

7 Supplementary Information

7.1 Estimating α and the Power of the method of selecting DEGs and comparing with Limma modulated t-test

In the following tables $R := \frac{1}{\mathcal{K}}(r_i^0 + r_i^1)$ as in Definition 2.2.

$\mathcal{K}$	Normal	Log-normal	Lévy
5	0.024667	0.129400	0.545067
10	0.000000	0.009067	0.410533
15	0.000000	0.000800	0.344333
20	0.000000	0.000067	0.304267
25	0.000000	0.000133	0.263533
30	0.000000	0.000000	0.250667
35	0.000000	0.000000	0.229000
40	0.000000	0.000000	0.220067
45	0.000000	0.000000	0.205000
50	0.000000	0.000000	0.196467

Table 15: $P(R > 2)$ for iid X, Y with different marginal distributions.

$\mathcal{K}$	Normal	Lognormal	Levy
5	0.055400	0.156975	0.344788
10	0.000737	0.035112	0.271150
15	0.000025	0.009350	0.233600
20	0.000000	0.002550	0.207100
25	0.000000	0.000700	0.191362
30	0.000000	0.000175	0.174200
35	0.000000	0.000087	0.161312
40	0.000000	0.000013	0.152300
45	0.000000	0.000025	0.145150
50	0.000000	0.000000	0.139263

Table 16: Estimated probabilities $P(\frac{r_i^0}{\mathcal{K}} > 1)$ for iid X, Y with different marginal distributions.

t	$(\mathcal{K} = 5)$	$(\mathcal{K} = 10)$	$(\mathcal{K} = 15)$
0.000	0.02450	0.00002	0.00000
1.111	0.16122	0.00770	0.00026
2.222	0.44240	0.11310	0.02498
3.333	0.67888	0.38126	0.19144
4.444	0.82580	0.64882	0.48872
5.556	0.90356	0.82682	0.74150
6.667	0.94676	0.91688	0.88806
7.778	0.96968	0.96366	0.95534
8.889	0.98108	0.98244	0.98214
10.000	0.98818	0.99160	0.99312

Table 17: $P(R > 2)$ with $Y \sim N(0, 1)$ fixed and $X \sim N(t, 1 + t)$.

t	$(\mathcal{K} = 5)$	$(\mathcal{K} = 10)$	$(\mathcal{K} = 15)$
0.000	0.05504	0.00094	0.00000
1.111	0.40886	0.12402	0.03502
2.222	0.75538	0.57042	0.41078
3.333	0.90926	0.86770	0.82164
4.444	0.96380	0.96562	0.96342
5.556	0.98404	0.99102	0.99318
6.667	0.99310	0.99774	0.99888
7.778	0.99646	0.99920	0.99968
8.889	0.99796	0.99974	0.99986
10.000	0.99882	0.99998	0.99996

Table 18: $P(\frac{r_i^0}{\mathcal{K}} > 1)$ with $X \sim N(0, 1)$ fixed and $Y \sim N(t, 1 + t)$.

$\mathcal{K}$ (per group)	Moderated df	Power
2	12	0.053
3	14	0.072
4	16	0.088
5	18	0.104
8	24	0.153
10	28	0.187
15	38	0.263
20	48	0.339
30	68	0.480
50	108	0.697

Table 19: Estimated power of a limma-style moderated two-sample t-test (two-sided, $\alpha = 0.05$) for a true mean difference $\delta = 0.5$ with $\sigma = 1$. Equal sample sizes per group. Empirical Bayes variance moderation with prior degrees of freedom $d_0 = 10$ and prior variance $s_0^2 = 1$. Power estimated via simulation (1000 genes per replicate, 300 replicates).

7.2 Distributions

The following distributions serve as reference for the location of the peaks:

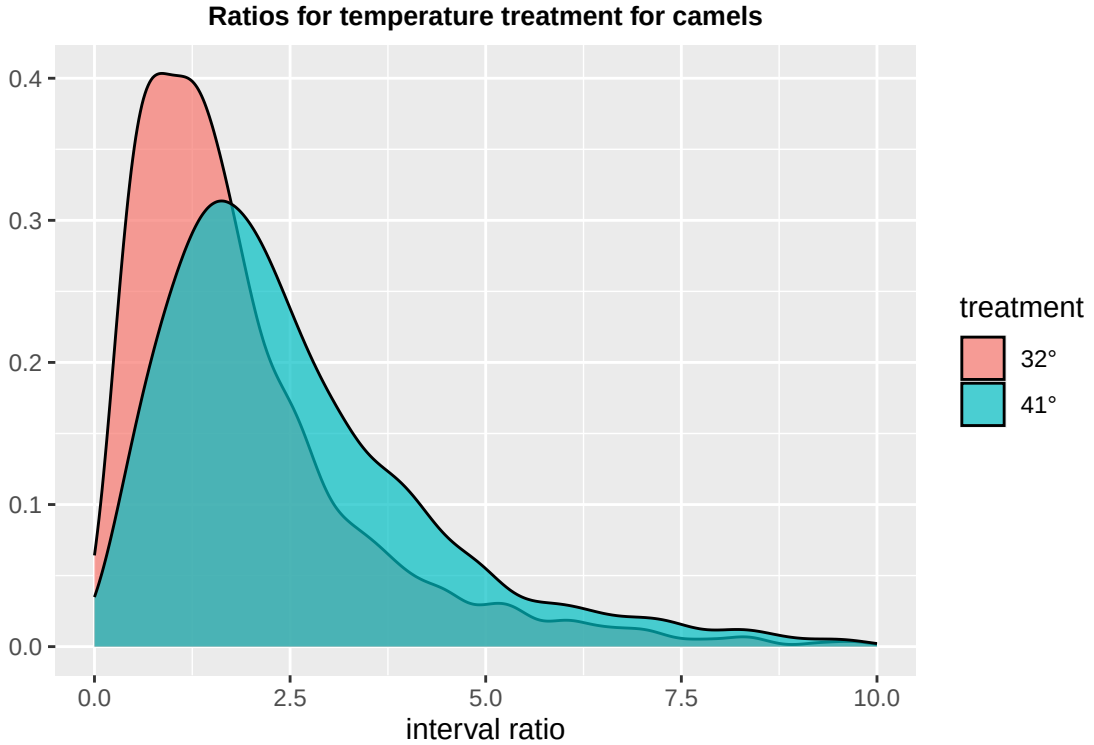


Figure 11: Distributions of the ratios of inter-individual variability before and after treatment for camels under the 32° and 41° treatments for all DEGs.

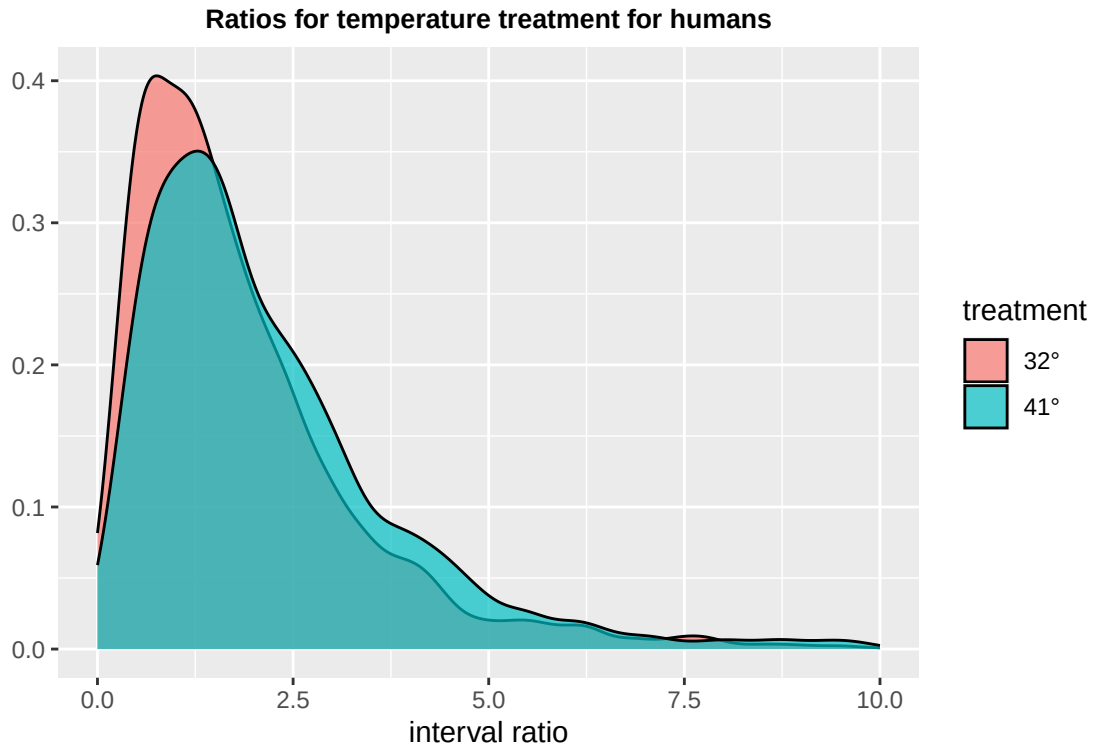


Figure 12: Distributions of the ratios of inter-individual variability before and after treatment for humans under the 32° and 41° treatments for all DEGs.

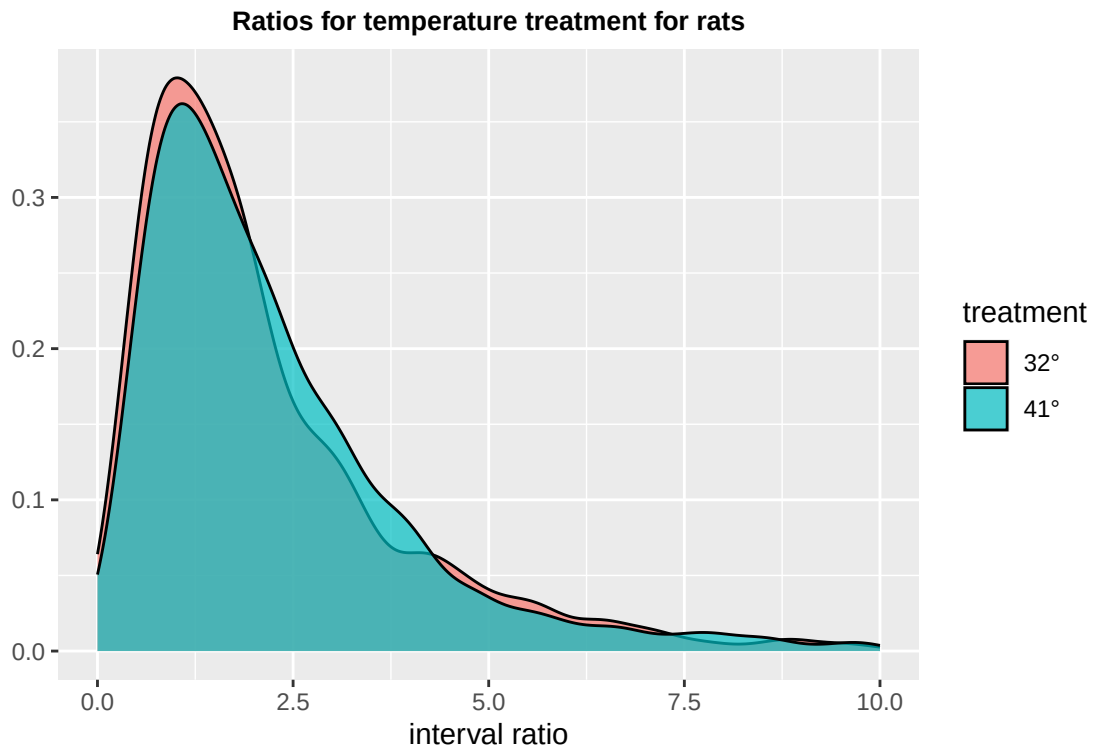


Figure 13: Distributions of the ratios of inter-individual variability before and after treatment for rats under the 32° and 41° treatments for all DEGs.

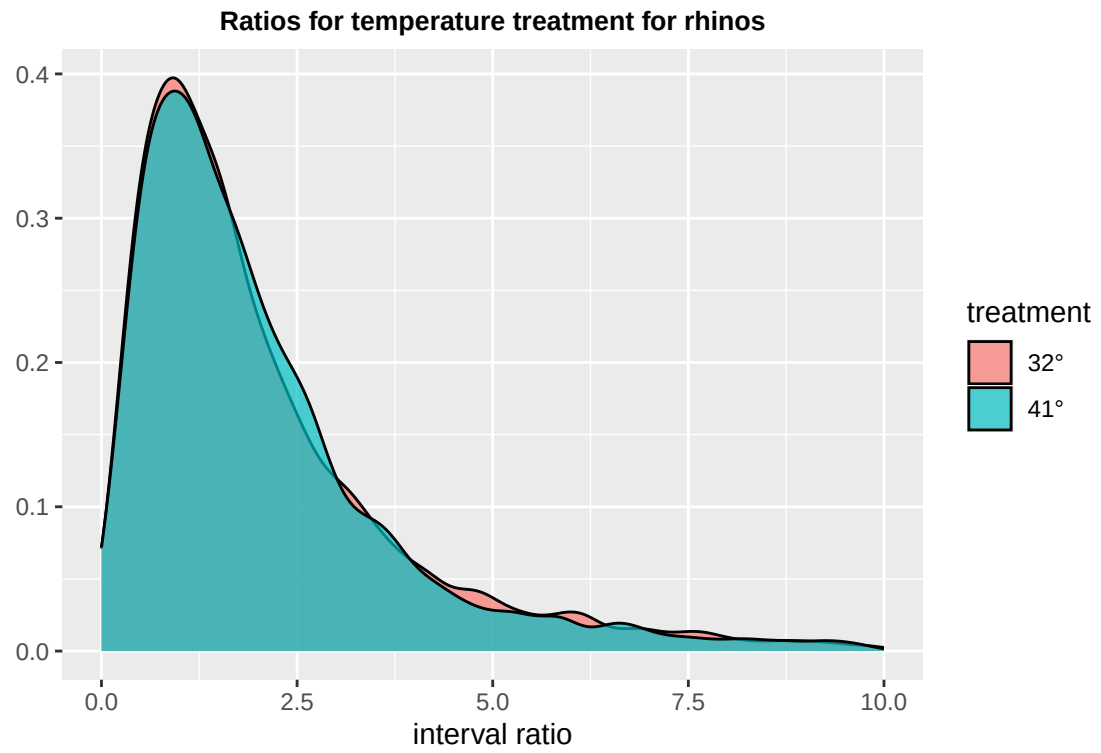


Figure 14: Distributions of the ratios of inter-individual variability before and after treatment for rhinos under the 32° and 41° treatments for all DEGs.

