

SUPPLEMENTARY TABLE: DNA Extraction and Cleaning Information

Species Code	Genus	Species	DNA Extraction Method	Sequencer	Quality Scoring	Quality Cutoff	Number of Individuals	Read Length	5' trim
Aamic	<i>Antarctophthirus</i>	<i>microchir</i>	Qiagen-Micro	HiSeq2500	Illumina 1.9	28	8	160 bp	yes
Hbarb	<i>Hoplopleura</i>	<i>arboricola</i>	Qiagen-Micro	HiSeq2500	Illumina 1.9	33	10	160 bp	yes
Hieur	<i>Haematopinus</i>	<i>eurysternus</i>	Phenol Chloroform	HiSeq2000	Illumina 1.5	64	5	100 bp	no
Ltspi	<i>Linognathus</i>	<i>spicatus</i>	Phenol Chloroform	HiSeq2000	Illumina 1.5	64	4	100 bp	no
Nepac	<i>Neohaematopinus</i>	<i>pacificus</i>	Qiagen-Micro	HiSeq2500	Illumina 1.9	33	10	160 bp	yes
PdhumCA	<i>Pediculus</i>	<i>humanus</i>	Phenol Chloroform	HiSeq2500	Illumina 1.9	33	5	100 bp	yes
PdhumHO	<i>Pediculus</i>	<i>humanus</i>	Phenol Chloroform	HiSeq2500	Illumina 1.9	33	5	100 bp	yes
PdschKE	<i>Pediculus</i>	<i>schaeffi</i>	Zymo MicroPrep	HiSeq2500	Illumina 1.9	33	5	160 bp	yes
PdschUG	<i>Pediculus</i>	<i>schaeffi</i>	Phenol Chloroform	HiSeq2000	Illumina 1.5	64	5	100 bp	no
Pnbad	<i>Pedicinus</i>	<i>badii</i>	Phenol Chloroform	HiSeq2000	Illumina 1.5	64	9	100 bp	no
Prflu	<i>Proechinophthirus</i>	<i>fluctus</i>	Phenol Chloroform	HiSeq2000	Illumina 1.5	64	6	100 bp	no
Ptgot	<i>Pthirus</i>	<i>gorillae</i>	Zymo MicroPrep	HiSeq2500	Illumina 1.9	33	2	160 bp	yes
Ptpub	<i>Pthirus</i>	<i>pubis</i>	Zymo MicroPrep	HiSeq2500	Illumina 1.9	33	6	160 bp	yes
Brant	<i>Bureelia</i>	<i>antiqua</i>	Phenol Chloroform	HiSeq2500	Illumina 1.9	33	50	100 bp	yes
Btmac	<i>Bothriometopus</i>	<i>macrocnemus</i>	Phenol Chloroform	HiSeq2000	Illumina 1.5	64	6	100 bp	no

SUPPLEMENTARY TABLE Information on the DNA extraction methods, sequencing runs and cleaning steps, for the 15 louse taxa represented in this manuscript. The FASTX Toolkit v0.0.14 (Hannon Lab) was used for all quality trimming steps. For libraries sequenced with IlluminaHiSeq version v1.8 or greater the first 3 bases were removed from the 5' end of the sequence read as they consistently had a lower quality score than the following nucleotides. All sequence reads were quality trimmed from the 3' end to remove bases with a phred score less than 28 using a sliding window of 1nt. Finally, any trimmed reads with fewer than 75nt in length were removed from the dataset