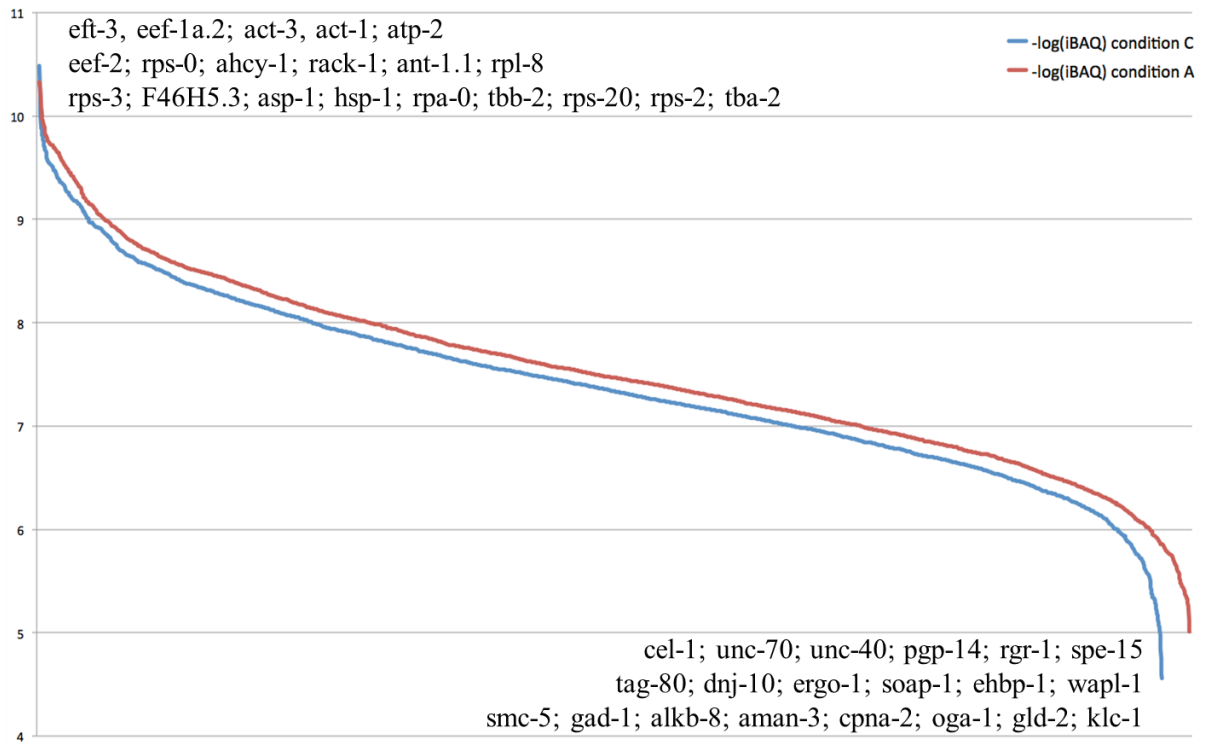


1 **Supplementary data**

2 **FIGURES**



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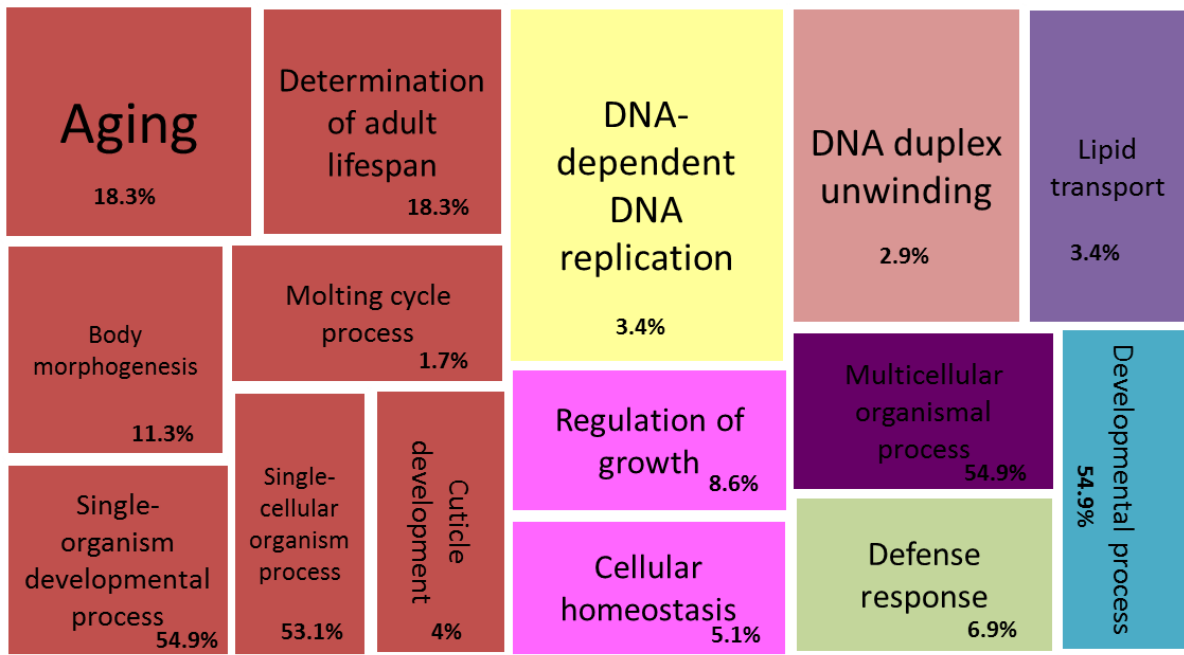
4 **Figure S1: -Log₁₀(iBAQ) for conditions acute (A) and chronic (C) with selected major and minor proteins detected in our**
5 **dataset. y=-Log₁₀(iBAQ) and x= protein ranking from the highest iBAQ to the lowest.**

