



Additional file 5. A heatmap describing the profiles of 351 differentially expressed genes (y-axis) between Patient Groups 2 and 4 (x-axis). Data displayed are log₂ transformation of normalised raw reads using *DESeq2*. The heatmap is divided into four sectors. Significant GO terms and/or KEGG pathways in each sector are shown in tables on the right. GO terms and/or KEGG pathways with adjusted *p*-value < 0.05 were deemed significant. The colour scale represents the expression level of DEGs: red (lower expression), black (higher expression). Patient Groups are labelled by colour beneath the dendrogram.