Supplementary document: A whole mitochondria analysis of the Tyrolean Iceman's leather provides insights into the animal sources of copper age clothing

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| Species Phylogeny (reference accession code) | Accession codes of Mitogenomes and associated haplogroup | Outgroups (accession codes) and species |
|---|---|---|
| **Sheep** (*Ovis aries*) **(AF010406)** | KF302447_B, KF302448_B1, AF010406_B1a1b_reference, EF490451_B1a_ 7G65F4, EF490454_B1a2_Oe173, EF490455_B1a_1LL2, EF490456_B1a_OLL15, HM236174_A1b_kk1, HM236175_A1b, HM236176_B1a4, HM236178_C_kk2, HM236179_C_mk4, HM236181_D, HM236182_E, HM236183_E, HM236185_B1a3_mouflon, KF302440_A1, KF302445_A1, KF302449_B1a1a, KF302450_B1a1a, KF302452_B1a2a, KF302453_B1a2a, KF302455_B1a2a, KF302457_B1a2a1a, KF302458_B1a2a1a, KF302459_B1a2a1a, KF302460_B1a2b, KF302461_B1a2b, KF302462_B1a2b, KF977845_B1a2_ Djallonke, KF977846_B1a1b_ Sahelian | HM236187_Ovis_vignei, HM236188_Ovis_ammon ,HM236189_Ovis_vignei |
| **Goat** (*Capra aegagrus hircus*) **(NC_005044.2)** | GU068049_A3, GU295658_B_isolate V07-146, KF952601_B, KJ192209_A2a, KJ192210_A2a1, KJ192211_A2a1, KJ192212_A2b2a, KJ192213_A2b2a, KJ192214_A2c1b, KJ192215_A2c1b, KJ192216_A1, KJ192217_A1b1a, KJ192218_A1a1a, KJ192219_A1a1a, KJ192220_A2b1a, KJ192221_A2b1a, KJ192222_A2b2b, KJ192223_A2b2b, KJ192224_A2c1a, KJ192225_A2c1a, KJ192226_A1a1, KJ192227_A1a, KJ192228_A2c, KJ192229_A2c, KJ192230_A1b2, KJ192231_A1b2, KJ192232_A2b1, KJ192234_A1b1a, | FJ207525_*Capra falconeri*, FJ207526_*Capra ibex* |

| | KJ192235_A1b1, KJ192236_C | |
|---|---|---|
| **Cattle** (***Bos taurus***) **(V00654)** | AY126697_I1, AY676861_T3d1, AY676862_T3r, AY676864_T3g, AY676873_T3o, DQ124375_T4a, DQ124376_T3k1, DQ124377_T4, DQ124391_T3n1, DQ124409_T3c, DQ124416_T3b, DQ124418_T3a1a, EU177824_T3p, EU177826_T3q1, EU177829_T3j, EU177852_T2d, EU177853_T2, EU177857_T2b, EU177860_T2c, EU177865_T5b, EU177868_I1, FJ971084_R1a, FJ971085_R1a, GU947012_T3f1, HQ184030_Q2, HQ184036_Q1, JN817304_T1d1, JN817309_T1c1a1, JN817313_T1a, JN817330_T1d1, JN817335_T1a1, JN817343_T1f, JN817348_T1b, JN817351_T1b1a, JQ437479_primigenius, GU985279_CPC98, JQ967333_T3s, KC153973_T1e, KF163072_T1c, KF163081_T1d, KF525852_C(Ancient Chinese Cattle) | EF494178.1_*Bos grunniens*, GU947006.1_*Bison bison*, JN632602.1_*Bison bonasus* |
| **Brown Bear** (***Ursus arctos***) **(HQ685964)** | AF303110_Eastern, AF303111_Ursus_maritimus, AJ428577.1_Greenland, EU497665.1_Western, GU573486_isolate_12WH,GU573487_isolate _A91-05,GU573488_Ursus_maritimus_,GU573489_ isolate_14KB_,GU573490_Ursus_maritimus_i solate_495, GU573491_isolate_76824,HQ685901_isolate _1,HQ685903.1_isolate_3, HQ685929_isolate_29,HQ685942_isolate_42, HQ685957_isolate_57,HQ685960_isolate_60, JX196367_isolate_KEN10-UAR100,JX196369_isolate_ABC1-051711,AP012559_isolate_834 | *Ursus spelaeus* (EU327344), *Ursus americanus* (NC_003426) and *Ursus thibetanus* (NC_011118) |
| **Roe Deer** (***Capreolus capreolus***) | KJ681480-KJ681491 | *Capreolus pygargus* (KJ681491- KJ681495), *Alces alces* (NC_020677) |

| (NC_020684) | | and *Hydropotes inermis* (NC_011821) |
| --- | --- | --- |

**Supplementary Table 1 | Accession codes for mitochondrial genomes downloaded from NCBI for phylogenetic tree construction.**

| SAMPLE | TOTAL SHOTGUN READS | SHOTGUN READS AFTER CLIPPING | SHOTGUN TOTAL MAPPED READS | FILTERED UNIQUE MAPPED READS | SHOTGUN MT COVERAGE (X) | TOTAL CAPTURED READS | CAPTURE READS AFTER CLIPPING | CAPTURE TOTAL MAPPED READS | FILTERED UNIQUE MAPPED READS | CAPTURE MT COVERAGE (X) | CAPTURE AVERAGE READ LENGTH |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 10304 | 824279 | 790340 | 15 | 14 | 0.04 | 1739134 | 1588194 | 38293 | 7028 | 20.6 | 55.7 |
| O314 | 870940 | 832339 | 3042 | 2763 | 7.99 | 1993094 | 1891808 | 1404087 | 29801 | 104.6 | 63 |
| OCA | 4947201 | 4734128 | 213 | 194 | 0.41 | 364953 | 313309 | 1512 | 822 | 2.0 | 53 |
| OCD | 723348 | 691219 | 6 | 6 | 0.02 | 2422032 | 2295615 | 23580 | 5141 | 15.5 | 65 |
| OCL2 | 533933 | 508963 | 5 | 5 | 0.01 | 594102 | 562100 | 6420 | 1,197 | 3.6 | 65 |
| OLC | 587776 | 561880 | 32 | 32 | 0.08 | 1287892 | 1225548 | 134420 | 14879 | 48.3 | 59 |
| OL | 962864 | 913673 | 103 | 102 | 0.34 | 4900933 | 4635327 | 847450 | 30782 | 110 | 64 |
| OSA | 13234516 | 12664087 | 2333 | 2169 | 5.92 | 72794 | 66300 | 16072 | 7398 | 22.4 | 54 |
| OH | NA | NA | NA | NA | NA | 21672 | 6960 | 1627 | 151 | 0.4 | 57 |

