



Supplemental Figure 1. Assignment of IGHD8-2 alleles. **A.** Fractions of ultralong CDRH3s with $diff$ exceeding $diff_{min}$ (x-axis) collected across 204 subjects. The selected value of $diff_{min} = 0.02$ and the fraction of used CDRH3s corresponding to it shown by grey lines. **B.** Animal 14053 classified as homozygous for allele IGHD8-2*01. Ultralong CDRH3s are shown as dots. The x-axis (y-axis) shows scores of alignments between ultralong CDRH3s and allele IGHD8-2*01 (IGHD8-2*02). The red line corresponds to $x=y$. CDRH3s were classified into three groups: (i) with $diff_{min} < 0.02$, (ii) with $diff_{min} \geq 0.02$, and (iii) $diff_{min} \geq 0.02$ and the mutation rate below 0.3 and colored them in blue, grey, and red, respectively. CDR3s from the third group were used for allele assignment. **C.** Animal 14015 classified as homozygous by allele IGHD8-2*02, with the legend as described in (B.). **D.** Animal 14363 classified as heterozygous, with the legend as described in (B.). **E.** The distribution of the fractions of non-discarded ultralong CDRH3s assigned to IGHD8-2*01 across 204 subjects. Subjects classified as homozygous for allele IGHD8-2*01, homozygous for allele IGHD8-2*02, or heterozygous were shown in blue, orange, or green, respectively.