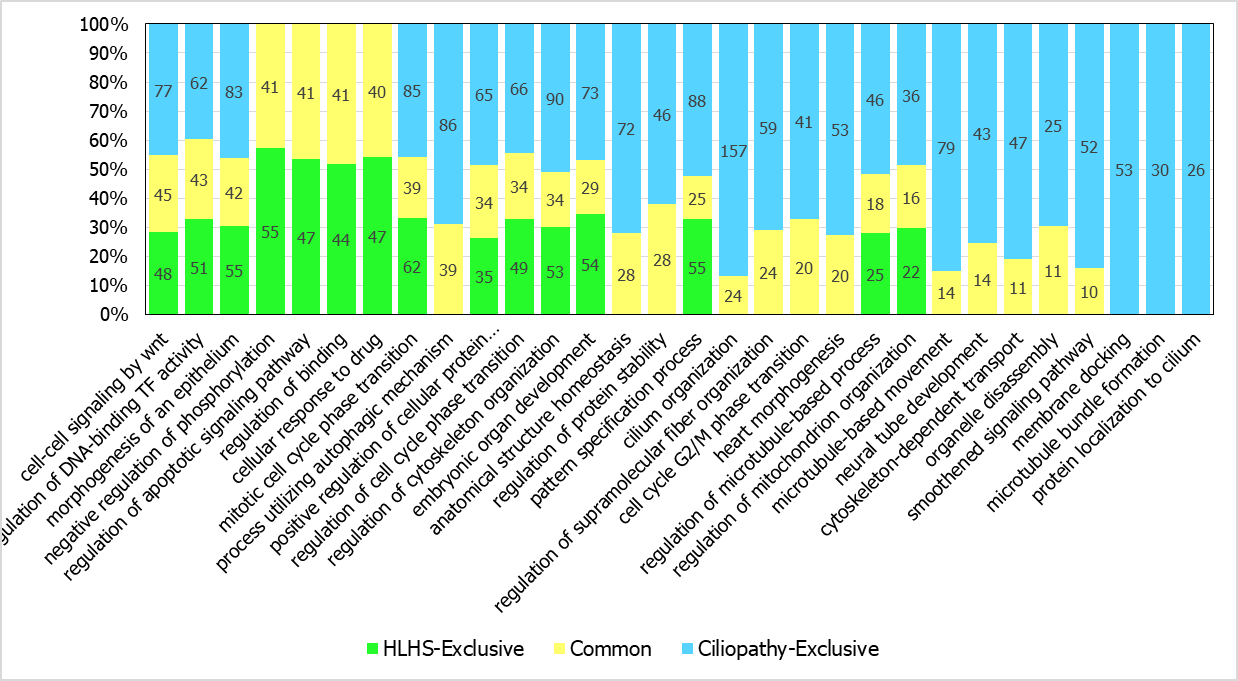
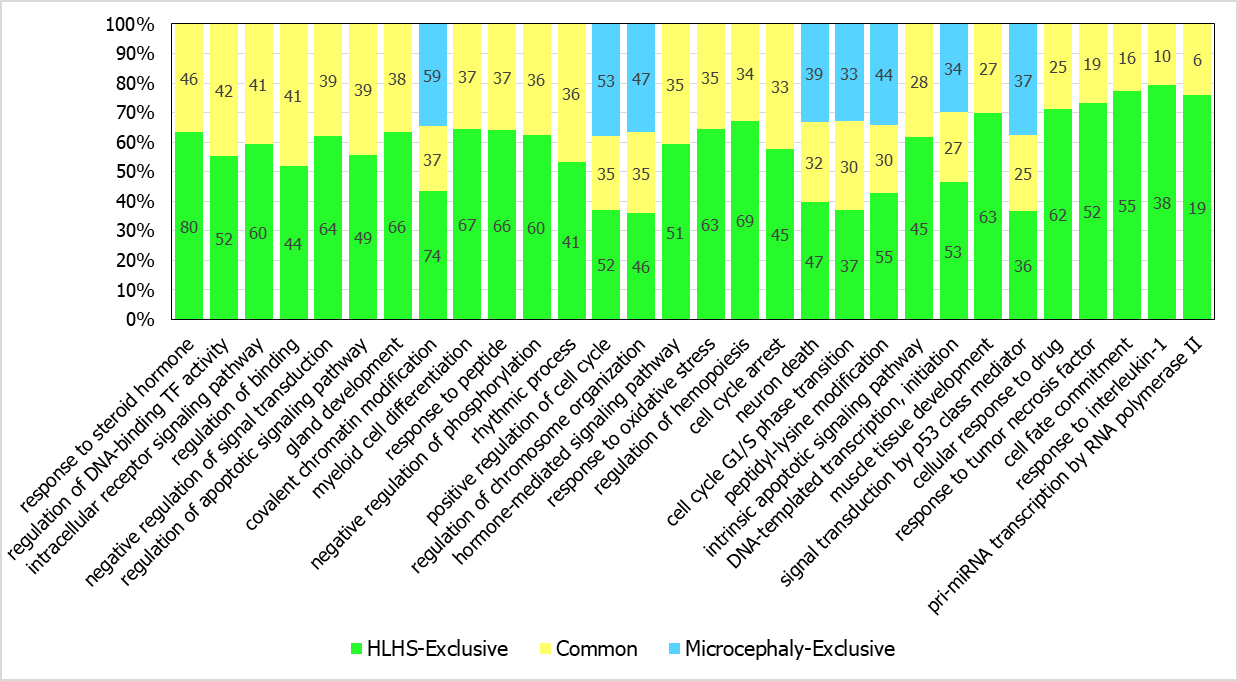
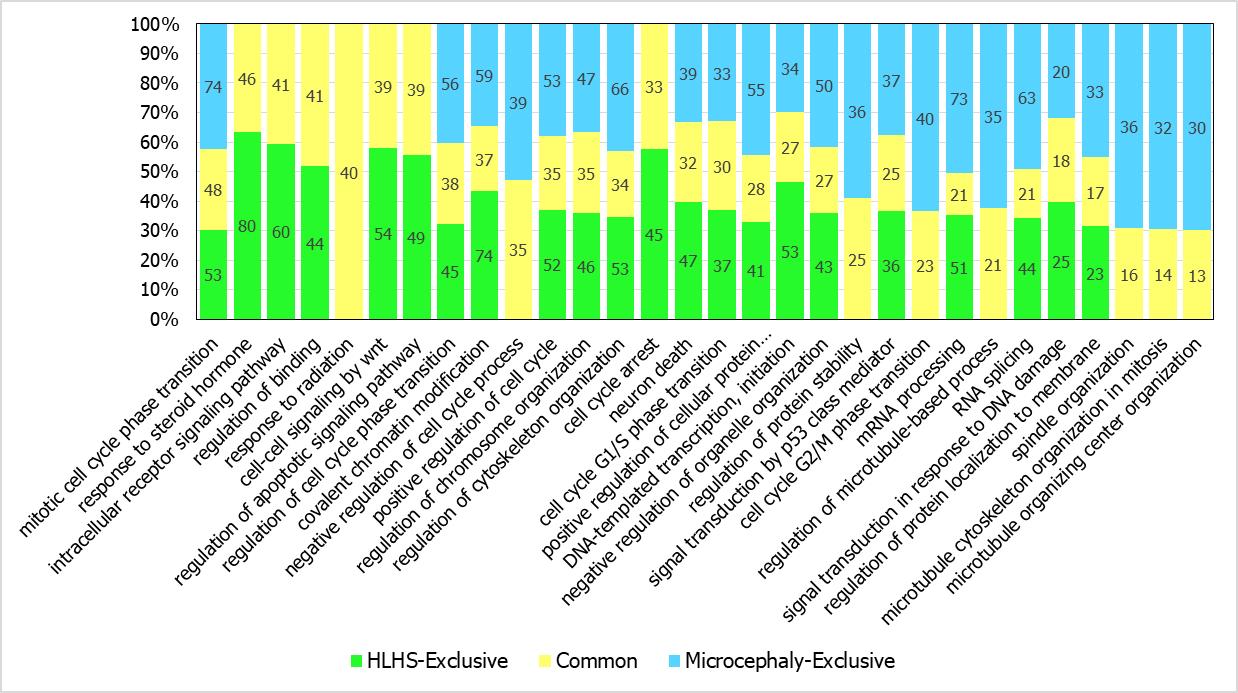
**Figure S1. Top-30 Gene Ontology Biological Processes associated with the hypoplastic left heart syndrome (HLHS) interactome in relation with the ciliopathy interactome:** Processes associated with the interactome were identified using WebGestalt (web-based gene set analysis toolkit). Statistical significance of GO enrichment was computed using Fisher's exact test, and corrected using the Benjamini-Hochberg method for multiple test adjustment. Shown here are the top-30 processes in the HLHS interactome, along with the number of genes associated exclusively with the HLHS interactome (green), exclusively with the ciliopathy interactome (blue) and common to both (yellow).

