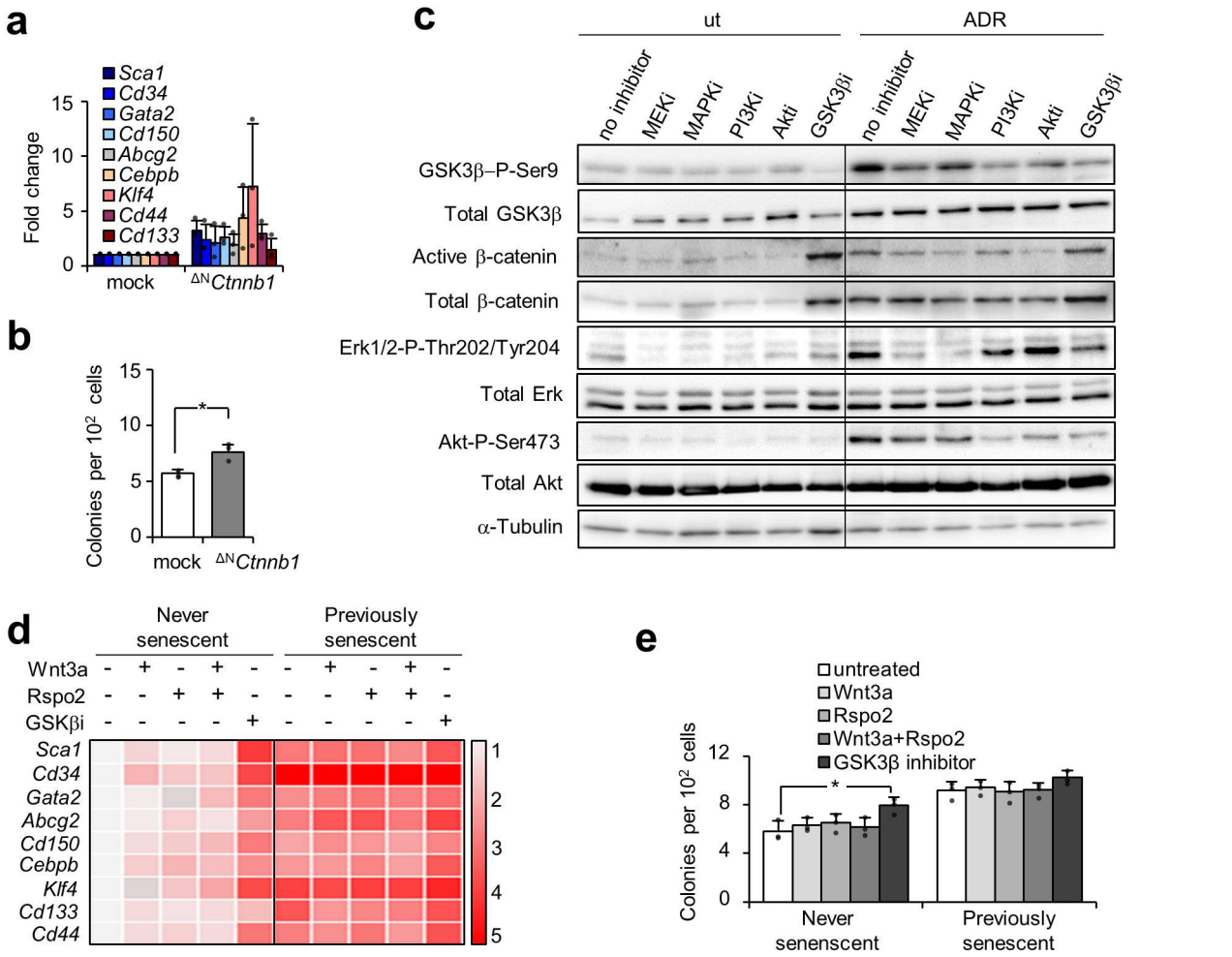

Extended Data Figure 6 | Cell-intrinsic activation of Wnt signalling cascade in TIS. a, **b**, Expression of indicated stem-cell-related transcripts by qPCR (**a**) and colony formation (**b**) in control;*Bcl2* lymphomas infected with a constitutively active Ctnnb1 mutant ($^{\Delta N}$Ctnnb1) or a mock retrovirus. Data represent mean expression fold change normalized to mock-infected cells and mean colony numbers, respectively ± s.d. ($n = 3$ biologically independent samples). Two-tailed, unpaired *t*-test with Welch's correction. $^{*}P < 0.05$. **c**, Immunoblot analysis of Ser9-phosphorylated (that is, inactivated) or total GSK3β, active or total β-catenin (as in Extended Data Fig. 5c), Thr202- and Tyr204-phosphorylated or total Erk1/2, and Ser473-phosphorylated or total Akt in control;*Bcl2* lymphoma cells treated with ADR for five days, together with pharmacological inhibitors targeting MAPK and PI3K kinase pathways. α-Tubulin was used as a loading control. One out of two independent experiments shown. For gel source data, see Supplementary Fig. 1. **d**, Expression of the indicated stem-cell-related transcripts by qPCR in never senescent and previously senescent *Suv39h1*$^{-}$;*Bcl2*;*Suv39h1*-ER^{T2} cells (passage 2) exposed to Wnt signalling agonists (Wnt3a, Rspo2, or GSK3β inhibitor) for two days. Colour scale represents mean fold change normalized to never senescent cells not exposed to Wnt agonists ± s.d. ($n = 3$ individual lymphomas). **e**, Colony formation of never senescent and previously senescent cells (as in **d**), after seven days in methylcellulose medium supplemented with the indicated Wnt agonists (mean colony numbers ± s.d., $n = 3$ individual lymphomas). Two-tailed, unpaired *t*-test with Welch's correction. $^{*}P < 0.05$.