It is suggested that SerRS self-aggregation is consequent to its too high number of connections to other amino acids, while the components of MaRS show lower number of connections. The number of aRS in MaRS is inversely proportional to the size of the subnetworks. Further details in [5,15].
Supplementary information 2. Thermal stability of anticodon pairs. The highest value among all pairs that can be formed by the triplets in each box is shown. Triplets in green are for single-meaning boxes, in red for multiple-meanings boxes.