

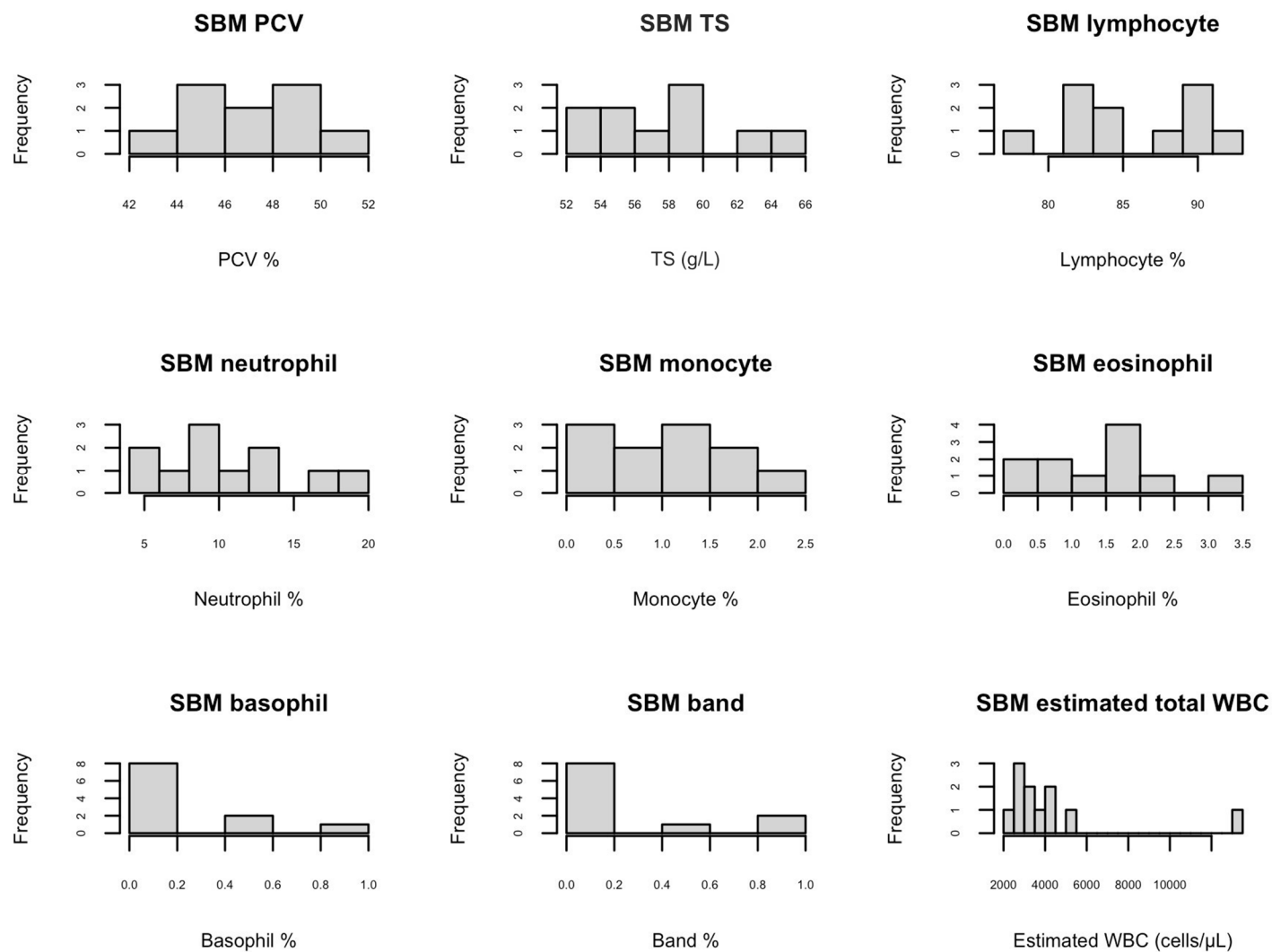


Figure S1: Histograms of haematology results of Shark Bay mice. TS = total solids; PCV = packed cell volume; WBC = white blood cell.

