

Supplemental Figure Legends

Figure S1. Annexin V-7AAD apoptosis assay by flow cytometry. A) Untreated cells were collected before treatment with Nutlin-3. “24h” and “48h” were collected, respectively, at 24 and 48 hours after treatment. Upper left quadrant, necrotic cells (Q1, annexin V^{low} and 7-AAD^{high}); upper right quadrant, dead cells (Q2, annexin V^{high} and 7-AAD^{high}); lower left quadrant, viable cells (Q3, annexin V^{low} and 7-AAD^{low}); lower right quadrant, early apoptotic cells (Q4, annexin V^{high} and 7-AAD^{low}). B) Western blot of samples representing a dilution series of RAJI cells, expressing TP53 in basal conditions, mixed with EHEB cells, not expressing TP53 in basal conditions, with the proportion of 0%, 5%, 10%, 20%, 50% and 100% of RAJI cells.

Figure S2. Western blot for CLL cases of the training cohort. Figure shows results from western blot assay of the 100 CLL cases of the training cohort subdivided in cases with a normal pattern (63 cases), cases with an intermediate pattern (19 cases) and cases with a mutant pattern (19 cases). The TP53 genotype is indicated: TP53 wild type (wt/wt), TP53 deleted only (del/wt), TP53 mutated only (mut/wt), TP53 deleted/mutated (del/mut). The TP53 antibody detect a major band of 53 kDa and, in some cases (e.g. T23, T27, T34, T36, T38, T90), a minor band of 48 kDa. This second band may correspond to the alternatively spliced form, TP53 β , described by Bourdon *et al* (2005). For cases showing a TP53 truncated form (e.g. T33, T69), the relative molecular weight is reported aside.

Figure S3. Lack of the gene expression signature associated with Nutlin-3 treatment in TP53^{del/t} CLL samples. A) Heat-map generated with 144 genes found to be differentially expressed by supervised analysis between Nutlin-3 treated (red bar under the tree) samples versus the respective untreated (blue bar under the tree) counterparts, of TP53^{wt/wt} CLL cases (13 cases), according to Zauli *et al* (2009) [1]. This signature was not shared by TP53^{del/mut} CLL cases (7 cases), as indicated by the heat-map that was not able to split the treated (yellow bar under the tree) from the untreated (cyan blue bar under the tree) counterparts of TP53^{del/mut} CLL cases. The colour scale identifies relative gene expression changes normalized by the standard deviation of 1 with 0 representing the mean expression level of a given gene.

