

Fig. S1: Catalase, Glutathione peroxidase, peroxiredoxin and superoxide dismutase activity is not correlative with lifespan.
(A) Catalase activity in primary fibroblasts from 12 species of rodents, 18 species of primates and 21 species of birds.
(B) Peroxiredoxin activity in primary fibroblasts from 17 species of rodents, 15 species of primates and 18 species of birds.
(C) Glutatione peroxidase activity in primary fibroblasts from 17 species of rodents, 15 species of primates and 18 species of birds.
(D) Superoxide dismutase activity in primary fibroblasts from 17 species of rodents, 15 species of primates and 18 species of birds.
(D) Superoxide dismutase activity in primary fibroblasts from 17 species of rodents, 15 species of primates and 18 species of birds.
Significance is based on simple linear regression analysis. Error bars if present represent multiple individuals assayed in a species.
Humans are shown with an 'H' but are excluded from statistical analysis. MLS = Maximum recorded species lifespan in years





ontidae PHRIKATNNKGKEK

Chinchillidae PHRIKATNIKGKE

(A) Contrast between antibody binding epitope and published sequences on NCBI for primate species. Note Otolemur garnettii and Tarsius syrichta were not listed as all species evaluated in figure 2 were contained within the Simiiformes infraorder of which these two species are outside . (B) Although the TXNRD3 epitope slightly differed for Hylobatidae this did not effect antibody binding affinity. Shown through an ELISA assay with custom produced peptides. (C) The primate species used in figure 2 span 8 families, although sequence data is only available of species in 5 of these families we consider coverage sufficient to assume the sequences are conserved accross all 8 families. (D) List of primate species in figure 2. We considered sequence data sufficient to include all species in analysis. (E) Contrast between antibody binding epitope and published sequences on NCBI for rodent species. Note Blesmols (mole rats) were excluded as these considered species were considered distinct from other rodent species. (F - H) Differences in antibody binding affinity determined by ELISA assay against custom synthesized peptides in some species led to the exclusion of some rodent groups from analysis in figure 2.

Caviidae PHRIKATNNKGKE

Erethizontidae

Sciuridae ATGERERYLGIEGDKEVCHADDLESLEW



Fig. S3: Mitochondrial but not cytosolic thioredoxin reductase activity correlates with lifespan.

Thioredoxin reductase activity in primary fibroblasts from 7 species primates, Cells were divided into mitochondrial and cytosolic fractions prior to assay.





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Fig. S4: Protein levels of glutathione reductase has a positive correlation with lifespan amongst primate and rodent species. (A) Representative immunoblots for primate species. (B) Scatterplot for GSR amongst primate species. (C) Representative immunoblots for rodent species. (D) Scatterplot for GSR amongst primate species. (E) Contrast between antibody binding epitope and published sequences on NCBI for primate species. (F) Contrast between antibody binding affinity in primates. Shown through an ELISA assay with custom synthesized peptides (H) Most epitope variations do not effect antibody binding affinity in rodents though antibody binding affinity was altered in Muridea species (I) Muridae species and Castoridae species were excluded from evaluation to differences in antibody binding affinity in Muridea and lack of sequence information in Castoridae.

