

**Supp. Fig. 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 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 linear, R2 = 0.82, y = 1 + 35x, while the dashed line is 5PL asymmetric sigmoidal, R2 = 0.92, y = = -6.54 + (17.5/((1+10^((-1.75538-X)×5.851))2.999^10)). X axis is log transformed.