Supplementary Material: Volatile odours reflect breeding status but not social group membership in captive Damaraland mole-rats

Results with peaks found in controls removed

In Tables S1 and S2, we present our results with peaks found in >1 control sample removed. All results remain qualitatively the same as the results in the main text, except for the interaction term between sex and breeding status for chemical diversity in the facial samples, which changes from being marginally significant ($P = 0.047$) to marginally nonsignificant ($P = 0.071$).

We used gas chromatography with flame ionization detector to analyse our profiles. This technique is more sensitive than gas chromatography-mass spectrometry in detecting organic compounds, but does not allow the identification of individual chemicals. This means that multiple chemicals can potentially be represented by a single peak. Peaks that are present in the control samples may therefore also include chemicals genuinely present in the samples. We therefore retain all peaks in the results presented in the paper.

Chemical differences associated with reproduction

Table S1

Results of permutational MANOVAs investigating chemical similarity based on sex and breeding status, modelled seperately for anogenital and facial samples

Sample area	Variable	*df*	SS	Pseudo-F	*P*
Anogenital	Sex	1	1666.8	0.773	0.64
	Breeding status	1	4884.4	2.266	0.03
	Sex: Breeding status	1	5612.9	2.604	0.02
Facial	Sex	1	3144.8	1.209	0.28
	Breeding status	1	3122.8	1.201	0.30
	Sex: Breeding status	1	2763.5	1.063	0.35

Models contained data from 35 individuals from eight social groups and the resulting *P* values were determined from 999 permutations of the data.

Table S2

Results of GLMMs of the effect of sex and breeding status on chemical diversity, modelled seperately for anogenital and facial samples

Sample area	Variable	Estimate	SE	z	*P*
Anogenital	(Intercept)	3.346	0.191	17.506	$<2 \times 10^{-16}$
	Sex (male)	0.454	0.275	1.647	0.100
	Status (nonbreeder)	0.686	0.274	2.506	0.012
	Sex (male), status (nonbreeder)	−0.062	0.368	−1.686	0.092
Facial	(Intercept)	3.888	0.224	17.345	$<2 \times 10^{-16}$
	Sex (male)	−0.433	0.331	−1.310	0.190
	Status (nonbreeder)	−0.716	0.334	−2.143	0.032

	Sex (male), status (nonbreeder)	0.813	0.450	1.807	0.071

Models contained data from 35 individuals from eight social groups.

Signals of group identity

No social group identity in facial samples. ANOSIM factor: group identity; Global R = −0.116, *P* = 0.97.

No social group identity in anogenital samples. ANOSIM factor: group identity; Global R = −0.057; *P* = 0.72.

No impact of colony size on chemical diversity in facial samples. GLMM; estimate = −0.0121, SE = 0.040, *z* = 0.301, *P* = 0.764.

No impact of colony size on chemical diversity in anogenital samples. GLMM; estimate = −0.0138, SE = 0.034, *z* = −0.412, *P* = 0.681.

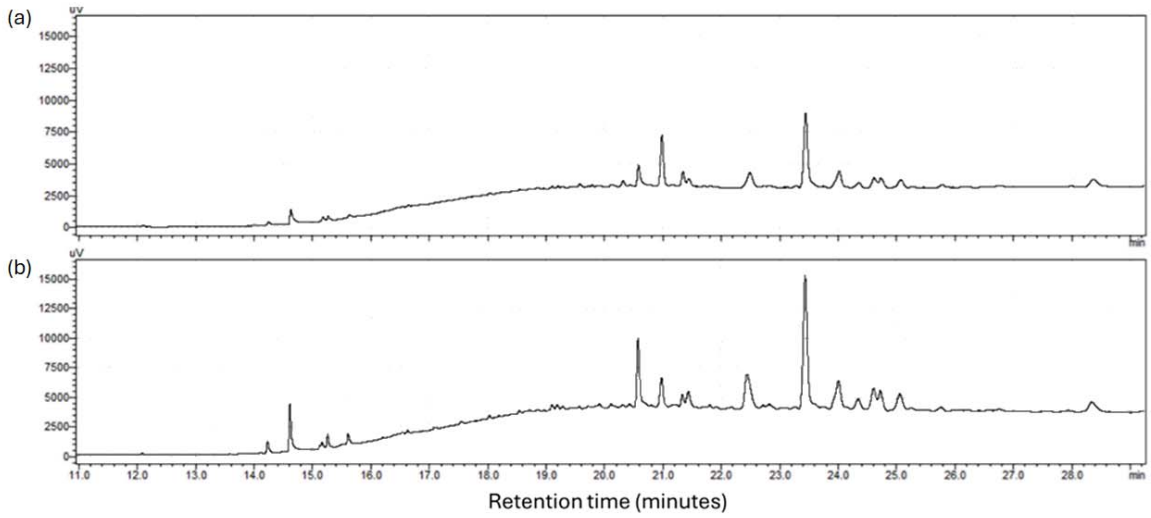

Figure S1. Chromatograms of the anogenital region of (a) a breeding female and (b) a nonbreeding female.

