



Supplemental Figure S5 (related to Fig. 4). **Functional enrichment of differentially expressed genes, including TP73-bound genes with highly conserved TP73 motifs, for ciliogenesis.**

(A and B) Hierarchical clustering of significantly enriched gene ontologies (GO) (WebGestalt, adjusted p-value ≤ 0.1) for genes that are differentially expressed at different time points of MTEC differentiation (ALI D0, 4, 7, 14), comparing WT and p73 KO samples. Genes are derived from the RNA-seq differential expression analysis and enrichment is calculated as the ratio of observed over expected genes per GO category. The magnitude of enrichment is displayed with colours ranging from white (no enrichment) to red (strong enrichment). Cilium-related terms during ALI D7 and D14 are highlighted in red.

(A) Enrichment of Biological Process (BP) functional categories. **(B)** Enrichment of Cellular Component (CC) functional categories.

Overall, ALI D7 and D14 cultures show strong enrichment for cilium-related terms due to a concerted downregulation of genes involved in ciliogenesis in p73KO vs. WT samples.

(C and D) Genomic distribution of motif distance from peaks and motif discovery within peaks.

(C) Distance of the predicted TP73 DNA-binding motif (*bottom*) from ChIP-seq peak centers. In general, the predicted motif lies narrowly within several bases of the peak center. **(D)** General motif quality. Frequency of estimated scores of the predicted TP73 DNA-binding motifs obtained from ChIP-seq peaks. Motif scores are calculated by taking the log-odds ratio of the predicted motif matrix. Thus, values higher than 0 indicate higher conservation and prevalence of the motif. Frequency is calculated by counting the number of times a given score is observed.

Overall, the predicted motifs have high scores indicating a highly conserved and prevalent TP73 motif.

(E) Hierarchical clustering of significantly enriched Biological Process (BP) gene ontologies (GO) (WebGestalt, adjusted p-value ≤ 0.1) for genes that are differentially expressed during MTEC differentiation (ALI D0, 4, 7, 14) and are bound by TP73. Enrichment is calculated as the ratio of observed over expected genes per GO category. The magnitude of enrichment is displayed with colours ranging from white (no enrichment) to red (strong enrichment). Cilium-related terms during ALI D7 and D14 are highlighted in red. Overall, ALI D7 and D14 cultures show strong enrichment of cilium-related terms due to a concerted downregulation of ciliogenesis genes in p73KO vs. WT samples.