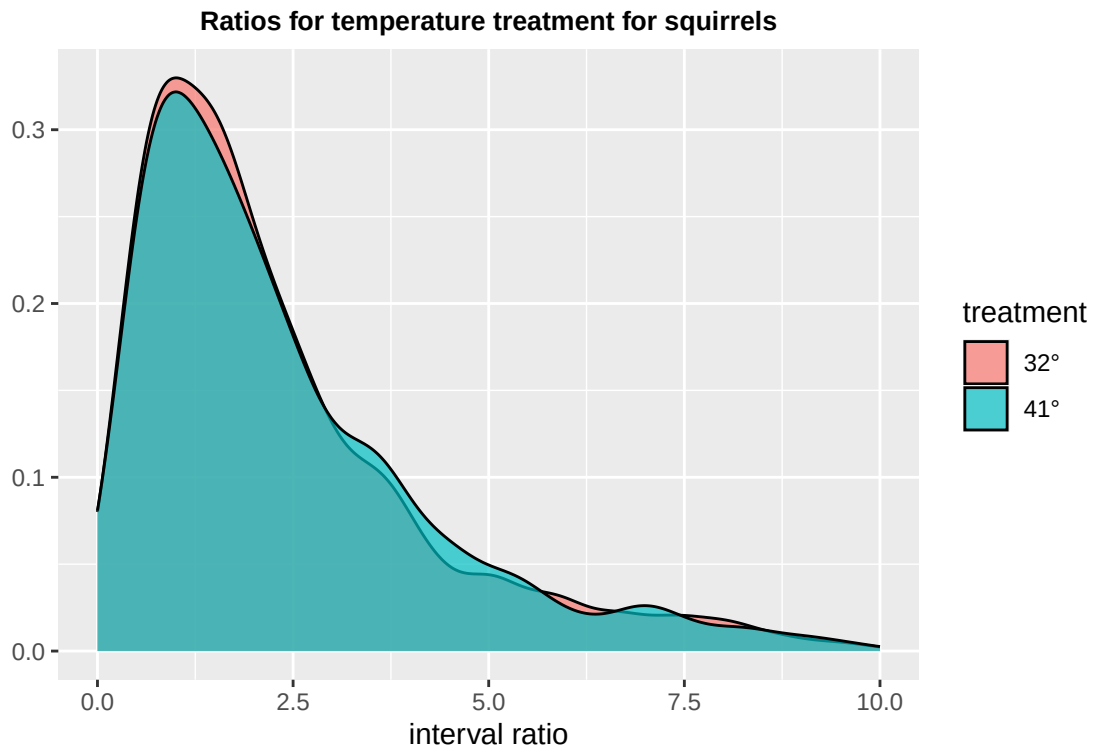


Figure 15: Distributions of the ratios of inter-individual variability before and after treatment for squirrels under the 32° and 41° treatments for all DEGs.

7 The figures below are useful for visualizing the peaks used to define the **extreme response**
8 **sets**. Recall that the Extreme response sets are defined in terms of their relative position in the
9 distributions of inter-individual variability at baseline and after treatment:

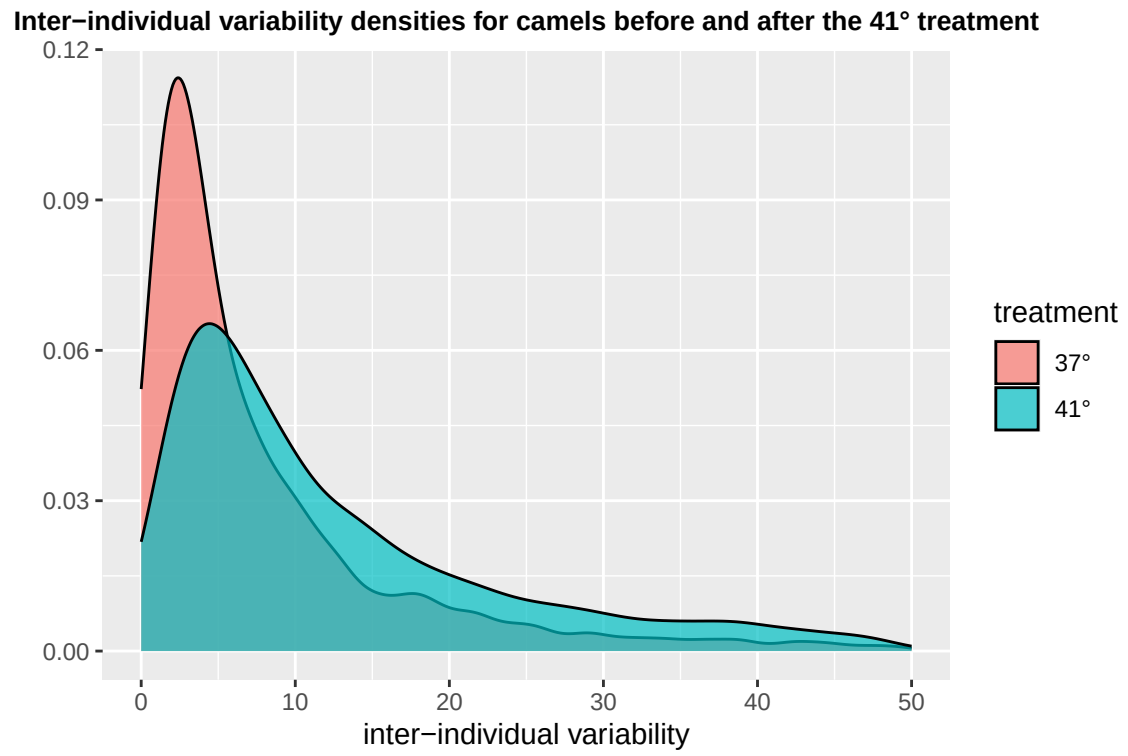


Figure 16: Distributions of the inter-individual variability for camels at 37°(baseline) and the 41° treatment for all DEGs.

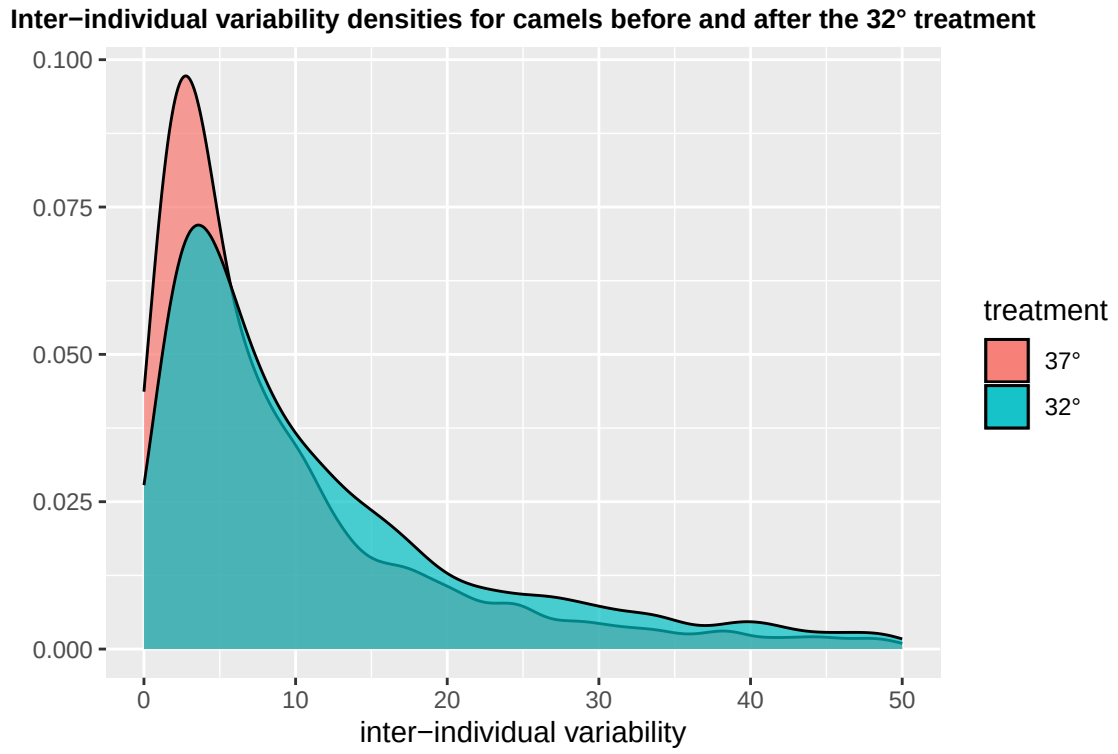


Figure 17: Distributions of the inter-individual variability for camels at 37°(baseline) and the 32° treatment for all DEGs.

Inter-individual variability densities for humans before and after the 41° treatment

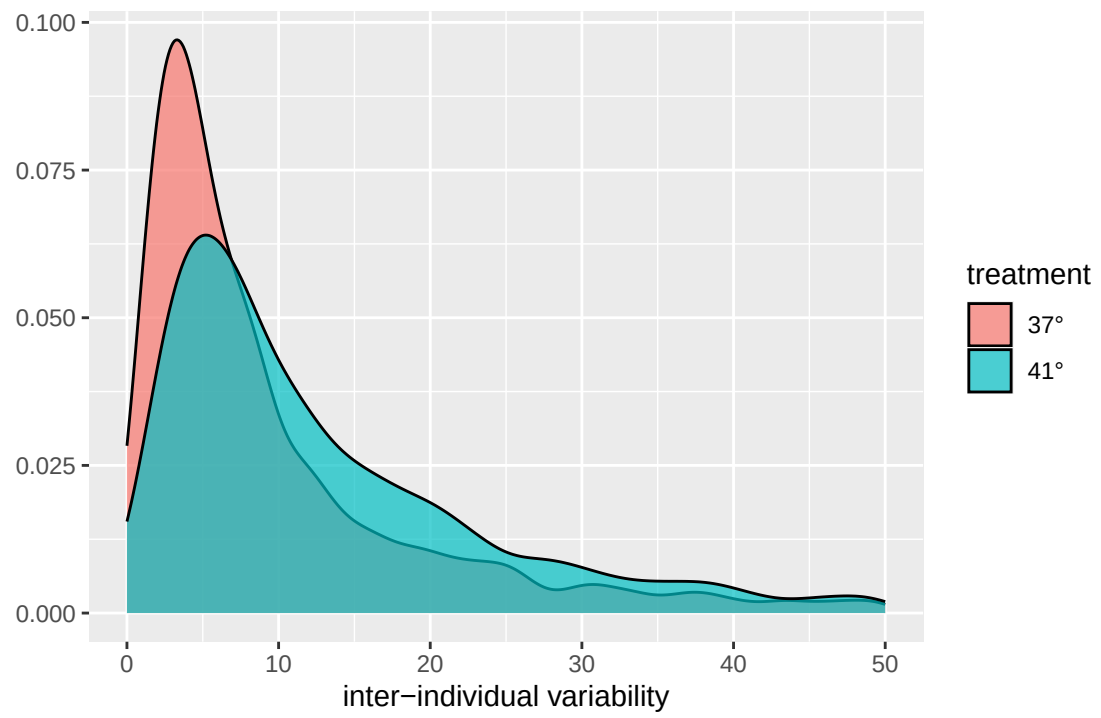


Figure 18: Distributions of the inter-individual variability for humans at 37°(baseline) and the 41° treatment for all DEGs.

Inter-individual variability densities for humans before and after the 32° treatment

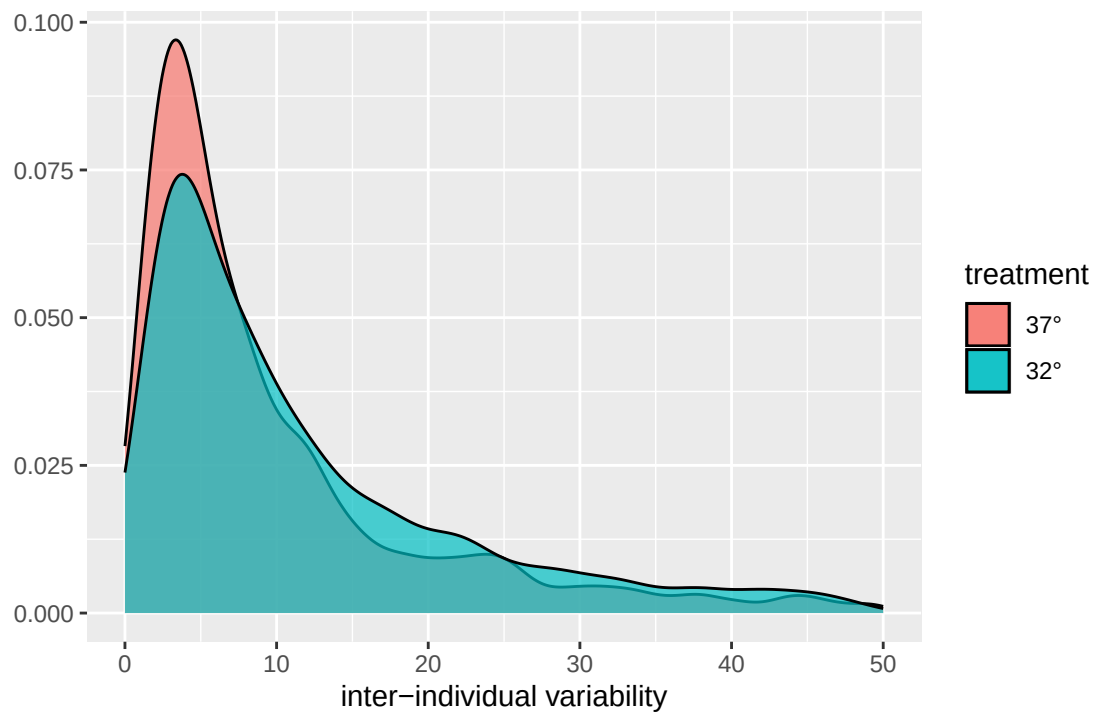


Figure 19: Distributions of the inter-individual variability for humans at 37°(baseline) and the 32° treatment for all DEGs.

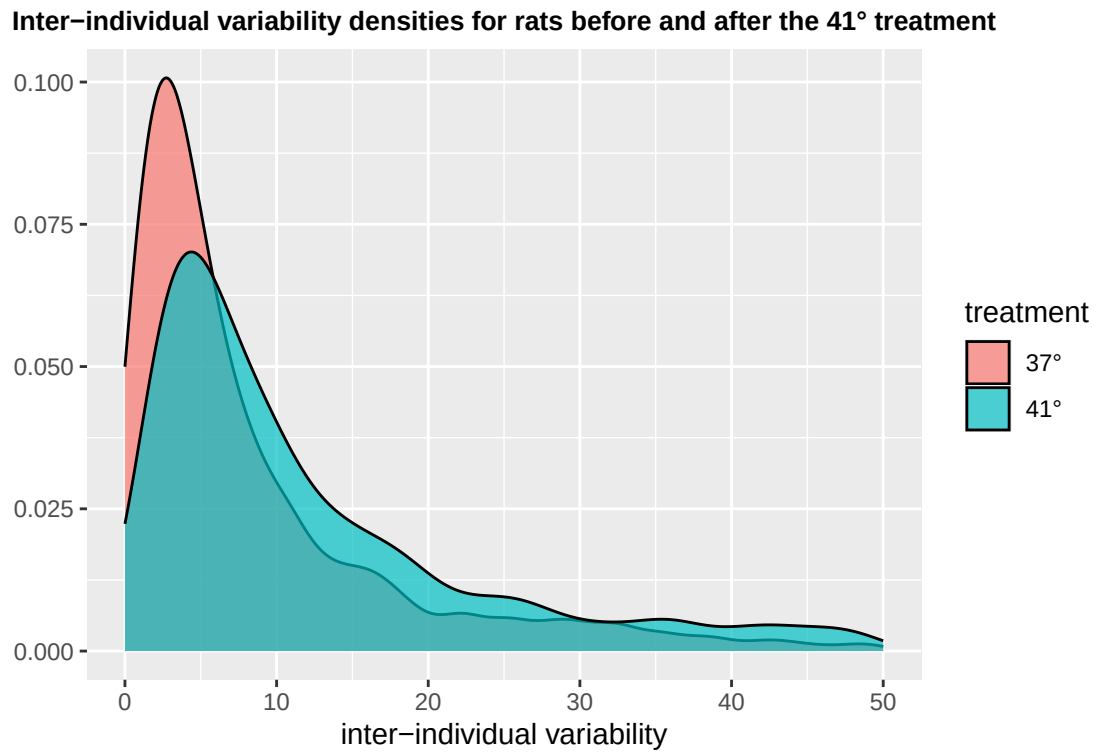


Figure 20: Distributions of the inter-individual variability for rats at 37°(baseline) and the 41° treatment for all DEGs.