**Supplementary table 2 | Sequencing output for shotgun and capture libraries.**

| Sample | Species | Haplogroups | Polymorphisms |
|---|---|---|---|
| **OSA** | Cattle | T3 | **169G,215+T,587+C,2536A,9682C,13310C,** 1599deletion |
| **O314** | Goat | A | **203C,1849T,2207C,2849C,3194G, 3468C,4032C,5601T,6096C, 7052A,7342A, 7660C,7839C,7885T,8055G, 8078T,8480C,8635C,8703T,8730C,8818C,8959T,9010T, 9826T,10479G,10638T,10686C,10813C, 11364C,11691G,11702A,11872G, 12383T,13100T,13178C,13280G,13286C,13681A, 13741C,13756T,13964A,14461T,14746C,14795A, 15004C,15220T,** 1119deletion, 7027T,15543C,15631A,15637T,15728G,15747A,15807T, 15811C,15843G,15893C,15913G,16045C,16083T,16232 C,16435A,16440C |
| **OL** | Goat | A | **203C,1849T,2207C,2849C,3194G, 3468C,4032C,5601T,6096C,7052A,7342A,7660C,7839C, 7885T, 8055G,8078T,8480C, 8635C,8703T,8730C,8818C,8959T, 9010T, 9826T,10479G,10638T,10686C,10813C, 11364C, 11691G,11702A,11872G,12383T, 13100T,13178C,13280G, 13286C,13681A,13741C,13756T, 13964A,14461T,14746C,14795A,15004C,15220T,** 1119deletion, 3222A,11558T, 12140A, 15462T,15543C,15631A,15637T,15728G,15747A,15807 T,15811C,15843G,15893C,15913G,16045C,16083T,162 32C,16458T,16485C,16504deletion,16515G |
| **10304** | Sheep | B1 | **281C,566+G,1729+C,3543A,6615A,7500A,8264C,8651T ,9375G,11668A,11710deletion,12539C,12571C,13199G, 13813C,14055C,15783T,15820T,16128T,16342+C,1634 3C,16472deletion,** 3092T,3230C,7983C,12494T,13375G,15579A,15923G,1 6147C,16440C,16466C |
| **OCD** | Sheep | B1 | **281C,566+G,1729+C,3543A,6615A,7500A,8264C,8651T ,9375G,11710deletion,11273T,11473G,11668A,12539C, 12571C,13199G,13813C,14055C,14653A,15721C,15783 T,15800T,15820T,16128T,16342+C,16343C,163472dele tion,** 6965T,6975T,14871C,15923G,16036A,16392C |
| **OCL2*** | Sheep | B1 | **281C,566+G,3543A,6615A,7500A,8264C, 8651T, 9375G,11668A,11710deletion,12539C,12571C,13199G, 14055C,15783T,16128T,16342+C,16343C,163472deleti on,** 1849A,2141A,2144G,2148T,2443T,2666T,5350C,7983C, 8927G,10615T,13549T,14530G,16392C |
| **OLC** | Sheep | B1 | **281C,566+G,1729+C,3543A,6615A,7500A,8264C,8651T ,9375G,11668A,11710deletion,12539C,12571C,13199G, 13813C,14055C,15800T,15820T,16128T,16342+C,1634 3C, 16472deletion,** 2801C,11273T,11473G,14653A,14871C,15923G,16036A ,16392C |

**Supplementary table 3 | Identified haplogroups for captured libraries made from consensus mapped reads.** Polymorphisms listed in bold are expected haplotypes for each haplogroup, polymorphisms in regular font are mutations not yet associated with identified haplogroups. All polymorphisms are relative to the mapped reference mitogenome, NCBI accession codes are in Supplementary table 4. *OCL2 is a partial reconstruction with low average coverage, missing sites include: 1-8np, 405-418np, 1678-1800np, 2216-2316np, 2855-

2930np, 3471-3514np, 5527-5556np, 5604-5639np, 6393-6415np, 6760-6784np, 7515-7541np, 7611-7644np, 8735-8794np, 9029-9067np, 11604-11634np, 12420-12466np, 12723-12767np, 13288-13362np, 16247-16289np.

| Species | Accession code |
|---|---|
| Brown bear (*Ursus arctos*) | HQ685964 |
| Chamois (*Rupicapra rupicapra*) | NC_020633 |
| Cattle (*Bos taurus*) | V00654 |
| Roe deer (*Capreolus capreolus*) | NC_020684 |
| Goat (*Capra aegagrus hircus*) | NC_005044.2 |
| Human (*Homo sapien*) | NC_012920 |
| Ibex (*Capra ibex*) | NC_020623 |
| Pig (*Sus scrofa*) | NC_012095 |
| Sheep (*Ovis aries*) | AF010406 |