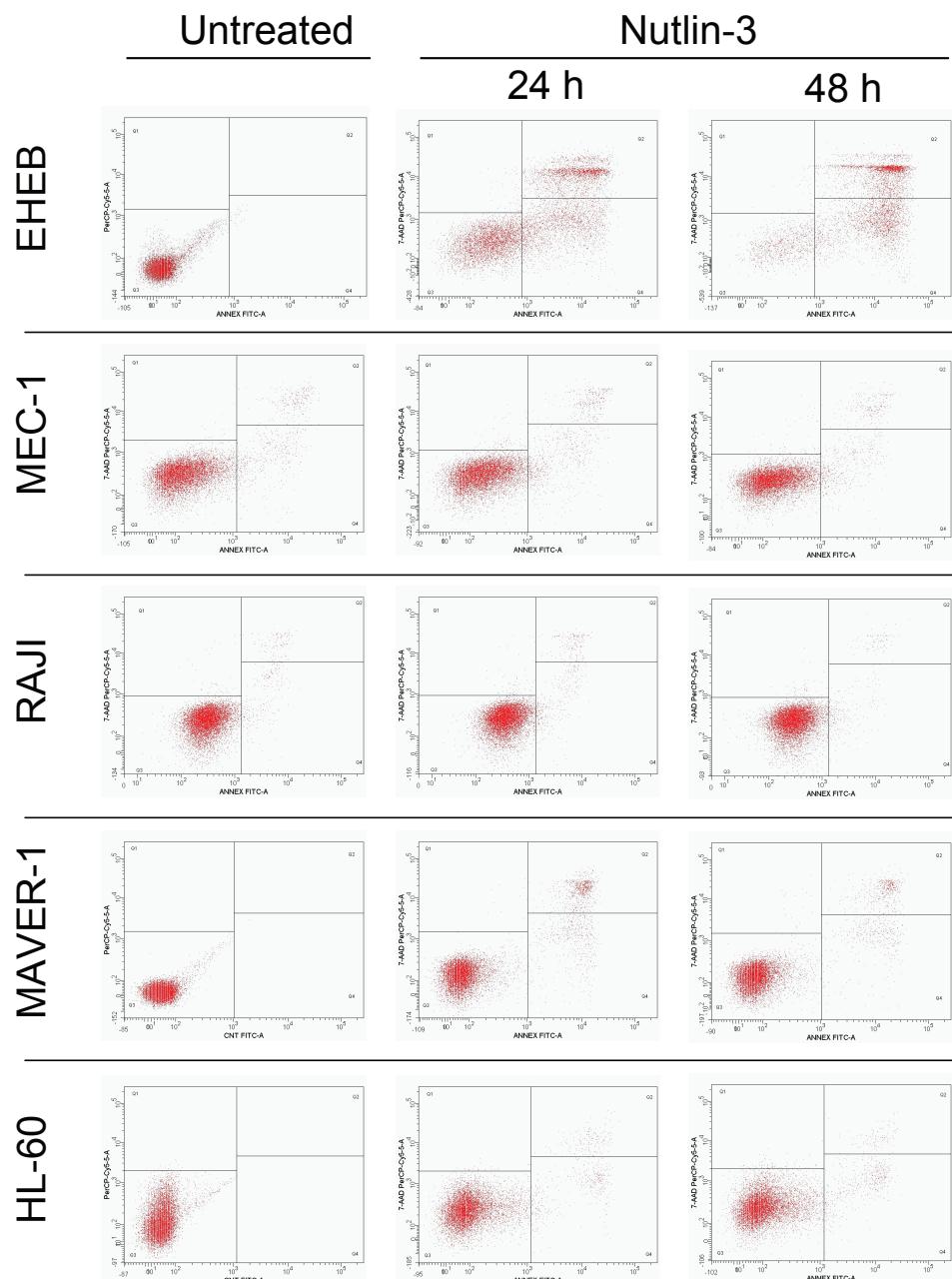
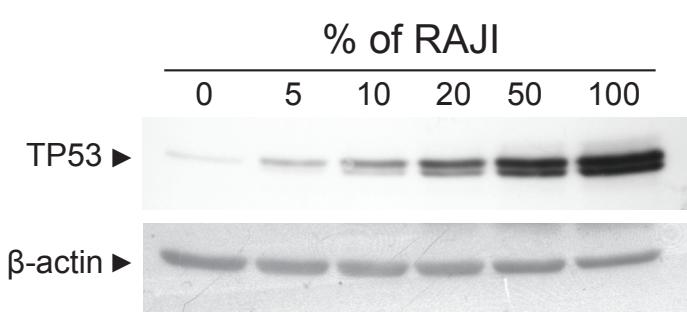
Figure S4. Western blot/qRT PCR assay for CLL cases of the validation cohort A)Figure shows results from western blot assay of the 40 CLL cases of the validation cohort. The TP53 genotype is indicated: TP53 wild type (wt/wt), TP53 deleted only (del/wt), TP53 mutated only (mut/wt), TP53 deleted/mutated (del/mut). The TP53 antibody detect a major band of 53 kDa and, in some cases (e.g. V6, V11, V20, V26, V29), a minor band of 48 kDa. This second band may correspond to the alternatively spliced form, TP53 β , described by Bourdon *et al* (2005) [2]. For cases showing a TP53 truncated form (e.g. V12, V13, V20, V28, V36), the relative molecular weight is reported aside. B) Histograms show data, obtained by qRT-PCR amplification, of CDKN1A fold increase expression for each CLL case of the validation cohort.

Figure S5. Comparison with alternative TP53 functional assays using combinatorial strategies with etoposide. A) Figure shows results from western blot/qRT PCR assay for the evaluation of TP53 and CDKN1A expression on the 4 cell lines EHEB, MEC-1, RAJI and HL60 at basal level or upon the alternative treatments with etoposide, etoposide plus Nutlin-3 or Nutlin-3. B) Figure shows results from western blot/qRT PCR assay for the evaluation of TP53 and CDKN1A expression on the comparison series of 10 CLL cases composed by 4 11q deleted (11q-)/TP53^{wt/wt}, 1 TP53^{del/mut}, 2 TP53^{mut/wt} and 3 TP53^{wt/wt} cases at basal level or upon the alternative treatments with etoposide, etoposide plus Nutlin-3 or Nutlin-3.

Figure S6. Comparison with evaluation of TP53 and CDKN1A protein expression levels by FACS analysis. A) Histograms show results from FACS assay for the evaluation of TP53 and CDKN1A protein expression on the 4 cell lines EHEB, MEC-1, RAJI and HL60 at basal level or upon Nutlin-3 treatment. B) Histograms show results from FACS assay for the evaluation of TP53 and CDKN1A protein expression on the comparison series of 10 CLL cases composed by 4 11q deleted (11q-)/TP53^{wt/wt}, 1 TP53^{del/mut}, 2 TP53^{mut/wt} and 3 TP53^{wt/wt} cases.

