





**Supplementary Figure 2. Systems analysis of NLS and TM domain of EGFR by phylogenetic tree.** Protein sequences of EGFR were taken from UniProt KnowledgeBase (59). Sequences of proteins from all animals, which have the protein discovered, were taken, excluding repeated entries for same species. Alignment of their NLS sequences and transmembrane sequences was carried out with MAFFT Multiple Sequence Alignment Tool (60). Finally, Jalview (61) was used for visualization, export of tables and phylogenetic trees.