Table S1: Growth of selected *Aureobasidium* strains on YNB medium, hemolytic activiy and siderophore production at 24 °C and 37 °C.

	growth on YNB		**hemolytic activity**		**siderophore production**	
Culture collection strain number	**24 °C**	**37 °C**	**24 °C**	**37 °C**	**24 °C**	**37 °C**
EXF-2481	+	NG	α	NG	1,15	NG
EXF-4632	+	NG	α	NG	2,41	NG
EXF-12298	+	NG	α	NG	1,28	NG
EXF-150	+	NG	α	NG	1,67	NG
EXF-3670	+	NG	α	NG	-	NG
EXF-10629	+	NG	α	NG	1,20	NG
EXF-11318	+	NG	α	NG	1,16	NG
EXF-5629	+	NG	α	NG	1,26	NG
EXF-3398	+	NG	α	NG	2,11	NG

Legend: + growth, - no production, NG – no growth.

Table S2: Assimilation of hydrocarbons (n-hexadecane and mineral oil) of selected *Aureobasidium* species.

Culture collection strain number	**n-hexadecane**	**mineral oil**
EXF-2481	-	-
EXF-4632	-	-
EXF-12298	-	-
EXF-150	-	-
EXF-3670	+	+
EXF-10629	-	-
EXF-11318	-	-
EXF-5629	-	-
EXF-3398	+	+

Legend: + assimilation, - no assimilation.

Table S3: Assimilation of neurotransmitters (acetylcholine – ACh, γ-aminobutyric acid – GABA, glycine – Gly, glutamate – Glu, dopamine – DA) of selected *Aureobasidium* species at 24 °C and 37 °C.

	24 °C					**37 °C**				
Culture collection strain number	**Ach**	**GABA**	**Gly**	**Glu**	**DA**	**Ach**	**GABA**	**Gly**	**Glu**	**DA**
EXF-2481	+	+	-	+	+	NG	NG	NG	NG	NG
EXF-4632	+	-	-	+	NG	NG	NG	NG	NG	NG
EXF-12298	+	+	+	+	=	NG	NG	NG	NG	NG
EXF-150	+	+	=	+	=	NG	NG	NG	NG	NG
EXF-3670	+	+	=	+	+	NG	NG	NG	NG	NG
EXF-10629	+	+	=	=	NG	NG	NG	NG	NG	NG
EXF-11318	+	+	=	=	=	NG	NG	NG	NG	NG
EXF-5629	+	-	-	-	NG	NG	NG	NG	NG	NG
EXF-3398	+	+		+	+	NG	NG	NG	NG	NG

Legend: + better growth, = similar growth, - worse growth, NG – no growth.

Table S4: Found non-ribosomal protein synthase (NRPS) genes with adenylation domains (A domains) similar to those of genes encoding proteins SidC and SidD in *A. melanogenum* genomes.

Present study number	**SidC**	**SidD**	**both**
1	1	1	2
2	1	2	3
3	1	1	2
4	1	1	2
5	1	1	2
6	2	2	4
7	1	1	2
8	2	2	4
9	3	2	5
10	2	2	4
11	1	1	2
12	1	1	2
13	1	1	2
14	1	1	2
15	1	1	2
16	3	2	5
17	3	2	5
18	1	1	2
19	2	2	4
20	3	2	5
21	3	2	5
22	3	2	5
23	3	2	5
24	3	2	5
25	1	1	2
26	2	2	4
27	1	1	2
28	2	1	3
29	2	2	4
30	2	2	4
31	3	2	5
32	2	1	3
33	3	2	5
34	2	2	4
35	1	2	3
36	2	2	4
37	3	2	5
38	1	2	3
39	2	2	4
40	1	1	2
41	2	2	4
42	2	2	4

43	3	2	5
44	3	2	5
45	3	2	5
46	3	2	5
47	1	2	3
48	1	1	2
49	3	2	5

Table S5: Found hemolysins homologues from three different groups in *A. melanogenum* genome.

