

SUPPLEMENTARY MATERIAL

## **Positive selection and centrality in the yeast and fly protein–protein interaction networks**

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**Table S1. Summary statistics of the networks used in the study**

Organism	Database	Number of proteins	Number of interactions
<i>S. cerevisiae</i>	BioGRID	5864	81,040
	STRING (score $\geq$ 40%)	6303	332,039
<i>D. melanogaster</i>	BioGRID	7968	36,589
	STRING (score $\geq$ 40%)	12,223	454,083

**Table S2. Network centralities of positively selected genes ( $P < 0.05$ ) and genes with no signatures of positive selection in *S. cerevisiae***

		BioGRID			STRING		
		Selected genes ( $n = 89$ )	Other genes ( $n = 1956$ )	$P$ -value	Selected genes ( $n = 91$ )	Other genes ( $n = 1976$ )	$P$ -value
Degree	Mean	18.01	27.23	0.016*	90.76	113.04	0.039*
	Median	13	14		68	78	
Betweenness	Mean	$6.73 \times 10^{-5}$	$1.90 \times 10^{-4}$	0.636	$1.02 \times 10^{-4}$	$1.74 \times 10^{-4}$	0.229
	Median	$1.21 \times 10^{-5}$	$2.34 \times 10^{-5}$		$6.36 \times 10^{-5}$	$7.40 \times 10^{-5}$	
Closeness	Mean	0.3869	0.3995	0.008**	0.4342	0.4449	0.014*
	Median	0.3943	0.4045		0.4485	0.4518	

$P$ -values correspond to the Mann–Whitney  $U$  test. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ .

**Table S3. Network centralities of positively selected genes ( $P < 0.01$ ) and genes with no signatures of positive selection in *S. cerevisiae***

		BioGRID			STRING		
		Selected genes ( $n = 31$ )	Other genes ( $n = 2014$ )	$P$ -value	Selected genes ( $n = 33$ )	Other genes ( $n = 2034$ )	$P$ -value
Degree	Mean	20.45	26.93	0.810	102.73	112.21	0.792
	Median	15	14		76	77	
Betweenness	Mean	$8.6 \times 10^{-5}$	$1.9 \times 10^{-4}$	0.540	$1.2 \times 10^{-4}$	$1.7 \times 10^{-4}$	0.475
	Median	$1.7 \times 10^{-5}$	$2.3 \times 10^{-5}$		$6.3 \times 10^{-5}$	$7.3 \times 10^{-5}$	
Closeness	Mean	0.4066	0.3989	0.350	0.4451	0.4444	0.718
	Median	0.4115	0.4037		0.4531	0.4515	

$P$ -values correspond to the Mann–Whitney  $U$  test.

**Table S4. Network centralities of positively selected genes ( $q < 0.1$ ) and genes with no signatures of positive selection in *S. cerevisiae***

		BioGRID			STRING		
		Selected genes ( $n = 5$ )	Other genes ( $n = 2040$ )	$P$ -value	Selected genes ( $n = 5$ )	Other genes ( $n = 2062$ )	$P$ -value
Degree	Mean	15.60	26.86	0.516	71.40	112.16	0.608
	Median	9	14		76	77	
Betweenness	Mean	$3.8 \times 10^{-5}$	$1.90 \times 10^{-4}$	0.764	$2.1 \times 10^{-4}$	$1.7 \times 10^{-4}$	0.782
	Median	$1.0 \times 10^{-5}$	$2.29 \times 10^{-5}$		$1.1 \times 10^{-4}$	$7.3 \times 10^{-5}$	
Closeness	Mean	0.4141	0.3990	0.369	0.4474	0.4444	0.818
	Median	0.4190	0.4037		0.4497	0.4516	

$P$ -values correspond to the Mann–Whitney  $U$  test.

**Table S5. Network centralities of positively selected genes ( $P < 0.05$ ) and genes with no signatures of positive selection in *D. melanogaster***

		BioGRID			STRING		
		Selected genes ( $n = 350$ )	Other genes ( $n = 6171$ )	$P$ -value	Selected genes ( $n = 247$ )	Other genes ( $n = 4167$ )	$P$ -value
Degree	Mean	10.49	9.19	0.049*	71.23	61.17	0.0004***
	Median	4	4		35	23	
Betweenness	Mean	$4.5 \times 10^{-4}$	$3.8 \times 10^{-4}$	0.008**	$1.3 \times 10^{-4}$	$1.1 \times 10^{-4}$	0.242
	Median	$5.0 \times 10^{-5}$	$3.0 \times 10^{-5}$		$4.0 \times 10^{-5}$	$2.0 \times 10^{-5}$	
Closeness	Mean	0.2418	0.2387	0.045*	0.3280	0.3214	0.0075**
	Median	0.2439	0.2406		0.3312	0.3243	

$P$ -values correspond to the Mann–Whitney  $U$  test. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ .

**Table S6. Network centralities of positively selected genes ( $P < 0.01$ ) and genes with no signatures of positive selection in *D. melanogaster***

		BioGRID			STRING		
		Selected genes ( $n = 139$ )	Other genes ( $n = 6373$ )	$P$ -value	Selected genes ( $n = 95$ )	Other genes ( $n = 4310$ )	$P$ -value
Degree	Mean	11.27	9.21	0.018*	80.57	61.32	$2.7 \times 10^{-5}***$
	Median	5	4		51	23	
Betweenness	Mean	$5.1 \times 10^{-4}$	$3.8 \times 10^{-4}$	0.053	$1.7 \times 10^{-4}$	$1.0 \times 10^{-4}$	0.022*
	Median	$6.2 \times 10^{-5}$	$3.2 \times 10^{-5}$		$6.2 \times 10^{-5}$	$2.0 \times 10^{-5}$	
Closeness	Mean	0.2456	0.2387	0.006**	0.3304	0.3215	0.006**
	Median	0.2473	0.2406		0.3359	0.3243	

$P$ -values correspond to the Mann–Whitney  $U$  test. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ .

**Table S7. Network centralities of positively selected genes ( $q < 0.1$ ) and genes with no signatures of positive selection in *D. melanogaster***

		BioGRID			STRING		
		Selected genes ( $n = 50$ )	Other genes ( $n = 6462$ )	$P$ -value	Selected genes ( $n = 33$ )	Other genes ( $n = 4167$ )	$P$ -value
Degree	Mean	10.16	9.25	0.542	102.15	61.42	$4.2 \times 10^{-4}***$
	Median	4	4		72	23	
Betweenness	Mean	$4.3 \times 10^{-4}$	$3.9 \times 10^{-4}$	0.717	$2.5 \times 10^{-4}$	$1.1 \times 10^{-4}$	0.002**
	Median	$3.1 \times 10^{-5}$	$3.2 \times 10^{-5}$		$9.4 \times 10^{-5}$	$2.1 \times 10^{-5}$	
Closeness	Mean	0.24612	0.23883	0.154	0.33877	0.32160	0.009**
	Median	0.24267	0.24070		0.34371	0.32445	

$P$ -values correspond to the Mann–Whitney  $U$  test. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ .