



Figure S4a: Functional predictions for the fecal microbiome of the PD-MCI, PD-NC and healthy groups. The KOs with significantly different abundances in the fecal microbiome identified using the software package PICRUSt are shown (FDR,  $P < 0.05$  are listed). \* $P < 0.05$ ; \*\* $P < 0.01$ .