

SUPPLEMENTARY DATA

Longevity vs. Healthy Longevity: Different Outcomes Underlain by Different Mechanisms

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Supplementary Materials

Supplementary 1. Samples filtration details.

All sequenced samples were screened for cross-contamination (i.e., the presence of another individual's DNA). Contamination levels were assessed using the allele ratio (AR) metric, as described by Dallavilla et al. [Dallavilla T. et al. *A fast, reliable and easy method to detect within-species DNA contamination*. *Acta Bio Medica Atenei Parm.* 2020; 91(Suppl 13): e2020019]. Using bcftools v1.21 (as of September 12, 2024) [29], we calculated the ratio of reads supporting one of the two alleles at biallelic positions relative to the total read count at that position, along with associated metrics. The applicability of this approach was demonstrated in a study by our colleagues, Feliz et al. [Feliz N.V. et al. *Experimental Evaluation of the Possibility to Detect Cross-Contaminated DNA Samples Based on Genetic Data*. *Russ. J. Genet.* 2023; 59(7): 719–728]. Samples with high contamination levels were excluded from further analysis.

For each sample, we also bioinformatically determined the Rh factor (based on RHD gene coverage) and sex (using DRAGEN's built-in "Ploidy estimator" tool). These results were cross-checked with the information provided in the patient questionnaires. Discrepancies between the bioinformatics analysis and the questionnaire data prompted further investigation and, in some cases, led to the exclusion of the sample from the database.

We screened all samples for duplicates using PICARD CrosscheckFingerprints v2.26.11. When duplicate samples were identified, we cross-referenced the donor questionnaires. If the sequenced samples were confirmed to originate from the same donor, only the sample with the highest quality metrics (average alignment coverage over the genome $\geq 30x$, GC content 38–40%, mapped reads $> 98\%$, duplicated reads $\leq 12\%$) was retained in the database. If the questionnaire information did not match, both samples were excluded.

Additionally, we calculated relatedness among samples using the kinship coefficient [Manichaikul A. et al. *Robust relationship inference in genome-wide association studies*. *Bioinformatics.* 2010; 26(22): 2867–2873]. For this calculation, we used the "FP_SNP.txt" variant set from the GRAF software [Jin Y. et al. *GRAF-pop: A Fast Distance-Based Method To Infer Subject Ancestry from Multiple Genotype Datasets Without Principal Components Analysis*. *G3 Genes|Genomes|Genetics.* 2019; 9(8): 2447–2461]. This set includes 10,000 genetic variants and is designed to identify duplicate samples and relatedness in large datasets [Jin Y. et al. *Quickly identifying identical and closely related subjects in large databases using genotype data*. *PLoS ONE.* 2017; 12(6): e0179106]. Pairwise calculations were performed for all sequenced samples, and the results were compared with the donor questionnaire data. Samples with discrepancies between computed and reported information were excluded from the database. To further assess ancestry and relatedness, we performed Y-chromosome and mtDNA typing using Yleaf v2.2 (March 16, 2020) and HaploGrep2 v2.2.5 (May 6, 2020), respectively.

Thus, only samples meeting the following criteria were included in the analysis:

- No contamination with another individual's DNA,
- Bioinformatics results (sex, Rh factor, relatedness) consistent with questionnaire data,
- No duplicates.

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Supplementary Table 1. Permutation feature importance for the PGS for longevity (random forest).

| Predictor | Permutation feature importance |
|-------------------------|--------------------------------|
| Sex | 0,087017855 |
| chr21 44286154 G C | 0,016483372 |
| chr5 61282896 ATACATG A | 0,013725167 |
| chr19 44908684 T C | 0,012195159 |
| chr1 7739222 A C | 0,012075964 |
| chr14 66984851 T G | 0,010999028 |
| chr5 152479903 G A | 0,0102969 |
| chr5 152479947 C G | 0,006840187 |
| chr5 152479860 C T | 0,006562267 |
| chr15 97195357 G C | 0,006334595 |
| chr2 120729349 G A | 0,005933963 |
| chr2 195012206 G A | 0,005552589 |
| chr19 44906745 G A | 0,005397087 |
| chr21 39677947 C G | 0,005310362 |
| chr4 107371106 G C | 0,005179511 |
| chr5 152479904 G T | 0,005105346 |
| chr15 51385831 A G | 0,004993572 |
| chr2 195019201 T C | 0,004940692 |
| chr19 44912678 G T | 0,00485263 |
| chr7 21246094 T A | 0,004806823 |
| chr2 195012780 C T | 0,004732533 |
| chr2 32501390 G T | 0,00471783 |
| chr19 44912456 G A | 0,004671329 |
| chr8 5644245 T C | 0,004534557 |
| chr2 195014152 TA T | 0,004418639 |
| chr10 132913337 G T | 0,004403473 |
| chr15 97178617 A T | 0,004381388 |
| chr7 121795684 T A | 0,004376826 |
| chr2 195011720 C A | 0,004297601 |
| chr21 35583167 C CA | 0,004287828 |
| chr15 97194729 C G | 0,004219787 |
| chr2 153479660 G A | 0,00387068 |
| chr20 291796 G A | 0,003813418 |
| chr2 195014826 C A | 0,003755558 |
| chr12 2951822 A G | 0,003748614 |
| chr4 106606538 G A | 0,003615704 |
| chr20 296976 C T | 0,003456427 |
| chr20 291169 TTCTC T | 0,00344264 |
| chr21 35568721 A G | 0,003441056 |
| chr12 2951608 A G | 0,003425002 |
| chr2 45352852 A G | 0,003403967 |
| chr17 49941182 CA C | 0,003397428 |
| chr15 97221677 C T | 0,003360997 |
| chr7 8083968 C A | 0,003343997 |
| chr2 153409390 A C | 0,003281478 |
| chr1 192791713 G A | 0,003156139 |
| chr2 204971350 A T | 0,003100439 |
| chr16 6123701 C T | 0,003018025 |
| chr12 2948970 T A | 0,002972988 |
| chr1 192751959 C T | 0,002930848 |

