1. Standard Analysis (Human or Mouse) with reference

Data Quality Control: filtering reads containing adapter or with low quality Statistics Analysis of Data Production and Quality Mapping Reads to Reference Genome Gene Expression Quantification Differential Expression Analysis (two or more groups of samples) GO Enrichment Analysis and KEGG Pathway Enrichment Analysis of Differentially Expressed Genes (DEGs) (two or more groups of samples) Protein Protein Interaction Analysis Functional Annotation of Transcription Factors Functional Annotation of Oncogene Alternative Splicing (AS) Quantification and Differential Expression Analysis Identification of anti-Transcript (Strand Specific Library Only) TSS and TSS Prediction (Strand Specific Library Only) SNP/InDel Analysis Fusion Gene Analysis (for tumor sample and cancer cell line)