**Supplementary table 4 | Reference mitogenomes used for species assignment**. Used default parameters of Fastq_screen (http://www.bioinformatics.babraham.ac.uk/projects/fastq_screen/) to find which references raw sequenced reads preferentially align.
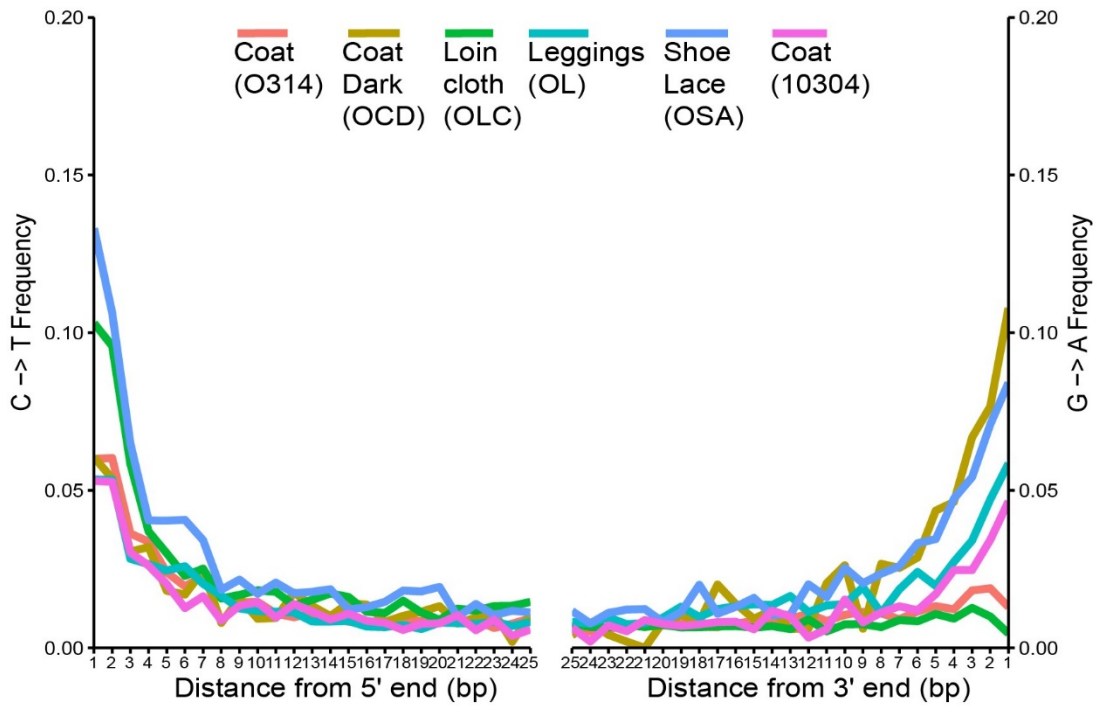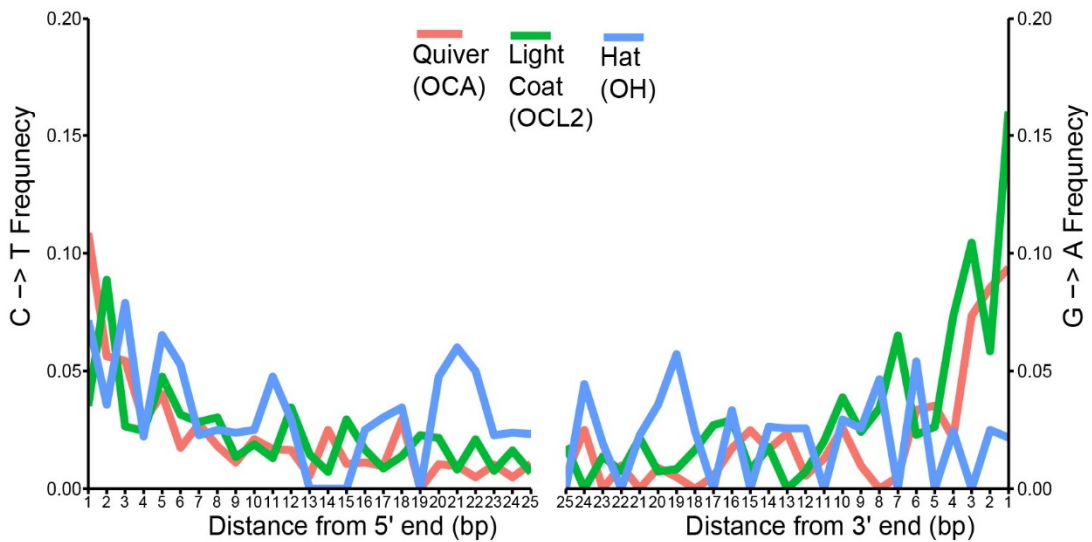
**Supplementary Figure 1 | mapDamage deamination plot.