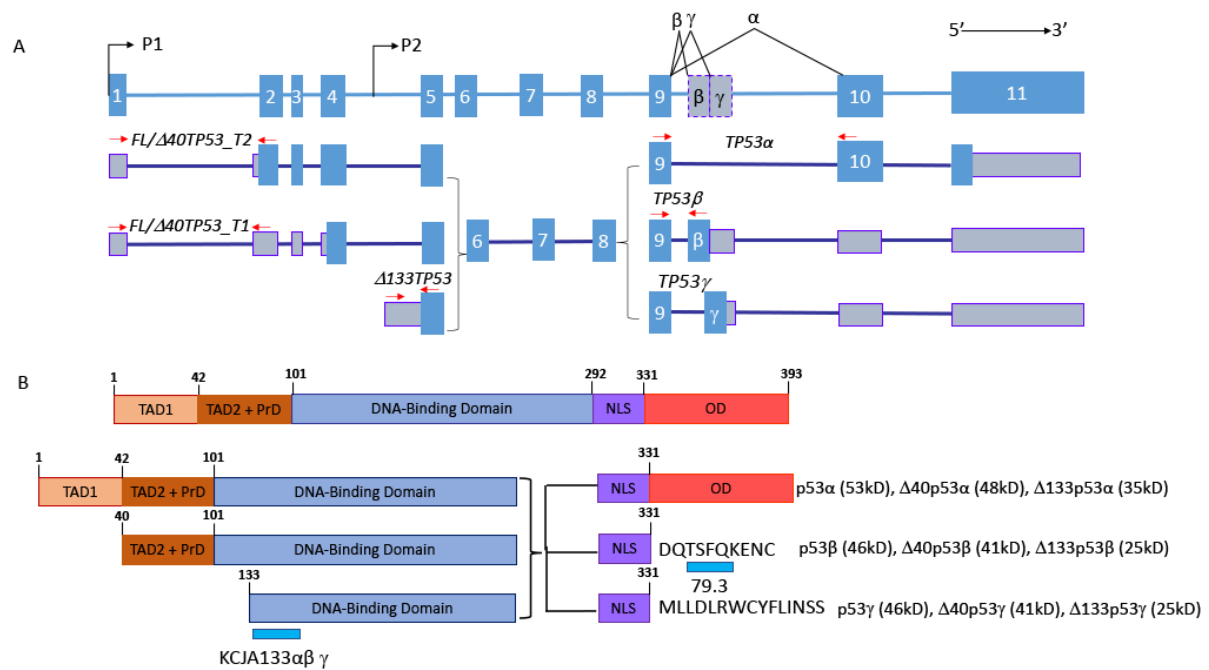
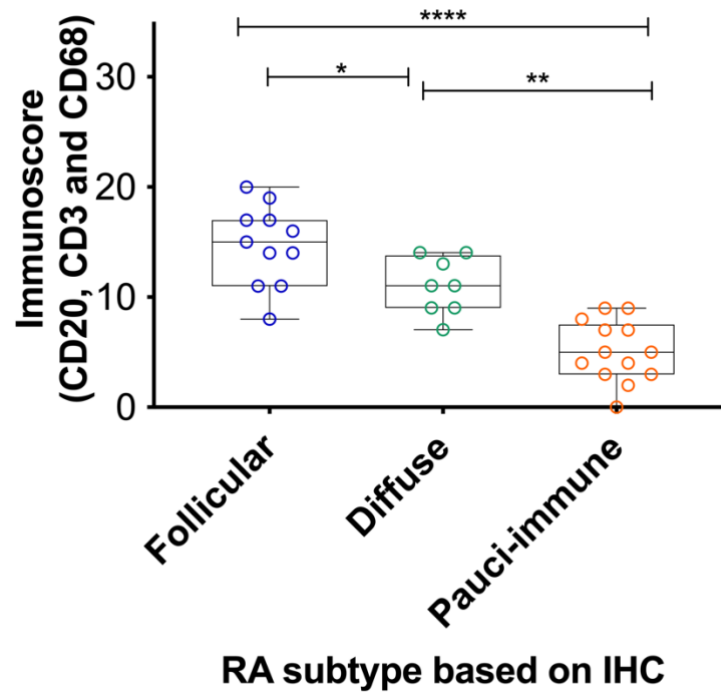


