Supplementary Figure 8. Transcription dependency of melanoma on MITF or MYC sensitizes toward TFIIH-CAK inhibition. 

**a.** Expression analysis of PMEL, MLANA and TYRP1 transcripts in 501 mel cells under retrovirus-driven c-MYC expression compared to empty vector (EV) and subsequent siSCR or siMITF1 RNA transfection. Relative expression was measured by qRT-PCR, normalized to GAPDH.
and given as mean ±SD from technical triplicates. b. Regression analysis of MITF and c-MYC transcript levels in genetically heterogeneous human melanoma cell lines. Relative expression was measured by qRT-PCR and normalized to GAPDH. c. Regression analysis of MITF and c-MYC protein levels in analogy to (b). Right panel: Immunoblot analysis of whole cell lysates showing MITF and c-MYC protein in primary neonatal human epidermal melanocytes (NHEM), immortalized human melanocytes (IHM), and various human melanoma cell lines analyzed analogous to (b). Actin used as loading control. d. Immunoblot analysis of whole cell lysates from n=18 human metastatic malignant melanomas exhibiting MITF and c-MYC protein expression. The asterisk (*) indicates tumors with low MITF/c-MYC expression ratio. Sample 187 was not quantifiable. e. Expression analysis of MITF and FUBP isoforms 1 and 3, which do not contain E box sequences in regulatory regions in contrast to FUBP2 (Fig 6G), upon MITF-directed RNAi using siMITF1 in 501 mel cells. Relative expression was measured by qRT-PCR, normalized to GAPDH and given as mean ±SD from technical triplicates. f. WST-1 based cell cytotoxicity assay under treatment with BET bromodomain inhibitor JQ1 for 48 hrs of a diverse set of melanoma cell lines compared to NCI-H69 lung carcinoma cell line as positive JQ1 sensitive control. g. WST-1-based cell cytotoxicity assay of a panel of genetically heterogeneous melanoma lines after treatment with covalent CDK7 inhibitor THZ1 for 48 hrs. Immortalized human melanocytes (IHM) and U87MG glioblastoma cells as THZ1-resistant controls. h. WST-1 based cell cytotoxicity assay of a panel of genetically heterogeneous melanoma lines after treatment with covalent CDK7 inhibitor THZ1 for 72 hrs. (f), (g) and (h); Graphs represent percentage cell viability relative to DMSO control. Data represent mean ±SD from technical triplicates.