Β

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	maximum lifespan (yrs)	(6)sew	logu(mass)	TXNRD2	mass predicted lifespan	mass predicted TXNRD2	mass independent lifespan	mass independent TXNRD2
Common Marmoset	17	255	2.41	19.56	17.56	10.10	-1.06	9.46
Pygmy Marmoset	19	124	2.09	25.43	13.17	4.86	5.43	20.57
Red Tamarin	21	501	2.70	19.26	21.66	15.00	-1.16	4.26
Noisy douroucouli	22	873	2.94	21.28	25.03	19.02	-2.93	2.26
L'Hoest's monkey	24	4700	3.67	16.42	35.25	31.24	-11.15	-14.82
Red titi	26	1120	3.05	14.10	26.54	20.83	-0.14	-6.73
Olive Baboon	28	24000	4.38	18.09	45.15	43.07	-17.65	-24.98
Common squirrel monkey	30	925	2.97	11.79	25.38	19.44	4.82	-7.66
Vervet	31	5620	3.75	13.87	36.33	32.53	-5.53	-18.66
Common woolly monkey	32	7650	3.88	14.93	38.21	34.77	-6.21	-19.84
Hamadryas Baboon	38	18000	4.26	16.70	43.40	40.98	-5.90	-24.28
Cynomolgus	39	6363	3.80	20.34	37.09	33.44	1.91	-13.10
Rhesus Macaque	40	8235	3.32	24.84	38.65	35.31	1.35	-10.47
Mandrill	40	23000	4.36	34.09	44.89	42.76	-4.89	-8.67
Bonobo	55	39925	4.60	76.85	48.24	46.76	6.76	30.03
Gorilla	55	139842	5.15	93.31	55.85	55.86	-0.45	37.46
White-handed gibbon	56	6810	3.83	82.13	37.50	33,93	18.50	48.20
Orangutan	59	64475	4.81	53.64	51.15	50.24	7.85	3.40
Chimpanzee	59	44984	4.65	41.10	48.97	47.63	10.43	-6.53

	maximum lifespan (yrs)	(6)ssew	(ssem)ngol	TXNRD activity	mass predicted lifespan	mass predicted TXNRD activity	mass independent lifespan	mass independent TXNRD activity
Common Marmoset	17	255	2.41	51.70	14.03	47.42	2.47	4.28
Coquerel's mouse lemur	17	311	2.49	37.50	15.37	50.38	2.05	-12.88
Red Tamarin	21	501	2.70	67.18	18.61	57.50	1.89	9.68
L'Hoest's monkey	24	4700	3.67	75.27	33.78	90.93	-9.68	-15.66
Red titi	26	1120	3.05	90.79	24.06	69.51	2.54	21.28
Olive Baboon	28	24000	4.38	83.77	44.84	115.28	-17.54	-31.51
Vervet	31	5620	3.75	49.35	35.00	93.60	-4.20	-44.25
Common woolly monkey	32	7650	3.88	107.30	37.09	98.20	-5.09	9.10
Hamadryas Baboon	38	18000	4.26	130.99	42.89	110.98	-5.39	20.01
Rhesus Macaque	40	8235	3.92	75.76	37.59	99.30	2.41	-23.54
Red-capped mangabey	46	9493	3.98	128.12	38.55	101.43	7.45	26.69
Bonobo	55	39925	4.60	146.13	48.29	122.88	6.71	23.25
Gorilla	55	139842	5.15	115.56	56.79	141.60	-1.59	-26.04
Orangutan	59	64475	4.81	133.72	51.54	130.04	7.46	3.68
Chimpanzee	59	44984	4.65	160.56	49.10	124.66	10.30	35,90

С

	maximum lifespan (yrs)	(6)sseu	log41(mass)	TXNRD2	mass predicted lifespan	mass predicted TXNRD2	mass independent lifespan	mass independent TXNRD2
mouse	4	21	1.31	70.62	5.56	40.89	-1.56	29.74
meadow vole	4	49	1.69	40.01	6.70	65.87	-2.70	-25.85
cotton rat	5	185	2.27	24.94	8.42	103.95	-3.22	-79.01
prairie vole	5	40	1.60	58.60	6.43	60.05	-1.13	-1.45
oldfield mouse	6	14	1.15	60.67	5.07	29.96	0.43	30.71
gerbil	6	53	1.73	44.78	6.80	68.22	-0.50	-23.44
nile kusu	7	110	2.04	124.52	7.75	89.05	-1.05	35.47
13-lined ground squirrel	8	173	2.24	121.66	8.33	101.98	-0.43	19.63
white footed mouse	8	23	1.36	38.13	5.71	44.19	2.19	-6.05
deer mouse	8	21	1.31	54.70	5.56	40.89	2.74	13.81
chipmunk	10	96	1.98	49.15	7.57	85.14	1.93	-35.93
red squirrel	10	200	2.30	90.08	8.52	106.18	1.28	-16.11
prairie dog	11	1125	3.05	187.77	10.76	155.70	0.24	32.07
guinea pig	12	728	2.86	163.65	10.20	143.22	1.80	26.43

