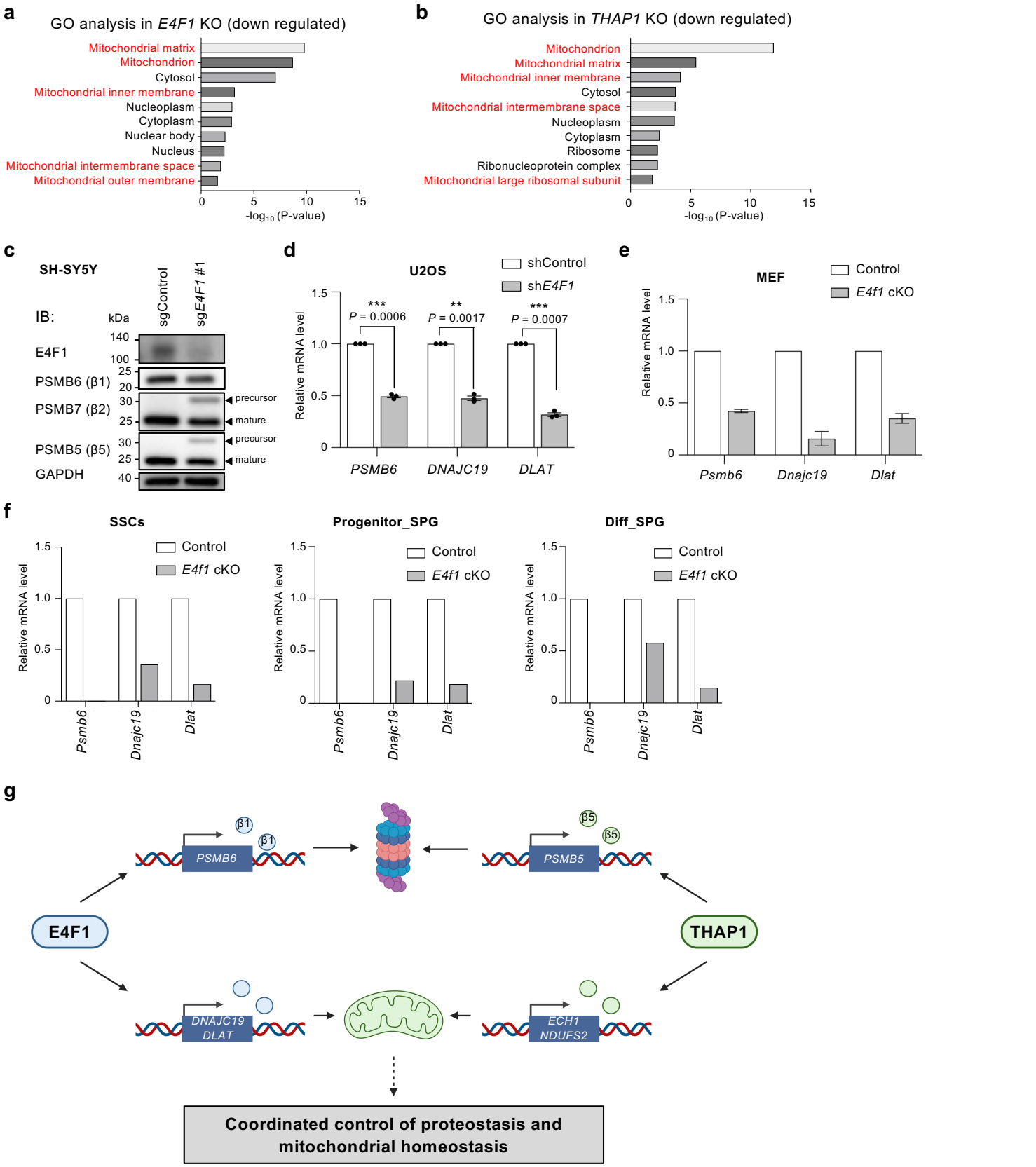

Supplementary Fig. 6. E4F1-dependent transcriptional regulation of *PSMB6* and mitochondrial genes is conserved across cell types

a Full Gene Ontology cellular component analysis of genes downregulated in *E4F1*-knockout HEK293T cells (fold change < 0.7 and $P < 0.005$). **b** Full Gene Ontology cellular component analysis of genes downregulated in *THAP1*-knockout HEK293T cells (fold change < 0.7 and $P < 0.005$). **c** Immunoblot analysis of SH-SY5Y cells transduced with the indicated sgRNAs using antibodies against the indicated proteins. **d** Expression levels of *PSMB6*, *DNAJC19*, and *DLAT* in control and *E4F1*-knockout U2OS cells from a previously published RNA-seq dataset. **e** Expression levels of *Psmb6*, *Dnajc19*, and *Dlat* in control ($E4f1^{+/flox;\ Cre\text{-}infected}$) and *E4f1* knockout ($E4f1^{-/flox;\ Cre\text{-}infected}$) MEFs from a previously published microarray dataset. **f** Expression levels of *Psmb6*, *Dnajc19*, and *Dlat* in control ($E4f1^{+/flox;\ Vasa\text{-}Cre}$) and *E4f1* knockout ($E4f1^{flox/flox;Vasa\text{-}Cre}$) spermatogonia from a previously published RNA-seq dataset. **g** Proposed model illustrating that distinct transcription factors independently regulate specific proteasome catalytic subunits together with non-overlapping mitochondrial gene programs. E4F1 and THAP1 selectively regulate *PSMB6* and *PSMB5*, respectively, together with distinct mitochondrial gene programs, supporting a modular transcriptional organization linking proteasome biogenesis with mitochondrial gene expression. All experiments were performed at least three biologically independent times with similar results. Source data are provided as a Source Data file.