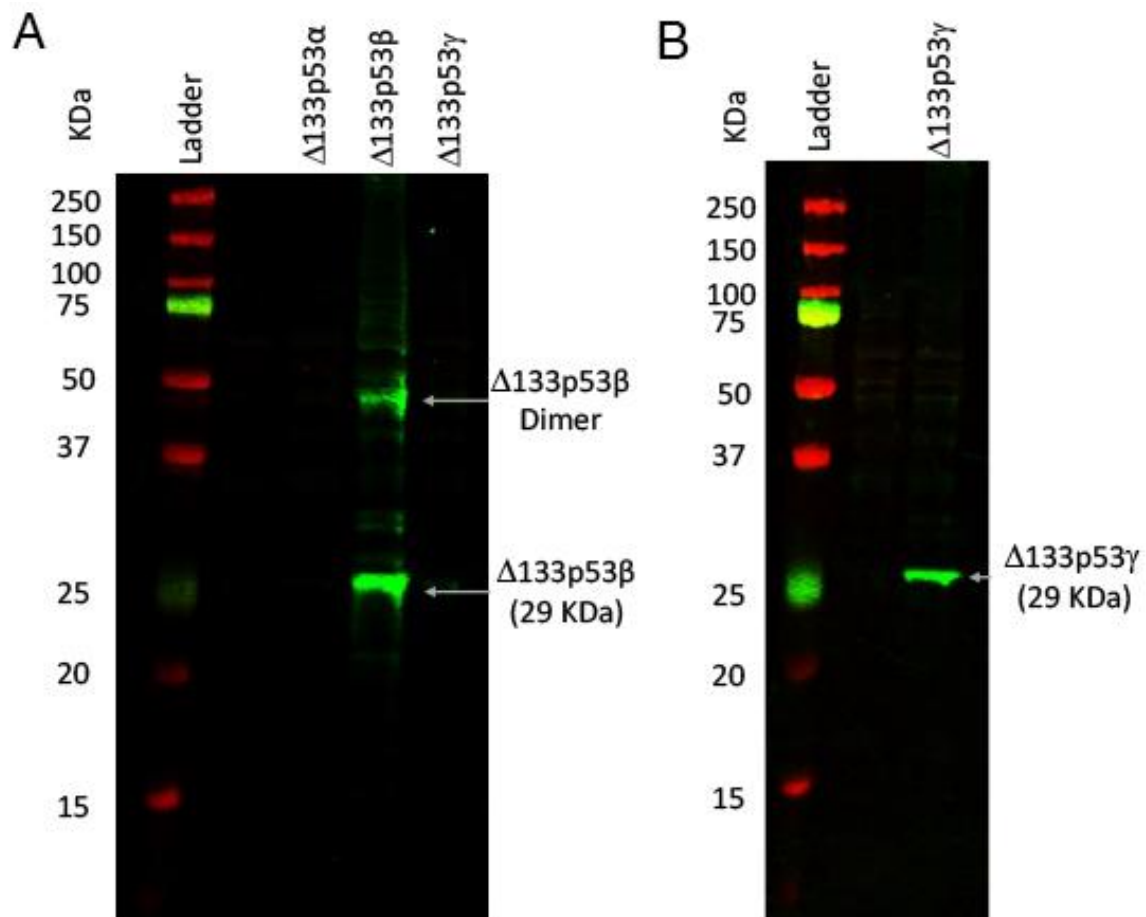


Supplementary Figure 1. Schematic of *TP53* transcripts and protein isoforms. **A** Top panel shows the gene structure of *TP53*. The bottom panel shows the 9 *TP53* transcripts resulting from alternative splicing (α , β , and γ) and alternative promoter usage (P1 and P2). RT-qPCR regions are shown as a red arrow that correspond to the 5' end of the *TP53* transcript for *FL/Δ40TP53_T1*, *FL/Δ40TP53_T2*, *Δ133TP53*, and those to the 3' end for *TP53α*, *TP53β* and *TP53γ*. Light blue region represents the coding exons; gray regions represent the untranslated regions. **B** Region recognized by the rabbit polyclonal antibody KCJA133αβγ and 79.3 designed to specifically detect the *Δ133p53* and *TP53β* isoform families respectively.

