

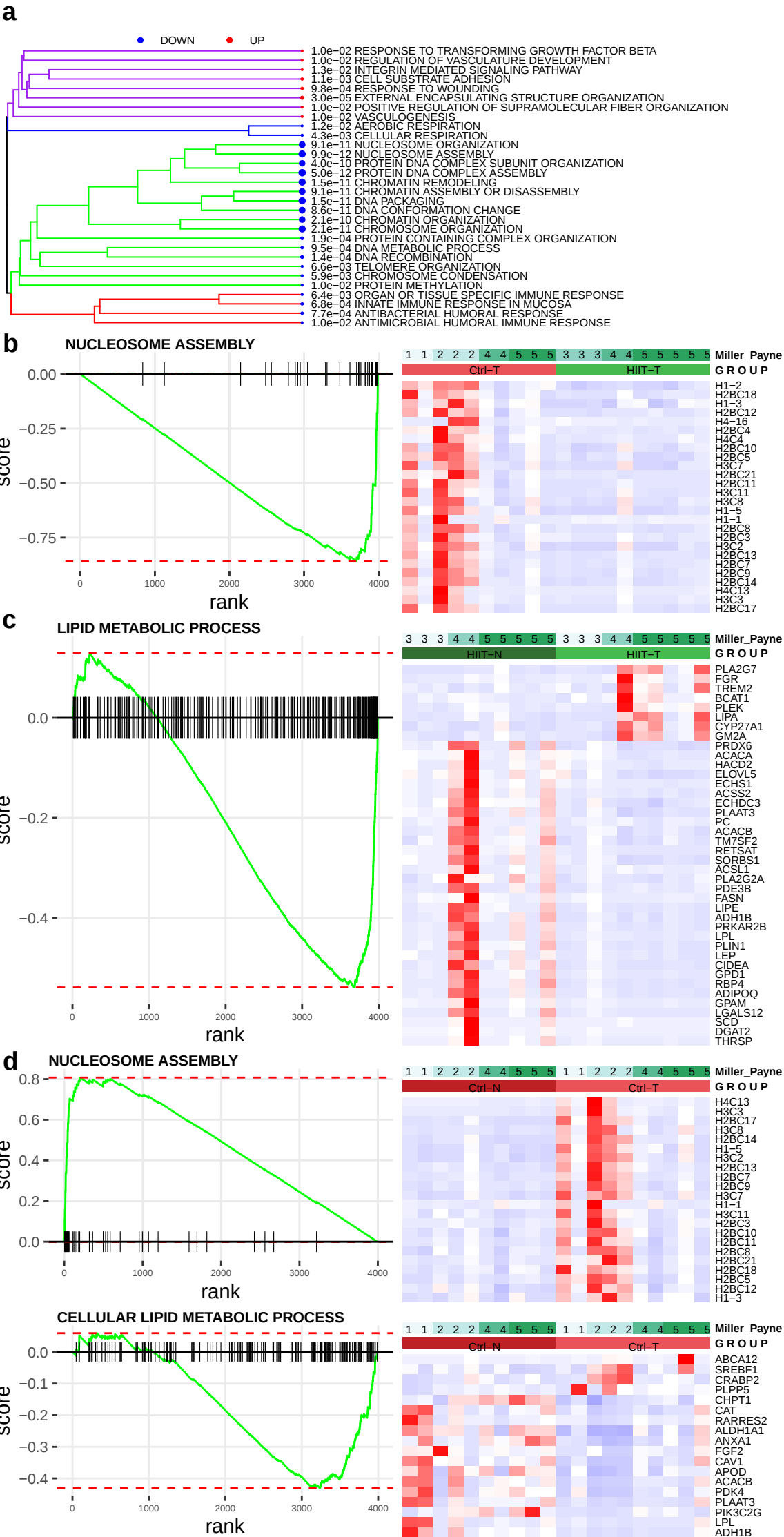


Fig. S2 Gene set enrichment analysis of differentially expressed genes between tumour and normal tissues from the HIIT and Ctrl groups. a Hierarchical clustering of the enriched gene sets based on the DEGs between HIIT and Ctrl-T. Blue dots designate pathways that are downregulated in the HIIT-T and red dots – pathways that are upregulated in the HIIT-T; dot size is proportional to p-values. b Heatmaps of DEGs representing 'nucleosome assembly' and gene set enrichment scores in HIIT-T vs Ctrl-T. Colour code of sample groups: green – HIIT-T, red – Ctrl-T. c Heatmap of DEGs representing 'lipid metabolic process' pathway and gene set enrichment score in HIIT-T vs N. Colour code of sample groups: dark green – HIIT-N, light green – HIIT-T. d Heatmaps of DEGs representing selected pathways and gene set enrichment score in Ctrl-T vs N. Colour code of sample groups: dark red – Ctrl-N, light red – Ctrl-T.