Description of Additional Supplementary Files:

Supplementary data 1: all functional SNVs and indels identified by WGS

Supplementary data 2: Characteristics of 32 HSRCC patients

Supplementary data 3: DAVID prediction of all altered genes (SNV/INDEL only) in non-hypo mutation group

Supplementary data 4: DAVID prediction of all altered genes in hypo mutation group

Supplementary data 5: SVs identified by whole-genome sequencing

Supplementary data 6: Characteristics of 797 validation patients

Supplementary data 7: DAVID prediction of all altered genes (SNV/INDEL, SVs, and SCNA) in non-hypo mutation group