

## Supplementary material

**Table S1.** PCR primers used to amplify and sequence the mitochondrial genomes of the domestic pig louse, *Haematopinus suis*, and the wild pig louse, *Haematopinus apri*

<b>Primer</b>	<b>Target gene or region</b>	<b>Sequence (5' to 3')</b>
mtd6	<i>cox1</i>	GGAGGATTTGGAAATTGATTAGTTCC
mtd11	<i>cox1</i>	ACTGTAAATATATGATGAGCTCA
12SA	<i>rrnS</i>	TACTATGTTACGACTTAT
12SB	<i>rrnS</i>	AAACTAGGATTAGATACCC
PGC1F	<i>cox1</i>	GGTTTTAGCGGGTGGGATTACTATATTGT
PGC1R	<i>cox1</i>	GGCAAAGAAAGTAACAGTAGGACAGCAGT
PG12SF	<i>rrnS</i>	TTTGTACACCGCTGTCGGAAGGTTGTGGA
PG12SR	<i>rrnS</i>	GACGTGCATTATCGATTACAAACATGGGT
PGseqF1	<i>rrnS</i>	TGTACTTTTCATAGGAGTTATTTTCTATGA
PGseqF2	<i>rrnS</i>	ATTGGGATGGTTTTACCCCAATTTTGGGG
PGseqF3	<i>cox1</i>	ACACTTCTTAGGTTTGAGAGGCATGCCACG
PGseqR1	<i>rrnS</i>	TTGGGCAATTTATAGCCCACTGTCGACTAC
PGseqR2	<i>cox1</i>	GCTGATATGAAGGTGTGTATCCGTCGATAG
PLF1	Non-coding region	GGAAGAGCATTTCGACGATTGTTACTTTAAC
PLR	Non-coding region	TAGCGATTTCTAAAAATCGTTATTGATCG

**Table S2.** PCR primers used to verify each mitochondrial minichromosome of the domestic pig louse, *Haematopinus suis*, and the wild pig louse, *Haematopinus apri*

<b>Primer</b>	<b>Target gene or region</b>	<b>Sequence (5' to 3')</b>
HS12SF	<i>rrnS</i>	GGTCCATGAAAACATAATAACATATGGCGGT
HS12SR	<i>rrnS</i>	AACCATTACTACCTTGATATGATACTTACG
HSCBF	<i>cob</i>	GGAGCAACTGTAATTACAAATTTGCTATCT
HSCBR	<i>cob</i>	GGTAAAACATAACCTAAGAATGCTGTTGCC
HSND1F	<i>nad1</i>	GCAACAGAGCGAATTGCCCCCATAGTTCTA
HSND1R	<i>nad1</i>	TCAATCTCTCTCATTTCGAGATTACATTTAG
HSND1F1	<i>nad1</i>	GGGTGTATACCGAATAGAAGCCTAAGTTTG
HSND1R1	<i>nad1</i>	TTCTTATGGATTACAACCTCCATTTCTTTCC
HSND2F	<i>nad2</i>	GCTGGGGTAATAGTATCCTTACCTAGGTCT
HSND2R	<i>nad2</i>	AATCCGACGAATTGACAGATCAATTGAACC
HSCX1F	<i>cox1</i>	CCAGAGCAACTATGGTTATTGCCATTCCCA
HSCX1R	<i>cox1</i>	ATCCATCCCTACTGTAAACATACGGTGTGC
HSND4LF	<i>nad4L</i>	GGGTAATGTTGGCAATGAGGGTTACTCACT
HSND4LR	<i>nad4L</i>	AGACAGAACTACCATTCTACACCTTGAAGC
HSND4LF2	<i>nad4L</i>	GGCAATGAGGGTTACTCACTATTGAATTGT
HSND4LR2	<i>nad4L</i>	CAGATAAAGACAGAACTACCATTCTACACC
HSCX3F	<i>cox3</i>	GCCGATAGTGTATGTGGTTCATTGTTTTAC
HSCX3R	<i>cox3</i>	CCTCAAACCTGAAACATAACAAACAACACTC
HSCX2F	<i>cox2</i>	GGATTCCTTGTTTCGCCTTTTGAAGTAGA
HSCX2R	<i>cox2</i>	TGACTTAACATGTATGAATCAAACCTCC
HS16SF	<i>rrnL</i>	CCTGCTCACTGCGTTGATAACGTAAATAGC
HS16SR	<i>rrnL</i>	TTAGTAAACAGTCAGACTAATTATTTGCCG

