

FGENES 1.6 Prediction of multiple genes in genomic DNA

Seq name: >gi|13907843|ref|NG_000007.1|

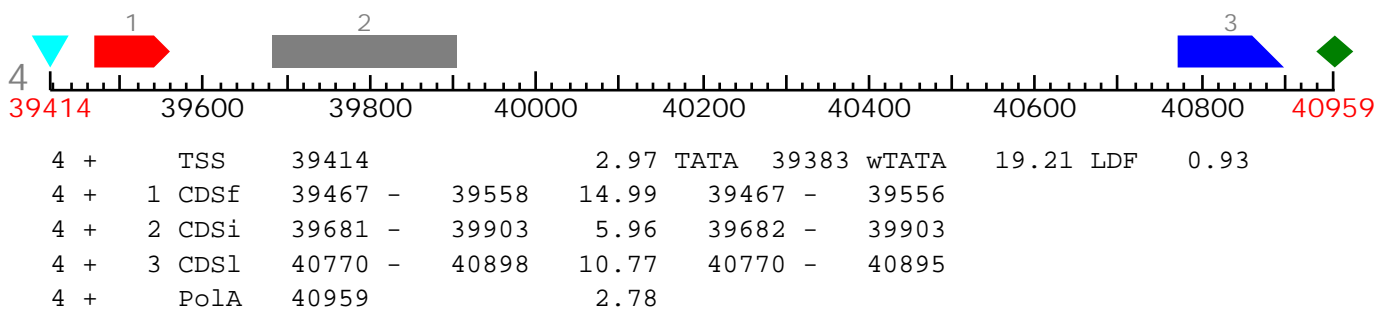
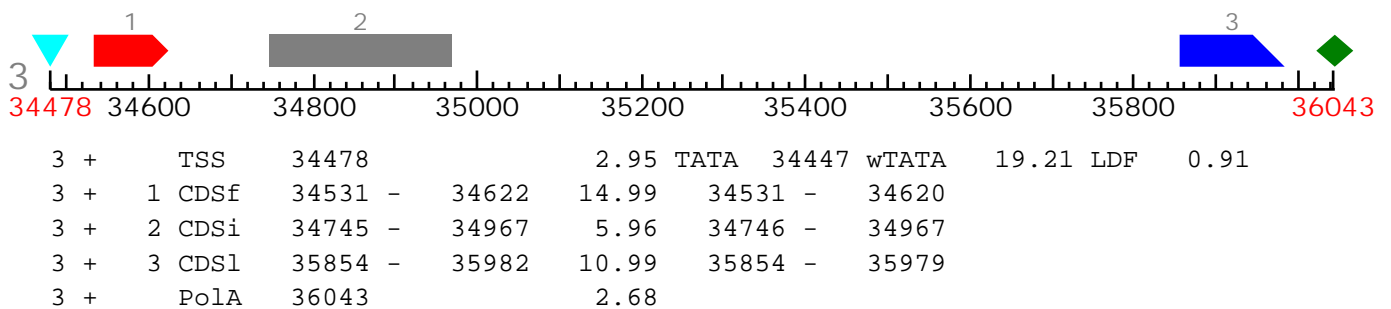
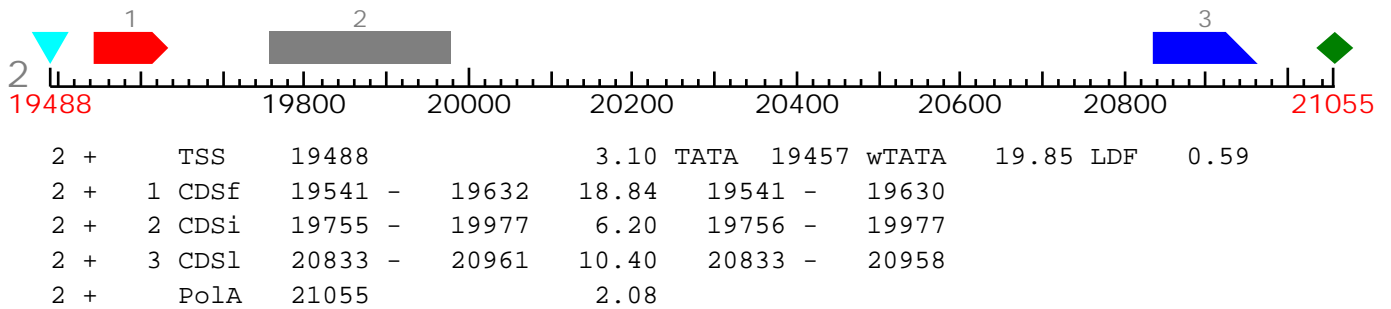
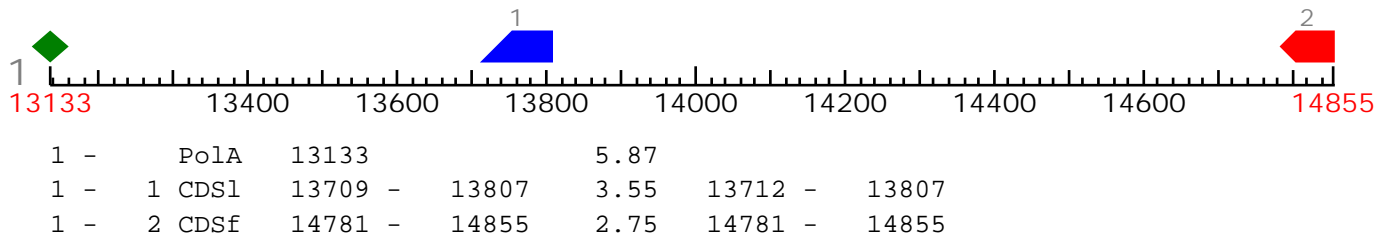
Length of sequence: 73308 GC content: 0.39 Zone: 1

