**Supplemental Tables**

**Table S1.** Length, estimated accuracy and subreads coverage in the 81 samples sequenced by SMRT Sequencing following Long Amplicon Analysis (LAA).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Run ID | Sample ID | Phasea | Length (bp) | Estimated  accuracy (%) | Subreads coverage |
| EUR1 | EUR029 | 0 | 3,007 | 100.00 | 500 |
|  | EUR030 | 1 | 3,005 | 100.00 | 296 |
|  |  | 2 | 3,007 | 100.00 | 202 |
|  | EUR032 | 1 | 3,024 | 99.92 | 257 |
|  |  | 2 | 3,028 | 99.99 | 238 |
|  | EUR035 | 1 | 3,008 | 100.00 | 313 |
|  |  | 2 | 3,008 | 100.00 | 180 |
|  | EUR036 | 1 | 3,039 | 100.00 | 230 |
|  |  | 2 | 3,038 | 99.99 | 267 |
|  | EUR039 | 1 | 3,006 | 100.00 | 267 |
|  |  | 2 | 3,006 | 99.99 | 218 |
|  | EUR040 | 1 | 3,006 | 100.00 | 244 |
|  |  | 2 | 3,008 | 100.00 | 255 |
|  | EUR042 | 1 | 3,004 | 100.00 | 282 |
|  |  | 2 | 3,003 | 99.99 | 215 |
|  | EUR043 | 0 | 3,023 | 99.99 | 500 |
|  | EUR044 | 1 | 3,011 | 99.99 | 252 |
|  |  | 2 | 3,012 | 99.95 | 244 |
| EUR2 | EUR001 | 1 | 3,006 | 100.00 | 291 |
|  |  | 2 | 3,006 | 100.00 | 206 |
|  | EUR002 | 1 | 3,006 | 100.00 | 245 |
|  |  | 2 | 3,008 | 99.99 | 251 |
|  | EUR003 | 1 | 3,006 | 99.99 | 257 |
|  |  | 2 | 3,007 | 100.00 | 239 |
|  | EUR004 | 1 | 3,006 | 100.00 | 241 |
|  |  | 2 | 3,007 | 100.00 | 256 |
|  | EUR005 | 0 | 3,004 | 100.00 | 500 |
|  | EUR006 | 1 | 3,007 | 100.00 | 235 |
|  |  | 2 | 3,007 | 100.00 | 263 |
|  | EUR007 | 1 | 3,007 | 100.00 | 247 |
|  |  | 2 | 3,006 | 100.00 | 249 |
|  | EUR008 | 1 | 3,007 | 100.00 | 241 |
|  |  | 2 | 3,007 | 100.00 | 252 |
|  | EUR009 | 1 | 3,007 | 100.00 | 334 |
|  |  | 2 | 3,008 | 100.00 | 162 |
|  | EUR010 | 1 | 3,006 | 100.00 | 282 |
|  |  | 2 | 3,008 | 100.00 | 217 |
|  | EUR011 | 1 | 3,007 | 99.99 | 240 |
|  |  | 2 | 3,008 | 99.98 | 259 |
|  | EUR012 | 0 | 3,013 | 99.99 | 499 |
|  | EUR013 | 1 | 3,005 | 100.00 | 234 |
|  |  | 2 | 3,007 | 100.00 | 261 |
|  | EUR014 | 1 | 3,007 | 99.98 | 229 |
|  |  | 2 | 3,006 | 99.99 | 268 |
|  | EUR015 | 1 | 3,007 | 100.00 | 256 |
|  |  | 2 | 3,008 | 100.00 | 236 |
|  | EUR016 | 1 | 3,005 | 100.00 | 245 |
|  |  | 2 | 3,005 | 100.00 | 243 |
|  | EUR018 | 1 | 3,006 | 100.00 | 246 |
|  |  | 2 | 3,007 | 100.00 | 250 |
|  | EUR022 | 1 | 3,009 | 100.00 | 247 |
|  |  | 2 | 3,010 | 99.99 | 248 |
|  | EUR023 | 1 | 3,007 | 100.00 | 269 |
|  |  | 2 | 3,008 | 100.00 | 226 |
|  | EUR024 | 1 | 3,008 | 100.00 | 275 |
|  |  | 2 | 3,008 | 100.00 | 218 |
|  | EUR026 | 1 | 3,006 | 100.00 | 269 |
|  |  | 2 | 3,007 | 100.00 | 225 |
|  | EUR027 | 0 | 3,006 | 100.00 | 497 |
|  | EUR028 | 1 | 3,005 | 99.99 | 266 |
|  |  | 2 | 3,006 | 99.99 | 227 |
|  | EUR033 | 0 | 3,006 | 100.00 | 495 |
|  | EUR034 | 0 | 3,007 | 99.99 | 499 |
|  | EUR037 | 1 | 3,006 | 100.00 | 263 |
|  |  | 2 | 3,007 | 100.00 | 234 |
|  | EUR038 | 1 | 3,006 | 99.99 | 237 |
|  |  | 2 | 3,006 | 99.94 | 257 |
|  | EUR041 | 1 | 3,008 | 100.00 | 230 |
|  |  | 2 | 3,007 | 100.00 | 266 |
| BRA | BRA002 | 1 | 3,007 | 100.00 | 271 |