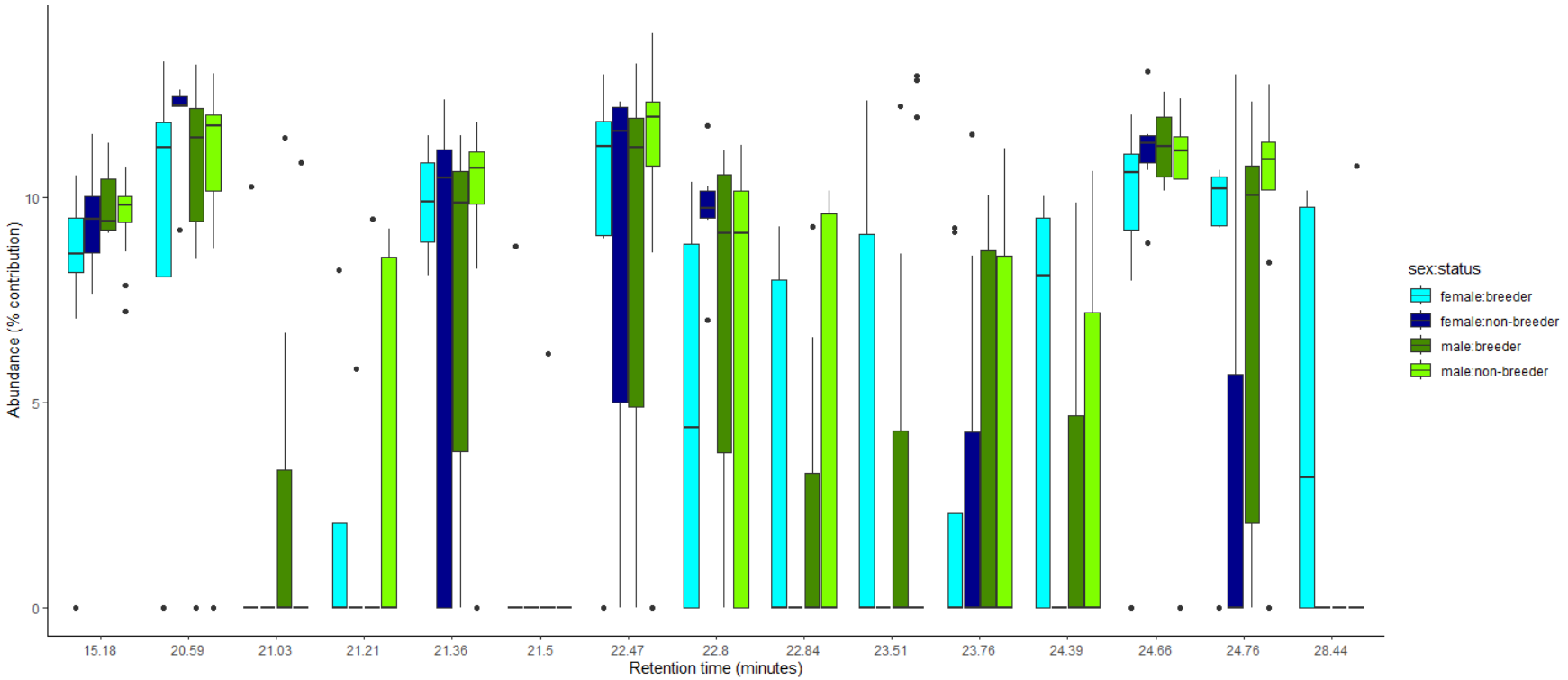

Figure S2. A summary of key differences in anogenital chemical profiles, displayed according to the sex and breeding status of the sampled individual. The box plots show the median and 25th and 75th percentiles; the whiskers indicate the values within 1.5 times the interquartile range and the circles are outliers. The 15 peaks with the highest percentage contribution are shown, based on the variable selection procedure in Primer 7, and are labelled according to their retention times. If we rerun our analysis based on only these substances, we find similar results as with the whole data set (i.e. significant interaction between sex and breeding status: *df* = 1; pseudo-F = 4.420; *P* = 0.005).