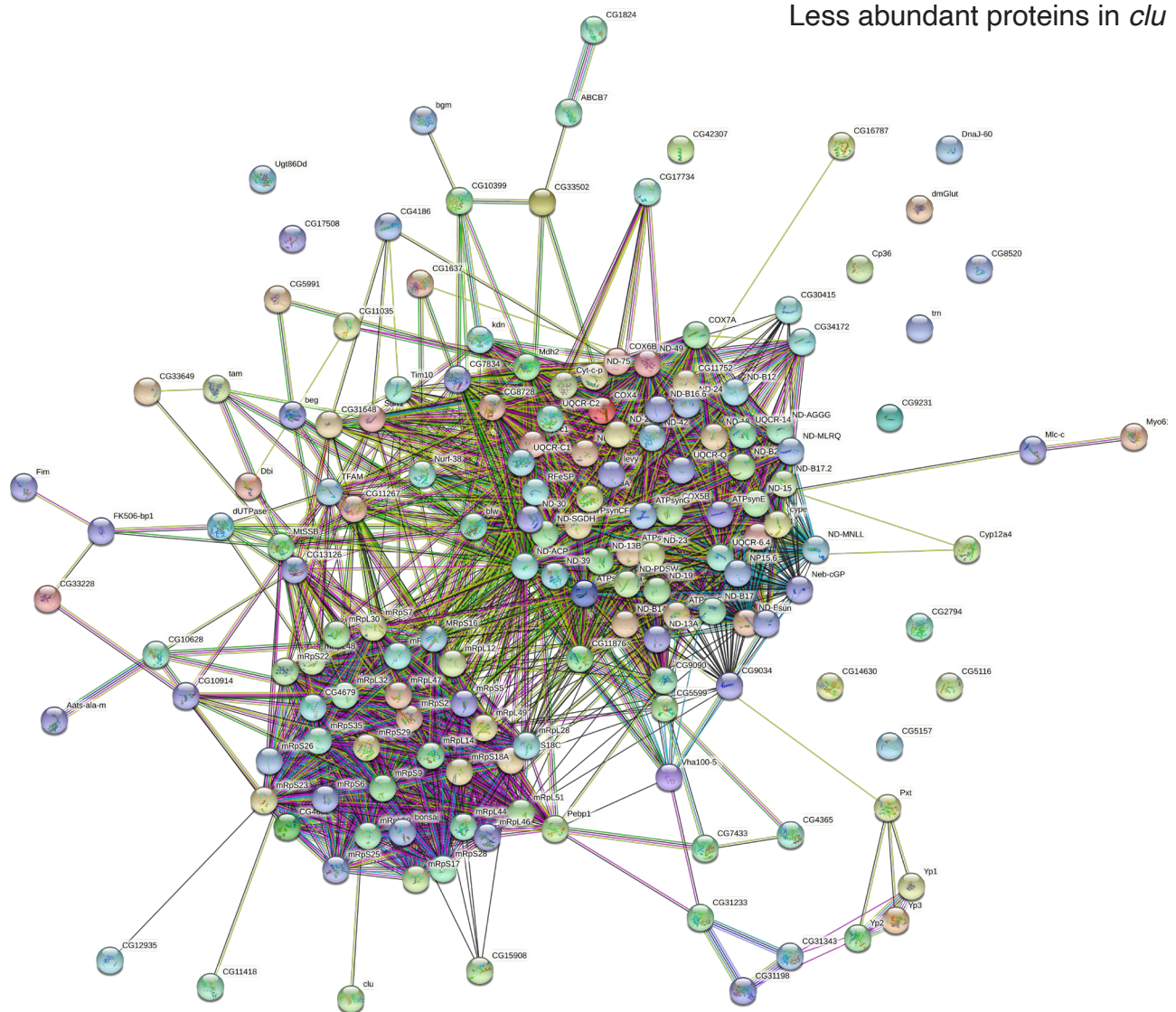
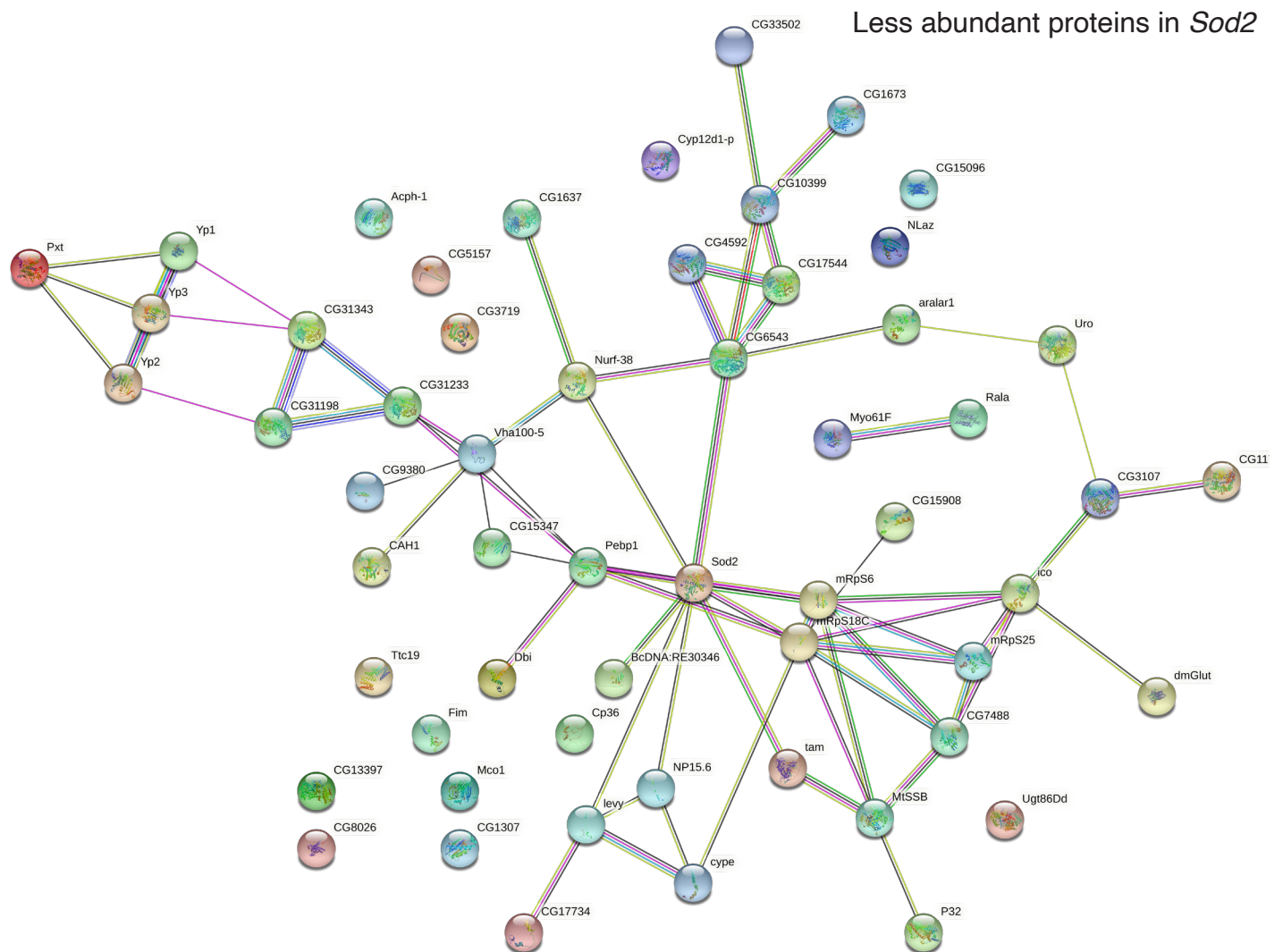