|  |  | 2 | 3,007 | 100.00 | 228 |
|  | BRA003 | 1 | 3,007 | 100.00 | 254 |
|  |  | 2 | 3,007 | 100.00 | 243 |
|  | BRA005 | 0 | 3,005 | 99.97 | 500 |
|  | BRA006 | 1 | 3,008 | 100.00 | 237 |
|  |  | 2 | 3,007 | 100.00 | 261 |
|  | BRA007 | 1 | 3,005 | 100.00 | 287 |
|  |  | 2 | 3,005 | 100.00 | 212 |
|  | BRA008 | 0 | 3,005 | 100.00 | 500 |
|  | BRA009 | 1 | 3,007 | 100.00 | 243 |
|  |  | 2 | 3,006 | 100.00 | 256 |
|  | BRA016 | 1 | 3,033 | 99.99 | 250 |
|  |  | 2 | 3,034 | 99.90 | 248 |
|  | BRA019 | 1 | 3,007 | 100.00 | 258 |
|  |  | 2 | 3,008 | 100.00 | 241 |
|  | BRA021 | 1 | 3,007 | 100.00 | 273 |
|  |  | 2 | 3,006 | 100.00 | 226 |
|  | BRA024 | 1 | 3,007 | 100.00 | 239 |
|  |  | 2 | 3,008 | 100.00 | 260 |
|  | BRA025 | 1 | 3,006 | 100.00 | 251 |
|  |  | 2 | 3,007 | 100.00 | 248 |
|  | BRA027 | 1 | 3,008 | 100.00 | 238 |
|  |  | 2 | 3,009 | 100.00 | 261 |
|  | BRA030 | 1 | 3,007 | 100.00 | 248 |
|  |  | 2 | 3,006 | 100.00 | 250 |
|  | BRA034 | 0 | 3,006 | 100.00 | 500 |
|  | BRA036 | 1 | 3,005 | 100.00 | 240 |
|  |  | 2 | 3,005 | 100.00 | 259 |
|  | BRA037 | 1 | 3,006 | 100.00 | 271 |
|  |  | 2 | 3,006 | 100.00 | 227 |
|  | BRA038 | 1 | 3,005 | 100.00 | 257 |
|  |  | 2 | 3,007 | 100.00 | 242 |
|  | BRA044 | 1 | 3,007 | 100.00 | 246 |
|  |  | 2 | 3,008 | 100.00 | 253 |
|  | BRA045 | 1 | 3,006 | 100.00 | 243 |
|  |  | 2 | 3,005 | 100.00 | 255 |
|  | BRA046 | 1 | 3,007 | 100.00 | 248 |
|  |  | 2 | 3,007 | 100.00 | 251 |
|  | BRA049 | 0 | 3,006 | 100.00 | 499 |
|  | BRA050 | 1 | 3,007 | 100.00 | 266 |
|  |  | 2 | 3,008 | 100.00 | 232 |
|  | BRA051 | 1 | 3,007 | 100.00 | 257 |
|  |  | 2 | 3,007 | 100.00 | 241 |
|  | BRA052 | 1 | 3,008 | 100.00 | 245 |
|  |  | 2 | 3,007 | 100.00 | 254 |
|  | BRA054 | 1 | 3,005 | 100.00 | 242 |
|  |  | 2 | 3,006 | 100.00 | 256 |
|  | BRA056 | 1 | 3,008 | 100.00 | 243 |
|  |  | 2 | 3,007 | 100.00 | 256 |
|  | BRA058 | 1 | 3,007 | 100.00 | 247 |
|  |  | 2 | 3,005 | 100.00 | 252 |
|  | BRA060 | 1 | 3,007 | 100.00 | 272 |
|  |  | 2 | 3,007 | 100.00 | 227 |
|  | BRA063 | 0 | 3,006 | 100.00 | 499 |
|  | BRA067 | 0 | 3,007 | 100.00 | 500 |
|  | BRA070 | 1 | 3,006 | 100.00 | 245 |
|  |  | 2 | 3,005 | 100.00 | 254 |
|  | BRA071 | 1 | 3,006 | 100.00 | 228 |
|  |  | 2 | 3,007 | 100.00 | 271 |
|  | BRA080 | 1 | 3,008 | 100.00 | 271 |
|  |  | 2 | 3,009 | 100.00 | 228 |
|  | BRA081 | 1 | 3,005 | 100.00 | 242 |
|  |  | 2 | 3,006 | 100.00 | 257 |
|  | BRA083 | 1 | 3,007 | 100.00 | 267 |
|  |  | 2 | 3,008 | 100.00 | 232 |
|  | BRA084 | 1 | 3,007 | 100.00 | 229 |
|  |  | 2 | 3,008 | 100.00 | 269 |
|  | BRA085 | 1 | 3,007 | 100.00 | 268 |
|  |  | 2 | 3,006 | 100.00 | 231 |
|  | BRA086 | 1 | 3,006 | 100.00 | 239 |
|  |  | 2 | 3,006 | 100.00 | 260 |
|  | BRA088 | 0 | 3,007 | 100.00 | 500 |
|  | BRA090 | 1 | 3,005 | 100.00 | 279 |
|  |  | 2 | 3,005 | 100.00 | 219 |
|  | BRA091 | 1 | 3,007 | 100.00 | 247 |
|  |  | 2 | 3,006 | 100.00 | 251 |
|  | BRA094 | 1 | 3,007 | 100.00 | 243 |
|  |  | 2 | 3,006 | 100.00 | 255 |