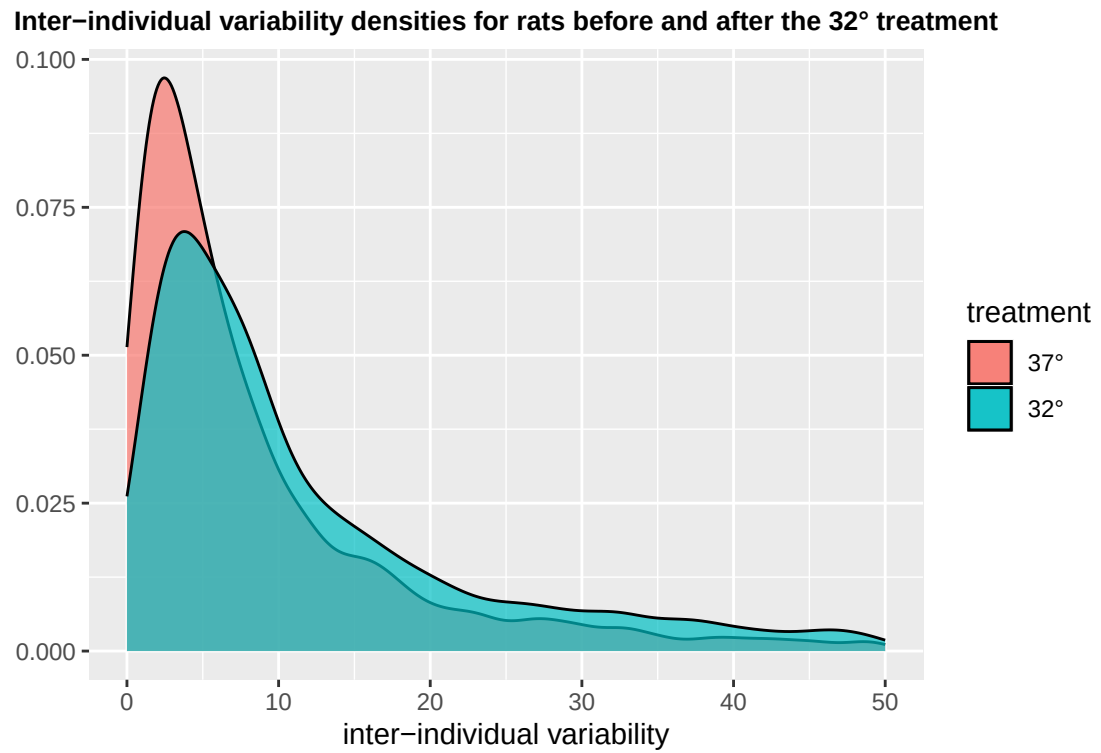


Figure 21: Distributions of the inter-individual variability for rats at 37°(baseline) and the 32° treatment for all DEGs.

Inter-individual variability densities for rhinos before and after the 41° treatment

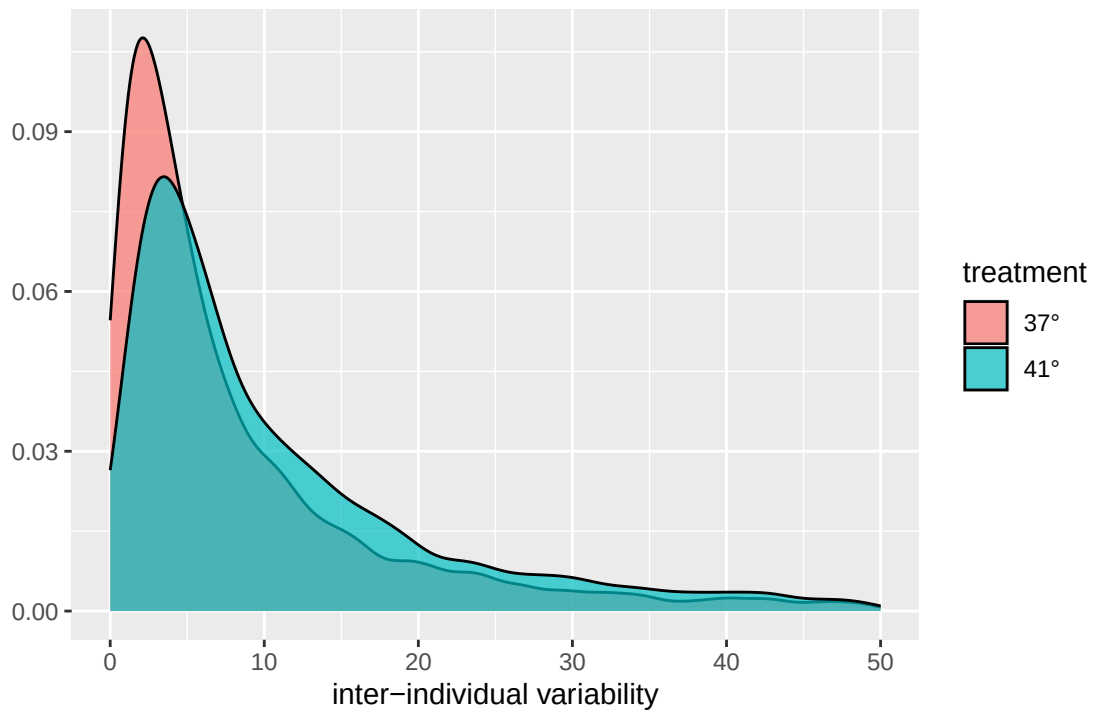


Figure 22: Distributions of the inter-individual variability for rhinos at 37°(baseline) and the 41° treatment for all DEGs.

Inter-individual variability densities for rhinos before and after the 32° treatment

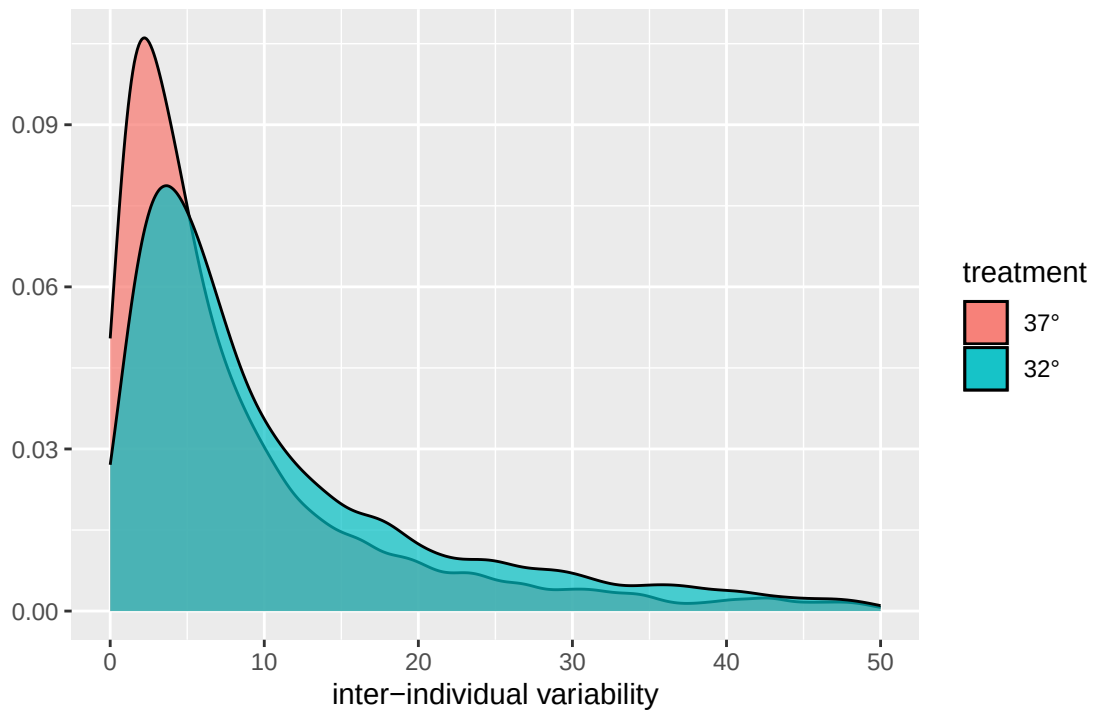


Figure 23: Distributions of the inter-individual variability for rhinos at 37°(baseline) and the 32° treatment for all DEGs.

Inter-individual variability densities for squirrels before and after the 41° treatment

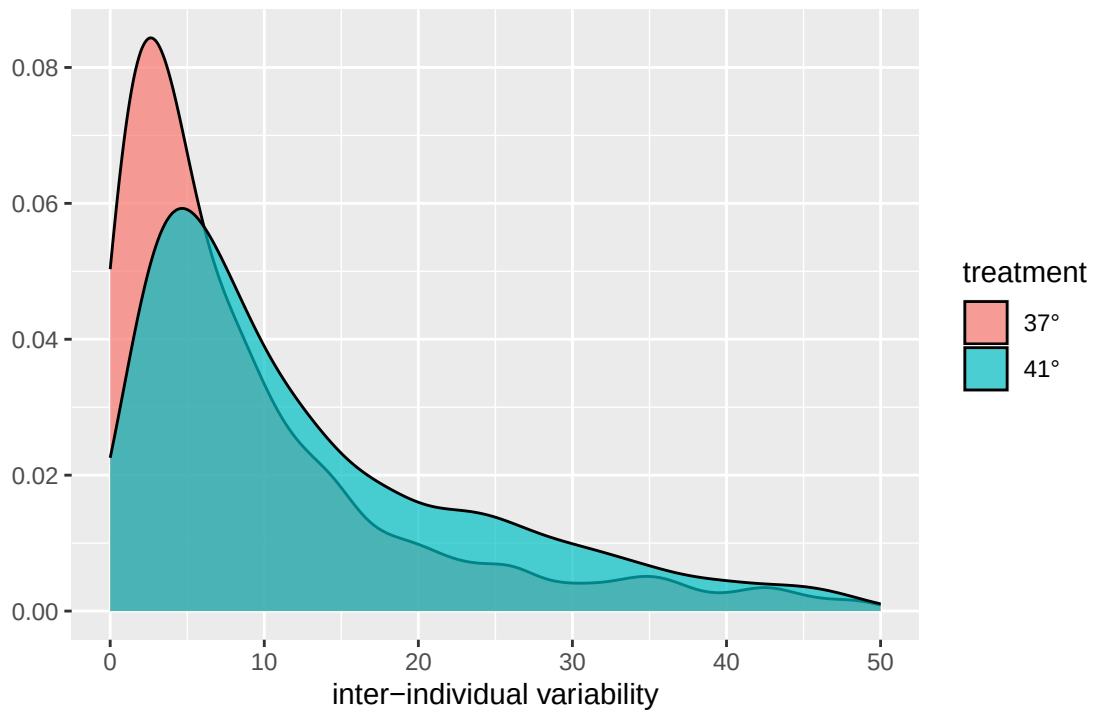


Figure 24: Distributions of the inter-individual variability for squirrels at 37°(baseline) and the 41° treatment for all DEGs.

Inter-individual variability densities for squirrels before and after the 32° treatment

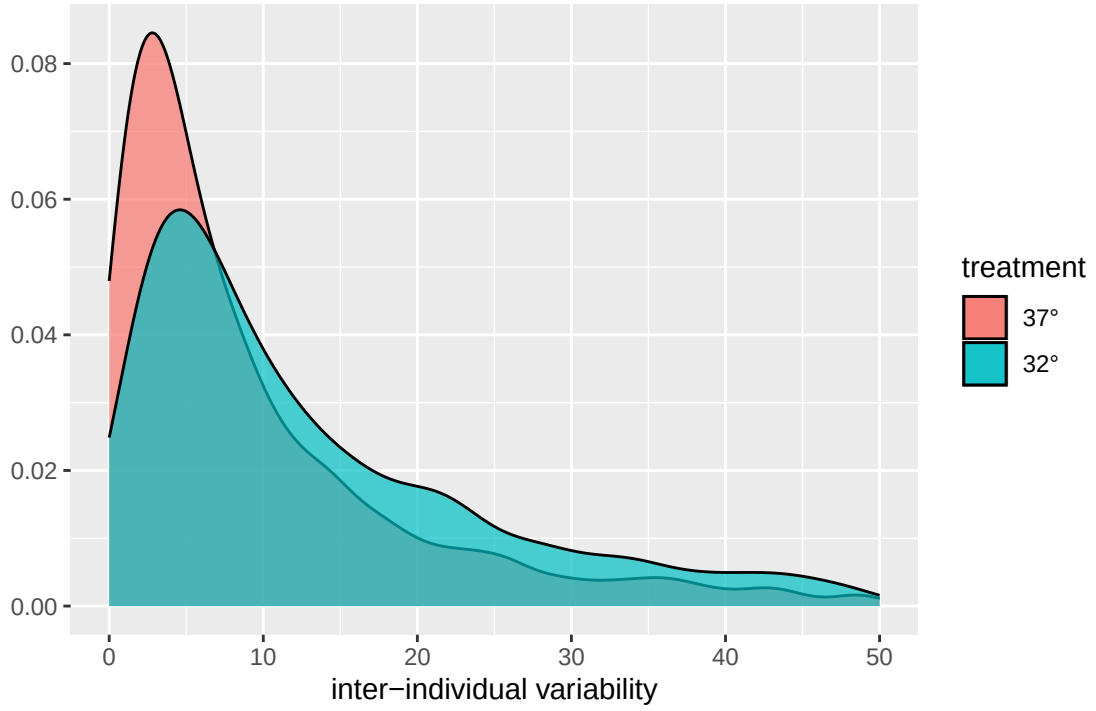


Figure 25: Distributions of the inter-individual variability for squirrels at 37°(baseline) and the 32° treatment for all DEGs.

7.3 Boxplots

For camels:

Quantiles	50%	95%
32°	0.3904	1.9444
41°	0.7574	2.2680

Table 20: Log quantiles for the 32° and 41° treatments for all DEGs according to the activity norm (6) for camels. The upper quantiles provide bounds for the ratios of the inter-individual variability of the DEGs.

The 95 percentile, for camels, for the 32° treatment is significantly smaller than for the 41° treatment.