	maximum lifespan (yrs)	(6)ssew	log4(mass)	TXNRD activity	mass predicted lifespan	mass predicted TXNRD activity	mass independent lifespan	mass independent TXNRD activity
Golden Hamster	4	105	2.02	72.57	9.19	133.12	-5.29	-60.55
Wild House Mouse	4	21	1.31	90.76	4.32	113.74	-0.32	-22.98
Cotton Rat	5	185	2.27	93.83	10.88	139.84	-5.68	-46.01
Gerbil	6	53	1.73	93.75	7.16	125.05	-0.86	-31.30
African Grass Rat	7	110	2.04	41.47	9.33	133.67	-2.63	-92.20
Cactus Mouse	7	25	1.40	140.83	4.91	116.09	2.49	24.73
13-lined Ground Squirrel	8	173	2.24	181.89	10.68	133.02	-2.78	42.87
Deer Mouse	8	21	1.31	121.11	4.32	113.74	3.98	7.37
Chipmunk	10	96	1.98	151.27	8.93	132.05	0.57	19.22
Red Squirrel	10	200	2.30	186.89	11.12	140.76	-1.32	46.13
Guinea Pig	12	728	2.86	153.24	14.98	156.09	-2.98	3.15
Degu	14	235	2.37	192.95	11.60	142.67	2.40	50.28
Fox Squirrel	16	800	2.90	213.74	15.26	157.21	0.74	56.53
Chinchilla	17	643	2.81	153.51	14.60	154.61	2.60	-1.10
American Beaver	23	20250	4.31	145.42	24.90	195.54	-1.50	-50.12
North American Porcupin	23	8600	3.93	180.48	22.35	185.38	1.05	-4.91
Gray squirrel	24	533	2.73	211.28	14.04	152.33	9.56	58.83

Fig. S5 Raw data for mass correction in figure 3. Raw and mass corrected data for: (A) TXNRD2 protein content amongst species of primates, (B) TXNRD2 protein content amongst species of rodent, (C) TXNRD activity amongst species of primates, (D) TXNRD activity amongst species of rodent. 'Predicted' values are based on the linear regression of Log10(species body mass) plotted against species maximum lifespan, TXNRD activity and TXNRD2 protein levels. "mass-independent' values are the predicted values subtracted from the actual values (residuals from the above plots).

B

C

	MLS	TXNRD activity
Marmoset	16.5	51.7
Coquerel's mouse lemur	17.4	37.5
Red tamarin	20.5	67.18
L'Hoest's monkey	24.1	75.27
Red titi	26.4	90.79
Olive baboon	27.5	83.77
Yervet	30.8	49.35
Vooliy monkey	32	107.3
Hamadryas baboon	37.5	130.99
Rhesus macaque	40	75.76
Red-capped mangabey	46	128.12
Bonobo	55	146.13
Gorilla	55.4	115.56
Orangutan	59	133.72
Chimpanzee	59.4	160.56

Hamadrias haboon
Dhama
Rnesus macaque
Red-capped mangabey
Bonobo
Gorilla
Orangutan
Chimpanzee

	MLS	TXNRD activity
American beaver	23.4	145.42
Vild house mouse	4	90.76
African grass rat	6.7	41.465
Gerbil	6.3	93.745
Cactus mouse	7.4	140.825
Deer mouse	8.3	121.105
Cotton rat	5.2	93.825
Golden hamster	3.9	72.565
Ground squirrel	7.9	181.885
Chipmunk	9.5	151.27
Red squirrel	9.8	186.89
Fox squirrel	16	213.74
Gray squirrel	23.6	211.28
Guinea pig	12	159.235
Porcupine	23.4	180.475
Chinchilla	17.2	153.51
Deau	14	192.95

