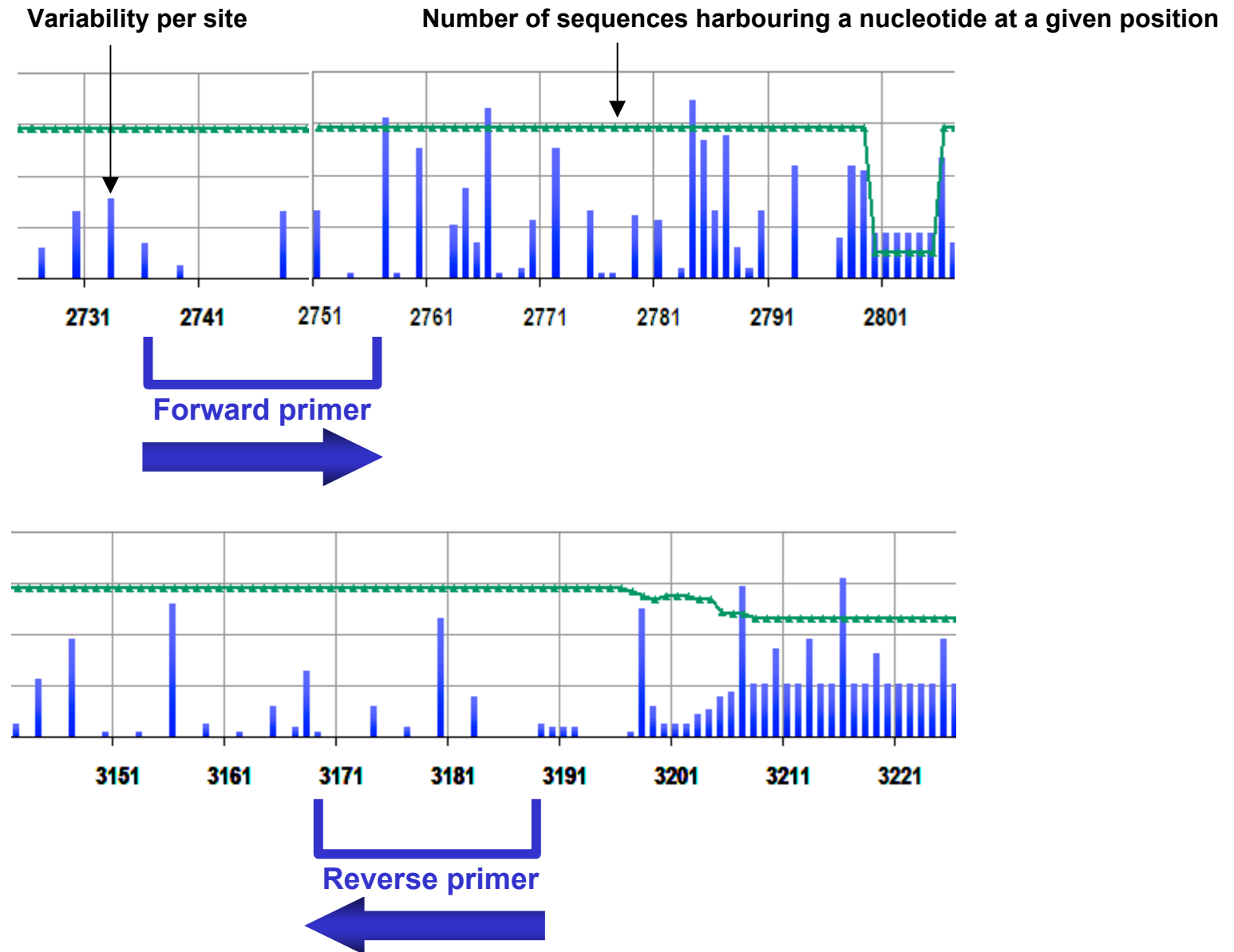
Corynebacterium species: variability in *rpoB*

« One shot » vizualisation of nucleotide site-by-site variability (nuc. 2001- 4000 of the alignment)