Three different runs were carried out: EUR1, n = 10 samples; EUR2, n = 28; BRA, n = 43.

Analysis parameters: minimum predicted accuracy ≥ 0.999; minimum and maximum subread lengths = 2,500 and 3,200, respectively; minimum allele/haplotype read fraction = 0.2; maximum phasing reads = 500.

a 0: a single haplotype (homozygous state) / the sample is considered to be carrying two copies of the same allele; 1 and 2: two different haplotypes (compound heterozygous state).

**Table S2.** Haplotypes obtained by SMRT Sequencing and respective phenotype in the 81 samples.

|  |  |  |  |
| --- | --- | --- | --- |
| Sample ID | Allele 1 | Allele 2 | Phenotype |
| EUR001 | *\*02\_02* | *\*02\_05* | Fy(a-b+) |
| EUR002 | *\*01\_01* | *\*02\_01* | Fy(a+b+) |
| EUR003 | *\*02\_01* | *\*02\_05* | Fy(a-b+) |
| EUR004 | *\*02\_04* | *\*02N.01\_01* | Fy(a-b+) |
| EUR005 | *\*02\_01* | *\*02\_01* | Fy(a-b+) |
| EUR006 | *\*01(714A)* | *\*02\_02* | Fy(a+b+) |
| EUR007 | *\*01\_01* | *\*01\_03* | Fy(a+b-) |
| EUR008 | *\*01\_03* | *\*02\_02* | Fy(a+b+) |
| EUR009 | *\*01\_01* | *\*02\_02* | Fy(a+b+) |
| EUR010 | *\*01\_01* | *\*02\_04* | Fy(a+b+) |
| EUR011 | *\*01\_01* | *\*02\_02* | Fy(a+b+) |
| EUR012 | *\*02\_02* | *\*02\_02* | Fy(a-b+) |
| EUR013 | *\*01\_01* | *\*02\_01* | Fy(a+b+) |
| EUR014 | *\*02\_03* | *\*02\_04* | Fy(a-b+) |
| EUR015 | *\*02\_01* | *\*02\_03* | Fy(a-b+) |
| EUR016 | *\*01\_03* | *\*02\_03* | Fy(a+b+) |
| EUR018 | *\*02\_01* | *\*02\_03* | Fy(a-b+) |
| EUR022 | *\*01\_02* | *\*02\_01* | Fy(a+b+) |
| EUR023 | *\*01\_01* | *\*02\_03* | Fy(a+b+) |
| EUR024 | *\*01\_02* | *\*02\_03* | Fy(a+b+) |
| EUR026 | *\*01\_01* | *\*02\_03* | Fy(a+b+) |
| EUR027 | *\*01\_02* | *\*01\_02* | Fy(a+b-) |
| EUR028 | *\*02\_01* | *\*02\_02* | Fy(a-b+) |
| EUR029 | *\*01\_01* | *\*01\_01* | Fy(a+b-) |
| EUR030 | *\*01\_01* | *\*02\_01* | Fy(a+b+) |
| EUR032 | *\*01\_01* | *\*02\_02* | Fy(a+b+) |
| EUR033 | *\*01\_03* | *\*01\_03* | Fy(a+b-) |
| EUR034 | *\*02\_01* | *\*02\_01* | Fy(a-b+) |
| EUR035 | *\*01\_02* | *\*02\_02* | Fy(a+b+) |
| EUR036 | *\*02\_04* | *\*02N.01\_01* | Fy(a-b+) |
| EUR037 | *\*01\_01* | *\*02\_06* | Fy(a+b+) |
| EUR038 | *\*02\_03* | *\*02\_05* | Fy(a-b+) |
| EUR039 | *\*02\_02* | *\*02\_03* | Fy(a-b+) |
| EUR040 | *\*01\_01* | *\*02\_01* | Fy(a+b+) |
| EUR041 | *\*01\_01* | *\*02\_02* | Fy(a+b+) |
| EUR042 | *\*02\_02* | *\*02\_04* | Fy(a-b+) |