		Predicted traits of ancestor		Phyloge	netic contrast	
Node	Species connected by node	MYA	MLS	TXNRD activity	MLS Contrast	TXNRD Contrast
Α	Marmoset to Tamerin	16	18.5	59.4	4.0	15.5
в	Node A to Voolly monkey	23	21.7	70.6	13.5	47.9
C	Node B to Red titi	26	22.1	72.7	4.8	20.2
D	L'Hoest's monkey to Vervet	7	27.5	62.3	6.7	-25.9
E	Olive baboon to Hamadryas baboon	1	32.5	107.4	10.0	47.2
F	Node E to Red-capped mangabey	5	38.5	116.6	13.5	20.7
G	Node F to Rhesus macaque	7	38.8	107.5	1.5	-40.8
н	Node D to Node G	10	33.1	84.9	11.4	45.2
- I	Bonobo to Chimpanzee	3	57.2	153.3	4.4	14.4
J	Node I to Gorilla	9	56.5	138.2	1.8	37.8
к	Node J to Orangutan	21	57.4	136.6	2.5	-4.5
L	Node H to Node K	31	49.6	119.9	24.3	51.7
м	Node C to Node L	43	38.2	100.4	27.4	47.2
- N	Node M to Mouse lemur	78	31.8	80.9	20.8	62.9

		Predicted traits of ancestor		Phylogenetic contrast		
Node	Species connected by node	MYA	MLS	TXNRD activity	MLS Contrast	TXNRD Contrast
Α	House mouse to African grass rat	11	5.4	66.1	2.7	-49.3
в	Node A to Gerbil	18	5.6	73.8	-1.0	-27.6
С	Cactus mouse to Deer mouse	7	7.9	131.0	0.9	-19.7
D	Node C to Cotton rat	18	6.8	116.9	2.7	37.1
Е	Node D to Golden hamster	20	6.6	112.8	2.9	44.3
F	Node B to Node E	21	6.3	103.1	1.0	39.0
G	Node F to American beaver	65	13.2	120.2	17.1	42.3
н	Guinea pig to Porcupine	37	17.7	169.9	11.4	21.2
- 1	Chinchilla to Degu	34	15.6	173.2	3.2	-39.4
J	Node H to Node I	38	17.3	170.5	2.1	-3.4
к	Fox squirrel to Grey squirrel	8	19.8	212.5	7.6	-2.5
L	Node K to Red squirrel	11	17.7	207.0	10.0	25.6
м	Ground squirrel to Chipmunk	11	8.7	166.6	1.6	-30.6
N	Node L to Node M	46	13.2	186.8	9.0	40.4
0	Node J to Node N	67	14.9	180.0	4.1	-16.3
Р	Node G to Node O	69	14.3	160.0	-1.1	-39.9

U		
	MLS	TXNRD2
Common Mamoset	16.5	19.56
Pigmy Marmoset	18.6	25.43
Red Tamerin	20.5	19.26
Noisy Douroucouli	22.1	21.28
L'Hoest's Monkey	24.1	16.42
Red Titi	26.4	14.10
Olive Baboon	27.5	18.09
Squirrel Monkey	30.2	11.79
Yervet	30.8	13.87
Voolly Monkey	32	14.93
Hamadryas Baboon	37.5	16.70
Cynomolgas	39	20.34
Mandrill	40	34.09
Rhesus Macaque	40	24.84
Bonobo	55	76.85
Gorilla	55.4	93.31
Gibbon	56	82.13
Orangutan	59	53.64
Chimnanzee	594	41 10

