Figure S1. The number of detected genes under different sequence depths. For both tumor and normal tissues in each patient, the percentage of genes in database being detected were plotted under different number of clean tag (after filtration) and unambiguous clean tag (clean tag that uniquely maps to the genome).
Figure S2. Kaplan-Meier survival plot for TNM staging and molecular indicators. (A) Cumulative survival curve of patients in the stage of T1, T2 and T3 using TNM staging indicators; (B-D) The association between the protein expressions of ALDH2 (B), CCNE1 (C) and SMAD3 (D) and survival rate of patients in the stage of T2 and T3. Mo: month.