Reference

- 1 Zauli G, di Iasio MG, Secchiero P, Dal Bo M, Marconi D, Bomben R, Del Poeta G, Gattei V: **Exposure of B cell chronic lymphocytic leukemia (B-CLL) cells to nutlin-3 induces a characteristic gene expression profile, which correlates with nutlin-3-mediated cytotoxicity.** *Curr.Cancer Drug Targets.* 2009, **9**:510-518.
- 2 Bourdon JC, Fernandes K, Murray-Zmijewski F, Liu G, Diot A, Xirodimas DP, Saville MK, Lane DP: **p53 isoforms can regulate p53 transcriptional activity.** *Genes Dev.* 2005, **19**:2122-2137.

A**B****Figure S1**

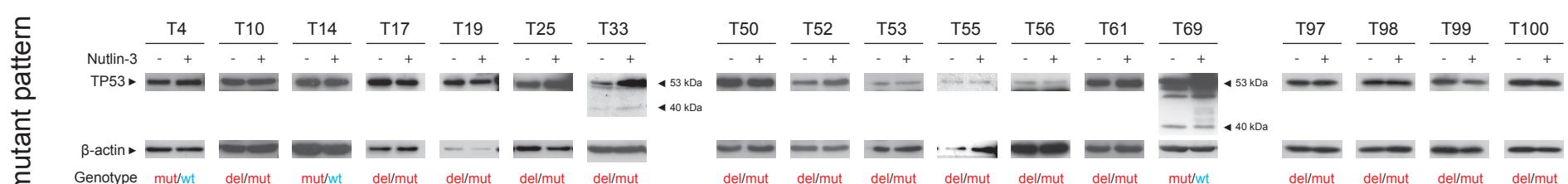
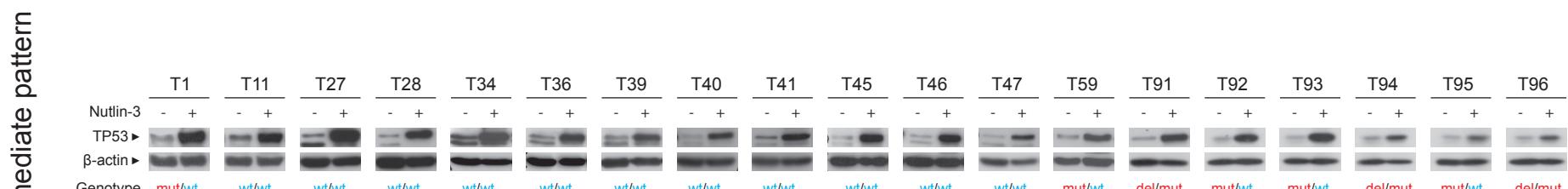
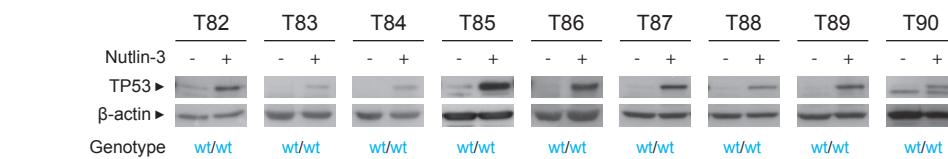
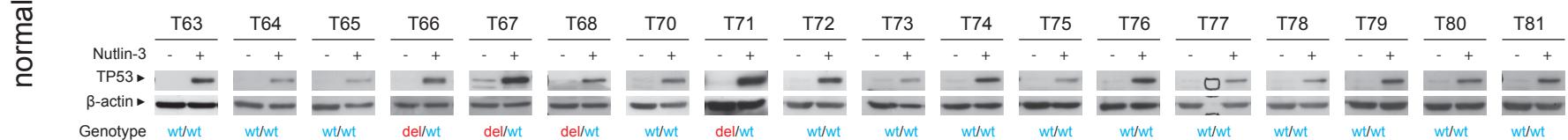
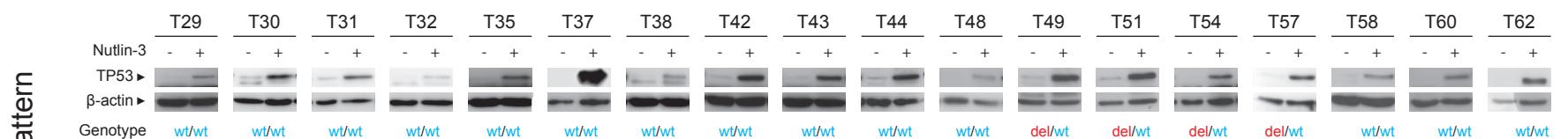
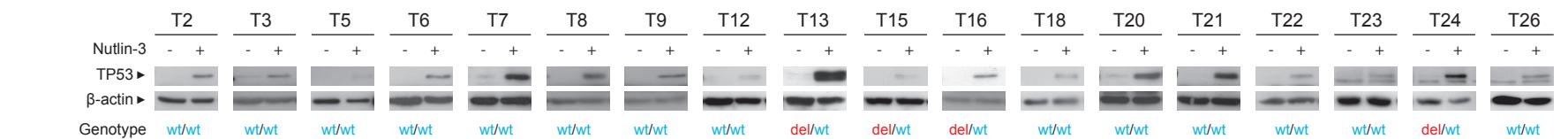


