

### Supplementary Methods

To compare the set of human (poly)phenol metabolite-binding proteins found within circulating exosomes with all human (poly)phenol metabolite-binding proteins (made available by Lacroix et al. 2018<sup>85</sup> and ExoCarta at the end of September 2021<sup>87</sup>), the graphical web application developed by Ge et al. 2020 using several R packages that automatically retrieves data from KEGG and STRING via API access was used.<sup>90</sup> Accordingly, the fold enrichment was calculated based on the distances between the two protein sets by  $1 - (N_i / N_u)$ , where  $N_i$  and  $N_u$  are the number of genes at the intersection and union of the two protein sets, respectively. The distance matrix thus computed subsequently allows for hierarchical clustering and for the estimation of relative GO term enrichment, using a cutoff of 0.05 after false discovery rate (FDR) correction.