Figure S1



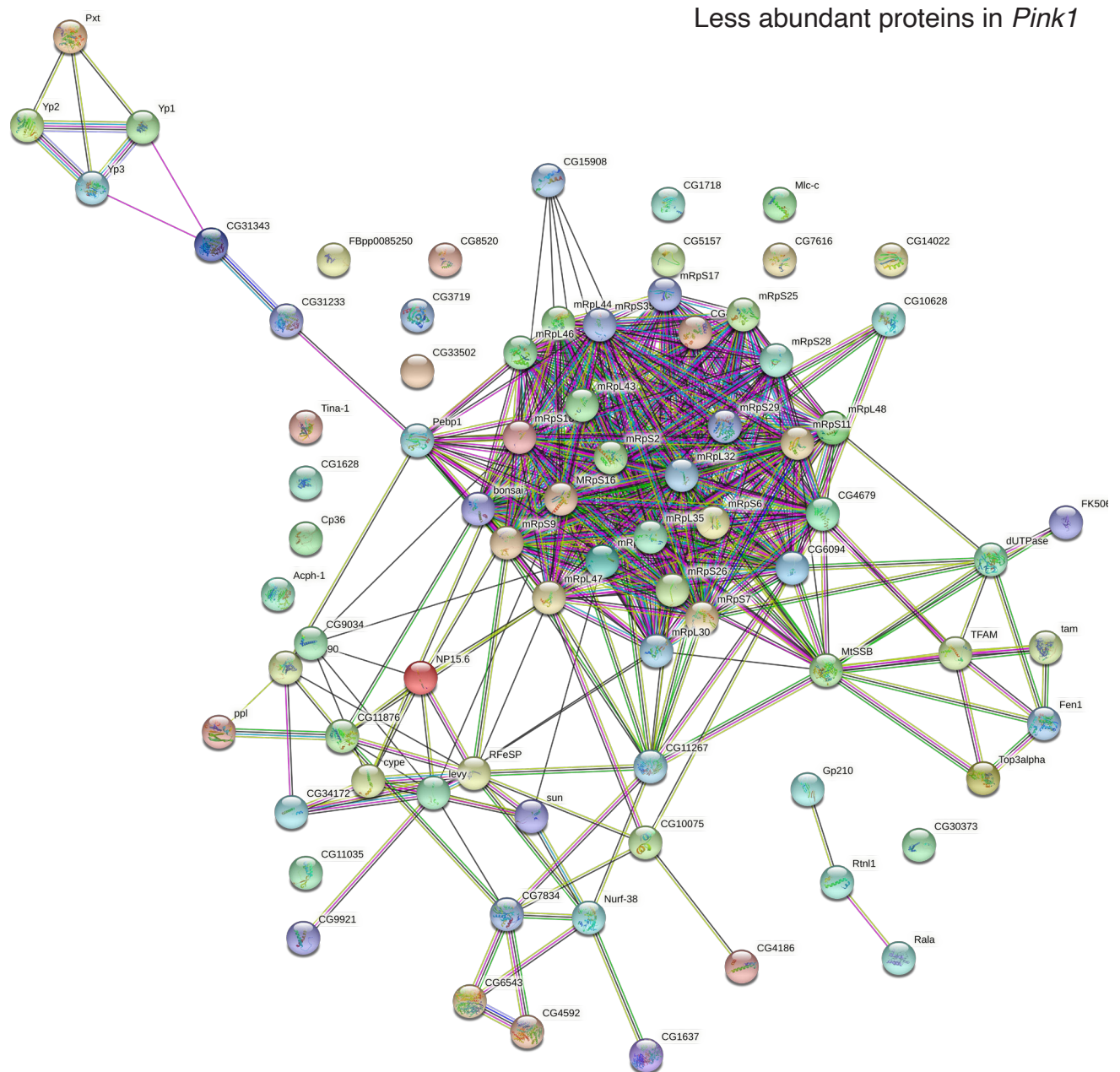
Supplemental Figure S1: The STRING protein-protein interaction (PPI) network showing the functional clustering features of less abundant proteins in *clu* mutants identified with TMT mass spectrometry analysis. The nodes (circles) represent proteins and edges (lines) denote interactions. The color of each nodes represents the nature of the interactions, e.g., known or predicted interaction. A detailed description of the nodes and the edges can be found at the STRING data base (http://version10.string-db.org/help/getting_started/).

