

Genetic architecture of gene regulation in Indonesian populations identifies QTLs associated with global and local ancestries

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Summary

Lack of diversity in human genomics limits our understanding of the genetic underpinnings of complex traits, hinders precision medicine, and contributes to health disparities. To map genetic effects on gene regulation in the underrepresented Indonesian population, we have integrated genotype, gene expression, and CpG methylation data from 115 participants across three island populations that capture the major sources of genomic diversity in the region. In a comparison with European datasets, we identify eQTLs shared between Indonesia and Europe as well as population-specific eQTLs that exhibit differences in allele frequencies and/or overall expression levels between populations. By combining local ancestry and archaic introgression inference with eQTLs and methylQTLs, we identify regulatory loci driven by modern Papuan ancestry as well as introgressed Denisovan and Neanderthal variation. GWAS colocalization connects QTLs detected here to hematological traits, and further comparison with European datasets reflects the poor overall transferability of GWAS statistics across diverse populations. Our findings illustrate how population-specific genetic architecture, local ancestry, and archaic introgression drive variation in gene regulation across genetically distinct and in admixed populations and highlight the need for performing association studies on non-European populations.

Introduction

As we move into the age of precision medicine, the systematic undersampling of global genetic diversity limits our ability to broadly apply biomedical research efforts across diverse ethnicities and population backgrounds.^{1,2} Indeed, the vast majority of human genomics studies to date have been conducted in individuals with European ancestry, who account for a minority of the global population.³ To gain a comprehensive understanding of the genetic architecture of complex diseases and deliver on the promise of genomic medicine, it is critical to expand human genomics studies into diverse populations. The collection of multi-modal genomic data from traditionally undersampled populations will allow for the mapping of genetic associations with molecular phenotypes and integration with genome-wide association studies (GWASs) to fully understand the degree to which population differences impact genetic architecture.⁴

The Indonesian archipelago is one such undersampled region, absent from all existing large-scale catalogs of human diversity. Genetically and geographically structured, with a genomic cline of Asian to Papuan ancestry stretching from west to east,^{5,6} Indonesia is the fourth largest country in

the world by population. Its tropical location makes it an epicenter of infectious disease diversity both past and present, making it possible that individuals from the region have adapted to local immune challenges over evolutionary time.⁷ We have previously described differences in gene expression and CpG methylation between Indonesian island populations associated with their genome-wide proportions of Papuan ancestry.⁸ To investigate the effects of modern and archaic local ancestry on gene regulation in Indonesians, here we integrate genome-wide genotype data with gene expression and DNA methylation measurements from 115 Indonesian individuals. Using this rich multi-modal dataset, we construct maps of eQTLs and methylQTLs and identify variants contributing to population differences—both within Indonesia and globally—in regulatory architecture.

Material and methods

Ethical approvals and dataset description

All samples were obtained from adult human male subjects. For full information about the new and published samples used in this study, refer to [Tables S1 and S2](#). All samples used in this study

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were previously collected by H.S., J. Stephen Lansing, and an Indonesian team from the Eijkman Institute for Molecular Biology, Jakarta, Indonesia, with the assistance of Indonesian Public Health clinic staff. Collections followed protocols for the protection of human subjects established by institutional review boards at the Eijkman Institute (EIREC #90 and EIREC #126) and the University of Melbourne (Human Ethics Sub-Committee approval 1851639.1). All individuals gave written informed consent for participation in the study. Permission to conduct research in Indonesia was granted by the Indonesian Institute of Sciences and by the Ministry for Research, Technology, and Higher Education. Whole blood sample collection was carried out as described.⁸ The gene expression and methylation data were previously published.⁸

Here, we report two new genomic datasets: (1) 42 samples genotyped with the Illumina Infinium Omni2.5-8 v1.3 BeadChip array, including five Korowai samples from New Guinea, 18 samples from Mentawai, western Indonesia, and 19 samples from Sumba, eastern Indonesia and (2) complete genomes for 70 samples, including 11 Korowai, 30 Mentawai, and 29 Sumba samples.

Whole-genome sequencing and data processing

Whole blood DNA from all individuals was extracted with Gentra Puregene for human whole blood kit (QIAGEN) and MagAttract HMW DNA kit (QIAGEN) according to the manufacturer's instructions. Approximately 1.3 µg of DNA from each of the 73 individuals were sent to Garvan and sequenced with TruSeq Nano v2.5 to an expected mean depth of 30×.

The newly generated genome sequences were processed closely following a previously described protocol⁶ with the resources of the University of Tartu High Performance Computing Center.⁹ Briefly, we first aligned the reads to the “decoy” version of the GRCh37 human reference sequence (hs37d5). After alignment, and keeping only properly paired reads that mapped to the same chromosome, the autosomal sequencing depth across the samples used in downstream analyses was as follows: min = 31.5×, Q1 = 35.3×, median = 36×, Q3 = 36.5×, max = 39.5×. Base-calling was undertaken with GATK best practices.^{10,11} Following the generation of per-sample gVCF files with GATK4 HaplotypeCaller, single sample gVCFs were combined into multi-sample files with CombineGVCFs, and joint genotyping was performed with GATK4 GenotypeGVCFs, outputting all sites to a multi-sample VCF. To maximize the SNP discovery and phasing power, we used approximately 900 complete genomes in a multi-sample calling pipeline. In addition to the newly generated genomes, these included complete genome sequences from SGDP¹² and IGD⁶ projects, Malaspinas et al.,¹³ Vernot et al.,¹⁴ Lan et al.,¹⁵ and the HiSeqX Diversity Cohort of Polaris project ([web resources](#)) as well as approximately 100 unpublished genome sequences from Estonia and Papua. SNP calling was performed on the combined dataset and published genomes were analyzed from raw reads exactly as they were for the new sequence data. Using bcftools v1.9,¹⁶ we applied the following filters to each genotype call in multisample VCF files: base depth (DP) ≥ 8× and ≤ 400× and genotype quality (GQ) ≥ 30. Only bi-allelic SNPs and invariable reference sites were kept.

The published data included seven Korowai and ten Mentawai samples, however, two first-degree relatives (MTW-024 and MTW-066) were excluded from further analysis.⁶ Our final whole-genome sequencing (WGS) dataset, therefore, included 84 samples from three target groups: 17 Korowai, 38 Mentawai, and 29 Sumba.

Next, modern human multi-sample VCF files were merged with two archaic individuals: Denisovan¹⁷ and Neanderthal.¹⁸ Positions with missing or low-quality calls (marked as “LowQual” in the original archaic VCF files) in one of the archaic samples were excluded during the merging procedure. We kept only sites that had high-quality variant calls in at least 99% of samples in the combined modern/archaic dataset. Applying this 99% call-rate filter yielded a total of 52,443,217 SNPs. However, we removed sites within segmental duplications, repeats, and low complexity regions, thus retaining 49,374,343 SNPs. These masks were downloaded from the UCSC and Broad Institute genome resources ([web resources](#)). Phasing was performed with Eagle v2.4.¹⁹ Because our final dataset included complete genomes from very diverse human populations together with a large number of local West Island Southeast Asian and Papuan groups, we did not use any reference datasets to avoid potential phasing bias.

Genotype array data processing

Approximately 1 µg of DNA from each of 42 individuals were sent to MacroGen for genotyping on the Illumina Infinium Omni2.5-8 v1.3 BeadChip array. Samples were processed according to the manufacturer's instructions. Array data was processed in PLINK v1.9.²⁰ The average missing rate per person in the raw dataset was around 0.45% (min 0.27%, max 2.5%); 2,194,297 autosomal positions were kept after excluding SNPs with more than 5% of missing data.

Array data were imputed with Beagle v5.1²¹ with complete genome sequences as a reference. Two imputation reference panels were generated containing both published⁶ and unpublished data. For the imputation of 18 Mentawai samples, we applied a reference panel that included 97 complete genome sequences from western Indonesia (Bali, Borneo, Java, Mentawai, Nias, Sulawesi, and Sumatra), the Philippines, and Taiwan. For the imputation of 24 Korowai and Sumba samples, we applied a reference panel made of 249 complete genomes sequence from eastern Indonesia (Alor, Flores, Kei, Lembata, Sumba, and Tanimbar) and Papua (Bougainville, New Britain, New Guinea, including Korowai, and New Ireland).

