Supplementary Data

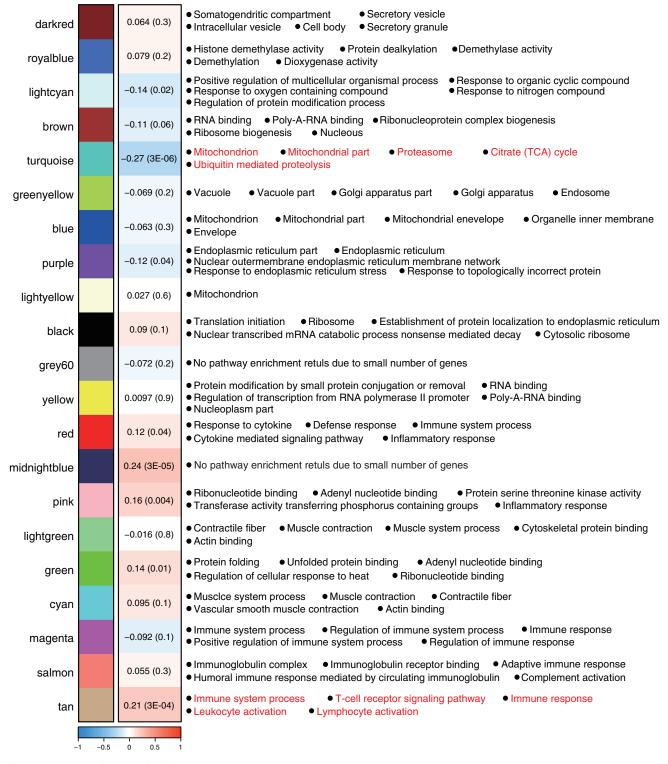| Module	Correlation	Pathways
darkred	0.064 (0.3)	● Somatogendritic compartment ● Secretory vesicle ● Intracellular vesicle ● Cell body ● Secretory granule
royalblue	0.079 (0.2)	● Histone demethylase activity ● Protein dealkylation ● Demethylase activity ● Demethylation ● Dioxygenase activity
lightcyan	−0.14 (0.02)	● Positive regulation of multicellular organismal process ● Response to organic cyclic compound ● Response to oxygen containing compound ● Response to nitrogen compound ● Regulation of protein modification process
brown	−0.11 (0.06)	● RNA binding ● Poly-A-RNA binding ● Ribonucleoprotein complex biogenesis ● Ribosome biogenesis ● Nucleous
turquoise	−0.27 (3E-06)	● Mitochondrion ● Mitochondrial part ● Proteasome ● Citrate (TCA) cycle ● Ubiquitin mediated proteolysis
greenyellow	−0.069 (0.2)	● Vacuole ● Vacuole part ● Golgi apparatus part ● Golgi apparatus ● Endosome
blue	−0.063 (0.3)	● Mitochondrion ● Mitochondrial part ● Mitochondrial enevelope ● Organelle inner membrane ● Envelope
purple	−0.12 (0.04)	● Endoplasmic reticulum part ● Endoplasmic reticulum ● Nuclear outermembrane endoplasmic reticulum membrane network ● Response to endoplasmic reticulum stress ● Response to topologically incorrect protein
lightyellow	0.027 (0.6)	● Mitochondrion
black	0.09 (0.1)	● Translation initiation ● Ribosome ● Establishment of protein localization to endoplasmic reticulum ● Nuclear transcribed mRNA catabolic process nonsense mediated decay ● Cytosolic ribosome
grey60	−0.072 (0.2)	● No pathway enrichment retuls due to small number of genes
yellow	0.0097 (0.9)	● Protein modification by small protein conjugation or removal ● RNA binding ● Regulation of transcription from RNA polymerase II promoter ● Poly-A-RNA binding ● Nucleoplasm part
red	0.12 (0.04)	● Response to cytokine ● Defense response ● Immune system process ● Cytokine mediated signaling pathway ● Inflammatory response
midnightblue	0.24 (3E-05)	● No pathway enrichment retuls due to small number of genes
pink	0.16 (0.004)	● Ribonucleotide binding ● Adenyl nucleotide binding ● Protein serine threonine kinase activity ● Transferase activity transferring phosphorus containing groups ● Inflammatory response
lightgreen	−0.016 (0.8)	● Contractile fiber ● Muscle contraction ● Muscle system process ● Cytoskeletal protein binding ● Actin binding
green	0.14 (0.01)	● Protein folding ● Unfolded protein binding ● Adenyl nucleotide binding ● Regulation of cellular response to heat ● Ribonucleotide binding
cyan	0.095 (0.1)	● Musclce system process ● Muscle contraction ● Contractile fiber ● Vascular smooth muscle contraction ● Actin binding
magenta	−0.092 (0.1)	● Immune system process ● Regulation of immune system process ● Immune response ● Positive regulation of immune system process ● Regulation of immune response
salmon	0.055 (0.3)	● Immunoglobulin complex ● Immunoglobulin receptor binding ● Adaptive immune response ● Humoral immune response mediated by circulating immunoglobulin ● Complement activation
tan	0.21 (3E-04)	● Immune system process ● T-cell receptor signaling pathway ● Immune response ● Leukocyte activation ● Lymphocyte activation

SUPPLEMENTARY FIG. S1. All constructed modules with pathway enrichment results. Top five the most significant GO or KEGG pathways are denoted for each module. The Pearson correlation coefficient and the correlation test *p*-value (in brackets) between age and the modules are presented.