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|----------------------|-------------|
| chr4 171903500 C G | 0,002929484 |
| chr15 95605210 G C | 0,002860544 |
| chr20 297051 C G | 0,002828802 |
| chr14 27988266 A C | 0,002794941 |
| chr3 123622928 A G | 0,002766189 |
| chr5 120592979 G A | 0,002761071 |
| chr1 230581065 A G | 0,002748541 |
| chr2 204976468 G A | 0,0027409 |
| chr6 37059185 T A | 0,002718604 |
| chr15 97203483 C T | 0,002695014 |
| chr7 8090098 G A | 0,002658343 |
| chr6 150650169 C T | 0,002648444 |
| chr16 6108260 A G | 0,002641933 |
| chr21 39046376 T C | 0,002579099 |
| chr17 13097235 A G | 0,002569842 |
| chr17 64338567 AT A | 0,002548702 |
| chr1 230630625 AAG A | 0,002502962 |
| chr2 153482195 A G | 0,002498757 |
| chr2 194983029 G A | 0,002482642 |
| chr3 113494646 C CA | 0,002473434 |
| chr16 6124794 G C | 0,002473289 |
| chr14 27989796 A C | 0,002416985 |
| chr16 6118101 G A | 0,002397981 |
| chr1 232649139 G C | 0,002387204 |
| chr6 9164502 A G | 0,002380864 |
| chr1 24897830 T C | 0,002364778 |
| chr7 24400646 T G | 0,002334129 |
| chr2 237352058 T A | 0,00232255 |
| chr19 44919689 A G | 0,002283697 |
| chr16 6097644 A G | 0,002277647 |
| chr2 195043993 C T | 0,002262539 |
| chr5 16963042 C T | 0,00225118 |
| chr1 77829821 G A | 0,002239812 |
| chr5 115410779 G T | 0,002231547 |
| chr3 49696771 C T | 0,002231302 |
| chr3 146366380 A C | 0,002229208 |
| chr20 297191 C T | 0,002217388 |
| chr2 77220386 C T | 0,002207026 |
| chr7 112393603 A T | 0,002193272 |
| chr20 52871483 G A | 0,002189424 |
| chr15 95603185 A C | 0,002187336 |
| chr3 1467110 T C | 0,002164675 |
| chr7 89107878 A G | 0,00216383 |
| chr13 37332098 T G | 0,0021519 |
| chr2 144467504 A G | 0,002151569 |
| chr16 6103850 C T | 0,002138454 |
| chr6 63439538 A T | 0,002096595 |
| chr9 123404417 T A | 0,002093241 |
| chr5 152479843 C T | 0,002091624 |
| chr9 38122775 T C | 0,002055873 |
| chr19 44921094 A T | 0,002054419 |
| chr7 112408714 C G | 0,002052094 |
| chr7 116680985 T C | 0,002028752 |
| chr22 42698334 G C | 0,002016293 |

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|--------------------------|-------------|
| chr15 25581859 C G | 0,002004094 |
| chr13 37328671 C T | 0,001985822 |
| chr20 55003272 C T | 0,001979896 |
| chr19 40822291 C T | 0,001955012 |
| chr14 51671038 T G | 0,001941906 |
| chr12 2951058 A C | 0,001924819 |
| chr16 3967566 T A | 0,001922557 |
| chr6 23366836 C T | 0,001921769 |
| chr10 110494824 G A | 0,001918773 |
| chr22 37750152 CAGAG C | 0,001913735 |
| chr2 193879986 T C | 0,001895662 |
| chr7 32240420 G A | 0,00189422 |
| chr15 97176173 C T | 0,001887989 |
| chr19 40823241 C CTGT | 0,00187765 |
| chr2 149083957 C CA | 0,001877342 |
| chr19 44918903 C G | 0,001870104 |
| chr4 10460338 A ACC | 0,001868669 |
| chr10 122074661 C T | 0,001859776 |
| chr3 1449151 C T | 0,001853054 |
| chr7 112407290 T C | 0,001851068 |
| chr11 78689474 C CT | 0,001850893 |
| chr11 44524101 A G | 0,00184379 |
| chr19 44919589 G A | 0,001841906 |
| chr22 42698919 G A | 0,001839326 |
| chr5 167435413 C T | 0,001832015 |
| chr7 9640892 C T | 0,001828375 |
| chr12 118587670 G A | 0,001826558 |
| chr2 144465588 C T | 0,001824547 |
| chr12 95697282 A G | 0,001821098 |
| chr7 24392336 T C | 0,001820394 |
| chr13 37330569 C T | 0,001819279 |
| chr16 3970731 C T | 0,001802857 |
| chr2 195019527 T C | 0,001797666 |
| chr5 167434063 A T | 0,001789973 |
| chr14 27314351 G GGCCAAA | 0,001789375 |
| chr1 109272630 A G | 0,001774385 |
| chr5 115009504 T C | 0,001772069 |
| chr19 36161845 C T | 0,001759754 |
| chr2 144466305 T C | 0,001758846 |
| chr7 112393732 T C | 0,001751955 |
| chr1 230630665 A G | 0,001751008 |
| chr5 167434683 G A | 0,001750789 |
| chr21 15412245 C CAT | 0,001750034 |
| chr5 167433117 A T | 0,001744167 |
| chr16 6122772 G A | 0,001742937 |
| chr2 494891 T C | 0,001735234 |
| chr7 116680832 C T | 0,001726605 |
| chr11 78702819 C T | 0,001711428 |
| chr2 153485761 A C | 0,001711021 |
| chr7 112410382 A G | 0,001706667 |
| chr5 167434758 A G | 0,001681205 |
| chr20 47769039 C T | 0,001678579 |
| chr10 67637008 C A | 0,001674683 |
| chr13 37350785 G T | 0,001664132 |

