 genomic scans for adaptive introgression S4 Power Analysis - 10 Mb Chromosome Derek Setter^{123°C}, Sylvain Mousset^{1°}, Xiaoheng Cheng⁴, Rasmus Nielsen⁵, Michael DeGiorgio^{6†}, Joachim Hermisson^{127†}, 1 Department of Mathematics, University of Vienna, Vienna, Austria 2 Vienna Graduate School of Population Genetics, Vienna, Austria 3 School of Biological Sciences, University of Edinburgh, Edinburgh, United Kingdom 4 Huck Institutes of the Life Sciences, Pennsylvania State University, University Park, PA, USA 5 Departments of Integrative Biology and Statistics, University of California, Berkeley, CA, USA 6 Department of Computer and Electrical Engineering and Computer Science, Florida Atlantic University, Boca Raton, FL, USA 7 Max F. Perutz Laboratories, University of Vienna, Vienna, Austria These authors contributed equally to this work. These authors also contributed equally to this work. These authors also contributed equally to this work. Current Address: School of Biological Sciences, University of Edinburgh, Edinburgh, United Kingdom *Correspondence: inachim hermisson@univie ac at (JH) mdegiorg@fau edu (MD) 	VolcanoFinder	
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	*Correspondence: joachim hermisson@univie ac at (JH) mdegiorg@fau edu (MD)	

S4 Human Data

Table D1

Candidate peaks ranked by the maximum log likelihood ratios in the VolcanoFinder scan of the European (CEU) sample.

