**Supplemental Information**

**Table S1.** Museum specimens used in this study. All are from the University of Alaska Museum (UAM). Sequences are deposited in NCBI SRA accession SRP151072.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **UAM #** | **Taxon** | **Age** | **Sex** | **Date** | **Locality** | **Field #** | **SRA #** |
| 7066 | *Plectrophenax hyperboreus* | AD | M | 25-Jul-97 | USA: Alaska: Bering Sea, St. Matthew Island | KSW1610 | SAMN09469434 |
| 7407 | *Plectrophenax hyperboreus* | AHY | F | 24-Jul-97 | USA: Alaska: Bering Sea, St. Matthew Island | KSW1588 | SAMN09469433 |
| 7524 | *Plectrophenax hyperboreus* | AD | F | 25-Jul-97 | USA: Alaska: Bering Sea, St. Matthew Island | KSW1611 | SAMN09469435 |
| 8200 | *Plectrophenax hyperboreus* | AD | F | 25-Jul-97 | USA: Alaska: Bering Sea, St. Matthew Island | KSW1617 | SAMN09469436 |
| 8474 | *Plectrophenax nivalis* | U | M | 22-Sep-98 | USA: Alaska: Alaska Peninsula, Cold Bay, Frosty Peak | KSW2691 | SAMN09469440 |
| 8476 | *Plectrophenax nivalis* | IM | F | 22-Sep-98 | USA: Alaska: Alaska Peninsula, Cold Bay, Frosty Peak | KSW2690 | SAMN09469439 |
| 11856 | *Plectrophenax nivalis* | AHY | F | 29-Jun-99 | USA: Alaska: Alaska Peninsula, Cold Bay, Frosty Peak | CLP163 | SAMN09469437 |
| 27725 | *Plectrophenax nivalis* | AD | M | 5-Jun-09 | USA: Alaska, Aleutian Islands, Kiska Island | JJW292 | SAMN09469438 |

**Supplemental Information, cont.**

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**Figure S1**. A 2D FS plot of the folded spectrum analyzed using δaδi, in which the color scale represents the logarithm of the number of variants (Gutenkunst et al. 2009).

**Figure S2**. Frequency distribution of locus lengths.

**Figure S3a**. Distribution of *FST* values among SNP sites between *Plectrophenax* *hyperboreus* and *P. nivalis* (excludes 7,662 sites with *FST* = 0).

**Figure S3b**. Distribution of *FST* values among 521 loci between *Plectrophenax* *hyperboreus* and *P.* *nivalis* (excludes 2,113 loci with *FST* = 0).

K

K

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K

**Figure S4**. Group assignments using Discriminant Analysis of Principal Components (DAPC) in adegenet (Jombart & Ahmed 2011). Cluster 1 is *P. nivalis*; cluster 2 is *P. hyperboreus*.

**Supplemental Information, cont.**

The five bunting loci with the highest *FST* values and the best BLAST match with the zebra finch genome:

**Query= uce-5659\_ALL\_buntings\_assembled\_contigs |uce-5659**

Length=1087

 Score E

Sequences producing significant alignments: (Bits) Value

ref|NC\_011475.1| Taeniopygia guttata isolate Black17 chromoso... 1869 0.0

ALIGNMENTS

>ref|NC\_011475.1| Taeniopygia guttata isolate Black17 chromosome 11, Taeniopygia\_guttata-3.2.4

Length=21403021

 Features flanking this part of subject sequence:

 292623 bp at 5' side: LOW QUALITY PROTEIN: iroquois-class homeodomain protein I...

 223208 bp at 3' side: alpha-ketoglutarate-dependent dioxygenase FTO

 Score = 1869 bits (1012), Expect = 0.0

 Identities = 1063/1088 (98%), Gaps = 1/1088 (0%)

**Query= uce-2530\_ALL\_buntings\_assembled\_contigs |uce-2530**

Length=1104

 Score E

Sequences producing significant alignments: (Bits) Value

ref|NC\_011468.1| Taeniopygia guttata isolate Black17 chromoso... 1709 0.0

ALIGNMENTS

>ref|NC\_011468.1| Taeniopygia guttata isolate Black17 chromosome 4A, Taeniopygia\_guttata-3.2.4

Length=20704505

 Features in this part of subject sequence:

 dachshund homolog 2 isoform X3

 dachshund homolog 2 isoform X1

 Score = 1709 bits (925), Expect = 0.0

 Identities = 1053/1112 (95%), Gaps = 20/1112 (2%)

**Query= uce-3157\_ALL\_buntings\_assembled\_contigs |uce-3157**

Length=1058

 Score E

Sequences producing significant alignments: (Bits) Value

ref|NC\_011466.1| Taeniopygia guttata isolate Black17 chromoso... 1491 0.0

ALIGNMENTS

>ref|NC\_011466.1| Taeniopygia guttata isolate Black17 chromosome 3, Taeniopygia\_guttata-3.2.4

Length=112617285

 Features flanking this part of subject sequence:

 25635 bp at 5' side: parkin coregulated gene protein

 23761 bp at 3' side: protein quaking

 Score = 1491 bits (807), Expect = 0.0

 Identities = 1000/1087 (92%), Gaps = 37/1087 (3%)

**Query= uce-1915\_ALL\_buntings\_assembled\_contigs |uce-1915**

Length=1038

 Score E

Sequences producing significant alignments: (Bits) Value

ref|NC\_011493.1| Taeniopygia guttata isolate Black17 chromoso... 1541 0.0

ALIGNMENTS

>ref|NC\_011493.1| Taeniopygia guttata isolate Black17 chromosome Z, Taeniopygia\_guttata-3.2.4

Length=72861351

 Features in this part of subject sequence:

 LOW QUALITY PROTEIN: doublesex- and mab-3-related transcr...

 Score = 1541 bits (834), Expect = 0.0

 Identities = 984/1051 (94%), Gaps = 32/1051 (3%)

**Query= uce-451\_ALL\_buntings\_assembled\_contigs |uce-451**

Length=1206

 Score E

Sequences producing significant alignments: (Bits) Value

ref|NC\_011465.1| Taeniopygia guttata isolate Black17 chromoso... 1971 0.0

ALIGNMENTS

>ref|NC\_011465.1| Taeniopygia guttata isolate Black17 chromosome 2, Taeniopygia\_guttata-3.2.4

Length=156412533

 Features flanking this part of subject sequence:

 419746 bp at 5' side: hepatocyte nuclear factor 4-gamma

 138007 bp at 3' side: zinc finger homeobox protein 4

 Score = 1971 bits (1067), Expect = 0.0

 Identities = 1164/1208 (96%), Gaps = 18/1208 (1%)