

1 Supplementary data for the manuscript:
2 Trans-species Polymorphism at Antimicrobial
3 Innate Immunity Cathelicidin Genes of Atlantic
4 cod and Related Species

5 Katrín Halldórsdóttir* and Einar Árnason

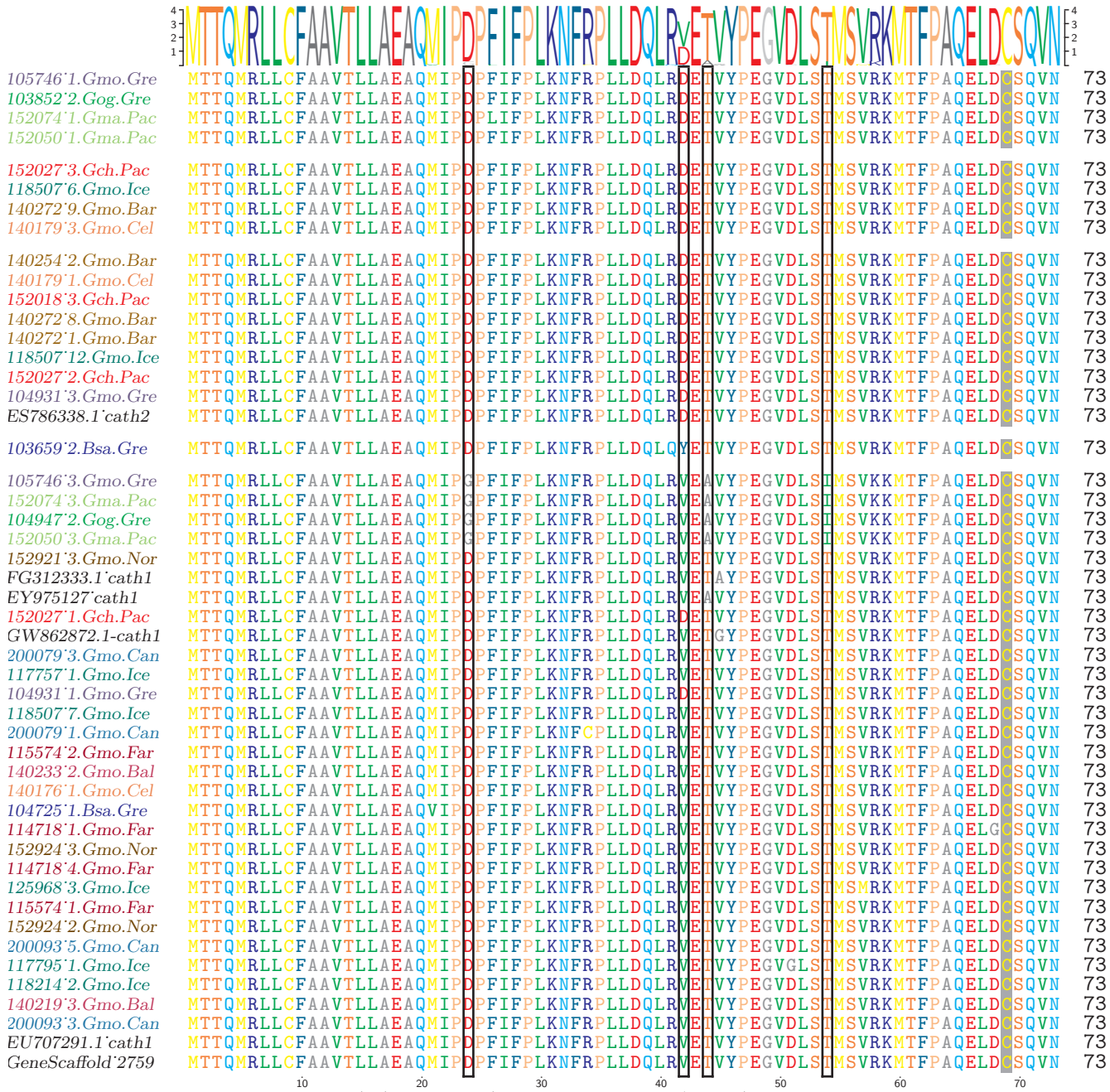
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Exon 1

Exon 2



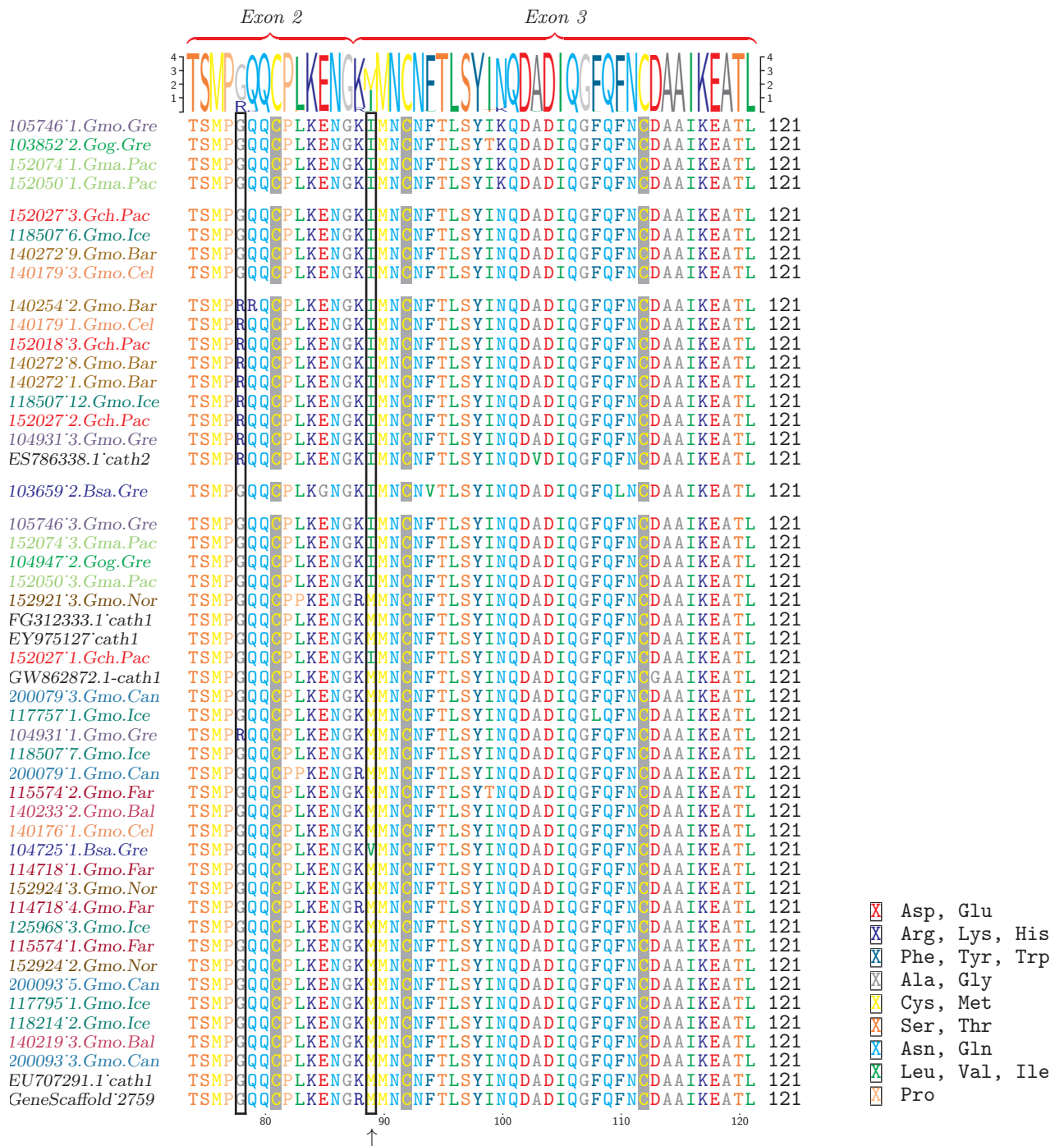
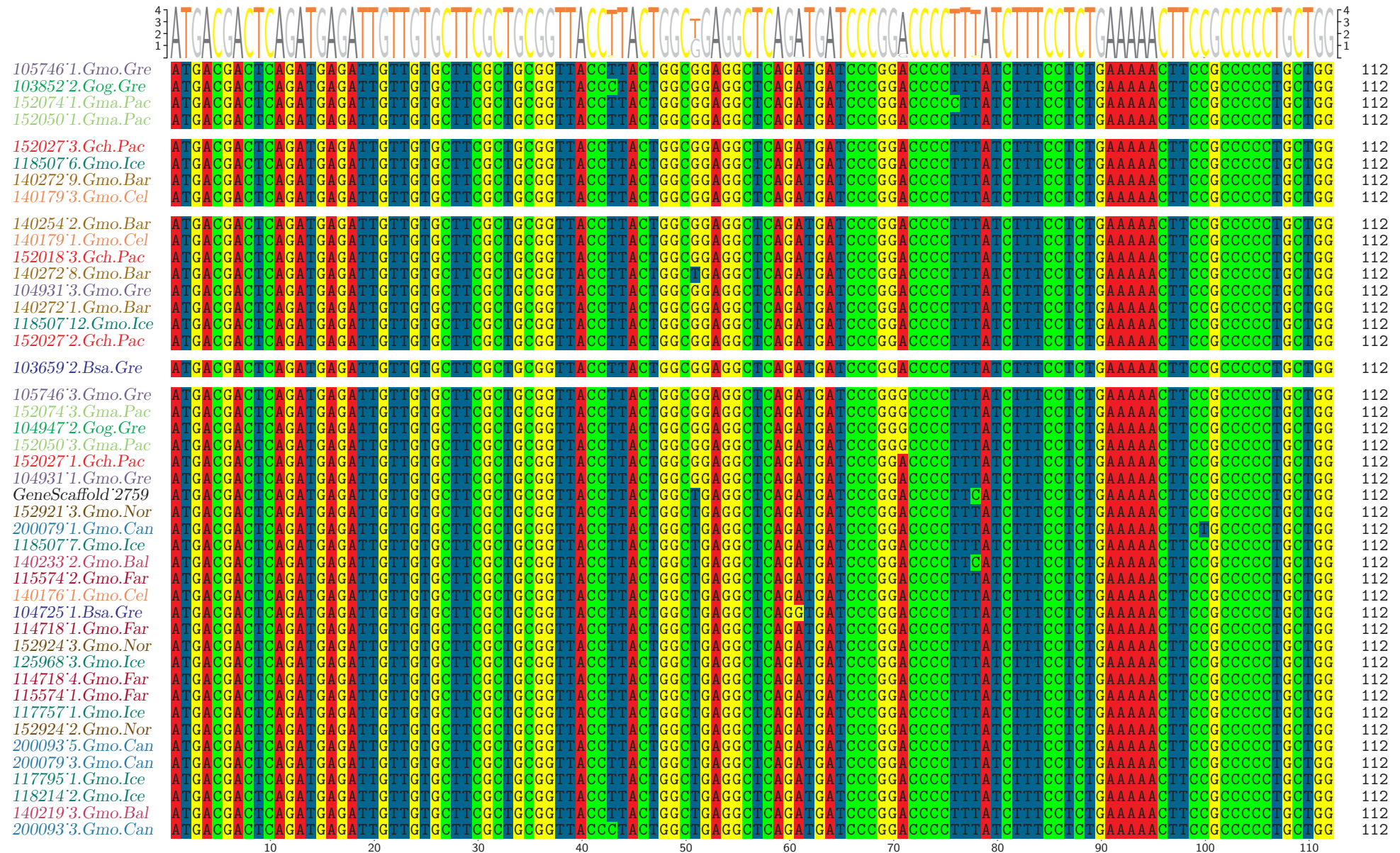


