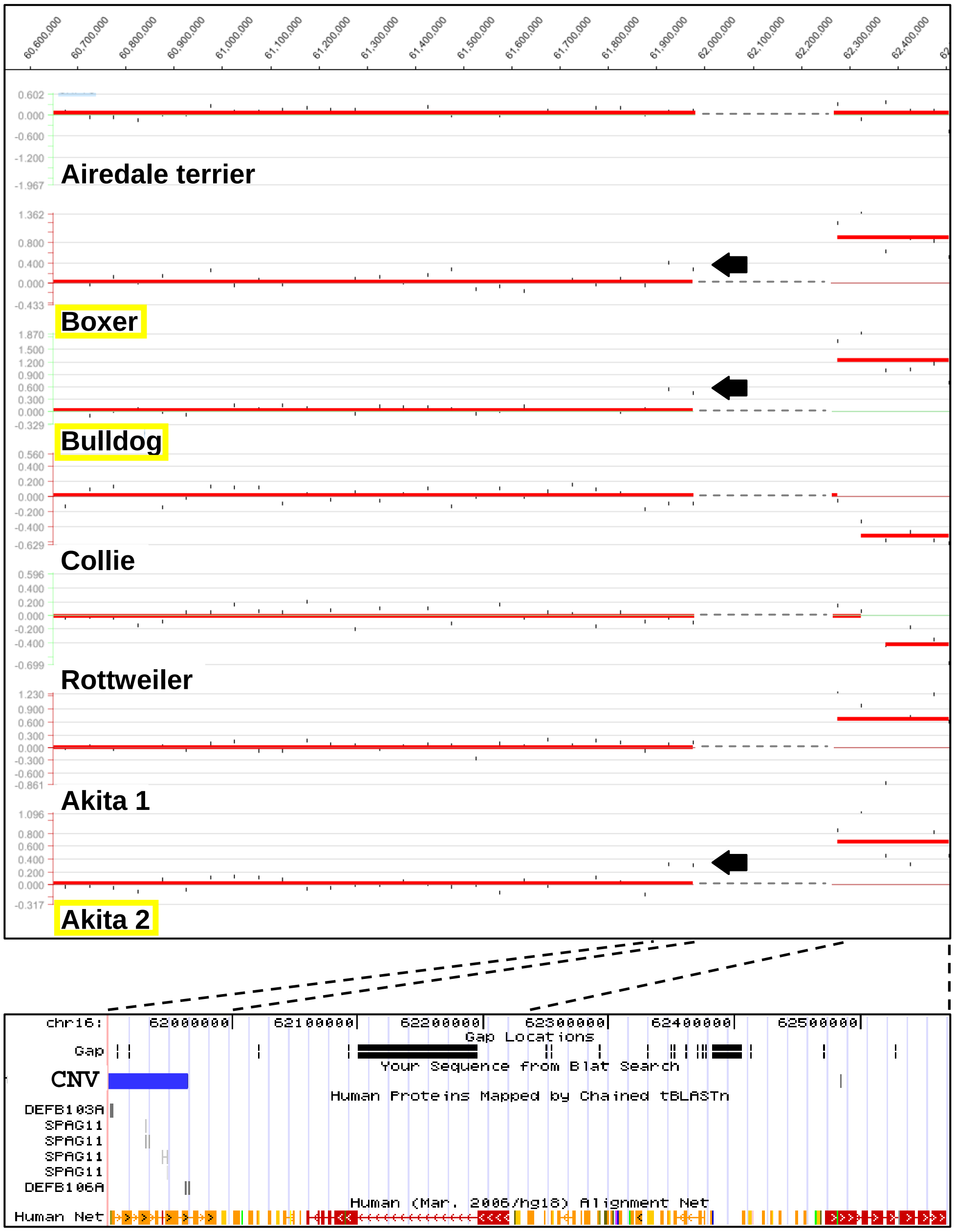

Supplemental Figure S1. DNA Structural variation affecting beta defensin *CBD103*. *Top)* Representative aCGH results. Signal is averaged in 50 kb windows; each dog is shown at a different optimized scale (SignalMap, Nimblegen). Genome coordinates are provided above results. The right edge represents the telomeric end of the assembly. A dashed line shows a gap in the oligonucleotide array coverage (partially due to an assembly gap). Black arrows point to the CNV gains called at high confidence. The Bulldog has a high gain and the Boxer/Akita have a lower gain. There is a great deal of copy number gain/loss with differing breakpoints in the most telomeric contig. *Bottom)* UCSC genome annotation is shown with genes taken from the track of human proteins mapped by chained tblastn. The *CBD103* CNV is shown in blue. The first gene, annotated as matching human *DEFB103A*, is in fact *CBD103* (the ortholog of human DEFB103B). The non-dog RefSeq track is not shown – for human, it illustrates *SPAG11* followed by *DEFB104B*, *DEFB106A*, *DEFB105A*, and *DEFB107A* (in that order, left to right). Genome assembly gaps are shown in the top track as black double bars.