

Supplementary methods: statistical analysis of count data

For the behavioral analysis, we first fitted generalized linear mixed models (GLMM) with Poisson or negative binomial distribution. In some cases, we found better model fits using hurdle models with zero-truncated Poisson or negative binomial distribution. These models generate two outputs: the zero-inflation model, which predicts the probability of zero count, and a conditional model, which fits positive (nonzero) counts. We report the findings from the conditional model except for courtship where we report the zero-inflation model due to the excess of zeros. In this case, we effectively show the probability of courtship display during a five-minute observation.

Supplementary Table S1

The total number of males that were tracked for social status and behavior are as follows. Dominant males: stable, *n*=24; unstable, *n*=25. Subordinate males: stable, *n*=43; unstable, *n*=52.

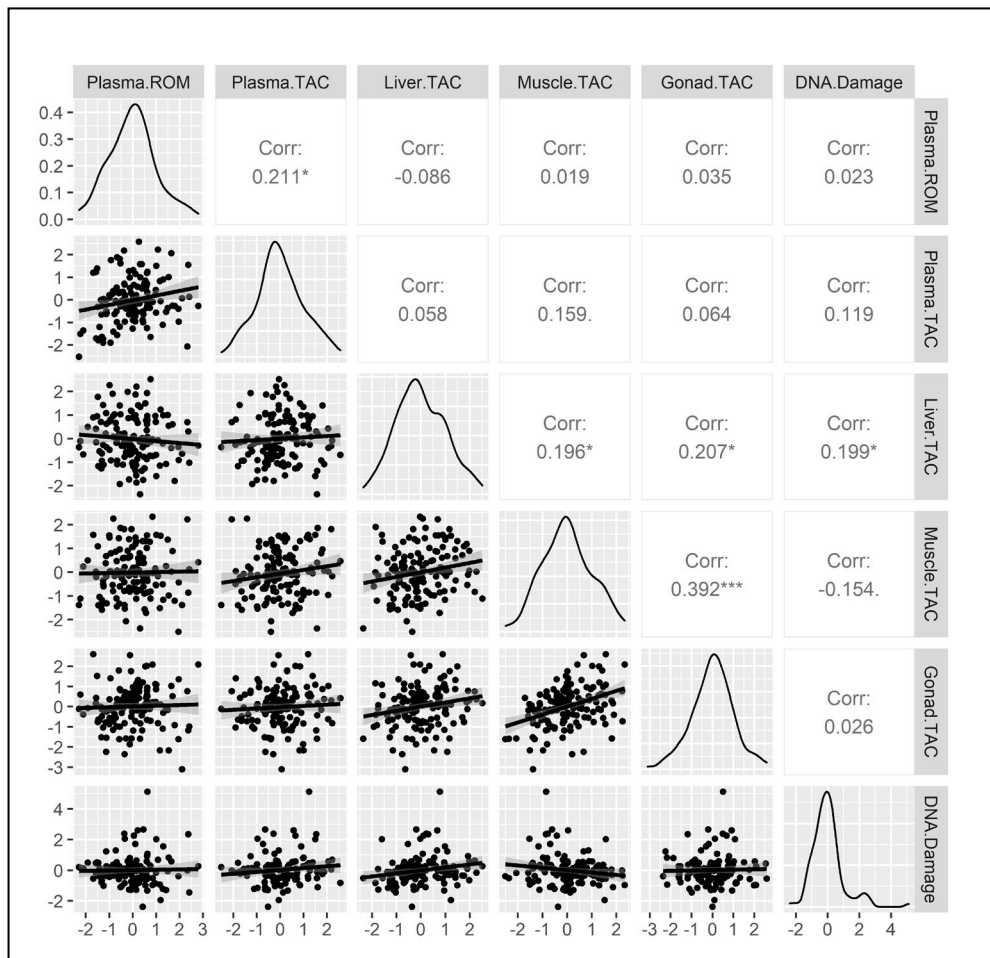
Samples sizes for each measurement of oxidative stress for dominant (DOM) and subordinate (SUB) males in each stability treatment varies depending on sample availability. Shown are reactive oxygen metabolites (ROM), total antioxidant capacity (TAC) and oxidative DNA damage based on 8-OHdG. Samples sizes vary depending on availability of blood/tissue for each measurement.