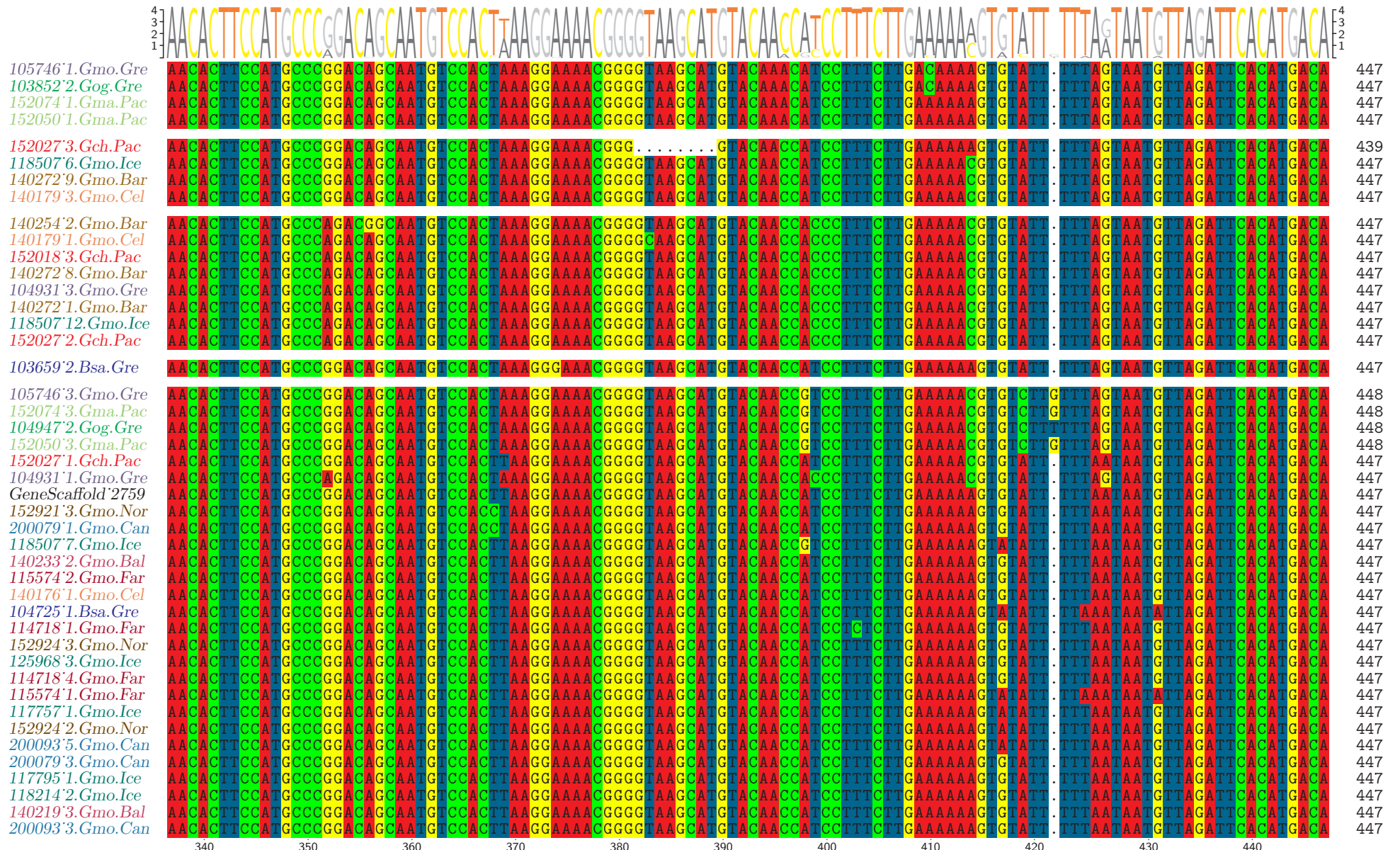
Figure S1. Alignment of amino acid sequences of exons 1, 2, and 3 combined, the conserved part of cathelicidin, from clones of various individuals of Atlantic cod and four closely related taxa. Highly polymorphic sites are boxed. The four conserved cysteine residues characterizing cathelicidin are shaded. Up arrows represent positively selected sites and down arrows negatively selected sites from Tables 1 and 2. Bsa.Gre (*Boreogadus saida*), Gch.Pac (*Gadus chalcogrammus*), Gma.Pac (*Gadus macrocephalus*), Gog.Gre (*Gadus ogac*) and Gmo (*Gadus morhua*) from various locations; Iceland (Gmo.Ice), Greenland (Gmo.Gre), Barents Sea (Gmo.Bar), Celtic Sea (Gmo.Cel), Baltic Sea (Gmo.Bal), Norway (Gmo.Nor), Faroe Islands (Gmo.Far), Canada (Gmo.Can).

