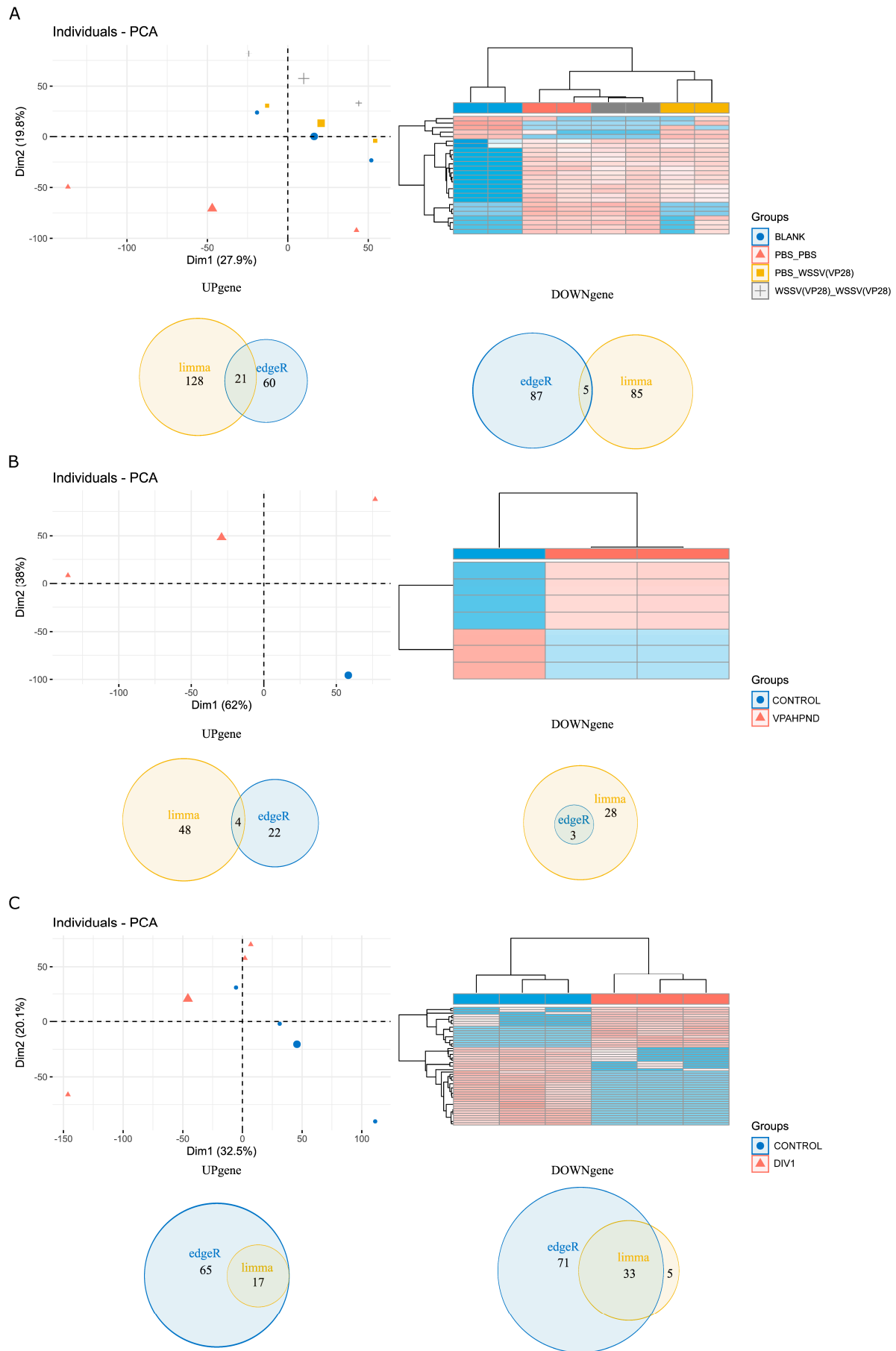
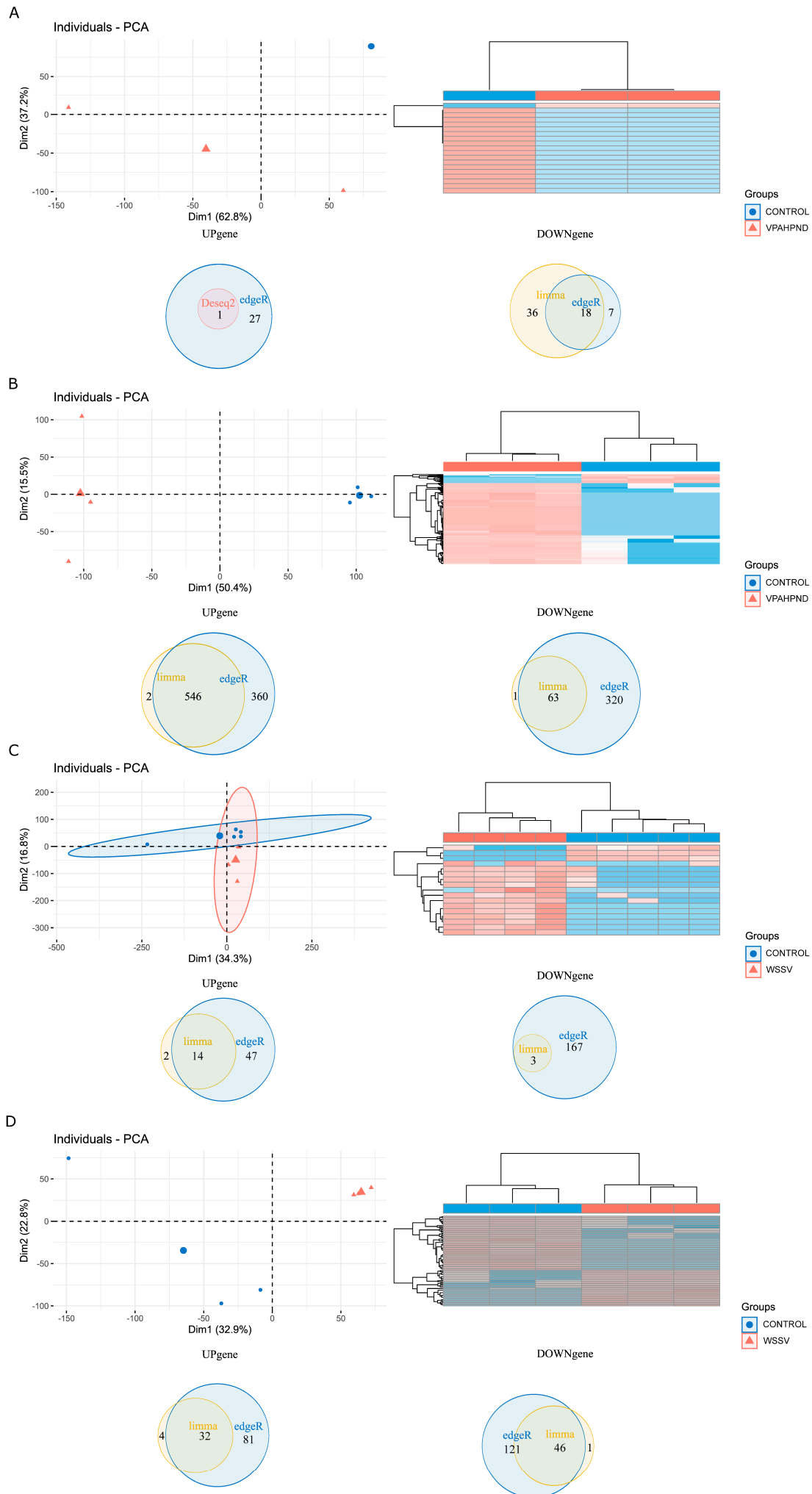


Supplementary Figure S1: Transcriptomic changes of gills infected by WSSV based on two studies (BioProject accession number: (A) PRJNA524934; (B) PRJNA716175), showing results from principal component analysis (PCA), gene abundance heat map, Wien diagrams showing number of differentially expressed candidate genes.



Supplementary Figure S2: Transcriptomic changes of haemolymph infected by WSSV, VP_{AHPND} and DIV1 based on two studies (BioProject accession number: (A) PRJNA233549; (B) PRJNA448614; (C) PRJNA612147), showing results from principal component analysis (PCA), gene abundance heat map, Wien diagrams showing number of differentially expressed candidate genes.



Supplementary Figure S3: Transcriptomic changes of hepatopancreas infected by WSSV and VP_{AHPND} based on two studies (BioProject accession number: (A) PRJNA413606; (B) PRJNA421143; (C) PRJNA428228; (D) PRJNA554075), showing results from principal component analysis (PCA), gene abundance heat map, Wien diagrams showing number of differentially expressed candidate genes.