Evaluating the influence of a G-quadruplex prone sequence on the transactivation potential by wild-type and/or mutant P53 family proteins through a yeast-based functional assay.

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Supplementary Figure S1. Relative activity of mutant P53 and P63 proteins. Comparison of wild-type TAP53 (full-length P53) or Δ NP63 (Δ NP63 α) variant activity with respect to the corresponding mutant protein (TAP53: R175H and R282W; Δ NP63 α : G134V and R204W) in yLFM-PUMA, yLFM-KSHV-PUMA, and yLFM-PUMA-KSHV strains. WT, wild-type. ns: not significant; ,* p < 0.05; ** p < 0.01; *** p < 0.001



Supplementary Figure S2. Fold change transactivation by co-expressed wild-type and mutant P53 proteins. Yeast cells co-expressing wild-type or wild-type and mutant TAP53 proteins were grown for 8 hours in Galactose 1% to evaluate the transactivation ability. **(A)** Evaluation of transcriptional activity from wild-type (i.e., constitutive pADH1-wild-type TAP53 + inducible pGal1,10-wild-type TAP53) or wild-type and mutant P53 (i.e., constitutive pADH1-wild-type TAP53 + inducible pGal1,10 TAP53 R175H or R282W) co-expression as fold change over empty vectors in presence of the p53 RE from the *PUMA* target gene (yLFM-PUMA) or a G4 prone sequence (yLFM-KSHV). **(B)** Evaluation of transcriptional activity as in panel A in presence of a G4 prone sequence upstream (yLFM-KSHV-PUMA) or downstream (yLFM-PUMA-KSHV) of the p53 RE from the *PUMA* target gene. WT, wild-type.



Supplementary Figure S3. Fold change transactivation by co-expressed wild-type and mutant P63 proteins. Yeast cells co-expressing wild-type or wild-type and mutant Δ NP63 proteins were grown for 8 hours in Galactose 1% to evaluate the transactivation ability. (A) Evaluation of transcriptional activity from wild-type (i.e., constitutive pADH1-wild-type Δ NP63 + inducible pGal1,10-wild-type Δ NP63) or wild-type and mutant P63 (i.e., constitutive pADH1-wild-type Δ NP63 + inducible pGal1,10 Δ NP63 G134V or R204W) co-expression as fold change over empty vectors in presence of the p53 RE from the *PUMA* target gene (yLFM-PUMA) or a G4 prone sequence (yLFM-KSHV). (B) Evaluation of transcriptional activity as in panel A in presence of a G4 prone sequence upstream (yLFM-KSHV-PUMA) or downstream (yLFM-PUMA-KSHV) of the p53 RE from the *PUMA* target gene. WT, wild-type