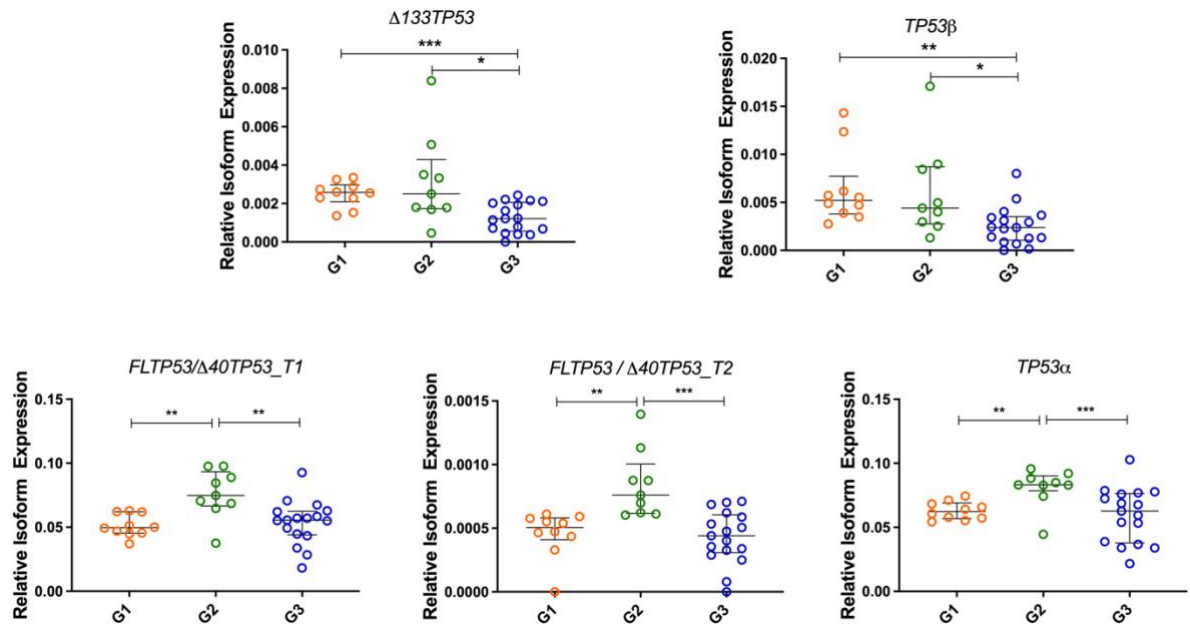


Supplementary Figure 2. Classification of RA subtype based on IHC.

Immunoscoring were assigned based on the following criteria: (i) B cell (CD20): Follicles: [0: none evident]; [1: <5]; [2: 5-10]; [3: >10]. (ii) Clusters: [0: negative]; [1: low]; [2: medium]; [3: high]. (iii) Scattered: [0: not present]; [1: <10%]; [2: 10-50%]; [3: >50%]. T cell (CD3): 'Clusters' and 'Scattered' as above for B cells. Macrophages: [0: negative]; [1: <10% low]; [2: 10-50% medium]; [3: >50% high] [28]. Synovia were classified into 3 pre-defined histopathological subtypes: (1) Follicular: predominantly lymphoid with ELS; (2) Diffuse: dominated by myeloid cells and T lymphocytes; and (3) Pauci-immune: fibroblast dominated, with minimal inflammatory infiltrate (36, 37).

