

GO term	no. genes	p-value
Protein modification (BP)	43	6.87e-6
Positive regulation of transcription (BP)	10	4.19e-5
Guanyl-nucleotide exchange factor activity (MF)	10	5.86e-5
Positive regulation of nucleobase, nucleoside, nucleotide, nucleic acid metabolism (BP)	10	6.19e-5
GTPase regulator activity (MF)	15	6.23e-5
ATP binding (MF)	37	1.53e-4
Biopolimer metabolism (BP)	63	1.56e-4
RNA capping (BP)	2	2.61e-4
mRNA capping (BP)	2	2.61e-4
Phosphorus metabolism (BP)	27	2.81e-4
Phosphate metabolism (BP)	27	2.81e-4
Positive regulation of cellular metabolism (BP)	11	2.94e-4
Regulation of cellular process (BP)	78	3.51e-4
Actin cytoskeleton (CC)	11	4.59e-4
Negative regulation of cellular physiological process (BP)	23	4.89e-4

Supplementary Table 1: List of top 15 enriched gene ontology categories for 311 genes uniquely associated with decreased bindings in OHT. MF(Molecular Function), BP(Biological Process), CC(Cellular Component)