**Table S1.** Optimal window size and overlap proportion with the \textit{wLOD} method in the simulated datasets.

| SNV subset | Scenario 1 | | Scenario 2 | |
|-------------|------------|---|------------|---|
|             | Window size | % overlap | Window size | % overlap |
| 18,000      | 60         | 7  | 70         | 5  |
| 50,000      | 70         | 18 | 80         | 19 |
| 80,000      | 80         | 28 | 90         | 22 |
| 125,000     | 80         | 29 | 100        | 26 |
| 750,000     | 130        | 37 | 120        | 32 |
Table S2. Optimal window sizes and overlap fractions with the LOD method in the simulated datasets.

| SNV subset | Scenario 1 | Scenario 2 |
|------------|------------|------------|
|            | Window size | % overlap | Window size | % overlap |
| 18,000     | 50         | 15        | 60         | 2         |
| 50,000     | 60         | 19        | 70         | 11        |
| 80,000     | 60         | 21        | 60         | 17        |
| 125,000    | 60         | 21        | 70         | 16        |
| 750,000    | 80         | 14        | 80         | 17        |
**Table S3.** Genomic regions encompassing genes with a median fraction of overlap with class 5 ROA of > 0.9 in at least one population.

| Chr | Begin (bp) | End (bp) | Genes          | Populations               |
|-----|------------|----------|----------------|---------------------------|
| 8   | 7,118,140  | 7,143,880| *LINC00965*    | ASW, LWK                  |
| 8   | 7,627,105  | 7,628,835| *FAM90A10P*    | LWK, TSI                  |
| 15  | 28,818,925 | 28,834,386| *HERC2P11*     | CEU                       |
| 21  | 9,825,831  | 9,826,263| *MIR3648, MIR3687* | CEU, JPT, LWK, TSI, GBR, CDX, GWD |
| 21  | 9,907,188  | 9968594  | *TEKT4P2*      | CDX                       |
| 21  | 11,020,841 | 11,098,937| *BAGE, BAGE2, BAGE3, BAGE4, BAGE5* | TSI, GBR, IBS, CLM, PUR |
| 21  | 14,982,497 | 15,013,906| *POTED*        | LWK, CDX                  |
**Table S4.** Genomic regions encompassing genes with a median fraction of overlap with class 4 ROA of > 0.9 in at least one population.