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| chr2 498698 C G | 0,001662474 |
| chr12 2952548 T G | 0,001655357 |
| chr2 499284 T C | 0,001648633 |
| chr4 95109793 T C | 0,001636414 |
| chr15 25573782 C G | 0,001633241 |
| chr3 55125536 A G | 0,001628983 |
| chr2 144466053 C T | 0,001628921 |
| chr2 195032546 AAAG A | 0,001626662 |
| chr10 131245991 G C | 0,001614119 |
| chr14 27315233 T G | 0,001612639 |
| chr8 5657395 C G | 0,00160244 |
| chr5 115008684 G A | 0,001596421 |
| chr19 40819294 T TA | 0,001588353 |
| chr3 5303506 G A | 0,001587507 |
| chr16 82695151 C T | 0,001574111 |
| chr22 42696845 A C | 0,001571248 |
| chr22 37874995 G A | 0,001570388 |
| chr2 195032251 A G | 0,001567019 |
| chr6 23360754 G A | 0,001558937 |
| chr3 182606184 A T | 0,001555492 |
| chr15 85940476 C T | 0,001551813 |
| chr10 125279703 T C | 0,001548235 |
| chr4 127540547 T C | 0,001539623 |
| chr11 44500979 G A | 0,001537999 |
| chr10 7190778 G A | 0,001534842 |
| chr2 195022107 T G | 0,001533781 |
| chr2 111058015 T A | 0,001529679 |
| chr12 95714434 C T | 0,001522849 |
| chr10 60279896 G C | 0,001509695 |
| chr11 78719400 T TATATA | 0,001503429 |
| chr9 16845532 T C | 0,001496481 |
| chr10 73672061 A AT | 0,00149612 |
| chr2 193860737 T C | 0,00147222 |
| chr3 135048582 C T | 0,001470198 |
| chr6 16050378 G C | 0,001469134 |
| chr11 78726770 C CT | 0,001464326 |
| chr1 109279386 G T | 0,001461439 |
| chr2 8380661 AAG A | 0,001459046 |
| chr1 3422621 G A | 0,001458371 |
| chr14 27298173 G T | 0,00145797 |
| chr10 7190307 G A | 0,001453331 |
| chr7 24421105 G A | 0,001453215 |
| chr17 75577062 GA G | 0,001450865 |
| chr3 184633518 G A | 0,001443525 |
| chr12 23062303 GAAGA G | 0,001440756 |
| chr13 37346522 C T | 0,001434437 |
| chr16 6098029 A G | 0,001426638 |
| chr10 118006870 C T | 0,001410097 |
| chr3 21681827 G GA | 0,001403586 |
| chr2 167908526 G A | 0,001399326 |
| chr4 171922535 AT A | 0,001398115 |
| chr3 146245489 G A | 0,001391918 |
| chr14 27345691 G T | 0,001391752 |
| chr2 144465675 G A | 0,001386126 |