		ceu traits	Predicted traits of ancestor		tic contrast
pecies connected by node	MYA	MLS	TXNRD2	MLS Contrast	TXNRD2
imy Marmoset to Common	5	17.6	22.5	2.1	5.9
amerin to Noisy Douroucouli	14	21.3	20.3	1.6	2.0
sus Macaque to Cynomolgas	4	39.5	22.6	1.0	4.5
Node A to Node B	16	20.7	20.6	3.8	-2.2
ode D to Squirrel monkey	20	22.9	18.6	9.5	-8.8
lode E to Voolly monkey	23	23.9	19.0	9.1	-3.7
Red titi to Node F	26	24.1	18.5	2.5	-4.9
baboon to Hamadryas baboon	1	32.5	17.4	10.0	-1.4
Node H to Mandrill	5	36.0	25.2	7.5	16.7
Node C to Node I	7	37.8	23.9	3.5	-2.6
ervet to L'hoesti monkey	7	27.5	15.1	6.7	-2.5
Node J to Node K	10	32.1	19.1	10.3	8.8
Chimpanzee to Bonobo	3	57.2	59.0	4.4	-35.8
Node M to Gorilla	9	56.5	72.8	1.8	-34.3
Node N to Orangutan	18	57.3	66.2	2.5	-19.2
Node O to Gibbon	21	57.2	68.2	1.3	-16.0
Node L to Node P	31	49.5	53.1	25.1	49.1
Node G to Node Q	43	38.8	38.5	25.4	34.6
	pecies connected by node mmy Marmoset to Common famerin to Noisy Douroucouli sus Macaque to Cynomolgas Node A to Node B lode D to Squirrel monkey Red titi to Node F baboon to Hamadryas baboon Node H to Mandrill Node C to Node I ervet to L'hoesti monkey Node J to Node K Chimpanzee to Bonobo Node M to Gorilla Node M to Gorilla Node N to Orangutan Node O to Gibbon Node C to Node P Node G to Node Q	pecies connected by node         MYA           mmy Marmoset to Common         5           famerin to Noisy Douroucouli         14           sus Macaque to Cynomolgas         4           Node A to Node B         16           lode D to Squirrel monkey         20           lode E to Voolly monkey         23           Red titi to Node F         26           baboon to Hamadrgas baboon         1           Node A to Node I         7           vervet to L'hoesti monkey         7           vervet to L'hoesti monkey         7           Node J to Node K         10           Chimpanzee to Bonobo         3           Node M to Garilla         9           Node O to Gibbon         21           Node L to Node P         31           Node G to Node Q         43	pecies connected by nodeMTAMLSprim Marmoset to Common517.6famerin to Noisy Douroucouli1421.3sus Macaque to Cynomolgas439.5Node A to Node B1620.7lode D to Squirrel monkey2022.9lode E to Voolly monkey2323.9Red titi to Node F2624.1baboon to Hamadryas baboon132.5Node A to Node I737.8vervet to L'hoesti monkey727.5Node J to Node K1032.1Chimpanzee to Bonobo357.2Node M to Gorilla956.5Node O to Gibbon2157.2Node C to Node P3149.5Node C to Node Q4338.8	Decise connected by node         MTA         MLS         TXNHU2           mmy Marmoset to Common         5         17.6         22.5           famerin to Noisy Douroucouli         14         21.3         20.3           sus Macaque to Cynomolgas         4         39.5         22.6           Node A to Node B         16         20.7         20.6           lode D to Squirrel monkey         20         22.9         18.6           lode E to Voolly monkey         23         23.9         19.0           Red titi to Node F         26         24.1         18.5           baboon to Hamadrigas baboon         1         32.5         17.4           Node H to Mandrill         5         36.0         25.2           Node C to Node I         7         37.8         23.9           ervet to L'hoesti monkey         7         27.5         15.1           Node M to Gorilla         9         56.5         72.8           Node N to Orangutan         18         57.2         68.2           Node N to Orangutan         20         53.1         Node G to Node P         31         49.5         53.1           Node G to Node Q         43         38.8         38.5         38.5	Decise connected by node         MTA         MLS         TXNHU2         MLS         Dit Sector           ming Marmoset to Common         5         17.6         22.5         2.1           famerin to Noisy Douroucouli         14         21.3         20.3         1.6           sus Macaque to Cynomolgas         4         39.5         22.6         1.0           Node A to Node B         16         20.7         20.6         3.8           lode D to Squirrel monkey         20         22.9         18.6         9.5           lode E to Voolly monkey         23         23.9         19.0         9.1           Red titi to Node F         26         24.1         18.5         2.5           baboon to Hamadrigas baboon         1         32.5         17.4         10.0           Node H to Mandrill         5         36.0         25.2         7.5           Node C to Node I         7         37.8         23.9         3.5           ervet to L'hoesti monkey         7         27.5         15.1         6.7           Node M to Gorilla         9         56.5         72.8         1.8           Node N to Orangutan         18         57.3         66.2         2.5