Figure S2

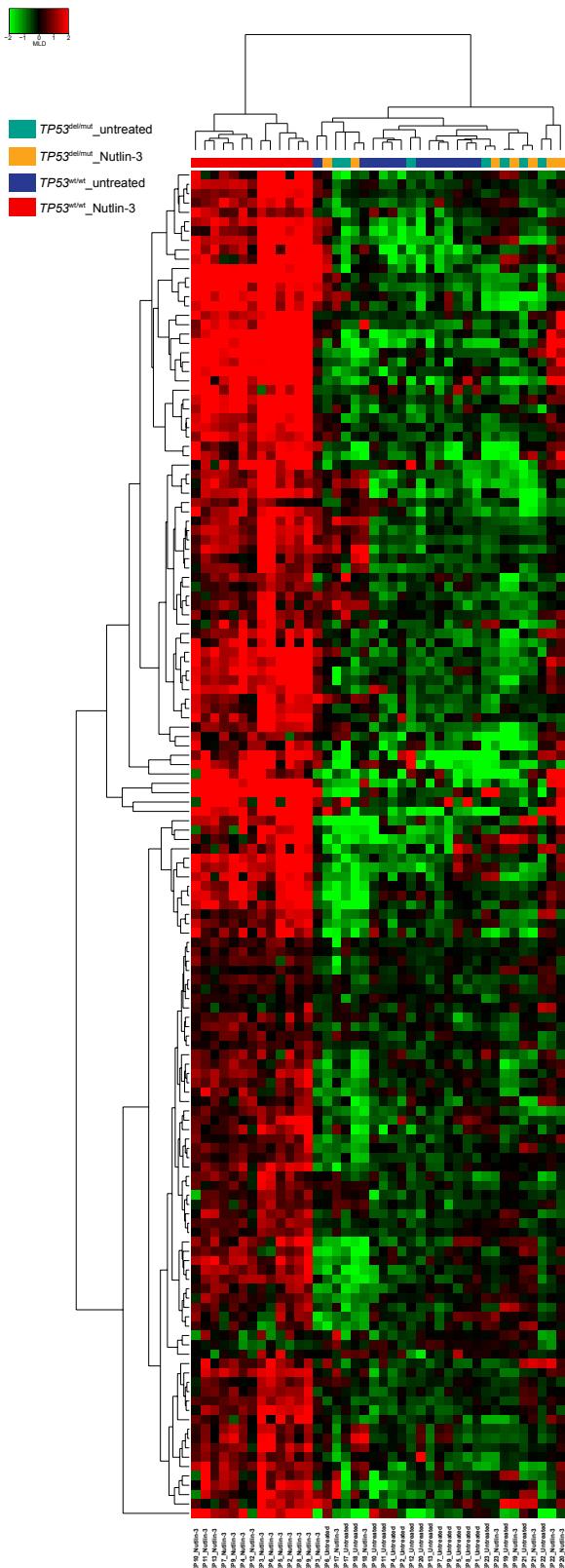
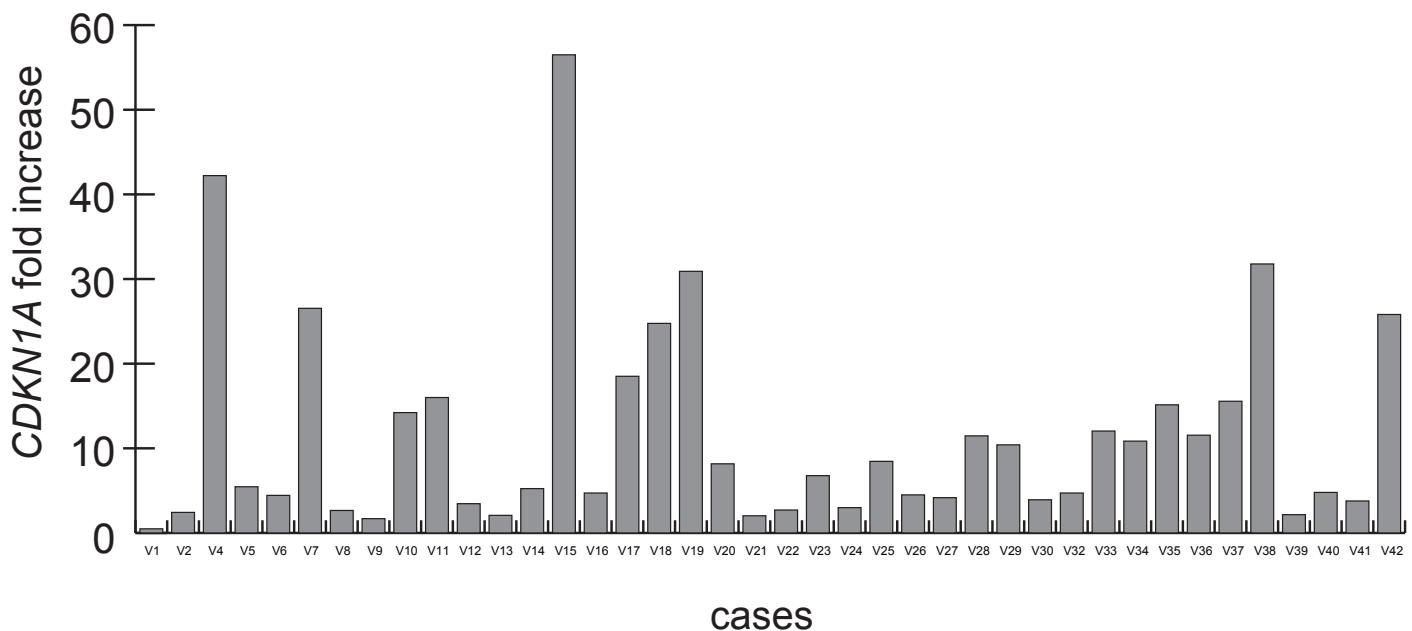