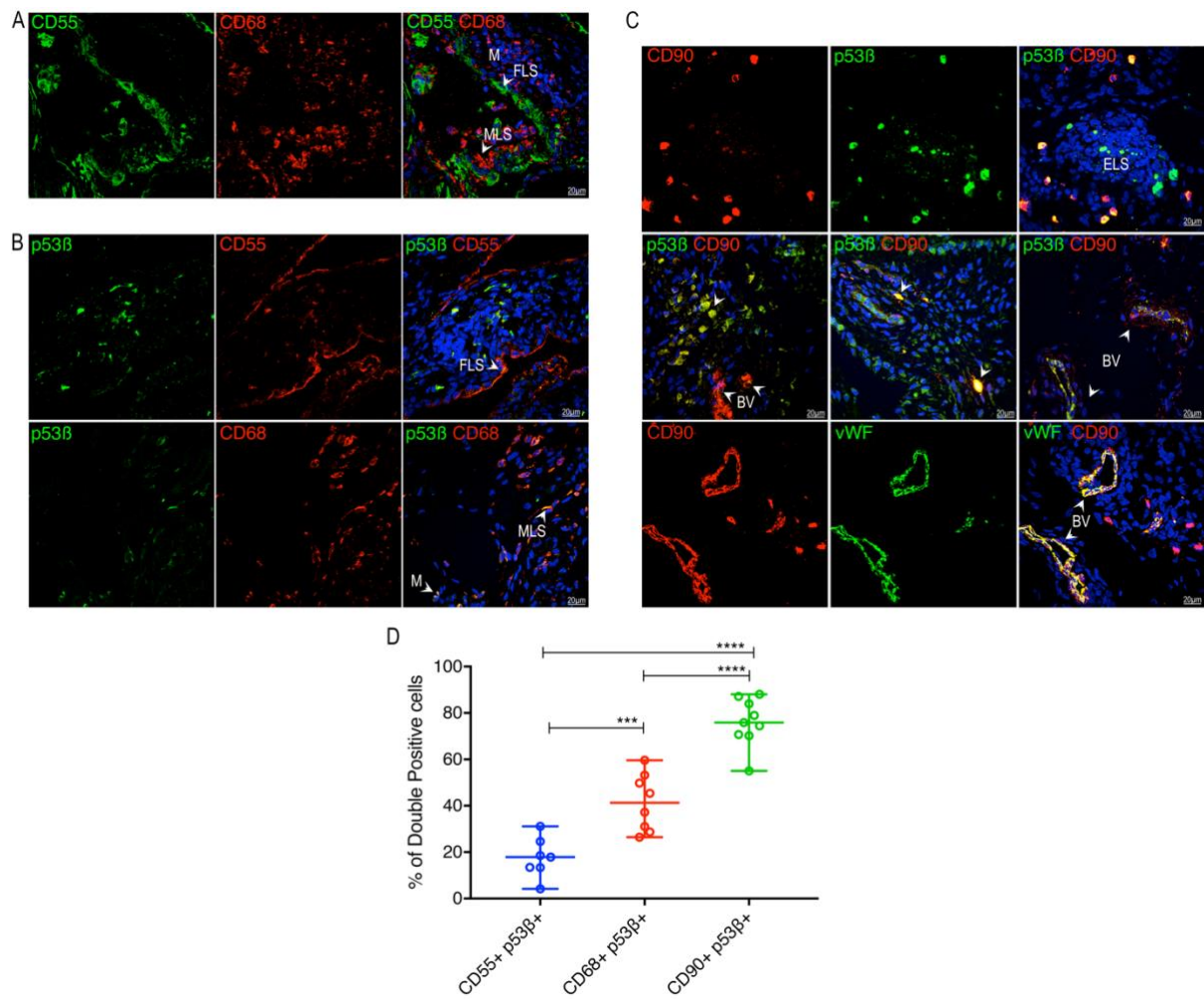


Supplementary Figure 3. Western Blot for isoform specific antibodies. **A** Western blot using the anti-p53 β antibody 79.3 (sourced from JC Bourdon lab) on total protein of PC-3 cells transfected with either control plasmid (Empty Vector) or a plasmid expressing either $\Delta 133p53\alpha$, $\Delta 133p53\beta$ or $\Delta 133p53\gamma$ isoforms respectively. **B** Western blot using KJCA133, an anti- $\Delta 133p53$ antibody (sourced from JC Bourdon lab) on total protein of PC-3 cells transfected with either control plasmid (Empty Vector) or a plasmid expressing $\Delta 133p53\gamma$.