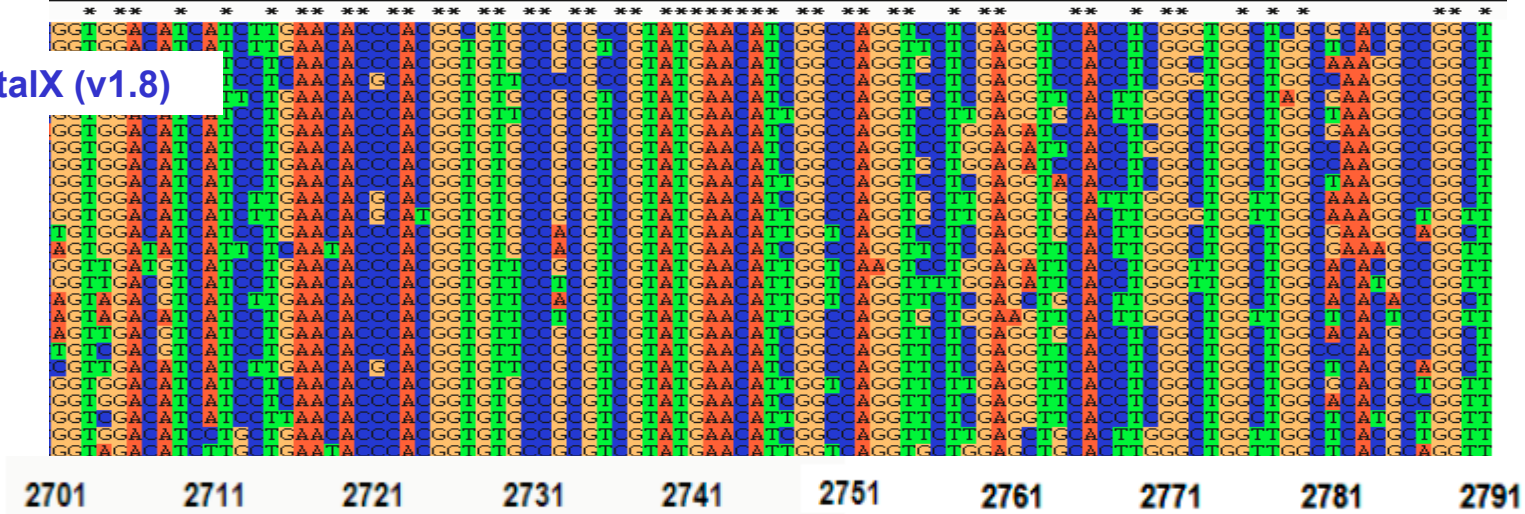
Corynebacterium* species: variability in *rpoB

Vizualisation of nucleotide site-by-site variability: primers hibridization regions