Exon 1



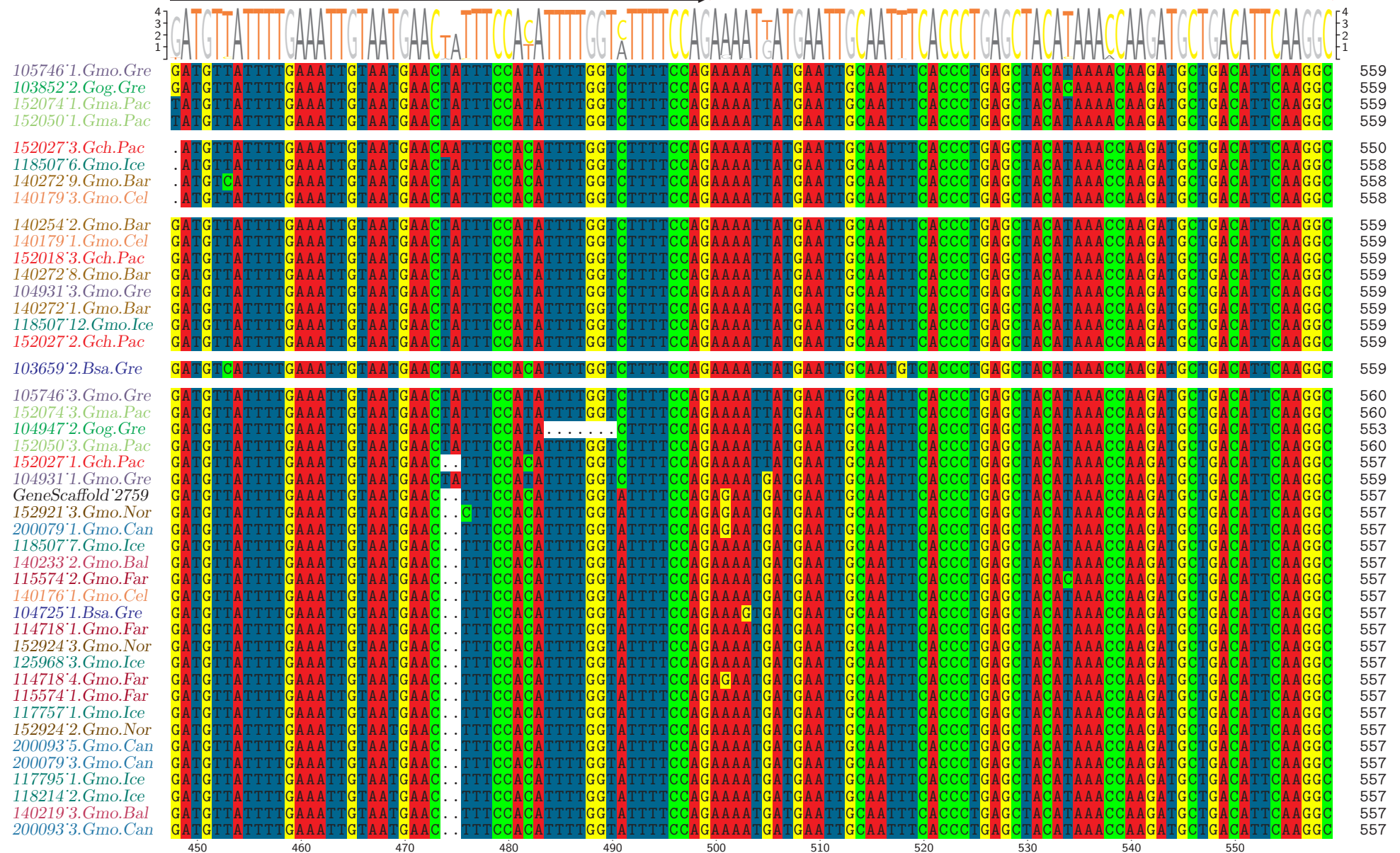
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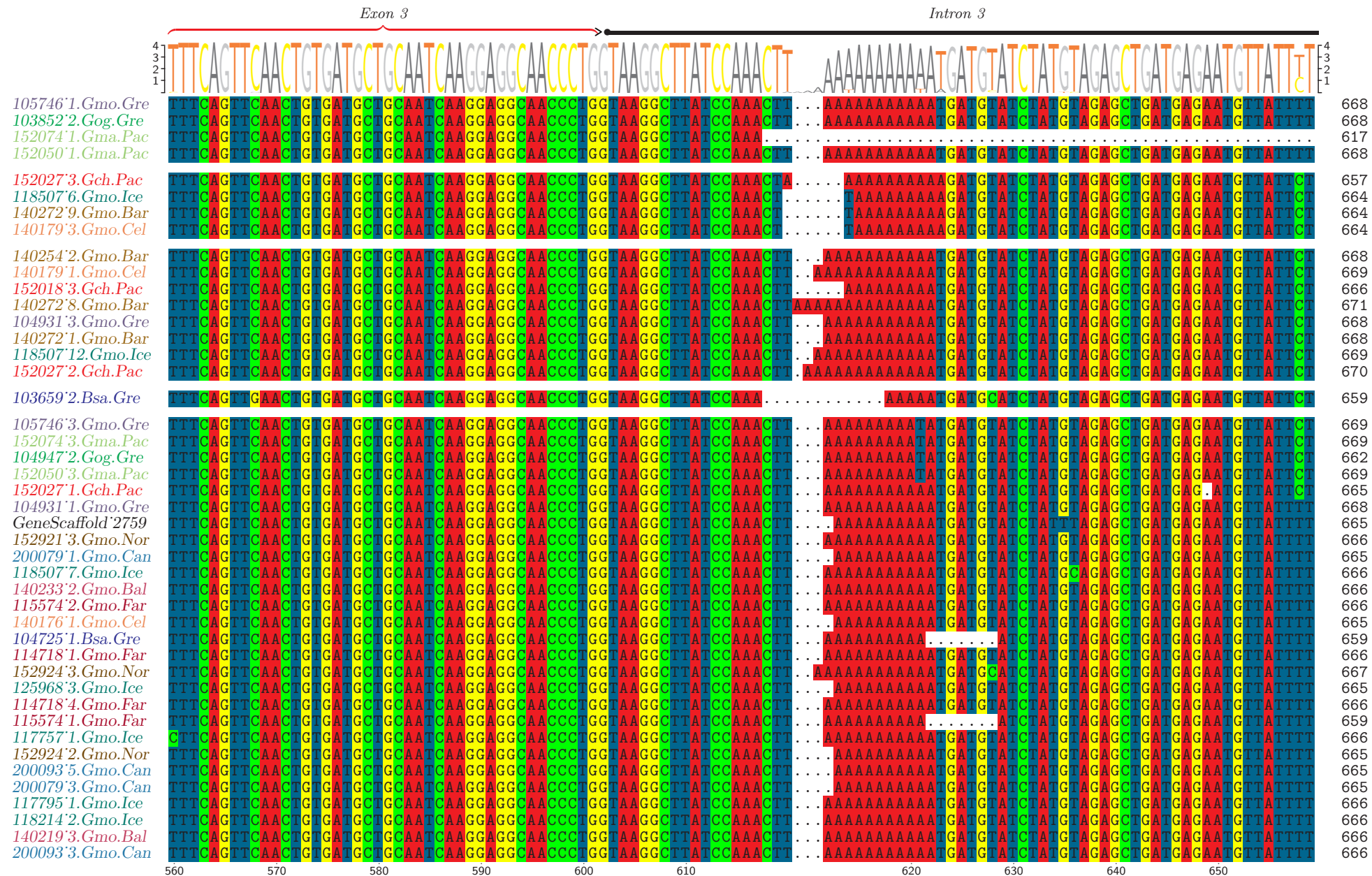
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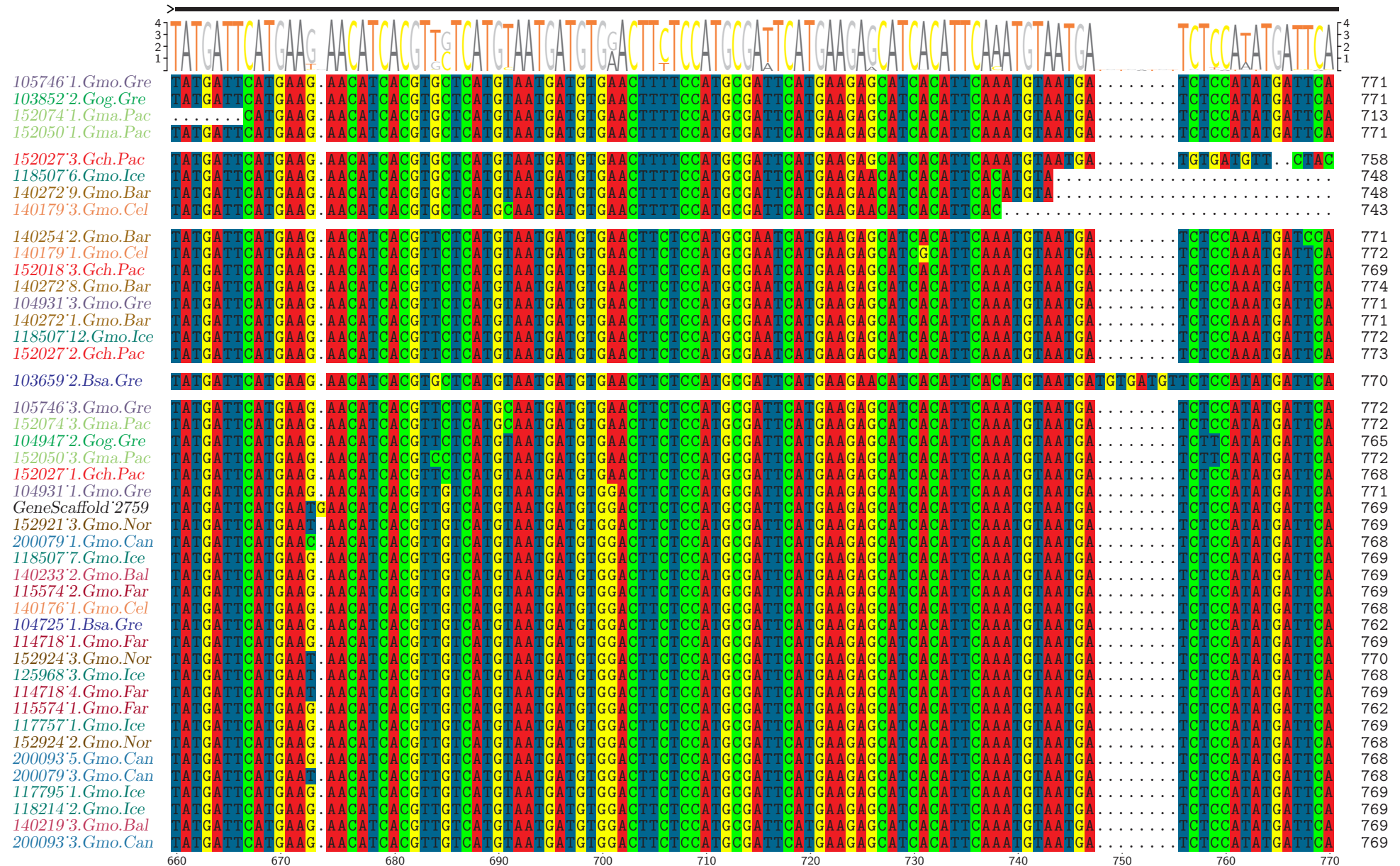
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Exon 3