Figure S2



Supplemental Figure S2: The STRING protein-protein interaction (PPI) network showing the functional clustering features of less abundant proteins in *Sod2* mutants identified with TMT mass spectrometry analysis. The nodes (circles) represent proteins and edges (lines) denote interactions. The color of each nodes represents the nature of the interactions, e.g., known or predicted interaction. A detailed description of the nodes and the edges can be found at the STRING data base (http://version10.string-db.org/help/getting_started/).

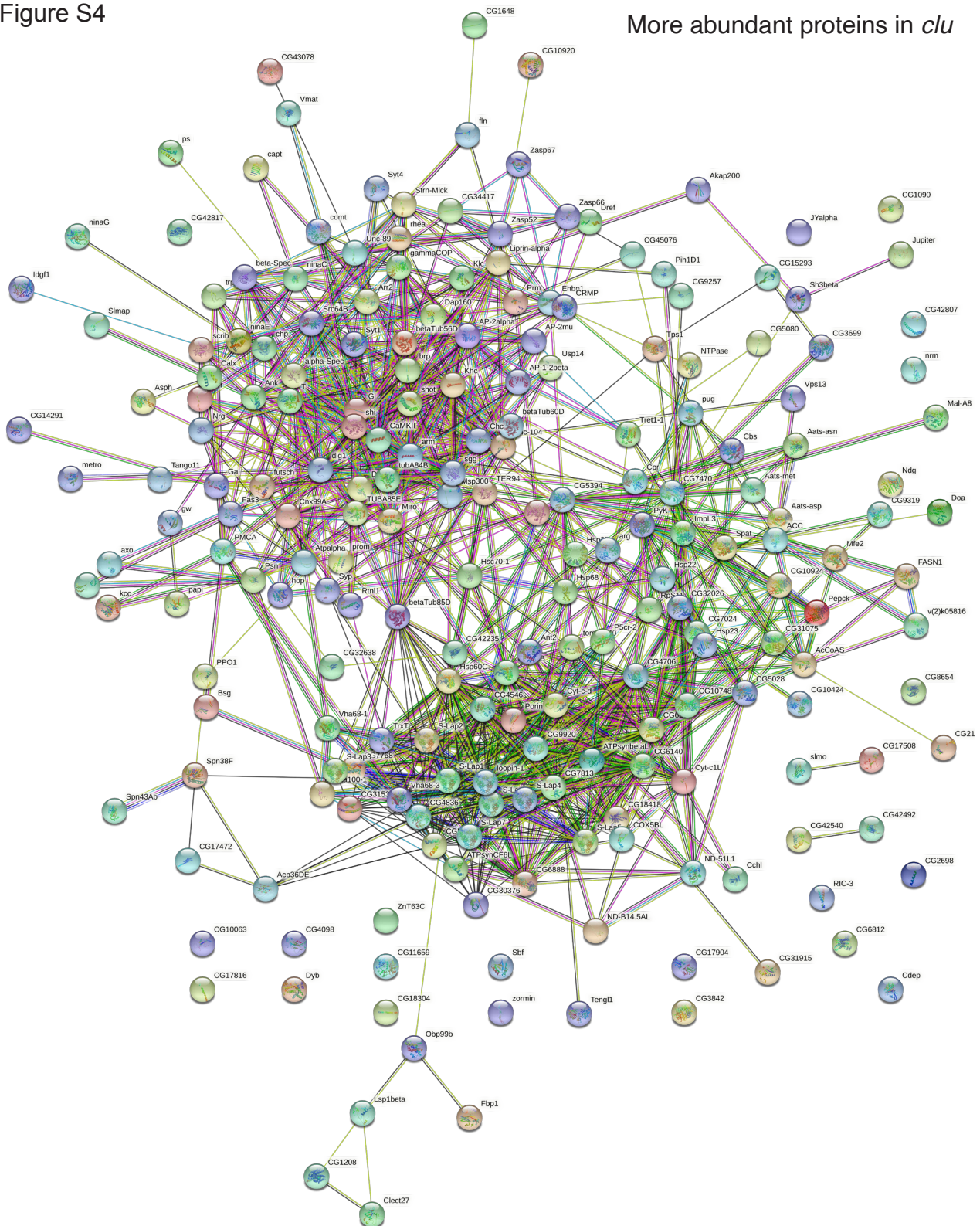
Figure S3



Supplemental Figure S3: The STRING protein-protein interaction (PPI) network showing the functional clustering features of less abundant proteins in *Pink1* mutants identified with TMT mass spectrometry analysis. The nodes (circles) represent proteins and edges (lines) denote interactions. The color of each nodes represents the nature of the interactions, e.g., known or predicted interaction. A detailed description of the nodes and the edges can be found at the STRING data base (http://version10.string-db.org/help/getting_started/).