** (**a**) Six high coverage enriched mitogenome libraries. (**b**) Three low coverage enriched mitogenome libraries.
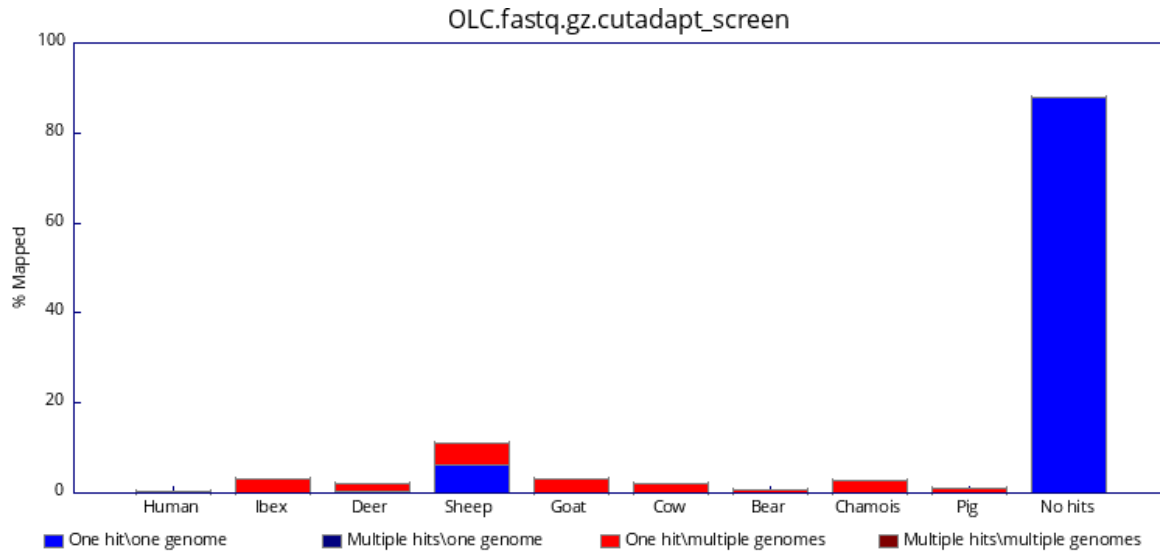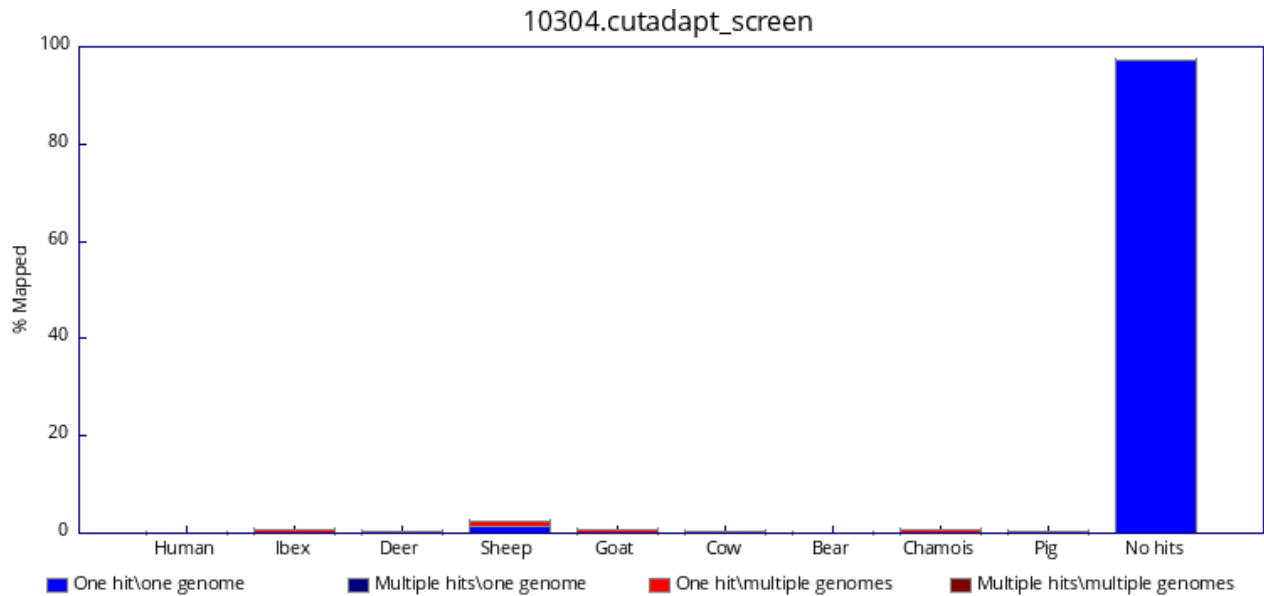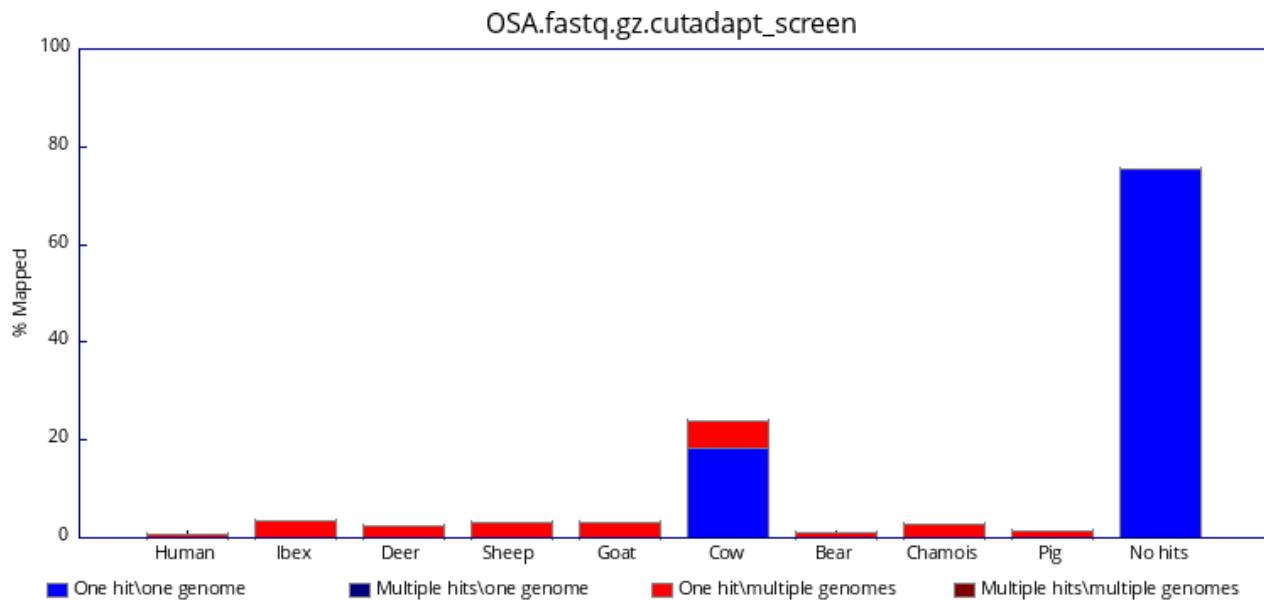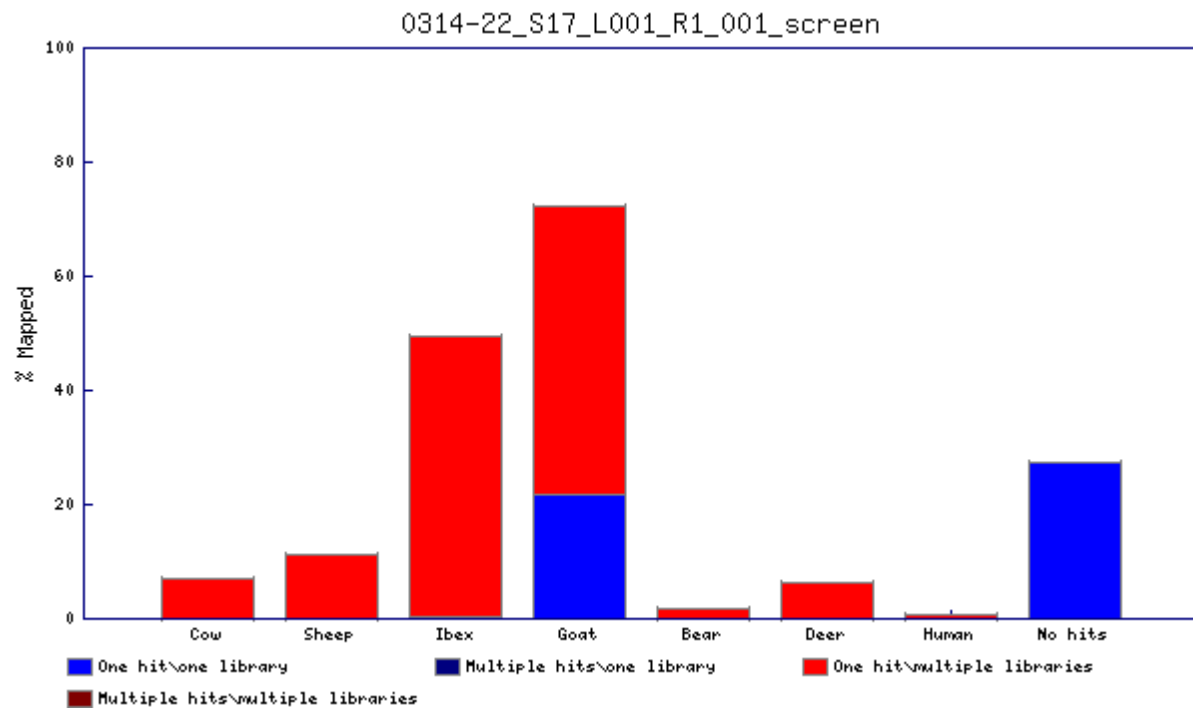
**Supplementary Figure 2 | Fastq_screen.** Initial species assignment for Loincloth from enriched library.
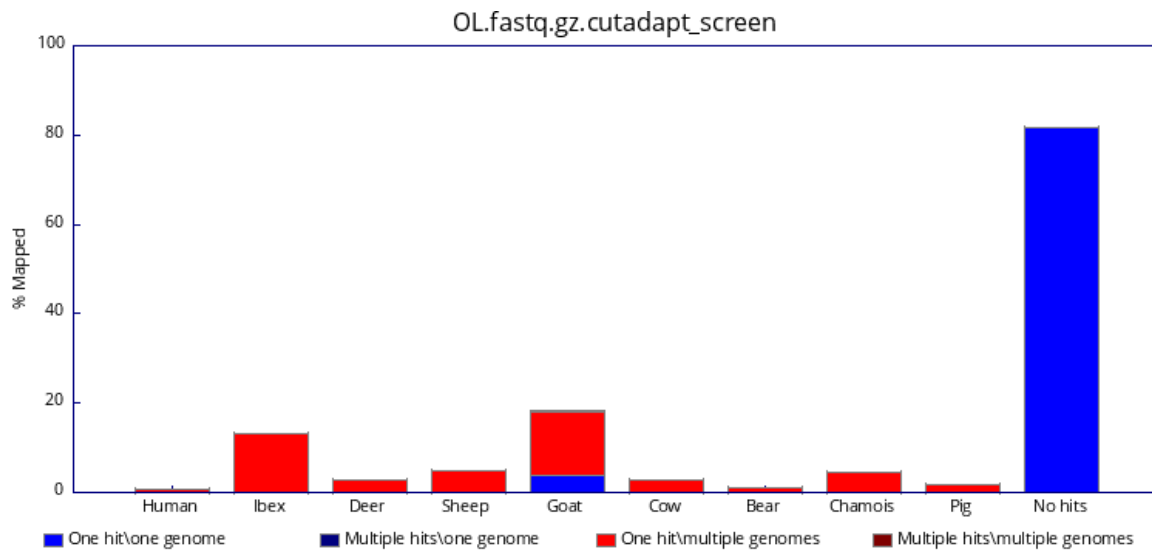