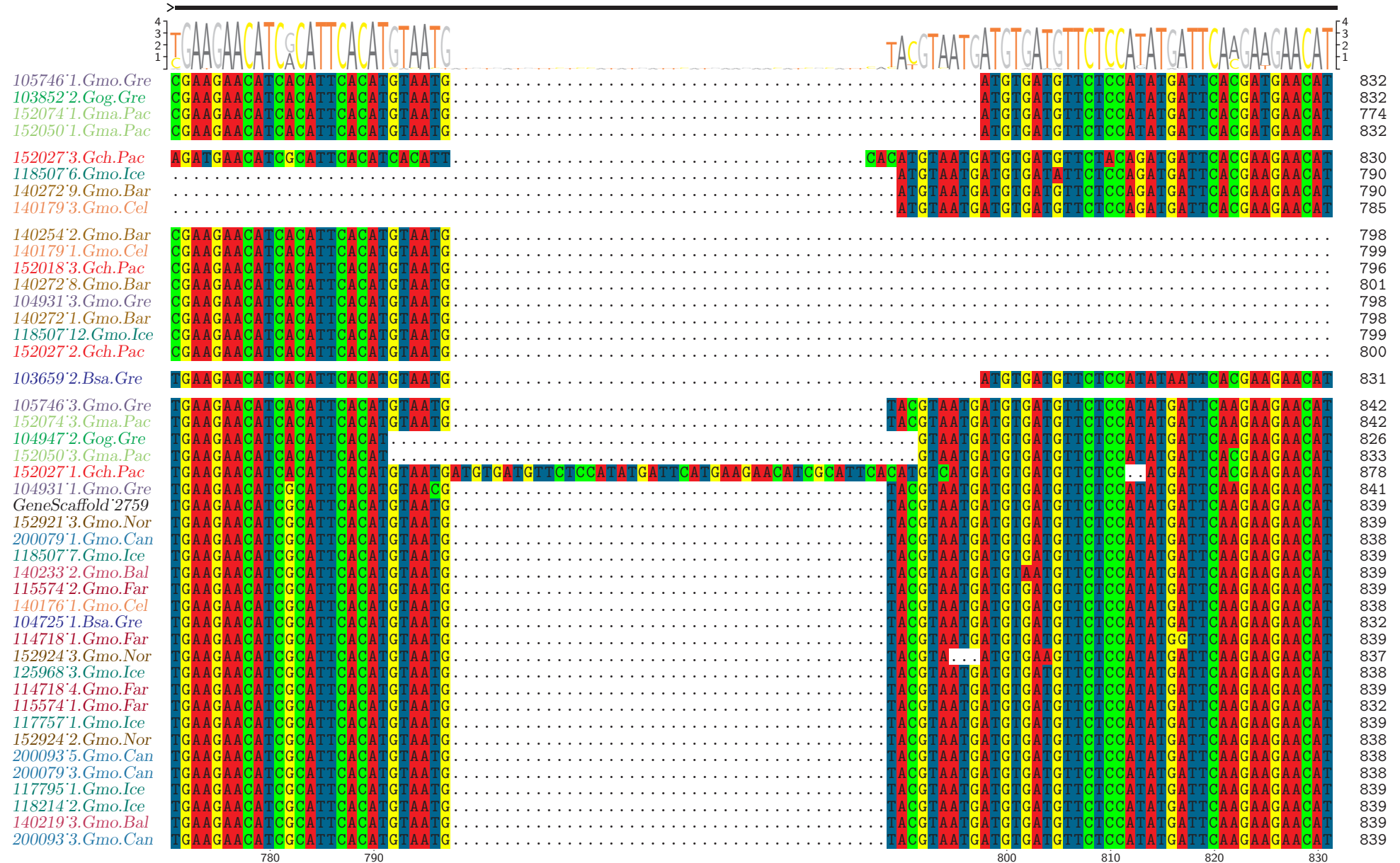




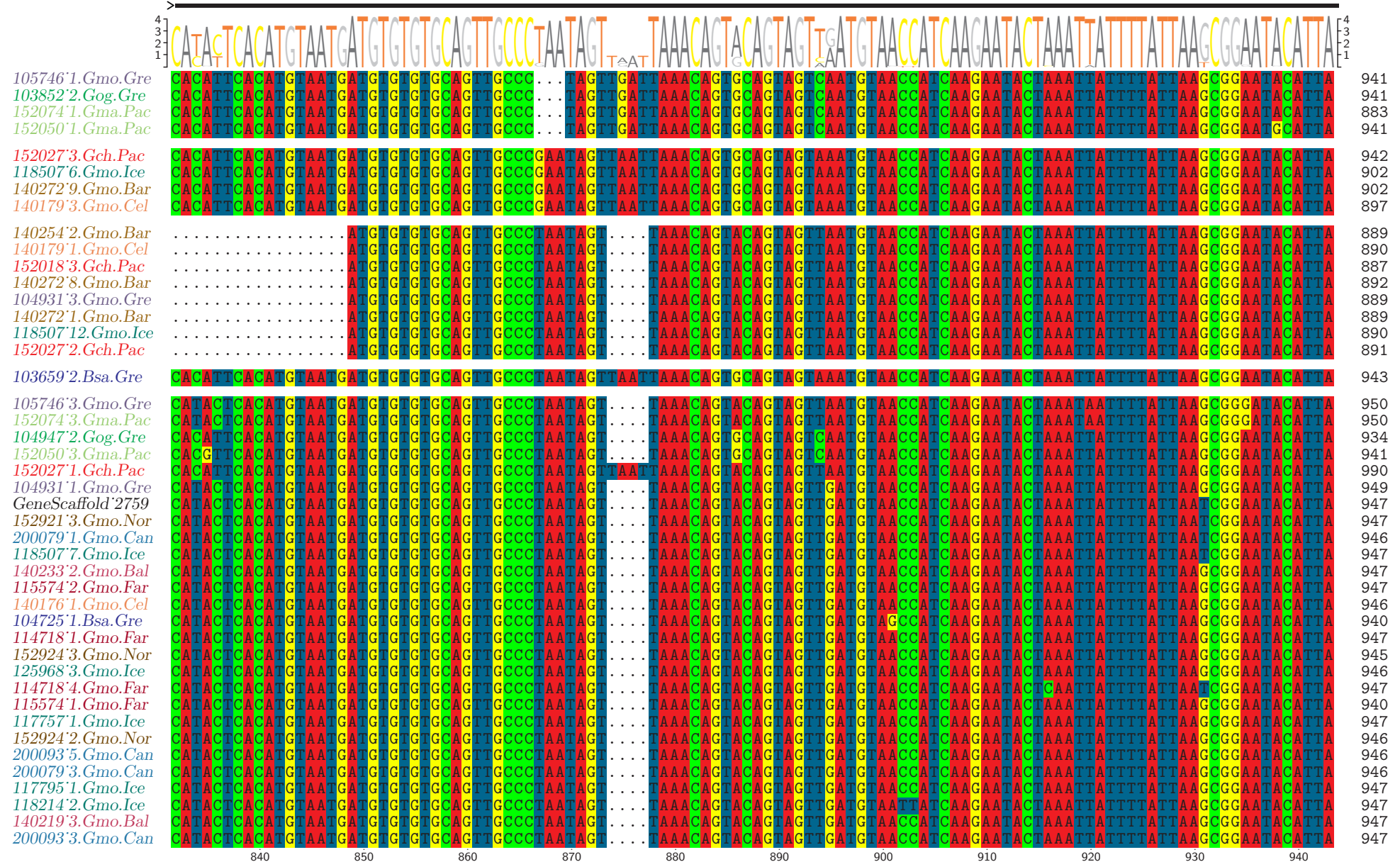
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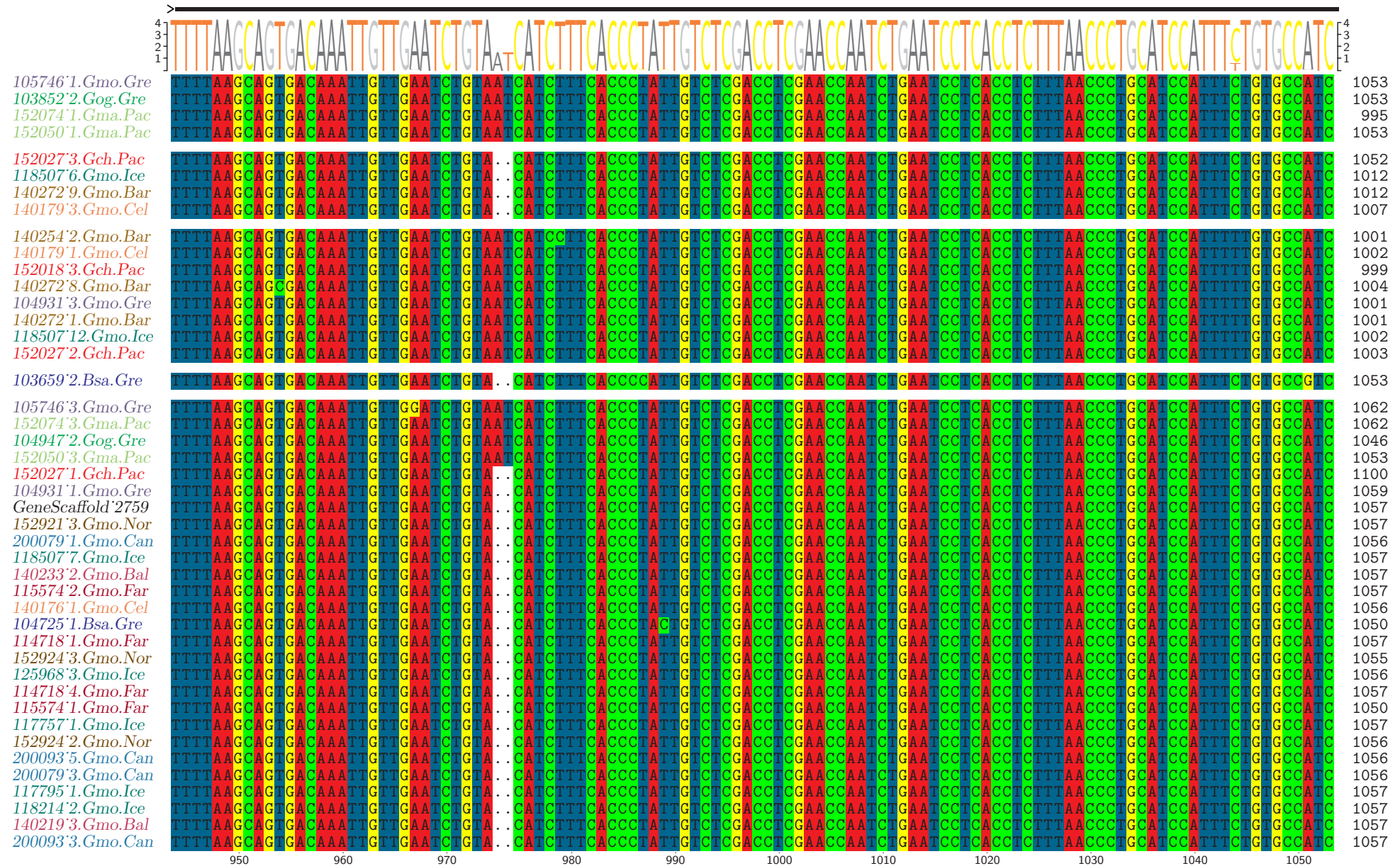
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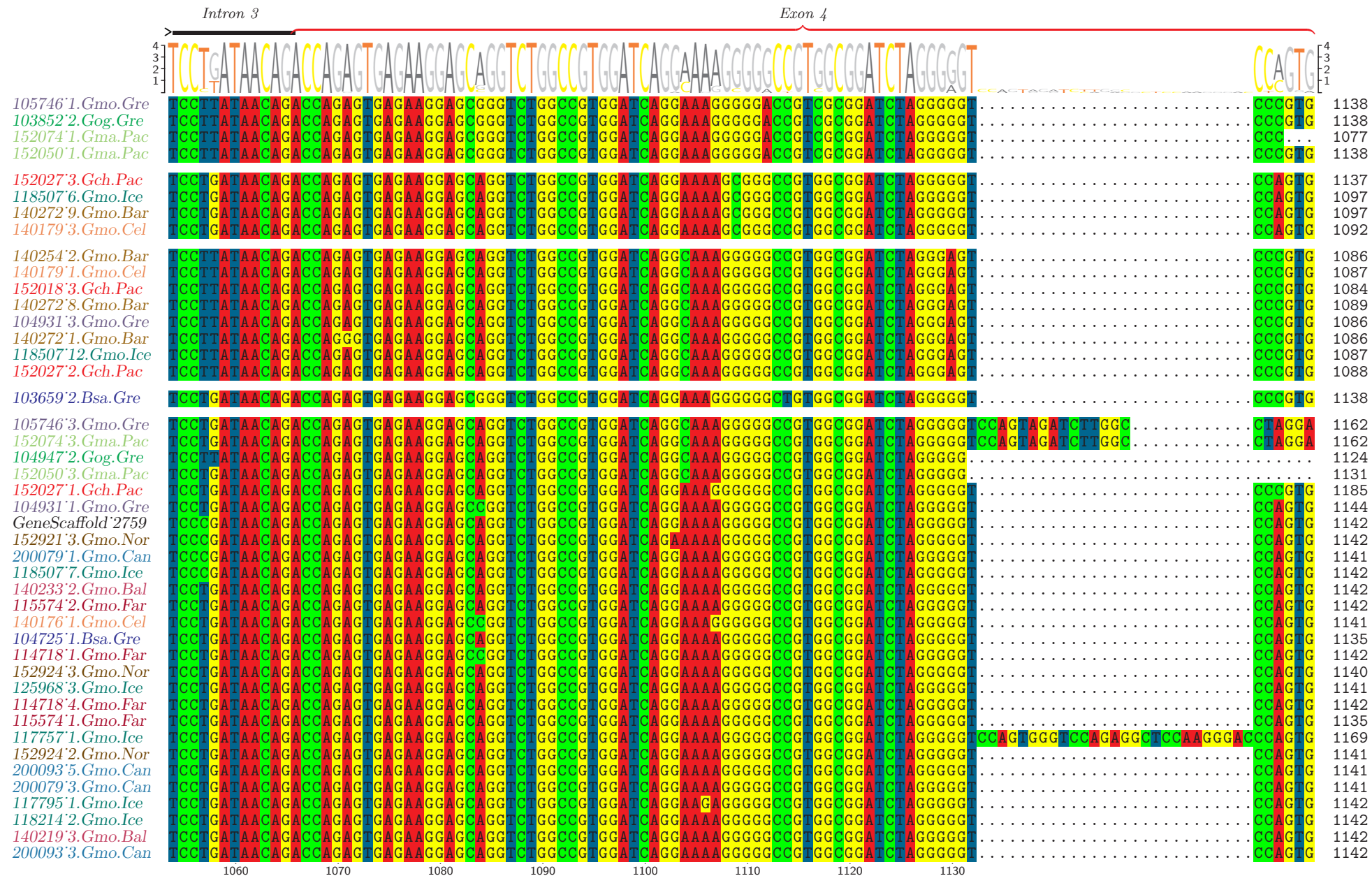


