**Figure 1. Human metastatic melanoma cell lines express higher levels of CHD7 protein compared to vertical growth phase melanoma cells and melanocytes.**

(A)   Western blot comparing CHD7 levels (330 kDa) in two invasive (A375 and WM1552) and vertical growth phase (WM115) human melanoma cell lines and melanocytes.

(B)   Immunostaining for CHD7 in A375 (upper panel) and WM115 (lower panel) human melanoma cell lines. Nuclei were counterstained with DAPI. Scale bar: 25 um.
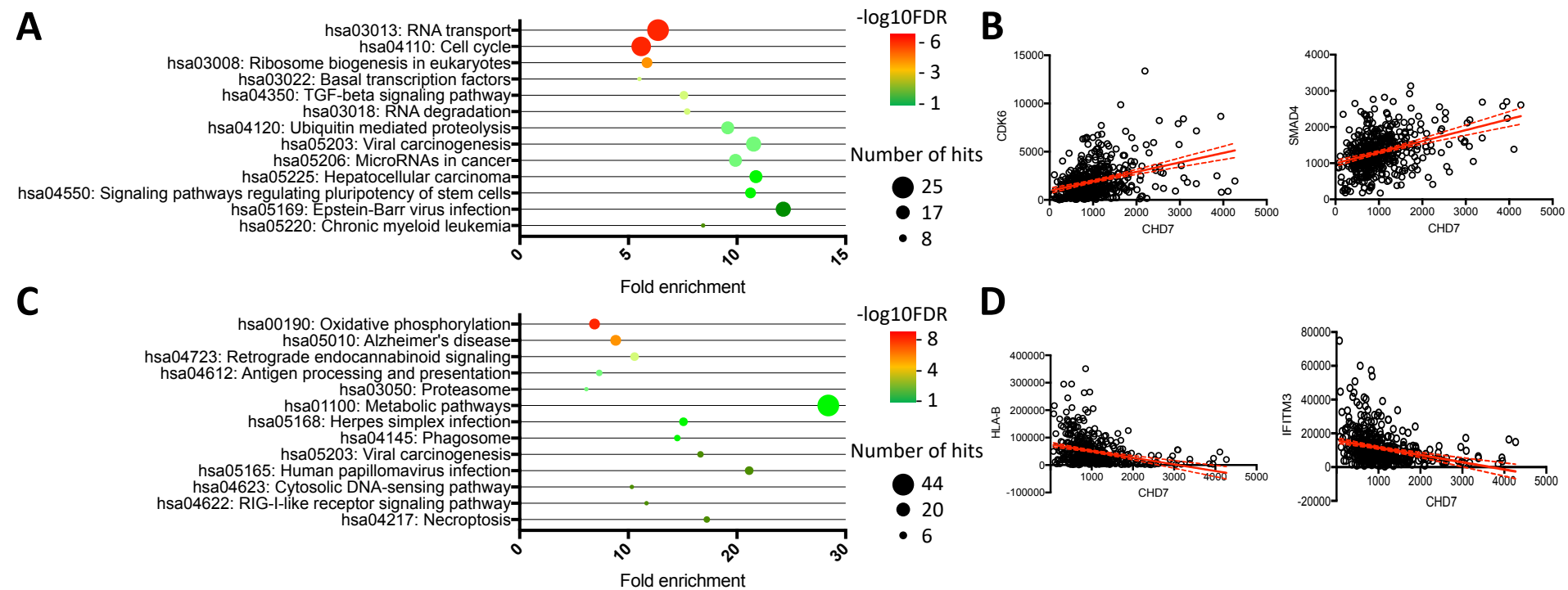
Figure 2. CHD7 expression positively correlates with genes associated to proliferative and invasive phenotype, while negatively correlates with immune-related genes.

(A) STRING functional enrichment analysis computed on genes which have been shown to positively correlates with CHD7 (Spearman r > 0.3; TCGA dataset, n = 472). Dot plot of the significant over-represented KEGG pathways (FDR < 0.05); the dot size is proportional to the number of genes associated with the pathway and the dot color gradients indicated the significance of the enrichment (-log10FDR).

(B) Scatter plots of rappresentative genes (normalized counts) with Spearman r > 0.3 from significantly enriched pathways. Linear fit with 95% CI is also reported in red.

(C) STRING functional enrichment analysis computed on genes which have been shown to positively correlates with CHD7 (Spearman r < -0.3; TCGA dataset, n = 472). Dot plot of the significant over-represented KEGG pathways (FDR < 0.05); the dot size is proportional to the number of genes associated with the pathway and the dot color gradients indicated the significance of the enrichment (-log10FDR).

(D) Scatter plots of rappresentative genes (normalized counts) with Spearman r < -0.3 from significantly enriched pathways. Linear fit with 95% CI is also reported in red.