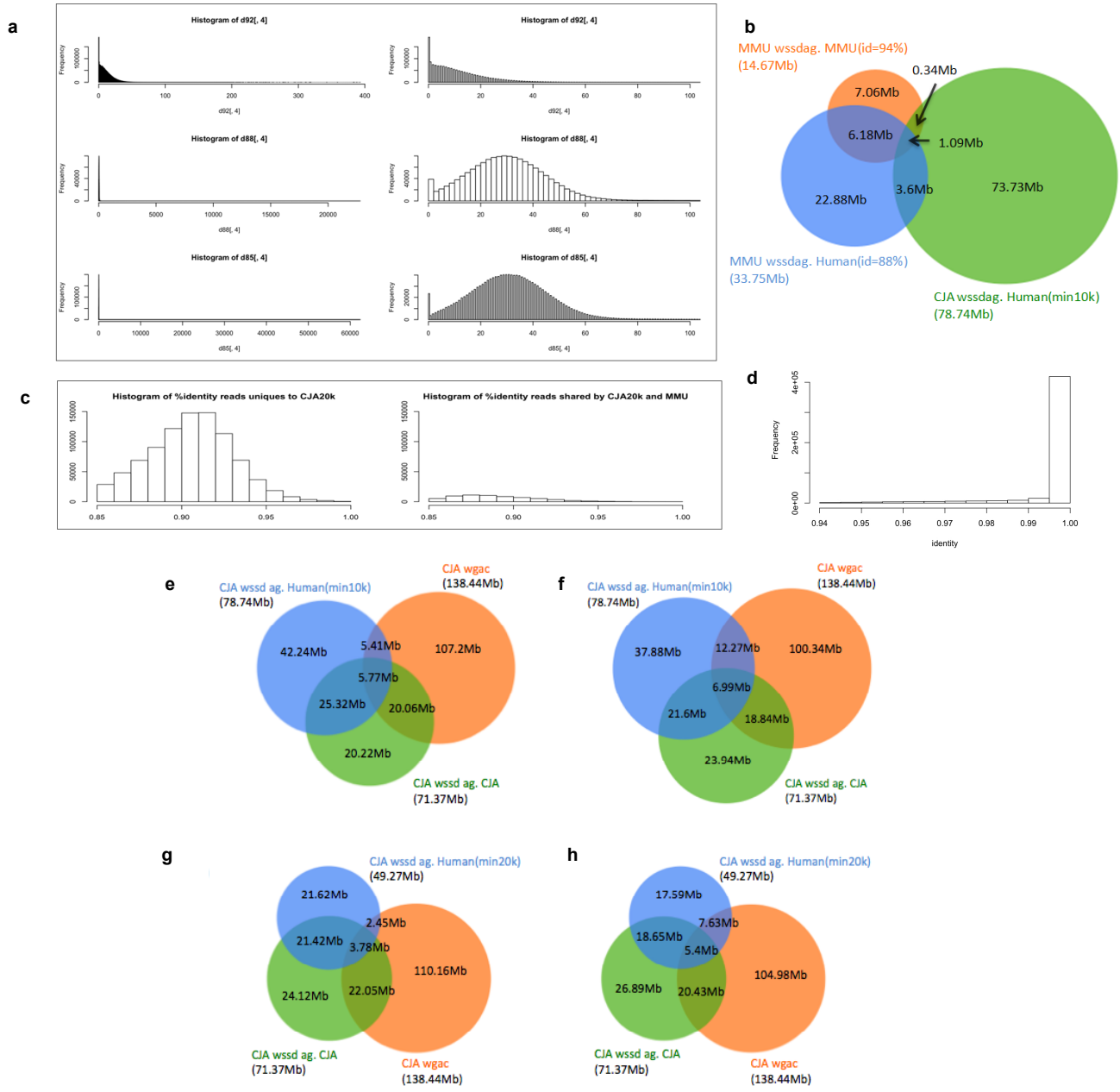

Supplementary Figure 4 | Summary of Structural Variation Data Part Two. **a**. Depth of coverage in 5 kb windows within control regions of single copy sequences in the human genome, shown with identity threshold of 92% (top), 88% (middle) and 85% (bottom), with full distribution on the left and windows with depth of coverage between 0 and 100 on the right. **b.** Shared versus specific duplications between macaque and marmoset genomes. "MMU WSSD against MMU(id=94%)" (orange) and "MMU WSSD against human (id=88%)" (blue) correspond to macaque duplications detected by WSSD using macaque reads aligned with >94% of identity against the human assembly and with >88% of identity against the macaque assembly, respectively. Both datasets are compared with marmoset duplicated sequences determined by WSSD against the human assembly using an identity threshold of 85% and a minimum length of 10 kb "CJA WSSD against human (min 10k)" (green). **c**. Histograms of aligned marmoset read identities between 85% and 100% within marmoset-specific duplications > 20kb (left) and duplications shared (>1 kb) between marmoset and macaque (right). **d.** Identities (94% to 100%) of reads aligned to the assembly in duplications shared with human. **e. through h.** Shared and marmoset-specific duplications detected by three different approaches. "CJA WSSD against CJA" (green) and "CJA WGAC" (orange) correspond to duplications detected in the marmoset assembly by WSSD using marmoset reads aligned with >94% of identity and WGAC respectively. Both datasets are compared with duplicated sequences determined by WSSD using an identity threshold of 85%. **e**. **and f.** Minimum length of 10 kb "CJA WSSD against human (min 10k)" (blue). **g. and h.** Minimum length of 20 kb "CJA WSSD against human (min 20k)" (blue). On the left **(e. and g)** duplicated sequences detected in the human assembly were aligned against the duplications identified on the marmoset assembly. On the right **(f and h)** is the converse, duplicated sequences from marmoset were mapped against duplicated sequences from the human assembly. Notice the consistency of the overlaps.