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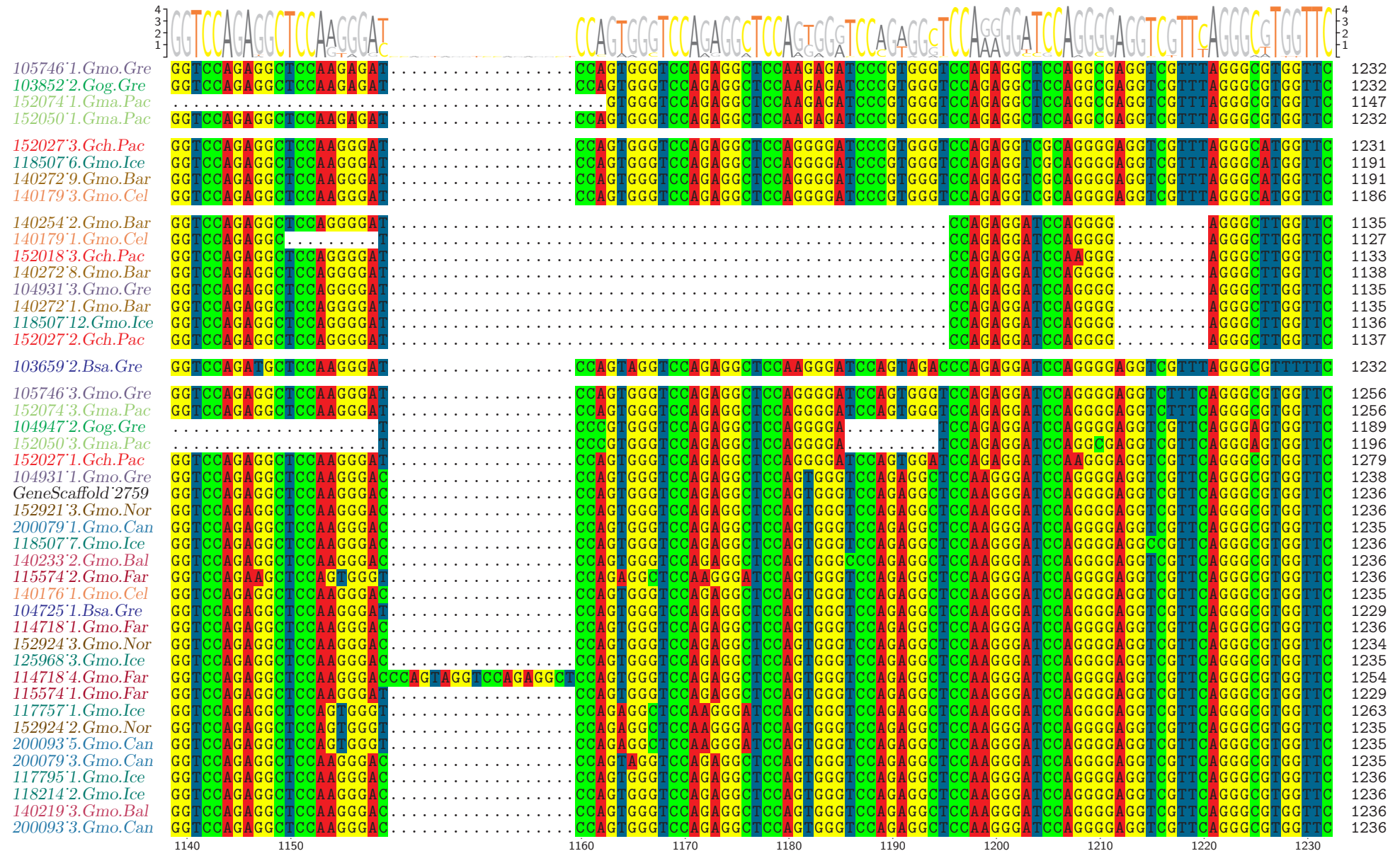