## D

	MLS	TXNRD2
House mouse	4	70.62
Nile kusu	6.7	124.52
Gerbil	6.3	44.78
Oldfield mouse	5.5	60.67
Deer mouse	8.3	54.70
White-footed mouse	7.9	38.13
Cotton rat	5.2	24.94
Meadow vole	4	40.01
Prairie vole	5.3	58.60
13-lined ground squirrel	7.9	121.66
Prairie dog	11	187.77
Chipmunk	9.5	49.15
Red squirrel	9.8	90.08
Guinea nig	12	169.65

		Predic	cted traits	of ancestor	Phylogenetic contrast		
Node	Species connected by node	MYA	MLS	TXNRD2	MLS Contrast	TXNRD2	
Α	Degu to Chinchilla	34	15.6	133.8	3.2	-31.1	
в	Node A to Guinea pig	38	15.3	137.0	3.6	-15.4	
С	Oldfield mouse to Deer mouse	1	6.9	98.1	2.8	35.5	
D	Node C to White-footed mouse	4	7.3	117.5	1.0	45.3	
E	Node D to Cotton rat	18	2.8	27.4	2.1	74.2	
F	Meadow vole to Prairie vole	1	4.7	72.9	1.3	-20.1	
G	Node E to Node F	19	3.0	31.2	1.9	45.5	
н	Node G to Gerbil	21	3.1	34.0	3.3	84.8	
- I	Ground squirrel to Prairie dog	9	9.5	154.1	3.1	39.5	
J	Node I to Chipmunk	11	9.5	152.0	0.1	-13.9	
ĸ	Node J to Red squirrel	46	9.6	141.1	0.3	-25.1	
L	Node B to Node K	67	12.0	139.4	5.7	-4.1	
м	Node H to Node I	63	11.6	124 5	89	105.4	

Fig. S6: Raw data for phylogenetic correction in figure 3. Raw and phylogenetically contrasted data for: (A) TXNRD activity amongst species of primates, (B) TXNRD activity amongst species of rodent, (C) TXNRD2 protein content amongst species of primates, (D) TXNRD2 protein content amongst species of rodent. A phylogeny was constructed for the species used in each data set (weighted based on millions of years, MYA, divergence). Values for common ancestors at each node were calculated. Phylogenetic contrasts were performed between each species and it's closest relative. All contrasts involved the subtraction of the shorter lived species from the longer lived species to reduce bias to the distribution.



Fig. S7: Correlation between thioredoxin reductase 2 protein level and lifespan remains significant after correction of mitochondrial load. (A) Representative immunoblots for primate species. (B) Contrast between porin antibody binding epitope and published sequences on NCBI for primate species. (C) Representative immunoblots for rodent species. (D) Contrast between porin antibody binding epitope and published sequences on NCBI for rodent species. (E) Scatterplot TXNRD2 for primates normalized to porin (F) Scatterplot TXNRD2 for rodents normalized to porin. (G – K) Thioredoxin reductase 2 protein levels in liver tissue from Snell dwarf, Papp-A, GHR-/-, liver-specific GHR-/- and NDGA treated mice normalized to porin. (L) p-value table of two-way ANOVA analysis for B-M). T-test were run only when a significant interaction term was observed. Values are shown in red when p < 0.05.



## Fig. S8: mRNA level of Glutatione reductase have no consistent trends in relation to lifespan in primate tissue.

Summarized scatterplots of GSR. Red lines represent trends which are significant at p < 0.05, red dashed lines p < 0.1, black lines p > 0.1. N varies from 6 – 12 species. Significance is based on simple linear regression analysis. Plots represents a secondary analysis of RNAseq data from (Peng et al., 2015). N varies from 6 – 12 species depending on tissue availability.



Fig. S9: TXNRD2 protein is unchanged in liver tissue from caloric restricted, rapamycin, 17- $\alpha$ -estradiol and acarbose treated mice. TXNRD2 protein levels in liver tissue from 12 month old mice treated with the above interventions (initiated at 4 months of age) N = 4.