**Supplementary Figure 3 | Fastq_screen.** Initial species assignment for leggings from the enriched library.

OH2.fastq.gz.cutadapt_screen
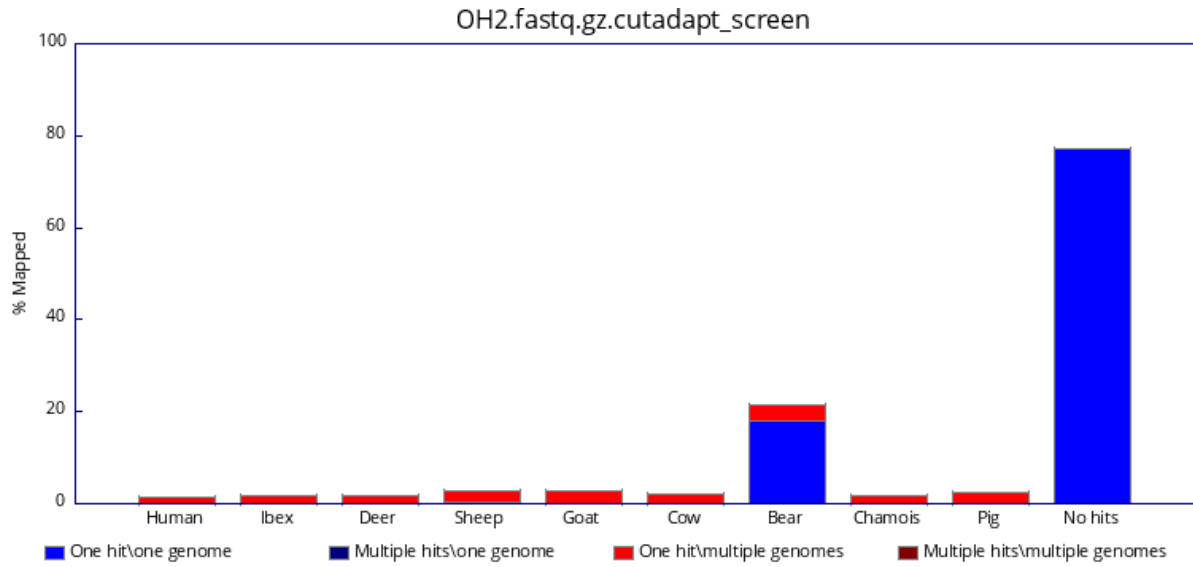
**Supplementary Figure 4 | Fastq_screen.** Initial species assignment for the hat from enriched library.



OCL2.fastq.gz.cutadapt_screen

Fuu
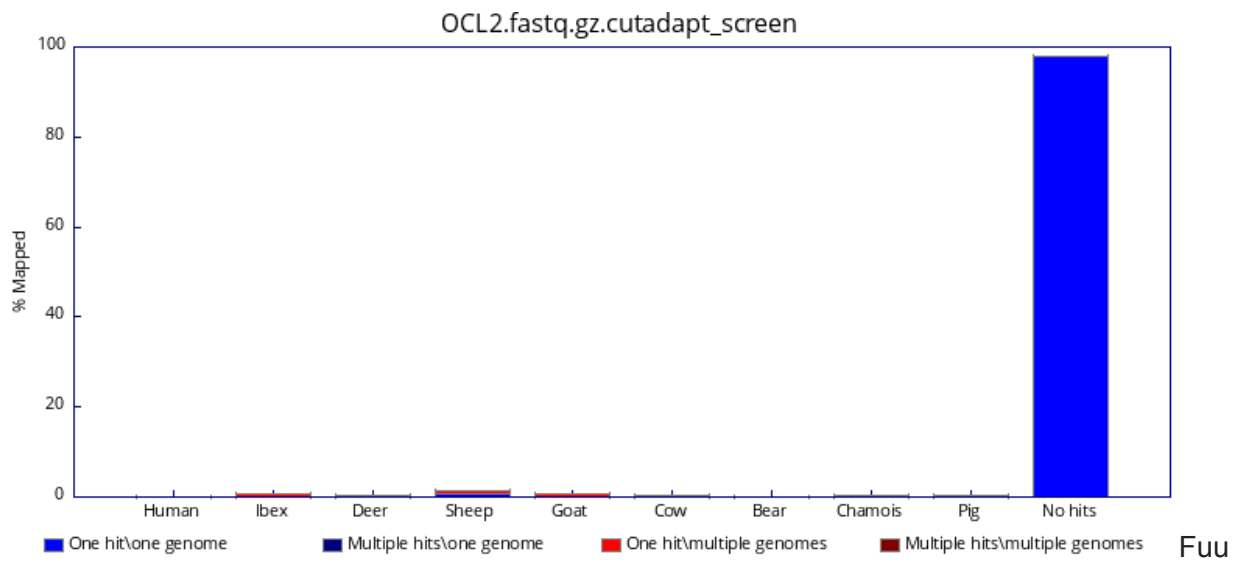
**Supplementary Figure 5 | Fastq_screen.** Initial species assignment for the light coat from enriched library.

**OCD.fastq.gz.cutadapt_screen**
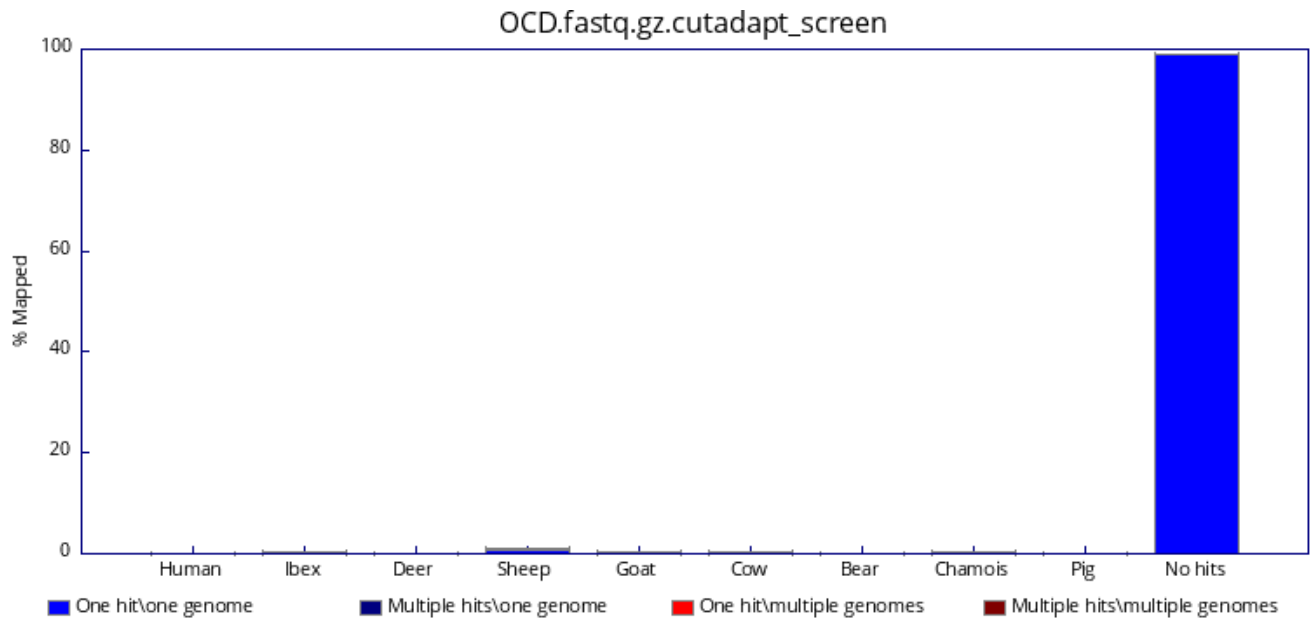
**Supplementary Figure 6 | Fastq_screen.** Initial species assignemnt for the dark coat from the enriched library.