HSND5F	<i>nad5</i>	GGAGTATCAGCACTTTGTGAAGTGGATTTA
HSND5R	<i>nad5</i>	ATTGACACTACCTTAAGTGCTTGTAACACC
HSATP6F	<i>atp6</i>	GGCTCTAATTCAGGCTTATGTGTTTCATAAG
HSATP6R	<i>atp6</i>	CAGCAAGAGTAATTACTIONTATGTGACCTGCTG
HA12SF	<i>rrnS</i>	GGTCCATGAAAATAATAACATATGGCGGT
HA12SR	<i>rrnS</i>	CATTGTATATAGTAGGGTATCTAATCCTAG
HAND1F1	<i>nad1</i>	GGGTGTATACCGAATAGAAGCCTAAGTTTG
HAND1R1	<i>nad1</i>	TTCTTATGGATTACAACCTCCATTTCTTCC
HAND4LF	<i>nad4L</i>	GGGTAATATTGGCAATGAGGGTTACTCATT
HAND4LR	<i>nad4L</i>	AGACAAAATACTACCATTCTACATCTTGATGC
HAND6F	<i>nad6</i>	CCTAATCCGGATTTAGGTGTTTTTAATAGA
HAND6R	<i>nad6</i>	TGAGTAACCCTCATTGCCAATATTACC
HAND4LF1	<i>nad4L</i>	CCTTAGGTTTGACCATTCTTGTTTCGACGA
HAND4LR1	<i>nad4L</i>	AATGATCTTGGGTAAACAAGAAAAAGG
HAND2F	<i>nad2</i>	GGTTC AATTGATCTGTCAATTCGTCGTATT
HAND2R	<i>nad2</i>	TAACATCACTACAACCGTTCCTCC
HACX1F	<i>cox1</i>	GCATATAATTATGGAGGAGAGAGGAA
HACX1R	<i>cox1</i>	ATGACCAAAAAACCAGAATAGATGCTGG
HA16SF	<i>rrnL</i>	GGTTTTACAAGACTAAGTCTGTCTCTGTGA
HA16SR	<i>rrnL</i>	TACTGCAGCTATTTACGTTATCAACG
HAND4F1	<i>nad4</i>	CCACTCTTTCTTACACACTCCTGATTA
HAND4R1	<i>nad4</i>	AAGGCTACTATTAATCCTAATGAGGAC
HAATP6F	<i>atp6</i>	CAGCAGGTCACATAGTAATTACTIONTCTT
HAATP6R	<i>atp6</i>	TTAAACTAATTGGCCGAATAACCAACC
HAND5F	<i>nad5</i>	GGTAGCTCTTTCTACACTGACCCATTTA

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HAND5R	<i>nad5</i>	ATCCACCTCACAAAGTGCTGACACTCCTGC
HACBF	<i>cob</i>	CGACTTTAGTACGGTTCTTTTCGTTTCATT
HACBR	<i>cob</i>	ATTCCTACAGAAAAACCTCCCCACAACC
HACX2F	<i>cox2</i>	GAGCAGGACTGCCAGCTATTTCTTTA
HACX2R	<i>cox2</i>	AAAGTCTCTGCACTTACAAGAAAACGG
HACX3F	<i>cox3</i>	GGAGTACCGTTTTTTGAATACTATGATCTT
HACX3R	<i>cox3</i>	ATATAATTCAAAGGCTGAATACCTACAGG

