Supplementary Figure Legends

Figure 1 Suppl. Secondary structure prediction of betaglycan.

The secondary structure of rat betaglycan was predicted using three distinct algorithms (as described in main text). Strands and helices are shown as solid bars and coils, respectively. Predicted signal peptide and transmembrane helices are indicated by a solid overbar. Regions shaded gray in the N- and C-terminal halves correspond to those that have significant homology with proteins endoglin and uromodulin, respectively (Blast E-value less than $1x10^{-8}$, Suppl Ref 1). Start and end points for Sol Δ10 and Sol Δ11 are indicated by right and leftward pointing arrowheads, respectively (filled for Sol Δ10 and open for Sol Δ11).

Figure 2 Suppl. SPR analysis of TGF-β1 binding activity of the Sol Δ10 and Sol Δ11 proteins.

(A) Sensorgrams and binding isotherms obtained as Sol Δ10 (left panels), Sol Δ11 (middle panels) and recombinant soluble betaglycan (Sol BG, right panels) were injected. Traces correspond to replicate measurements of 2 fold serial dilutions of the receptors with concentrations 0-2 μM for both Sol Δ10 and Sol Δ11 and 0-0.2 μM for Sol BG. Binding isotherms correspond to plots of the response at equilibrium as a function of receptor concentration, which were fit to a hyperbolic equation using Scrubber 2 software.

(B) Sensorgrams and binding isotherms obtained for coinjection experiments for Sol Δ11 binding to TGF-β1 in the presence of 2 μM Sol Δ10. Traces correspond to replicate measurements of 2 fold serial dilutions of SolΔ11 with concentrations 0-2 μM. Left panel represents the original sensorgrams; middle panel represents the sensorgrams after subtracting the binding response of 2

μM Sol Δ10; right panel represents the binding isotherms corresponding to plots of the response at equilibrium (taken from middle panel) as a function of receptor concentration fit to Eq. 1.

Figure 3 Suppl. SPR analysis of TGF-β3 binding activity of the Sol Δ10 and Sol Δ11 proteins.

(A) Sensorgrams and binding isotherms obtained as Sol Δ10 (left panels), Sol Δ11 (middle panels) and recombinant soluble betaglycan (Sol BG, right panels) were injected. Traces correspond to replicate measurements of 2 fold serial dilutions of the receptors with concentrations 0-2 μM for both Sol Δ10 and Sol Δ11 and 0-0.2 μM for Sol BG. Binding isotherms correspond to plots of the response at equilibrium as a function of receptor concentration, which were fit to a hyperbolic equation using Scrubber 2 software.

(B) Sensorgrams and binding isotherms obtained for coinjection experiments for Sol Δ11 binding to TGF-β3 in the presence of 2 μM Sol Δ10. Traces correspond to replicate measurements of 2 fold serial dilutions of Sol Δ11 with concentrations 0-2 μM. Left panel represents the original sensorgrams; middle panel represents the sensorgrams after subtracting the binding response of 2 μM Sol Δ10; right panel represents the binding isotherms corresponding to plots of the response at equilibrium (taken from middle panel) as a function of receptor concentration fit to Eq. 1.

Supplementary Reference:

1. Altschul, S. F., Gish, W., Miller, W., Myers, E. W., and Lipman, D. J. (1990) Basic local alignment search tool. *J Mol Biol* 215, 403-410