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| AS1, SNORA7B, EF-
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- | RPL32P3, H1FX, H1FX- AS1, SNORA7B, EF- CAB12 CAB12 | 5 -
6 -
7 AS1, SNORA7B, EF-
CAB12
- | 3 -
3 RPL32P3, H1FX, H1FX-
4S1, SNORA7B, EF-
CAB12
- | 3 MYO9B, USE1, OCEL1
3 -
3 -
5 -
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6 -
7 -
8 RPL32P3, H1FX, H1FX-
AS1, SNORA7B, EF-
CAB12
- | S LGR5, ZFC3H1
MYO9B, USE1, OCEL1
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8 RPL32P3, H1FX, H1FX-
AS1, SNORA7B, EF-
CAB12
- | LGR5, ZFC3H1 LGR5, ZFC3H1 MYO9B, USE1, OCEL1 - - RPL32P3, H1FX, H1FX-
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CAB12 - | 3 KBTBD12 - - 5 - 3 MY09B, USE1, OCEL1 3 - 3 - 4 - 5 - 5 - 6 - 7 - 8 RPL32P3, H1FX, H1FX- AS1, SNORA7B, EF- CAB12 - - - | CDH13 KBTBD12 K
 | GCDH13 KBTBD12 KBTBD12 LGR5, ZFC3H1 MY09B, USE1, OCEL1 MY09B, H1FX, H1FX- RPL32P3, H1FX, H1FX- AS1, SNORA7B, EF- CAB12 | GTF2IRD1 GTF2IRD1 GDH13 KBTBD12 LGR5, ZFC3H1 LGR5, ZFC3H1 MY09B, USE1, OCEL1 MY09B, H1FX, H1FX, H1FX- AS1, SNORA7B, EF- CAB12 | 3 TLK1 3
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 | MCF2L2, B3GNT5 TFCP2L1 TLK1 GTF2IRD1 GTF2IRD1 KBTBD12 LGR5, ZFC3H1 KBTBD12 RPL32P3, H1FX, H1FX- AS1, SNORA7B, EF- CAB12 | <i>KCNE4</i>
<i>MCF2L2, B3GNT5</i>
<i>TFCP2L1</i>
<i>TLK1</i>
<i>GTF2IRD1</i>
<i>GTF2IRD1</i>
<i>CDH13</i>
<i>KBTBD12</i>
<i>CDH13</i>
<i>KBTBD12</i>
<i>LGR5, ZFC3H1</i>
<i>MYO9B, USE1, OCEL1</i>
<i>MYO9B, USE1, OCEL1</i>
<i>AS1, SNORA7B, EF-CAB12</i>
<i>CAB12</i> | ITSN2 KCNE4 MCF2L2, B3GNT5 TFCP2L1 TLK1 GTF2IRD1 GTF2IRD12 KBTBD12 LGR5,
ZFC3H1 MY09B, USE1, OCEL1 MY09B, H1FX, H1FX-
AS1, SNORA7B, EF-
CAB12 | CHODL, CHODL-AS1
ITSN2 KCNE4
MCF2L2, B3GNT5
TFCP2L1 TLK1
GTF2IRD1 GTF2IRD1 CDH13
KBTBD12 LGR5, ZFC3H1 MYO9B, USE1, OCEL1 MYO9B, H1FX, H1FX-
AS1, SNORA7B, EF-
CAB12 | TSHR CHODL, CHODL-AS1 ITSN2 KCNE4 MCF2L2, B3GNT5 TFCP2L1 TLK1 GTF2IRD1 GTF2IRD1 LGR5, ZFC3H1 MY09B, USE1, OCEL1 MY09B, H1FX, H1FX-
AS1, SNORA7B, EF-
CAB12 | KCNE4 TSHR CHODL, CHODL-AS1 ITSN2 KCNE4 MCF2L2, B3GNT5 TFCP2L1 TLK1 GTF2IRD1 GTF2IRD12 LGR5, ZFC3H1 MY09B, USE1, OCEL1 MY09B, H1FX, H1FX-
AS1, SNORA7B, EF-
CAB12
 | CHRNB3, CHRNA6 KCNE4 TSHR CHODL, CHODL-AS1 ITSN2 KCNE4 MCF2L2, B3GNT5 TFCP2L1 TLK1 GTF2IRD1 GTF2IRD1 GTF2IRD12 CDH13 KBTBD12 LGR5, ZFC3H1 MYO9B, USE1, OCEL1 RPL32P3, H1FX, H1FX-
AS1, SNORA7B, EF-
CAB12 CAB12 |
| <i>NORA7B, EF</i> - NR_020
NORA7B, EF- NR_020
 | , H1FX, H1FX- NR_00;
NORA7B, EF- NR_020
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<i>USE1, OCEL1</i> NM_00
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, <i>H1FX, H1FX</i> - NM_02
<i>NORA7B, EF</i> - NR_02
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<i>rC3H1</i> NM_00
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<i>USE1, OCEL1</i> NM_02
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<i>NORA7B, EF-</i> NR_02
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<i>VSE1, OCEL1</i> NM_00
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NORA7B, EF- NR_02
NM_02 | 1. NM_01
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<i>FC3H1</i> NM_02
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| I LOZI S, HIFA, HIFA- INCOM
SI, SNORA7B, EF- NR_020
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 | CDH13 NM_00 CBTBD12 NM_20 CGR5, ZFC3H1 NM_00 AYO9B, USE1, OCEL1 NM_00 AYO9B, USE1, OCEL1 NM_02 LSL32P3, H1FX, H1FX- - LS1, SNORA7B, EF- NR_02 AB12 - | TTF2IRD1 NM_00 CDH13 NM_00 CBTBD12 NM_00 GR5, ZFC3H1 NM_00 AYO9B, USE1, OCEL1 NM_02 ISL, SNORA7B, EF- - NR_02 - AB12 - - - </td <td>TF2IRD1 NM_01 TF2IRD1 NM_00 CDH13 NM_00 CBTBD12 NM_02 CGR5, ZFC3H1 NM_02 AYO9B, USE1, OCEL1 NM_02 SPL32P3, H1FX, H1FX- NM_02 IS1, SNORA7B, EF- NR_02 AB12 -</td> <td><i>IFCP2L1</i> NM_01 <i>ILK1</i> NM_01 <i>JTF2IRD1</i> NM_02 <i>GR5, ZFC3H1</i> NM_02 <i>AY09B, USE1, OCEL1</i> NM_02 <i>RPL32P3, H1FX, H1FX, H1FX-</i> NM_02 <i>RPL32P3, H1FX, H1FX, H1FX-</i> NR_02 <i>AB12</i> - - -<!--</td--><td>ACF2L2, B3GNT5 NM.01 IFCP2L1 NM.01 TLK1 NM.01 TF2IRD1 NM.01 TF2IRD1 NM.00 CBTBD12 NM.00 GR5, ZFC3H1 NM.00 AYO9B, USE1, OCEL1 NM.00 IS1, SNORA7B, EF- - NR.02 - AB12 - - -</td><td>CCNE4 NM.08 ACF2L2, B3GNT5 NM.01 IFCP2L1 NM.00 IFF2IRD12 NM.00 CBTBD12 NM.00 CBF5, ZFC3H1 NM.00</td><td>TSN2 NML00 CCNE4 NML01 ACF2L2, B3GNT5 NML01 PFCP2L1 NML01 PFCP2L1 NML01 PTF2IRD1 NML00 CBTBD12 NML00 CBFBD12 NML00 CBF5, ZFC3H1 NML00 AYO9B, USE1, OCEL1 NML00 SPL32P3, H1FX, H1FX- NML00 IS1, SNORA7B, EF- NRL00 AB12 -</td><td>CHODL, CHODL-AS1 NM.00 TSN2 NM.00 CCNE4 NM.00 ACF2L2, B3GNT5 NM.01 PFCP2L1 NM.02 CDH13 NM.00 CBTBD12 NM.00 CBT5, ZFC3H1 NM.00 AYO9B, USE1, OCEL1 NM.02 AYO9B, USE1, OCEL1 NM.02 SI, SNORA7B, EF- - PL32P3, H1FX, H1FX- NR.00 AB12 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - <!--</td--><td>ISHR NM.00 CHODL, CHODL-AS1 NM.00 TSN2 NM.00 CCNE4 NM.00 ACF2L2, B3GNT5 NM.01 PFCP2L1 NM.01 PFCP2L1 NM.01 PTF2IRD1 NM.01 CDH13 NM.00 CBTBD12 NM.00 GR5, ZFC3H1 NM.00 AYO9B, USE1, OCEL1 NM.02 IS1, SNORA7B, EF- - AB12 -</td><td>CONE4 NML08 CSHR NML00 TSN2 NML00 CONE4 NML00 ACF2L2, B3GNT5 NML00 CONE4 NML00 ACF2L2, B3GNT5 NML00 PFCP2L1 NML01 PTF2IRD1 NML00 GR5, ZFC3H1 NML00 AYO9B, USE1, OCEL1 NML00 AYO9B, USE1, OCEL1 NML00 SNORA7B, EF- NR_00 AB12 NR_00</td><td>$\begin{array}{llllllllllllllllllllllllllllllllllll$</td></td></td> | TF2IRD1 NM_01 TF2IRD1 NM_00 CDH13 NM_00 CBTBD12 NM_02 CGR5, ZFC3H1 NM_02 AYO9B, USE1, OCEL1 NM_02 SPL32P3, H1FX, H1FX- NM_02 IS1, SNORA7B, EF- NR_02 AB12 -
 | <i>IFCP2L1</i> NM_01 <i>ILK1</i> NM_01 <i>JTF2IRD1</i> NM_02 <i>GR5, ZFC3H1</i> NM_02 <i>AY09B, USE1, OCEL1</i> NM_02 <i>RPL32P3, H1FX, H1FX, H1FX-</i> NM_02 <i>RPL32P3, H1FX, H1FX, H1FX-</i> NR_02 <i>AB12</i> - - - </td <td>ACF2L2, B3GNT5 NM.01 IFCP2L1 NM.01 TLK1 NM.01 TF2IRD1 NM.01 TF2IRD1 NM.00 CBTBD12 NM.00 GR5, ZFC3H1 NM.00 AYO9B, USE1, OCEL1 NM.00 IS1, SNORA7B, EF- - NR.02 - AB12 - - -</td> <td>CCNE4 NM.08 ACF2L2, B3GNT5 NM.01 IFCP2L1 NM.00 IFF2IRD12 NM.00 CBTBD12 NM.00 CBF5, ZFC3H1 NM.00</td> <td>TSN2 NML00 CCNE4 NML01 ACF2L2, B3GNT5 NML01 PFCP2L1 NML01 PFCP2L1 NML01 PTF2IRD1 NML00 CBTBD12 NML00 CBFBD12 NML00 CBF5, ZFC3H1 NML00 AYO9B, USE1, OCEL1 NML00 SPL32P3, H1FX, H1FX- NML00 IS1, SNORA7B, EF- NRL00 AB12 -</td> <td>CHODL, CHODL-AS1 NM.00 TSN2 NM.00 CCNE4 NM.00 ACF2L2, B3GNT5 NM.01 PFCP2L1 NM.02 CDH13 NM.00 CBTBD12 NM.00 CBT5, ZFC3H1 NM.00 AYO9B, USE1, OCEL1 NM.02
AYO9B, USE1, OCEL1 NM.02 SI, SNORA7B, EF- - PL32P3, H1FX, H1FX- NR.00 AB12 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - <!--</td--><td>ISHR NM.00 CHODL, CHODL-AS1 NM.00 TSN2 NM.00 CCNE4 NM.00 ACF2L2, B3GNT5 NM.01 PFCP2L1 NM.01 PFCP2L1 NM.01 PTF2IRD1 NM.01 CDH13 NM.00 CBTBD12 NM.00 GR5, ZFC3H1 NM.00 AYO9B, USE1, OCEL1 NM.02 IS1, SNORA7B, EF- - AB12 -</td><td>CONE4 NML08 CSHR NML00 TSN2 NML00 CONE4 NML00 ACF2L2, B3GNT5 NML00 CONE4 NML00 ACF2L2, B3GNT5 NML00 PFCP2L1 NML01 PTF2IRD1 NML00 GR5, ZFC3H1 NML00 AYO9B, USE1, OCEL1 NML00 AYO9B, USE1, OCEL1 NML00 SNORA7B, EF- NR_00 AB12 NR_00</td><td>$\begin{array}{llllllllllllllllllllllllllllllllllll$</td></td> | ACF2L2, B3GNT5 NM.01 IFCP2L1 NM.01 TLK1 NM.01 TF2IRD1 NM.01 TF2IRD1 NM.00 CBTBD12 NM.00 GR5, ZFC3H1 NM.00 AYO9B, USE1, OCEL1 NM.00 IS1, SNORA7B, EF- - NR.02 - AB12 - - - | CCNE4 NM.08 ACF2L2, B3GNT5 NM.01 IFCP2L1 NM.00 IFF2IRD12 NM.00 CBTBD12 NM.00 CBF5, ZFC3H1 NM.00 | TSN2 NML00 CCNE4 NML01 ACF2L2, B3GNT5 NML01 PFCP2L1 NML01 PFCP2L1 NML01 PTF2IRD1 NML00 CBTBD12 NML00 CBFBD12 NML00 CBF5, ZFC3H1 NML00 AYO9B, USE1, OCEL1 NML00 SPL32P3, H1FX, H1FX- NML00 IS1, SNORA7B, EF- NRL00 AB12 -
 | CHODL, CHODL-AS1 NM.00 TSN2 NM.00 CCNE4 NM.00 ACF2L2, B3GNT5 NM.01 PFCP2L1 NM.02 CDH13 NM.00 CBTBD12 NM.00 CBT5, ZFC3H1 NM.00 AYO9B, USE1, OCEL1 NM.02 AYO9B, USE1, OCEL1 NM.02 SI, SNORA7B, EF- - PL32P3, H1FX, H1FX- NR.00 AB12 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - </td <td>ISHR NM.00 CHODL, CHODL-AS1 NM.00 TSN2 NM.00 CCNE4 NM.00 ACF2L2, B3GNT5 NM.01 PFCP2L1 NM.01 PFCP2L1 NM.01 PTF2IRD1 NM.01 CDH13 NM.00 CBTBD12 NM.00 GR5, ZFC3H1 NM.00 AYO9B, USE1, OCEL1 NM.02 IS1, SNORA7B, EF- - AB12 -</td> <td>CONE4 NML08 CSHR NML00 TSN2 NML00 CONE4 NML00 ACF2L2, B3GNT5 NML00 CONE4 NML00 ACF2L2, B3GNT5 NML00 PFCP2L1 NML01 PTF2IRD1 NML00 GR5, ZFC3H1 NML00 AYO9B, USE1, OCEL1 NML00 AYO9B, USE1, OCEL1 NML00 SNORA7B, EF- NR_00 AB12 NR_00</td> <td>$\begin{array}{llllllllllllllllllllllllllllllllllll$</td> | ISHR NM.00 CHODL, CHODL-AS1 NM.00 TSN2 NM.00 CCNE4 NM.00 ACF2L2, B3GNT5 NM.01 PFCP2L1 NM.01 PFCP2L1 NM.01 PTF2IRD1 NM.01 CDH13 NM.00 CBTBD12 NM.00 GR5, ZFC3H1 NM.00 AYO9B, USE1, OCEL1 NM.02 IS1, SNORA7B, EF- - AB12 - | CONE4 NML08 CSHR NML00 TSN2 NML00 CONE4 NML00 ACF2L2, B3GNT5 NML00 CONE4 NML00 ACF2L2, B3GNT5 NML00 PFCP2L1 NML01 PTF2IRD1 NML00 GR5, ZFC3H1 NML00 AYO9B, USE1, OCEL1 NML00 AYO9B, USE1, OCEL1 NML00 SNORA7B, EF- NR_00 AB12 NR_00 | $\begin{array}{llllllllllllllllllllllllllllllllllll$
 |
| CAB12 CAB12 NORA7B, EF- NR_020 | .0015 – – –
.0023 <i>RPL32P3, H1FX, H1FX-</i> NR_00;
<i>AS1, SNORA7B, EF-</i> NR_020
<i>CAB12</i> NM_20 | .001500150023 <i>RPL32P3, H1FX, H1FX-</i> NR_003 <i>AS1, SNORA7B, EF-</i> NR_026 <i>CAB12</i> NM_20 | .0023 | .0023 MYO9B, USE1, OCEL1 NM_00
.0023
.0015
.0023 RPL32P3, H1FX, H1FX- NR_005
AS1, SNORA7B, EF- NR_026
CAB12 NM_20 | .0038 LGR5, ZFC3H1 NM_00 .0023 MYO9B, USE1, OCEL1 NM_02 .0023 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - NR_002 - .0023 RPL32P3, HIFX, HIFX, HIFX- NR_003 AS1, SNORA7B, EF- NR_026 CAB12 NM_20 - | .0015 | .0023 <i>KBTBD12</i> NM.20