| Genomic region | Genes | Populations |
|----------------|-------|-------------|
| Chr | Begin (bp) | End (bp) | |
| 1 | 12,998,504 | 13,002,353 | **PRAMEF9** | TSI |
| 1 | 206,317,458 | 206,332,104 | **CTSE** | JPT, CHS |
| 2 | 111,132,685 | 111,142,113 | **LINC01106** | TSI |
| 2 | 131,220,388 | 131,357,148 | **POTEI, CFC1** | TSI, CLM, PUR |
| 4 | 9,212,382 | 9,370,796 | **USP17L5, USP17L10, USP17L11, USP17L12, USP17L13, USP17L15, USP17L17, USP17L18, USP17L19, USP17L20, USP17L21, USP17L22, USP17L24, USP17L26, USP17L27, USP17L28, USP17L29, USP17L30, USP17L6P, USP17L9P** | TSI |
| 4 | 41,937,136 | 41,988,484 | **TMEM33, DCAF4L1** | CDX |
| 4 | 70,146,216 | 70,160,768 | **LOC653080, SERF1A, SERF1B, SMN1, SMN2, SMA4, GTF2H2B, SMA5, LOC441081, GUSBP9, NAIP, GTF2H2, LOC647859** | ASW, LWK, YRI, ACB, ESN, GWD |
| 5 | 69,140,495 | 74,867,509 | **LOC647859** | CDX |
| 7 | 74,572,383 | 74,867,509 | **NCF1C, CASTOR2** | CDX |
| 8 | 7,118,140 | 7,143,880 | **LINC00965** | PJL |
| 8 | 7,812,534 | 7,946,611 | **FAM66E, USP17L8, MIR548I3, FOXD4L5** | CDX, BEB, ITU, PJL |
| 10 | 17,794,259 | 18,134,122 | **TMEM236, MIR511** | CDX |
| 10 | 48,155,942 | 48,158,691 | **CTSLP2** | LWK, GWD |
| 10 | 51,253,907 | 51,371,344 | **PARGPI** | MXL, CDX, ITU |
| 14 | 101,391,157 | 101,454,566 | **SNORD113-1, SNORD113-2, SNORD113-4, SNORD113-5, SNORD113-6, SNORD113-7, SNORD113-9, SNORD114-1, SNORD114-2, SNORD114-3, SNORD114-4, SNORD114-5, SNORD114-6, SNORD114-7, SNORD114-8, SNORD114-9, SNORD114-10, SNORD114-11, SNORD114-12, SNORD114-13, SNORD114-14, SNORD114-15, SNORD114-16, SNORD114-17, SNORD114-18, SNORD114-19, SNORD114-20, SNORD114-21, SNORD114-22, SNORD114-23, SNORD114-24, SNORD114-25, SNORD114-26, SNORD114-27** | JPT, CDX |
| 14 | 106,383,837 | 106,438,358 | **FAM30A, ADAM6** | CEU, CHB, CIH, JPT, MXL, TSI, FIN, GBR, IBS, CLM, PUR, BEB, ESN, GWD, MSL |
| 15 | 30,653,442 | 30,782,516 | **CHRFAM7A, GOLGA8R, LOC100288203** | CDX |
| 15 | 120,462,344 | 120,463,262 | **OR4F4** | LWK, GWD |
| 16 | 21,413,454 | 21,445,776 | **NPIPB3, LOC100190986** | PUR |
| 19 | 110,678 | 202,209 | **OR4F17, LINC01002** | CDX |
| 19 | 55,280,873 | 55,360,024 | **ZNF81BP, LOC101928804, KIR2DL1, KIR3DL1, KIR2DS4** | TSI, GBR, CDX, PEL, BEB, ITU, PJL |
| 21 | 17,911,408 | 17,912,231 | **MIR99A, MIRLET7C** | CDX |

*OMIM autosomal recessive genes are in bold.*
Additional File 2: Weighted Likelihood Inference of Autozygosity

Table S5. Genomic regions encompassing genes with a median fraction of overlap with class 3 ROA of > 0.9 in at least one population.

| Chr | Begin (bp) | End (bp) | Genes              | Populations         |
|-----|------------|----------|--------------------|---------------------|
| 1   | 248,756,130| 248,790,429| *OR2T10, OR2T11*  | ASW, LWK, YRI, ACB, GWD, MSL |
| 2   | 114,256,660| 114,258,727| *FOXD4L1*         | CDX                 |
| 4   | 70,146,216 | 70,160,768 | *UGT2B28*         | CEU, MXL, TSI, GBR, IBS, BEB, ITU, PJL, PEL |
| 9   | 46,116,942 | 46,168,270 | *LOC105376064, FAM27E2* | TSI |
| 11  | 61,567,096 | 61,582,712 | *FADS1, MIR1908*  | ITU, STU |
| 13  | 19,582,398 | 19,586,774 | *LINCO0442*       | PEL |
| 16  | 2,688,982  | 2,696,130 | *FLJ42627*        | CDX |
| 16  | 21,413,454 | 21,445,776 | *NPiPB3, LOC100190986* | CDX |
| 19  | 43,715,942 | 43,752,798 | *LOC284344*       | KHV |
**Additional File 2: Weighted Likelihood Inference of Autozygosity**

**Table S6.** Genomic regions encompassing genes with a median fraction of overlap with class 2 ROA of > 0.9 in at last one population.

