



Supplementary Figure S1. Distribution of copy number variation (CNV) in 85 endometrial carcinomas (ECs). The samples are sorted in ascending order of CNV size calculated from the sum of the loss (CNV ≤ 1.5), gain (CNV ≥ 2.5) and copy neutral loss of heterozygosity (cnLOH) in the genome, estimated by whole exome sequencing. The ECs with a CNV size greater than the 75th percentile ($>Q3$) were defined as copy number (CN)-high.