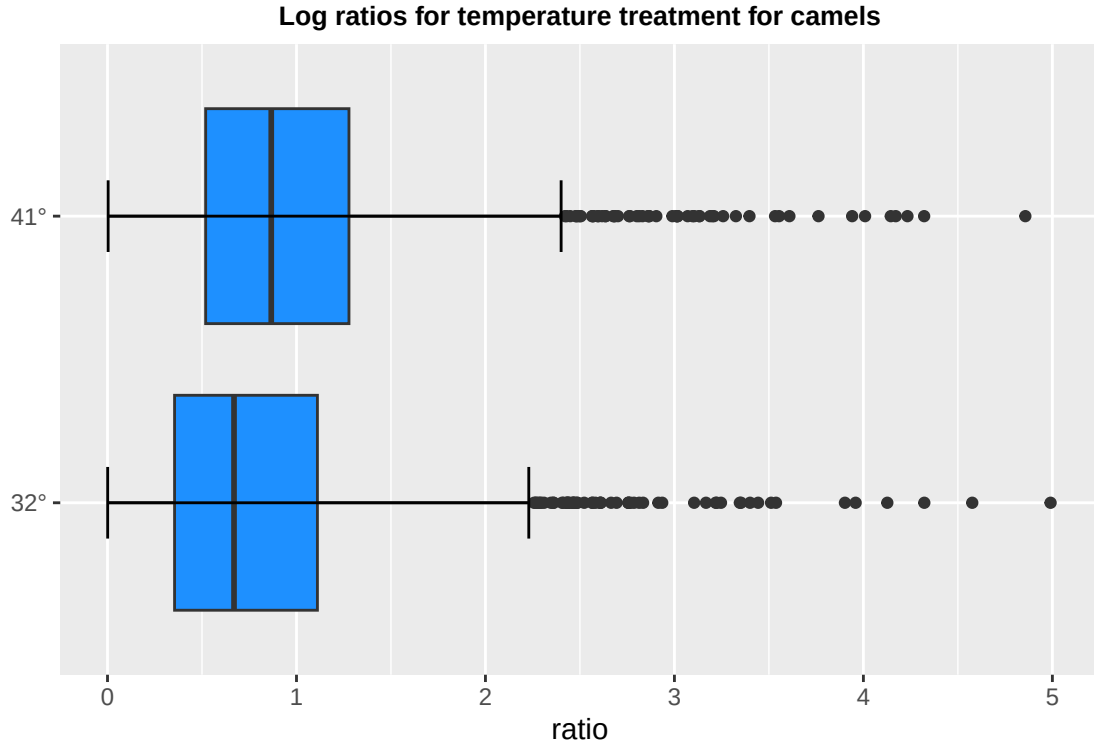


Figure 26: Boxplots of log ratios of inter-individual variability before and after treatment for camels under the 32° and 41° treatments for all DEGs. The 32° distribution is visibly more shifted to the left.

$D = 0.217$, p-value $< 2e-16$

$W = 2577087$, p-value $< 2e-16$

14 For humans:

Quantiles	50%	95%
32°	0.3638	1.5797
41°	0.5373	1.7092

Table 21: Log quantiles for the 32° and 41° treatments for all DEGs according to the activity norm (6) for humans. The upper quantiles provide bounds for the ratios of the inter-individual variability of the DEGs.

15 The ratios for humans are significantly smaller for the 32° than for the 41° treatment.

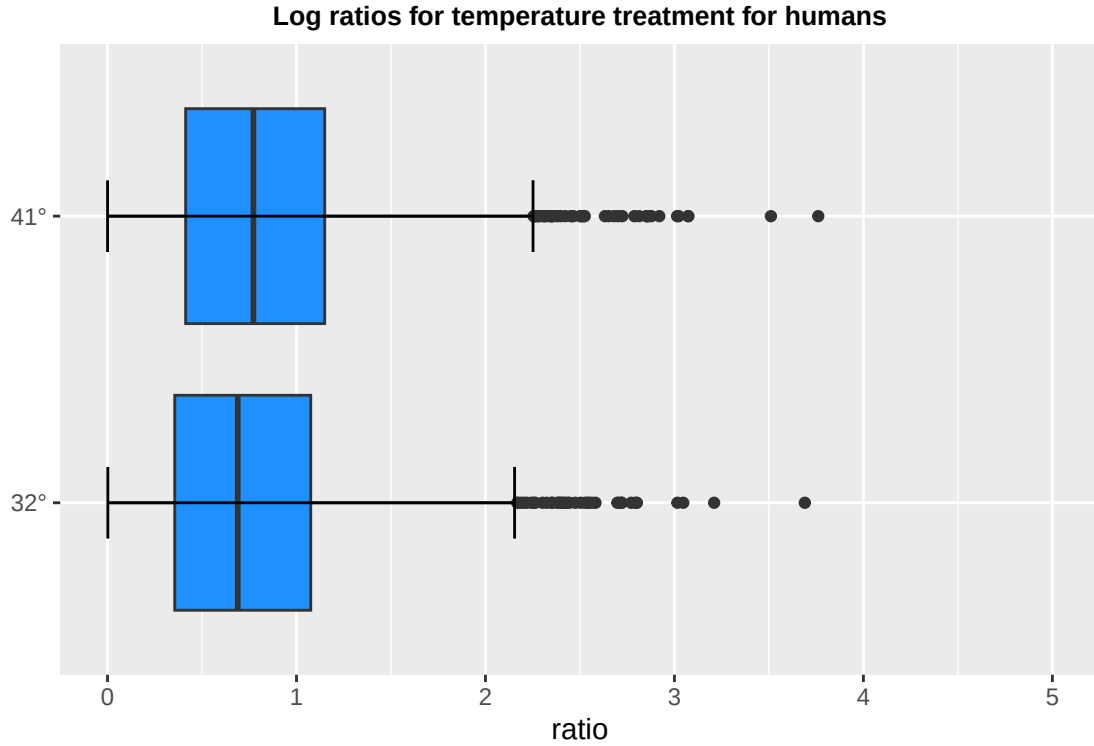


Figure 27: Boxplots of log ratios of inter-individual variability before and after treatment for humans under the 32° and 41° treatments for all DEGs. The 32° distribution is visibly more shifted to the left.

$D = 0.477$, p-value $< 2e-16$

$W = 3398677$, p-value $< 2e-16$

16 For rats:

Quantiles	50%	95%
32°	0.5377	2.8549
41°	0.5980	2.7749

Table 22: Log quantiles for the 32° and the 41° treatment for all DEGs according to the activity norm (6) for rats. The upper quantiles provide bounds for the ratios of the inter-individual variability of the DEGs.

17 For rats the 95 percentile, for the 32° treatment is larger than for the 41° treatment, indicating
 18 the possibility that rats are better acclimated to the latter treatment.

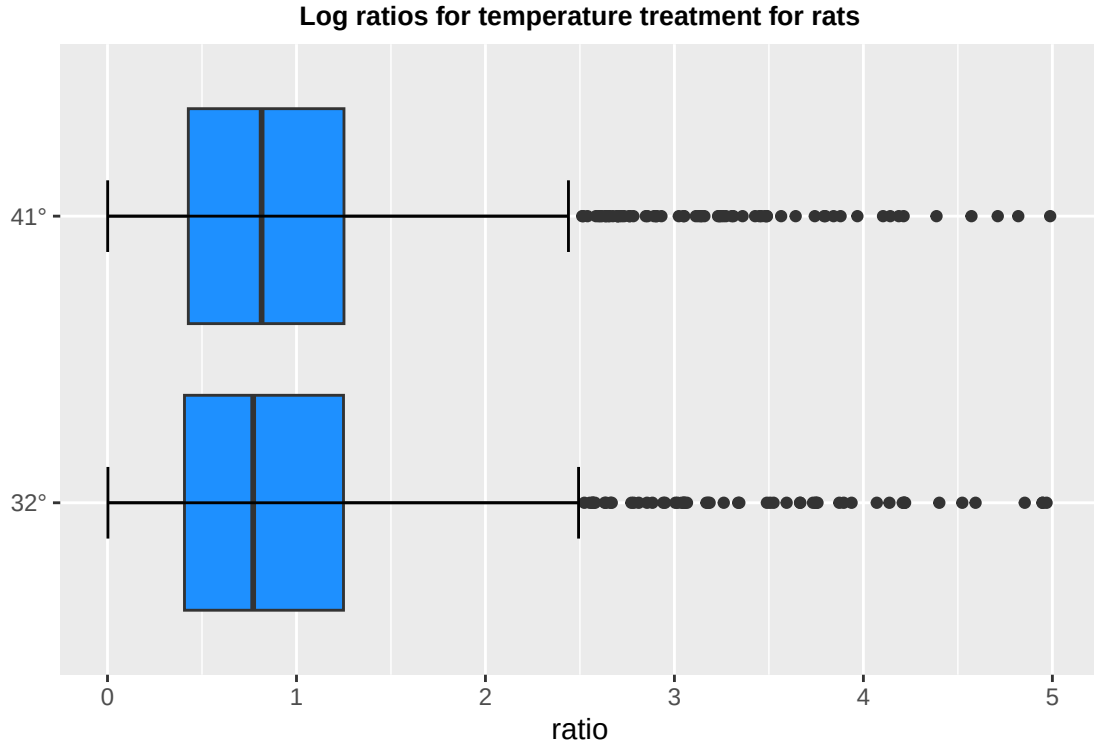


Figure 28: Boxplots of log ratios of inter-individual variability before and after treatment for rats under the 32° and 41° treatments for all DEGs.

$D = 0.515$, $p\text{-value} < 2e-16$

$W = 1299915$, $p\text{-value} < 2e-16$

19 For rhinos:

Quantiles	50%	95%
32°	0.4538	2.1447
41°	0.5016	2.2095

Table 23: Log quantiles for the 32° and 41° treatments for all active genes according to the activity norm (6) for rhinos. The upper quantiles provide bounds for the ratios of the inter-individual variability of the DEGs.

20 For rhinos, the ratios for the 32° treatment are again less than for the 41° treatment.

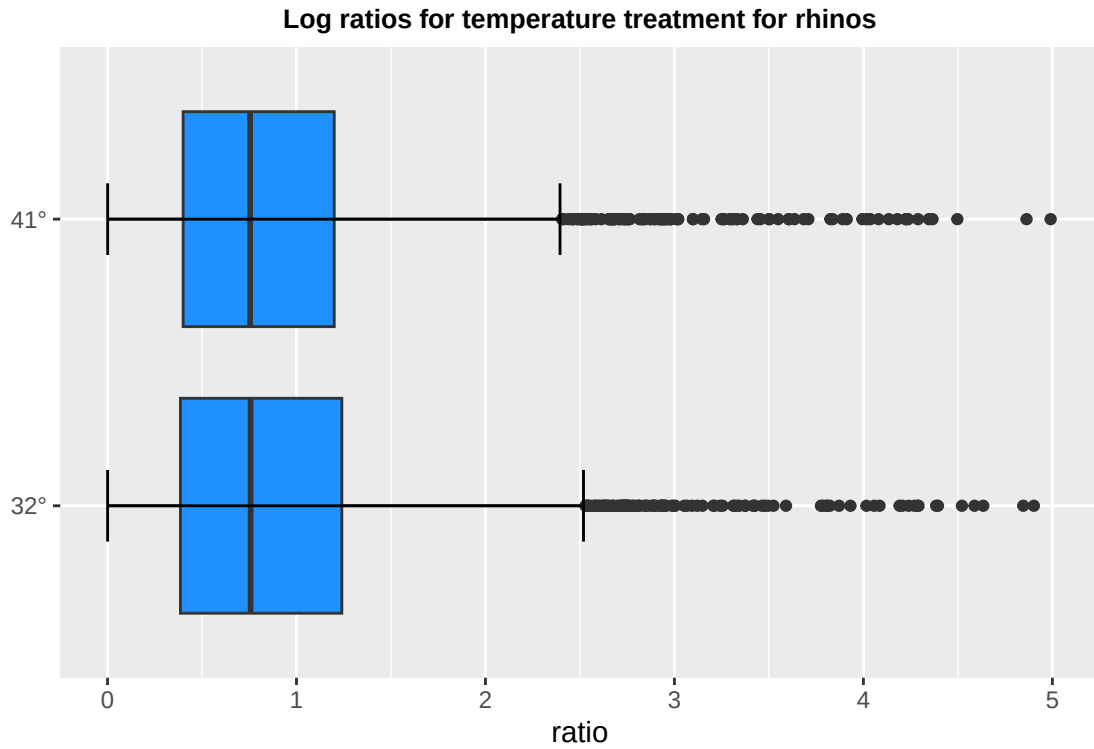


Figure 29: Boxplots of log ratios of inter-individual variability before and after treatment for rhinos under the 32° and 41° treatments for all DEGs.

$D = 0.497$, p-value $< 2e-16$

$W = 4090204$, p-value $< 2e-16$

21 7.4 Common DEGs

22 Below is the diagram of the common DEGs for the high temperature (41°) treatment listed
 23 according to their rank (7) for humans.

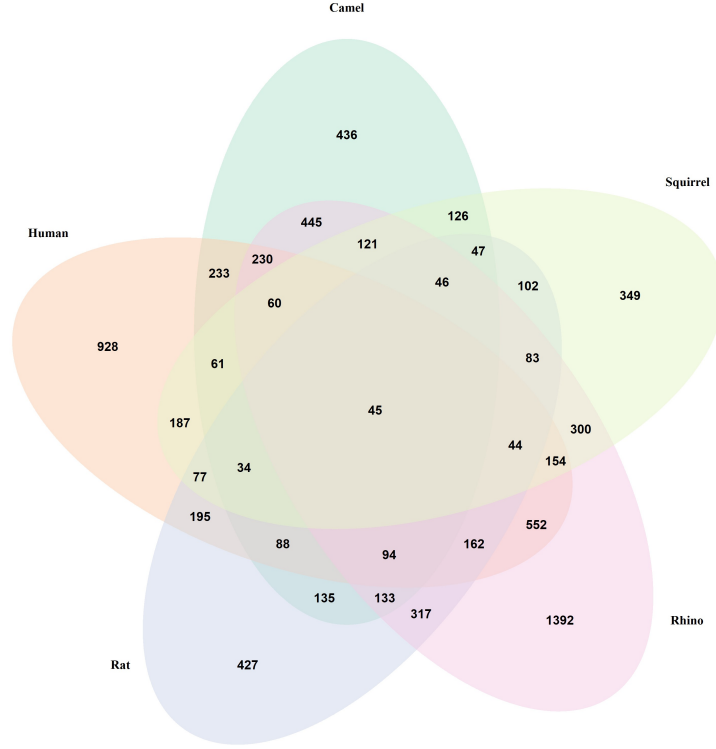


Figure 30: Diagram constructed from all DEGs for the 41° treatment.

The genes in the intersection (i.e., DEGs common to all species) are listed according to their rank (ordering) by (7) for humans: [1] "ENSG00000130724" "ENSG00000100591" "ENSG00000186480" "ENSG00000169710" "ENSG00000076067" [6] "ENSG00000102317" "ENSG00000120656" "ENSG00000167772" "ENSG00000124587" "ENSG00000088986" [11] "ENSG00000011451" "ENSG00000092199" "ENSG00000155660" "ENSG00000149257" "ENSG00000004478" [16] "ENSG00000068745" "ENSG00000110921" "ENSG00000122884" "ENSG00000144647" "ENSG00000109919" [21] "ENSG00000145919" "ENSG00000160752" "ENSG00000221821" "ENSG00000117500" "ENSG00000141002" [26] "ENSG00000007392" "ENSG00000137288" "ENSG00000120437" "ENSG00000272047" "ENSG00000086061" [31] "ENSG00000167508" "ENSG00000171148" "ENSG00000130638" "ENSG00000134262" "ENSG00000198146" [36] "ENSG00000100982" "ENSG00000198911" "ENSG00000265491" "ENSG00000188706" "ENSG00000107669" [41] "ENSG00000170345" "ENSG00000052841" "ENSG00000184557" "ENSG00000117394" "ENSG00000141013"

Below is the diagram of the common DEGs for the 32° treatment according to their rank (7) for humans.

