



Supplemental Fig. 2. Family alignment of extracellular domain modules. (A) Family alignment (ClustalW, standard PAM 250 parameters) of the CUB domain, (B) the pentraxin domain, (C) and the GPS motif. h=human, dr=*Drosophila*, l=limpo, x=Xenla. A consensus sequence is given at the bottom of each motif alignment. Black and grey boxes indicate identical and similar (conserved) amino-acid residues, respectively. VIGR (GenBank accession no. AF216967), TSG6 (GenBank accession no. P98066), TLD (GenBank accession no. P25723), PCO1 (GenBank accession no. Q15113), NRP1 (GenBank accession no. NP003864), NRP2 (GenBank accession no. NP061004), CRAR (GenBank accession no. P48740), C1S (GenBank accession no. NP001725), C1R (GenBank accession no. NP001724), BMP1 (GenBank accession no. AAA51833), NPX2 (GenBank accession no. P47972), CRP (GenBank accession no. P02741), CRP4 (GenBank accession no. P06206), PXN1 (GenBank accession no. P49263), BAI3 (GenBank accession no. NP001695), BAI1 (GenBank accession no. NP001693), CD97 (GenBank accession no. P48960), EMR2 (GenBank accession no. AAF21974), Ig-HEPTA (GenBank accession no. NP620810), C1RL1 (GenBank accession no. NP055736), HE6 (GenBank accession no. AAN33056), TM7XN1 (GenBank accession no. CAB37294), EMR1 (GenBank accession no. Q14246), C1RL3 (GenBank accession no. NP570835), CELSR1 (GenBank accession no. Q9NYQ6), BAI2 (GenBank accession no. NP001694).

