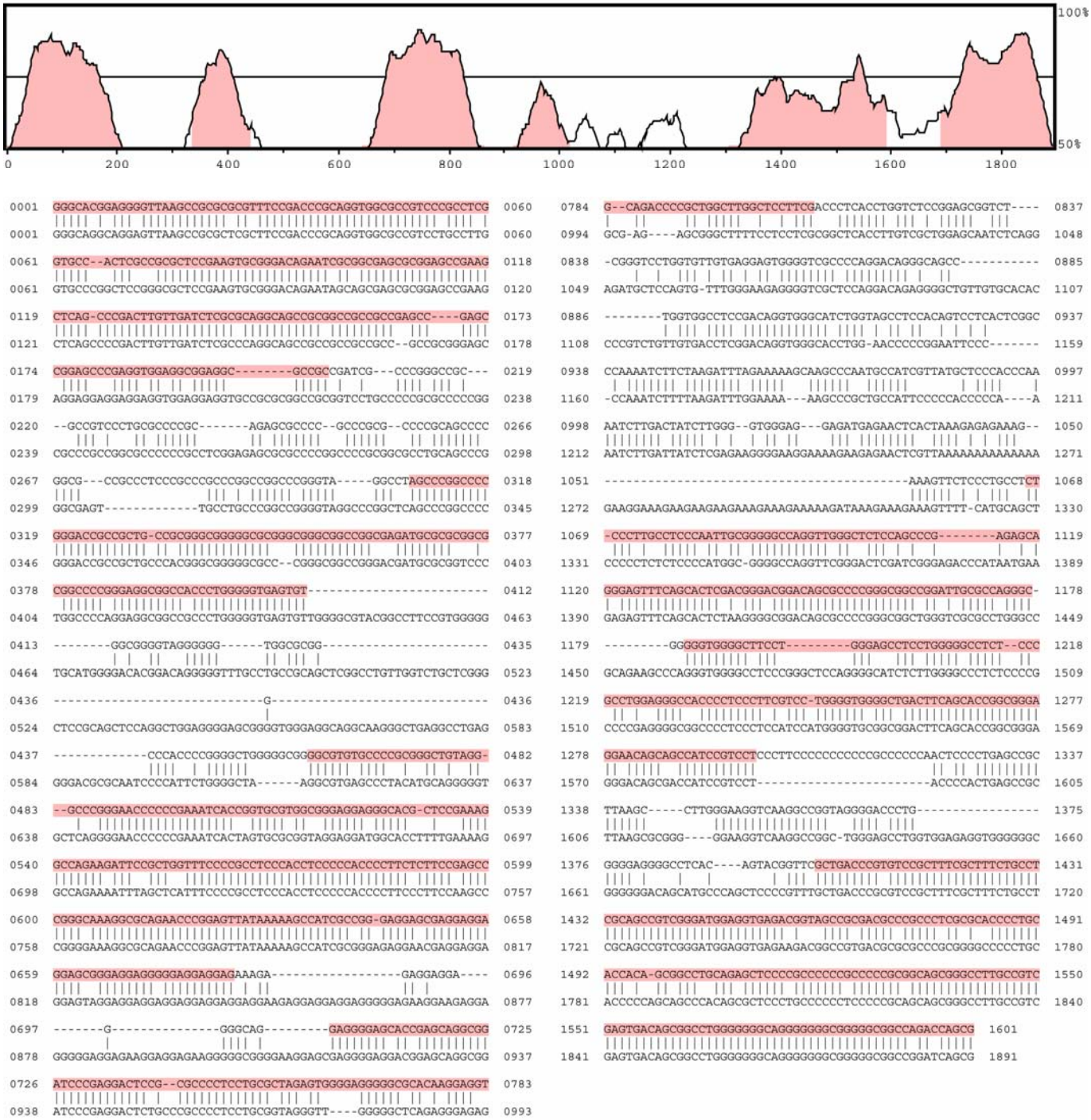
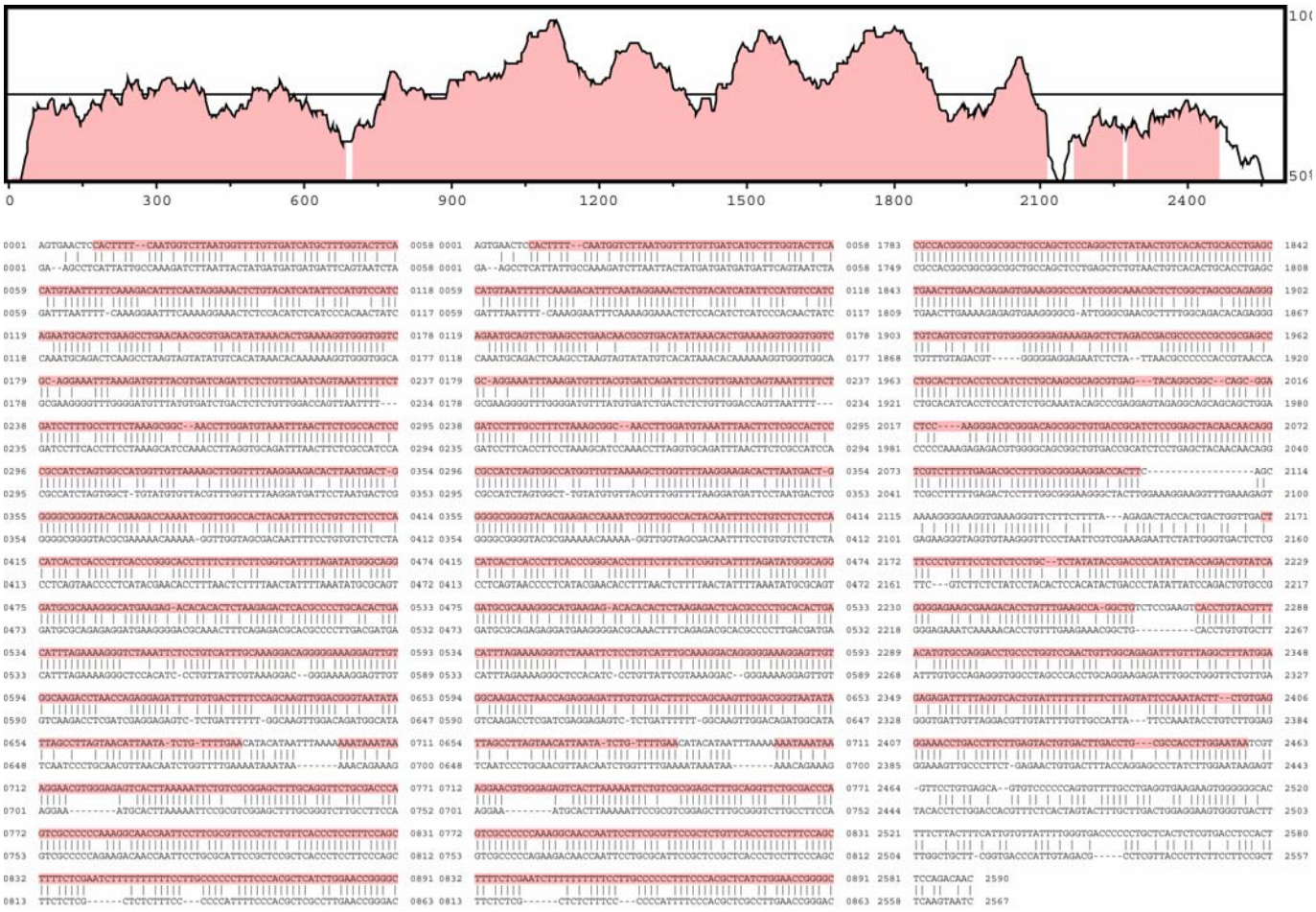
Supplementary Material

Figure 7



Comparison of the upstream regulatory sequences of the mouse and human Kv2.1 genes performed using the Vista alignment program (mouse is upper sequence in the sequence alignment). In the alignment a set of highly conserved features were found to be separated by poorly conserved sequences. The conserved sequences provided unambiguous landmarks for comparisons between the sequences. The selected regions were not identical in length. Differences in length were largely due to insertions or deletions in non-conserved or highly repetitive regions. The selected sequences extend to the initiator methionine of exon 1 of the Kv2.1 gene and makes no assumptions about the exact location of the transcription start site.

Figure 8



Comparison of the upstream regulatory sequences of the mouse and human Kv4.2 genes performed using the Vista alignment program (mouse is upper sequence in the sequence alignment). A similar approach was used to select regions of the Kv4.2 gene for functional analysis as was used for the Kv2.1 genes. There is greater sequence similarity in the proximal promoter region of the Kv4.2 gene than the Kv2.1 gene and the sequences selected for functional analysis were very similar in length. The selected sequences extend to the initiator methionine of exon 1 of the Kv4.2 gene and makes no assumptions about the exact location of the transcription start site.

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