



Supplementary Figure S2 Whole-genome siCHILD/Haplarithmis haplotyping and copy number typing outcomes (digynic-triploidy). **(A)** Shown here are the digynic triploidy profiles for two embryos. The genomic signatures representing genome-wide haplotypes (haplarithms) and copy number states (haplarithms and normalized Log-R plot) were obtained by implementing siCHILD/Haplarithmis on single blastomeres as previously described (Zamani Esteki *et al.*, 2015; Dimitriadou *et al.*, 2017). **(B)** Schematic interpretation of the maternal and paternal haplarithm profiles corresponding to digynic triploidy. Shown in this example is the profile of one chromosome. In the case of genome-wide digynic triploidy—as in panel A—the distance between the blue and the red lines (e.g. 0.67 for the paternal and 0.33 for the maternal) remain constant along the entire genome.