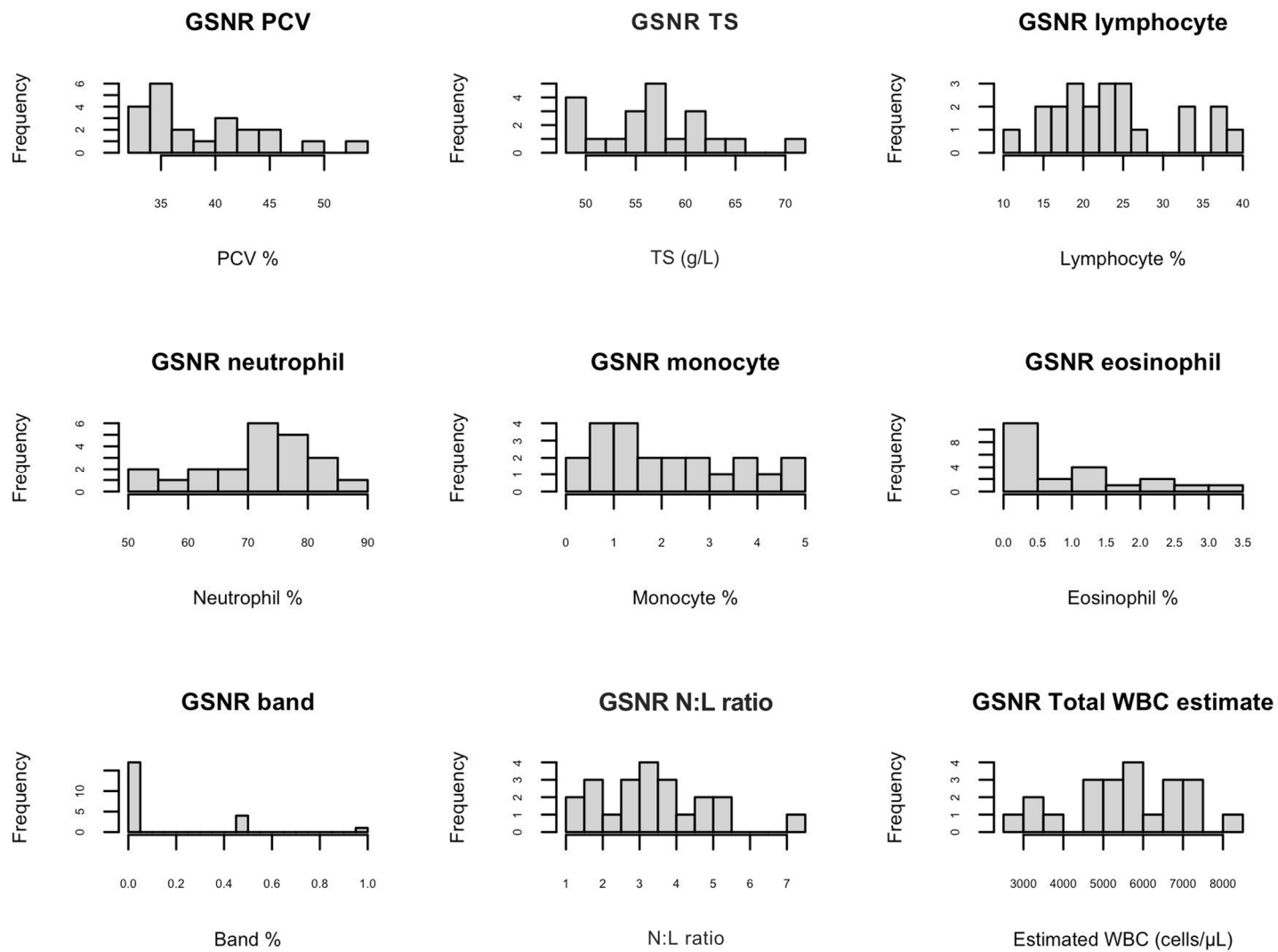


Figure S2: Histograms of haematology results of greater stick-nest rats. TS = total solids; PCV = packed cell volume; WBC = white blood cell.

Table S1: Faecal parasitology apparent prevalence (AP) across species and cohorts. 37.2% of GSNR and 27% of SBM were positive for at least one taxon by faecal flotation. There was no statistically significant difference of apparent prevalence of faecal parasites between cohorts of GSNR (Fisher's exact, $p = 0.158$), or SBM ($\chi^2 = 0.12$, $df = 1$, $p = 0.73$), noting only a small number of faecal samples ($n = 12$) were collected from the Franklin Islands. Species identification was not possible through our methods, although in most cases, parasites were identified to a family/genus level.