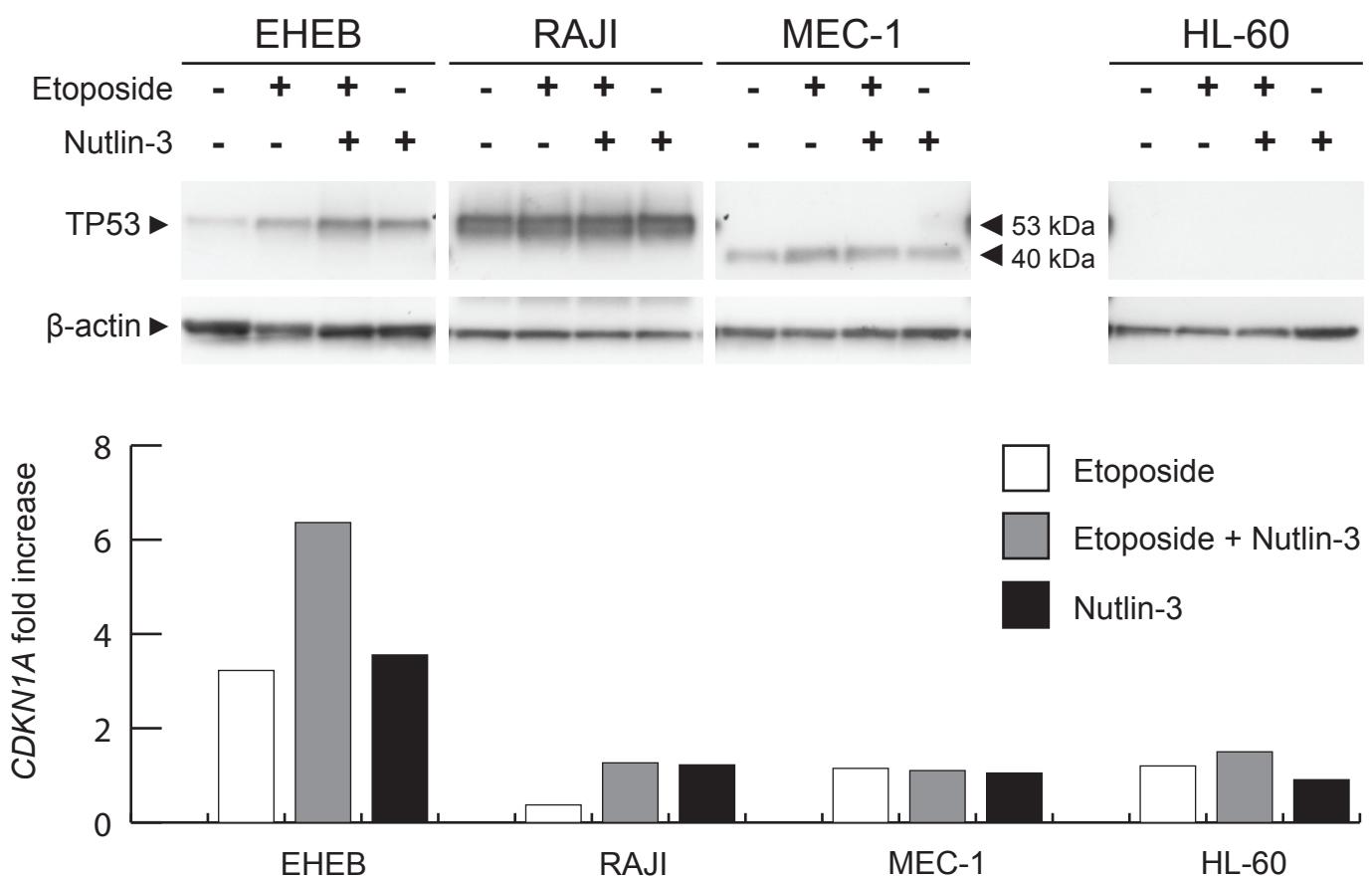