| Chr | Begin (bp) | End (bp) | Genes          | Populations |
|-----|------------|----------|----------------|-------------|
| 8   | 41,284,173 | 41,284,246| **SNORD65B**   | CHB         |
| 9   | 44,384,584 | 44,391,314| **LOC101927827** | MXL, BEB, ITU |
| 11  | 62,334,482 | 62,334,543| **MIR6747**    | CDX         |
| 15  | 25,440,067 | 25,440,148| **SNORD115-14**| CLM         |
| 20  | 62,159,775 | 62,168,723| **PTK6**       | CHB         |
### Table S7. Genomic regions encompassing genes with a median fraction of overlap with class 1 ROA of > 0.9 in at least one population.

| Chr | Begin (bp) | End (bp) | Genes | Populations |
|-----|------------|----------|-------|-------------|
| 1   | 16,860,385 | 16,866,530 | LINC01783, FAM231B | CDX |
| 1   | 50,883,222 | 50,889,119 | DMRTA2 | JPT, CHS, CDX |
| 1   | 120,839,004 | 120,855,681 | FAM72B | MXL, CDX |
| 1   | 142,697,420 | 142,713,605 | ANKRD20A12P | CDX |
| 2   | 91,824,708 | 91,970,153 | LOC654342, GGT8P | MXL, CDX |
|     |            |           |        | CHB, GIH, JPT, MXL, TSI, GBR, CHS, PUR, CDX, PEL, KHV, BEB, ITU, PJL, STU |
| 3   | 48,658,274 | 52,029,958 |                | CEU, JPT, MXL, TSI, IBS, CHS, CDX, PEL |
| 4   | 86,386,724 | 86,387,377 | SNHG5, SNORD50A, SNORD50B | CDX |
| 5   | 27,168,125 | 27,170,399 | HOXA4 | ITU |
| 6   | 10,524,487 | 10,524,580 | MI4286 | CHB |
| 7   | 42,691,816 | 42,751,412 | THAP1, MIR4469 | TSI, JPT, FIN, IBS, ITU |
| 8   | 43,603,172 | 43,630,730 | FAM74A7, SPATA31A6 | CEU, TSI, YRI, FIN, GBR, IBS, CDX, ACB, ITU, STU |
| 9   | 44,384,584 | 44,391,314 | LOC101927827 | CDX |
| 10  | 66,494,268 | 66,555,601 | PTGER4P2-CDK2AP2P2, LOC728673 | TSI, IBS, GWD, STU |
| 10  | 99,671,356 | 99,704,572 | LOC441454, NUTM2G | CEU, GBR, IBS, CLM, PUR |
| 10  | 74,720,206 | 75,193,319 | NUDT13, SNORA11F, ECD, DNAJC9, MRPS16, MSS51 | MXL, TSI, FIN, GBR, IBS, PUR, PEL, STU |
| 10  | 75,404,638 | 75,415,863 | SYNPO2L | TSI |
| 11  | 38,670,407 | 38,676,799 | LINC01493 | MXL, TSI |
| 11  | 46,624,855 | 46,638,777 | HARB1 | PEL |
| 11  | 50,003,008 | 50,004,071 | OR4C12 | MXL, CDX |
| 11  | 51,411,377 | 51,516,211 | OR4CA5, OR4C46 | MXL |
| 11  | 55,110,676 | 55,433,572 | OR4A16, OR4C11, OR4P4, OR4S2, OR4G6 | ASW, CEU, GIH, LWK, MXL, TSI, YRI, GBR, CLM, PUR, CDX, ACB, BEB, GWD, ITU, MSL, PJL, STU |
| 11  | 55,606,227 | 57,429,337 | OR5D16, OR5I1, OR10AG1, OR7ESP, OR5F1, OR5A51, OR8I2, OR8H2, OR8H3, OR8J3, OR5J2, OR5T1, OR8K3, OR8K1, OR8U8, OR8U1, OR5AL1, OR5I1, OR5MB, OR5M11, OR5M10, OR5M1, TIMM10, MIR130A, CLP1 | MXL, CDX, PEL, KHV |
| 11  | 89,819,117 | 89,820,299 | UBTFL1 | CDX |
| 12  | 34,175,215 | 34,181,236 | ALG10 | JPT, CHS, CDX, KHV |
Additional File 2: Weighted Likelihood Inference of Autozygosity