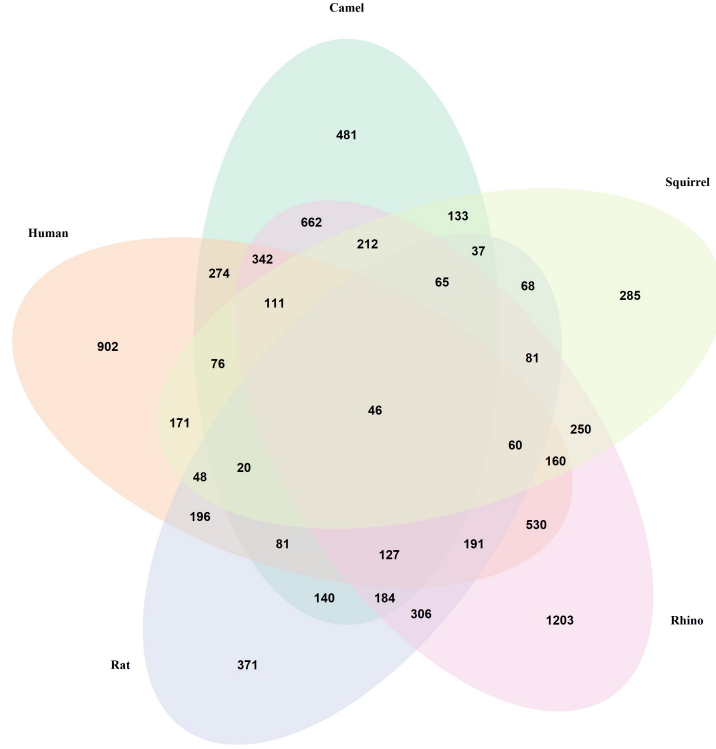


Figure 31: Diagram constructed from the active genes for the 32° treatment.

The genes in the intersection for the 32° treatment are listed according to their rank (7) for humans: [1] "ENSG00000139613" "ENSG00000112685" "ENSG00000198642" "ENSG00000241973" "ENSG00000105576" [6] "ENSG00000138413" "ENSG00000186480" "ENSG00000139514" "ENSG00000115486" "ENSG00000169710" [11] "ENSG00000070423" "ENSG00000163156" "ENSG00000114956" "ENSG00000196284" "ENSG00000103544" [16] "ENSG00000198001" "ENSG00000126249" "ENSG00000113070" "ENSG00000161920" "ENSG00000136100" [21] "ENSG00000108528" "ENSG00000158019" "ENSG00000145029" "ENSG00000001630" "ENSG00000121058" [26] "ENSG00000198911" "ENSG00000117758" "ENSG0000012061" "ENSG00000175467" "ENSG00000145919" [31] "ENSG00000172725" "ENSG00000102317" "ENSG00000131475" "ENSG00000185115" "ENSG00000120129" [36] "ENSG00000137207" "ENSG00000117505" "ENSG00000142039" "ENSG00000104549" "ENSG00000113845" [41] "ENSG00000166295" "ENSG00000136146" "ENSG00000136485" "ENSG00000160310" "ENSG00000187024" [46] "ENSG00000115226"

7.5 Extreme response sets

Below we present the number genes in each of the extreme sets for Camels, Humans, Rats, Rhinos, and Squirrels, including different criteria for "large" in the definitions of the extreme response groups :

	Camels	Humans	Rats	Rhinos	Squirrels
DEGs	2334	3144	2029	4178	1836
Key-Response	352	412	296	518	245

Table 24: Numbers of active genes belonging to the Key-Response set at 41° for camels, humans, rats, rhinos, squirrels.

	Camels	Humans	Rats	Rhinos	Squirrels
DEGs	2334	3144	2029	4178	1836
Treatment-specific 50%	46	82	55	104	38
Treatment-specific 60%	23	45	22	53	19
Treatment-specific 70%	6	22	10	28	4
Treatment-specific 80%	0	10	6	8	0
Treatment-specific 90%	0	1	2	3	0

Table 25: Numbers of active genes belonging to the Treatment-Specific set at 41° for camels, humans, rats, rhinos, and squirrels.

	Camels	Humans	Rats	Rhinos	Squirrels
DEGs	2334	3144	2029	4178	1836
Support 50%	298	334	176	333	140
Support 60%	237	257	135	244	140
Support 70%	166	186	98	180	59
Support 80%	104	124	59	109	38
Support 90%	48	59	24	52	18

Table 26: Numbers of active genes belonging to the Support set at 41° for camels, humans, rats, rhinos, and squirrels.

	Camels	Humans	Rats	Rhinos	Squirrels
DEGs	2334	3144	2029	4178	1836
Noisy 50%	69	77	62	112	63
Noisy 60%	40	33	36	78	47
Noisy 70%	23	10	24	44	33
Noisy 80%	13	1	9	21	13
Noisy 90%	5	0	4	6	5

Table 27: Numbers of active genes belonging to the Noisy set at 41° for camels, humans, rats, rhinos, and squirrels.

	Camels	Humans	Rats	Rhinos	Squirrels
DEGs	2991	3335	2021	4530	1462
Key-Response	406	426	264	548	149

Table 28: Numbers of active genes belonging to the Key-Response set at 32° for camels, humans, rats, rhinos, and squirrels.

	Camels	Humans	Rats	Rhinos	Squirrels
DEGs	2991	3335	2021	4530	1462
Treatment-specific 50%	73	97	42	136	52
Treatment-specific 60%	37	47	23	64	25
Treatment-specific 70%	12	20	12	27	10
Treatment-specific 80%	1	9	3	7	6
Treatment-specific 90%	0	1	1	1	1

Table 29: Numbers of active genes belonging to the Treatment-Specific set at 32° for camels, humans, rats, rhinos, and squirrels.

	Camels	Humans	Rats	Rhinos	Squirrels
DEGs	2991	3335	2021	4530	1462
Support 50%	234	266	167	330	100
Support 60%	166	189	124	234	77
Support 70%	114	129	85	159	54
Support 80%	63	76	41	87	39
Support 90%	35	28	17	38	14

Table 30: Numbers of active genes belonging to the Support set at 32° for camels, humans, rats, rhinos, and squirrels.

	Camels	Humans	Rats	Rhinos	Squirrels
DEGs	2991	3335	2021	4530	1462
Noisy 50%	98	102	68	129	72
Noisy 60%	59	44	44	73	46
Noisy 70%	35	15	26	35	23
Noisy 80%	17	3	15	20	13
Noisy 90%	9	0	8	8	8

Table 31: Numbers of active genes belonging to the Noisy set at 32° for camels, humans, rats, rhinos, and squirrels.

7.6 Network predictions

In the tables below we show the results from training neural networks with the Key-Response group, the Treatment-Specific group, and the Noisy group for humans and camels for the 32° and 41° treatments. Humans and camels are chosen as representatives for the strict and flexible homeostasis mammals respectively, in order to compare their networks. The Response Prediction column shows the intervals containing the output of the trained networks with baseline conditions as input. The Stability Prediction column shows the intervals containing the output of the trained networks with observations after treatment used as the input conditions. Response Prediction assesses how well the networks represent the response of the species, whereas Stability Prediction measures how well homeostasis is approximated after treatment. In particular, in the case of the Treatment-Specific group and the Noisy group Stability Prediction indicates whether the intervals continue to contract, expand, or are stable.

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000151881	[11.063, 18.834]	[10.9, 18.325]	0.022	[10.874, 17.957]	0.036
ENSG00000109572	[16.057, 18.547]	[13.671, 20.802]	0.134	[13.57, 20.441]	0.127
ENSG00000142330	[8.972, 12.256]	[6.751, 13.272]	0.152	[6.77, 13.012]	0.139
ENSG00000136478	[15.246, 21.338]	[15.118, 23.135]	0.053	[15.13, 22.665]	0.039
ENSG00000164168	[13.155, 14.962]	[10.081, 18.052]	0.219	[10.023, 17.527]	0.203
ENSG00000176994	[7.299, 9.314]	[5.028, 11.205]	0.251	[5.043, 11.035]	0.239
ENSG00000101407	[6.193, 9.446]	[4.051, 10.357]	0.195	[4.071, 10.168]	0.182
ENSG00000132330	[4.142, 5.417]	[1.485, 8.045]	0.553	[1.479, 7.778]	0.526
ENSG00000082516	[6.613, 8.814]	[3.749, 10.486]	0.294	[3.824, 10.245]	0.274
ENSG00000093217	[1.421, 3.127]	[-0.0, 5.355]	0.802	[-0.0, 5.071]	0.74

Table 32: Inter-individual variability intervals for the Key-Response genes for Humans at 32° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000133104	[19.197, 26.009]	[21.748, 27.212]	0.083	[18.763, 19.921]	0.144
ENSG00000127948	[38.091, 50.447]	[38.619, 50.449]	0.006	[37.843, 40.558]	0.114
ENSG00000154803	[16.398, 19.8]	[16.843, 18.817]	0.039	[16.388, 16.79]	0.083
ENSG00000117614	[72.455, 89.65]	[70.811, 91.606]	0.022	[58.198, 62.925]	0.253
ENSG00000138801	[45.56, 52.936]	[47.068, 54.114]	0.027	[35.259, 38.842]	0.248
ENSG00000075420	[55.156, 57.33]	[50.535, 60.568]	0.07	[44.3, 46.467]	0.193
ENSG00000052802	[16.91, 24.462]	[19.96, 24.564]	0.076	[17.87, 18.876]	0.158
ENSG00000134108	[12.002, 23.902]	[17.734, 21.301]	0.232	[18.503, 19.595]	0.301
ENSG00000102032	[0.594, 2.675]	[0.54, 1.079]	0.505	[0.749, 0.875]	0.598
ENSG00000138078	[5.105, 9.103]	[5.699, 6.531]	0.223	[5.941, 6.154]	0.266

Table 33: Inter-individual variability intervals for the Treatment-Specific genes for Humans at 32° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000113812	[25.157, 44.798]	[31.714, 34.901]	0.235	[29.651, 37.985]	0.162
ENSG00000182872	[19.306, 29.141]	[19.871, 21.947]	0.16	[18.17, 23.896]	0.132
ENSG00000109220	[50.979, 78.179]	[56.321, 65.479]	0.14	[51.152, 74.007]	0.034
ENSG00000011007	[14.222, 40.918]	[21.593, 30.927]	0.315	[17.16, 37.803]	0.11
ENSG00000221821	[15.52, 34.153]	[19.618, 23.446]	0.298	[16.893, 26.558]	0.181
ENSG00000227057	[66.175, 79.663]	[66.426, 76.097]	0.026	[62.21, 83.848]	0.056
ENSG00000124875	[1.414, 21.149]	[8.017, 11.235]	0.732	[7.025, 14.177]	0.558
ENSG00000026559	[6.352, 23.306]	[15.13, 18.696]	0.451	[13.307, 21.808]	0.285
ENSG00000181915	[12.845, 24.9]	[16.838, 18.832]	0.267	[15.283, 20.472]	0.182
ENSG00000182180	[23.254, 41.483]	[22.966, 25.855]	0.246	[21.329, 28.605]	0.229

Table 34: Inter-individual variability intervals for the Noisy genes for Humans at 32° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000105514	[6.644, 11.372]	[6.578, 14.253]	0.164	[5.267, 15.789]	0.322
ENSG00000163961	[8.362, 11.999]	[5.722, 13.086]	0.183	[4.56, 14.611]	0.315
ENSG00000074582	[28.946, 33.559]	[27.674, 38.276]	0.096	[26.269, 40.869]	0.16
ENSG00000126705	[21.513, 25.189]	[18.777, 28.376]	0.127	[17.427, 30.402]	0.199
ENSG00000109118	[16.651, 18.682]	[12.711, 21.758]	0.199	[11.344, 23.946]	0.299
ENSG00000184602	[7.984, 15.332]	[6.509, 15.098]	0.073	[5.129, 18.87]	0.274
ENSG00000096968	[8.278, 13.187]	[5.791, 13.416]	0.127	[4.658, 15.144]	0.26
ENSG00000108262	[37.114, 44.58]	[33.797, 46.668]	0.066	[31.951, 49.704]	0.126
ENSG00000183665	[8.19, 12.351]	[5.043, 12.331]	0.154	[3.749, 13.855]	0.289
ENSG00000130758	[20.569, 24.657]	[17.984, 27.186]	0.113	[16.739, 29.251]	0.186

Table 35: Inter-individual variability intervals for the Key-Response genes for Humans at 41° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000230124	[17.656, 22.366]	[17.652, 19.115]	0.081	[17.838, 18.321]	0.106
ENSG00000118960	[21.334, 26.062]	[22.183, 25.127]	0.038	[22.029, 22.884]	0.082
ENSG00000154803	[17.802, 26.947]	[21.818, 25.741]	0.117	[21.099, 22.22]	0.179
ENSG00000139428	[6.516, 11.384]	[8.482, 9.58]	0.211	[8.887, 9.266]	0.251
ENSG00000102032	[0.39, 1.142]	[0.406, 1.203]	0.05	[0.645, 0.9]	0.325
ENSG00000145390	[7.972, 11.553]	[9.129, 10.78]	0.099	[9.053, 9.608]	0.155
ENSG00000090487	[62.85, 71.837]	[61.308, 74.283]	0.03	[58.458, 62.224]	0.104
ENSG00000179604	[36.008, 41.285]	[35.822, 40.411]	0.014	[34.882, 36.136]	0.081
ENSG00000126767	[44.606, 52.648]	[43.758, 51.118]	0.024	[42.489, 44.51]	0.105
ENSG00000103353	[32.337, 44.014]	[38.679, 44.338]	0.087	[36.99, 38.459]	0.134

Table 36: Inter-individual variability intervals for the Treatment-Specific genes for Humans at 41° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000026559	[19.335, 34.83]	[28.121, 31.471]	0.224	[26.056, 36.131]	0.148
ENSG00000116685	[65.525, 95.388]	[69.489, 79.099]	0.126	[65.347, 94.424]	0.007
ENSG00000175387	[18.342, 69.288]	[17.06, 52.976]	0.201	[17.996, 103.054]	0.389
ENSG00000176454	[34.389, 56.251]	[36.215, 40.38]	0.195	[34.832, 45.981]	0.118
ENSG00000182872	[49.825, 61.927]	[49.244, 55.647]	0.061	[45.435, 59.332]	0.063
ENSG00000171497	[45.237, 70.254]	[50.874, 60.913]	0.13	[51.963, 78.545]	0.13
ENSG00000182180	[19.797, 36.477]	[20.725, 22.189]	0.27	[19.371, 23.995]	0.229
ENSG00000122965	[18.576, 34.204]	[19.232, 20.576]	0.271	[18.126, 22.397]	0.232
ENSG00000136478	[24.664, 39.739]	[26.498, 28.654]	0.201	[25.353, 31.968]	0.131
ENSG00000163320	[63.244, 86.488]	[68.261, 79.704]	0.079	[66.656, 87.734]	0.031

Table 37: Inter-individual variability intervals for the Noisy genes for Humans at 41° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000113240	[5.587, 8.642]	[4.316, 11.119]	0.263	[3.442, 12.002]	0.387
ENSG00000204843	[-0.0, 3.113]	[-0.0, 4.148]	0.333	[-0.0, 4.963]	0.594
ENSG00000055332	[-0.0, 2.198]	[-0.0, 4.733]	1.153	[-0.0, 5.62]	1.557
ENSG00000025772	[23.283, 27.519]	[21.23, 29.87]	0.087	[20.047, 30.518]	0.123
ENSG00000174437	[1.098, 1.512]	[-0.0, 5.33]	1.883	[-0.0, 6.577]	2.36
ENSG00000156502	[6.732, 10.555]	[6.232, 12.775]	0.157	[5.238, 13.572]	0.261
ENSG00000122033	[7.142, 7.78]	[4.377, 10.71]	0.382	[3.593, 11.678]	0.499
ENSG00000130021	[15.477, 20.038]	[14.431, 21.223]	0.063	[13.671, 22.048]	0.107
ENSG00000143373	[15.629, 18.579]	[13.093, 21.015]	0.145	[11.998, 22.007]	0.206
ENSG00000113272	[11.956, 15.628]	[9.703, 17.366]	0.145	[8.779, 18.197]	0.208