Present study number	First group	Second group	Third group
1	1	1	2
2	0	1	2
3	1	1	2
4	1	1	2
5	1	1	2
6	2	2	6
7	1	1	2
8	2	2	3
9	1	2	4
10	1	2	4
11	1	1	2
12	1	1	2
13	1	1	2
14	1	1	2
15	1	1	2
16	0	2	4
17	1	1	4
18	1	1	2
19	1	2	4
20	2	1	4
21	2	2	4
22	2	2	4
23	2	2	4
24	1	1	4
25	1	1	2
26	1	3	4
27	1	1	2
28	1	1	4
29	2	1	4
30	2	1	4
31	2	2	4
32	2	1	4
33	2	2	4

34	1	2	4
35	0	1	1
36	2	2	6
37	1	2	4
38	0	1	2
39	1	2	4
40	1	1	2
41	2	2	6
42	2	1	4
43	1	2	4
44	1	3	4
45	1	2	4
46	1	2	4
47	1	1	2
48	1	1	2
49	1	2	4

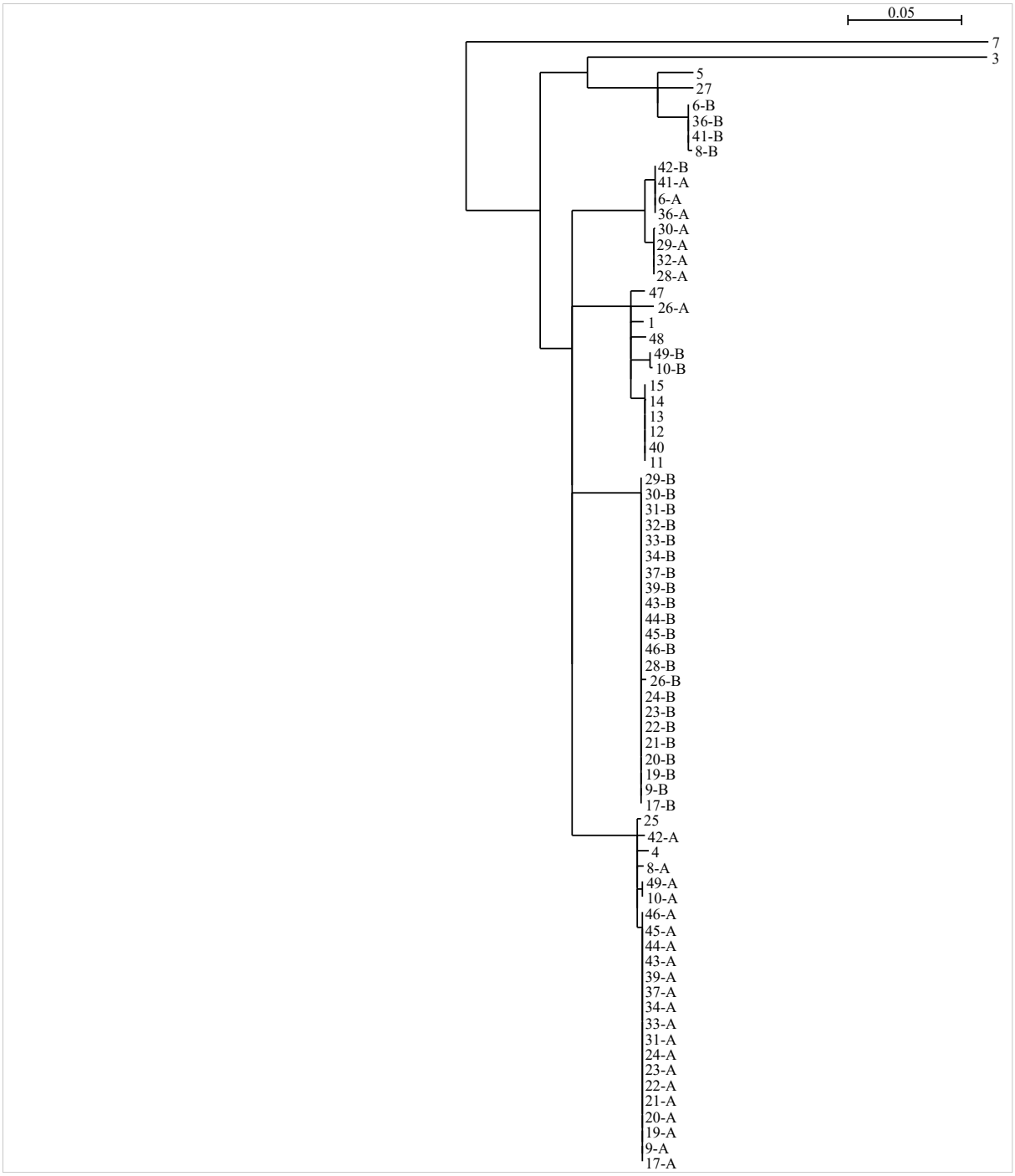

Figure S1: Majority rule consensus tree of *A. melanogenum* Benchmarking Universal Single-Copy