Intron 3





Exon 4



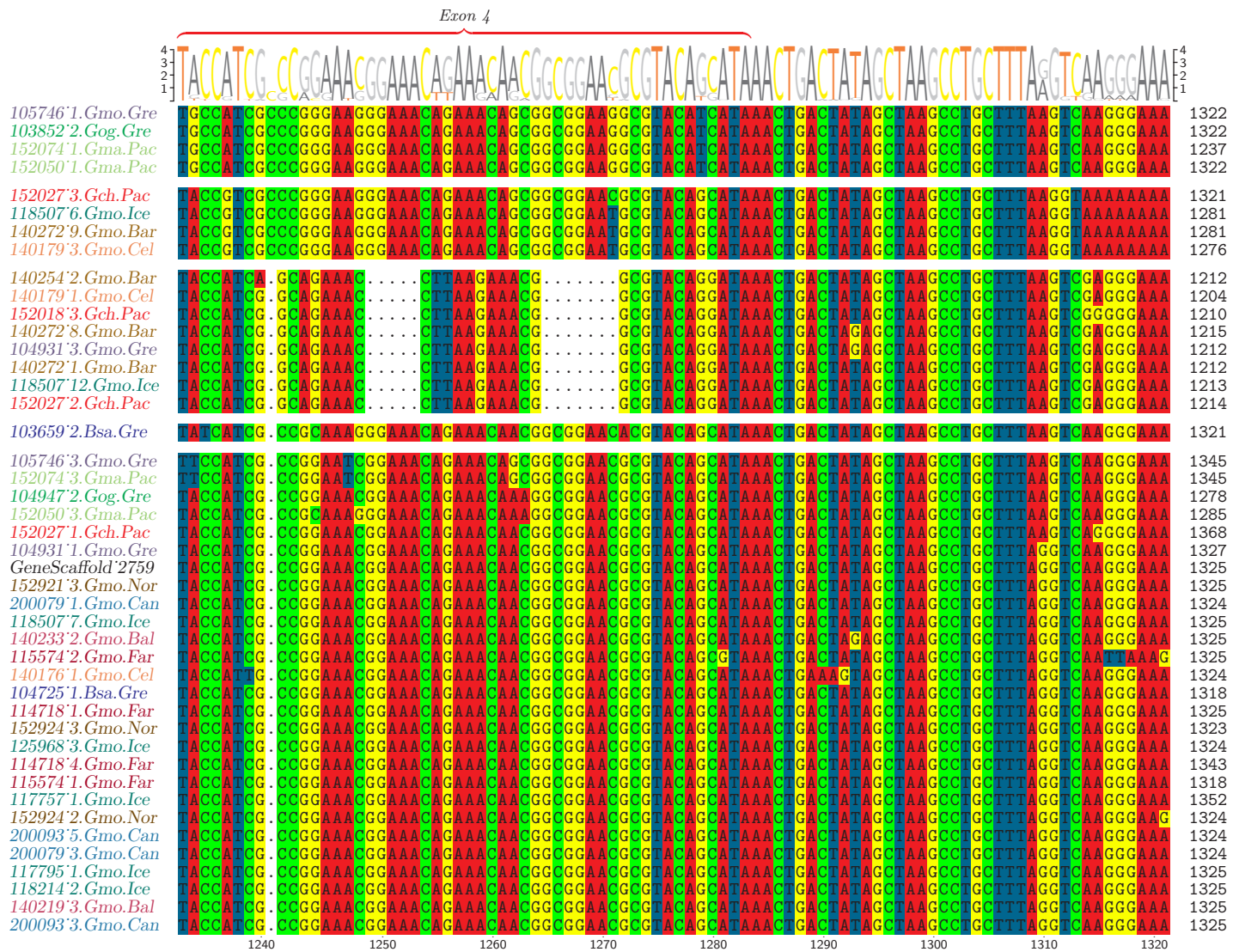


Figure S2. Alignment of nucleotide sequences of cathelicidin among clones from various individuals of Atlantic cod and four closely related taxa. Bsa.Gre (*Boreogadus saida*), Gch.Pac (*Gadus chalcogrammus*), Gma.Pac (*Gadus macrocephalus*), Gog.Gre (*Gadus ogac*) and Gmo (*Gadus morhua*) from various locations; Iceland (Gmo.Ice), Greenland (Gmo.Gre), Barents Sea (Gmo.Bar), Celtic Sea (Gmo.Cel), Baltic Sea (Gmo.Bal), Norway (Gmo.Nor), Faroe Islands (Gmo.Far), Canada (Gmo.Can).

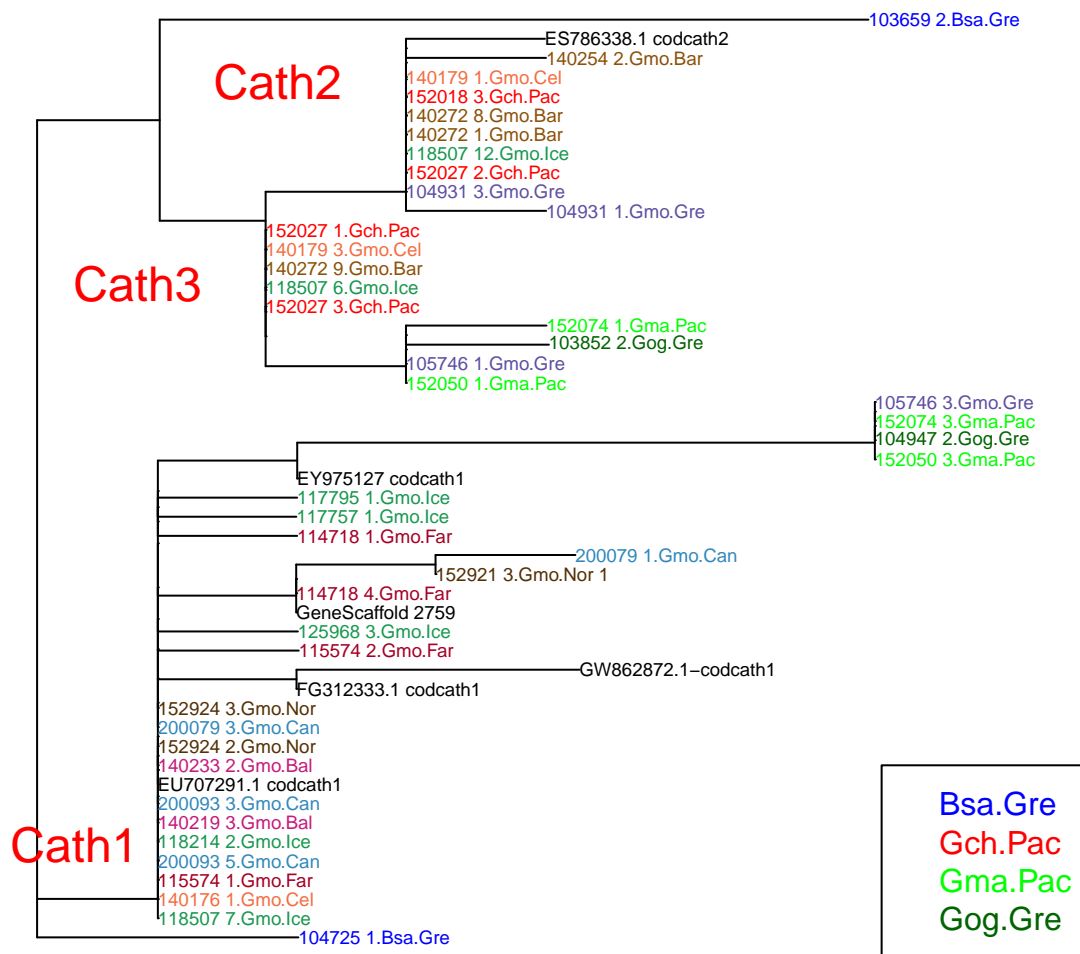


Figure S3. Maximum likelihood phylogenetic tree of Cathelicidin amino acid sequences of the conserved part. Phylogenetic tree built on amino acid sequences in exons 1, 2, and 3 combined, the conserved part of cathelicidin, of clones from various individuals of Atlantic cod and four closely related taxa. Bsa.Gre (*Boreogadus saida*), Gch.Pac (*Gadus chalcogrammus*), Gma.Pac (*Gadus macrocephalus*), Gog.Gre (*Gadus ogac*) and Gmo (*Gadus morhua*) from various locations; Iceland (Gmo.Ice), Greenland (Gmo.Gre), Barents Sea (Gmo.Bar), Celtic Sea (Gmo.Cel), Baltic Sea (Gmo.Bal), Norway (Gmo.Nor), Faroe Islands (Gmo.Far), Canada (Gmo.Can).

