Supplemental Figure 2. PCR-based validation of a chimpanzee-specific CNV comprised of clones Chr8tp-11E7 and Chr8tp-16F1. (a) This CNV overlaps a ~6 kb gap in an alignment of the chimpanzee genome sequence (panTro2) to the human genome sequence (hg18). (b) The chimpanzee log2 ratios for these two clones, along with a relative loss identified in this region in the reference chimpanzee Clint compared to the human reference individual in our between-species aCGH experiment, suggested that this ~6 kb region might be polymorphically deleted in chimpanzees (Clint was the reference individual for our study and the donor for the chimpanzee genome sequence) and represent the source of the detected CNV. We designed a PCR-based assay (shown in panel a) to test this hypothesis. (c) Results of the PCR-based assay on a 1.2% agarose gel with ethidium bromide staining confirmed the presence of a polymorphic deletion. (d) The PCR-based copy number estimates are generally consistent with the aCGH data. There is some overlap among the log2 ratios for PCR-estimated 1 and 2 copy number states, which suggests that a ~6 kb deletion may be at or near the resolution limit for the WGTP platform.