|   |   |   |   |   |   |
|---|---|---|---|---|---|
| 12 | 111,374,405 | 111,395,622 | LINCO1405, LOC10536980 | CDX, PEL |
| 12 | 123,745,516 | 123,756,863 | CDK2AP1 | JPT |
| 14 | 59,930,239 | 59,972,124 | GPR135, L3HYPDH, JKAMP | CHB, CDX |
| 14 | 67,908,571 | 67,908,647 | MIR5694 | CDX |
| 15 | 24,686,273 | 24,693,114 | PWRN3 | ASW, CEU, JPT, LWK, TSI, FIN, IBS, CLM, PUR, ACB, BEB, GWD, ITU, MSL, PJL |
| 15 | 42,491,767 | 42,491,864 | MIR627 | IBS |
| 15 | 72,668,453 | 72,879,654 | TMEM202, MIR630 | GIH, CDX, BEB, PJL, STU |
| 16 | 14,397,823 | 14,403,228 | MIR193B, MIR365A | CDX |
| 16 | 32,888,796 | 32,896,463 | SLC6A1OP | BEB |
| 16 | 33,961,051 | 33,962,503 | LINCO0273 | CEU, GIH, TSI, IBS, CLM, PUR, CDX, BEB, ITU, PJL, STU |
| 16 | 34,403,801 | 34,404,762 | UBE2MP1, FRG2DP | MHL, TSI, GWD, STU |
| 16 | 46,723,557 | 46,920,386 | ORC6, SNORD14B | CDX, PEL, KHV |
| 16 | 47,999,599 | 48,005,598 | LINCO2134 | IBS, CDX, BEB |
| 16 | 67,906,925 | 68,267,402 | EDC4, NNR11, PSMB10, LCAT, DPEP3, ESRP2, MIR6773 | CHS, CDX, CHB |
| 17 | 28,951,335 | 28,953,825 | SH3GL1P2 | TSI, GBR, IBS |
| 19 | 28,281,400 | 28,284,848 | LINCO0662 | CHB, CDX |
| 20 | 25,593,572 | 26,188,914 | NANP, LINCO1733, NCOR1P1, MIR663A | CDX |
| 20 | 29,637,583 | 30,619,984 | MLLT10P1, DEFB121, 1D1, MIR3193, COX4I2, ABALON, CCM2 | CEU, CHB, GIH, MXL, IBS, CHS, CDX, PEL, KHV, BEB, ITU, PJL, STU |
| 20 | 34,020,826 | 34,288,902 | GDF5OS, MIR1289-1, RBM12, ROMO | JPT, CDX, PEL, IBS, CLM |
| 22 | 42,086,546 | 42,094,140 | C22orf46 | JPT |
| 22 | 43,608,679 | 43,609,667 | LOC105373051 | CDX |

OMIM autosomal dominant genes are underlined.
OMIM autosomal recessive genes are in bold.
### Table S8. Genomic regions marginally enriched for autozygosity signals in the GIH, ITU, and PJL subgroups

