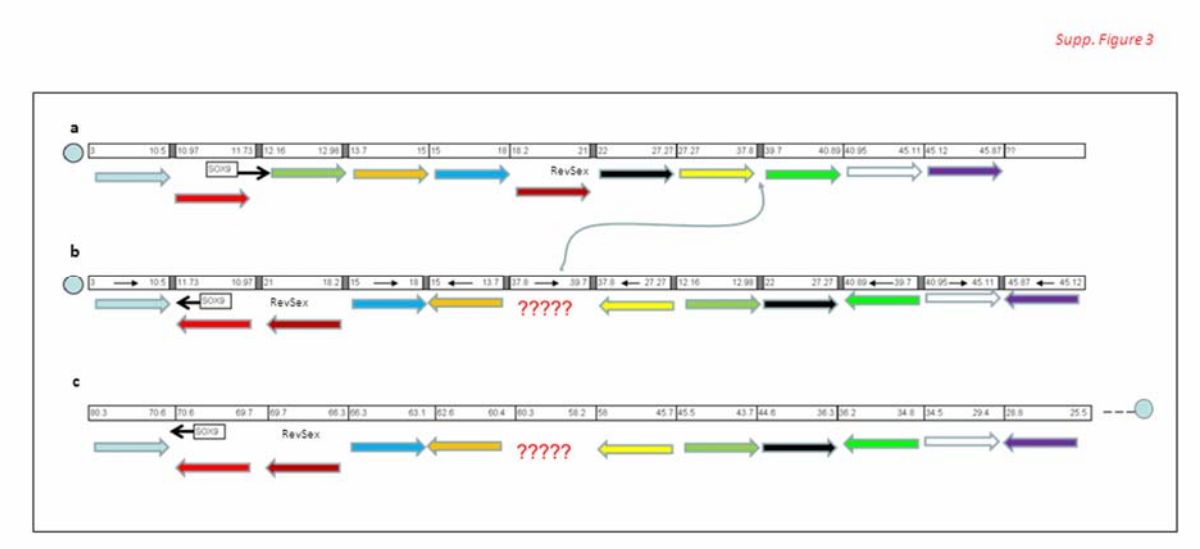
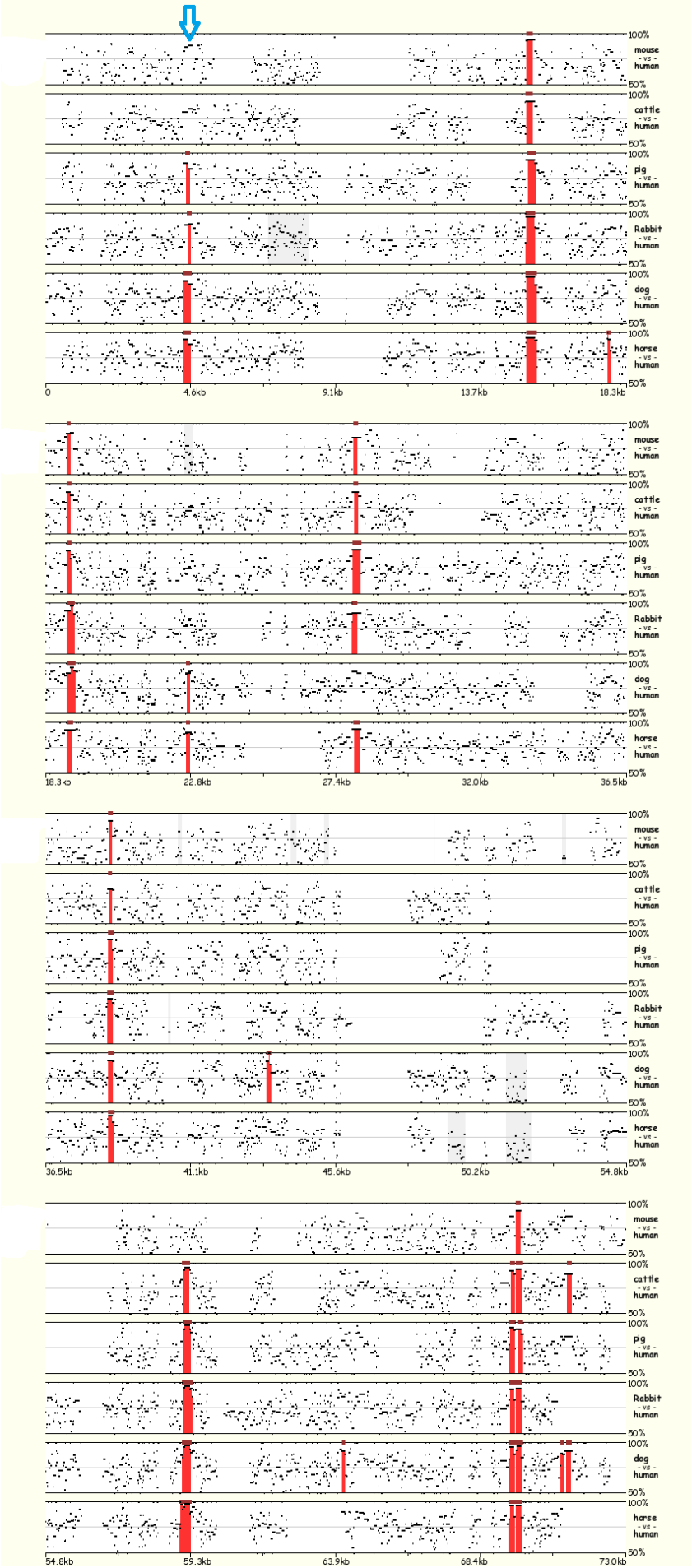
Supplementary Figure 1
ECRs in the *RevSex* genomic region.
The conserved regions included in the human 73-Kb *RevSex* genomic region versus the ortholog regions of mouse, cattle, pig, rabbit, dog, and horse are presented. The positions of these regions on the available genome assemblies are reported in Table 3. Only ECRs with a similitude higher than 95% are reported. Mulan software parameters are presented in the Material and Methods section. The blue arrow indicates the localization of the conserved SOX binding site reported in Table 4.



Supplementary Figure 3

Preliminary Bioinformatic reconstruction of dog chromosome 9 assembly considering the human hg19 genome assembly.

The preliminary bioinformatic analysis of the CF9 genome assembly in comparison with the hg19 human genome assembly is presented. (a) canFam2 genome assembly up to 46 Mb. (b) The proposed reconstruction of CF9 following homologies with the HS17 hg19 assembly. (c) HS17 hg19 genome assembly. The number indicates the bp position in Mb. Round circles denote the centromere position. Note that the canFam3 possess the same order of canFam2 (here reported) but all are moved 3 Mb close to centromere (In fact, in the version 3 the first 3 Mb of the version 2, which were empty, have been removed).


100%
mouse
- vs -
human
50%
cattle
pig
Rabbit
dog
horse
0
4.6kb
9.1kb
13.7kb
18.3kb
22.8kb
27.4kb
32.0kb
36.5kb
41.1kb
45.6kb
50.2kb
54.8kb
59.3kb
63.9kb
68.4kb
73.0kb