Table 38: Inter-individual variability intervals for the Key-Response genes for Camels at 32° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000118816	[56.735, 61.825]	[53.014, 65.81]	0.065	[50.367, 56.01]	0.103
ENSG00000100417	[10.271, 14.917]	[10.59, 13.399]	0.073	[10.68, 11.997]	0.132
ENSG00000100403	[35.349, 47.615]	[37.143, 48.337]	0.03	[37.397, 42.177]	0.09
ENSG00000126545	[17.886, 22.241]	[17.915, 21.573]	0.017	[17.828, 19.372]	0.073
ENSG00000048828	[62.446, 66.18]	[58.171, 72.008]	0.079	[54.749, 60.813]	0.102
ENSG00000185761	[26.272, 29.618]	[25.798, 30.112]	0.017	[25.906, 27.761]	0.04
ENSG00000180354	[13.18, 16.621]	[13.116, 15.44]	0.042	[13.386, 14.338]	0.083
ENSG00000135521	[32.671, 41.319]	[35.503, 44.021]	0.075	[33.596, 37.359]	0.066
ENSG00000164062	[12.921, 16.589]	[13.317, 17.066]	0.03	[13.183, 14.912]	0.066
ENSG00000285025	[36.267, 45.838]	[40.404, 46.728]	0.061	[36.082, 41.169]	0.059

Table 39: Inter-individual variability intervals for the Treatment-Specific genes for Camels at 32° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000060762	[-0.0, 224.047]	[-0.0, 250.247]	0.117	[-0.0, 253.88]	0.133
ENSG00000127922	[-0.0, 160.942]	[-0.0, 169.151]	0.051	[-0.0, 188.016]	0.168
ENSG00000205581	[-0.0, 107.072]	[-0.0, 108.682]	0.015	[-0.0, 108.216]	0.011
ENSG00000023734	[-0.0, 63.777]	[-0.0, 65.249]	0.023	[-0.0, 64.476]	0.011
ENSG00000149428	[-0.0, 58.468]	[-0.0, 75.264]	0.287	[-0.0, 84.724]	0.449
ENSG00000179889	[-0.0, 40.623]	[-0.0, 42.074]	0.036	[-0.0, 41.422]	0.02
ENSG00000204628	[-0.0, 1157.682]	[-0.0, 1157.733]	0.0	[-0.0, 1157.926]	0.0
ENSG00000100568	[47.771, 61.505]	[45.326, 62.156]	0.028	[43.88, 67.474]	0.09
ENSG00000122705	[-0.0, 61.838]	[-0.0, 80.188]	0.297	[-0.0, 89.969]	0.455
ENSG00000011478	[45.341, 68.772]	[45.273, 66.225]	0.023	[44.857, 72.788]	0.039

Table 40: Inter-individual variability intervals for the Noisy genes for Camels at 32° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000109654	[-0.0, 4.083]	[0.874, 4.77]	0.382	[-0.0, 6.019]	0.474
ENSG00000065883	[-0.0, 3.747]	[-0.0, 3.768]	0.006	[-0.0, 5.194]	0.386
ENSG00000143776	[-0.0, 3.774]	[-0.0, 3.238]	0.142	[-0.0, 4.661]	0.235
ENSG00000137817	[10.446, 12.86]	[8.884, 12.86]	0.067	[7.552, 14.233]	0.183
ENSG00000125818	[0.149, 3.982]	[-0.0, 3.568]	0.136	[-0.0, 5.137]	0.316
ENSG00000175387	[19.807, 29.375]	[25.45, 30.669]	0.141	[24.034, 32.629]	0.152
ENSG00000110013	[5.446, 10.195]	[5.84, 10.406]	0.039	[4.311, 12.009]	0.188
ENSG00000132604	[24.061, 28.816]	[24.279, 29.794]	0.023	[22.428, 31.705]	0.086
ENSG00000041988	[9.143, 14.735]	[10.495, 14.746]	0.057	[9.21, 16.315]	0.069
ENSG00000100023	[0.0, 2.189]	[-0.0, 2.302]	0.052	[-0.0, 3.379]	0.544

Table 41: Inter-individual variability intervals for the Key-Response genes for Camels at 41° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000168710	[70.823, 85.673]	[73.771, 84.688]	0.025	[71.678, 77.537]	0.057
ENSG00000156875	[37.437, 43.681]	[39.589, 42.485]	0.041	[39.486, 41.181]	0.056
ENSG00000110921	[14.585, 21.737]	[19.7, 20.327]	0.18	[19.799, 20.131]	0.188
ENSG00000179163	[74.041, 93.539]	[80.193, 90.545]	0.055	[76.907, 83.382]	0.078
ENSG00000104976	[25.445, 29.776]	[27.518, 28.775]	0.056	[27.501, 28.198]	0.066
ENSG00000120137	[11.298, 14.705]	[12.637, 13.043]	0.115	[12.678, 12.892]	0.123
ENSG00000156535	[30.0, 41.923]	[34.046, 37.924]	0.112	[34.657, 36.848]	0.135
ENSG00000182973	[24.9, 34.438]	[29.353, 30.435]	0.143	[29.206, 29.83]	0.15
ENSG00000198912	[43.092, 47.649]	[44.01, 46.862]	0.019	[44.069, 45.515]	0.034
ENSG00000160803	[25.443, 31.457]	[27.357, 28.587]	0.084	[27.341, 28.015]	0.094

Table 42: Inter-individual variability intervals for the Treatment-Specific genes for Camels at 41° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

Gene	Observation	Response Prediction	Error 1	Stability Prediction	Error 2
ENSG00000127922	[-0.0, 162.926]	[122.398, 163.831]	0.757	[95.797, 166.951]	0.613
ENSG00000114850	[-0.0, 148.288]	[27.22, 190.509]	0.468	[25.599, 337.806]	1.451
ENSG00000122705	[-0.0, 58.442]	[22.292, 56.732]	0.411	[5.203, 60.34]	0.122
ENSG00000168883	[-0.0, 21.301]	[10.275, 14.524]	0.801	[9.508, 14.819]	0.751
ENSG00000137710	[-0.0, 43.779]	[-0.0, 28.836]	0.341	[-0.0, 32.468]	0.258
ENSG00000100650	[15.445, 44.225]	[27.732, 34.748]	0.365	[25.906, 37.494]	0.288
ENSG00000087502	[0.607, 34.171]	[6.165, 9.84]	0.859	[5.491, 11.146]	0.803
ENSG00000165410	[-0.0, 19.264]	[4.616, 6.294]	0.913	[3.744, 7.078]	0.827
ENSG00000127415	[28.815, 57.777]	[42.181, 46.376]	0.286	[38.914, 50.334]	0.203
ENSG00000143436	[-0.0, 20.913]	[11.281, 14.486]	0.847	[9.896, 17.035]	0.659

Table 43: Inter-individual variability intervals for the Noisy genes for Camels at 41° for the top 10 genes. Comparison of observed intervals vs predicted by trained networks. The fractional errors, Error 1 and Error 2, are computed according to formulas (13) and (14).

7.7 Strong interactions

We can visualize and compare the strengths of the interactions by graphing the ordered interaction profile for all the DEGs. Explicitly, we compute the interaction for all genes on a fixed j th gene, order them from smallest to largest, and graph these values as a curve. To demonstrate how DEG interaction strengths vary among treatments and species, we plot curves for Key-Response genes for humans and camels at 32°C and 41°C.

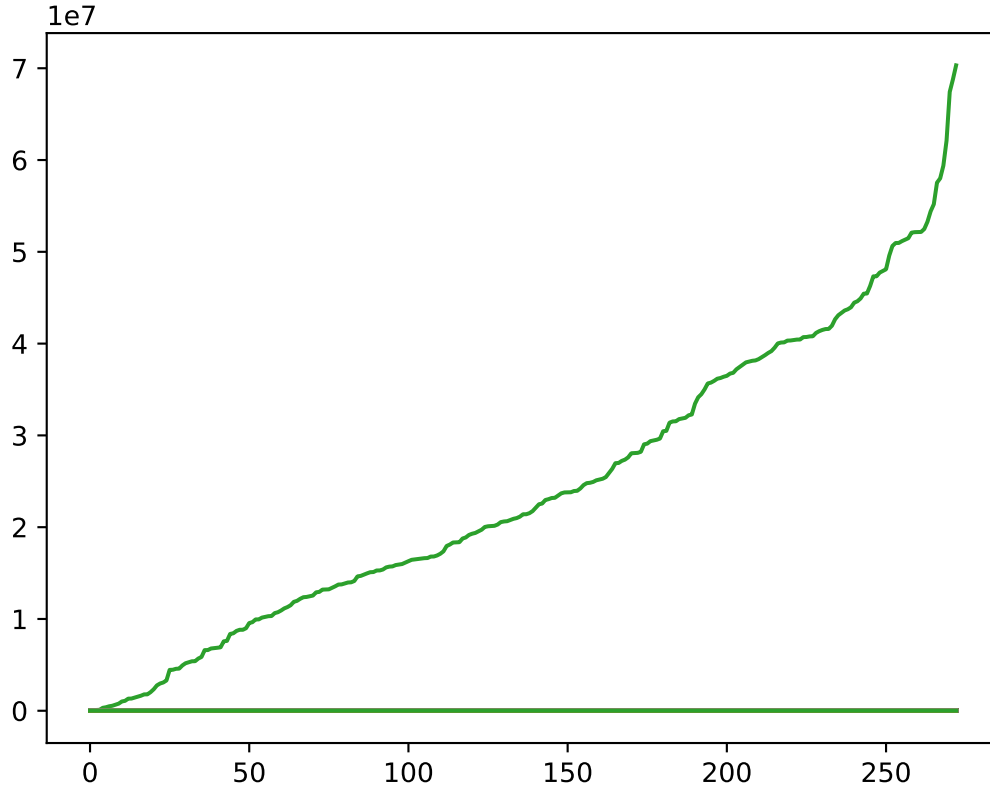


Figure 32: Interaction profiles for Key-Response genes for humans at 32°. Each profile has been sorted. The x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

At this scale only two groups of profiles are distinguishable for humans at 32°. We present below the strongest pairs of interacting genes.

ENSG00000204138	ENSG00000104728
ENSG00000152620	"ENSG00000104728
ENSG00000188277	ENSG00000104728
ENSG00000099822	ENSG00000104728
ENSG00000165312	ENSG00000104728
ENSG00000185220	ENSG00000104728
ENSG00000135945	ENSG00000104728
ENSG00000124523	ENSG00000104728
ENSG00000211454	ENSG00000164944
ENSG00000104728	ENSG00000104728

Table 44: Top 10 interaction pairs among Key-Response genes for humans at 32°.

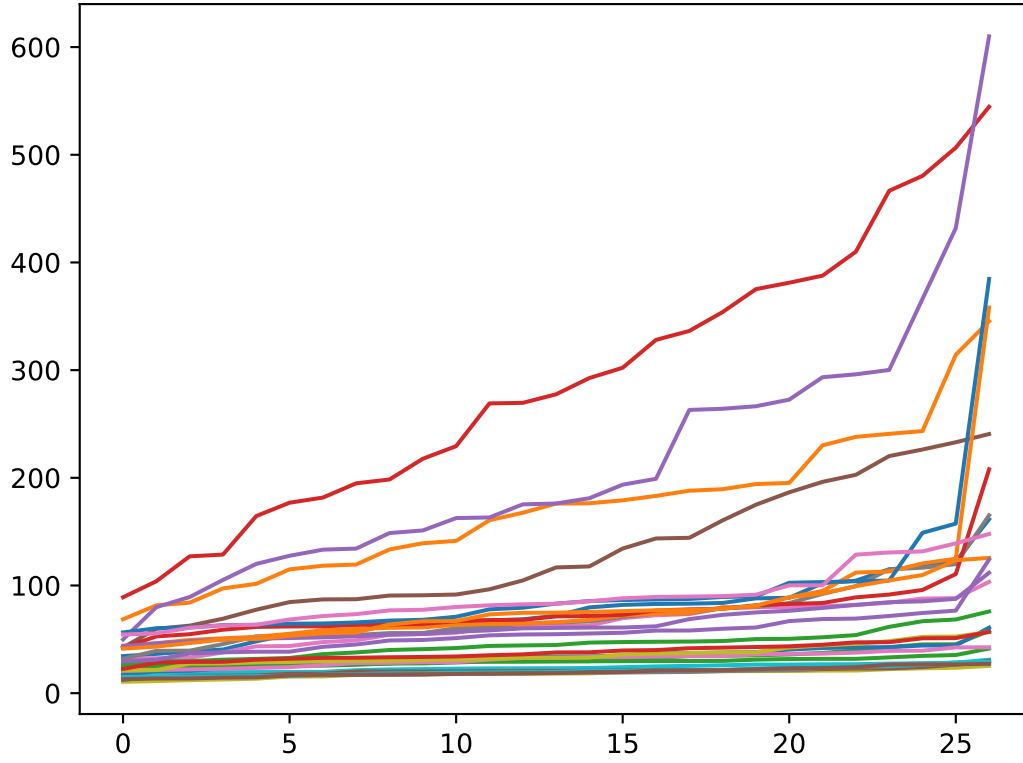


Figure 33: Interaction profiles for Treatment-Specific genes for humans at 32°. Each profile has been sorted. The x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

ENSG00000138801	ENSG00000052802
ENSG00000117614	ENSG00000117614
ENSG00000099949	ENSG00000052802
ENSG00000177868	ENSG00000052802
ENSG00000127948	ENSG00000134108
ENSG00000075420	ENSG00000117614
ENSG00000119048	ENSG00000052802
ENSG00000134108	ENSG00000052802
ENSG00000133104	ENSG00000052802
"ENSG00000241839	ENSG00000154803

Table 45: Top 10 interaction pairs among Treatment-Specific genes for humans at 32°.

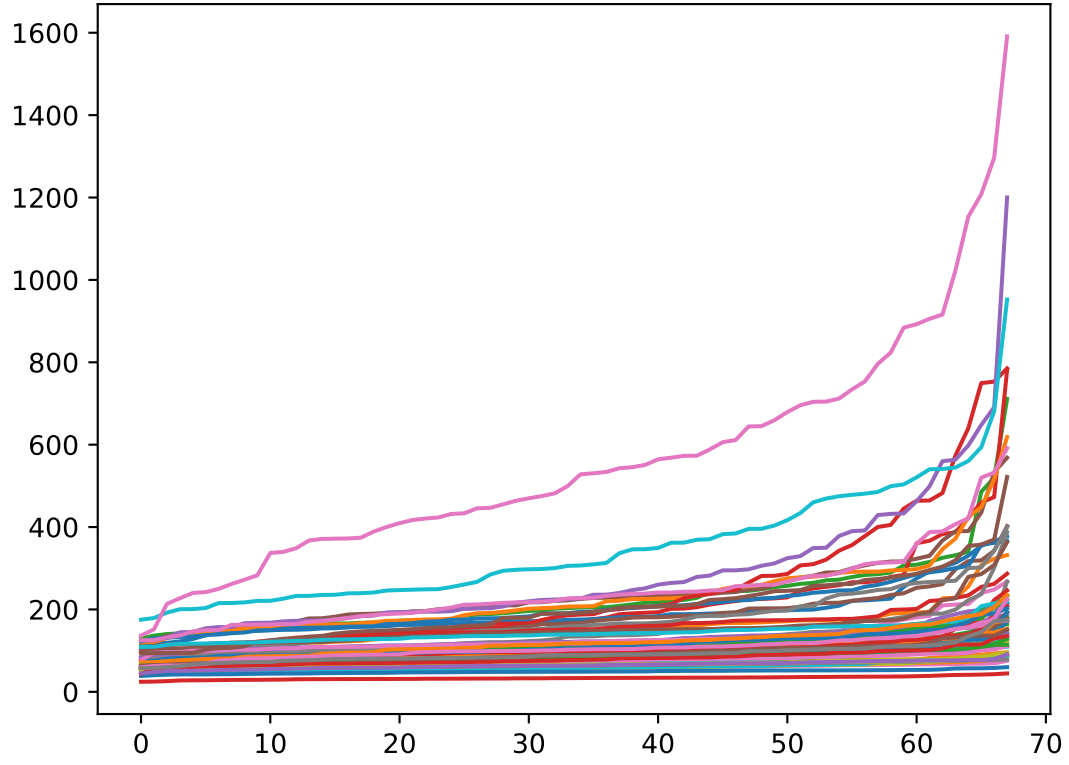


Figure 34: Interaction profiles for Noisy genes for humans at 32°. Each profile has been sorted. The x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

ENSG00000100029	ENSG00000100029
ENSG00000187678	ENSG00000109111
ENSG00000168002	ENSG00000100029
ENSG00000130304	ENSG00000168002
ENSG00000011007	ENSG00000109111
ENSG00000109220	ENSG00000109111
ENSG00000184557	ENSG00000109111
ENSG00000109111	ENSG00000168002
ENSG00000227057	ENSG00000109111
ENSG00000150760	ENSG00000100029

Table 46: Top 10 interaction pairs among Noisy genes for humans at 32°.