| EUR043 | *\*01\_03* | *\*01\_03* | Fy(a+b-) |
| EUR044 | *\*01\_02* | *\*02\_01* | Fy(a+b+) |
| BRA002 | *\*01\_02* | *\*02N.01\_01* | Fy(a+b-) |
| BRA003 | *\*02\_05* | *\*02N.01\_01* | Fy(a-b+) |
| BRA005 | *\*02N.01\_01* | *\*02N.01\_01* | Fy(a-b-) |
| BRA006 | *\*01\_01* | *\*02N.01\_01* | Fy(a+b-) |
| BRA007 | *\*02\_03* | *\*02N.01\_01* | Fy(a-b+) |
| BRA008 | *\*02N.01\_02* | *\*02N.01\_02* | Fy(a-b-) |
| BRA009 | *\*02\_01* | *\*02N.01(V266M)* | Fy(a-b+) |
| BRA016 | *\*01\_02* | *\*02N.01\_01* | Fy(a+b-) |
| BRA019 | *\*01\_01* | *\*02N.01\_01* | Fy(a+b-) |
| BRA021 | *\*02\_01* | *\*02N.01\_01* | Fy(a-b+) |
| BRA024 | *\*01\_01* | *\*02N.01\_01* | Fy(a+b-) |
| BRA025 | *\*02\_07* | *\*02N.01\_01* | Fy(a-b+) |
| BRA027 | *\*01\_01* | *\*02N.01\_01* | Fy(a+b-) |
| BRA030 | *\*01\_01* | *\*02N.01\_01* | Fy(a+b-) |
| BRA034 | *\*02N.01\_01* | *\*02N.01\_01* | Fy(a-b-) |
| BRA036 | *\*02\_03* | *\*02N.01\_01* | Fy(a-b+) |
| BRA037 | *\*01\_02* | *\*02N.01\_01* | Fy(a+b-) |
| BRA038 | *\*02\_03* | *\*02N.01\_02* | Fy(a-b+) |
| BRA044 | *\*01\_01* | *\*02N.01\_01* | Fy(a+b-) |
| BRA045 | *\*02\_08* | *\*02N.01\_02* | Fy(a-b+) |
| BRA046 | *\*02\_03* | *\*02N.01\_03* | Fy(a-b+) |
| BRA049 | *\*02N.01\_01* | *\*02N.01\_01* | Fy(a-b-) |
| BRA050 | *\*01\_01* | *\*02N.01\_01* | Fy(a+b-) |
| BRA051 | *\*02N.01\_01* | *\*02N.01\_06* | Fy(a-b-) |
| BRA052 | *\*01\_01* | *\*02N.01\_03* | Fy(a+b-) |
| BRA054 | *\*02\_01* | *\*02N.01\_01* | Fy(a-b+) |
| BRA056 | *\*01\_01* | *\*02N.01\_03* | Fy(a+b-) |
| BRA058 | *\*02\_03* | *\*02N.01\_02* | Fy(a-b+) |
| BRA060 | *\*02\_02* | *\*02N.01\_01* | Fy(a-b+) |
| BRA063 | *\*02N.01\_01* | *\*02N.01\_01* | Fy(a-b-) |
| BRA067 | *\*02N.01\_01* | *\*02N.01\_01* | Fy(a-b-) |
| BRA070 | *\*02\_01* | *\*02N.01\_01* | Fy(a-b+) |
| BRA071 | *\*02\_01* | *\*02N.01\_01* | Fy(a-b+) |
| BRA080 | *\*01\_01* | *\*02N.01\_01* | Fy(a+b-) |
| BRA081 | *\*02\_04* | *\*02N.01\_02* | Fy(a-b+) |
| BRA083 | *\*01\_01* | *\*02N.01\_01* | Fy(a+b-) |
| BRA084 | *\*01\_01* | *\*02N.01\_01* | Fy(a+b-) |
| BRA085 | *\*02\_04* | *\*02N.01\_01* | Fy(a-b+) |
| BRA086 | *\*01\_02* | *\*02N.01\_05* | Fy(a+b-) |
| BRA088 | *\*02N.01\_01* | *\*02N.01\_01* | Fy(a-b-) |
| BRA090 | *\*01\_02* | *\*02N.01\_01* | Fy(a+b-) |
| BRA091 | *\*02\_04* | *\*02N.01\_04* | Fy(a-b+) |
| BRA094 | *\*02\_01* | *\*02N.01\_01* | Fy(a-b+) |

