



Supplementary Figure 1. Putative fly cationic transporters and their human orthologues are structurally distinct from System L-like transporter light chains Alignment of hydropathy plots for putative fly cationic amino acid transporters <http://genome.ucsc.edu/cgi-bin/pbGateway> (Slif has been shown to act as a cationic amino acid transporter [20]) and their mammalian orthologues show the conservation of 14 transmembrane domains and an architecture that is distinctly different from the *Drosophila* System L transporter family light chains (with 12 TM domains) described in this paper, e.g. Mnd [21] and see Figure 3. Within each sequence the position of cysteine residues is indicated by vertical blue bars and glycosylation sites by vertical red bars. Arrow and dashed line indicates the position of a cysteine, which was used to align the sequences shown to each other, as it is present in a conserved position in all of the cationic amino acid transporters shown here and also the light chains in Figure 3. Only CG5535 has a cysteine in an equivalent position to the cysteine present in all light chains (e.g. Mnd) that is required for covalent linkage to cD98hc. The human cationic amino acid transporters are ordered according to their SLC number and the fly cationic amino acid transporters according to similarity to Slif.