.0015
.0038 <i>LGR5, ZFC3H1</i> NM.00
.0023 <i>MYO9B, USE1, OCEL1</i> NM.00
.0023
.0015
.0015 <i>RPL32P3, H1FX, H1FX-</i> NR_00
<i>AS1, SNORA7B, EF-</i> NR_02
<i>CAB12</i> NM.20 | .0015 CDH13 NM_00 .0023 KBTBD12 NM_20 .0015 - - .0023 LGR5, ZFC3H1 NM_00 .0023 MYO9B, USE1, OCEL1 NM_02 .0023 - - .0015 - - .0023 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0016 - NR_02 </td <td>.00230015 CDH13 NM_00
.0023 KBTBD12 NM_20
.0038 LGR5, ZFC3H1 NM_00
.0023 MYO9B, USE1, OCEL1 NM_00
.0015</td> <td>.0030 GTF2IRD1 NM.00 .0023 - - - .0015 CDH13 NM.00 .0023 KBTBD12 NM.20 .0015 - - .0015 - - .0015 - - .0015 - - .0038 LGR5, ZFC3H1 NM.00 .0023 MYO9B, USE1, OCEL1 NM.02 .0023 - - - .0015 - - - .0023 AS1, SNORATB, EF- NR.02 .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0023 RPL32P3, H1FX, H1FX- NR.00 AS1, SNORATB, EF- NM.20</td> <td>.0023 TLK1 NM_01 .0030 GTF2IRD1 NM_00 .0023 - - .0015 CDH13 NM_00 .0023 KBTBD12 NM_02 .0015 - NM_02 .0023 KBTBD12 NM_02 .0015 - - .0023 MYO9B, USE1, OCEL1 NM_02 .0023 - - .0023 - - .0023 - - .0023 - - .0023 - - .0023 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0016 - - .0017 RPL32P3, H1FX, H1FX- NR_02 .0023<td>.0015 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0015 CDH13 NM.02 .0015 CDH13 NM.02 .0015 CDH13 NM.02 .0015 - - .0015 - NM.20 .0015 - NM.02 .0015 - - .0015 - - .0023 MY09B, USE1, OCEL1 NM.02 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0023 RPL32P3, H1FX, H1FX, H1FX- NR_02 .0024 AS1, SNORA7B, EF- NR_02</td><td>.0023 MCF2L2, B3GNT5 NM.01 .0015 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0015 CDH13 NM.00 .0023 - - .0015 CDH13 NM.00 .0023 KBTBD12 NM.20 .0015 - - .0015 - - .0015 - NM.00 .0015 - - .0023 MY09B, USE1, OCEL1 NM.02 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0023 RPL32P3, H1FX, H1FX, H1FX- NR.00 .0015 - - .0023 RPL32P3, M15X, M16X, M16X, M16X, M1.20</td><td>.0030 KCNE4 NM.08 .0023 MCF2L2, B3GNT5 NM.01 .0015 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0015 CDH13 NM.00 .0023 KBTBD12 NM.00 .0015 CBR5, ZFC3H1 NM.00 .0023 LGR5, ZFC3H1 NM.00 .0015 - - .0015 - - .0023 MYO9B, USE1, OCEL1 NM.02 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0023
 RPL32P3, H1FX, H1FX, H1FX- NR.00 AS1, SNORA7B, EF- <</td><td>.0015 ITSN2 NML0 .0030 KCNE4 NML0 .0023 MCF2L2, B3GNT5 NML01 .0015 TFCP2L1 NML01 .0023 TLK1 NML01 .0023 TLK1 NML01 .0023 TLK1 NML01 .0023 TLK1 NML00 .0023 CDH13 NML00 .0015 CDH13 NML00 .0015 CBTSD12 NML00 .0015 - - .0015 - - .0015 - - .0015 - - .0023 MYO9B, USE1, OCEL1 NML00 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - -</td><td>0015 CHODL, CHODL-AS1 NM.00 0015 ITSN2 NM.00 0023 MCF2L2, B3GNT5 NM.01 0023 MCF2L2, B3GNT5 NM.01 0023 TFCP2L1 NM.01 0023 TFCP2L1 NM.01 0023 TFCP2L1 NM.01 0023 TFCP2L1 NM.01 0023 GTF2IRD1 NM.00 0015 CDH13 NM.00 0015 CDH13 NM.00 0015 - - 0015 KBTBD12 NM.02 0015 - - 0015 - - 0023 MYO9B, USE1, OCEL1 NM.02 0015 - - 0015 - - 0015 - - 0015 - - 0015 - - 0015 - - 0015 - - 0015 - -</td><td></td><td>.0061 KCNE4 NM.08 .0023 TSHR NM.00 .0015 CHODL, CHODL-AS1 NM.00 .0015 ITSN2 NM.00 .0023 MCF2L2, B3GNT5 NM.01 .0023 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0023 FCDH13 NM.01 .0023 - - .0015 LGR5, ZFC3H1 NM.02 .0023 - - .0023 - - .0023 - - .0023 - - .0023 - - .0023 - - .0015 - - .0016 - - .0017 - - .0023 AYO9B, USE1, OCEL1 NM.02 .0015 - -<</td><td>.0023 CHRNB3, CHRNA6 NM.00 .0023 TSHR NM.00 .0015 CHODL, CHODL-AS1 NM.00 .0015 CHODL, CHODL-AS1 NM.00 .0015 TTSN2 NM.00 .0023 MCF2L2, B3GNT5 NM.01 .0023 TFCP2L1 NM.01 .0023 TFCP2L1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0015 CDH13 NM.02 .0015 CDH13 NM.02 .0023 KBTBD12 NM.02 .0015 - - .0023 KBTBD12 NM.02 .0015 - - .0023 MYO9B, USE1, OCEL1 NM.02 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0023</td></td> | .00230015 CDH13 NM_00
.0023 KBTBD12 NM_20
.0038 LGR5, ZFC3H1 NM_00
.0023 MYO9B, USE1, OCEL1 NM_00
.0015 | .0030 GTF2IRD1 NM.00 .0023 - - - .0015 CDH13 NM.00 .0023 KBTBD12 NM.20 .0015 - - .0015 - - .0015 - - .0015 - - .0038 LGR5, ZFC3H1 NM.00 .0023 MYO9B, USE1, OCEL1 NM.02 .0023 - - - .0015 - - - .0023 AS1, SNORATB, EF- NR.02 .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0015 - - - .0023 RPL32P3, H1FX, H1FX- NR.00 AS1, SNORATB, EF- NM.20