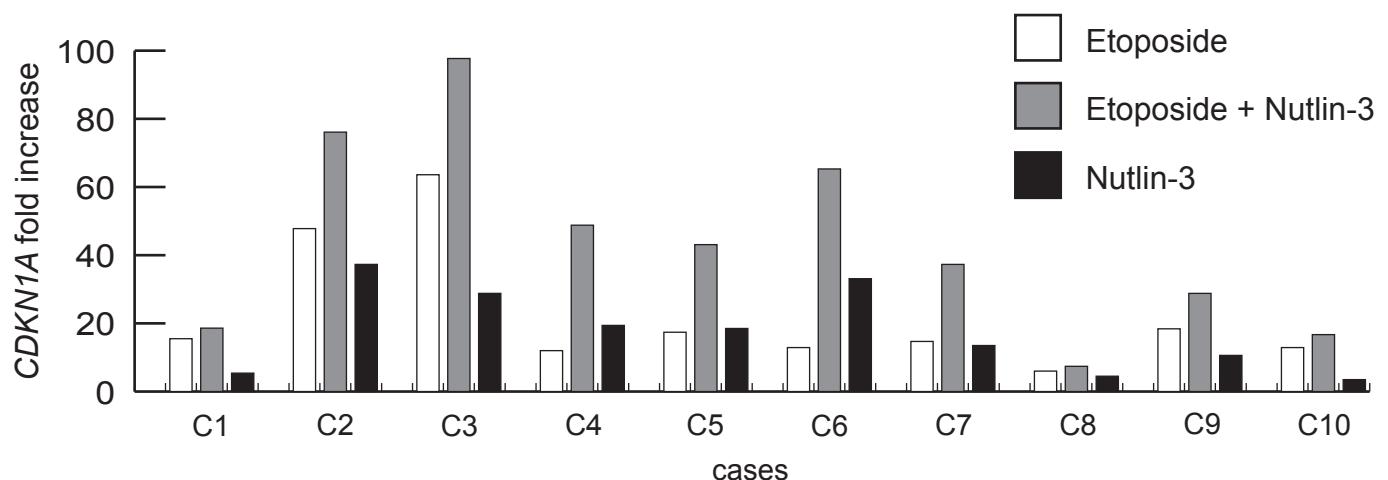
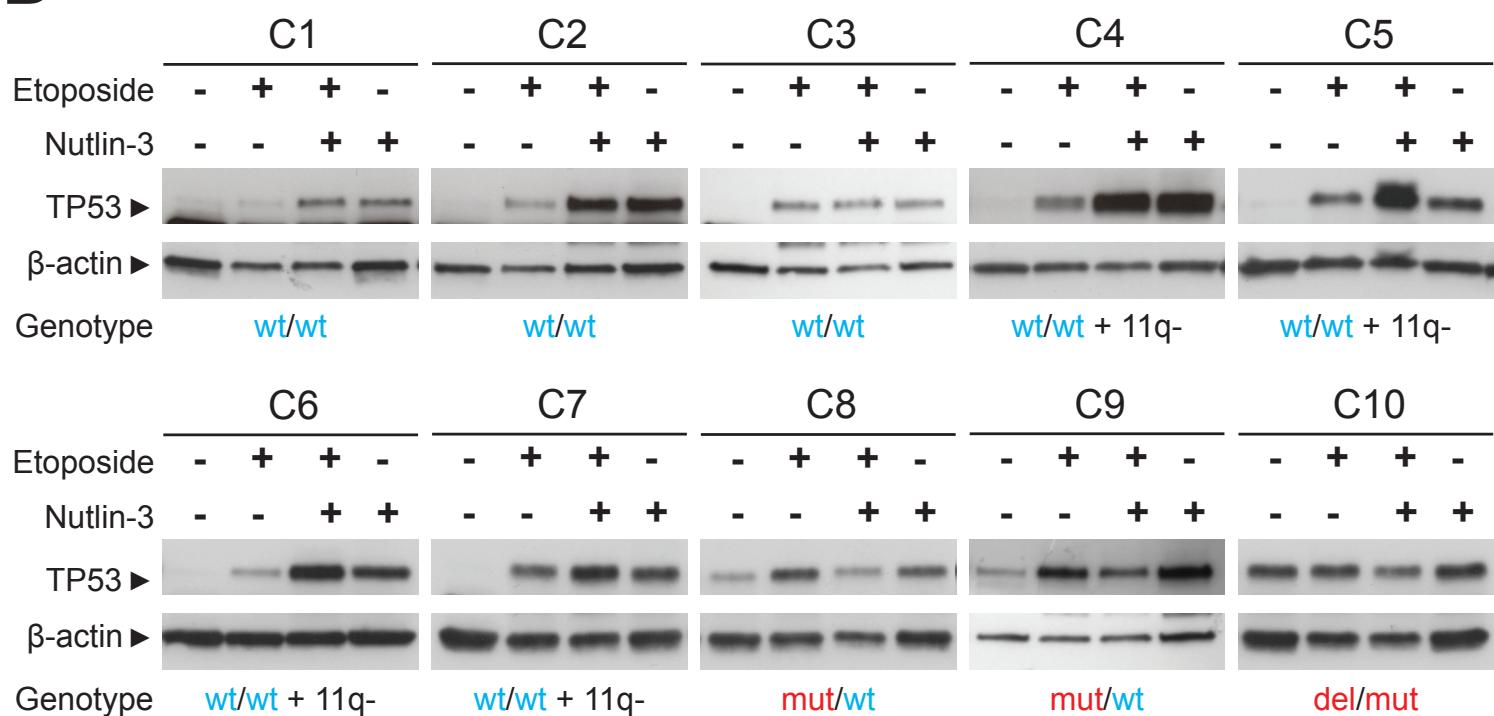