Taxa	GSNR	Salutation Island	Franklin Islands	SBM	Bernier Island	Northwest Island
	AP % (95% CI and total)	AP % (95% CI and total)	AP % (95% CI and total)	AP % (95% CI and total)	AP % (95% CI and total)	AP % (95% CI and total)
Any	37.21 (24.38–52.14; $n = 16/43$)	45.16 (29.16–62.23; $n = 14/31$)	16.67 (4.7–44.8; $n = 2/12$)	26.97 (18.84–37; $n = 24/89$)	24.49 (14.6–38.09; $n = 12/49$)	30 (18.07–45.43; $n = 12/40$)
<i>Entamoeba</i>	27.91 (16.75–42.69; $n = 12/43$)	35.48 (21.12–53.05; $n = 11/31$)	8.33 (0.43–35.39; $n = 1/12$)	2.25 (0.62–7.83; $n = 2/89$)	2.04 (0.1–10.69; $n = 1/49$)	2.5 (0.13–12.88; $n = 1/40$)
Unidentified protozoan	20.93 (11.42–35.21; $n = 9/43$)	25.81 (13.7–43.25; $n = 8/31$)	8.33 (0.43–35.39; $n = 1/12$)	1.12 (0.06–6.09; $n = 1/89$)	2.04 (0.1–10.69; $n = 1/49$)	0 (0–8.76; $n = 0/40$)
Coccidian	2.33 (0.12–12.06; $n = 1/43$)	3.22 (0.17–16.19; $n = 1/31$)	0 (0–24.25; $n = 0/12$)	-	-	-
<i>Chilomastix</i>	6.98 (2.4–18.61; $n = 3/43$)	9.68 (3.35–24.9; $n = 3/31$)	0 (0–24.25; $n = 0/12$)	-	-	-
Trichomonidae	-	-	-	21.35 (14.11–30.95, $n = 19/89$)	18.37 (9.98–31.36; $n = 9/49$)	25 (14.19–40.19; $n = 10/40$)
Spiruroid	-	-	-	1.12 (0.06–6.09; $n = 1/89$)	0 (0–7.27; $n = 0/49$)	2.5 (0.13–12.88; $n = 1/40$)
<i>Protospirura</i> or <i>Mastophurus</i>	-	-	-	1.12 (0.06–6.09; $n = 1/89$)	0 (0–7.27; $n = 0/49$)	2.5 (0.13–12.88; $n = 1/40$)
Unidentified cestode	-	-	-	1.12 (0.06–6.09; $n = 1/89$)	2.04 (0.1–10.69; $n = 1/49$)	0 (0–8.76; $n = 0/40$)
Multiple burdens	16.28 (8.12–29.97; $n = 7/43$)	22.58 (11.4–39.81; $n = 7/31$)	0 (0–24.25; $n = 0/12$)	2.25 (0.62–7.83; $n = 2/89$)	2.04 (0.1–10.69; $n = 1/49$)	2.5 (0.13–12.88; $n = 1/40$)

Table S2: Nucleotide sequences obtained from amplification of the *Orthoherpesviridae* DNA polymerase catalytic subunit gene region from rodent swabs collected during this study.

Species	Nucleotide sequence
SBM	ATGGCCGGCGGTCGCGAGCGACATATCCCTGCTGATCTTGGTGATAAAAGCGGC
GSR	ACGGGGGTGGCCAGTGGCATCTTGCCCTGCGTCAAGATCGCCGAGACGGTGACTTTCGTGGGCCGACGGATGCTGGGAG CCTCGATGGACCTGGTGAATCCCTGTCGCTGGAGCGACTCGAGGAGATTACGGGGCGCCGCTGCCGCGCGGCGAGGG GGCCTCGCTCCGAGTGATCTACGGCGACACGGACTCTG

Table S3: Nucleotide sequences obtained from amplification of the *Mollicutes* 16S rRNA gene region from rodent swabs collected during this study.

Species	Year sourced	Nucleotide sequence
SBM	2021/2022	GGTAGTCCACGCCGTAAACGATGATCATTAGTTGGTAGAAATAATTTACTAACGCAGCTAACGCATTAAATGATCCGCCT GAGTAGTATGCTCGCAAGAGTGAAACTTAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTTGA AGATACGCGTAGAACCTTACCCACTCTTGACATCCTTTGCAAAGTTATAGAGATATAATG
GSR	2021	GCCCCCGTGAATAATATGCTCACGGGAGTGACTCTTAGGAGATTTGACGCAGACCCACACACGGGGTGGAACGTGTTTT TTATTTTGAATATACGCATAAAATCTTACCCACTCTTGACCTCTTCTGCAACTATATAAATATATAGTG
GSR	2021/2022	GGTAGTCCACGCCGTAAACGATGATCATTAGTTGGTAGAAGAATTTACCGACGCAGCTAACGCATTAAATGATCCGCCTG AGTAGTATGCTCGCAAGAGTGAAACTTAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTTGAA GATACGCGTAGAACCTTACCCACTCTTGACATCTTCTGCAAAAATATAGAGATATATTG
GSR	2022	ATTCATCGGCGCAGCTAACGCATTAAATGATCCGCCTGAGTAGTACGTTTCGCAAGAATAAACTTAAAGGAATTGACGGGGAT CCGCACAAGCGGTGGAGCATGTGGTTTAATTTGAAGATACGCGTAGAACCTTACCCACTCTTGACTTCTTCTGCAATGCTATGG AGACATAGCG