Figure S1. The genes that were affected by OTU Deubiquitinase 7A (*OTUD7A*) overexpression. To identify the genes that were affected by *OTUD7A* overexpression, primary goose hepatocytes transfected with empty pcDNA3.1 (+) vector (control) or pcDNA3.1 (+) containing goose *OTUD7A* coding sequence (overexpression) were used in RNA-Sequencing analysis (RNA-Seq). The mapped reads of each gene were calculated and presented as Reads Per Kb per Million reads (RPKM). The significance was determined using DESeq. Genes with max RPKM value > 2, fold change of treatment over control > 2 or < 0.5, and *P*-value < 0.05 were assigned as differential expressed genes. Red dots represent up-regulated genes, blue dots represent down-regulated genes, and gray dots represent non-significantly differentially expressed genes after *OTUD7A* overexpression in goose primary hepatocytes. There are six replicates for each treatment.
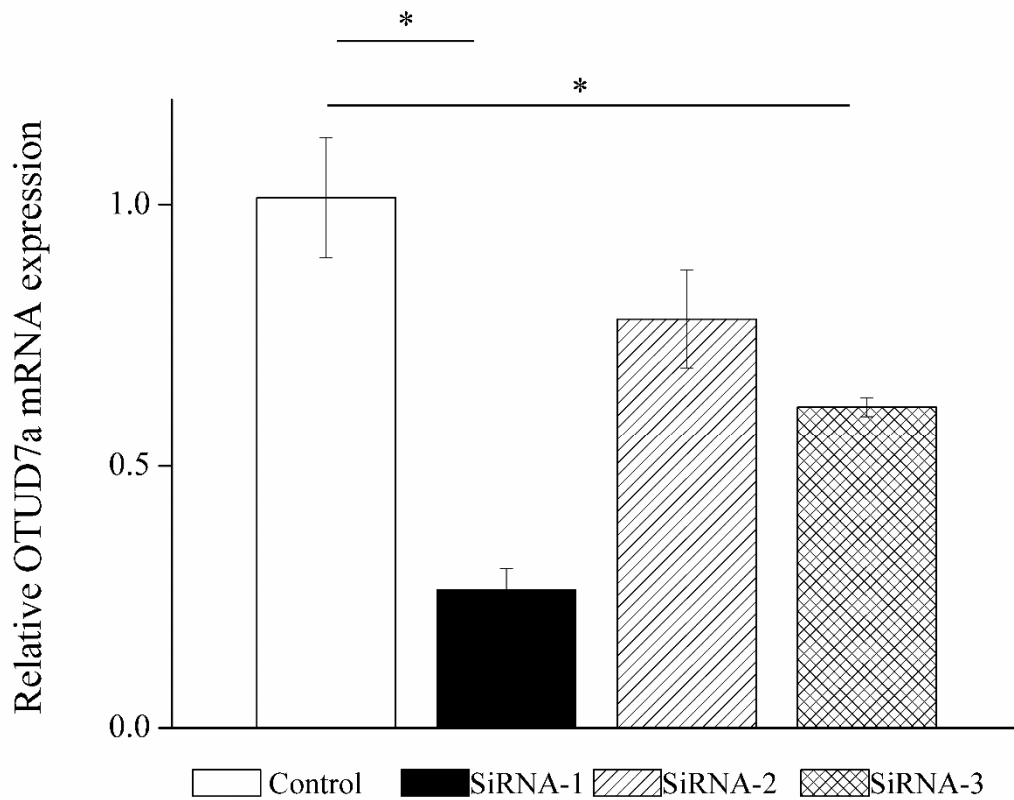
Figure S2. The screening of small interfering RNAs (siRNAs) for OTU Deubiquitinase 7A (*OTUD7A*). Three different siRNAs were designed to target the goose *OTUD7A* CDS. The siRNAs were separately transfected into goose primary hepatocytes cultured in serum-free and antibiotic-free Opti-MEM using Lipofectamine 2000. The Opti-MEM was replaced with complete culture medium after 6 h of transfection. Cells were cultured for 24 h at 37°C in 5% CO_2 incubator. Scrambled siRNA was used as a negative control and three replicates for each treatments were used. The sense strand sequence and antisense strand sequence were 'GCGUGUACAGUGAAGAUUUTT' and 'AAAUCUUCACUGUACACGCTT' for siRNA-1, 'CCAUCUGUAGUAAUUCCAATT' and 'UUGGAAUUACUACAGAUGGTT' for siRNA-2, ' GCACUGAAUGGGUCAUCUATT' and 'UAGAUGACCCAUUCAGUGCTT' for siRNA-3, respectively.