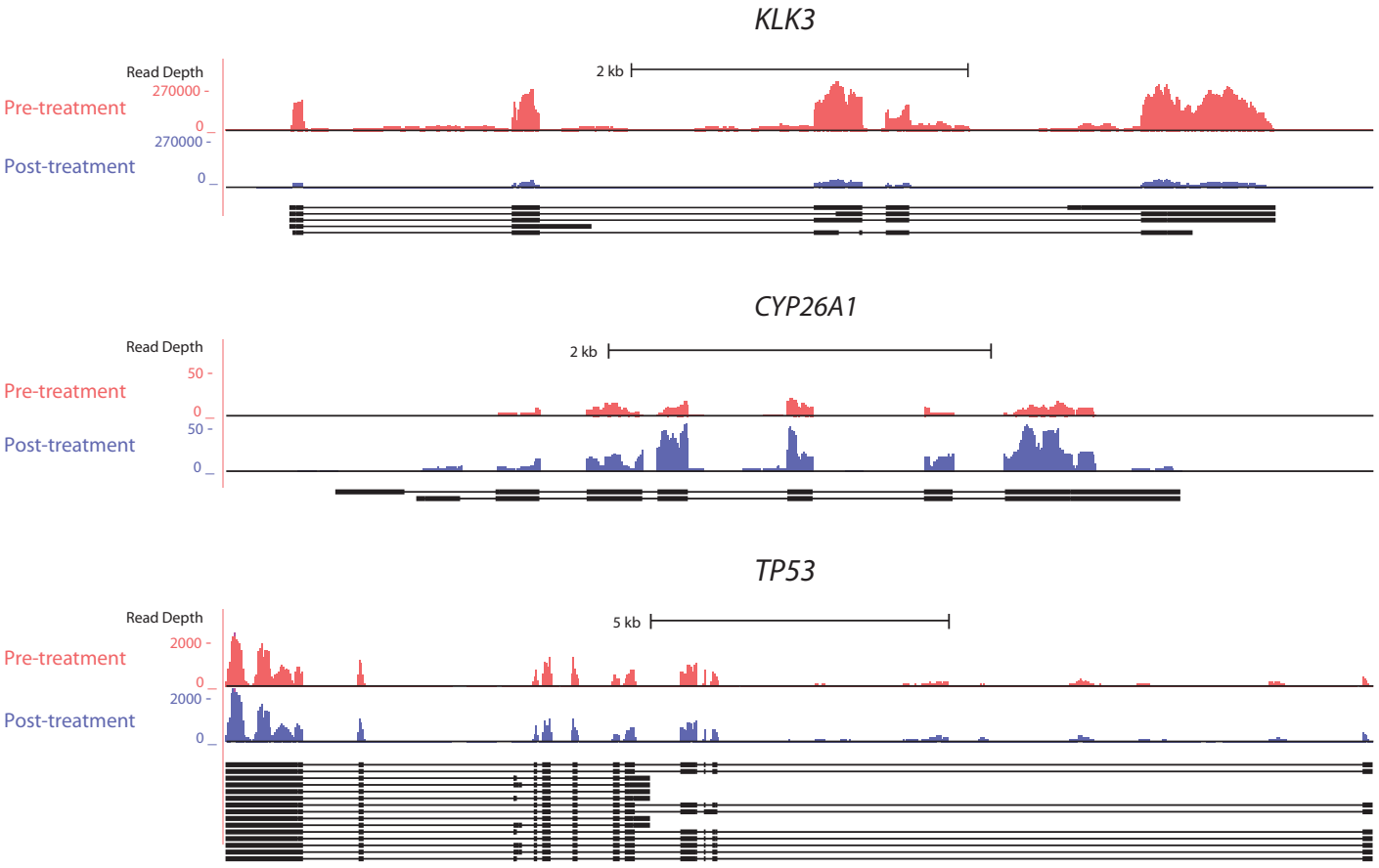
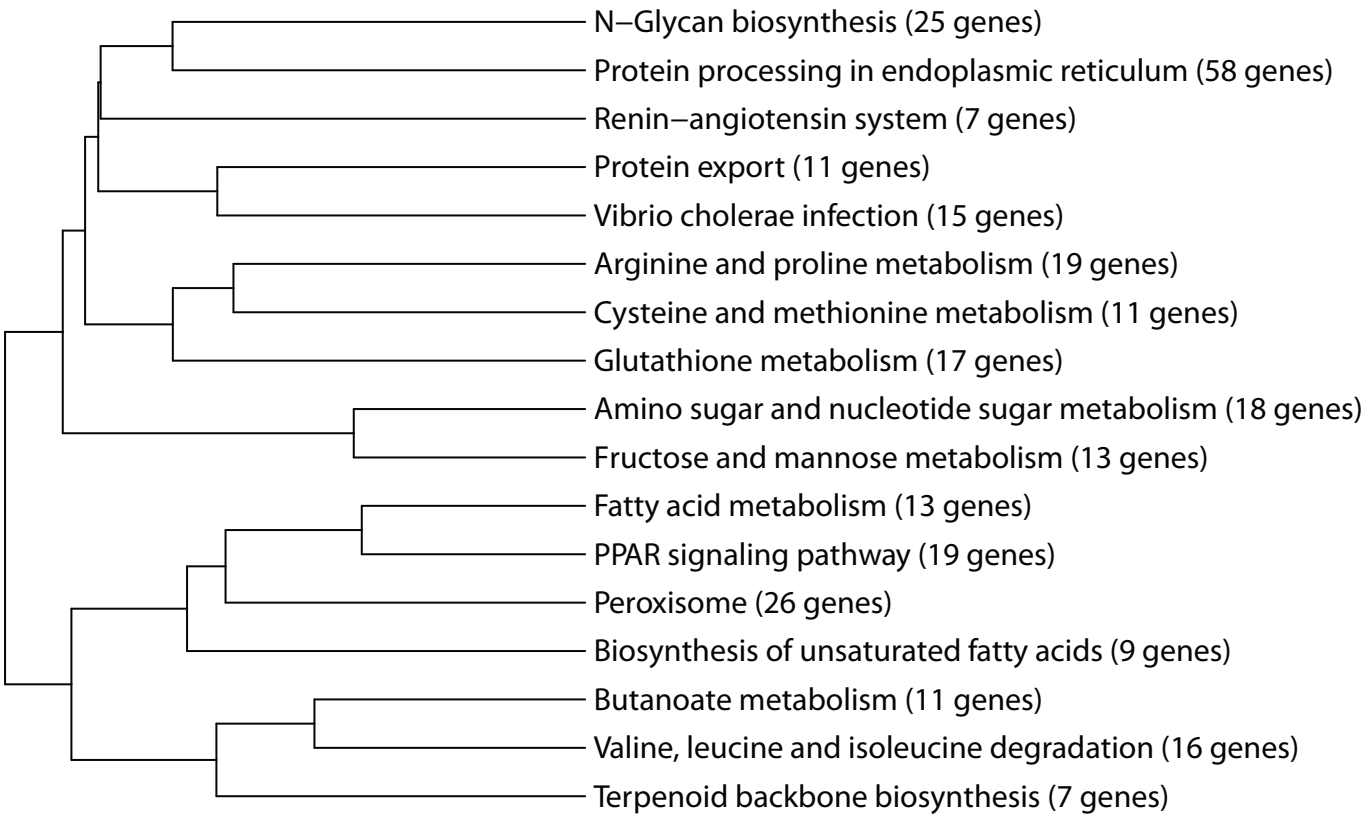