Figure S4

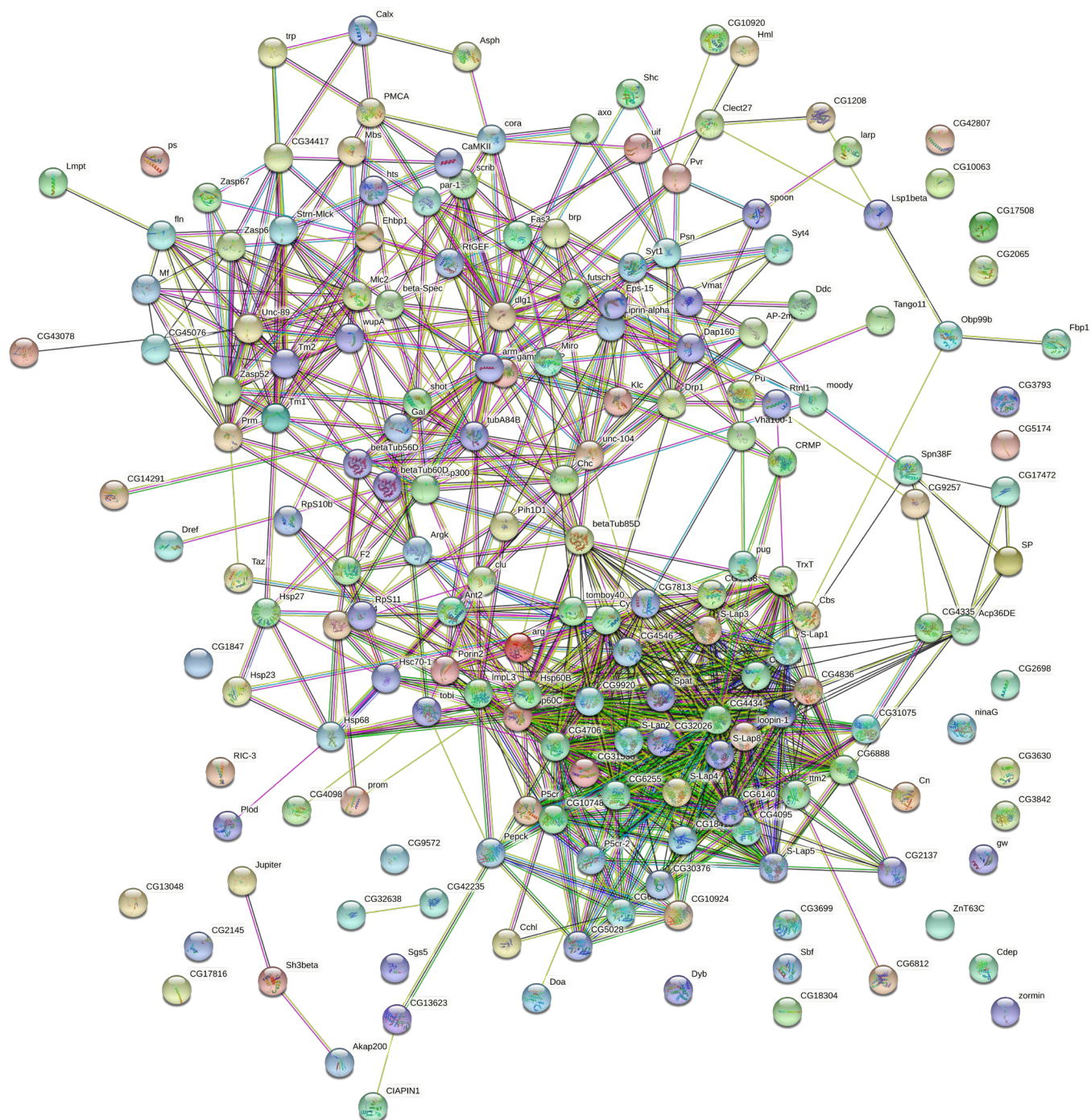
More abundant proteins in *clu*



Supplemental Figure S4: The STRING protein-protein interaction (PPI) network showing the functional clustering features of more abundant proteins in *clu* mutants identified with TMT mass spectrometry analysis. The nodes (circles) represent proteins and edges (lines) denote interactions. The color of each nodes represents the nature of the interactions, e.g., known or predicted interaction. A detailed description of the nodes and the edges can be found at the STRING data base (http://version10.string-db.org/help/getting_started/).

