

**Supplemental Figure 1. Reduced DACH1 mRNA in NSCLC.** Relative abundance of DACH1 mRNA in human lung cancer derived from Oncomine. The data bases of distinct groups comparing normal lung and lung adenocarcinoma are shown for separate experimental patient groups as indicated in the Figure. Data are shown as log 2 median centered intensity.

**Supplemental Figure 2. DACH1 and p53 co-localized in a nuclear extranucleolar location.** (A) Immunohistochemical staining for DACH1 and p53 in H1299 and (B) HCT116 cells, shown at higher magnification than Fig. 2 A,C.

**Supplemental Figure 3.** Western blot analysis of H1299 cells treated with 5-Aza-2'-deoxycytidine (5MM) for 5 days and Trichostatin A (1MM, 8hrs). Antibodies are directed to DACH1 and GAPDH (SE shorter exposure, LE longer exposure)

**Supplemental Figure 4. EGFR and DACH1 expression in NSCLC vs. SCLC.** Expression profiles of DACH1, EGFR in NSCLC (N=251) and SCLC (N=38). (A) EGFR and DACH1 expression value differences from the corresponding sample means, (B) EGFR and DACH1 expression values divided by the sample means to obtain the fold change. (C) Expression value differences from the sample mean, divided by the sample mean to obtain the normalized expression values. Data are for ADC (adenocarcinoma), LCC, SCC and SCLC (small cell lung cancer). (D) The P value for the correlation coefficient for each tumor sub type is shown. (E). Survival probability comparing the EGFR.DACH1 in upper left quadrant of (A) compared with the other 3 quadrants, shows trend towards reduced survival. Low DACH1 and high EGFR predicted an approximately 1 year worse prognosis compared with other tumors.

**Supplemental Table 1. Genes binding both P53 and DACH1 in ChIP Seq.** Sets of genes binding p53 in IMR90 lung fibroblasts in ChIP Seq (36) were compared with genes binding DACH1, in ChIP Seq (36). A total of 743 binding sites for p53 and 1844 binding sites for DACH1 were identified. 112 genes bound by both DACH1 and p53 were identified ( $p < 1E^{-16}$ ).