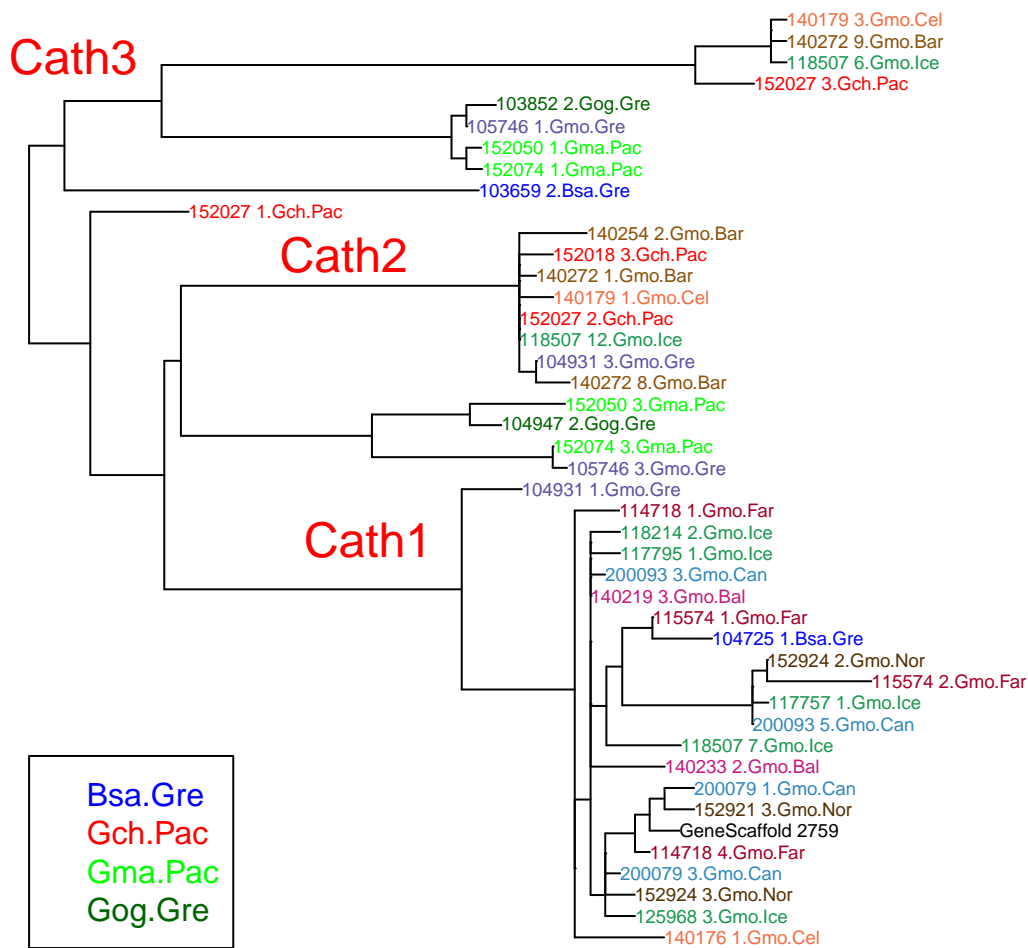


Figure S4. Maximum likelihood phylogenetic tree of nucleotide sequences. Phylogenetic tree of nucleotide sequences of the cathelicidin gene from 43 representative clones of various individuals of Atlantic cod and four sister taxa. Bsa.Gre (*Boreogadus saida*), Gch.Pac (*Gadus chalcogrammus*), Gma.Pac (*Gadus macrocephalus*), Gog.Gre (*Gadus ogac*) and Gmo (*Gadus morhua*) from various locations; Iceland (Gmo.Ice), Greenland (Gmo.Gre), Barents Sea (Gmo.Bar), Celtic Sea (Gmo.Cel), Baltic Sea (Gmo.Bal), Norway (Gmo.Nor), Faroe Islands (Gmo.Far), Canada (Gmo.Can).

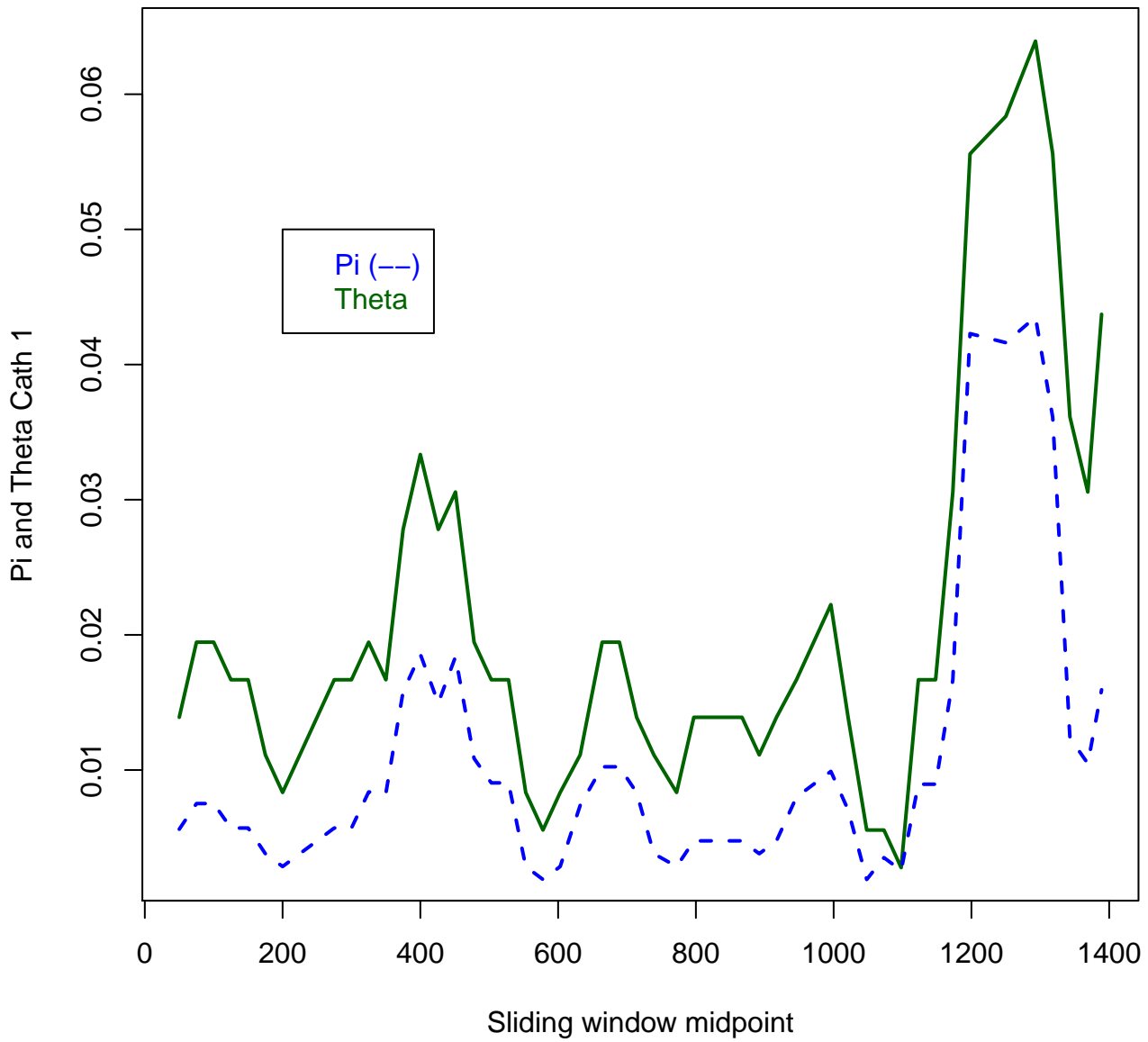


Figure S5. Sliding window analysis of nucleotide diversity π and the scaled mutation rate θ for Cath1. Window length was 100 bp with a 25 bp step size.