Figure S5

More abundant proteins in *Sod2*



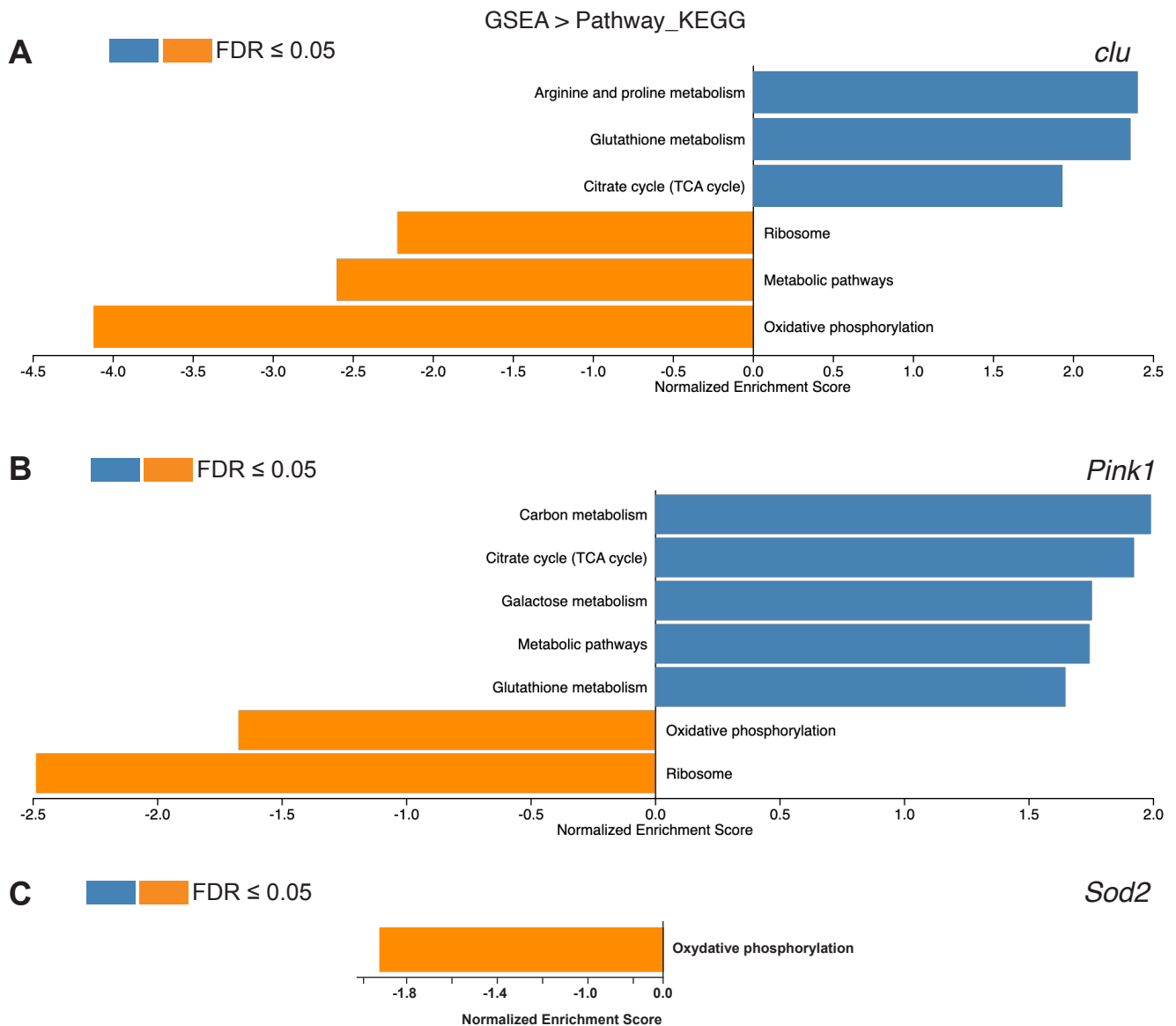
Supplemental Figure S5: The STRING protein-protein interaction (PPI) network showing the functional clustering features of more abundant proteins in *Sod2* mutants identified with TMT mass spectrometry analysis. The nodes (circles) represent proteins and edges (lines) denote interactions. The color of each nodes represents the nature of the interactions, e.g., known or predicted interaction. A detailed description of the nodes and the edges can be found at the STRING data base (http://version10.string-db.org/help/getting_started/).