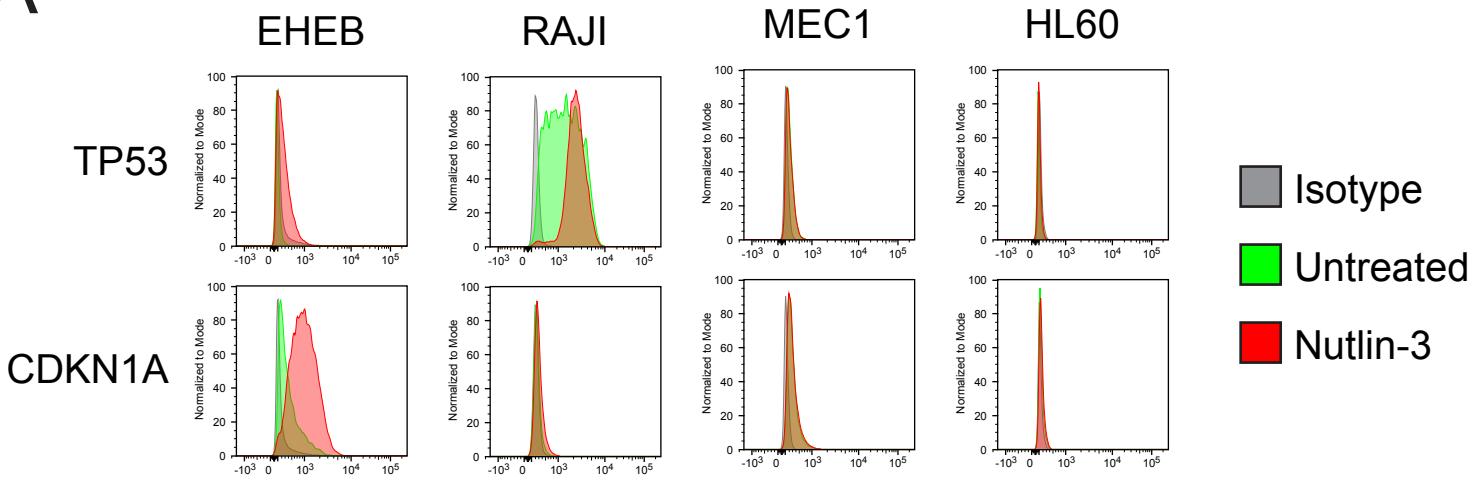
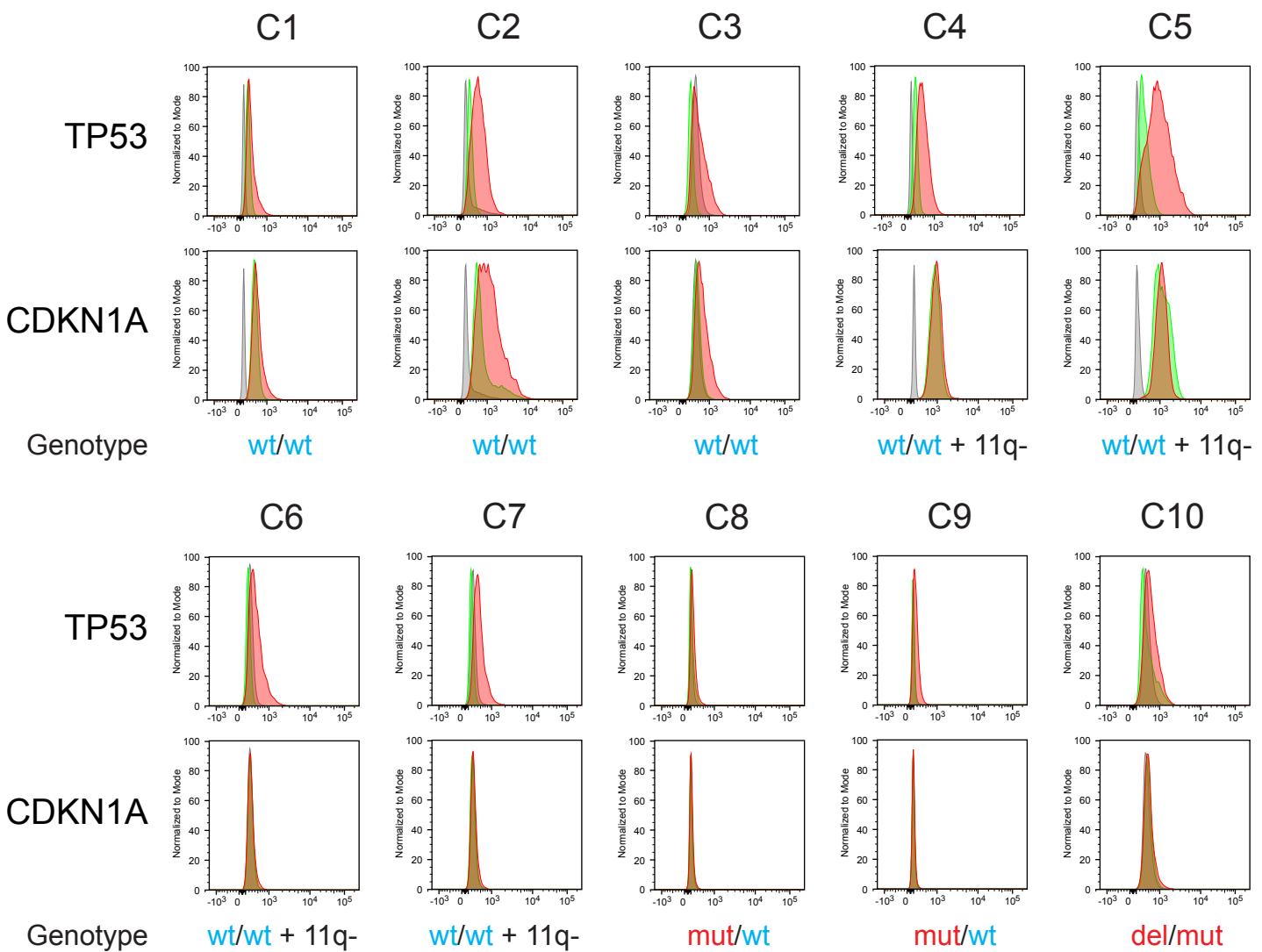


Figure S3

A**B****Figure S4**

A**B****Figure S5**

A**B****Figure S6**