Supplemental Data for:

Biophysical and biochemical characterization of avian secretory component provides structural insights into the evolution of the polymeric Ig receptor

Running title: Biophysical characterization of avian secretory component

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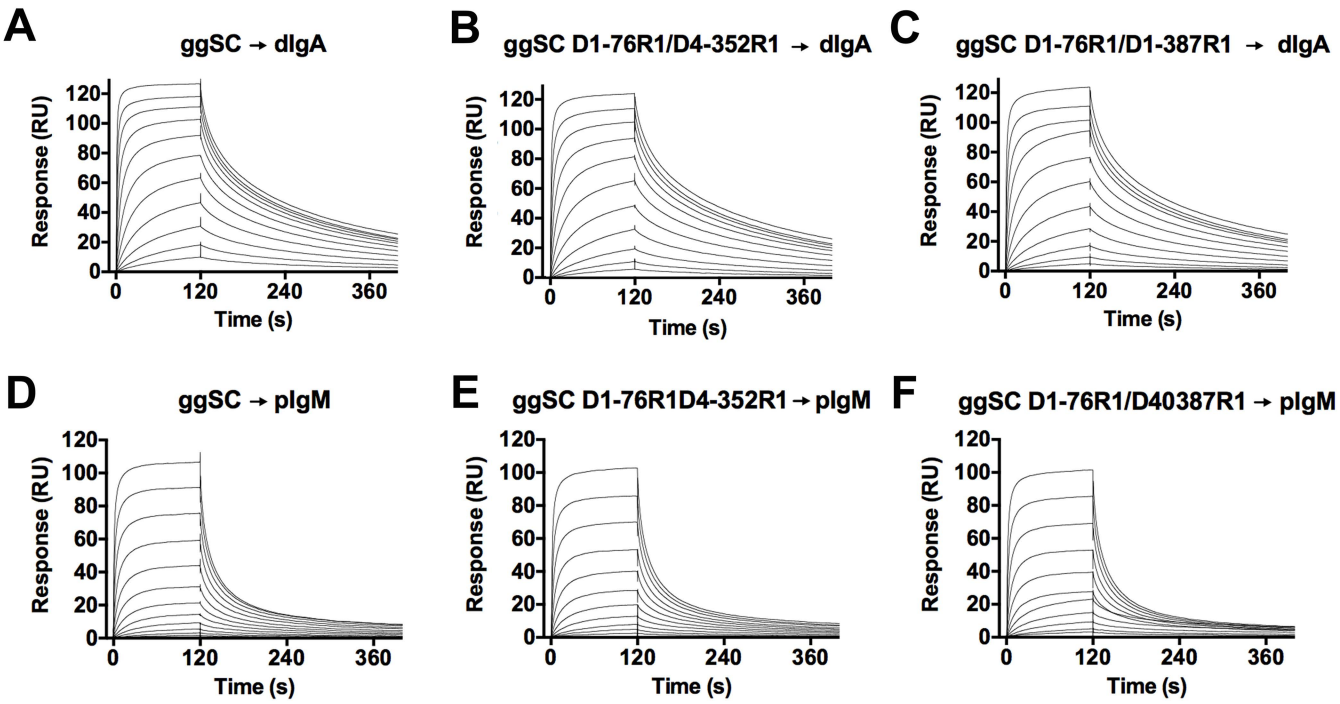

Figure S1. Spin-labeled ggSC binding to human dIgA and pIgM. Sensorgrams showing ggSC and nitroxide-labeled ggSC binding to dIgA (A-C) and pIgM (D-F). High concentrations shown are 1024uM and 512uM for dIgA and pIgM, respectively.