We filtered variant sites with bcftools and VCFtools²² to retain only high-quality imputed sites with dosage $R^2 > 0.95$ (estimated squared correlation between the estimated allele dose and the true allele dose, DR2). We extracted these positions from the complete genomes from Korowai, Mentawai, and Sumba ($n = 84$) to produce a new combined SNP set made of imputed and WGS data. We filtered these data to retain SNPs with a proportion of missing data < 0.3 and minor allele frequency (MAF) > 0.05, which resulted in 4,077,164 variants. Imputed genotypes were further filtered to retain genotypes with genotype probability (GP) > 0.90.

RNA sequencing and data processing

RNA sequencing and data processing were carried out as previously described.⁸ Whole blood RNA was collected and extracted with the Tempus Blood RNA tube and Tempus Spin RNA Isolation Kit (Invitrogen). The quality and concentration of all extracted RNA samples were assessed with a Bioanalyzer 2100 (Agilent) and a Qubit device (Life Technologies). We selected samples for sequencing on the basis of their RIN (RNA integrity number) by focusing on villages with at least 10 samples with $RIN \geq 6$. Library preparation was performed by MacroGen (South Korea) with 750 ng of RNA and the Globin-Zero Gold rRNA Removal Kit (Illumina) according to the manufacturer's instructions. Samples were

sequenced with a 100 bp paired-end configuration on an Illumina HiSeq 2500 to an average depth of 30 million read pairs per individual in three batches (Table S2).

FASTQ read files underwent quality control with FastQC v0.11.5 (web resources), and leading and trailing bases below a Phred score of 20 were removed with Trimmomatic v0.36.²³ Reads were aligned to the human genome (GRCh38 Ensembl release 90, web resources) with STAR v2.5.3a²⁴ and a two-pass alignment mode. Read counts were quantified with featureCounts v1.5.3²⁵ against a subset of GENCODE basic (release 27) annotations²⁶ (web resources) that included only transcripts with support levels 1–3. Coordinates were converted to hg19 with the R package liftOver v1.8.0 (web resources). Gene expression data were filtered to retain 12,539 genes with FPKM (fragments per kilobase of transcript per million mapped reads) > 0.1 and a read count of >6 in at least 50 samples. The distributions of FPKM in each sample and gene were transformed into the quantiles of the standard normal distribution.

DNA methylation data processing

1 µg of DNA from each sample was shipped to MacroGen, bisulfite-converted, and hybridized to Illumina EPIC BeadChips according to the manufacturer's instructions. We randomized samples with respect to village and island across two array batches, and three samples were processed on both batches to control for technical variation (Table S1). DNA methylation data were obtained and processed as previously described⁸ with *minfi* v1.30.0²⁷. We combined and preprocessed the two arrays to correct for array background signal. Signal strength across all probes was evaluated and probes with signal $p < 0.01$ in >75% of samples were retained. To avoid potential spurious signals due to differences in probe hybridization affinity, we discarded 6,072 probes overlapping known SNPs segregating in any of the study populations based on previously published genotype data.⁶ The final number of probes retained was 859,404. Subset-quantile within array normalization (SWAN) was carried out with the “preprocessSWAN” function.²⁸ Methylated and unmethylated signals were quantile normalized with *lumi* v2.36.0.²⁹

Local ancestry inference

We used ChromoPainter v2³⁰ (CP) to perform local ancestry (LA) inference and detect Asian and Papuan ancestry in all published and newly generated complete genomes from Korowai ($n = 17$), Mentawai ($n = 38$), and Sumba ($n = 29$). This method relies on phased haplotype data and describes each individual recipient chromosome as a mixture of genetic blocks from the set of predefined donor individuals.

First, East Asian and Papuan reference panels were generated to assign local genomic ancestry in target samples. We selected unadmixed East Asian and Papuan samples by running ADMIXTURE v1.3³¹ at $K = 3$ with all available East and Southeast Asian, European, and Papuan samples from the combined WGS dataset. For the East Asian reference panel, we kept only Asian samples ($n = 102$) with less than 0.05% of non-East Asian ancestry. For the Papuan reference panel, we kept only Papuan samples ($n = 63$) with less than 0.05% of non-Papuan ancestry and excluded all Korowai samples. To balance the sample size of the two reference panels, we randomly selected 63 East Asian samples from the unadmixed reference dataset.

Next, we painted each of 84 target genomes individually with the East Asian and Papuan reference panels as donors. We used the following protocol.

- (1) We performed the initial CP run with ten expectation-maximization steps to estimate prior copying probabilities for each individual and chromosome separately.
- (2) Estimated prior copying probabilities were averaged across the genome for each individual. The main CP run was performed with a recombination scaling constant and global mutation probability from the first step and genome-wide average prior copying probability.
- (3) Either East Asian or Papuan ancestry was then assigned to individual SNPs with a probability threshold of 0.85. Unknown ancestry was assigned to SNPs with intermediate copying probability.

Identifying archaic introgression

We defined the high-confidence Denisovan archaic haplotypes as outlined previously⁶ but with a larger group of sub-Saharan African individuals (61 sub-Saharan Africans in total, Table S3). For each individual, we started with Denisovan-introgressed haplotypes as inferred by CP, then filtered out those that did not overlap (by >0.001%) the Denisovan-introgressed haplotypes as inferred by a previously published hidden Markov model (HMM),⁶ then filtered out those that did not overlap (by >0.001%) archaic introgressed haplotypes inferred by another HMM approach,³² and finally filtered out any of the remaining haplotypes that did overlap (by >0.001%) Neanderthal-introgressed haplotypes as inferred by CP. We then annotated each SNP found in several target sample groups (i.e., monomorphic SNPs in that group are skipped, as are any that are masked out by the alignability/gap mask) according to how often the reference/alternative (REF/ALT) state appears on an inferred high-confidence Denisovan-introgressed haplotype in that group. This was done for three separate groups: (1) all Korowai individuals, (2) all Korowai individuals and Sumba individuals and those Mentawai individuals who are from the new dataset, and (3) all individuals in the “Papuan” continental group, which includes all Papuans and Melanesians except Baining. We used an analogous process to annotate Neanderthal ancestry SNPs, beginning instead with Neanderthal-introgressed haplotypes inferred by CP before requiring intersection with Neanderthal-introgressed haplotypes inferred by the HMM and archaic haplotypes inferred by HMM_{Archaic} and removing those intersecting CP Denisovan haplotypes.

Accounting for population structure and non-genetic sources of variation in the QTL analyses

Principal-component analysis (PCA) of the genotype data was carried out with the R package *SNPRelate* v1.18.1.³³ We included five genotype principal components (PCs) as covariates in QTL analyses to account for population structure. We used a probabilistic estimation of expression residuals³⁴ (PEER) to infer hidden sources of variation in expression and methylation data. These latent factors were used as surrogate variables for unknown technical batch effects and included as covariates in the QTL analyses. 29 hidden factors (25% of the number of samples) were included in models, as recommended in Stegle et al. (2012)³⁴ (for technical details, see Stegle et al. [2010]³⁵).

eQTL and methylQTL analyses

Variant effects on gene expression and CpG methylation were identified by linear regression as implemented in QTLtools.³⁶ Genotype, gene expression, and methylation data were available for

115 individuals: 48 Mentawai, 48 Sumba, and 19 Korowai (Tables S1 and S2). Variants within 1 Mb of the gene/CpG under investigation were considered for testing. p values of top associations adjusted for the number of variants tested in *cis* were obtained from 10,000 permutations. We calculated false discovery rate (FDR)-adjusted p values to adjust for multiple phenotypes tested. Significant associations were selected with an FDR-adjusted p value threshold of 0.01. Nominal p values for all sites within the *cis*-window were obtained with the QTLtools nominal pass. QTL power calculations were carried out with the R package *powerEQTL* v0.1.7.³⁷

Variant annotation and variant set enrichment analyses

To understand the genomic context of the putative eQTLs and methylQTLs, we annotated top SNPs from the permutation-based analyses and the target CpGs of methylQTLs by using the R package *annotatr* v1.10.0.³⁸ Genic annotations (1–5 kb upstream of the transcription start site (TSS), the promoter [<1 kb upstream of the TSS], 5' UTR, first exons, exons, introns, coding sequences [CDS], 3' UTR, and intergenic regions) were obtained with the *TxDb.Hsapiens.UCSC.hg19.knownGene* R package v3.2.2 (web resources), CpG annotations with the *AnnotationHub* R package v2.16.1 (web resources), and enhancer annotations from FANTOM5.³⁹