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| chr10 117997312 T C | 0,001376332 |
| chr19 46637798 T A | 0,001373642 |
| chr1 109274623 C T | 0,001372906 |
| chr7 24420917 T G | 0,001370955 |
| chr2 205168316 A T | 0,001363998 |
| chr5 103576593 A G | 0,001362794 |
| chr16 15219642 G T | 0,001358363 |
| chr4 127539873 A G | 0,001350191 |
| chr3 49398273 C T | 0,001349534 |
| chr20 47760554 C A | 0,001346526 |
| chr12 95697577 A T | 0,001339613 |
| chr19 44750325 G A | 0,001333274 |
| chr2 194998703 G A | 0,001330219 |
| chr4 188602666 A AC | 0,001316975 |
| chr10 87420173 A G | 0,001315804 |
| chr14 27346327 A C | 0,001307478 |
| chr19 40818173 G A | 0,001304913 |
| chr11 58247417 C A | 0,001293486 |
| chr1 3686723 G A | 0,001291642 |
| chr7 28306644 T C | 0,001286828 |
| chr16 70684409 T TC | 0,001286756 |
| chr11 81072837 C T | 0,001285613 |
| chr1 237833280 A AT | 0,001284087 |
| chr16 68303895 T A | 0,001279544 |
| chr16 78634173 C T | 0,001276702 |
| chr6 41201941 G T | 0,001272747 |
| chr6 159727378 G A | 0,001268212 |
| chr2 193860742 A G | 0,001267619 |
| chr3 135049171 C T | 0,001267417 |
| chr18 73741021 T C | 0,001265296 |
| chr4 106540161 T C | 0,001265032 |
| chr16 72691858 AAAAC A | 0,001263613 |
| chr1 226411585 G GA | 0,001262759 |
| chr2 8381150 G A | 0,00126266 |
| chr11 81073165 C T | 0,001258733 |
| chr13 37332174 T A | 0,001243483 |
| chr1 52730842 T TA | 0,001242734 |
| chr20 11552689 A G | 0,001242067 |
| chr8 91826427 C T | 0,001232615 |
| chr2 19588450 C T | 0,001232112 |
| chr12 95706474 G A | 0,001222928 |
| chr4 127533455 G A | 0,001220124 |
| chr5 116920846 G A | 0,001219726 |
| chr2 111052260 T C | 0,001217459 |
| chr9 41482376 C T | 0,001214436 |
| chr2 193834381 A C | 0,001214381 |
| chr19 44892457 T C | 0,001212831 |
| chr18 73740233 G C | 0,001212072 |
| chr10 60175146 C A | 0,001209518 |
| chr12 54063491 A AGT | 0,001203052 |
| chr2 195012324 G C | 0,001200299 |
| chr7 24416609 G A | 0,001193564 |
| chr2 19586059 C T | 0,001191031 |
| chr4 106760744 C T | 0,001190948 |

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| chr6 16475605 T A | 0,001190132 |
| chr5 115003061 C A | 0,001188609 |
| chr4 127543659 AG A | 0,001187081 |
| chr1 109276674 C A | 0,001179376 |
| chr4 188111068 G A | 0,001178518 |
| chr9 38114860 C CA | 0,001171387 |
| chr16 82703090 C G | 0,001167657 |
| chr19 44888997 C T | 0,001161888 |
| chr4 106786092 A T | 0,001161729 |
| chr10 67680091 C A | 0,001157374 |
| chr2 193850604 T C | 0,001157296 |
| chr7 40727165 T G | 0,001154232 |
| chr2 167909170 A G | 0,001153979 |
| chr12 54052659 T G | 0,001151326 |
| chr2 193841832 A G | 0,001148241 |
| chr11 74340999 G C | 0,001127091 |
| chr7 521813 G A | 0,001124456 |
| chr2 111060228 T C | 0,001123633 |
| chr20 47769038 G T | 0,001123144 |
| chr4 127546726 G A | 0,00112262 |
| chr11 74510778 T TG | 0,001121814 |
| chr5 150298733 A G | 0,00111956 |
| chr6 9169258 C G | 0,001118461 |
| chr2 111060950 A G | 0,001112577 |
| chr4 188602367 A ACT | 0,001108842 |
| chr10 117984213 C T | 0,001105505 |
| chr11 44502208 T A | 0,001101822 |
| chr4 106702296 C T | 0,001101097 |
| chr2 195018718 T C | 0,001099623 |
| chr7 522076 C G | 0,001092186 |
| chr1 226421638 A C | 0,001086991 |
| chr4 127501245 G A | 0,001084243 |
| chr4 188111111 A ATATT | 0,001083018 |
| chr2 8380491 A G | 0,001082643 |
| chr9 78779946 A G | 0,001081514 |
| chr2 193843546 GA G | 0,001080867 |
| chr2 193222506 C T | 0,001080803 |
| chr4 188111627 G A | 0,00108065 |
| chr4 188111803 C T | 0,00108012 |
| chr8 60051152 C A | 0,001079146 |
| chr2 111068709 C T | 0,001074787 |
| chr4 188602571 C CAA | 0,001073545 |
| chr13 38847631 T C | 0,001070134 |
| chr6 37197609 G A | 0,001054591 |
| chr2 195028848 G A | 0,001052139 |
| chr4 25967903 G A | 0,001050347 |
| chr20 57721771 G A | 0,001045693 |
| chr19 40821881 T C | 0,001044886 |
| chr20 11551246 C T | 0,001037163 |
| chr2 111057740 A G | 0,001034019 |
| chr4 155912369 C T | 0,001027644 |
| chr7 24401906 T C | 0,001026329 |
| chr9 38090224 G A | 0,001017174 |
| chr6 22077868 G A | 0,00101707 |