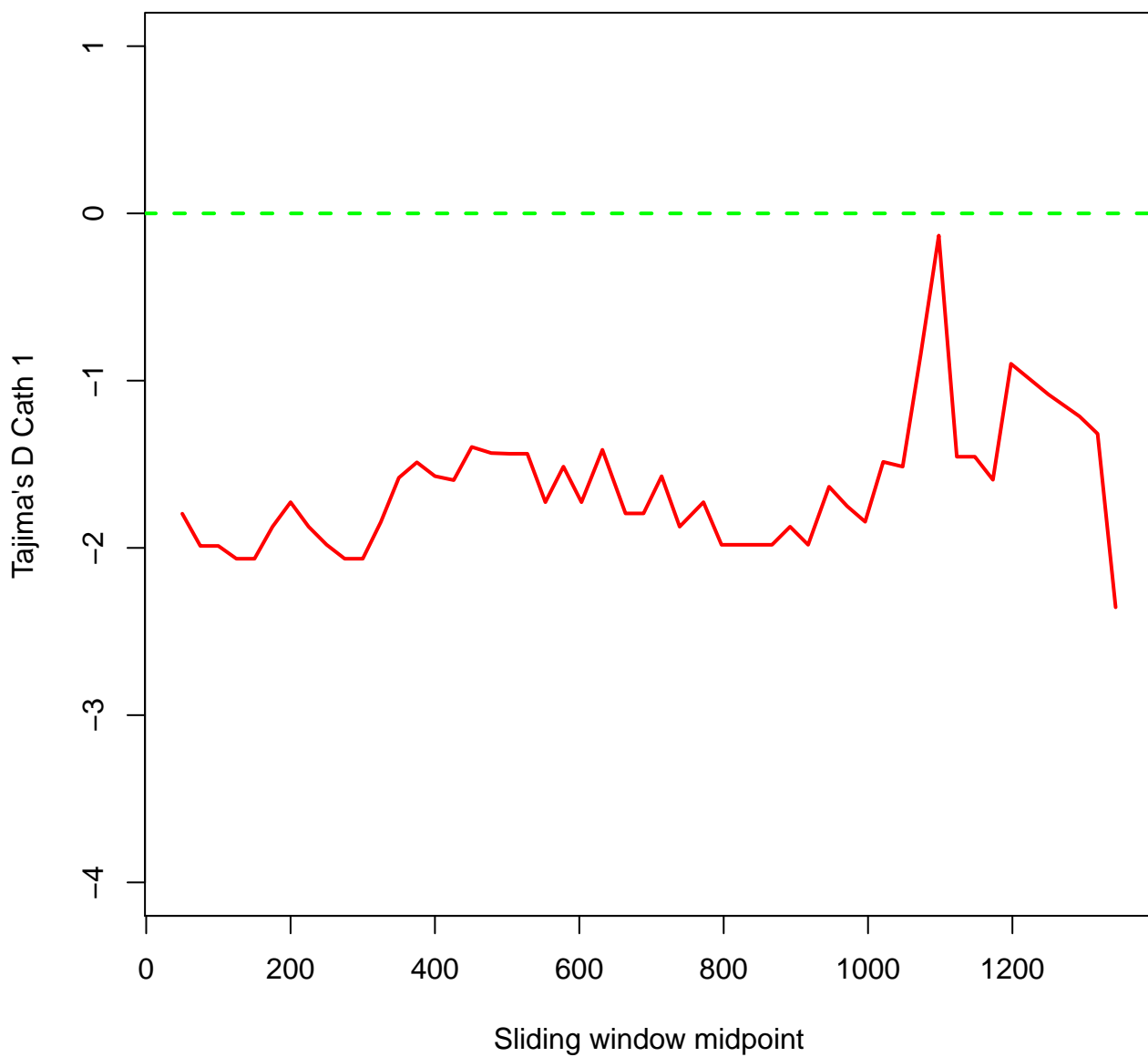


Figure S6. Sliding window Tajima's D for Cath1. Window length was 100 bp with a 25 bp step size.

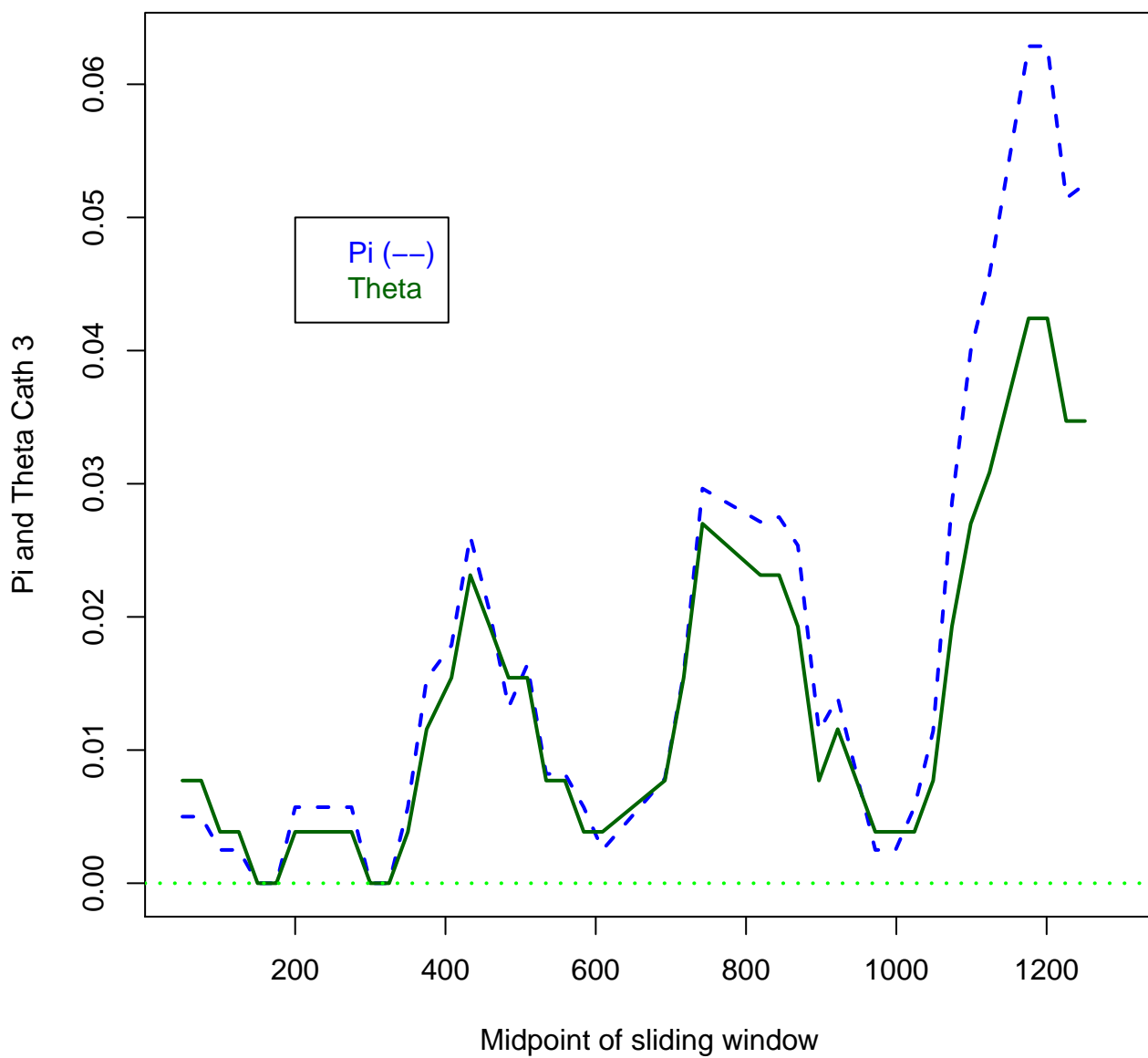


Figure S7. Sliding window analysis of nucleotide diversity π and the scaled mutation rate θ for Cath3. Window length was 100 bp with a 25 bp step size.

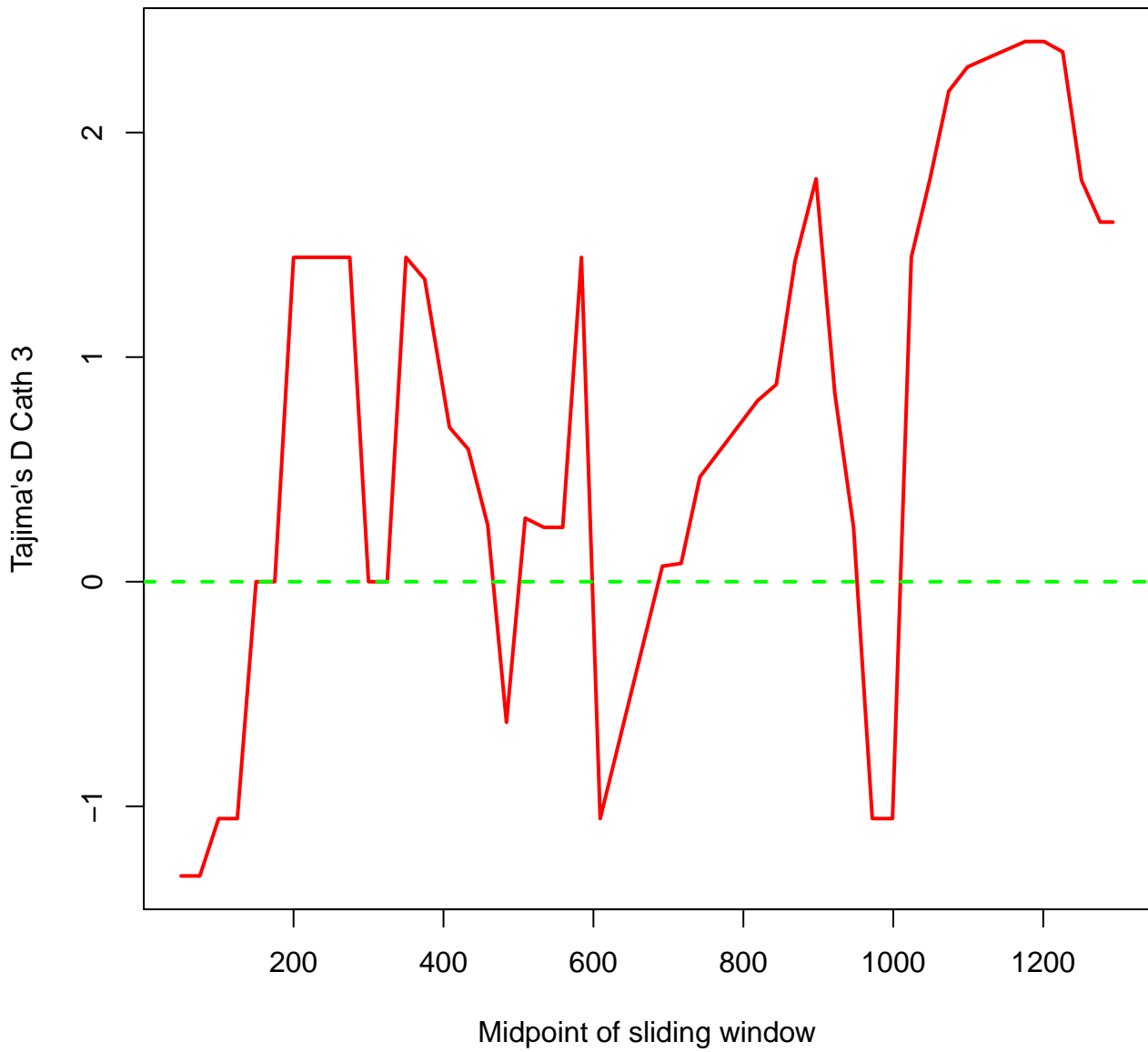


Figure S8. Sliding window Tajima's D for Cath3. Window length was 100 bp with a 25 bp step size.