**OCA.fastq.cutadapt_screen**
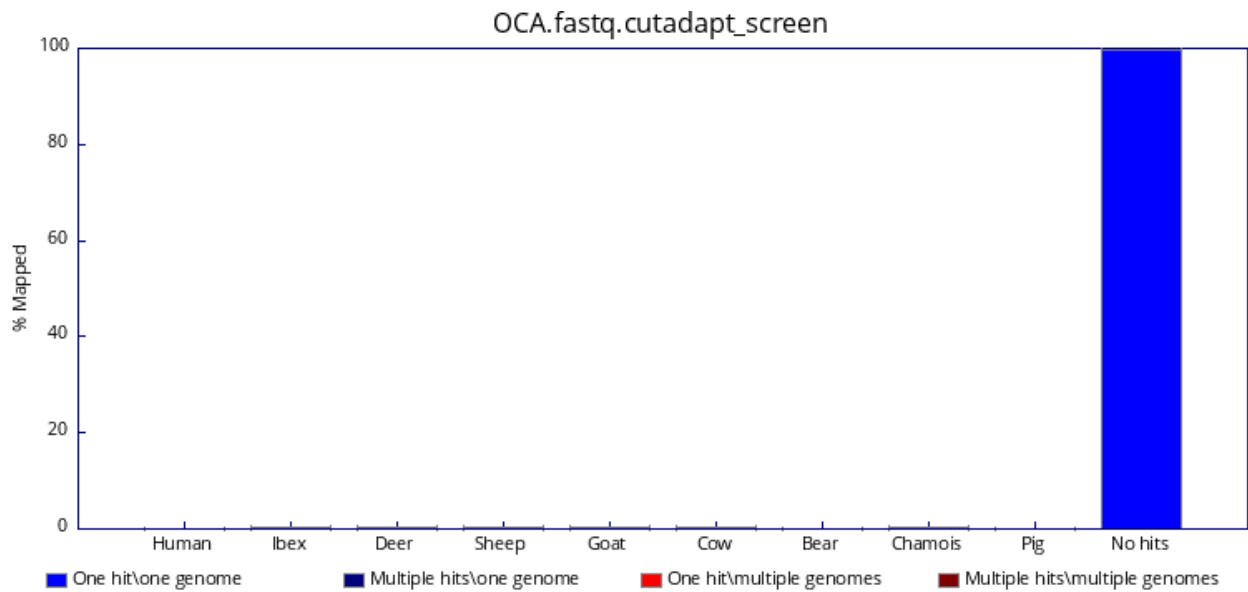
**Supplementary Figure 7 | Fastq_screen.** Initial species assignment for the quiver from enriched library.

**Supplementary Figure 8 | Fastq_screen.** Initial species assignment for coat sample 10304 from the enriched library.



**Supplementary Figure 9 | Fastq_screen.** Initial species assignment for the shoelace sample from the enriched library.

**Supplementary Figure 10 | Fastq_screen.** Initial species assignment for the coat sample 0314 from the enriched library.
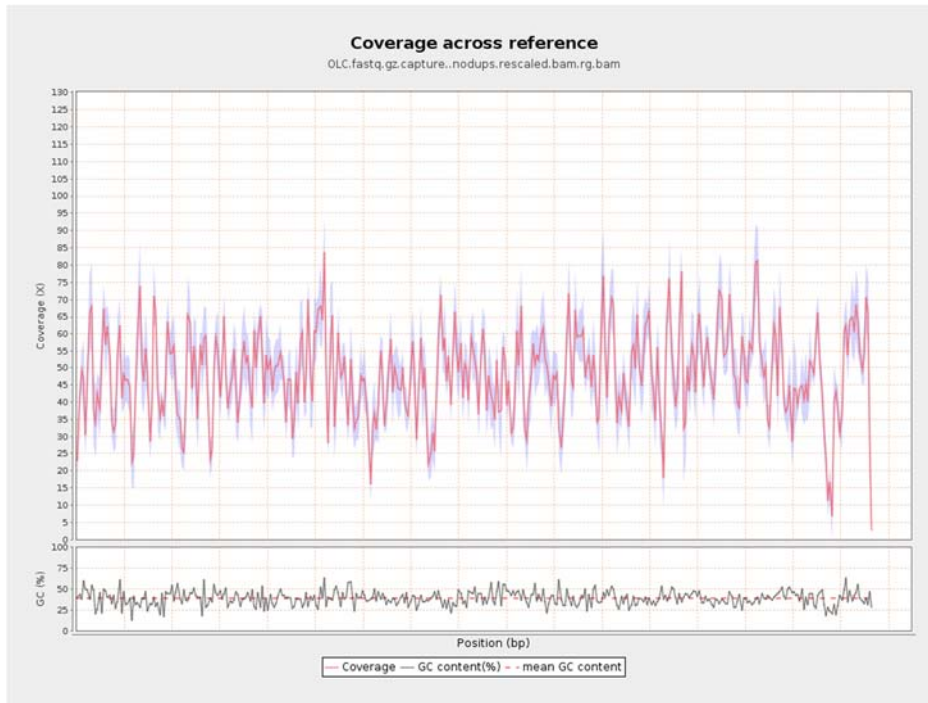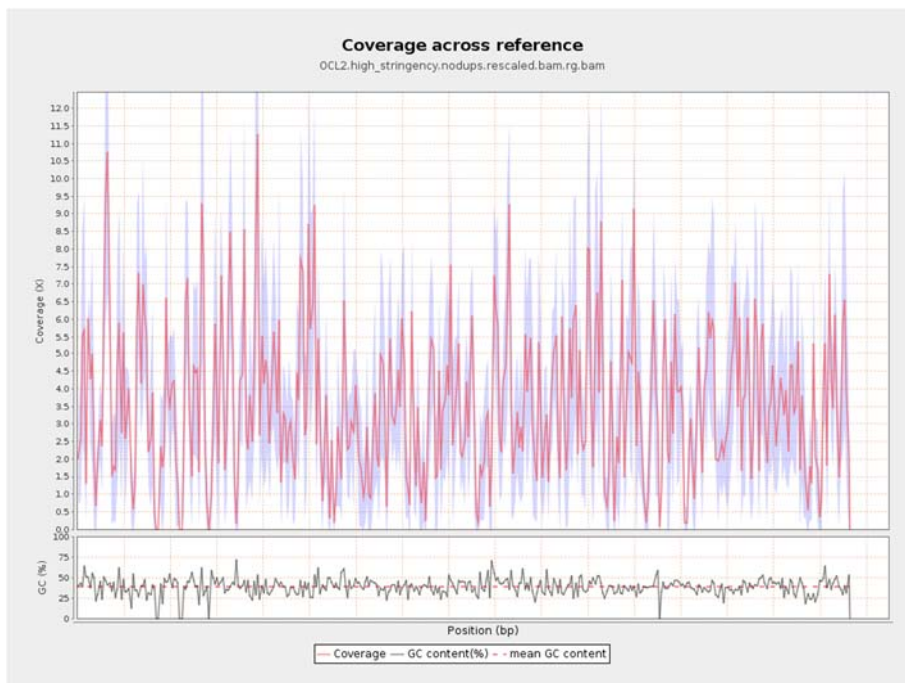
**Supplementary Figure 11 | Coverage across the reference**. Captured loincloth library (OLC).
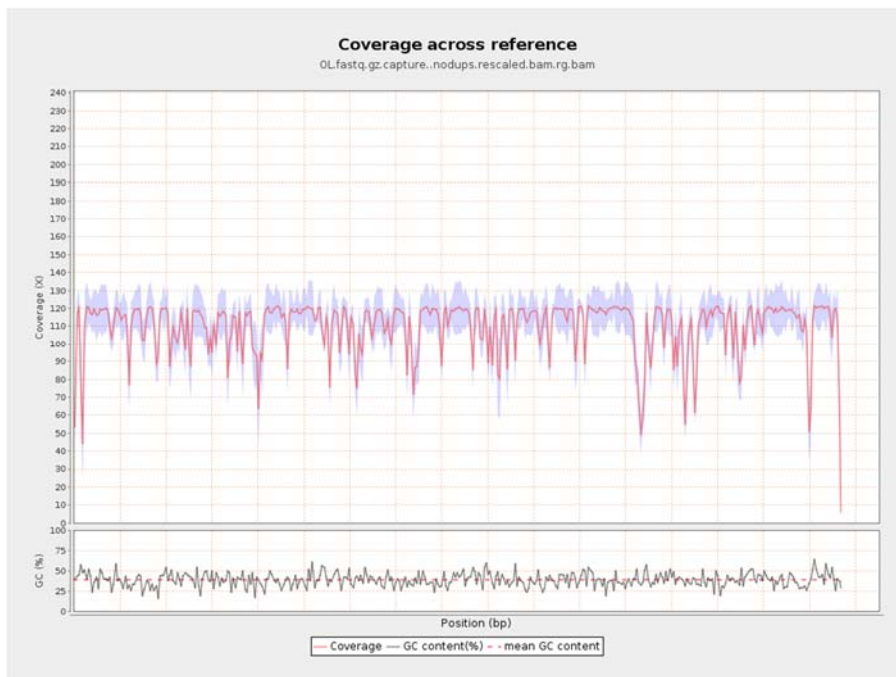