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| chr6 29298720 G A | 0,001010059 |
| chr4 106864721 G A | 0,001007744 |
| chr4 188112316 C G | 0,001006903 |
| chr4 188111787 A G | 0,001002699 |
| chr16 66326150 G A | 0,000997256 |
| chr12 8625415 C T | 0,00099598 |
| chr11 65707180 CTT C | 0,000993718 |
| chr2 19585164 C T | 0,000979041 |
| chr2 193852578 CT C | 0,000973238 |
| chr16 82706623 C T | 0,000966462 |
| chr19 44892962 C T | 0,000962047 |
| chr4 188110522 C T | 0,000959198 |
| chr2 193857043 A G | 0,00095778 |
| chr10 87421320 G A | 0,000951487 |
| chr2 111068812 C T | 0,000943405 |
| chr10 67935982 T C | 0,000939973 |
| chr10 68034982 C T | 0,00093907 |
| chr4 127468740 T C | 0,000935448 |
| chr6 16300593 A C | 0,000934026 |
| chr16 66321930 T A | 0,000931993 |
| chr9 18943812 C T | 0,000929123 |
| chr7 24421015 C G | 0,000926986 |
| chr6 16488202 C T | 0,000924359 |
| chr3 147998711 T C | 0,000920822 |
| chr10 67233854 G C | 0,000912681 |
| chr9 78804491 C T | 0,000911997 |
| chr2 19585146 C G | 0,00091178 |
| chr9 75657928 G A | 0,000906459 |
| chr4 25970593 A G | 0,000904973 |
| chr19 44891712 T G | 0,000902184 |
| chr16 70669587 G A | 0,000898487 |
| chr4 25973489 C T | 0,00089779 |
| chr19 20087874 A G | 0,000891221 |
| chr21 35871495 T C | 0,000890138 |
| chr3 75965499 G A | 0,000889078 |
| chr9 78784485 C T | 0,000888032 |
| chr4 106595630 T C | 0,00088633 |
| chr12 54058214 G C | 0,000885446 |
| chr2 111067015 A G | 0,000883502 |
| chr16 75813049 CT C | 0,000880051 |
| chr4 127499115 G C | 0,00087757 |
| chr11 19703993 G A | 0,000874673 |
| chr9 108163090 C T | 0,000872025 |
| chr10 87726727 T C | 0,00087009 |
| chr4 188112110 G A | 0,000867418 |
| chr9 78784938 C T | 0,000866993 |
| chr16 82713405 G A | 0,000865905 |
| chr14 33066812 G T | 0,000865879 |
| chr19 54855608 TCTC T | 0,000864732 |
| chr9 5906186 T TA | 0,000863467 |
| chr4 190041312 G C | 0,000858712 |
| chr4 106658282 G A | 0,000857152 |
| chr10 124658836 C G | 0,000855545 |
| chr2 195006046 C A | 0,000854765 |

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| | |
|------------------------|-------------|
| chr19 44909521 CT C | 0,000854211 |
| chr4 127468627 T C | 0,000853893 |
| chr9 78785435 C T | 0,000852736 |
| chr3 131953645 C T | 0,000849697 |
| chr16 78628198 G A | 0,000849341 |
| chr4 188112365 C T | 0,000847286 |
| chr3 182774673 G T | 0,000847175 |
| chr6 11193627 G A | 0,000846323 |
| chr2 8369906 G A | 0,000842076 |
| chr7 90578951 T TATA | 0,000837313 |
| chr12 95697179 C CA | 0,000834057 |
| chr4 188602574 C A | 0,000831205 |
| chr12 88825399 A G | 0,000831063 |
| chr2 8388491 G C | 0,000829854 |
| chr16 66322465 G A | 0,000824816 |
| chr6 11194743 G T | 0,000824348 |
| chr4 188112326 C T | 0,000822374 |
| chr3 123632227 C T | 0,000821417 |
| chr17 7846692 G C | 0,00082117 |
| chr9 78783420 C G | 0,000820966 |
| chr11 19683686 C T | 0,000819799 |
| chr8 59894757 C A | 0,000817453 |
| chr16 78628189 C T | 0,000817167 |
| chr2 195004544 T C | 0,000816465 |
| chr16 78616559 C A | 0,000816342 |
| chr6 90850414 T C | 0,000810481 |
| chr2 8375645 A T | 0,00080437 |
| chr16 78631069 A G | 0,000803959 |
| chr9 123394981 C T | 0,000803183 |
| chr2 111059463 T C | 0,000801194 |
| chr7 12207894 T G | 0,000798917 |
| chr16 66321878 A G | 0,000796662 |
| chr3 132730054 GAT G | 0,000795821 |
| chr2 8373938 G T | 0,000794979 |
| chr2 195002375 A T | 0,00079416 |
| chr1 8891970 C T | 0,00079356 |
| chr8 59804399 G A | 0,000792164 |
| chr7 24390756 C T | 0,000791696 |
| chr6 170450076 G T | 0,000789405 |
| chr7 160956 A G | 0,000788586 |
| chr6 11192672 C T | 0,000788282 |
| chr7 89551760 G GTA | 0,000786343 |
| chr2 111052443 C G | 0,00078586 |
| chr11 8700066 G T | 0,000785273 |
| chr16 66327250 G A | 0,000785101 |
| chr22 25085739 G A | 0,000780907 |
| chr4 155908871 A G | 0,000779218 |
| chr12 42563194 A T | 0,000774461 |
| chr1 25066140 T TCTCCC | 0,000774317 |
| chr4 188602744 G A | 0,000773496 |
| chr13 75981352 G C | 0,000771885 |
| chr2 8372282 C G | 0,000769159 |
| chr3 129417341 C A | 0,000766775 |
| chr10 87426834 A G | 0,000766548 |