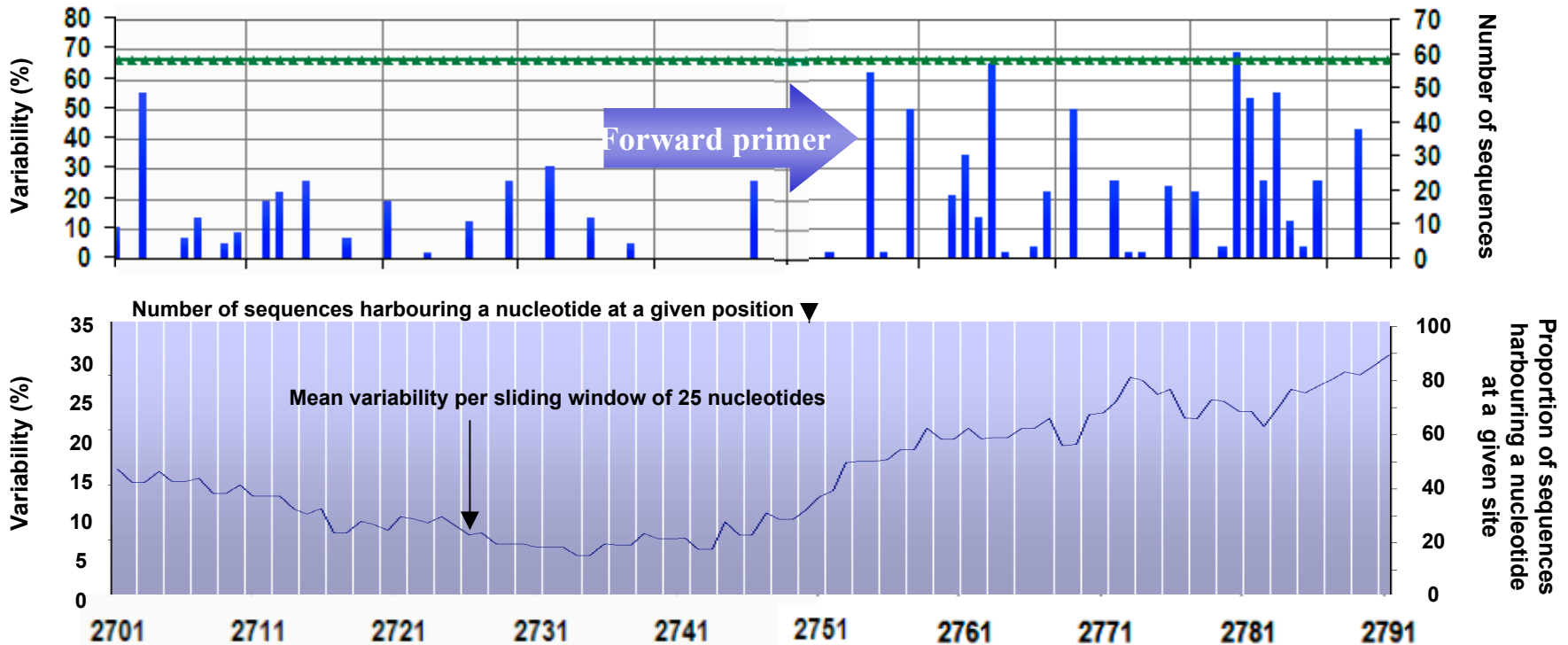


Corynebacterium species: variability in *rpoB*

■ ClustalX (v1.8)



■ SVARAP: analysis of variability per site and per sliding window of 25 nucleotides