Orthologs (BUSCOs). Strains 2, 16, 18, and 38 were excluded from the analysis due to a large share of their BUSCOs predicted as single-copy instead of in the expected two copies and strain 35 was excluded due to its large phylogenetic distance to other strains.

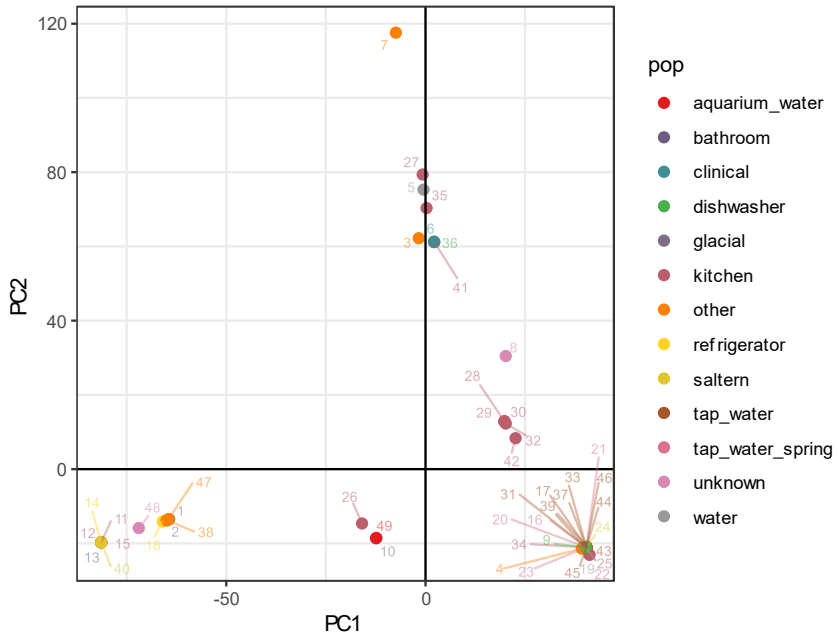

Figure S3: Clustering of *A. melanogenum* genomes. Principal component analysis of SNP data estimated by comparing the genomes to the reference *A. melanogenum* genome (EXF-3378). The genomes are represented by circles, the colour corresponds to the habitat. The axes explain 33,11% (horizontal) and 19,85% (vertical) of variation.