SUPPLEMENTARY DATA

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| chr7 173155 A G | 0,00076317 |
| chr9 78802548 T G | 0,000762609 |
| chr16 20481621 G A | 0,000762008 |
| chr10 124665923 C T | 0,000761585 |
| chr7 24401750 C T | 0,000761443 |
| chr2 8373158 A G | 0,000759494 |
| chr7 24399983 C T | 0,000756264 |
| chr7 24392535 G A | 0,000753426 |
| chr7 118558957 T A | 0,000753133 |
| chr16 78626011 A C | 0,000752834 |
| chr4 155913776 T C | 0,00075271 |
| chr6 170450078 C T | 0,00075261 |
| chr4 190041082 G A | 0,000749564 |
| chr7 89546963 GAA G | 0,000743458 |
| chr10 68089587 C T | 0,000742089 |
| chr7 148227229 A G | 0,000736451 |
| chr2 195013623 CTGAG C | 0,000731254 |
| chr2 193840042 G A | 0,000724327 |
| chr2 8378569 A T | 0,00071706 |
| chr4 160743071 G A | 0,000707677 |
| chr17 31889490 G A | 0,00070569 |
| chr13 51239832 GTAGA G | 0,00070468 |
| chr7 24405158 C T | 0,000703251 |
| chr10 87423284 A G | 0,000702514 |
| chr4 106650766 C T | 0,000701484 |
| chr6 29160931 C A | 0,000700105 |
| chr16 66326599 A G | 0,000695869 |
| chr3 135052344 G A | 0,000693735 |
| chr7 194618 C T | 0,00069364 |
| chr7 118293784 C G | 0,000693012 |
| chr14 25000109 C T | 0,000692241 |
| chr7 188634 C A | 0,000691266 |
| chr7 164282 A G | 0,000688196 |
| chr19 51797963 C A | 0,000687141 |
| chr7 24380807 CAT C | 0,000682733 |
| chr7 143680 G A | 0,000677887 |
| chr7 118510547 G T | 0,000674246 |
| chr7 112444742 A T | 0,000672189 |
| chr1 8501227 C T | 0,000671296 |
| chr10 87425405 A G | 0,000671185 |
| chr7 148229402 G A | 0,000666893 |
| chr3 132005102 T C | 0,00066687 |
| chr11 73508073 C T | 0,000666497 |
| chr2 111067944 A G | 0,000666262 |
| chr2 215972305 T TA | 0,00066427 |
| chr2 111060806 T C | 0,000662909 |
| chr9 78790332 C G | 0,000662146 |
| chr7 24416337 C T | 0,000659735 |
| chr7 24399995 C T | 0,000658408 |
| chr2 195011181 A G | 0,000657432 |
| chr2 205175586 G A | 0,000657077 |
| chr6 11194828 C G | 0,000656209 |
| chr9 78806155 T C | 0,00065527 |
| chr9 78796836 A G | 0,000653465 |

SUPPLEMENTARY DATA

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| chr4 25969855 C T | 0,000651397 |
| chr1 101229388 A G | 0,000650675 |
| chr4 188973055 C CT | 0,000649447 |
| chr7 24403488 G C | 0,000647052 |
| chr11 73373989 T C | 0,000642397 |
| chr9 108163459 C CTG | 0,000642287 |
| chr4 127477661 T A | 0,0006387 |
| chr18 57932503 AC A | 0,000638643 |
| chr9 78801847 C T | 0,000635659 |
| chr11 73516316 T C | 0,000632407 |
| chr7 24403908 C G | 0,00063231 |
| chr2 111068715 G C | 0,000631055 |
| chr9 123389887 C T | 0,00062806 |
| chr4 155913754 T G | 0,00062366 |
| chr16 50820507 G A | 0,000622847 |
| chr11 19691449 C T | 0,000619951 |
| chr7 90575986 A G | 0,000618148 |
| chr14 53511385 A AAAAC | 0,000613679 |
| chr4 155913072 T C | 0,000605283 |
| chr2 8373697 C T | 0,000597683 |
| chr10 67265630 C T | 0,000590917 |
| chr9 78807342 G A | 0,00059045 |
| chr2 8377479 C G | 0,000587049 |
| chr7 24416362 G A | 0,000585361 |
| chr8 3497518 T C | 0,000581595 |
| chr16 82710576 T A | 0,000578648 |
| chr16 82671348 C G | 0,000578636 |
| chr10 124711816 T C | 0,000577597 |
| chr10 87425075 T C | 0,00057714 |
| chr2 8369450 T C | 0,000576192 |
| chr9 78784551 A G | 0,000574288 |
| chr2 8378146 A G | 0,000572916 |
| chr16 78615850 A C | 0,000572226 |
| chr10 124662511 C A | 0,000567688 |
| chr14 53517725 C T | 0,000565987 |
| chr11 73591723 T C | 0,000565354 |
| chr11 73513376 AT A | 0,000554217 |
| chr8 3473553 A G | 0,000554086 |
| chr9 78796164 G A | 0,000551942 |
| chr10 124664398 C G | 0,000550665 |
| chr10 124679399 C T | 0,000550276 |
| chr3 129499420 AAGC A | 0,000541189 |
| chr13 51236817 A G | 0,00053718 |
| chr9 101495392 C G | 0,000536716 |
| chr4 127545545 A G | 0,00053473 |
| chr15 74583031 C CA | 0,000531177 |
| chr16 66329136 G A | 0,000531015 |
| chr7 24403292 G A | 0,000523435 |
| chr8 3471792 A G | 0,000518768 |
| chr4 106700050 TTTTG T | 0,000518641 |
| chr11 73537628 A C | 0,000513413 |
| chr10 124679589 A G | 0,000513237 |
| chr10 87422258 C CT | 0,000511298 |
| chr3 123486696 G A | 0,000508099 |