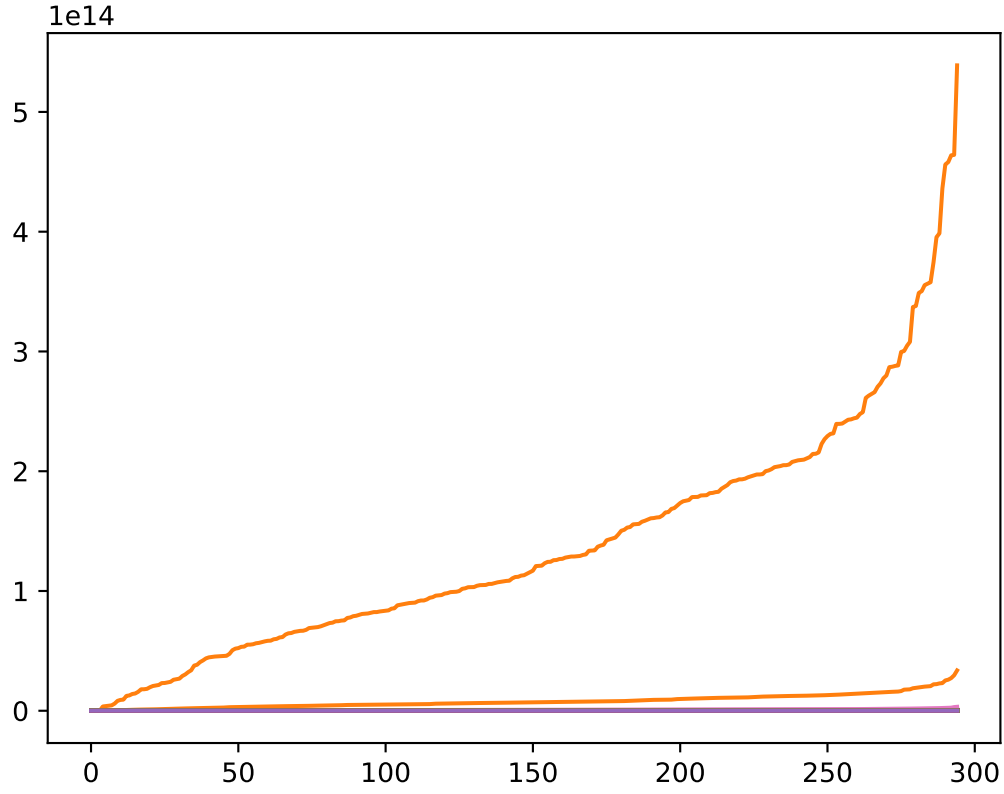


Figure 35: Interaction profiles for Key-Response genes for humans at 41° . Each profile has been sorted. The x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

ENSG00000078403"	"ENSG000000136451
"ENSG000000127870"	"ENSG000000127870"
"ENSG000000100426"	"ENSG000000127870"
"ENSG000000204228"	"ENSG000000127870"
"ENSG000000181915"	"ENSG000000127870"
"ENSG000000198794"	"ENSG000000127870"
"ENSG000000167625"	"ENSG000000127870"
"ENSG000000165312"	"ENSG000000127870"
"ENSG000000126705"	"ENSG000000136451"
"ENSG000000221995"	"ENSG000000136451"

Table 47: Top 10 interaction pairs among Key-Response genes for humans at 41° .

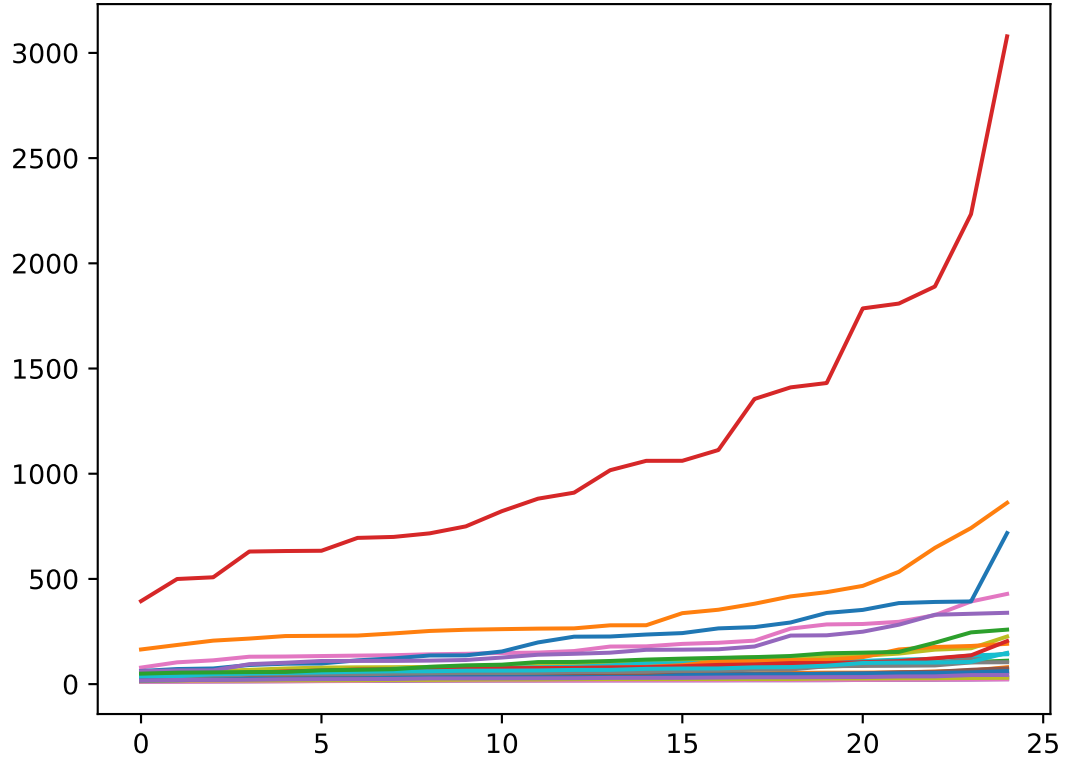


Figure 36: Interaction profiles for Treatment-Specific genes for humans at 41°. Each profile has been sorted. The x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

ENSG00000117298	ENSG00000117298
ENSG00000178913	ENSG00000117298
ENSG00000159461	ENSG00000117298
ENSG00000090487	ENSG00000090487
ENSG00000117448	ENSG00000121769
ENSG00000119986	ENSG00000117298
ENSG00000126767	ENSG00000117298
ENSG00000103249	ENSG00000117298
ENSG00000083099	ENSG00000178913
ENSG00000141447	ENSG00000117298

Table 48: Top 10 interaction pairs among Treatment-Specific genes for humans at 41°.

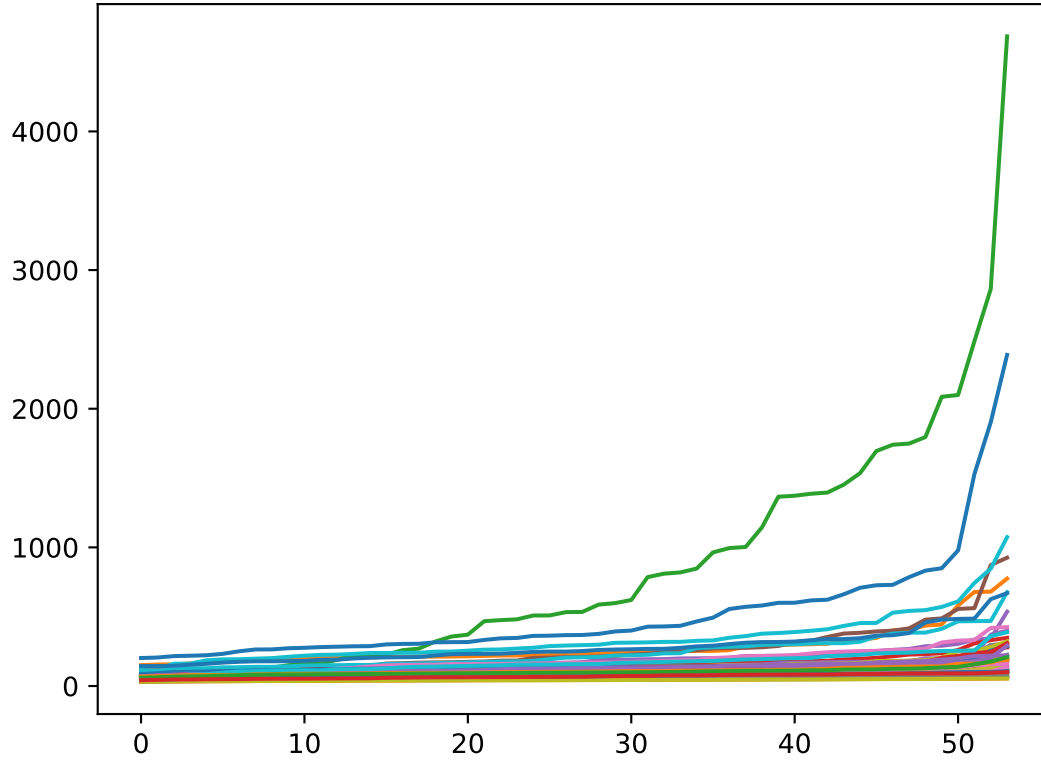


Figure 37: Interaction profiles for Noisy genes for humans at 41°. Each profile has been sorted. The x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

ENSG00000175387	ENSG00000182180
ENSG00000100029	ENSG00000120963
ENSG00000163320	ENSG00000168002
ENSG00000116685	ENSG00000100029
ENSG00000116685	ENSG00000100029
ENSG00000154545	ENSG00000182180
ENSG00000168002	ENSG00000168002
ENSG00000182872	ENSG00000100029
ENSG00000163512	ENSG00000163320
ENSG00000147852	ENSG00000120963

Table 49: Top 10 interaction pairs among Noisy genes for humans at 41°.

72 In the case of Camels the pictures are considerably different, and there is more spread in the
73 profiles.

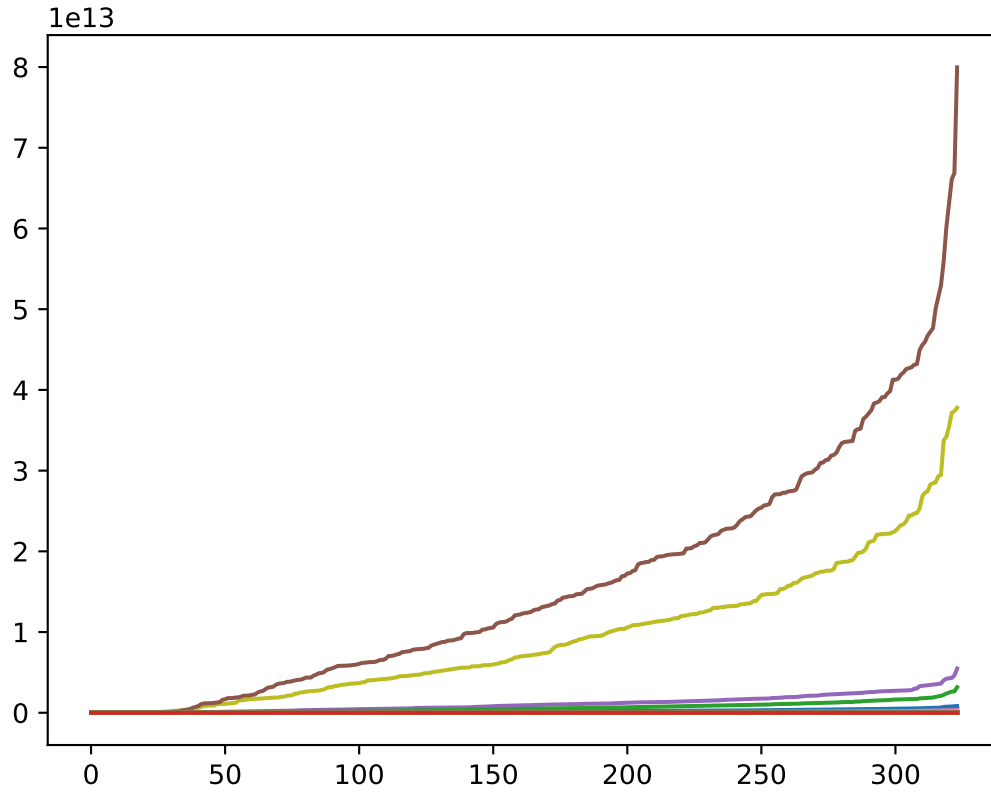


Figure 38: Interaction profiles for Key-Response genes for Camels at 32°. Each profile has been sorted and the x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

"ENSG00000151151"	"ENSG00000100151"
"ENSG00000182224"	"ENSG00000167202"
"ENSG00000196155"	"ENSG00000100151"
"ENSG00000170502"	"ENSG00000100151"
"ENSG00000109686"	"ENSG00000167202"
"ENSG00000138231"	"ENSG00000100151"
"ENSG00000145331"	"ENSG00000167202"
"ENSG00000105323"	"ENSG00000100151"
"ENSG00000121481"	"ENSG00000100151"
"ENSG00000048028"	"ENSG00000167202"

Table 50: Top 10 interaction pairs among Key-Response genes for camels at 32°.