 | .0023 TLK1 NM_01 .0030 GTF2IRD1 NM_00 .0023 - - .0015 CDH13 NM_00 .0023 KBTBD12 NM_02 .0015 - NM_02 .0023 KBTBD12 NM_02 .0015 - - .0023 MYO9B, USE1, OCEL1 NM_02 .0023 - - .0023 - - .0023 - - .0023 - - .0023 - - .0023 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0016 - - .0017 RPL32P3, H1FX, H1FX- NR_02 .0023 <td>.0015 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0015 CDH13 NM.02 .0015 CDH13 NM.02 .0015 CDH13 NM.02 .0015 - - .0015 - NM.20 .0015 - NM.02 .0015 - - .0015 - - .0023 MY09B, USE1, OCEL1 NM.02 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0023 RPL32P3, H1FX, H1FX, H1FX- NR_02 .0024 AS1, SNORA7B, EF- NR_02</td> <td>.0023 MCF2L2, B3GNT5 NM.01 .0015 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0015 CDH13 NM.00 .0023 - - .0015 CDH13 NM.00 .0023 KBTBD12 NM.20 .0015 - - .0015 - - .0015 - NM.00 .0015 - - .0023 MY09B, USE1, OCEL1 NM.02 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0023 RPL32P3, H1FX, H1FX, H1FX- NR.00 .0015 - - .0023 RPL32P3, M15X, M16X, M16X, M16X, M1.20</td> <td>.0030 KCNE4 NM.08 .0023 MCF2L2, B3GNT5 NM.01 .0015 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0015 CDH13 NM.00 .0023 KBTBD12 NM.00 .0015 CBR5, ZFC3H1 NM.00 .0023 LGR5, ZFC3H1 NM.00 .0015 - - .0015 - - .0023 MYO9B, USE1, OCEL1 NM.02 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0023 RPL32P3, H1FX, H1FX, H1FX- NR.00 AS1, SNORA7B, EF- <</td> <td>.0015 ITSN2 NML0 .0030 KCNE4 NML0 .0023 MCF2L2, B3GNT5 NML01 .0015 TFCP2L1 NML01 .0023 TLK1 NML01 .0023 TLK1 NML01 .0023 TLK1 NML01 .0023 TLK1 NML00 .0023 CDH13 NML00 .0015 CDH13 NML00 .0015 CBTSD12 NML00 .0015 - - .0015 - - .0015 - - .0015 - - .0023 MYO9B, USE1, OCEL1 NML00 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - -</td> <td>0015 CHODL, CHODL-AS1 NM.00 0015 ITSN2 NM.00 0023 MCF2L2, B3GNT5 NM.01 0023 MCF2L2, B3GNT5 NM.01 0023 TFCP2L1 NM.01 0023 TFCP2L1 NM.01 0023 TFCP2L1 NM.01 0023 TFCP2L1 NM.01 0023 GTF2IRD1 NM.00 0015 CDH13 NM.00 0015 CDH13 NM.00 0015 - - 0015 KBTBD12 NM.02 0015 - - 0015 - - 0023 MYO9B, USE1, OCEL1 NM.02 0015 - - 0015 - - 0015 - - 0015 - - 0015 - - 0015 - - 0015 - - 0015 - -</td> <td></td> <td>.0061 KCNE4 NM.08 .0023 TSHR NM.00 .0015 CHODL, CHODL-AS1 NM.00 .0015 ITSN2 NM.00 .0023 MCF2L2, B3GNT5 NM.01 .0023 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0023 FCDH13 NM.01 .0023 - - .0015 LGR5, ZFC3H1 NM.02 .0023 - - .0023 - - .0023 - - .0023 - - .0023 - - .0023 - - .0015 - - .0016 - - .0017 - - .0023 AYO9B, USE1, OCEL1 NM.02 .0015 - -<</td> <td>.0023 CHRNB3, CHRNA6 NM.00 .0023 TSHR NM.00 .0015 CHODL, CHODL-AS1 NM.00 .0015 CHODL, CHODL-AS1 NM.00 .0015 TTSN2 NM.00 .0023 MCF2L2, B3GNT5 NM.01 .0023 TFCP2L1 NM.01 .0023 TFCP2L1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0015 CDH13 NM.02 .0015 CDH13 NM.02 .0023 KBTBD12 NM.02 .0015 - - .0023 KBTBD12 NM.02 .0015 - - .0023 MYO9B, USE1, OCEL1 NM.02 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0023</td> | .0015 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0015 CDH13 NM.02 .0015 CDH13 NM.02 .0015 CDH13 NM.02 .0015 - - .0015 - NM.20 .0015 - NM.02 .0015 - - .0015 - - .0023 MY09B, USE1, OCEL1 NM.02 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0023 RPL32P3, H1FX, H1FX, H1FX- NR_02 .0024 AS1, SNORA7B, EF- NR_02
 | .0023 MCF2L2, B3GNT5 NM.01 .0015 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0015 CDH13 NM.00 .0023 - - .0015 CDH13 NM.00 .0023 KBTBD12 NM.20 .0015 - - .0015 - - .0015 - NM.00 .0015 - - .0023 MY09B, USE1, OCEL1 NM.02 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0023 RPL32P3, H1FX, H1FX, H1FX- NR.00 .0015 - - .0023 RPL32P3, M15X, M16X, M16X, M16X, M1.20 | .0030 KCNE4 NM.08 .0023 MCF2L2, B3GNT5 NM.01 .0015 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0015 CDH13 NM.00 .0023 KBTBD12 NM.00 .0015 CBR5, ZFC3H1 NM.00 .0023 LGR5, ZFC3H1 NM.00 .0015 - - .0015 - - .0023 MYO9B, USE1, OCEL1 NM.02 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0023 RPL32P3, H1FX, H1FX, H1FX- NR.00 AS1, SNORA7B, EF- <
 | .0015 ITSN2 NML0 .0030 KCNE4 NML0 .0023 MCF2L2, B3GNT5 NML01 .0015 TFCP2L1 NML01 .0023 TLK1 NML01 .0023 TLK1 NML01 .0023 TLK1 NML01 .0023 TLK1 NML00 .0023 CDH13 NML00 .0015 CDH13 NML00 .0015 CBTSD12 NML00 .0015 - - .0015 - - .0015 - - .0015 - - .0023 MYO9B, USE1, OCEL1 NML00 .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - .0015 - - | 0015 CHODL, CHODL-AS1 NM.00 0015 ITSN2 NM.00 0023 MCF2L2, B3GNT5 NM.01 0023 MCF2L2, B3GNT5 NM.01 0023 TFCP2L1 NM.01 0023 TFCP2L1 NM.01 0023 TFCP2L1 NM.01 0023 TFCP2L1 NM.01 0023 GTF2IRD1 NM.00 0015 CDH13 NM.00 0015 CDH13 NM.00 0015 - - 0015 KBTBD12 NM.02 0015 - - 0015 - - 0023 MYO9B, USE1, OCEL1 NM.02 0015 - - 0015 - - 0015 - - 0015 - - 0015 - - 0015 - - 0015 - - 0015 - - | | .0061 KCNE4 NM.08 .0023 TSHR NM.00 .0015 CHODL, CHODL-AS1 NM.00 .0015 ITSN2 NM.00 .0023 MCF2L2, B3GNT5 NM.01 .0023 TFCP2L1 NM.01 .0023 TLK1 NM.01 .0023 TLK1 NM.01 .0023 GTF2IRD1 NM.01 .0023 - - .0023 FCDH13 NM.01 .0023 - - .0015 LGR5, ZFC3H1 NM.02 .0023 - - .0023 - - .0023 - - .0023 - - .0023 - - .0023 - - .0015 - - .0016 - - .0017 - - .0023 AYO9B, USE1, OCEL1 NM.02 .0015 - -<
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June 8, 2020