| Population | Name    | Group | Chr | Begin (bp) | End (bp) | Length (bp) | Number of windows | Minimum $P_{perm}$ | RefSeq Genes & miRNA |
|------------|---------|-------|-----|------------|----------|-------------|-------------------|-------------------|----------------------|
| GIH Gujarati | 2 | 2 | 242,977,775 | 243,178,150 | 200,376 | 42 | 0.064 | LOC728323 |
| GIH Gujarati | 2 | 20 | 2,799,801 | 2,893,954 | 94,154 | 32 | 0.067 | PCED1A, VPS16, PTPRA |
| ITU Telugu | 1 | 2 | 169,745,523 | 169,865,984 | 120,462 | 39 | 0.084 | G6PC2, ABCB11 |
| ITU Telugu | 1 | 6 | 137,323,081 | 137,441,791 | 118,711 | 3 | 0.083 | IL20RA |
| ITU Telugu | 1 | 12 | 100,036,343 | 100,203,990 | 167,648 | 43 | 0.055 | ANKS1B, FAM71C, TMEM104, GRIN2C, FDXR, FADS6, USH1G, OTOP2, OTOP3 |
| ITU Telugu | 1 | 17 | 72,781,311 | 72,933,576 | 152,266 | 32 | 0.051 | SNAI3, RNF166, CTU2, MIR4722, PIEZO1 |
| PJL Punjabi | 1 | 16 | 88,737,170 | 88,812,876 | 75,707 | 12 | 0.087 | |
**Table S9.** The 68 individuals removed during individual quality control check due to relatedness, likely erroneous sex assignment, or who did not cluster genetically with other members of their population.

| Population | Individual ID | Reason for removal |
|------------|---------------|--------------------|
| ASW        | NA19625       | Intra-population AV relationship with NA20274 |
| ASW        | NA19904       | Intra-population PO relationship with NA19913 |
| ASW        | NA20317       | Intra-population PO relationship with NA20318 |
| ASW        | NA20320       | Intra-population PO relationship with NA20231 |
| ASW        | NA20355       | Intra-population PO relationship with NA20334 |
| ASW        | NA20362       | Intra-population PO relationship with NA20359 |
| GIH        | NA20900       | Intra-population PO relationship with NA20882 & NA20891 (trio G001 in Pemberton et al. [207]) |
| GIH        | NA21109       | Intra-population AV relationship with NA21135 |
| LWK        | NA19042       | Intra-population AV relationship with NA19042 |
| LWK        | NA19334       | Intra-population FS relationship with NA19331 |
| ACB        | HG02479       | Intra-population FS relationship with HG02429 |
| ITU        | HG03873       | Intra-population AV relationship with NA19042 |
| STU        | HG03733       | Intra-population FS relationship with HG03899 |
| STU        | HG03750       | Intra-population PO relationship with HG03754 |
| STU        | HG03998       | Intra-population FS relationship with HG03873 |
| YRI        | NA18870       | Clusters with Esan (ESN) individuals |
| ESN        | HG03294       | Clusters with Yoruban (YRI) individuals |
| CDX        | HG01798       | Clusters with Han (CHB and CHS) and Kinh (KHV) individuals |
| CEU        | NA11932       | Lies far from CEU cluster in comparisons with East Asian populations |
| CEU        | NA12383       | Lies far from CEU cluster in comparisons with East Asian populations |
| CHB        | NA18550       | Lies far from CHB cluster in comparisons with East Asian populations |
| CHB        | NA18628       | Lies far from CHB cluster in comparisons with East Asian populations |
| JPT        | NA18976       | Lies intermediate between JPT and the Han Chinese (CHB/CHS) cluster |
| MXL        | NA19648       | Lies far from MXL cluster and within the CLM/PUR clusters |
| MXL        | NA19679       | Lies far from MXL cluster and within the CLM/PUR clusters |
| GBR        | HG00116       | Lies far from GBR cluster in comparisons with European and East Asian populations |
| GBR        | HG00120       | Lies far from GBR cluster in comparisons with European and East Asian populations |
| CHS        | HG00475       | Lies far from CHS cluster in comparisons with East Asian populations |
## Additional File 2: Weighted Likelihood Inference of Autozygosity