We tested for the enrichment of the eQTL and methylQTL variants among genomic features by using the *VSE* R package v0.99.⁴⁰ A null-distribution was constructed on the basis of 100 matched random variant sets. Consolidated chromatin immunoprecipitation sequencing (ChIP-seq) peaks for histone marks derived from primary mononuclear cells from peripheral blood were downloaded from the NIH Epigenomics Roadmap FTP site.⁴¹ Additionally, annotations for DNaseI hypersensitivity peaks and histone marks for K562 and GM12878 cell lines were downloaded from the ENCODE portal.⁴²

We tested for the overrepresentation of the population-specific eGenes among Gene Ontology (GO) terms and canonical pathways by using *clusterProfiler* 3.14.3.⁴³ We used a background set of all eGenes to test for overrepresentation.

eQTL-methylQTL colocalization analysis

We used a Bayesian test, as implemented in the R package *coloc* v4,^{44,45} to assess the probability of colocalization of methylQTL and eQTL signals between 3,057 pairs of CpGs and genes. We used masking to allow for multiple causal loci for each trait. Masking implemented in *coloc* allows for multiple causal variants per trait with the assumption that if multiple causal variants exist for any individual trait, they are in linkage equilibrium. All SNPs independently associated within a dataset were identified with the function “*finemap.signals*.” For the pairs of CpGs and genes with multiple signals, colocalization analysis was performed for each pair of signals, restricting the search space to SNPs not in linkage disequilibrium (LD) with any-but-one of each signal SNP. The p value threshold for calling a signal was set to 1×10^{-6} , and the maximum r^2 between two SNPs for them to be considered independent was 0.01.

Pairs with the posterior probability for a common causal variant (CCV) > 0.8 and the ratio of the posterior probability for a CCV and different causal variants (DCVs) $\text{CCV}/\text{DCV} > 5$ were considered to show strong evidence of colocalization. As the posterior probability for colocalization is dependent on the prior probability, we used the *coloc* post hoc sensitivity analysis to determine the range of prior probabilities (1.0×10^{-8} to 1.0×10^{-4}) for

which colocalization is supported. Pairs passing the colocalization threshold with a range of ppCCV values from $<1.0 \times 10^{-6}$ to 1.0×10^{-4} (lower bound of ppCCV below 1.0×10^{-6}) were considered as showing robust support for colocalization.

eQTL sharing with European eQTLs

Similarly to eQTL-methylQTL colocalization, we used *coloc* v4 to test for colocalization between 3,300 permutation-based eQTLs detected here with an FDR-adjusted $p < 0.10$ and three European whole blood eQTL studies: GTEx⁴⁶ ($n = 670$), the Estonian Biobank cohort⁴⁷ ($n = 491$), and Twins UK⁴⁸ ($n = 384$). The European eQTL summary statistics were obtained from the EBI eQTL catalog.⁴⁹ The methods used to call the eQTLs in the EBI eQTL catalog are comparable to the methods used in this study. Out of the 3,300 genes selected for testing, 3,049 were present in the European data and had shared variants with the Indonesian data. We identified colocalized genes with the threshold $\text{CCV} > 0.8$ and a ratio $\text{CCV}/\text{DCV} > 5$. To identify genes that do not show support for colocalization even with a relaxed threshold, we used a threshold of $\text{CCV} > 0.5$ and $\text{CCV}/\text{DCV} > 2$.

To compare the alternative and minor allele frequencies of eSNPs between populations, European genotype data were obtained from the 1000 Genomes dataset.⁵⁰ After subsetting the VCFs for the samples belonging to the European superpopulation, alternative allele counts and frequencies were recalculated with VCFtools.²² Minor allele frequencies in Indonesia and Europe were calculated in relation to the minor allele in the Indonesian data.

Estimating and testing for differences in effect sizes between populations

We used multivariate adaptive shrinkage as implemented in the R package *mashr*⁵¹ to more reliably estimate effect sizes and to identify shared and population-specific eQTLs. The model was fit with both data-driven and canonical covariances. The data-driven covariance matrix was constructed by identifying strong signals based on a significance threshold of 0.05, by obtaining the initial data-driven covariance matrix for the first two PCs of the strong signals, and then applying the built-in extreme deconvolution algorithm. To facilitate computational limitations, we fit the model by using a random subset of 100,000 SNP-gene pairs. For the calculation of pairwise sharing of eQTLs, an eQTL was considered shared between datasets if the effects are the same sign and within a factor of 0.5.

Colocalization with blood trait GWAS loci

To connect the QTLs detected here to blood traits, we tested for colocalization between the FDR-significant permutation-based QTLs ($\text{FDR-}p < 0.1$ eQTLs and $\text{FDR-}p < 0.01$ methylQTLs) and 36 hematological traits by using genome-wide summary statistics from Astle et al.⁵² GWAS summary statistics were downloaded from the GWAS catalog.⁵³ As no LD information was available, these colocalization analyses were carried out without allowing for multiple causal variants. Similarly, eQTL-GWAS colocalization analysis was carried out with the European datasets.

Selection scan

We performed a selection scan using a haplotype-based statistic (number of segregating sites by length, nSL),⁵⁴ as implemented in Selscan v1.2.0.⁵⁵ This test identifies ongoing positive selection in the genome by looking for the tracts of extended haplotype

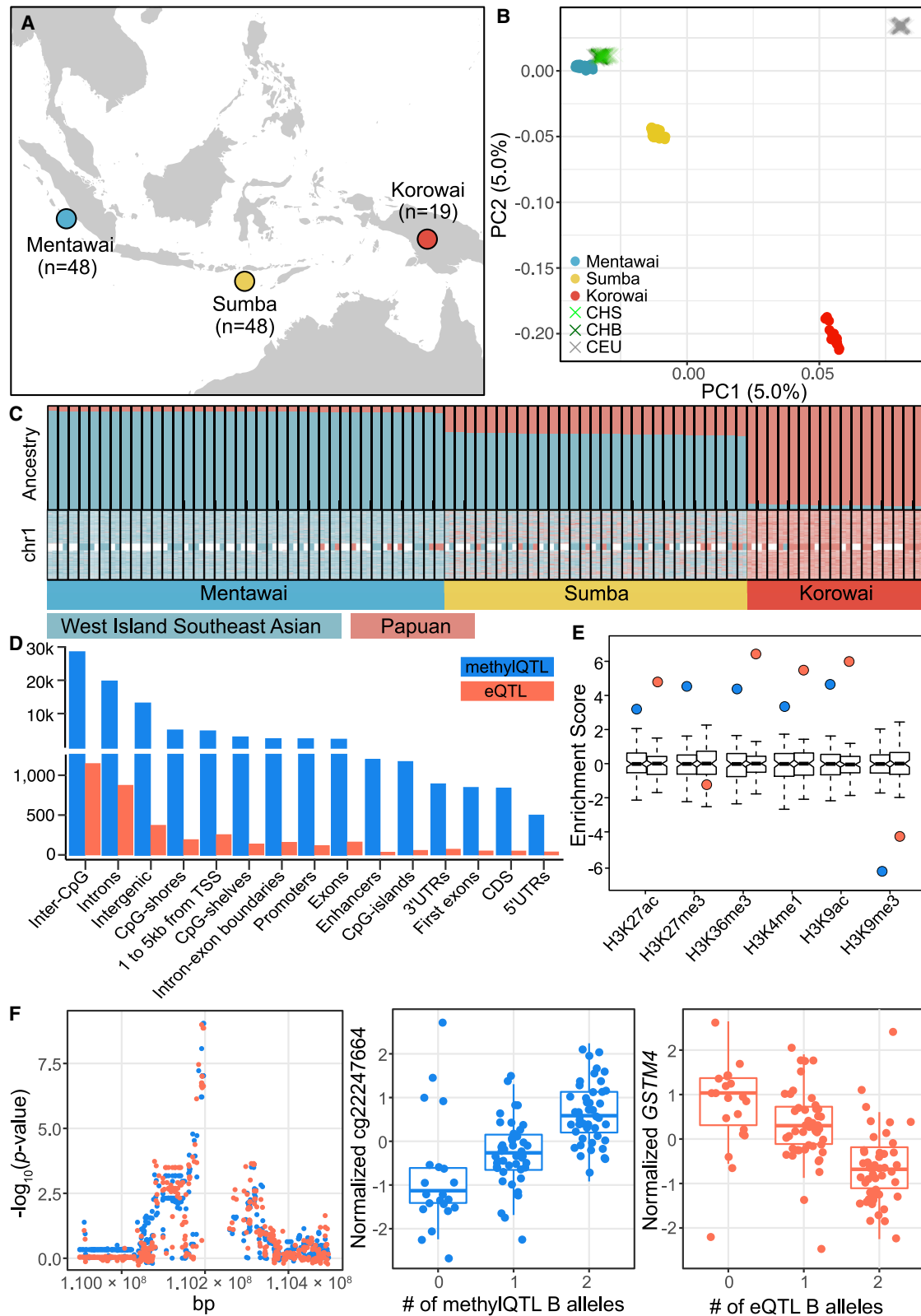


Figure 1. Genetic ancestry and QTL features across 115 Indonesian individuals

(A) Map of the sampling locations of the three study populations: Mentawai, blue; Sumba, yellow; Korowai, red. The numbers of samples used in the QTL analyses are indicated.