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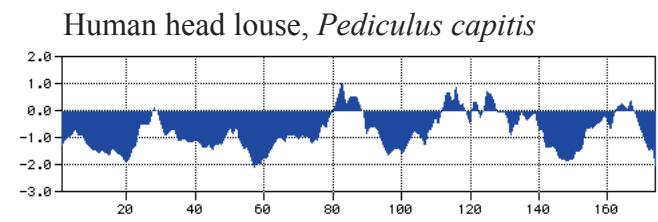
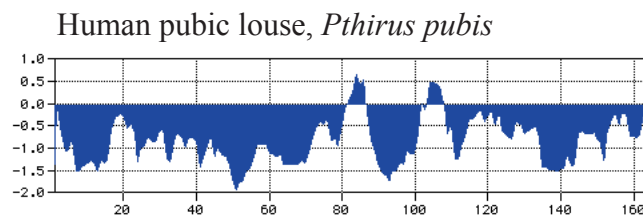
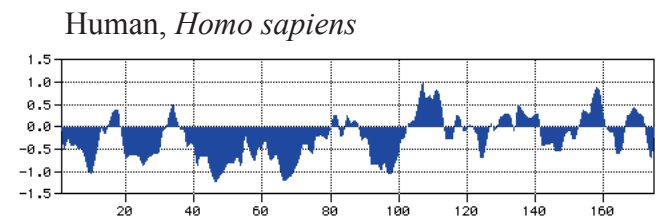
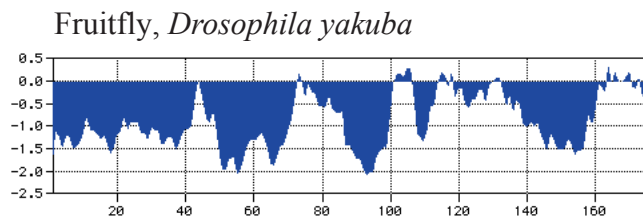
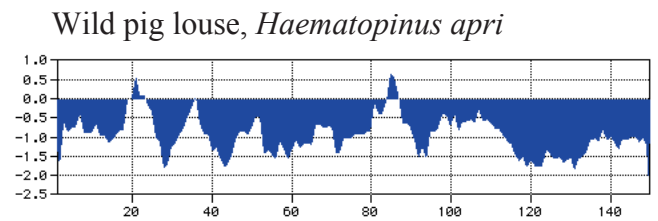
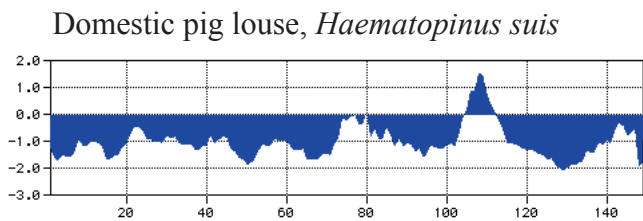


Fig. S1. Hopp/Woods hydrophilicity profiles of NAD6 proteins of *Haematopinus suis* and *H. apri* with four other animals. Amino acids are along the horizontal lines. Hydrophilicity values of amino acids are along the vertical lines.

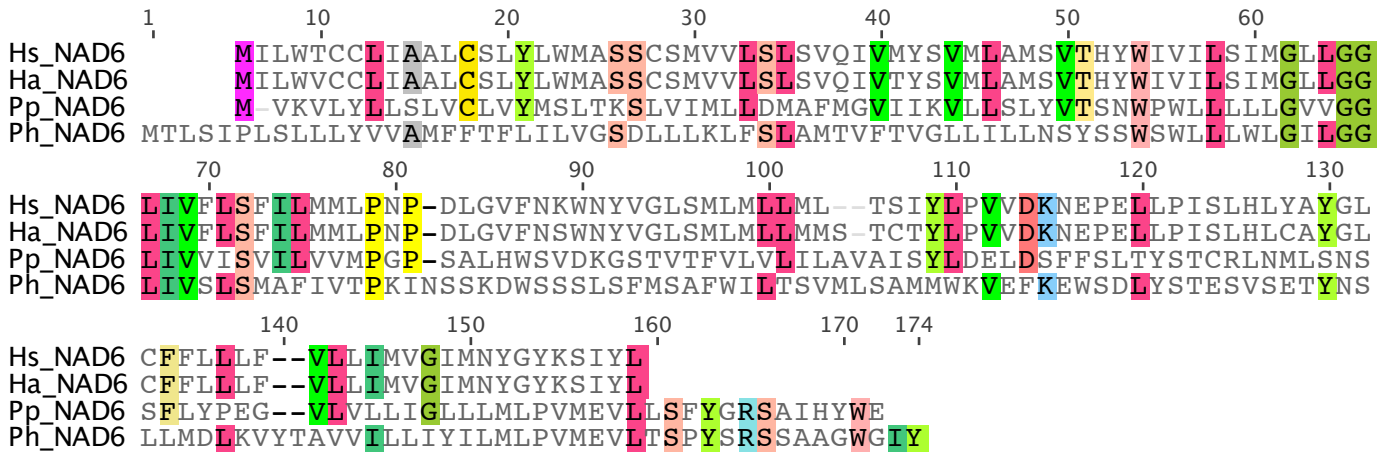


Fig. S2. Alignment of the putative amino acid sequences of mitochondrial NAD6 proteins of sucking lice. Conserved amino acid sequences were highlighted in colors. Abbreviations of species names are: Hs – *Haematopinus suis* (domestic pig louse), Ha – *Haematopinus apri* (wild pig louse), Pp – *Pthirus pubis* (human pubic louse), and Ph – *Pediculus humanus* (human body louse). Alignment was with Geneious 6.1.2 (Kearse et al. 2012). BLOSUM cost matrix was used; gap open cost was 10 and gap extend cost was 6.6.