



**Supplementary Figure 3 | Summary of Structural Variation Data.** **a.** Pairwise length (left) and Identity (right) distribution of marmoset assembly intrachromosomal (blue) and interchromosomal (red) segmental duplications. Length distributions are partitioned into 1kb to 10kb in 1kb increments and 10 kb to 50 kb in 10 kb increments. Identity distributions are shown for 90 to 100% identity. Note the depletion of duplication with identity >99.5% and excess of short duplication in comparison to other assemblies. **b.** Histograms of the aligned marmoset reads mapped to the human genome. Bins of percent identity between 85% and 100%, showing number of reads in each bin, for reads mapped to regions without a known CNV in any previously analyzed primate (left) and the entire genome (right). In both cases, the mean is 91% and there are relatively few reads mapped with an identity <85%. **c.** Examples of FISH, clones CH259-366A22 (left) and CH259-290F14 (right) selected in WGAC positive regions. **d.** Global view of SDs in the mapped marmoset genome (WGAC). Blue lines are pairs of duplication within the same chromosome, and red lines are the interchromosomal duplications. Each line is a chromosome, chromosome 1 at top and X and Y at the bottom. Only scaffolded chromosomes data are shown. **e.** As in (d) with unplaced scaffolds mapped to each chromosome included at the right. **f.** As in (d) with unmapped scaffolds (ChrUn) included at the bottom.