(B) PCA of genotype data from study samples as well as Han Chinese from Beijing (CHB), Southern Han Chinese (CHS), and individuals of European ancestry (CEU) from the 1000 Genomes project.

(legend continued on next page)

homozygosity and is capable of identifying both sweeps from standing variation and incomplete sweeps. To identify the traces of positive selection in three target populations, we used our combined dataset of WGS and imputed genotyping array data represented by approximately 4M SNPs. The following Selscan parameters were used: the maximum allowed gap between loci of 50 kb, the gap scale parameter of 5 kb, and the maximum extent of haplotype homozygosity decay curve of 1,333 loci (approximately 1 Mb given the obtained SNP density). Raw nSL results were normalized with Selscan's norm package in 50 kb non-overlapping genomic windows with ten allele frequency bins. Windows with less than 21 SNPs were discarded. The proportion of absolute nSL scores > 2 in each 50 kb genomic window was used as a test statistic. Windows with a proportion of SNPs with an absolute nSL > 2 of 30% were considered to be outliers and showing evidence of past positive selection.

To identify regulatory loci under positive selection, we used a colocalization-based method to detect shared signals between the QTL p values and nSL values. We calculated empirical p values for the nSL values by using an outlier approach by sorting all the scores genome-wide and then dividing the rank by the total number of values in the distribution.

Identifying eQTL effects driven by local ancestry

We calculated the variance explained by modern LA in the genotype of each significant (FDR- $p < 0.01$) permutation-based eQTL and methylQTL as previously described.⁵⁶ For each eVariant and methylVariant, we fit the linear model $V = \alpha \times \text{PAP} + \beta$, where V is the genotype vector (number of QTL B alleles) and PAP is the LA covariate, representing the number of alleles assigned to the Papuan population. This analysis was carried out with the 73 WGS (30 Mentawai, 29 Sumba, 14 Korowai) samples included in the LA inference. Variants with an absolute $R^2 > 0.7$ were considered to exhibit a high correlation with LA. Similarly, we calculated the variance explained by archaic Denisovan and Neanderthal ancestry.

Results

Genetic determinants of gene expression and CpG methylation levels in Indonesia

To contextualize the genetic diversity in our dataset, we began by clustering the 115 Indonesian samples (Figure 1A) through PCA of genotype data, along with European and Han Chinese samples from the 1000 Genomes project. The first two PCs clearly separate the three study populations (Figure 1B). The Mentawai, of West Island Southeast Asian ancestry, cluster closest to mainland Chinese populations, whereas the Korowai, representative of

Papuan ancestry (not well represented in existing public datasets), form a distinct cluster from all other populations. Individuals from Sumba—a mixture of the two ancestries—fall between Mentawai and Korowai, as expected.⁸

We genotyped our samples by using two separate platforms, whole-genome sequencing (WGS, $n = 73$) and the Illumina Omni 2.5M genotyping array ($n = 42$; [material and methods, Table S1](#)). Using only the complete genome sequences, we inferred patterns of global and local ancestry (LA) and archaic introgression across the three populations. On average, the proportion of the genome for which we can make a confident ancestry assignment is 80% for Mentawai, 71% for Sumba, and 85% for Korowai. The average proportion of ancestry-called individual haploid genomes assigned as Papuan is 5.3% in Mentawai, 26.8% in Sumba, and 95.0% in Korowai (Figure 1C). In addition, we were able to identify Denisovan-introgressed haplotypes covering, on average, 0.13%, 0.48%, and 1.44%, of each haploid genome in Mentawai, Sumba, and Korowai, respectively, consistent with a previous study⁶ showing a high frequency of Denisovan sequence in Korowai (Figure S1). Proportions of inferred Papuan ancestry and Denisovan introgression are highly correlated (Pearson's $r = 0.995$, Figure S1). Further, we identified Neanderthal-introgressed haplotypes covering on average 1.08%, 1.19%, and 1.40% of each haploid genome from the three study populations, raising the possibility that either archaic ancestry source has made contributions to gene regulatory architecture in these populations.

To identify genetic variants associated with changes in expression (eQTL) and methylation (methylQTL) levels, we used a linear regression-based approach ([material and methods](#)). At an FDR of 0.01, we detect a total of 1,975 significant *cis*-eQTLs (Data S1) and 48,014 *cis*-methylQTLs (Data S2). As expected, the majority of QTLs are located in non-coding parts of the genome, enriched among transcriptionally active histone marks and accessible chromatin, and mostly depleted from marks associated with heterochromatin and repression of transcription across three blood cell lines (Figures 1D and 1E, Figure S2). We then tested for colocalization between 4,639 pairs of CpGs and genes that potentially harbor a common causal variant by using a Bayesian approach ([material and methods, supplemental note 1](#)) to better understand how genetic regulation of methylation levels contributes to the regulation of gene expression. Over a wide range of

(C) Global and local ancestry across 73 Indonesian individuals (bars) with available WGS data. The top plot shows the average proportion of West Island Southeast Asian and Papuan ancestry genome wide. The bottom plot shows patterns of local ancestry across the two haplotypes in each individual in chr1.

(D) Genomic locations of eQTLs (orange) and methylQTLs (blue). Each QTL can have multiple annotations.

(E) Enrichment of eQTLs (orange) and methylQTLs (blue) among histone marks derived from primary mononuclear cells from peripheral blood in the Epigenomics Roadmap project compared to a null-distribution of 100 matched random variant sets.

(F) An example of a colocalized eQTL-methylQTL pair exhibiting an opposing effect direction on the target trait. The left-side plot shows the $-\log_{10}(p \text{ values})$ of the associations between variants in *cis* and *GSTM4* expression (orange) or cg22247664 methylation (blue). The middle plot shows the relationship between the top-SNP genotype and cg22247664 methylation, and the right-side shows the relationship between the top-SNP genotype and *GSTM4* expression.

prior probabilities, 720 (15.5%) of the tested pairs show robust support for a common causal variant (material and methods, Figure S3, Data S4), corresponding to 621 unique CpGs and 222 unique genes. As expected, CpGs located on promoters are more likely to show an opposite direction of effect with the gene than CpGs located outside regulatory regions (Fisher's test $p = 3.835 \times 10^{-6}$, Figure 1F, supplemental note 1, Figure S4); additionally, we had previously identified 80 (36.0%) of the 222 genes as showing a negative correlation between expression and promoter methylation levels.⁸

Population specificity of Indonesian eQTLs

The bulk of eQTL studies to date have been carried out in European populations. To better understand the impact of ancestry on the genetic architecture of gene regulation, we compared eQTLs detected here with those identified in three comparable mostly European datasets with publicly available genome-wide summary statistics: GTEx⁴⁶ ($n = 670$), the Estonian Biobank cohort⁴⁷ ($n = 491$), and Twins UK⁴⁸ ($n = 384$). While 996 (9.8%) of the 10,214 unique eGenes were shared across cohorts, the same number of eGenes were detected in all European cohorts but not in Indonesia (Figure 2A). Furthermore, 698 (6.8%) were only detected in the Indonesian data. After relaxing our FDR threshold to $p < 0.10$ to account for differences in power, we tested 3,300 Indonesian eGenes for eQTL colocalization with any of the European datasets. On average, 26.9% of tested genes showed some evidence of colocalization and 6.71% showed robust support across a wide range of prior probabilities with each European dataset (Table S4). In total, 1,177 (35.7%) of tested genes showed some evidence of colocalization and 318 (9.6%) robust support for colocalization with a wide range of prior probabilities for a common causal variant with at least one European dataset. Of these, 105 (33.0%) genes (Table S4), including Ras suppressor *RSU1* (Figure 2E, Figure S5), showed robust support for colocalization between Indonesia and all European datasets. In contrast, we found much higher levels of colocalization when comparing between European datasets at a similarly relaxed FDR: on average, 46.3% of tested genes colocalized across at least one pair of datasets with some support and 17.8% with robust support (Table S4). These results suggest a true difference in eQTL architecture between the Indonesian and European data. Indeed, 1,081 (32.8%) of genes exhibited no evidence of colocalization between Indonesia and any European dataset, even with relaxed thresholds (material and methods). We followed up on these results by using a multivariate adaptive shrinkage model (material and methods) that enables joint analysis of all the datasets simultaneously and is geared toward more accurately estimating effect sizes and identifying shared and specific effects. Concordant with the colocalization results above, we found eQTL effects were largely shared between the European datasets (Figure 2B). We also identified 2,411 Indonesia-specific eSNP-eGene pairs, corresponding to a total of 1,599 eGenes. To generate

a robust set of Indonesia-specific eQTLs, we intersected the results from the colocalization and multivariate analyses and identified 245 genes that harbored Indonesia-specific eQTLs and had no evidence of colocalization with European eQTLs. It should be noted that these Indonesia-specific eQTLs are likely to be present in some unsurveyed populations and thus specific to particular populations and not only Indonesia. As our comparison using the available datasets is between European and Indonesian eQTLs, we are calling this set of eQTLs Indonesia specific in the current study.