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Table D2

Candidate peaks ranked by the maximum log likelihood ratios in the VolcanoFinder scan of the Yoruban (YRI) sample.

Chr.	Peak Position	LR	$-\log_{10}\hat{\alpha}$	D	Nearest Gene(s)	Respective RefSeq ID
19	41473015	45.2	3.49	0.0020	CYP2B7P, CYP2B6	NR_001278.1, NM_000767.4
1	152102007	37.3	3.48	0.0030	LOC100131107, TCHHL1,	NM_001310142.1, NM_001008
					TCHH, RPTN	NM_007113.3, NM_001122965.
12	59033128	32.1	3.56	0.0020	LOC101927653,	NR_120452.1, NR_126341.1
					LOC100506869	
ಬ	33007016	32.0	3.48	0.0030	CCR4, GLB1	NM_005508.4, NM_001079811.:
2	$170\ 442\ 117$	28.7	3.25	0.0020	FASTKD1, PPIG	NM_001322046.1, NM_004792.:
2	235174117	25.1	3.09	0.0020	I	I
4	$101\ 771\ 036$	22.9	3.53	0.0020	I	I
4	78105036	ე ე ე	ວ ວາງ 1	0.0030	CCNCO	NIN DI LE

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Whole-genome Manhattan plot of the maximum likelihood ratio test statistic for the European (CEU) population computed from Model 1 of VolcanoFinder on data on within-CEU polymorphism and substitutions with respect to chimpanzee, and annotated with the top 18 gene candidates.