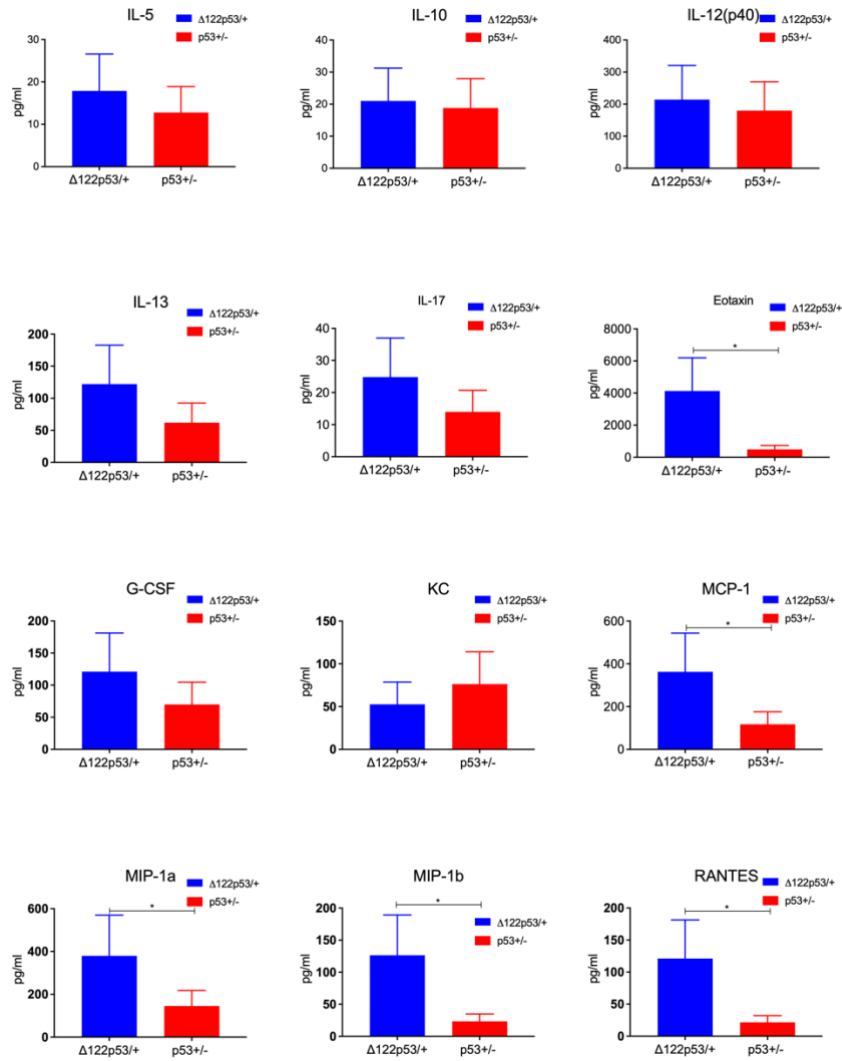
Supplementary Figure 4. Distribution of mRNA expression levels of *FL/Δ40TP53_T1*, *FL/Δ40TP53_T2*, *Δ133TP53*, *TP53α*, *TP53β* in OA and RA synovial tissue.

Dots represent data from individuals in each group. Lines represent mean and SD. Significance was determined using unpaired t-test with Welch's correction. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



Supplementary Figure 5. p53β protein co-localises with CD55⁺ fibroblast-like synoviocytes (FLS), CD68⁺ macrophage-like synoviocytes (MLS) and macrophages, and CD90⁺ cells.

Panels 1 through to 4 describe panels left to right. **A** FLS are CD55⁺; MLS and macrophages (M) are CD68⁺ **B** p53β expressing cells (green, panel 1), CD55⁺/CD68⁺ expressing cells (red, panel 2), Merged (panel 3) showing co-localisation of p53β⁺ with either CD55⁺ or CD68⁺ cells (yellow) and nuclei (blue). 400x magnification; scale bar 50μm. **C** p53β is highly expressed in CD90⁺ cells surrounding ELS (top row). p53β is expressed in cells that are CD90⁺ that resemble plasma cells (middle row, panel 1; arrowed) and adjacent to p53β⁺ endothelium (middle row, panel 2) and in endothelial cells (middle row, panel 3). CD90⁺ and vWF⁺ cells in endothelial and sub-endothelial layer (bottom row) **D** The percentage of CD55⁺, CD68⁺, and CD90⁺ cells that also co-express p53β. Each dot represents results from each individual image field and a minimum of 100 cells. The lines represent the mean and SD. Significance was determined using unpaired t test with Welch's correction (***p < 0.001; ****p < 0.0001). CD90⁺/p53β⁺ vs CD68⁺/p53β⁺, p<0.0001; CD90⁺/p53β⁺ vs CD55⁺/p53β⁺, p<0.0001; CD68⁺/p53β⁺ vs CD55⁺ p53β⁺, p<0.0004.



Supplementary Figure 6. MCP-1, MIP-1a, MIP-1b and RANTES were elevated in the serum from $\Delta 122p53/+$ (blue) compared to $p53+/-$ (red) mice.

The bars represent the concentration of the individual cytokines from 4 pooled serum samples. The error bars represent 97% CI. Significance was determined using unpaired t-test with Welch's correction; * $p < 0.05$.