Corynebacterium species: variability in *rpoB*

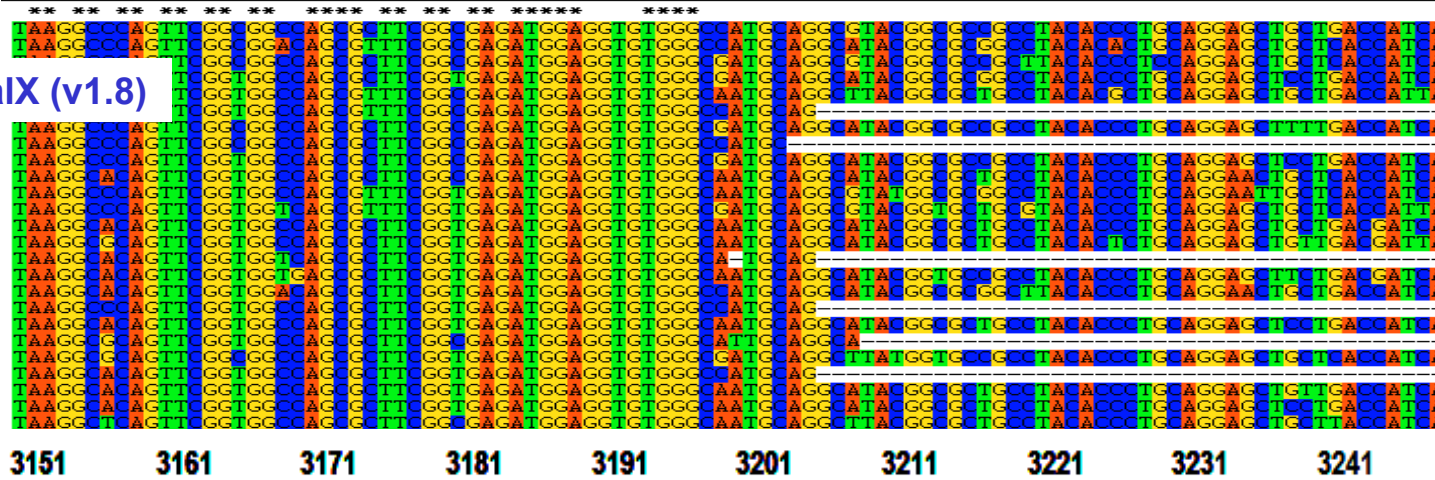
Forward primer

Defined positions	2736	2737	2738	2739	2740	2741	2742	2743	2744	2745	2746	2747	2748	2749	2750	2751	2752	2753	2754	2755	2756	2757	2758	2759	
Number of sequences	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	
Consensus	T	C	G	T	A	T	G	A	A	C	A	T	C	G	G	C	C	A	G	G	T	G	C	T	
Absolute values																									
A	0	0	0	2	58	0	0	58	58	0	58	0	0	0	0	0	0	58	1	0	0	0	0	0	
C	8	58	0	1	0	0	0	0	0	58	0	0	43	0	0	43	58	0	0	0	0	21	57	0	
T	50	0	0	55	0	58	0	0	0	0	0	58	15	0	0	14	0	0	0	0	58	15	1	58	
G	0	0	58	0	0	0	58	0	0	0	0	0	0	58	58	1	0	0	57	58	0	22	0	0	
Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
%																									
A	0	0	0	3	100	0	0	100	100	0	100	0	0	0	0	0	0	100	2	0	0	0	0	0	
C	14	100	0	2	0	0	0	0	0	100	0	0	74	0	0	74	100	0	0	0	0	36	98	0	
T	86	0	0	95	0	100	0	0	0	0	0	100	26	0	0	24	0	0	0	0	100	26	2	100	
G	0	0	100	0	0	0	100	0	0	0	0	0	0	100	100	2	0	0	98	100	0	38	0	0	
Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Nb of distinct variations</i>	1	0	0	2	0	0	0	0	0	0	0	0	1	0	0	2	0	0	1	0	0	2	1	0	
Variability	14	0	0	5	0	0	0	0	0	0	0	0	26	0	0	26	0	0	2	0	0	62	2	0	

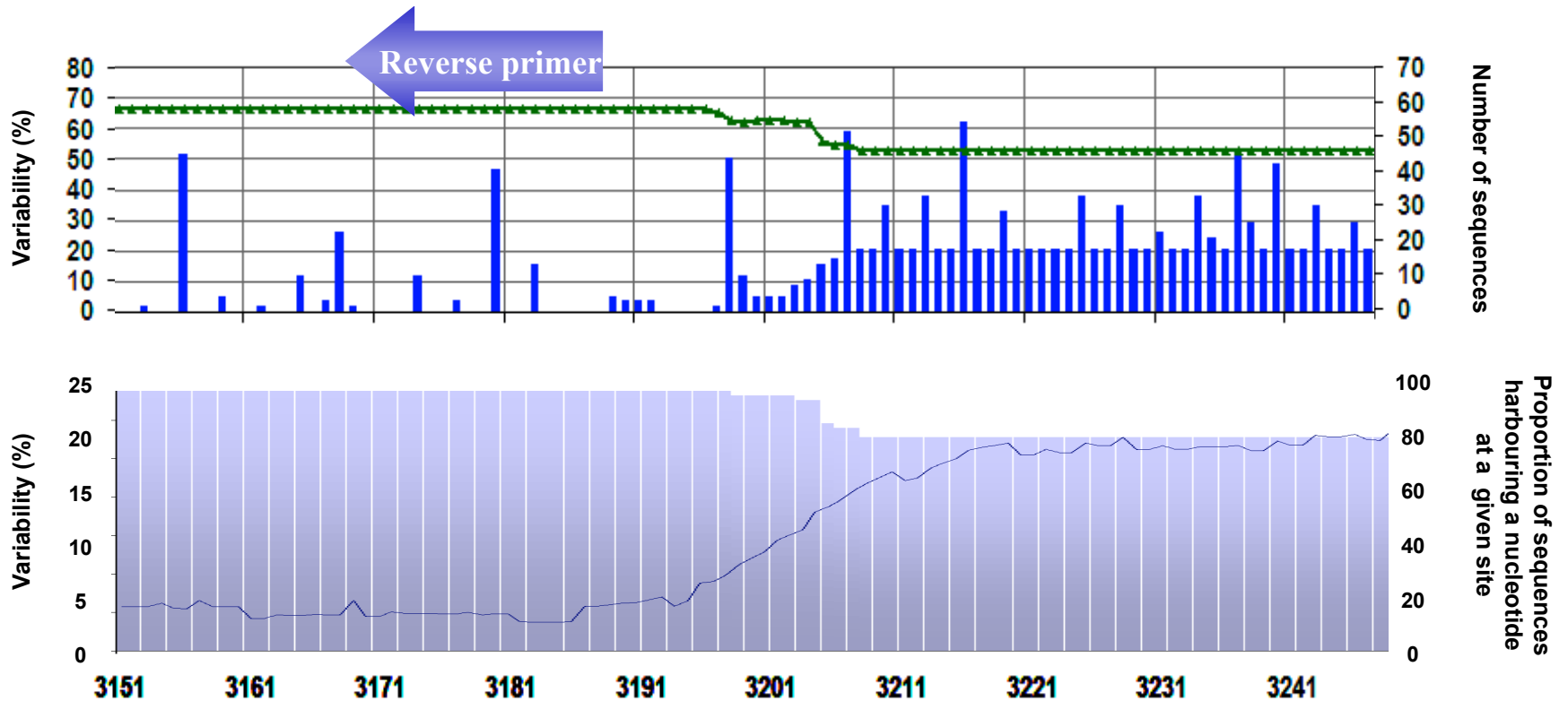
[Link to MAIN PAGE](#)