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Introgression sweep signals, parameter estimates, and sequencing properties across the 100 kb region on chromosome 22 covering APOL gene cluster in YRI.

A. Likelihood ratio test statistic computed from Model 1 of VolcanoFinder on data on within-YRI polymorphism and substitutions with respect to chimpanzee. Horizontal dark gray, medium gray, and light gray bars correspond to regions that were filtered based on Hardy-Weinberg equilibrium (HWE) test. Gene tracts and labels for key genes are depicted below the plot, with the wider bars representing exons. B. Values for α and divergence D corresponding to the maximum likelihood estimate of the data. Black line corresponds to $-\ln(\alpha)$ and vertical gray bars correspond to estimated D. C. Likelihood ratio test statistic computed from T_2 of BALLET on data on within-YRI polymorphism and substitutions with respect to chimpanzee using windows of 100 (black) or 22 (gray) informative sites on either side of the test site. **D.** Mean pairwise sequence difference (θ_{π}) computed in five kb windows centered on each polymorphic site. E. Mappability uniqueness scores for 35 nucleotide sequences across the region. F. Mean sequencing depth across the 108 YRI individuals as a function of genomic position, with the gray ribbon indicating standard deviation. The background heatmap displays the number of individuals devoid of sequencing reads as a function of genomic position, with darker shades of red indicating a greater number of individuals with no sequencing reads.



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Introgression sweep signals, parameter estimates, and sequencing properties across the 100 kb region on chromosome 22 covering APOL4 gene in CEU, matching the same region in YRI.

A. Likelihood ratio test statistic computed from Model 1 of VolcanoFinder on data on within-CEU polymorphism and substitutions with respect to chimpanzee. Horizontal 74 dark gray, medium gray, and light gray bars correspond to regions that were filtered based on Hardy-Weinberg equilibrium (HWE) test. Gene tracts and labels for key genes are depicted below the plot, with the wider bars representing exons. B. Values for α and divergence D corresponding to the maximum likelihood estimate of the data. Black line corresponds to $-\ln(\alpha)$ and vertical gray bars correspond to estimated D. C. Likelihood ratio test statistic computed from T_2 of BALLET on data on within-CEU polymorphism and substitutions with respect to chimpanzee using windows of 100 (black) or 22 (gray) informative sites on either side of the test site. **D.** Mean pairwise sequence difference $(\hat{\theta}_{\pi})$ computed in five kb windows centered on each polymorphic site. **E.** Mappability uniqueness scores for 35 nucleotide sequences across the region. F. Mean sequencing depth across the 108 YRI individuals as a function of genomic position, with the gray ribbon indicating standard deviation. The background heatmap displays the number of individuals devoid of sequencing reads as a function of genomic position, with darker shades of red indicating a greater number of individuals with no sequencing reads.



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Introgression sweep signals, parameter estimates, and sequencing properties across the one Mb region on chromosome 7 covering the PTPRN2 gene region in YRI.

A. Likelihood ratio test statistic computed from Model 1 of VolcanoFinder on data 94 on within-YRI polymorphism and substitutions with respect to chimpanzee. Horizontal 95 dark gray and light gray bars correspond to regions that were filtered based on either mean CRG score or mean CRG score and proximity to a telomere, respectively. Gene 97 tracts and labels for key genes are depicted below the plot, with the wider bars 98 representing exons. B. Values for α and divergence D corresponding to the maximum 99 likelihood estimate of the data. Black line corresponds to $-\ln(\alpha)$ and vertical gray bars 100 correspond to estimated D. C. Likelihood ratio test statistic computed from T_2 of 101 BALLET on data on within-YRI polymorphism and substitutions with respect to 102 chimpanzee using windows of 100 (black) or 22 (gray) informative sites on either side of 103 the test site. **D.** Mean pairwise sequence difference (θ_{π}) computed in five kb windows 104 centered on each polymorphic site. E. Mappability uniqueness scores for 35 nucleotide 105 sequences across the region. F. Mean sequencing depth across the 108 YRI individuals 106 as a function of genomic position, with the gray ribbon indicating standard deviation. 107 The background heatmap displays the number of individuals devoid of sequencing reads 108 as a function of genomic position, with darker shades of red indicating a greater number 109 of individuals with no sequencing reads. 110



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Introgression sweep signals, parameter estimates, and sequencing properties across the one Mb region on chromosome 19 covering region surrounding PCAT19 and CEACAM4 genes in YRI.

A. Likelihood ratio test statistic computed from Model 1 of VolcanoFinder on data 116 on within-YRI polymorphism and substitutions with respect to chimpanzee. Horizontal 117 dark gray and light gray bars correspond to regions that were filtered based on 118 Hardy-Weinberg equilibrium (HWE) test. Gene tracts and labels for key genes are 119 depicted below the plot, with the wider bars representing exons. B. Values for α and 120 divergence D corresponding to the maximum likelihood estimate of the data. Black line 121 corresponds to $-\ln(\alpha)$ and vertical grav bars correspond to estimated D. C. Likelihood 122 ratio test statistic computed from T_2 of BALLET on data on within-YRI polymorphism 123 and substitutions with respect to chimpanzee using windows of 100 (black) or 22 (gray) 124 informative sites on either side of the test site. **D.** Mean pairwise sequence difference 125 (θ_{π}) computed in five kb windows centered on each polymorphic site. E. Mappability 126 uniqueness scores for 35 nucleotide sequences across the region. F. Mean sequencing 127 depth across the 108 YRI individuals as a function of genomic position, with the gray 128 ribbon indicating standard deviation. The background heatmap displays the number of 129 individuals devoid of sequencing reads as a function of genomic position, with darker 130 shades of red indicating a greater number of individuals with no sequencing reads. 131



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Introgression sweep signals, parameter estimates, and sequencing properties across the one Mb region on chromosome 17 covering IGFBP1 and B4GALNT2 in YRI.