**Figure S2. Top-30 Gene Ontology Biological Processes associated with the ciliopathy interactome in relation with the hypoplastic left heart syndrome (HLHS) interactome:** Processes associated with the interactome were identified using WebGestalt (web-based gene set analysis toolkit). Statistical significance of GO enrichment was computed using Fisher's exact test, and corrected using the Benjamini-Hochberg method for multiple test adjustment. Shown here are the top-30 processes in the HLHS interactome, along with the number of genes associated exclusively with the HLHS interactome (green), exclusively with the ciliopathy interactome (blue) and common to both (yellow).



**Figure S3. Top-30 Gene Ontology Biological Processes associated with the hypoplastic left heart syndrome (HLHS) interactome in relation with the microcephaly interactome:** Processes associated with the interactome were identified using WebGestalt (web-based gene set analysis toolkit). Statistical significance of GO enrichment was computed using Fisher's exact test, and corrected using the Benjamini-Hochberg method for multiple test adjustment. Shown here are the top-30 processes in the HLHS interactome, along with the number of genes associated exclusively with the HLHS interactome (green), exclusively with the microcephaly interactome (blue) and common to both (yellow).



**Figure S4. Top-30 Gene Ontology Biological Processes associated with the microcephaly interactome in relation with the hypoplastic left heart syndrome (HLHS) interactome:** Processes associated with the interactome were identified using WebGestalt (web-based gene set analysis toolkit). Statistical significance of GO enrichment was computed using Fisher's exact test, and corrected using the Benjamini-Hochberg method for multiple test adjustment. Shown here are the top-30 processes in the HLHS interactome, along with the number of genes associated exclusively with the HLHS interactome (green), exclusively with the microcephaly interactome (blue) and common to both (yellow).