74 In the case of Camels the pictures are considerably different, and there is more spread in the
75 profiles.

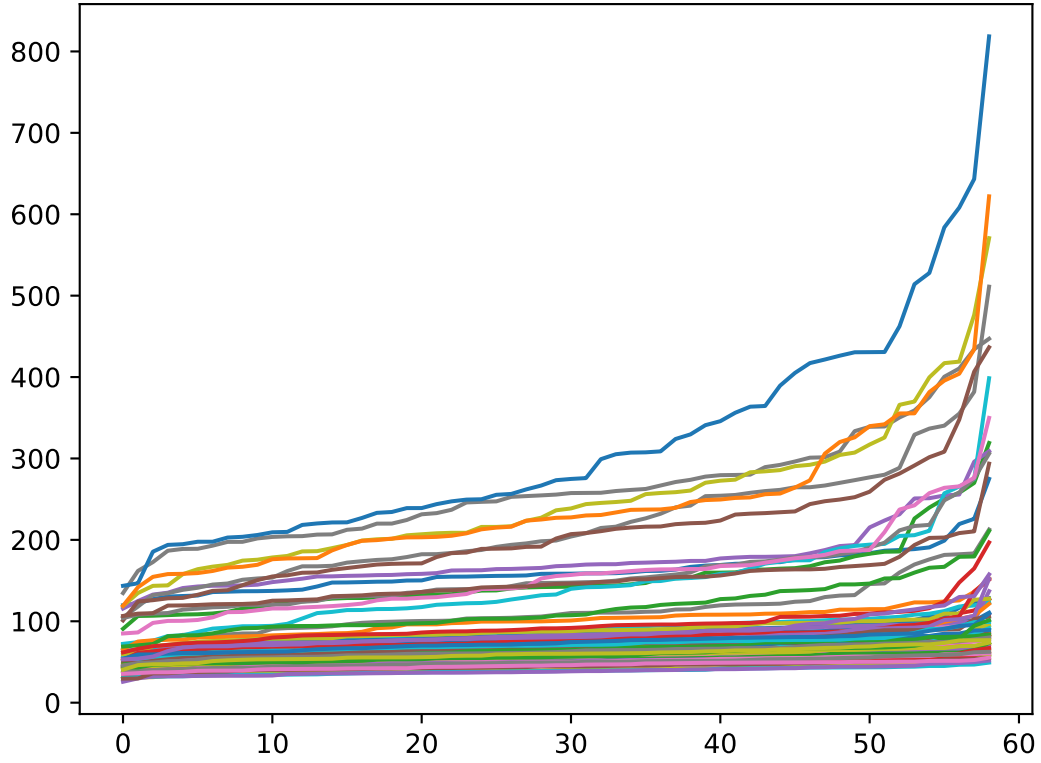


Figure 39: Interaction profiles for Treatment-Specific genes for Camels at 32°. Each profile has been sorted and the x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

ENSG00000134330	ENSG00000118816
ENSG00000100811	ENSG00000118816
ENSG00000135441	ENSG00000118816
ENSG00000147471	ENSG00000118816
ENSG00000239789	ENSG00000118816
ENSG00000060971	ENSG00000118816
ENSG00000285025	ENSG00000118816
ENSG00000125734	ENSG00000118816
ENSG00000100403	ENSG00000048828
ENSG00000048828	ENSG00000118816

Table 51: Top 10 interaction pairs among Treatment-Specific genes for camels at 32°.

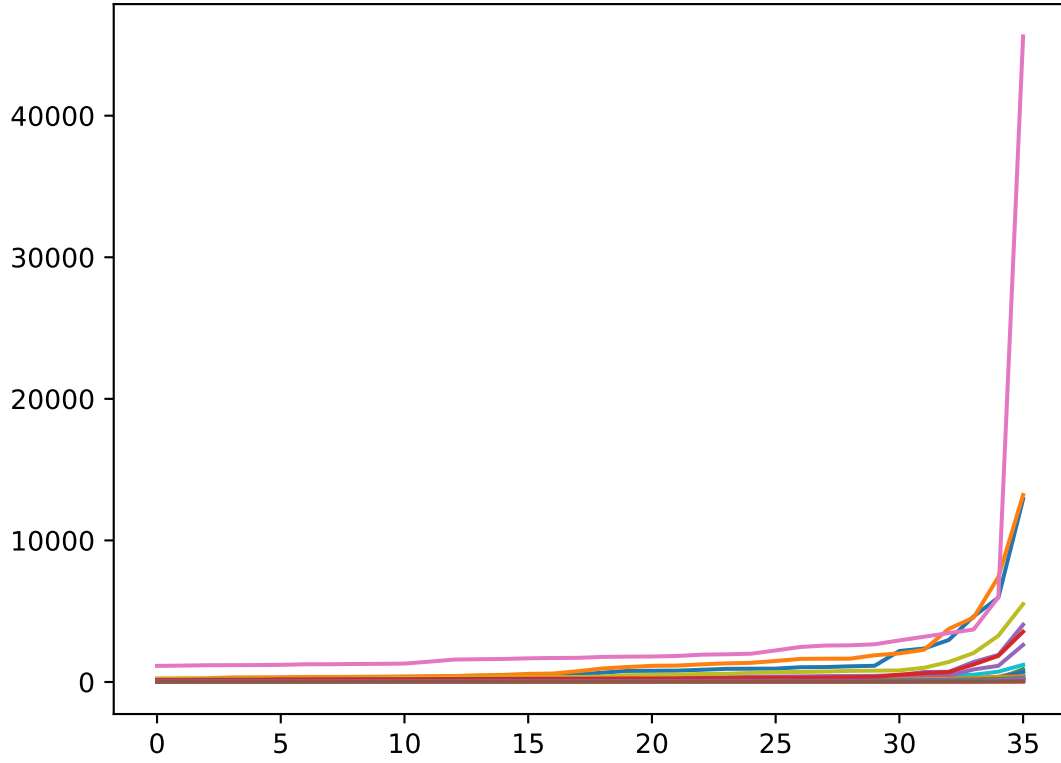


Figure 40: Interaction profiles for Noisy genes for Camels at 32°. Each profile has been sorted and the x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

ENSG00000204628	ENSG00000204628
ENSG00000127922	ENSG00000205581
ENSG00000060762	ENSG00000205581
ENSG00000122705	ENSG00000205581
ENSG00000149428	ENSG00000205581
ENSG00000165410	ENSG00000205581
ENSG00000170445	ENSG00000205581
ENSG00000011478	ENSG00000205581
ENSG00000205581	ENSG00000204628
ENSG00000100568	ENSG00000205581

Table 52: Top 10 interaction pairs among Noisy genes for camels at 32°.

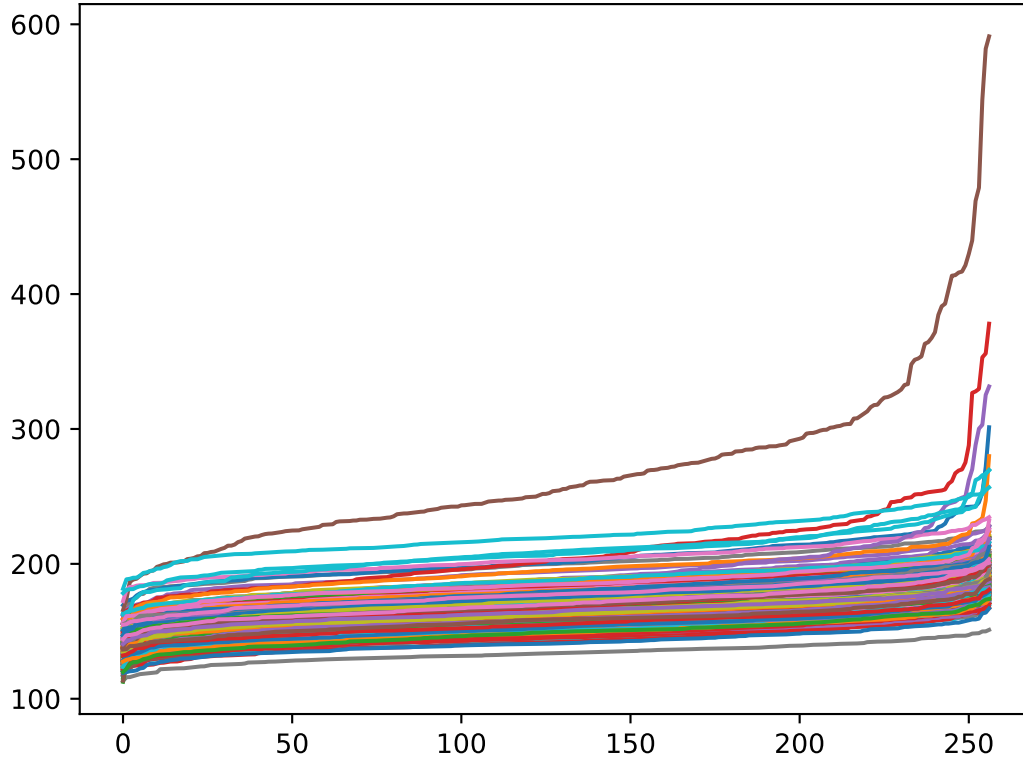


Figure 41: Interaction profiles for Key-Response genes for Camels at 41°. Each profile has been sorted and the x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

"ENSG00000164190"	"ENSG00000086232"
"ENSG00000164291"	"ENSG00000134882"
"ENSG00000106089"	"ENSG00000134882"
"ENSG00000100151"	"ENSG00000134882"
"ENSG00000142733"	"ENSG00000134882"
"ENSG00000197024"	"ENSG00000134882"
"ENSG00000086232"	"ENSG00000164920"
"ENSG00000134882"	"ENSG00000134882"
"ENSG00000033011"	"ENSG00000099875"
"ENSG00000136159"	"ENSG00000255072"

Table 53: Top 10 interaction pairs among Response genes for camels at 41°.

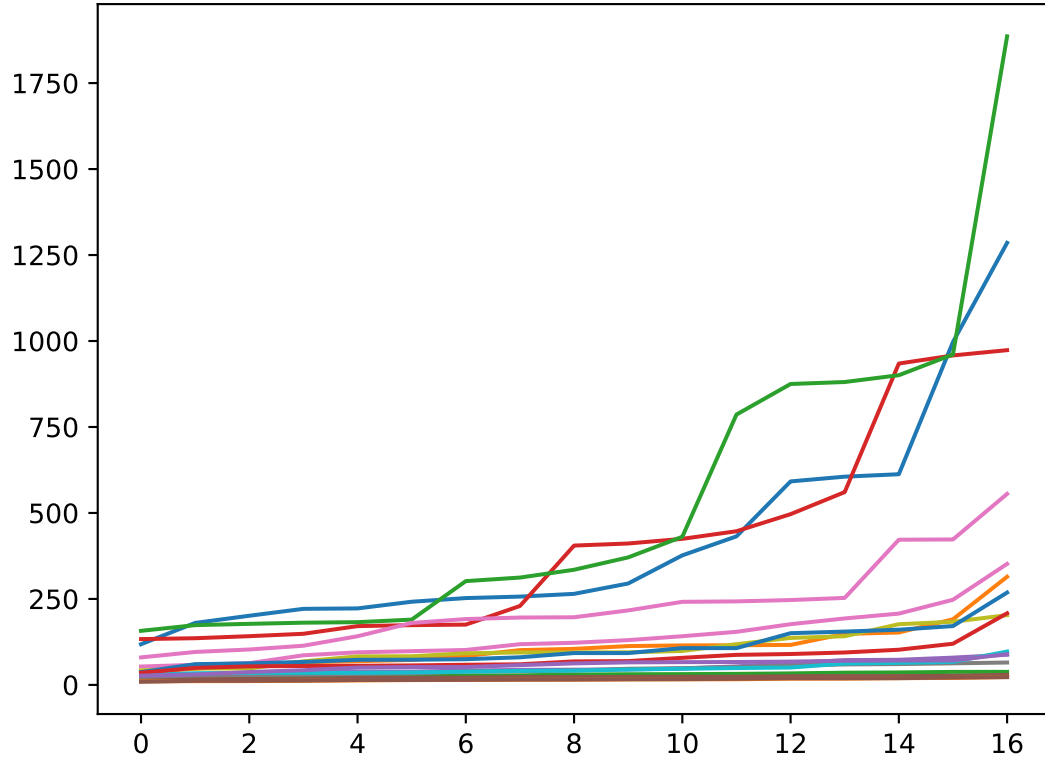


Figure 42: Interaction profiles for Treatment-Specific genes for Camels at 41°. Each profile has been sorted and the x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

ENSG00000101152	ENSG00000168710
ENSG00000168710	ENSG00000101152
ENSG00000179163	ENSG00000179163
ENSG00000084652	ENSG00000101152
ENSG00000156535	ENSG00000168710
ENSG00000156875	ENSG00000101152
ENSG00000101473	ENSG00000168710
ENSG00000168303	ENSG00000101152
ENSG00000198912	ENSG00000101152
ENSG00000160803	ENSG00000101152

Table 54: Top 10 interaction pairs among Treatment-Specific genes for camels at 41°.

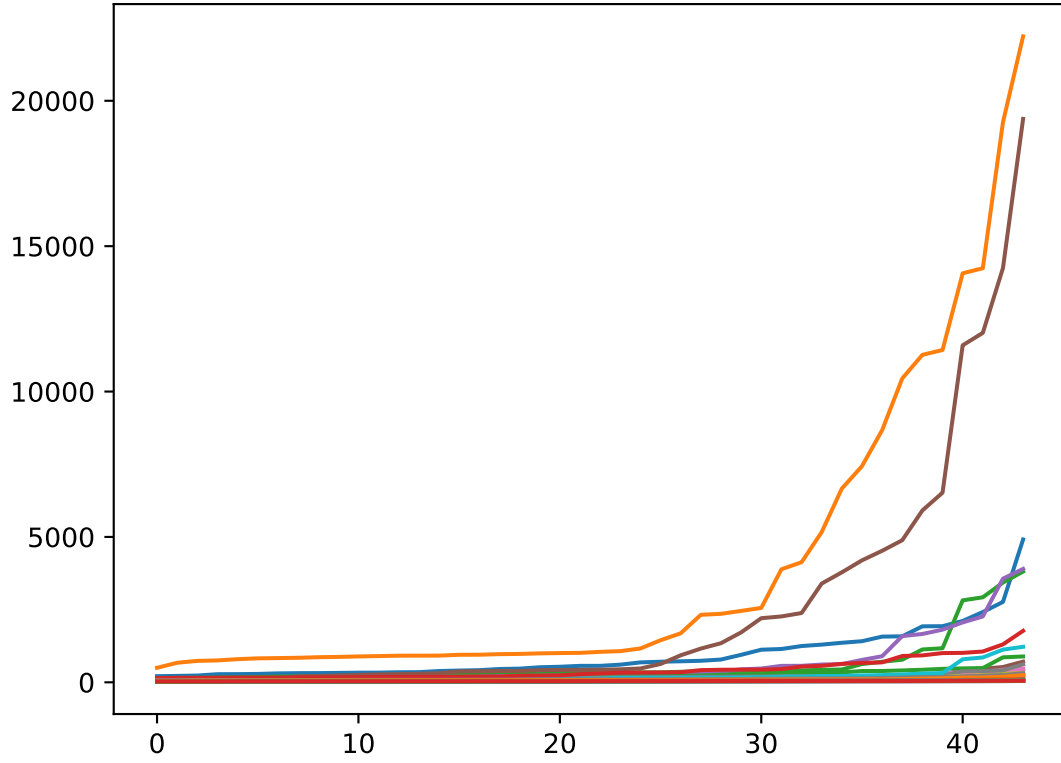


Figure 43: Interaction profiles for Noisy genes for Camels at 41° . Each profile has been sorted and the x axis denotes the rank of the interaction. The y axis denotes the relative strength of the interaction.

ENSG00000114850	ENSG00000146278
ENSG00000265972	ENSG00000146278
ENSG00000127922	ENSG00000100650
ENSG00000137710	ENSG00000146278
ENSG00000122705	ENSG00000100650
ENSG00000100568	ENSG00000100568
ENSG00000141295	ENSG00000100650
ENSG00000227057	ENSG00000146278
ENSG00000100650	ENSG00000100650
ENSG00000146278	ENSG00000100650

Table 55: Top 10 interaction pairs among Noisy genes for camels at 41° .

76 **7.8 Network Entropy**

	G1	G2	G4
Humans	0.621	-8.528	1.082
Camels	-4912.596	1.247	-0.382

Table 56: Network entropy for humans and camels at 32°.

	G1	G2	G4
Humans	-20514.161	-20.082	0.348
Camels	1.558	-35.239	-5.492

Table 57: Network entropy for humans and camels at 41°.