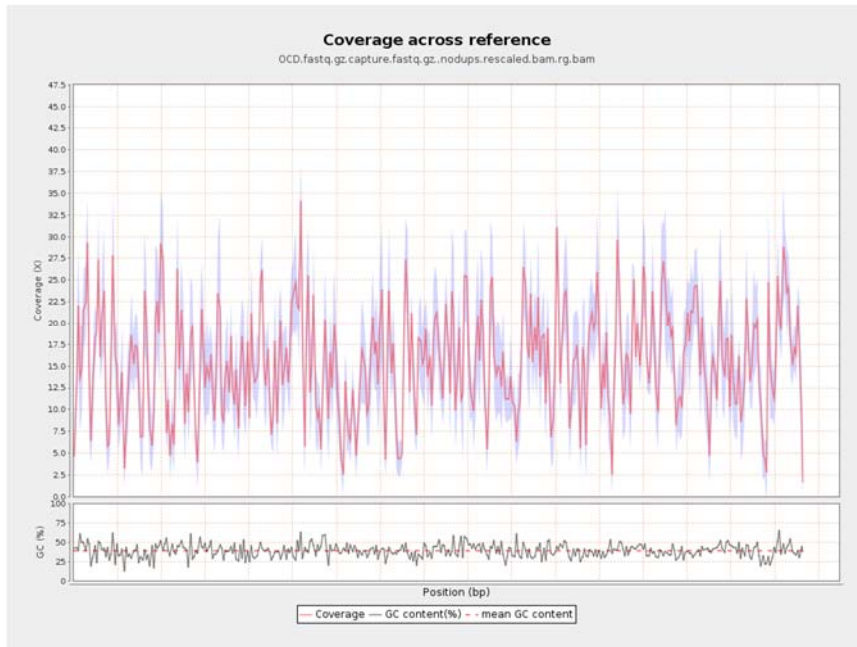**Supplementary Figure 12 | Coverage across the reference.** Captured leggings library (OL).
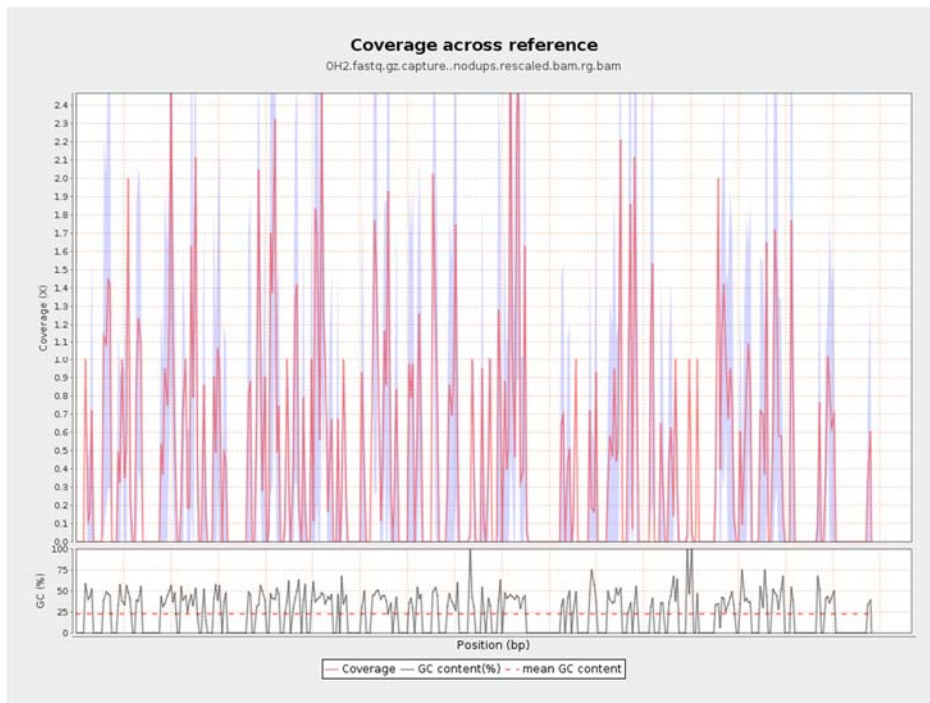
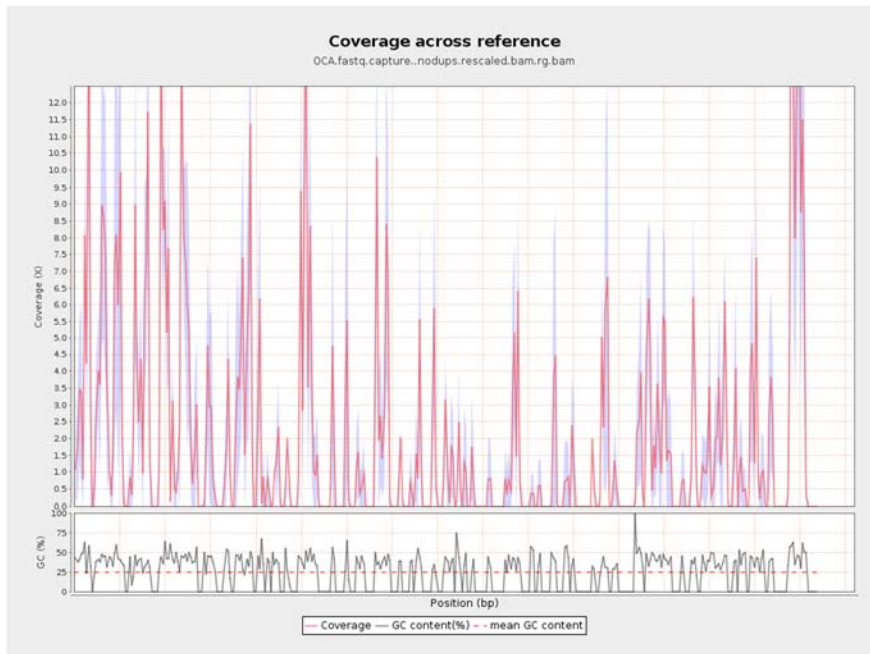**Supplementary Figure 13 | Coverage across the reference.** Captured hat library (OH).