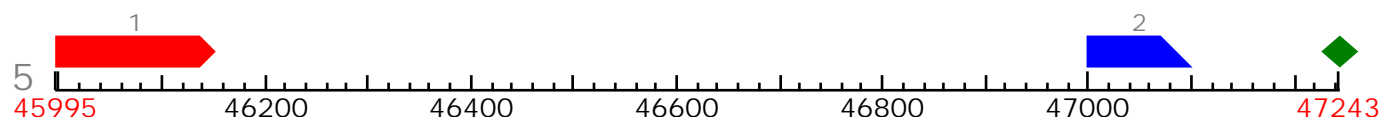
Number of predicted genes: 7 In +chain: 6 In -chain: 1

Number of predicted exons: 19 In +chain: 17 In -chain: 2

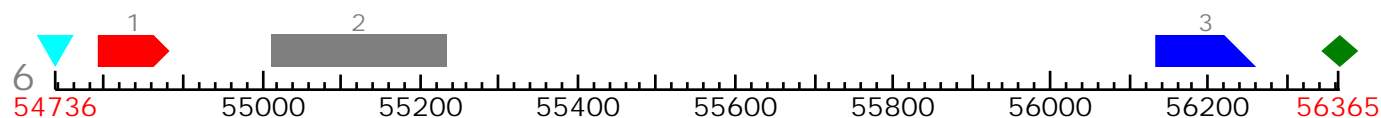
Positions of predicted genes and exons:

▶ CDSf
 ■ CDSi
 ▵ CDSl
 ■ CDSs
 ◆ PolA
 ▼ TSS

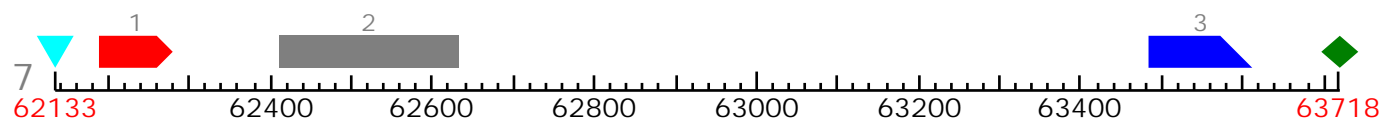




5 +	1	CDSf	45995 -	46151	5.25	45995 -	46150
5 +	2	CDSl	46997 -	47100	4.21	46999 -	47097
5 +		PolA	47243		2.75		



6 +		TSS	54736		3.22	TATA	54708	wTATA	20.47	LDF	0.24
6 +	1	CDSf	54790 -	54881	15.25		54790 -	54879			
6 +	2	CDSi	55010 -	55232	5.60		55011 -	55232			
6 +	3	CDSl	56131 -	56259	8.87		56131 -	56256			
6 +		PolA	56365		1.07						



7 +		TSS	62133		2.88	TATA	62105	wTATA	19.79	LDF	0.41
7 +	1	CDSf	62187 -	62278	16.52		62187 -	62276			
7 +	2	CDSi	62409 -	62631	6.64		62410 -	62631			
7 +	3	CDSl	63482 -	63610	11.44		63482 -	63607			
7 +		PolA	63718		4.72						

Predicted proteins:

>FGENES 1.6 >gi|13907843|re 1 Multiexon gene 13709 - 14855 57 a Ch-MCSHHLASNCCFRSVPLPHLSRSLQEFVLKVNFNHNRKCLIEAKASVKERNISSKPLCC

>FGENES 1.6 >gi|13907843|re 2 Multiexon gene 19541 - 20961 147 a Ch+MVHFTAEEKAAVTSLWSKMNVEEAGGEALGRLLVVYPWTQRFFDSFGNLSSPSAILGNPKVKAHGKKVLTSFGDAIKNMDNLKPAFAKLSELHCDKLHVDPENFKLLGNVMVILATHFGKEFTPEVQAAWQKLVSVAIALAHKYH

>FGENES 1.6 >gi|13907843|re 3 Multiexon gene 34531 - 35982 147 a Ch+MGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFFDSFGNLSSASAIMGNPKVKAHGKKVLTSFGDAIKHLDDLKGTFAQLSELHCDKLHVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMVTGVASALSSRYH

>FGENES 1.6 >gi|13907843|re 4 Multiexon gene 39467 - 40898 147 a Ch+MGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFFDSFGNLSSASAIMGNPKVKAHGKKVLTSFGDAIKHLDDLKGTFAQLSELHCDKLHVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMVTAVASALSSRYH

>FGENES 1.6 >gi|13907843|re 5 Multiexon gene 45995 - 47100 86 a Ch+MGNPKVKAHGKKVLISFGKAVMLTDDLKGTFFATLSDLHCNKLHVDPENFLVSTLRQRDIDCFGNPLQRGFYPTDTGFLAVTNKCCG

>FGENES 1.6 >gi|13907843|re 6 Multiexon gene 54790 - 56259 147 a Ch+MVHLTPEEKTAVNALWGKVNVDAGGEALGRLLVVYPWTQRFFESFGDLSSPDAVMGNPKVKAHGKKVLGAFSDGLAHLNKLKGTFSQLSELHCDKLHVDPENFRLLGNVLVCVLARNFG

KEFTPQMQAAYQKVVAGVANALAHKYH

>FGENES 1.6 >gi|13907843|re 7 Multiexon gene 62187 - 63610 147 a Ch+

MVHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDVVMGNPK

VKAHGKKVLGAFSDGLAHLNDNLKGTFFATLSELHCDKLHVDPENFRLLGNVLCVLAHHFG

KEFTPPVQAAYQKVVAGVANALAHKYH