SUPPLEMENTARY DATA

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| chr10 87437746 C T | 0,000507636 |
| chr16 66328334 T C | 0,000507505 |
| chr3 123563679 A T | 0,000507141 |
| chr16 89407985 G A | 0,000506322 |
| chr9 78793387 C T | 0,000503601 |
| chr14 53517990 C T | 0,000503096 |
| chr10 87437236 C G | 0,000501956 |
| chr9 78787709 T C | 0,000501507 |
| chr16 78627486 T G | 0,000500767 |
| chr16 82678132 A C | 0,000496644 |
| chr14 53513512 T C | 0,000493848 |
| chr19 20085282 C T | 0,000493159 |
| chr1 100876005 A C | 0,000492102 |
| chr9 78798783 A G | 0,00049091 |
| chr11 73538333 AC A | 0,000490841 |
| chr1 173561854 CAG C | 0,000487927 |
| chr10 87415334 T A | 0,000486415 |
| chr7 140707 C G | 0,00048559 |
| chr9 78785970 C T | 0,000484021 |
| chr7 522862 T C | 0,000483353 |
| chr11 73377449 G A | 0,000482 |
| chr7 24398790 A G | 0,000478222 |
| chr9 78792317 G A | 0,000477153 |
| chr7 161290 C T | 0,000476768 |
| chr3 123997777 A C | 0,000469495 |
| chr9 78790172 G C | 0,00046905 |
| chr16 82677828 G C | 0,000465291 |
| chr7 24414414 A G | 0,000465154 |
| chr9 78793915 A C | 0,000461871 |
| chr11 73496903 A ACACG | 0,000455433 |
| chr3 129516804 G C | 0,000455017 |
| chr14 53514004 C T | 0,000453745 |
| chr16 82672962 G T | 0,000450467 |
| chr22 27195458 G T | 0,000448785 |
| chr9 78794843 G A | 0,00044558 |
| chr16 82675921 C G | 0,00044556 |
| chr16 82676935 G A | 0,000445291 |
| chr3 182765339 G T | 0,000444462 |
| chr14 53518204 A T | 0,000438876 |
| chr11 73508633 T C | 0,000432456 |
| chr16 82677264 C T | 0,000430318 |
| chr7 82637664 G A | 0,000428938 |
| chr19 44892652 C G | 0,000428214 |
| chr16 82678710 A G | 0,000424665 |
| chr11 73324754 T C | 0,000423605 |
| chr6 29292698 C T | 0,000422784 |
| chr17 31986830 G A | 0,000419856 |
| chr17 32023822 T G | 0,000414328 |
| chr3 28807221 C T | 0,000412075 |
| chr16 66328543 G C | 0,000410717 |
| chr14 53520432 TG T | 0,000410337 |
| chr14 53517773 G A | 0,000408493 |
| chr11 73553611 C T | 0,000408004 |
| chr7 24389290 A G | 0,000400975 |

SUPPLEMENTARY DATA

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| chr7 132919 CCTAT C | 0,000400415 |
| chr6 170450031 C A | 0,000400141 |
| chr10 124690834 T G | 0,0003967 |
| chr9 74659785 T G | 0,000388976 |
| chr7 169091 C T | 0,000387739 |
| chr3 28795938 T C | 0,000387709 |
| chr13 51236376 T G | 0,00038673 |
| chr16 82679161 T A | 0,000381577 |
| chr2 195000320 C T | 0,000379199 |
| chr11 73350187 A T | 0,000377823 |
| chr16 82675874 G C | 0,000373355 |
| chr9 78799274 T A | 0,000373346 |
| chr6 48345856 T TAC | 0,000367089 |
| chr11 36128723 C T | 0,000365455 |
| chr9 78789626 A T | 0,000359969 |
| chr11 73535873 AT A | 0,000359316 |
| chr2 8376809 G T | 0,000358719 |
| chr11 73569910 GA G | 0,000356419 |
| chr15 28737988 G A | 0,000355916 |
| chr19 44891079 T C | 0,00035582 |
| chr16 62754721 G A | 0,000354515 |
| chr10 124689272 G C | 0,000354513 |
| chr10 124703530 G A | 0,000354236 |
| chr10 124706424 C G | 0,000353773 |
| chr14 53521954 T C | 0,000349344 |
| chr11 73584178 CT C | 0,00034587 |
| chr14 53517464 A G | 0,000345161 |
| chr16 82691128 T A | 0,000344003 |
| chr6 18425723 A G | 0,000342569 |
| chr11 54748607 T G | 0,000338921 |
| chr11 73350860 C G | 0,000336062 |
| chr6 23029705 A G | 0,000335513 |
| chr7 130346 C G | 0,000328984 |
| chr11 73579118 A G | 0,000317207 |
| chr10 124720089 G A | 0,000313842 |
| chr11 73533185 C T | 0,000313606 |
| chr10 124693783 C T | 0,000312947 |
| chr11 73549418 A C | 0,000301415 |
| chr8 59945604 A G | 0,000287105 |
| chr10 124661772 A G | 0,000286192 |
| chr11 73374789 T C | 0,000285973 |
| chr9 78798153 T C | 0,000285167 |
| chr11 73561146 A G | 0,000282174 |
| chr7 161547 C T | 0,000278893 |
| chr16 82675875 C G | 0,000274307 |
| chr19 40419251 AGAchrA | 0,000270821 |
| chr6 18460927 A C | 0,000262212 |
| chr11 73572945 T A | 0,000261812 |
| chr11 73561901 T G | 0,000261459 |
| chr13 41399599 ATT A | 0,000257748 |
| chr22 27194733 G T | 0,000250116 |
| chr9 78786721 A G | 0,000249226 |
| chr11 73583433 T C | 0,000239025 |
| chr6 18435483 AG A | 0,000235519 |