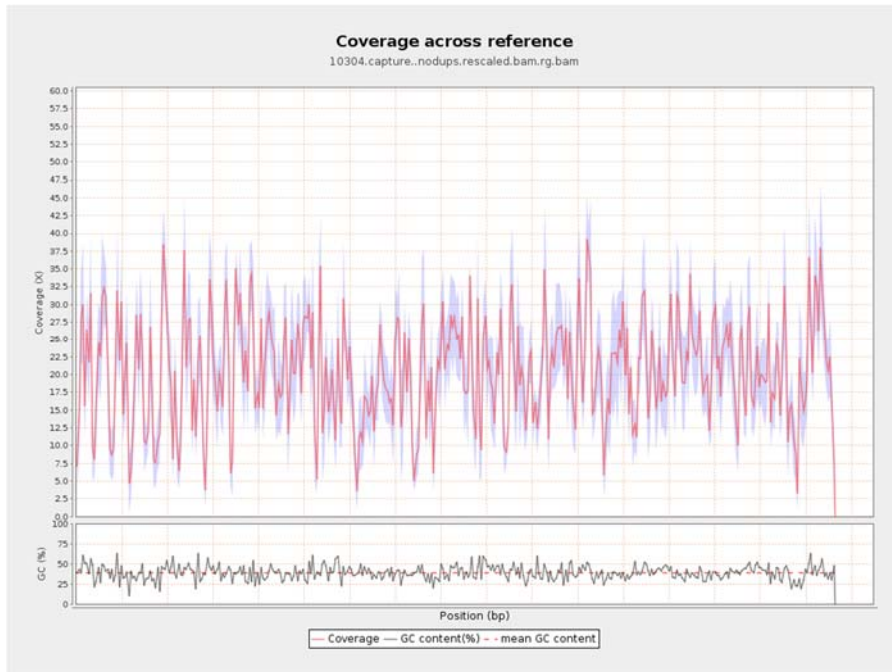**Supplementary Figure 14 | Coverage across the reference.** Captured light coat library (OCL2).
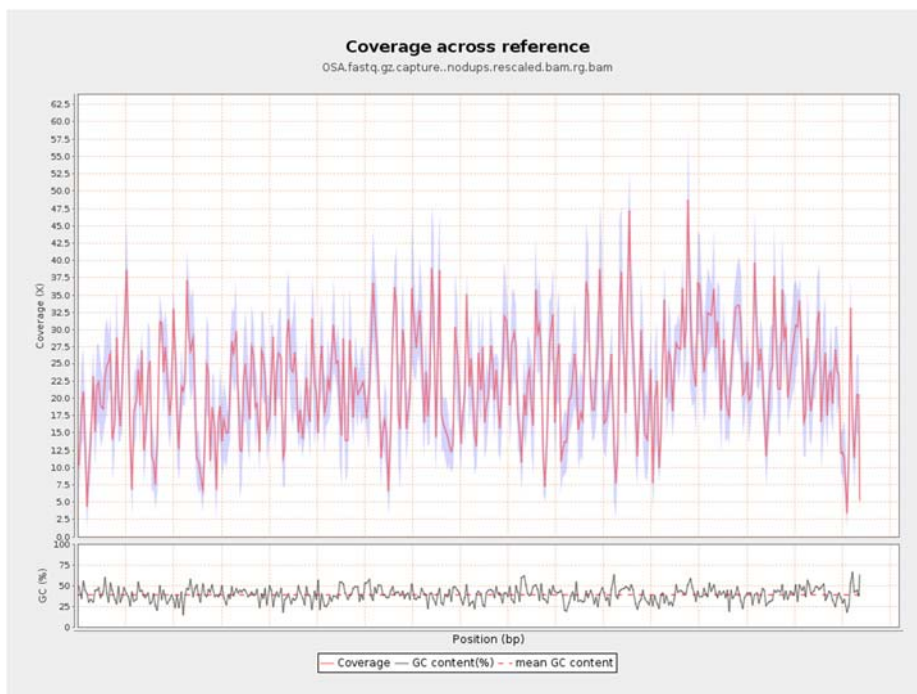
**Supplementary Figure 15 | Coverage across the reference**. Captured dark coat library (OCD).
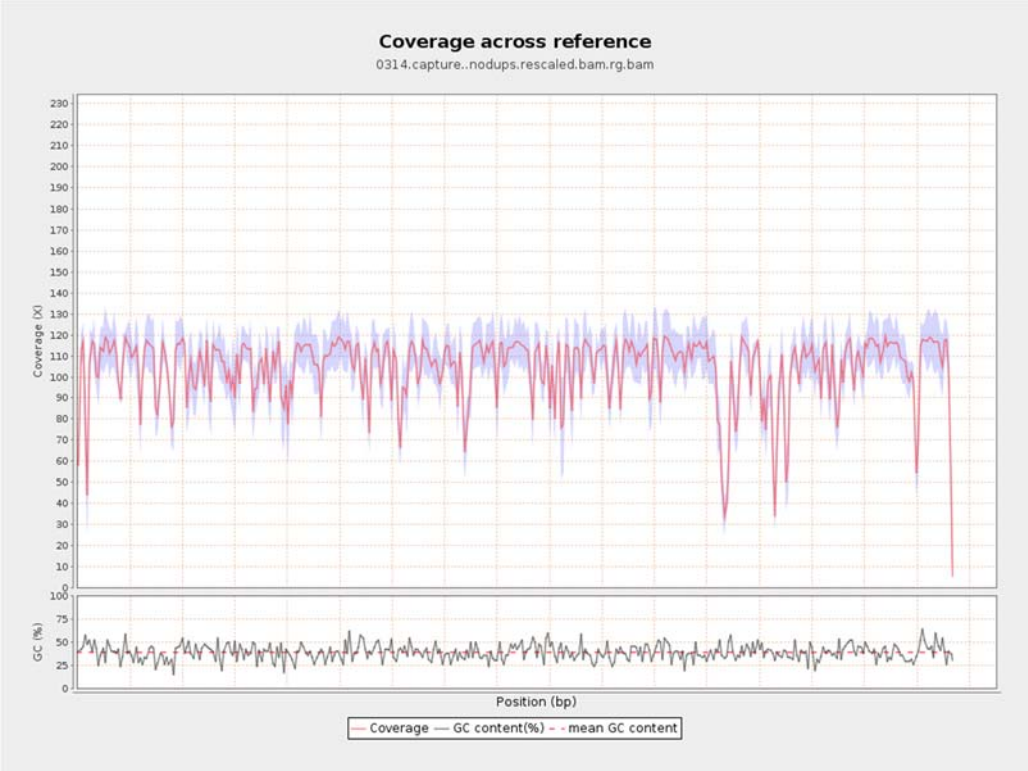


**Supplementary Figure 16 | Coverage across the reference**. Captured quiver library (OCA).

**Supplementary Figure 17 | Coverage across the reference.** Captured coat library (10304).



**Supplementary Figure 18 | Coverage across the reference**. Captured shoe library (OSA).

**Supplementary Figure 19 | Coverage across the reference**. Captured coat library (O314).