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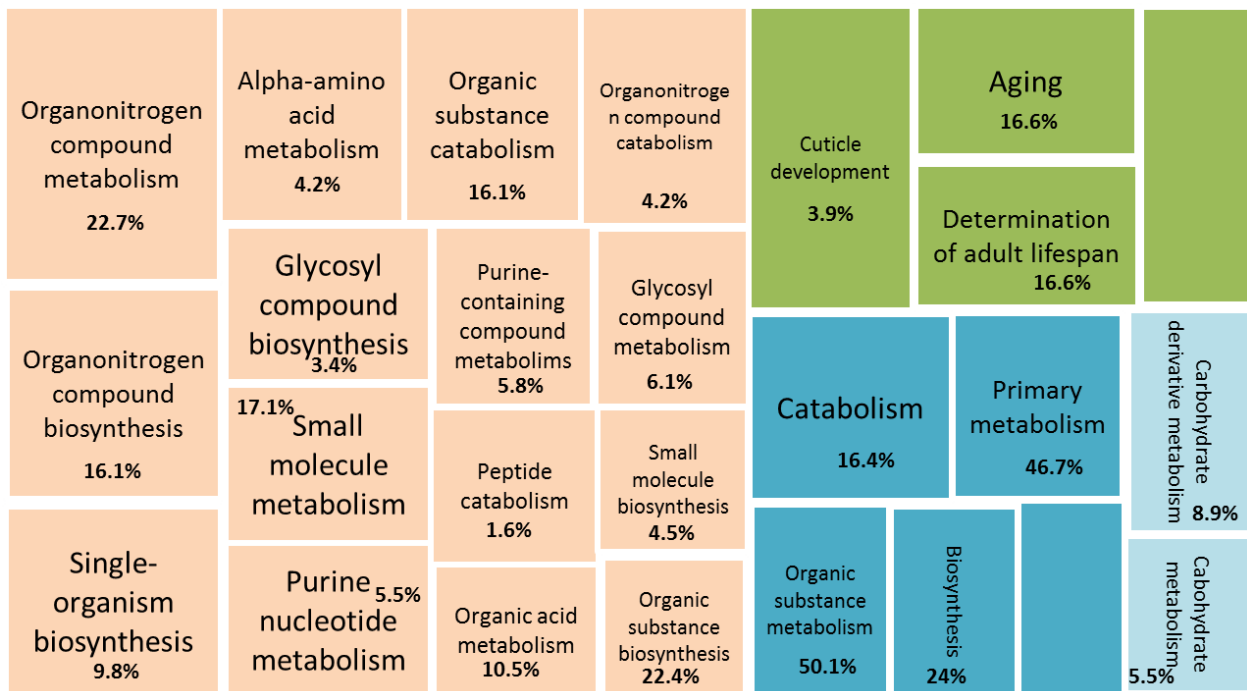


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11 Figure S1 : Independent DAVID gene functional enrichment analysis based on results of all proteins identified as
 12 significant after chronic irradiation (ANOVA). Significant GO-term biological processes (p. value <0.05) were then
 13 summarized using REVIGO. The % of significant proteins involved in the process is written in each case. Tree maps show a
 14 two-level hierarchy of GO terms (main clusters and cluster members); the size of the rectangles is relative to the log₁₀ (p.
 15 value) absolute. With a same color, biological processes belonging to one main head process: determination of adult
 16 lifespan (red), regulation of growth (pink).

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20 **Figure S3: Independent DAVID gene functional enrichment analysis based on results of all proteins identified as**
 21 **significant after acute irradiation (ANOVA). Significant GO-term biological processes (p. value <0.05) were then**
 22 **summarized using REVIGO. The % of significant proteins involved in the process is written in each case. Tree maps show a**
 23 **two-level hierarchy of GO terms (main clusters and cluster members); the size of the rectangles is relative to the log10 (p.**
 24 **value) absolute. With a same color, biological processes belonging to one main head process: alpha-amino acid**
 25 **metabolism (pale orange), cuticle development (green), catabolism (blue), carbohydrate derivative metabolism (pale**
 26 **blue).**

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