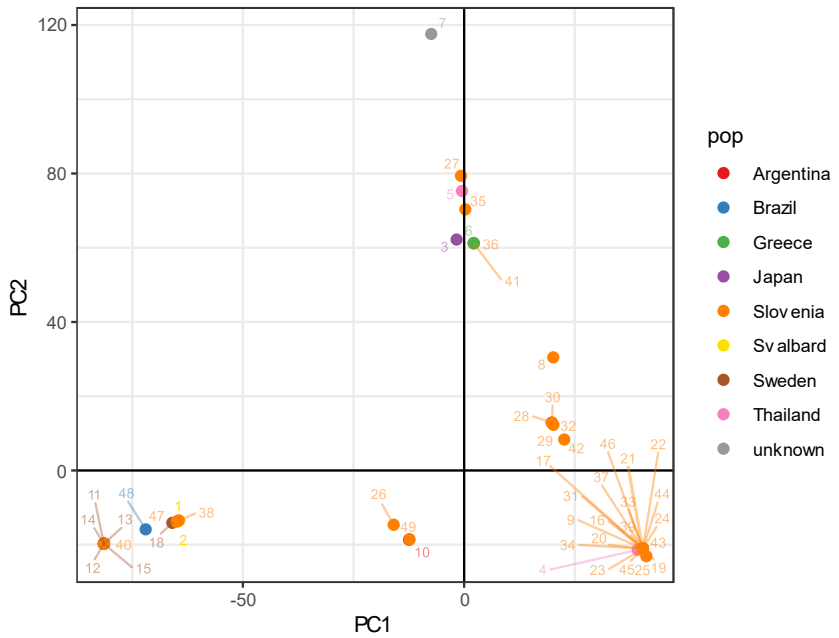

Figure S4: Clustering of *A. melanogenum* genomes. Principal component analysis of SNP data estimated by comparing the genomes to the reference *A. melanogenum* genome (EXF-3378). The genomes are represented by circles, the colour corresponds to the sampling location. The axes explain 33,11% (horizontal) and 19,85% (vertical) of variation.

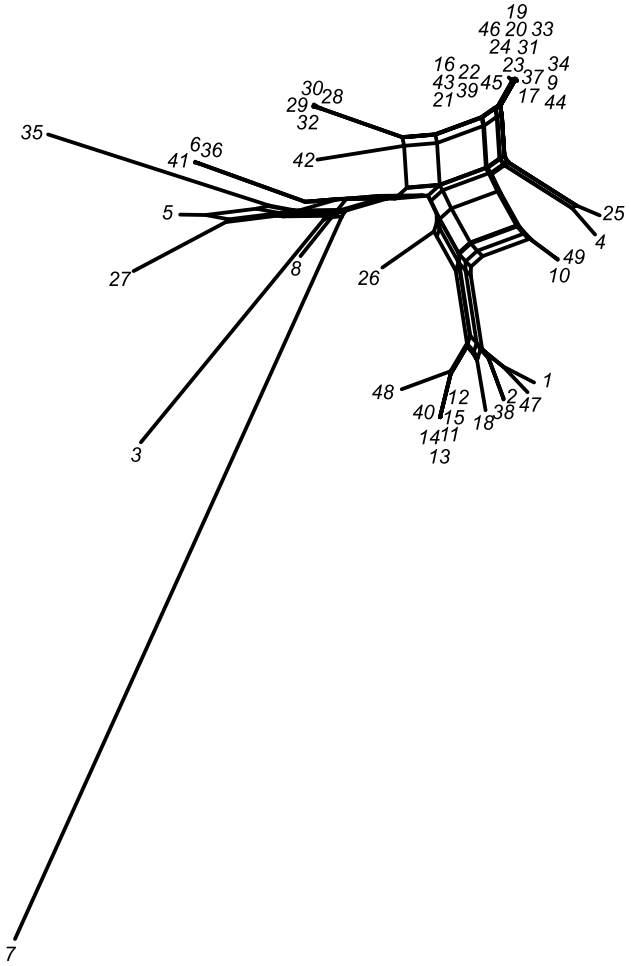

Figure S2: Phylogenetic network of sequenced *A. melanogenum* strains, reconstructed with the Neighbor-Net algorithm based on the dissimilarity distance matrix calculated from the SNP data.