SUPPLEMENTARY DATA

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| chr16 79466400 C A | 0,00023542 |
| chr19 2676700 G C | 0,000235035 |
| chr7 33980357 G A | 0,000232616 |
| chr14 65561347 G A | 0,000229502 |
| chr6 35378089 C G | 0,000225596 |
| chr11 73495684 C T | 0,000189786 |
| chr11 73587453 C T | 0,000179882 |
| chr6 18466177 G A | 0,000176925 |
| chr6 35334758 A C | 0,000170719 |
| chr6 18437789 C A | 0,000168546 |
| chr6 18435573 A C | 0,000167348 |
| chr7 23467021 T G | 0,000167058 |
| chr6 35323680 C G | 0,000164135 |
| chr6 18423561 G A | 0,000162941 |
| chr6 18432498 A G | 0,000162367 |
| chr11 73560943 T C | 0,000157757 |
| chr6 18457930 G GT | 0,000157119 |
| chr11 73472957 C T | 0,000154721 |
| chr6 18423847 A G | 0,000154604 |
| chr2 104307765 AT A | 0,000148453 |
| chr10 124703241 G A | 0,000147292 |
| chr11 73404269 A G | 0,000146559 |
| chr10 107913716 C T | 0,00014314 |
| chr1 201156817 A G | 0,000142815 |
| chr11 73422787 CGA C | 0,000139982 |
| chr7 134201 A G | 0,00013672 |
| chr1 201153148 C G | 0,0001318 |
| chr11 73399623 T C | 0,000129495 |
| chr22 16056701 A C | 0,000124928 |
| chr11 73474329 AT A | 0,000123762 |
| chr6 18444045 T C | 0,000122316 |
| chr11 73447074 T C | 0,000120598 |
| chr11 73449544 A G | 0,000112529 |
| chr6 18440891 C CA | 0,000110047 |
| chr6 35363914 ATATAT A | 0,000105381 |
| chr4 35083979 T C | 0,000101333 |
| chr6 35359584 G A | 0,000100403 |
| chr10 124655826 T C | 9,9871E-05 |
| chr6 35373827 C T | 9,98679E-05 |
| chr6 18423517 A G | 9,59735E-05 |
| chr6 18451501 T C | 9,37224E-05 |
| chr6 35368525 G A | 9,31345E-05 |
| chr11 73496472 T C | 9,10037E-05 |
| chr4 35082793 G A | 8,96826E-05 |
| chr11 73430582 C G | 8,84611E-05 |
| chr4 35082023 T A | 8,83191E-05 |
| chr11 73410827 C G | 8,76361E-05 |
| chr4 35047065 TA T | 8,66742E-05 |
| chr6 35325543 A G | 8,43249E-05 |
| chr4 35087605 A G | 8,30303E-05 |
| chr7 23495299 C CA | 8,16498E-05 |
| chr6 18419208 C T | 8,14168E-05 |
| chr6 18418577 G A | 7,54757E-05 |
| chr4 35087162 T C | 7,32098E-05 |

SUPPLEMENTARY DATA

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| chr6 35378810 A T | 7,11928E-05 |
| chr4 35084493 T A | 7,08178E-05 |
| chr6 35325178 G A | 6,60869E-05 |
| chr6 35365000 C T | 6,598E-05 |
| chr11 73425216 A T | 6,39271E-05 |
| chr6 18456996 G A | 6,10924E-05 |
| chr11 73428071 T C | 6,04413E-05 |
| chr4 35084045 A G | 5,57212E-05 |
| chr4 35076273 C T | 5,56318E-05 |
| chr11 73464865 A T | 5,30318E-05 |
| chr4 35081708 A T | 4,88038E-05 |
| chr4 35081959 G A | 4,83761E-05 |
| chr4 35082196 G T | 4,68958E-05 |
| chr11 73413396 A G | 4,38983E-05 |
| chr4 35076137 G A | 4,3451E-05 |
| chr9 136045417 G A | 4,21254E-05 |
| chr4 35085720 C T | 3,77687E-05 |
| chr6 18425109 G A | 3,77561E-05 |
| chr4 35087456 A G | 3,73576E-05 |
| chr4 35064100 A AAT | 3,68888E-05 |
| chr6 35371318 G A | 3,63221E-05 |
| chr6 35377990 C T | 3,42442E-05 |
| chr4 35084363 T A | 3,35948E-05 |
| chr6 18418717 A G | 3,25379E-05 |
| chr7 23507859 A G | 3,09603E-05 |
| chr4 35083272 A G | 2,94146E-05 |
| chr6 18425472 G C | 2,7003E-05 |
| chr4 35083467 G A | 2,55168E-05 |
| chr4 35085184 C A | 2,52622E-05 |
| chr6 35369494 C T | 2,43801E-05 |
| chr4 35077638 T C | 1,86639E-05 |