To identify the attributes of Indonesia-specific eQTLs, we compared these 245 genes to the set of 105 genes with robust support for colocalization between Indonesia and all European datasets. Although there is no overall enrichment for GO or KEGG terms among Indonesian-specific eGenes, there are clinically relevant genes in this set (Table S5), including the *NRAS* proto-oncogene (Figure 2F, Figure S5). Concordant with previous reports, eQTLs that are shared between populations exhibit larger effect sizes than other eQTLs (t test $p < 2.2 \times 10^{-16}$), and most (97%–100%) shared eQTLs show the same direction of effect in both populations⁵⁷ (Figure S6). Indonesia-specific eQTLs exhibit significantly larger effect sizes in Indonesia than in the European datasets, while colocalized eQTLs show no statistically significant differences in effect sizes between datasets, as expected (Figure 2D). We hypothesized that differences in genetic trait architecture may underlie these population-specific eQTLs. Indeed, when we compared the MAF of eSNPs between Indonesians and Europeans, we found no significant difference among the colocalized eQTLs but a significantly higher MAF in Indonesians for the Indonesian-specific eQTLs (t test; mean MAF in Indonesia 0.26; in the 1000 Genomes European super population 0.22; $p = 0.0099$), suggesting population differences in haplotype structure contribute to our observation. However, they alone were insufficient to explain the entirety of Indonesia-specific eQTLs. Thus, we also examined the role of gene expression levels—i.e., whether a gene is highly expressed in Indonesian samples but expressed at low levels or not at all in European ones. Indeed, as with MAF, we observed no significant difference in expression levels of colocalized eGenes across the datasets, but there was a significant increase in expression of the Indonesia-specific eGenes (t test; mean $\log_2(\text{TPM})$ in Indonesia 3.5, in GTEx whole blood 2.6, $p < 2.8 \times 10^{-12}$, Figure S7). Interestingly, there were a number of Indonesia-specific eQTLs where little or no difference in MAF or gene expression was observed, highlighting the need for a deeper mechanistic investigation of these loci (Figure S8).

While some of the population specificity we detect may be attributable to limited statistical power across all datasets, our findings illustrate the value of performing analyses on diverse populations to achieve a comprehensive understanding of the genetic regulation of molecular traits. Importantly, of all datasets under consideration,

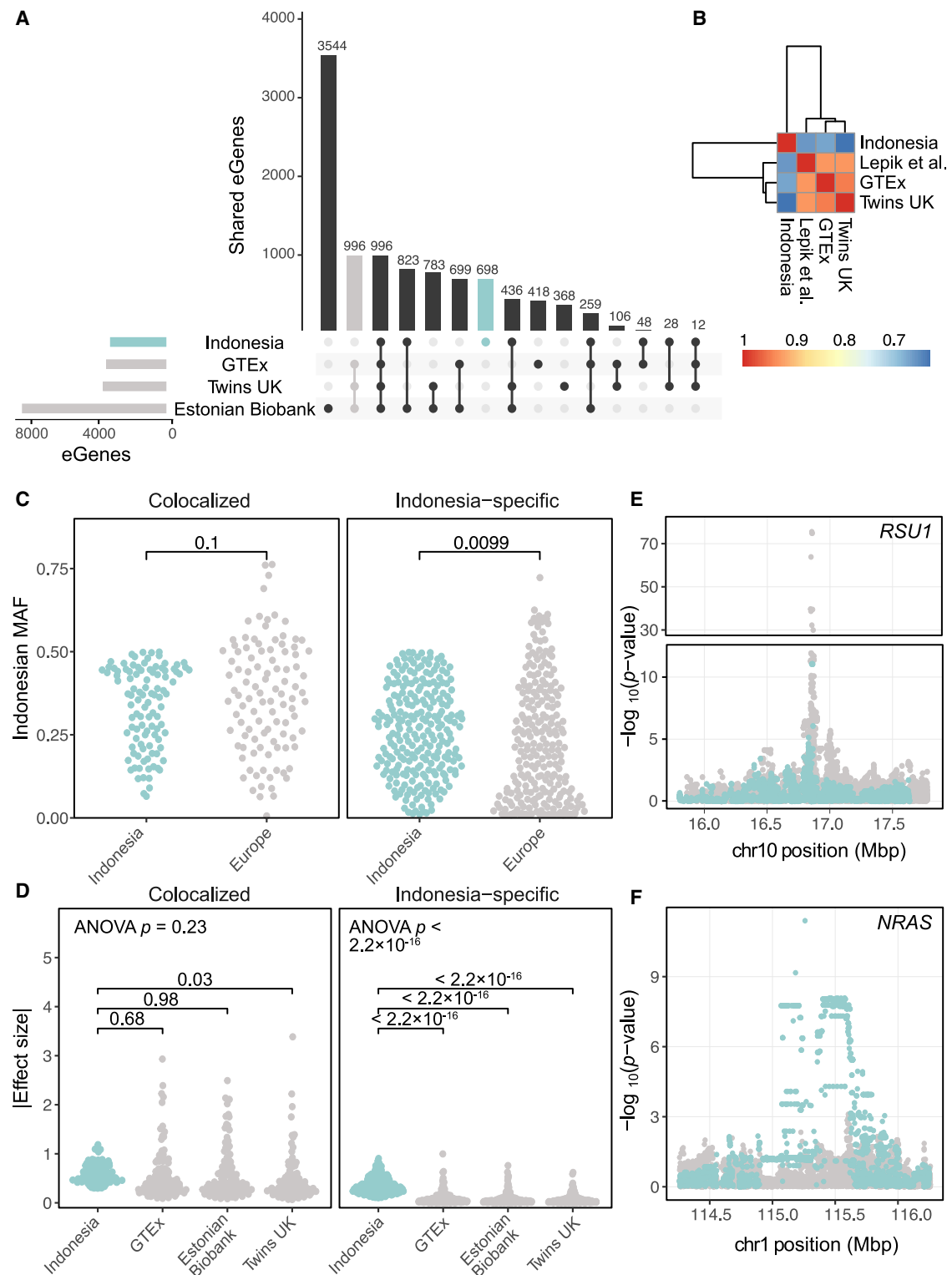


Figure 2. Sharing of eQTLs between Indonesian and European populations

(A) Overlap of permutation-significant (FDR- $p < 0.1$) eGenes between Indonesia and three European eQTL cohorts.
 (B) Pairwise sharing of eQTLs between the datasets across all tested SNP-gene pairs.
 (C) Minor allele frequencies of shared and Indonesia-specific eSNPs in Indonesia and the 1000 Genomes European super-population. MAFs are reported relative to the minor allele in Indonesia.
 (D) Absolute effect sizes of the shared and Indonesia-specific eQTLs. In (C) and (D), ANOVA p values and t test p values between Indonesia and the European datasets are indicated.
 (E) An example of a colocalized gene, *RSU1*.
 (F) An example of an Indonesia-specific eQTL for the gene *NRAS*. In (E) and (F), $-\log_{10}(p\text{ values})$ for Indonesia are indicated in blue and for the European datasets are indicated in gray.