More abundant proteins in *Pink1*

The diagram illustrates a complex network of protein interactions. Nodes are represented by small circular icons with different colors and patterns, and they are connected by a dense web of lines. The network is highly interconnected, with many nodes having multiple connections. The nodes are labeled with various protein names and identifiers, including: Zasp67, CG34417, AP-2, Eps-15, Syt4, Dap160, Syt1, Liprin-alpha, PihiD1, Doa, CG10920, CG1801, DmelCG44243, CG17904, CG17816, ninaG, ZnT63C, CG43078, CG13623, CG8665, Cyp6a20, CG2065, CG6812, CG42235, CG2698, CG2145, CG2137, CG18418, CG4095, CG6140, CG6149, CG6148, CG6147, CG6146, CG6145, CG6144, CG6143, CG6142, CG6141, CG6140, CG6139, CG6138, CG6137, CG6136, CG6135, CG6134, CG6133, CG6132, CG6131, CG6130, CG6129, CG6128, CG6127, CG6126, CG6125, CG6124, CG6123, CG6122, CG6121, CG6120, CG6119, CG6118, CG6117, CG6116, CG6115, CG6114, CG6113, CG6112, CG6111, CG6110, CG6109, CG6108, CG6107, CG6106, CG6105, CG6104, CG6103, CG6102, CG6101, CG6100, CG6099, CG6098, CG6097, CG6096, CG6095, CG6094, CG6093, CG6092, CG6091, CG6090, CG6089, CG6088, CG6087, CG6086, CG6085, CG6084, CG6083, CG6082, CG6081, CG6080, CG6079, CG6078, CG6077, CG6076, CG6075, CG6074, CG6073, CG6072, CG6071, CG6070, CG6069, CG6068, CG6067, CG6066, 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Supplemental Figure S6: The STRING protein-protein interaction (PPI) network showing the functional clustering features of more abundant proteins in *Pink1* mutants identified with TMT mass spectrometry analysis. The nodes (circles) represent proteins and edges (lines) denote interactions. The color of each nodes represents the nature of the interactions, e.g., known or predicted interaction. A detailed description of the nodes and the edges can be found at the STRING data base (http://version10.string-db.org/help/getting_started/).