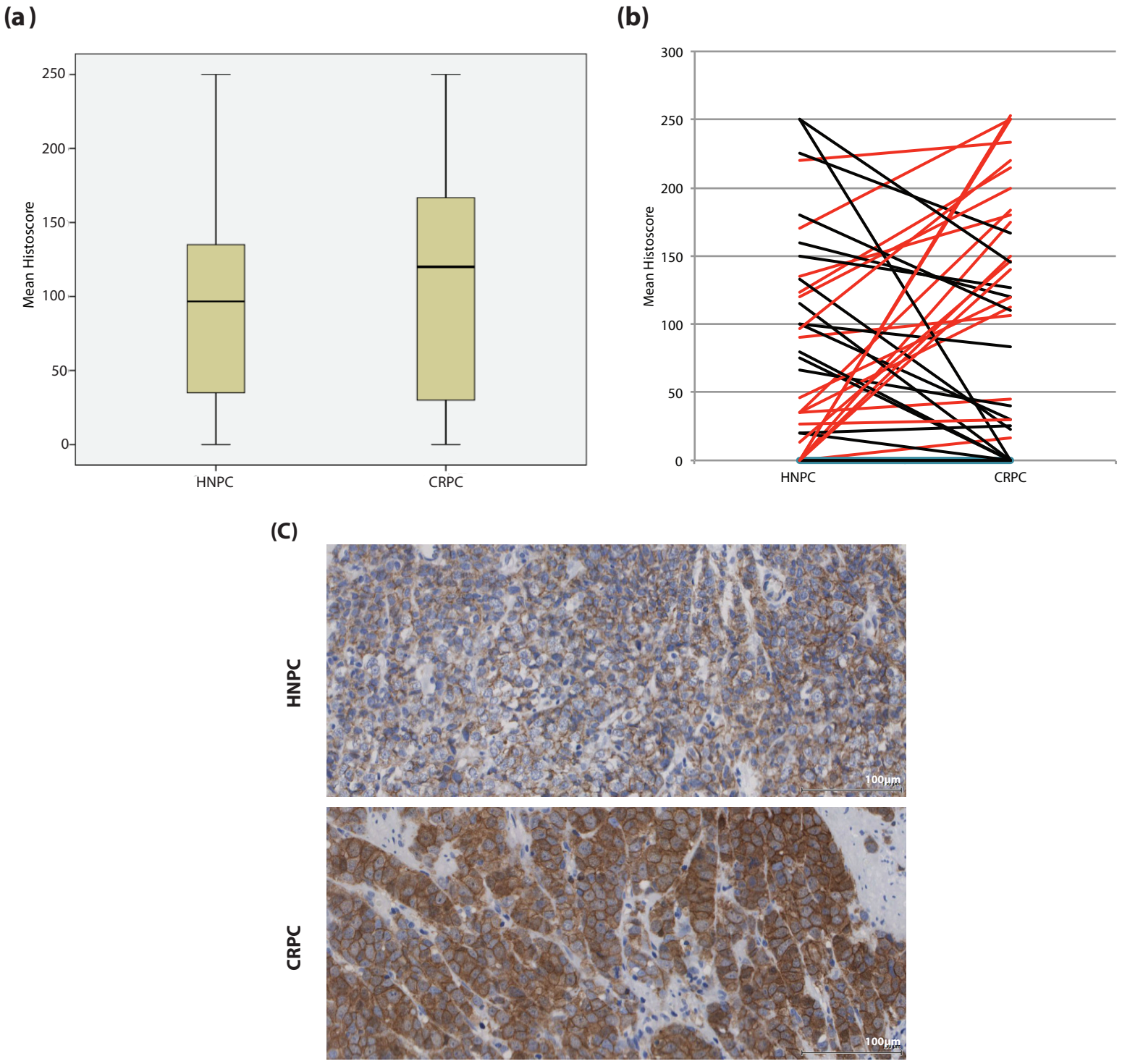
(a)



