

**Supplementary Figure 1.** **The relationship between the selenocysteine content within specific domains of selenoprotein P and selenium requirements.** The solid lines with the solid circles (●) is the best fit model for the number of Sec residues found upstream and including the APOER2 binding site in the C-terminal of SEPP1 versus the selenium requirements (mg Se/kg DM) in mammals, birds and bony fish. The broken lines represents the same data modelled with an additional five bony fish species with known Se requirement levels (○), but unannotated genomes as described in Fig. 2. The solid line is second order polynomial, R2 = 0.77, y = -2.3 + 88x - 164x2, while the dashed line is 5PL asymmetric sigmoidal, R2 = 0.86, y = -10.4 + (21.3/((1+10^((-2.27097-X) × 4.728))5.331^10)). X axis is log transformed.