



**Figure 3.** Genomic landscape surrounding the bovine pseudoautosomal boundary: pseudoautosomal region (red), X-specific sequences (green), Y-specific sequences (blue), and pseudoautosomal boundary (orange). (CG%) [G+C] content calculated in a 200-bp sliding window; the horizontal line corresponds to 50% [G+C]. (CpG Islands) CpG islands defined according to Gardiner-Garden and Frommer (1987). (RepeatMasker) Repetitive elements identified with RepeatMasker (A.F.A Smit and P. Green, <http://repeatmasker.genome.washington.edu>): LTRs (orange), SINEs (blue), LINEs (green), simple repeats (red), tRNAs and snRNAs (black). (Genes) Protein-encoding genes are transcribed from *right to left* (strand +) or *left to right* (strand -); gene names are given adjacent to the corresponding boxed gene. (ESTs) ESTs BLASTing to the region with an identity >95% and an  $E$ -value <  $10^{-50}$ . Most ESTs correspond to identified exons with the notable exception of a cluster of ESTs located between *OFD1Y* and *AMELY*. Although very similar, these ESTs show some differences with the genomic sequence and with each other. They probably originate from paralogous loci.