S7 Table. Analysis details for RNA-seq in Tfg1-HA vs. Tfg1-K60,61R-HA strains

RNA-seq in Tfg1-HA and Tfg1-K60,61R-HA strains	
Samples and conditions	Two independent replicates were prepared from cultures grown in SC medium at 30°C. 1 – Tfg1-HA 2 – Tfg1-K60,61R
Library synthesis	NEB Ultra II directional mRNA library prep (PolyA enrichment)
Sequencing	Illumina HiSeq 2500; Paired-end reads; 2x 126 nt; 30 million reads/sample
Quality control	FastQC (0.11.9)
Genome alignment	HISAT2 (2.1.0) ***Parameters:*** Default options; UCSC annotaion file: sacCer3.ncbiRefSeq.gtf
Transcript counting	Transcripts counted using featureCounts from Subread (2.0.0) ***Parameters:*** Default options; -p (paired)
Differential expression analysis	edgeR (3.32.1) ***Parameters:*** Library sizes were normalized using calcNormFactors; dispersions were estimated with estimateDisp with robust argument; likelilhood ratio tests for differential expression were performed with glmFit and glmLRT.