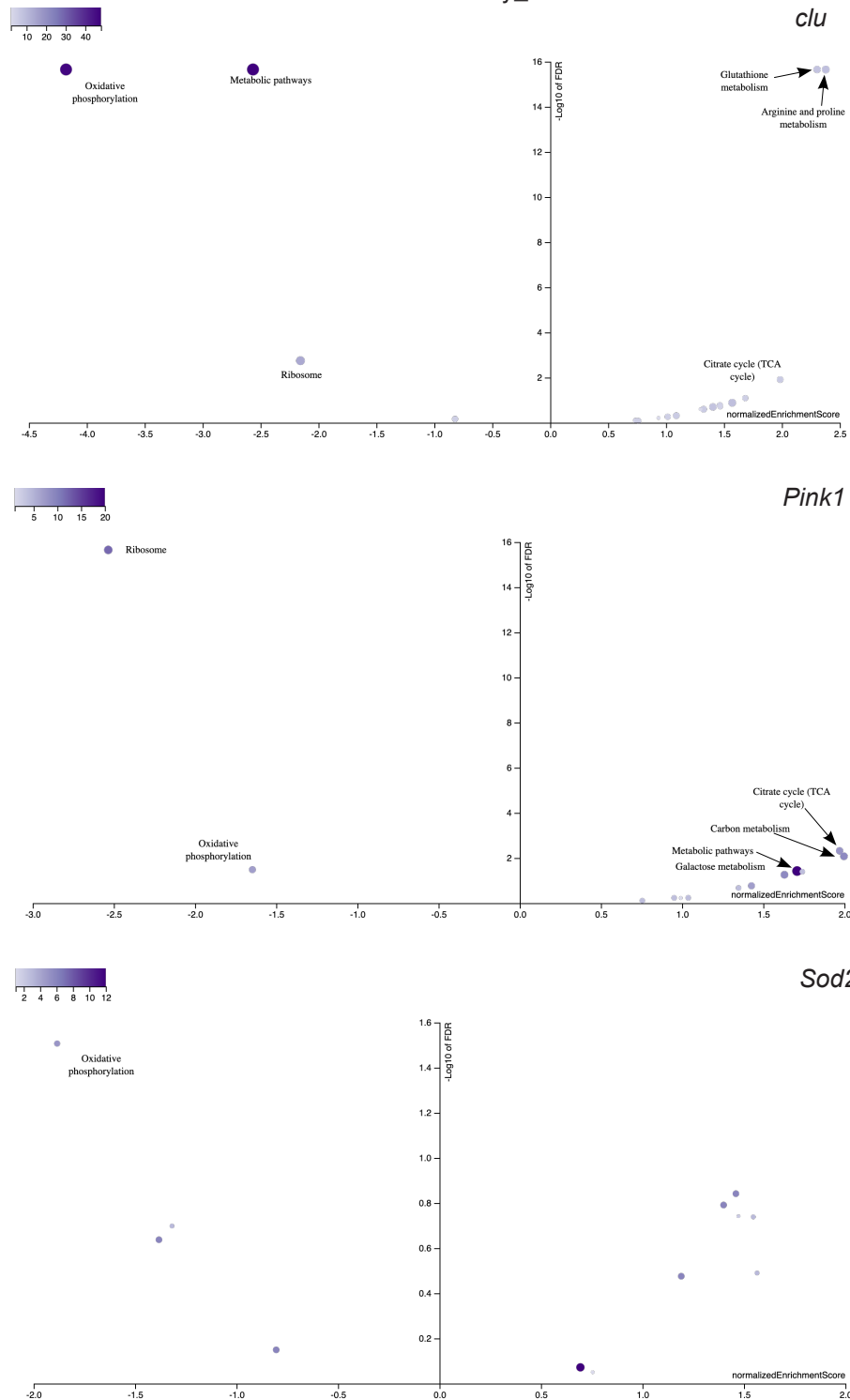
Figure S7



Supplemental Figure S7. The Gene Set Enrichment Analysis (GSEA) for less and more abundant proteins from *clu* (A), *Pink1* (B), and *Sod2* (C) mutants. KEGG Pathway analysis shows enrichment of pathways from less abundant proteins (in orange bars) and more abundant proteins (in blue bars). The names of each pathway are indicated next to each bar. The normalized enrichment scores are shown on the y-axis. Parameters for enrichment analysis are as follow: Minimum number of IDs in the category: 5, Maximum number of IDs in the category: 2000, Significance Level: FDR < 0.05, Number of permutations: 1000. FDR = False Discovery Rate.