Fig. S10 Lifespan extension from thioredoxin reductase 2 overexpression is robust in both male and female flies. (A) Trxr-2 mRNA levels in GS-Da-*GAL4>yw* mated female flies in the absence and presence of the RU486 which serves to induce the transgene. N = 12 per condition. (B) Thioredoxin reductase activity in GS-Da-*GAL4>yw* mated *fe*male flies. N = 12 per condition. (C) Lifespan of GS-Da- *GAL4>yw mated* male flies, N  $\approx$  200. (D) Trxr-2 mRNA levels GS-Da-*GAL4>yw* mated male flies. Flies are of the same genetic background as those in A - C minus the transgene this serves as a control for off target effects. N = 12 per condition. (E) Thioredoxin reductase activity in GS-Da- *GAL4>yw mated* male flies. N = 12 per condition. (F) Lifespan of GS-Da-*GAL4>yw* mated male flies, N  $\approx$  250. (G-H) Two independent repeats of the lifespan of GS-Da-*GAL4>UAS-Trxr-2* mated female flies. (I) Independent repeats of the lifespan of GS-Da-*GAL4>UAS-Trxr-2* mated male flies. (J) Lifespan of w<sup>1118</sup>>UAS-*Trxr-2* mated female flies, N  $\approx$  250 (control for off target effects).



## Fig. S11: Overexpression of Trxr-1 (orthologue of TXNRD1) does not increase lifespan in flies.

(A) Trxr-1 mRNA levels in GS-Da-GAL4>UAS-Trxr-1A mated female flies in the absence and presence of the RU486 inducer. N = 3 per condition. (B) Trxr-1 mRNA levels in GS-Da-GAL4>UAS-Trxr-1B mated female flies in the absence and presence of the RU486 inducer. N = 3 per condition. (C) Trxr-1 mRNA levels in GS-Da-GAL4>UAS-Trxr-1C mated female flies in the absence and presence of the RU486 inducer. N = 3 per condition.

		2-w	T-test			
		Туре	Sex	Type* Sex	ď	Q
TXNRD2	Snell	< 0.001	0.723	0.761		
	Papp-A	< 0.001	0.051	0.342		
	GHR-/-	< 0.001	< 0.001	0.510		
	Li_GHR-/-	0.450	< 0.001	0.453		
	NDGA	0.008	0.018	0.433		
TXNRD activity	Snell	< 0.001	< 0.001	0.012	0.037	0.065
	Papp-A	0.009	0.311	0.413		
	GHR-/-	0.011	0.217	0.022	0.036	0.131
	Li_GHR-/-	0.9	0.192	0.922		
	NDGA	0.069	0.001	0.035	0.022	0.311

**Table S1.** p-value table of two-way ANOVA analysis for figure 4. T-tests were run only when a significant interaction term was observed. Values are shown in red when p < 0.05.

		GS-Da-GAL4		GS-Tub5-GAL4		GS-elav-GAL4		GS-tigs-GAL4	
		Median (50%)	Maximum (90%)	Median (50%)	Maximum (90%)	Median (50%)	Maximum (90%)	Median (50%)	Maximum (90%)
UAS-Trxr-2	Median (% change)	+ 9.7	+ 5.8	- 0.5	+ 3.7	+ 3.7	+ 0.7	+ 2.6	+ 2.3
		(average of 3 lifespans)							
	Logrank (p-value)	< 0.001		0.04		0.02		< 0.001	
UAS-Trxr-1A	Median (% change)	+ 0.9	+ 0.2	+ 0.2	+ 0.1				
	Logrank (p-value)	0.03		0.265					
UAS-Trxr-1B	Median (% change)	- 1.1	+ 2.3	+ 2.9	+ 5.3	- 0.5	+ 0.4	+ 0.5	0.0
	Logrank (p-value)	0.53		< 0.001		0.937		0.241	
UAS-Trxr-1C	Median (% change)	+ 1.0	+ 2.6	- 3.0	- 0.2				
	Logrank (p-value)	0.331		0.01					
yw	Median (% change)	- 0.6	+ 0.3	- 3.4	- 0.3	+ 1.0	+ 2.1	- 2.0	0.0
	Logrank (p-value)	0.51		0.84		0.124		0.265	

Table S2: Table of % change in fly median & maximum lifespan as well as log-rank significance. Median lifespan is defined as the age at which 50% of flies have died. Maximum lifespan is defined as the age at which 90% of flies have died.