| Population | Sample ID | Description |
|------------|-----------|-------------|
| CHS Han Chinese (Southern) | HG00500 | Lies far from CHS cluster in comparisons with East Asian populations |
| CHS Han Chinese (Southern) | HG00542 | Lies far from CHS cluster in comparisons with East Asian populations |
| CLM Colombian | HG01342 | Lies far from CLM cluster in comparisons with European, East Asian, and Admixed populations |
| CLM Colombian | HG01390 | Lies far from CLM cluster in comparisons with European, East Asian, and Admixed populations |
| CLM Colombian | HG01462 | Lies far from CLM cluster in comparisons with European, East Asian, and Admixed populations |
| CLM Colombian | HG01485 | Lies far from CLM cluster in comparisons with European, East Asian, and Admixed populations |
| CLM Colombian | HG01551 | Lies far from CLM cluster in comparisons with European, East Asian, and Admixed populations |
| PUR Puerto Rican | HG01108 | Lies far from PUR cluster and within ASW/ACB clusters |
| PUR Puerto Rican | HG01242 | Lies far from PUR cluster and within ASW/ACB clusters |
| PUR Puerto Rican | HG01063 | Clusters with HG01108 and HG01242 and apart from the PUR cluster |
| PEL Peruvian | HG02006 | Lies far from PEL cluster in all comparisons |
| KHV Kinh | HG02122 | Lies intermediate between KHV and the Chinese (CHB/CHS/CDX) cluster |
| KHV Kinh | HG02029 | Lies intermediate between KHV and CHS clusters |
| KHV Kinh | HG02032 | Lies intermediate between KHV and CHS clusters |
| KHV Kinh | HG02082 | Lies intermediate between KHV and CHS clusters |
| ACB Afro-Caribbean | HG02429 | Lies far from ACB cluster in all comparisons except with MXL |
| BEB Bengali | HG04161 | Lies far from BEB cluster in comparisons with European and East Asian populations |
| BEB Bengali | HG04162 | Lies far from BEB cluster in comparisons with European and East Asian populations |
| ESN Esan | HG03343 | Lies far from ESN cluster in comparisons with African, European, and East Asian populations |
| ESN Esan | HG03352 | Lies far from ESN cluster in comparisons with African, European, and East Asian populations |
| ESN Esan | HG03366 | Lies far from ESN cluster in comparisons with African, European, and East Asian populations |
| GWD Gambian | HG02610 | Lies far from GWD cluster in comparisons with European and East Asian populations |
| GWD Gambian | HG02624 | Lies far from GWD cluster in comparisons with European and East Asian populations |
| GWD Gambian | HG02642 | Lies far from GWD cluster in comparisons with European and East Asian populations |
| GWD Gambian | HG02666 | Lies far from GWD cluster in comparisons with European and East Asian populations |
| MSL Mende | HG03449 | Lies far from MSL cluster in comparisons with African, European, and East Asian populations |
| MSL Mende | HG03464 | Lies far from MSL cluster in comparisons with African, European, and East Asian populations |
| MSL Mende | HG03469 | Lies far from MSL cluster in comparisons with African, European, and East Asian populations |
| MSL Mende | HG03478 | Lies far from MSL cluster in comparisons with African, European, and East Asian populations |
| MSL Mende | HG03484 | Lies far from MSL cluster in comparisons with African, European, and East Asian populations |
| STU Sri Lankan | HG03898 | Lies far from MSL cluster in comparisons with African, European, and East Asian populations |
### Additional File 2: Weighted Likelihood Inference of Autozygosity

|   | Population   | Sample ID   | Autozygosity Status                  |
|---|--------------|-------------|--------------------------------------|
| STU | Sri Lankan   | HG03955     | Lies far from MSL cluster in comparisons with African, European, and East Asian populations |
| STU | Sri Lankan   | HG03991     | Lies far from MSL cluster in comparisons with African, European, and East Asian populations |
| LWK | Luhya        | NA19332     | Female with ~100% homozygosity on X chromosome |
| TSI | Toscani      | NA20506     | Female with ~100% homozygosity on X chromosome |
| TSI | Toscani      | NA20530     | Female with ~100% homozygosity on X chromosome |
| TSI | Toscani      | NA20533     | Female with ~100% homozygosity on X chromosome |
| FIN | Finnish      | HG00361     | Female with ~100% homozygosity on X chromosome |
| ESN | Esan         | HG03511     | Female with ~100% homozygosity on X chromosome |