

**Supplementary Figure 1.** Summary of genomic changes on the entire chromosomes in a total of 29 PDAC samples, determined by 1 Mb-spaced CGH arrays. “Genetic gains” are shown as green bars and “losses” as red bars according to the genomic positions (Ensembl Ver39). Thick bars are used to depict HAs and HDs. The regions surrounded by rectangles indicate all MCRs of genetic alterations identified by MSA. At the bottom, the information of regions of copy number variation was integrated from the published data by Redon *et al* (<http://projects.tcag.ca/variation/downloads/Redon2006.txt>)[31].

**Supplementary Figure 2.** Two representative array CGH profiles in PC8 (Ch8) and SUI2 (Ch9), analysed by the SPOT software [26]. The red lines were used to depict inferred copy numbers by aCGH-Smooth [27]. (A) HA at 8q24.13 was detected in PC8. The size of this amplicon is approximately 1.32 Mb and it includes the *MYC* gene (*arrow*). (B) The 2.1 Mb region of HD including the entire *PTPRD* gene (9p23) was detected in SUI2 line (*arrow*).