

## Supplementary material: Details of statistical analysis performed in R Studio and R commander (version 3.4.1, 2017)

Call:

```
glm(formula = friendly_lat_index ~ age + domestication_num + gender_num +  
group_num + rank + social_index, family = gaussian(identity),  
data = Dataset)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.25847	-0.05255	-0.01936	0.06754	0.17684

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.457774	0.128112	-3.573	0.00154 **
age	0.001554	0.003878	0.401	0.69219
domestication_num	0.053735	0.095284	0.564	0.57802
gender_num	0.050475	0.052285	0.965	0.34398
group_num	0.007565	0.037812	0.200	0.84312
rank	0.088735	0.095671	0.928	0.36290
social_index	0.102087	0.076831	1.329	0.19644

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 0.01225402)

Null deviance: 0.41659 on 30 degrees of freedom  
Residual deviance: 0.29410 on 24 degrees of freedom  
AIC: -40.419

Number of Fisher Scoring iterations: 2

**Spearman correlations:**

	age	friendly_lat_index
age	1.0000	0.0517
friendly_lat_index	0.0517	1.0000

Number of observations: 31

Pairwise two-sided p-values:

	age	friendly_lat_index
age		0.7824
friendly_lat_index	0.7824	

**wilcoxon rank sum test** with continuity correction

data: friendly\_lat\_index by domestication

W = 65, p-value = 0.09425

alternative hypothesis: true location shift is not equal to 0

RcmdrMsg: [6] WARNUNG: warning in wilcox.test.default(x = c(-0.09, -0.08, -0.33,

RcmdrMsg+ -0.45, -0.35, :

RcmdrMsg+ cannot compute exact p-value with ties