**Supplemental Table 1 | Sample information.** Samples from 13 black bears were used in this study. A sample from a single male bear (JAX001) was used to sequence and assemble the initial draft genome.

|  |  |  |
| --- | --- | --- |
| Sample | Sex | Origin |
| JAX001 | male | Maine (Patten) |
| JAX101 | male | Maine (T2R8) |
| JAX103 | male | Maine (Grindstone) |
| JAX106 | female | Maine |
| JAX113 | female | Maine (Mattamiscontis) |
| JAX118 | female | Maine (Patten) |
| JAX134 | female | Maine |
| JAX136 | female | Maine |
| JAX140 | male | Maine |
| JAX141 | male | Maine |
| JAX146 | male | Maine |
| JAX160 | female | Maine (Orono) |
| JAX165 | male | Maine |

**Supplemental Table 2 | Raw read filtering statistics Illumina for JAX001**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sequencing** | **Total reads** | **HQ Filtered reads** | **Percentage HQ Filtered Reads** | **After SOAP Correction** | **Coverage for Analysis (X)** |
| PE Lane3 | 670,082,334 | 481,339,036 | 71.83 | 481,290,964 |  |
| PE Lane4 | 671,035,938 | 484,058,076 | 72.14 | 484,008,138 | 47.47 |
|  |  |  |  |  |  |
| MP Lane1 | 411,843,244 | 307,749,866 | 74.73 | 216,745,240 |  |
| MP Lane2 | 412,026,660 | 311,016,074 | 75.48 | 218,066,406 | 15.78 |

**Supplemental Table 3 | Raw read filtering statistics PacBio for JAX001**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Number of SMRT Cells** | **Number of Bases** | **Number of Sub-Reads** | **N50 Read Length** | **Mean Read Length** | **Coverage for Analysis (X)** |
| 23 | 12,175,034,146 | 1,922,053 | 8,108 | 6,334 | ~4.81 |

**Supplemental Table 4 | Details of the assembled sequence length for JAX001.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Assembly type** | **Total scaffolds** | **Min length** | **Max length** | **N50** | **N90** | **N95** | **N99** | **Total BP** |
| Original Scaffold Assembly with 1KBP contigs | 105,002 | 297 | 1,787,317 | 198,844 | 17,829 | 7,871 | 1,189 | 2,572,828,434 |
| Broken Scaffold Assembly (reapr) | 142,288 | 100 | 1,238,834 | 123,915 | 10,550 | 3,687 | 1,095 | 2,548,747,558 |
| Merging with Pacbio (Final Assembly) | 113,759 | 100 | 2,352,914 | 189,858 | 18,798 | 7,125 | 1,132 | 2,588,744,122 |

**Supplemental Table 5 | Summary of RNA-Seq Sequencing and quality control**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sample** | **Collection date** | **Sequenced Reads** | **Percentage Uniquely mapping reads to Genome (Star mapping Stats)** | **Percentage Multi-mapping reads to Genome (Star Mapping Stats)** |
| JAX118 | 9/14/15 | 61,004,520 | 74.30 | 6.49 |
| JAX134 | 9/10/15 | 58,776,952 | 75.32 | 6.52 |
| JAX141 | 9/07/15 | 57,689,672 | 76.92 | 6.24 |
| JAX146 | 9/04/15 | 63,803,702 | 77.89 | 5.45 |
| JAX160 | 9/05/15 | 51,170,413 | 74.81 | 6.13 |
| JAX165 | 9/05/15 | 47,090,896 | 80.14 | 5.09 |
| JAX101 | 5/19/15 | 63,466,747 | 77.89 | 5.66 |
| JAX103 | 5/18/15 | 62,141,996 | 75.07 | 6.05 |
| JAX106 | 5/18/15 | 58,707,521 | 78.18 | 5.85 |
| JAX113 | 6/03/15 | 56,682,528 | 72.00 | 6.66 |
| JAX136 | 6/04/15 | 65,514,196 | 69.30 | 7.07 |
| JAX140 | 5/28/15 | 65,002,266 | 69.86 | 6.26 |