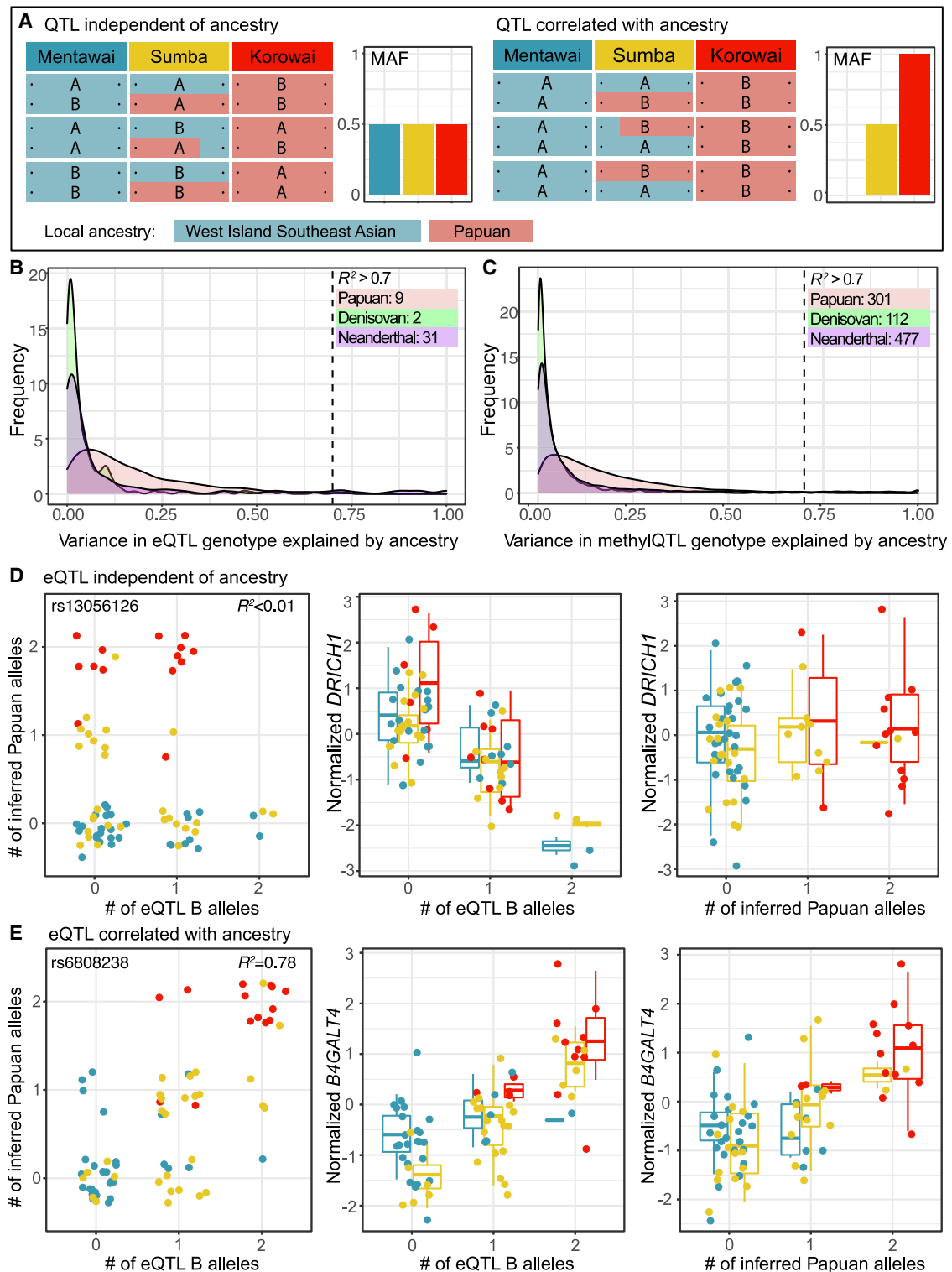


Figure 3. Integrating local ancestry inference at regulatory loci to detect QTLs driven by ancestry and archaic introgression

(A) Schematic illustrations of variation in QTL genotype (A = major allele, B = minor allele) and local ancestry are shown across the two haplotypes in three individuals in three populations. In the first example, QTL genotype variation is independent of local ancestry and allele frequencies are equal between populations. In the second example, QTL B allele closely segregates with the ancestry informative marker and allele frequencies differ between populations. There is an expected correlation between the genotype and the molecular trait, as well as inferred ancestry and the trait.

(B and C) Linear regression between the numbers of QTL B alleles and numbers of inferred Papuan, Denisovan, and Neanderthal alleles reveal subsets of (B) eQTLs and (C) methylQTLs largely driven by modern LA and archaic introgression. The numbers of QTLs exceeding the R^2 threshold of 0.7 are indicated.

(D) An example of an eQTL independent of modern LA.

(legend continued on next page)

the Indonesian one is the smallest, making our inability to replicate Indonesian eQTLs in European studies more likely to be biologically meaningful and clear candidates for functional follow-up.

Subsets of expression and methylation QTLs are largely driven by modern local ancestry and archaic introgression

In addition to differences between Indonesians and Europeans, we sought to understand the extent to which the two distinct sources of LA in modern Indonesians, as well as introgression from archaic hominins, have impacted gene regulatory architecture. We examined the haplotype background on which our QTLs occur and asked whether there was a relationship between the inferred ancestral source of the genotype and expression/methylation levels (material and methods, Figures 3A, 3D, and 3E). We find nine, two, and 31 instances where variance in eQTL genotype is largely driven ($R^2 > 0.7$) by modern LA, archaic Denisovan introgression, and archaic Neanderthal introgression, respectively (Figure 3B, Data S5, Data S6, Data S7), directly linking ancestry-informative alleles to expression differences between individuals. Similarly, we find 301, 112, and 477 instances where the methylQTL genotype is driven by modern LA, Denisovan introgression, and Neanderthal introgression, respectively (Figure 3C, Data S8, Data S9, Data S10). In total, 2.1% of eQTLs and 2.29% of methylQTLs are driven by modern LA or archaic introgression; given the unbalanced representation of the two ancestries in our dataset (Figure S1) this number represents only a lower boundary, and the true number is likely to be much greater.

Of the nine and 373 unique Papuan-driven QTL target genes and CpGs, we had previously identified seven (77.8%) and 270 (72.4%) as differentially expressed/methylated in at least one of the pairwise comparisons between the three study populations.⁸ Further, 42 out of the 122 (34.4%) Denisovan-driven methylQTL targets were differentially methylated and seven (22.6%) and 149 (25.6%) of the Neanderthal-driven eQTL and methylQTL targets are differentially expressed/methylated. However, despite multiple lines of evidence suggesting that some introgressed Neanderthal and Denisovan alleles have been positively selected for in human populations,^{58–60} we were unable to identify evidence of recent positive selection among these loci (supplemental note 3, Table S6, Table S7). Altogether, our findings highlight the potential for local sources of genetic ancestry, whether modern or archaic, to variably impact gene expression architecture across populations and again emphasize the importance of truly diverse sampling.

Connecting regulatory variants to complex traits

Differences in genetic architecture between populations, including differences in allele frequencies and patterns of LD, are known to limit the transferability of GWASs and polygenic risk scores across populations.^{1,4} Thus, we sought to examine how the differences in QTL architecture between Indonesian and European populations propagate through to the genetic underpinnings of complex traits.

First, using the same Bayesian methodology as above, we tested for colocalization between the significant Indonesian QTLs and 36 hematological traits by using genome-wide summary statistics from a GWAS on 173,480 participants of European ancestry.⁵² We detected 30 (1.5%) and 614 (1.3%) unique eGenes and methylCpGs, respectively, that colocalize with at least one trait (Table S8); in total, we identified 78 significant trait-eGene pairs. The genes and CpGs colocalized with the most unique traits were *ITGA4* and cg18815117, colocalizing with ten and 16 traits, respectively. *ITGA4* has been previously implicated in blood trait GWASs across diverse populations.^{61–65} The CpG cg18815117 is located in the body of *CRHR1*, an important regulator of the hypothalamic–pituitary–adrenal (HPA) axis. Epigenetic changes in the body and promoter of *CRHR1* have been found to be highly predictive of major depressive disorder and panic disorder in some cohorts.^{66–68}

Next, we repeated the GWAS colocalization analysis, this time by using the three European eQTL datasets alone. Compared to the 30 eGenes that colocalized with at least one GWAS trait, here we found an average of 55 unique eGenes colocalizing with at least one trait (45 in GTEx, 48 in TwinsUK, and 77 in the Estonian Biobank). Focusing on pairs of colocalized GWAS-eQTLs—rather than unique eGenes—we found that 72 (28%) of the 257 unique significant trait-gene pairs detected across all datasets were shared across all three European datasets (Figure 4A) and an average of 25.7% of colocalized genes were shared between datasets for a given trait (Table S9). Furthermore, 31 GWAS-eQTL pairs (12%) were shared between all three European datasets and Indonesia. The GWAS-eQTLs shared between Indonesia and Europe show robust support for eQTL colocalization, indicative of a shared genetic architecture underlying the regulation of these genes and the biological association identified by GWAS (Figure 4B). Among the shared GWAS-eQTLs, we identify *SLC12A7*, which colocalized with red blood cell distribution width, a biomarker representing the variability in the size of circulating erythrocytes (Figure 4C). Variants annotated with *SLC12A7* have previously been uncovered in GWASs on this and other datasets.^{52,69,70}

In addition to these population-shared GWAS-eQTLs, we also identified population-specific colocalized pairs of

(E) An example of an eQTL highly correlated with modern LA. In (D) and (E), the leftmost plot shows the correlation between the number of inferred Papuan alleles and eQTL B alleles. rs ID and R^2 are indicated. The middle plot shows the effect of the eQTL B allele dosage on the normalized expression level of the target gene. The rightmost plot shows the effect of the inferred Papuan allele dosage on the target gene.