Corynebacterium species: variability in *rpoB*

■ ClustalX (v1.8)



■ SVARAP: analysis of variability per site and per sliding window of 25 nucleotides



Corynebacterium species: variability in *rpoB*

Reverse primer

Defined positions	3167	3168	3169	3170	3171	3172	3173	3174	3175	3176	3177	3178	3179	3180	3181	3182	3183	3184	3185	3186	3187	3188	3189	3190	
Number of sequences	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	58	
Consensus	C	C	C	A	G	C	G	C	T	T	C	G	G	C	G	A	G	A	T	G	G	A	G	G	
Absolute values																									
A	0	6	0	58	0	0	0	0	0	0	0	0	0	1	0	58	9	58	0	0	0	58	3	0	
C	56	43	57	0	0	58	0	51	0	0	56	0	0	31	0	0	0	0	0	0	0	0	0	0	
T	2	9	0	0	0	0	0	7	58	58	2	0	0	26	0	0	0	0	58	0	0	0	0	2	
G	0	0	1	0	58	0	58	0	0	0	0	58	58	0	58	0	49	0	0	58	58	0	55	56	
Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
%																									
A	0	10	0	100	0	0	0	0	0	0	0	0	0	2	0	100	16	100	0	0	0	100	5	0	
C	97	74	98	0	0	100	0	88	0	0	97	0	0	53	0	0	0	0	0	0	0	0	0	0	
T	3	16	0	0	0	0	0	12	100	100	3	0	0	45	0	0	0	0	100	0	0	0	0	3	
G	0	0	2	0	100	0	100	0	0	0	0	100	100	0	100	0	84	0	0	100	100	0	95	97	
Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Nb of distinct variations</i>	1	2	1	0	0	0	0	1	0	0	1	0	0	2	0	0	1	0	0	0	0	0	1	1	
Variability	3	26	2	0	0	0	0	12	0	0	3	0	0	47	0	0	16	0	0	0	0	0	5	3	

SVARAP download :

- Philippe Colson, Unité des Rickettsies, CNRS UMR 6020, IFR 48, Faculté de Médecine, Université de la Méditerranée, Marseille, France.
- http://ifr.free.fr/recherche/jeu_cadre/jeu_rickettsie.html
- Hypertext link « Téléchargement »