Stable communities:

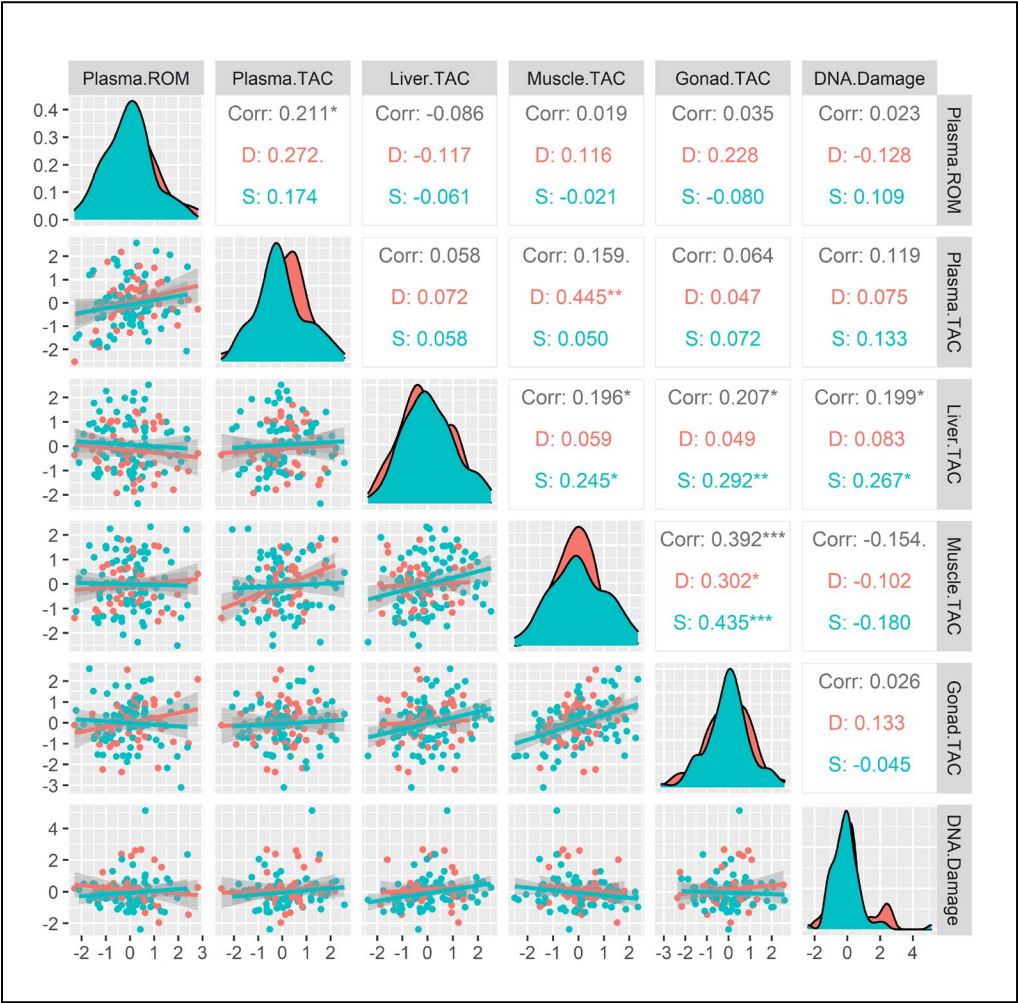
	Plasma ROM	Plasma TAC	Liver TAC	Muscle TAC	Gonad TAC	Liver DNA
DOM	23	23	24	24	24	20
SUB	42	41	43	41	40	37

Unstable communities:

	Plasma ROM	Plasma TAC	Liver TAC	Muscle TAC	Gonad TAC	Liver DNA
DOM	25	24	25	25	24	20
SUB	50	47	52	52	52	43



**Fig. S1A. Correlations across different measurements of oxidative stress.** There were several significant correlations across the different oxidative stress measurements and all significant correlations were positive. Plasma ROM was significantly correlated with plasma TAC but it did not correlate with the other measurements. Plasma TAC only showed a significant correlation with muscle TAC. Tissue TAC measurements were generally correlated and liver TAC was correlated with liver DNA damage. Before analysis, we standardized all measurements by calculating z-scores, which were obtained by subtracting the entire sample mean from each observation and dividing by the standard deviation. Shown are the Pearson correlation coefficient and significance level (\*  $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ ) for each pairwise correlation. Variables shown are plasma reactive oxygen metabolites (ROM), plasma total antioxidant capacity (TAC), and liver oxidative DNA damage based on 8-OHdG.



**Fig. S1B.** Same as supplementary figure 1A but now shown for dominant (D) and subordinate (S) males separately.