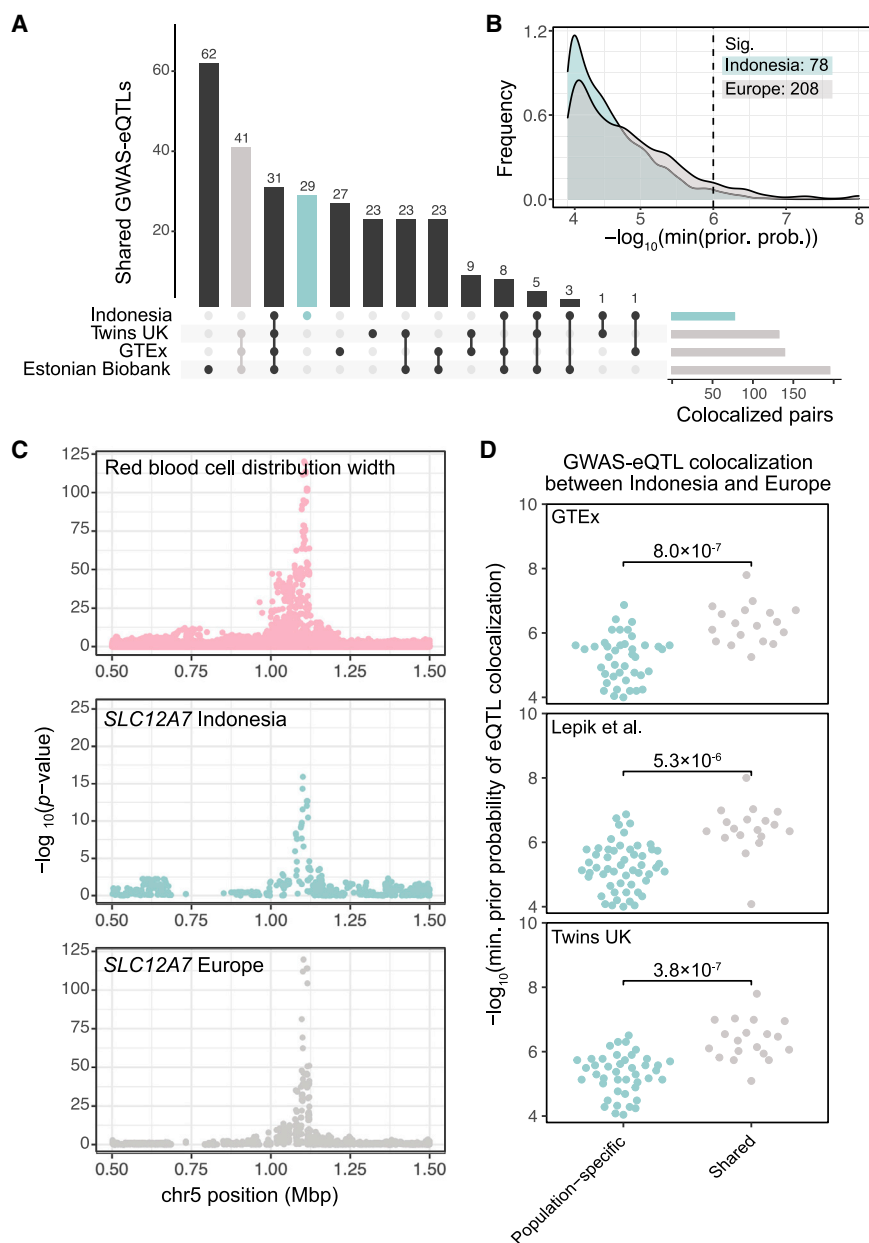


Figure 4. GWAS colocalization with eQTLs from diverse populations identifies shared and population-specific variant-gene-trait associations

(A) Overlap of colocalized trait-gene pairs. The horizontal bar plot shows the numbers of significant colocalized pairs for each dataset. The dot plot shows the intersections and the vertical bar plot shows the numbers of shared trait-gene pairs for each intersection.

(B) European GWAS shows more colocalization with European eQTLs than Indonesian eQTLs. The x axis shows the $-\log_{10}$ of the lower bound of the prior probability of colocalization where the gene passes the colocalization threshold, and larger values indicate a more robust support for eQTL colocalization. The minimum prior probability threshold of 1.0×10^{-6} for robust colocalization is indicated.

(C) An example of a GWAS-eQTL significantly colocalized across Indonesia and all European datasets. $-\log_{10}(p\text{ values})$ for red blood cell component distribution width (top), *SLC12A7* eQTLs in Indonesia (middle), and *SLC12A7* eQTLs in the three European datasets (bottom) are shown.

(D) Population-specific GWAS-colocalized eGenes are less likely to show eQTL colocalization between Indonesia and Europe than shared GWAS-genes. The y axis shows the $-\log_{10}$ of the lower bound of the prior probability of colocalization where the gene passes the colocalization threshold, and larger values indicate more robust support for eQTL colocalization.

genes in question in contributing to the overall trait. The striking difference in GWAS colocalization between European and Indonesian eQTLs reflects the poor transferability of genetic association studies between populations.

GWAS-eQTLs. Overall, European eQTLs show more evidence for colocalization with GWAS traits than Indonesian eQTLs (Figures 4A and 4B). Indeed, 208 (80.9%) of the 257 unique eGene-trait pairs that were detected across at least one of the European datasets could not be replicated in Indonesia. Intriguingly, although the GWAS was performed in a predominantly European sample, 29 GWAS-eQTL pairs colocalized exclusively in the Indonesian data and not in any of the European datasets (Figure 4A). Out of these, eight were not colocalized in any of the European datasets even with a relaxed significance threshold (see material and methods). Reassuringly, these population-specific GWAS genes show low support for eQTL colocalization (Figure 4D), again strongly arguing for differences in the genetic architecture underlying gene regulation, while simultaneously supporting the importance of the

ancestry or archaic introgression-driven QTLs that are associated with hematological traits. Among the GWAS-colocalizing QTLs were a Papuan-driven methylQTL that colocalizes with hemoglobin measurements, and notably, four Denisovan-associated methylQTLs that colocalize with platelet count. We further examined these four methylQTLs to gain insight into possible mechanisms underlying the connection with platelet count (supplemental note 4, Table S10). All four target CpGs are located near the *HLA* superlocus. While these methylQTLs do not significantly colocalize with eQTLs in our data, all four methylSNPs are nominally associated with the expression of the nearby gene *ZFP57* (lowest $p\text{ value} = 5.85 \times 10^{-6}$). *ZFP57* is a transcriptional regulator known to have an important role in DNA methylation, epigenetic regulation, and imprinting during development.⁷¹ Expression of *ZFP57* is dependent

on underlying genetic variation, and while the biology of *ZFP57* in adults is not well studied, it has been implicated as the causal gene connecting some GWAS variants to cancer and HIV/AIDS progression.⁷² As above, the geographically restricted ancestry of the methylSNPs and their linkage structure suggests that the regulatory interactions may not be fully shared between populations. Further GWASs and functional studies on diverse populations are needed for the fine-mapping of causal variants underlying gene regulation and complex traits.