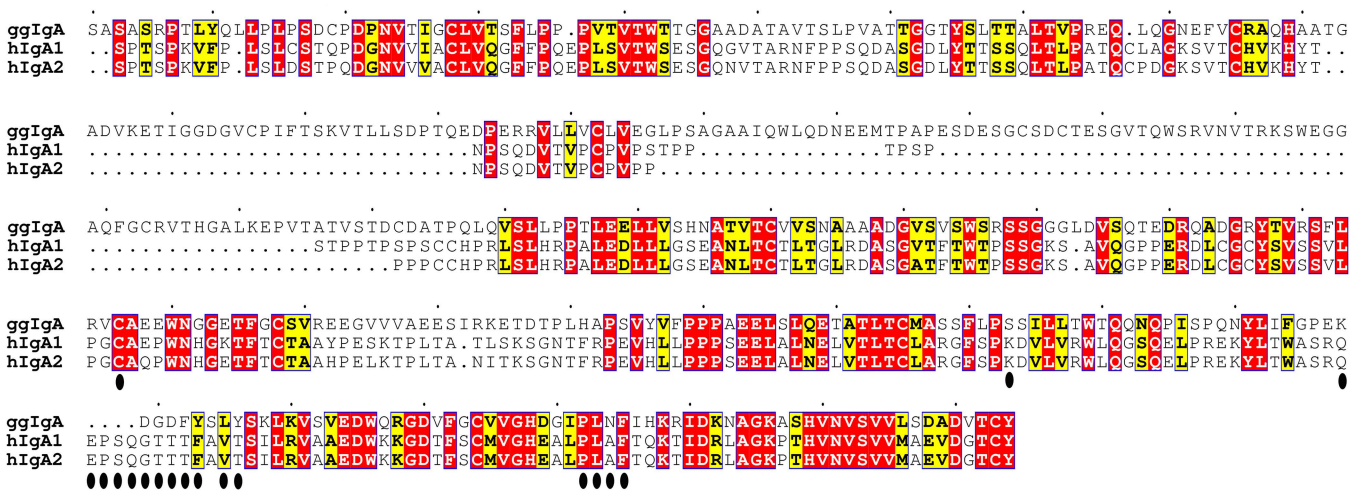

Figure S2. Human and avian IgA sequences. Sequence alignment of the IgA heavy chain constant regions from birds (ggIgA) and humans (hIgA1 and hIgA2). Residues implicated in mammalian SC binding to pIgA (1) are indicated by black ovals.

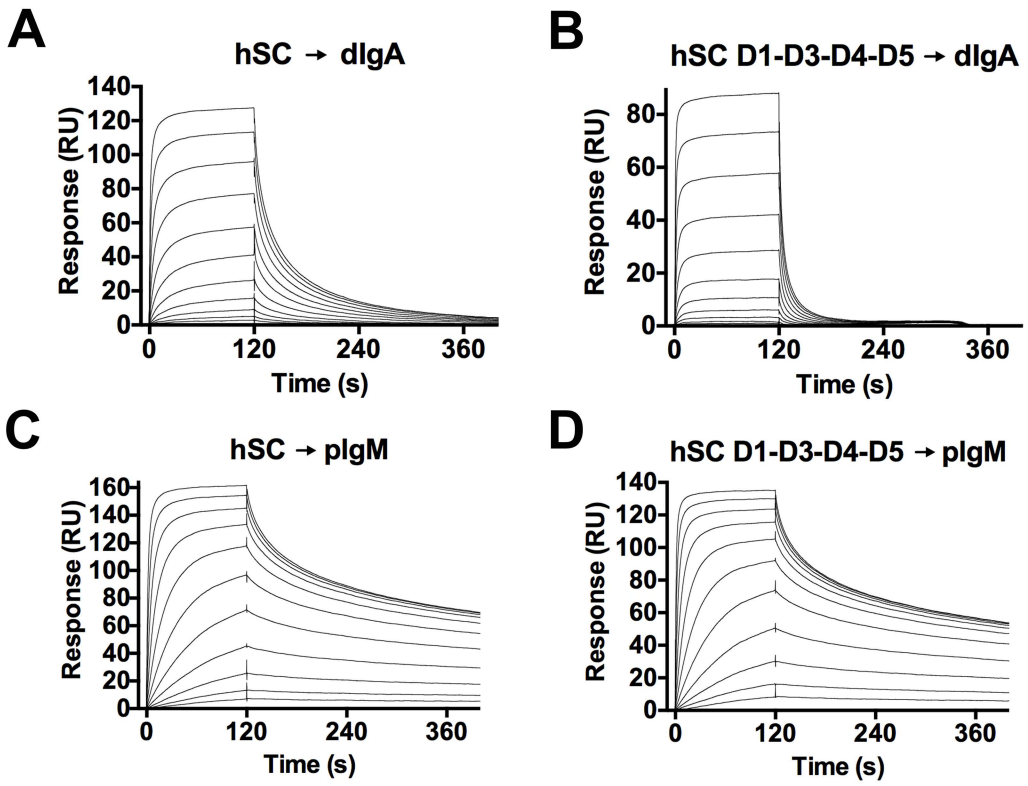

Figure S3. hSC and hSC D1-D3-D4-D5 binding to human dIgA and pIgM. (A-D) Senorgrams showing the response (RU) of hSC and hSC D1-D3-D4-D5 binding to human dIgA and pIgM. High concentrations shown are 1024uM and 512uM for dIgA and pIgM, respectively.

SUPPLEMENTAL REFERENCES

1. Woof, J. M., and Russell, M. W. (2011) Structure and function relationships in IgA. *Mucosal Immunol* **4**, 590-597.