A. Likelihood ratio test statistic computed from Model 1 of VolcanoFinder on data 137 on within-YRI polymorphism and substitutions with respect to chimpanzee. Horizontal 138 dark gray and light gray bars correspond to regions that were filtered based on 139 Hardy-Weinberg equilibrium (HWE) test. Gene tracts and labels for key genes are 140 depicted below the plot, with wider bars representing exons. B. Values for α and 141 divergence D corresponding to the maximum likelihood estimate of the data. Black line 142 corresponds to $-\ln(\alpha)$ and vertical grav bars correspond to estimated D. C. Likelihood 143 ratio test statistic computed from T_2 of BALLET on data on within-YRI polymorphism 144 and substitutions with respect to chimpanzee using windows of 100 (black) or 22 (gray) 145 informative sites on either side of the test site. **D.** Mean pairwise sequence difference 146 (θ_{π}) computed in five kb windows centered on each polymorphic site. E. Mappability 147 uniqueness scores for 35 nucleotide sequences across the region. F. Mean sequencing 148 depth across the 108 YRI individuals as a function of genomic position, with the gray 149 ribbon indicating standard deviation. The background heatmap displays the number of 150 individuals devoid of sequencing reads as a function of genomic position, with darker 151 shades of red indicating a greater number of individuals with no sequencing reads. 152



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Introgression sweep signals, parameter estimates, and sequencing properties across the 100 kb region on chromosome 19 covering the gene MUC4 in CEU.

A. Likelihood ratio statistic computed from Model 1 of VolcanoFinder on the data of within-CEU polymorphism and substitutions with respect to the chimpanzee. Gray bars immediately below indicate the type of filters, and the longest gene transcripts are depicted with thick bars standing for exons. B. Values for α and divergence Dcorresponding to the maximum likelihood estimate of the data. Black line corresponds to $-\ln(\alpha)$ and vertical gray bars correspond to estimated D. C. Likelihood ratio test statistic computed from T_2 of BALLET on data on within-CEU polymorphism and substitutions with respect to chimpanzee using windows of 100 (black) or 22 (gray) informative sites on either side of the test site. D. Mean pairwise sequence difference $(\hat{\theta}_{\pi})$ computed in five kb windows centered on each polymorphic site. E. Mappability uniqueness scores for 35 nucleotide sequences across the region. F. Mean sequencing depth across the 99 CEU individuals as a function of genomic position, with the gray ribbon indicating standard deviation. The background heatmap displays the number of individuals devoid of sequencing reads as a function of genomic position, with darker shades of red indicating a greater number of individuals with no sequencing reads.



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Introgression sweep signals, parameter estimates, and sequencing properties across the 100 kb region on chromosome 19 covering the gene CYP2B6 and CYP2B7 in YRI.

A. Likelihood ratio statistic computed from Model 1 of VolcanoFinder on the data 178 of within-YRI polymorphism and substitutions with respect to the chimpanzee. Gray 179 bars immediately below indicate the type of filters, and the longest gene transcripts are 180 depicted with the wider bars standing for exons. B. Values for α and divergence D 181 corresponding to the maximum likelihood estimate of the data. Black line corresponds 182 to $-\ln(\alpha)$ and vertical gray bars correspond to estimated D. C. Likelihood ratio test 183 statistic computed from T_2 of BALLET on data on within-YRI polymorphism and 184 substitutions with respect to chimpanzee using windows of 100 (black) or 22 (gray) 185 informative sites on either side of the test site. **D.** Mean pairwise sequence difference 186 $(\hat{\theta}_{\pi})$ computed in five kb windows centered on each polymorphic site. E. Mappability 187 uniqueness scores for 35 nucleotide sequences across the region. F. Mean sequencing 188 depth across the 108 YRI individuals as a function of genomic position, with the gray 189 ribbon indicating standard deviation. The background heatmap displays the number of 190 individuals devoid of sequencing reads as a function of genomic position, with darker 191 shades of red indicating a greater number of individuals with no sequencing reads. 192



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Evidence for adaptive introgression on the one Mb genomic region covering gene BNC2 in CEU.

A. Likelihood ratio test statistic computed from Model 1 of VolcanoFinder on data 197 on within-CEU polymorphism and substitutions with respect to chimpanzee. Horizontal 198 light gray bars correspond to regions that were filtered based on mean CRG and 199 Hardy-Weinberg equilibrium (HWE) test. Gene tracts and labels for key genes are 200 depicted below the plot, with the wider bars representing exons. Tracks of putative 201 regions with Neanderthal (above the horizontal line) or Denisovan (below the horizontal 202 line) ancestry are located below gene diagrams. Higher probabilities of Neanderthal or 203 Denisovan ancestry are depicted with darker colored bands (data from [1]). 204 Non-synonymous mutations with Neanderthal are indicated in red. **B.** Values for α and 205 divergence D corresponding to the maximum likelihood estimate of the data. Black line 206 corresponds to $-\ln(\alpha)$ and vertical gray bars correspond to estimated D. C. Likelihood 207 ratio test statistic computed from T_2 of BALLET on data on within-CEU polymorphism 208 and substitutions with respect to chimpanzee using windows of 100 (black) or 22 (gray) 209 informative sites on either side of the test site. **D.** Mean pairwise sequence difference 210 (θ_{π}) computed in five kb windows centered on each polymorphic site. **E.** Mappability 211 uniqueness scores for 35 nucleotide sequences across the region. F. Mean sequencing 212 depth across the 99 CEU individuals as a function of genomic position, with the gray 213 ribbon indicating standard deviation. The background heatmap displays the number of 214 individuals devoid of sequencing reads as a function of genomic position, with darker 215 shades of red indicating a greater number of individuals with no sequencing reads. 216



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References

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