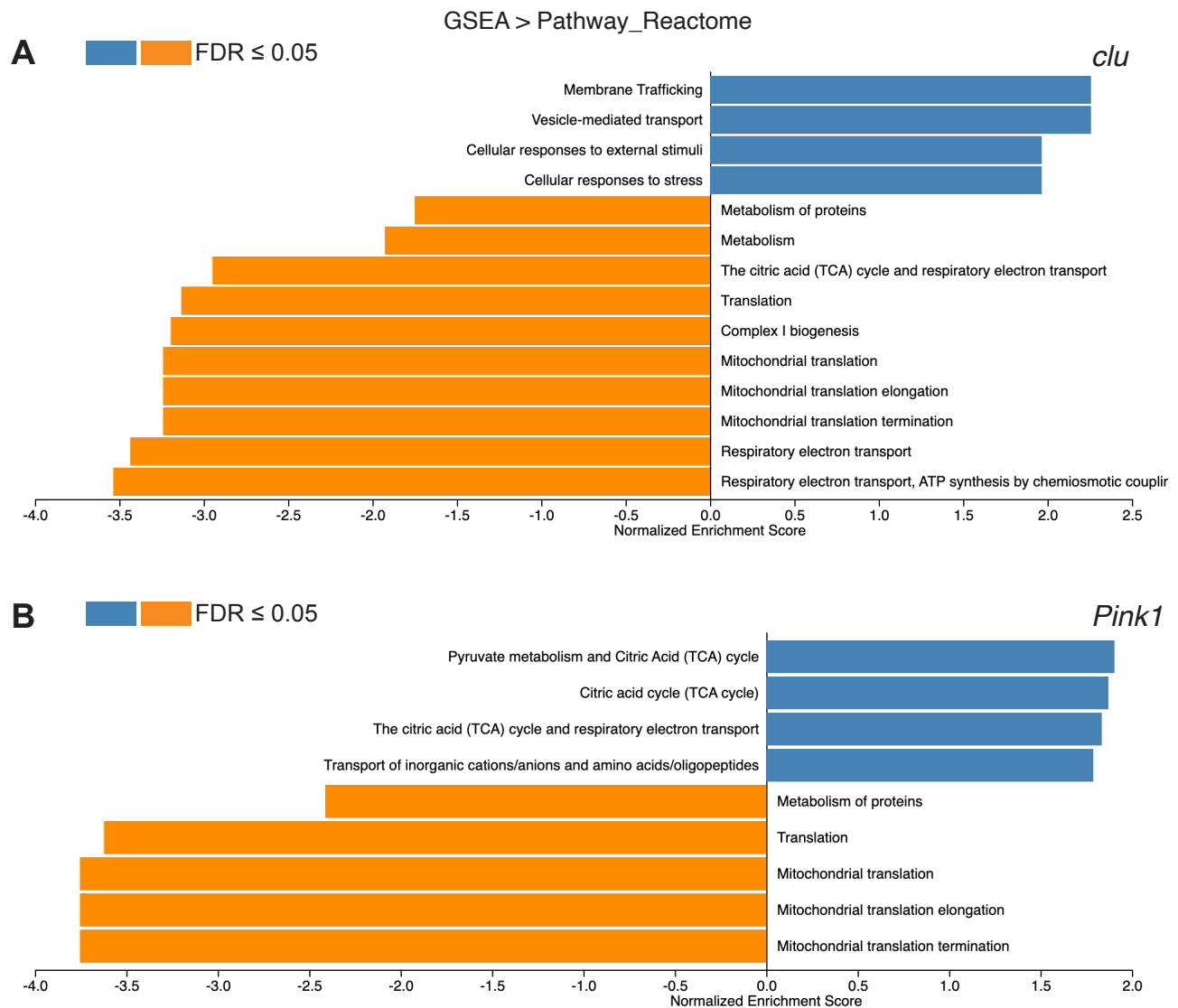
Figure S8

GSEA > Pathway_KEGG



Supplemental Figure S8. The Gene Set Enrichment Analysis (GSEA) for less and more abundant proteins from *clu* (A), *Pink1* (B), and *Sod2* (C) mutants. KEGG Pathway analysis shows enrichment of pathways from less abundant proteins using volcano plots. The names of each pathway are indicated next to each dot. Statistically insignificant pathways are shown as unlabeled dots. The -Log₁₀ of FDR is shown on the x-axis and the normalized enrichment scores are shown on the y-axis. Parameters for enrichment analysis are as follow: Minimum number of IDs in the category: 5, Maximum number of IDs in the category: 2000, Significance Level: FDR < 0.05, Number of permutations: 1000. FDR = False Discovery Rate.

Figure S9



Supplemental Figure S9. The Gene Set Enrichment Analysis (GSEA) for less and more abundant proteins from *clu* (A) and *Pink1* (B). Reactome Pathway analysis shows enrichment of pathways from less abundant proteins (in orange bars) and more abundant proteins (in blue bars). Reactome Pathway analysis did not find any significant changes for *Sod2* mutants. The names of each pathway are indicated next to each bar. The normalized enrichment scores are shown on the y-axis. Parameters for enrichment analysis are as follow: Minimum number of IDs in the category: 5, Maximum number of IDs in the category: 2000, Significance Level: FDR < 0.05, Number of permutations: 1000. FDR = False Discovery Rate.

Figure S10: List of primers used one step RT-PCR analysis

Primers	Sequences
Tom20 forward	CACCATGATTGAAATGAACAAAACCTGCAATCGGC
Tom20 reverse	TTCGAGGTCGTCGATACTTGCG
ND-19 forward	CACCATGGTCATCACCAACAACAC
ND-19 reverse	CTCCAGCCAGTGGAAGCGGGAACC
ND-ASH1 forward	CACCATGTCTGGCGTTTGTGAAAAC
ND-ASH1 reverse	CTTCTCGAAGGTGTAGTGC
ND-SGDH forward	CACCATGGTCGGTTGGAGCCGTTTGC
ND-SGDH reverse	GTCTCCGCGCAGAGCCTCCAG
UQCR-14 forward	CACCATGTCTGAACCTATATTGCCAG
UQCR-14 reverse	GTGGATCTTTTCCCAGTCCTCACG
COX5B forward	CACCATGGCATCGATCTGTGGACGC
COX5B reverse	AACAGCTGCCTTCTCCACCAGC
ATPsynCF6 forward	CACCATGCTGTCGCAATCCCTGCTG
ATPsynCF6 reverse	CTGTGGGGCCTGGGTGATGGGATC
ND-42 forward	CACCATGACCGCCGTGTTCCGCGTAGG
ND-42 reverse	TCGAGGACAACACCCTGGCCGG
ND-23 forward	CACCATGTCTGCTAACTATGCGAATTTTCACC
ND-23 reverse	AGCTCCTCGTGCCTCTCCGTGG
COX4 forward	CACCATGGCCCTGCGACTACTCAACAG
COX4 reverse	TGGAGGTCAATCCGGTGACGGGG
Levy forward	CACCATGTCCGCTATTCTAAACCACGC
Levy reverse	GTGCTCGTAGCCGTCGGGCAGGG
UQCR-Q forward	CACCATGCGTCTATCCTCGATCCTG
UQCR-Q reverse	TTCGTCTGTTTCGCGTAGTCAGCGG
mRpS16 forward	CACCATGTCTCTATCGCCAGCCAGTGG
mRpS16 reverse	TGCGGTTGATTCCGCCTTTTCTGG
HSP22 forward	CACCATGCGTTTCTTACCGATGTTTTGG
HSP22 reverse	CTGACTGGCGGCTTTGTCATTTGGC