**Supplemental Table 6 | Summary of differentially expressed genes**

Excel file

**Supplemental Table 7 | Summary of genome sequencing and quality control**

|  |  |  |  |
| --- | --- | --- | --- |
| Sample | Sequenced Reads | Quality trimmed/Adaptor Removed Reads | % High Quality Reads |
| Bear101 | 80,042,724 | 47,594,138 | 59.46 |
| Bear103 | 82,046,702 | 38,560,514 | 46.99 |
| Bear113 | 98,393,474 | 57,456,262 | 58.39 |
| Bear118 | 87,022,484 | 51,120,894 | 58.74 |
| Bear134 | 75,863,344 | 45,992,142 | 60.62 |
| Bear160 | 79,015,868 | 46,268,154 | 58.56 |

**Supplemental Table 8 | Summary of coding transcripts with RNA-editing.** Editing was observed in all 12 samples except for *ZNF688* in which we only observed editing in the spring samples. Sites indicated in bold were confirmed with Sanger sequencing of the RNA transcript.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Contig** | **Position** | **Ref base** | **Alt base** | **Feature** | **AA change** | **Remark\*** |
| *PTCD1* | 3060 | 216894 | A | I | 5’UTR |  |  |
| ***SYNE2*** | **11596** | **1608** | **A** | **I** | **CDS** | L-to-L |  |
| ***IDH1*** | **660** | **132419** | **C** | **U** | **3’UTR** |  |  |
| *NMNAT1* | 7555 | 90746 | A | I | 3’UTR |  |  |
| *SLC25A51* | 408 | 343378 | A | I | 5’UTR |  |  |
| *KCNIP2* | 283 | 43560 | A | I | 3’UTR |  |  |
| *PAICS* | 3388 | 17253 | A | I | 3’UTR |  | Human |
| *TOR1AIP2* | 8765 | 12215 | A | I | 3’UTR |  |  |
| *TRPM3* | 3807 | 132928 | C | U | 3’UTR |  |  |
| *ENSCAFG00000040594* | 20747 | 50545 | A | I | exon |  |  |
| ***FLNB*** | **1255** | **165746** | **C** | **U** | **CDS** | M-to-V | Human, Mouse |
| ***ALDH1A1*** | **26346** | **24965** | **A** | **I** | **CDS** | G-to-G |  |
| *HMGA1* | 10323 | 68028 | A | I | 3’UTR |  |  |
| *ENSCAFG00000013809* | 267 | 1095 | A | I | CDS |  |  |
| ***IST1*** | **818** | **78551** | **A** | **I** | **3’UTR** |  |  |
| *ZHX2* | 4067 | 112564 | A | I | CDS | K-to-R |  |
| ***GPRC5B*** | **4938** | **128686** | **A** | **I** | **CDS** | T-to-T | Human |
| *MICAL3* | 8064 | 249651 | A | I | 3’UTR |  |  |
| *ENSCAFG00000022297* | 1496 | 321379 | A | I | exon |  |  |
| *CPN2* | 20 | 146998 | A | I | CDS | Q-to-R |  |
| *NBEAL2* | 179 | 269038 | A | I | CDS | A-to-A |  |
| *HOMER2* | 432 | 515746 | C | U | 3’UTR |  |  |
| ***ENSCAFG00000014154*** | **440** | **66585** | **A** | **I** | **exon** |  |  |
| *PLEKHM3* | 660 | 328758 | C | U | CDS | D-to-D |  |
| *USP39* | 875 | 493475 | C | U | CDS | Y-to-Y |  |
| *NFKB1* | 1339 | 289908 | A | I | CDS | A-to-A |  |
| *USP46* | 1582 | 132480 | A | I | 3’UTR |  |  |
| ***TMED3*** | **2155** | **45921** | **A** | **I** | **3’UTR** |  |  |
| *FEM1B* | 3491 | 152656 | A | I | 5’UTR |  |  |
| *ENSCAFG00000030572* | 4212 | 309670 | A | I | exon |  |  |
| *WWTR1* | 5646 | 16741 | A | I | 3’UTR |  | Human |
| *ZNF217* | 5967 | 51298 | A | I | CDS | K-to-R |  |
| *CEP95* | 7197 | 19854 | A | I | 3’UTR |  |  |
| *CTSO* | 7856 | 89886 | A | I | CDS | T-to-A |  |
| *MPP7* | 9440 | 111224 | C | U | 3’UTR |  |  |
| *GTPBP1* | 10248 | 93709 | A | I | CDS | T-to-T | Human |
| ***ZNF688*** | **76864** | **76864** | **A** | **I** | **3’UTR** |  |  |

\*RNA-editing is observed in the human or mouse orthologs gene, but not at the same position