Discussion

Indonesia is the world's fourth most populous country and a region that has been vastly understudied, but it is also one that is undergoing a rapid demographic and lifestyle shift giving rise to an expanding middle class and where non-infectious, complex diseases are already contributing substantially to mortality and morbidity. As is happening elsewhere in the Global South, this transition accelerates the need to understand the molecular underpinnings of complex disease, and in this context, our study adds to a growing literature demonstrating the importance of characterizing functional genomics within traditionally understudied populations.^{73,74}

We have explored the degree to which functional variation differs between Europeans and Indonesians, and more broadly, the difficult problem of translating eQTL knowledge across populations. Focusing largely on a set of eQTLs that had strong evidence of being colocalized between populations and a set of eQTLs with strong evidence of being specific to Indonesia, we were able to examine potential drivers of population specificity. At least some portion of the population-specific effects we observe are explained by population-specific genomic architecture at *cis*-regulatory regions. The future identification of such eQTLs is fully contingent on performing large-scale QTL studies in underrepresented populations, and our work demonstrates the value of such approaches. Other drivers of population differences in architecture are likely to include *trans* effects (themselves most likely driven by population-specific *cis* effects),⁷⁵ as well as environmental differences between populations.⁷⁶ The identification of 245 putative population-specific eQTLs—a number of which implicate genes involved with biological processes such as immunity and cancer progression—coupled with the insights gained from exploring the genetic underpinnings of these eQTLs advances our understanding of the genetic architecture of gene regulation. In the future, the collection of multi-modal data and mapping of QTLs across tissues and diverse populations can allow a more comprehensive assessment of population specificity and the exact mechanisms underlying population differences in gene regulation. In particular, future surveys across South East Asia can further clarify the genomic and environmental drivers of gene regulatory variation in the area.

In addition to comparisons between Indonesian and European populations, we were able to leverage the unique cline of Asian and Papuan ancestry in Indonesia to identify both QTLs driven by local ancestry or introgression from archaic hominin species. A large proportion of the target genes and CpGs of these LA-driven QTLs were previously identified as differentially expressed or methylated between islands, demonstrating how between-island differences in genetic ancestry can contribute to differences in molecular phenotypes in the region. Notably, these loci, which might *a priori* appear to be prime candidates for local adaptation, showed no evidence of having been targets of positive selection. This suggests that the relationship between trait architecture, demographic history, and adaptation to local pressures such as pathogens is not straightforward. However, our analysis demands a strong correlation between allelic state and ancestry, making our estimates of LA-driven QTLs highly conservative and identifies loci that have evolved under specific scenarios, e.g., drift to high frequency in the Papuan population. Relaxing these demands may lead to the discovery of other regulatory variants that arose within Papua after divergence from Asia. Furthermore, our analysis is limited by the small sample size. Future sample collection efforts across diverse populations will address this limitation. Understanding how complex gene regulatory landscapes and the polygenicity of most traits constrain the action of natural selection is an open challenge in human genomics, one underscored by the difficulty many studies of genome-wide positive selection in humans have encountered in linking evidence of selection at the DNA level to tangible phenotypes.^{77,78}

Similarly, the modest overlap of GWAS hits with the population-specific QTLs represents a non-trivial challenge in the field of functional genomics: how do we connect population-specific functional variation to loci associated with complex traits identified in European populations? From a practical perspective, we do not anticipate a robust expansion of traditional GWASs' being carried out in understudied populations. To this end, the field will need to move away from simple intersections of GWASs and QTL hits, which rely upon shared LD structure, and instead integrate genetic variation, GWAS results, context-specific multi-omics (in simulated or actual disease states and in a range of cell types), and robust functional validations to define common sets of regulatory elements that contribute to disease and are shared across populations.

Data and code availability

All genotype data, RNA sequencing reads, and Illumina Epic iDat files are available through the Data Access Committee of the official data repository at the European Genome-phenome Archive (EGA; [web resources](#)). Illumina Omni 2.5M genotyping array data are deposited in study EGA: EGAS00001003670 and the whole-genome data are deposited in study EGA: EGAS00001003654. The RNA sequencing data are deposited in study EGA:

EGAS00001003671 and the methylation data are deposited in study EGA: EGAS00001003653. Matrices of unfiltered read counts (<https://doi.org/10.26188/5d12023f77da8>) and M-values (<https://doi.org/10.26188/5d13fb401e305>) for all samples, including replicates, are freely available on Figshare ([web resources](#)). The nominal eQTL statistics for all tested SNP-gene pairs are available as [Data S3](#) and the nominal methylQTL statistics for all SNPs tested for the targets of the permutation-significant methylQTLs are available at Mendeley Data: <https://doi.org/10.17632/z7rgf54jd6.2>. The code generated during this study is available on GitHub ([web resources](#)).

Supplemental information

Supplemental information can be found online at <https://doi.org/10.1016/j.ajhg.2021.11.017>.

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Declaration of interests

The authors declare no competing interests.

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Web resources

ADMIXTURE v1.3, <https://dalexander.github.io/admixture/>
 AnnotationHub v2.16.1, <https://bioconductor.org/packages/release/bioc/html/AnnotationHub.html>
 annotatr v1.10.0, <https://bioconductor.org/packages/release/bioc/html/annotatr.html>
 bcftools v1.9, <https://samtools.github.io/bcftools/>
 Beagle v5.1, <https://faculty.washington.edu/browning/beagle/beagle.html>
 BLAST, https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastSearch
 Broad Institute genome annotations, http://software.broadinstitute.org/software/genomestrip/node_ReferenceMetadata.html
 ChromoPainter v2, https://people.maths.bris.ac.uk/~madjl/finestructure-old/chromopainter_info.html
 clusterProfiler v3.14.3, <https://bioconductor.org/packages/release/bioc/html/clusterProfiler.html>
 coloc v4, <https://chr1swallace.github.io/coloc/>
 Eagle v2.4, <https://alkesgroup.broadinstitute.org/Eagle/>
 ENCODE portal, <https://www.encodeproject.org/>
 eQTL catalog, <https://www.ebi.ac.uk/eqtl/>
 European Genome-Phenome Archive, <https://ega-archive.org/>

FANTOM5, <https://fantom.gsc.riken.jp/data/>
 FastQC v0.11.5, <https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>
 featureCounts v1.5.3, <http://subread.sourceforge.net/>
 FigShare, <https://figshare.com>
 GATK4, <https://gatk.broadinstitute.org/hc>
 GENCODE release 27, https://www.gencodegenes.org/human/release_27.html
 GitHub repository for this publication, https://github.com/heinin/Indonesia_QTL
 GRCh37 human reference sequence (hs37d5), ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/technical/reference/phase2_reference_assembly_sequence
 GRCh38 Ensembl release 90 August 2017, ftp://ftp.ensembl.org/pub/release-90/gtf/homo_sapiens/Homo_sapiens.GRCh38.90.chr.gtf.gz
 GWAS catalog, <https://www.ebi.ac.uk/gwas/>
 liftOver v1.8.0, <https://www.bioconductor.org/packages/release/workflows/html/liftOver.html>
 lumi v2.36.0, <https://www.bioconductor.org/packages/release/bioc/html/lumi.html>
 mashr v0.2.50, <https://cran.r-project.org/web/packages/mashr/index.html>
 MatchIt v3.0.2, <https://cran.r-project.org/web/packages/MatchIt/>
 minfi v1.30.0, <https://bioconductor.org/packages/release/bioc/html/minfi.html>
 NIH Epigenomics Roadmap FTP, <ftp://ftp.ncbi.nlm.nih.gov/pub/geo/DATA/roadmap/epigenomics/>
 PEER v1.3, <https://github.com/PMBio/peer>
 PLINK v1.9, <https://www.cog-genomics.org/plink/>
 powerEQTl v0.1.7, <https://cran.r-project.org/web/packages/powerEQTl/index.html>
 QTLtools v1.0, <https://qtltools.github.io/qtltools/>
 Selscan v1.2.0, <https://github.com/szpiech/selscan>
 SNPRelate v1.18.1, <https://www.bioconductor.org/packages/release/bioc/html/SNPRelate.html>
 STAR v2.5.3a, <https://github.com/alexdobin/STAR>
 The Polaris Project, <https://github.com/Illumina/Polaris>
 Trimmomatic v0.36, <http://www.usadellab.org/cms/?page=trimmomatic>
 TxDb.Hsapiens.UCSC.hg19.knownGene v3.2.2, <https://bioconductor.org/packages/release/data/annotation/html/TxDb.Hsapiens.UCSC.hg19.knownGene.html>
 UCSC genome annotations, <http://hgdownload.soe.ucsc.edu/goldenPath/hg19/database/genomicSuperDups.txt.gz>
 Uniquely mappable regions with various kmers, <https://bismap.hoffmanlab.org/>
 VCftools v0.1.13, <https://vcftools.github.io/index.html>
 VSE v0.99, <https://cran.r-project.org/src/contrib/Archive/VSE/>

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