(b)



Supplemental Figure 1



Supplemental Figure 2

Supplemental Fig. 1 – Clustering of overlapping Kyoto Encyclopaedia of Genes and Genomes (KEGG) pathways. (a) Examples of upregulated (*CYP26A1*) and downregulated (*KLK3*) genes along with an example of a gene for which there is no evidence of a change following androgen-deprivation therapy (*TP53*). *KLK3* was, on average, downregulated 5.9-fold. Tracks show aggregate coverage over the length of each gene in the pre- and post-treatment conditions. Transcript structure is show below the gene. Images from the UCSC Genome Browser (http://genome.ucsc.edu), human reference genome hg19. (b) Hierarchical clustering of KEGG pathways enriched in downregulated gene sets. Dendrograms show clustering of KEGG terms based on the number of differentially expressed genes two pathways have in common as a proportion of the total number of differentially regulated genes in the two pathways combined.

Supplemental Fig. 2 – Expression β-catenin protein in human prostate cancer (PCa). (a) Histoscore populations are graphically represented using a box and whisker plot, as these data are not normally distributed. Statistical analysis revealed overall no statistically significant difference in β-catenin protein expression between matched hormone-naïve PCa (HNPC) and castration-resistant PCa (CRPC) tumours ($p = 0.327$), but there was a cohort of 16 tumours (b) that demonstrated upregulation of expression (shown as red lines) as compared with downregulation or no change (shown as black lines). Representative images from β-catenin immunostaining (c) are shown for the same patient at the time of diagnosis and prior to androgen-deprivation therapy (HNPC) and following progression (CRPC).