Allele details are provided in Table 2.

**Table S3.** Potential similar *ACKR1* haplotypes found in previous studies.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| This study | | |  | Previous studies | | | | |
| Designationa |  | GenBankb |  | Designationa |  | GenBankb |  | Reference |
| *\*01\_01* |  | MK813892 |  | *\*01:1* |  | JN251907 |  | [6] |
| *\*01\_02* |  | MK813894 |  | *\*01:2* |  | JN251908 |  | [6] |
|  |  |  |  | *\*01:2* |  | JN251909 |  | [6] |
| *\*02\_01* |  | MK813896 |  | *\*02:4* |  | JN251913 |  | [6] |
| *\*02\_02* |  | MK813897 |  | *\*04:1* |  | JN251916 |  | [6] |
| *\*02\_03* |  | MK813898 |  | *\*02:1* |  | JN251910 |  | [6] |
| *\*02\_05* |  | MK813900 |  | *\*02:2* |  | JN251911 |  | [6] |
| *\*02N.01\_01* |  | MK813902 |  | *\*03:1* |  | JN251914 |  | [6] |
|  |  |  |  | N/A |  | MG932622 |  | [7] |
|  |  |  |  | N/A |  | MG932623 |  | [7] |
|  |  |  |  | N/A |  | MG932624 |  | [7] |
|  |  |  |  | N/A |  | MG932625 |  | [7] |
|  |  |  |  | N/A |  | MG932632 |  | [7] |
| *\*02N.01\_03* |  | MN259535 |  | N/A |  | MG932631 |  | [7] |

a Unofficial haplotype designation. N/A: not applicable.

b GenBank Accession Number (www.ncbi.nlm.nih.gov/genbank/).

Overlapped regions between this study and reference [6]: 2,253 bp ; Chr1:159,174,224-159,176,476 in the human GRCh37.p13/hg19 reference genome.

Overlapped regions between this study and reference [7]: 3,008 bp ; Chr1:159,173,469-159,176,476 in the human GRCh37.p13/hg19 reference genome.

**Table S4.** Frequency of variations in the LR-PCR primers.

|  |  |  |  |
| --- | --- | --- | --- |
| Primer ID | Primer sequence (5’→3’)a | dbSNPb | Minor allele frequencyc |
| ACKR1\_e1-2F | ACAAATGAAACAGCGTCCCC | rs776148234 | 1.28e-4 |
|  |  | rs572653927 | 3.19e-5 |
| ACKR1\_e1-2R | TCTCCCTTGAGATGGCCGTG | rs185605233 | 5.99e-3 |
|  |  | rs1340666753 | 6.38e-5 |
|  |  | rs374967750 | 3.19e-5 |
|  |  | rs138795069 | 1.28e-4 |
|  |  | rs192256602 | 4.15e-4 |

a Polymorphic positions are underlined.

b NCBI database of genetic variation (URL: www.ncbi.nlm.nih.gov/snp).

c MAF: minor allele frequency in the general populations (gnomAD v2.1.1 [20]).