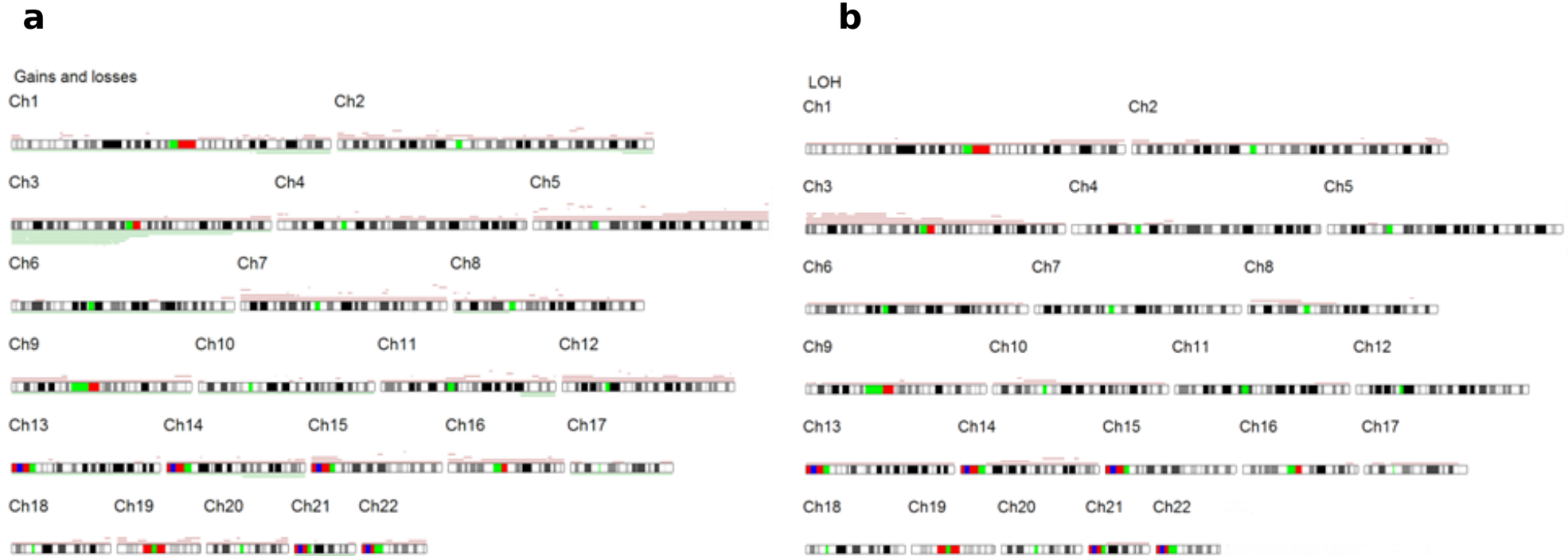


**Additional File 1.** Whole-genome maps of CN alterations and LOH events in the nine ccRCC primary cultures, using CNAG v3.0 software.



Chromosomes are represented from p to q end (from left to right), with cytobands (black and white blocks), centromeres (green blocks) and heterocromatic regions (red and blue blocks). **(a)** Starting from the HMM-CN state data, regions of CN gain (upper red traces) and CN loss (lower green traces) are represented along each chromosome (from 1 to 22). **(b)** Regions of statistically significant LOH (with LOH likelihood higher than 30) are represented with red traces along each chromosome. Chromosome X was excluded from analyses.

