**Supplementary:**

[**A**] Various exon 24 clones generated from heterogeneous populations of PTCH1 suppressed NEB1 cells show reduced PTCH1 and increased GLI1 mRNA expression. [**B**] Both human and mouse SMO protein sequences contain predicted nuclear and nucleolar localisation signals located within the C-terminal region, non-matching amino acids are highlighted in red. Site directed mutagenesis was employed to alter the N(o)LS by changing each amino acid to alanine for the mNLS construct, mNLS2 was used for Figures 2B and 2C. [**C**] NEB1-shCON cells and to a greater extent NEB1-shPTCH1 cells transfected with EGFP-SMO and EGFP-SMO-M2 show upregulation of GLI1 mRNA expression that is then reduced to below basal levels upon mutation of N(o)LS sequences, particularly mNLS2. qPCR analysis for GLI1 expression in [**D**] NEB1 and [**E**] N/Tert exon 3 and exon 24 shPTCH1 clones treated with both KAAD-Cyc and SANT-1 show all shPTCH1 clones are unresponsive to SMO pharmacological inhibitors. [**F**] qPCR on NEB1-shPTCH1 exon 3 clone and N/Tert-shPTCH1 cells to validate the results for cancer related genes obtained from the microarray analysis. [**G**] Immunofluorescence staining of NEB1 cells with three different SMO antibodies. [**Table 1**] List of differentially expressed zinc-finger protein genes. \*P≤0.05 and \*\*P≤0.01 (as calculated by Student’s *t* test), error bars represent standard deviation, n=6.