Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for *RBPMS* in Erythropoiesis

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Genome-wide association studies (GWASs) have identified loci for erythrocyte traits in primarily European ancestry populations. We conducted GWAS meta-analyses of six erythrocyte traits in 71,638 individuals from European, East Asian, and African ancestries using a Bayesian approach to account for heterogeneity in allelic effects and variation in the structure of linkage disequilibrium between ethnicities. We identified seven loci for erythrocyte traits including a locus (*RBPMS/GTF2E2*) associated with mean corpuscular hemoglobin and mean corpuscular volume. Statistical fine-mapping at this locus pointed to *RBPMS* at this locus and excluded nearby *GTF2E2*. Using zebrafish morpholino to evaluate loss of function, we observed a strong in vivo erythropoietic effect for *RBPMS* but not for *GTF2E2*, supporting the statistical fine-mapping at this locus and demonstrating that *RBPMS* is a regulator of erythropoiesis. Our findings show the utility of trans-ethnic GWASs for discovery and characterization of genetic loci influencing hematologic traits.

Introduction

Erythrocyte disorders are common worldwide, contributing to substantial morbidity and mortality.[1] Erythrocyte counts and indices are heritable (estimated h^2 = 0.40–0.90[2–4]), exhibit different patterns across ethnic groups, and have been influenced by selection in various ethnic groups, most notably for protection against infection by parasites such as those that cause malaria.[5–7] Erythrocyte traits have been studied most extensively in European

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ancestry populations,[8–10] with smaller studies in non-European populations, and have shown both shared and distinct genetic loci influencing erythrocyte traits.[11,12]

Trans-ethnic meta-analysis of genome-wide association studies (GWASs) offers improved signal detection in a combined meta-analysis when heterogeneity of allelic effects, allele frequencies, and differences in linkage disequilibrium (LD) between ethnicities are accounted for. Trans-ethnic meta-analysis can also enable fine-mapping of association intervals by evaluating differences in LD structure between diverse populations, thereby enhancing the detection of causal variants.[13]

We conducted trans-ethnic GWAS meta-analyses with the goal of elucidating the genetic architecture of erythrocyte traits and to evaluate (1) whether combining data across populations of diverse ancestry may improve power to detect associations for erythrocyte traits and (2) whether differences in LD structure can be exploited to identify causal variants driving the observed associations with common SNPs. In this study, we analyzed GWAS summary statistics from 71,638 individuals from three diverse populations of European (EUR), East Asian (EAS), and African (AFR) ancestry. We conducted replication analyses in independent samples and performed functional testing to support our approach to fine-mapping.

Subjects and Methods

Study Samples

We aggregated HapMap-imputed GWAS results from 71,638 individuals represented in 23 cohorts embedded in the CHARGE Consortium (40,258 individuals of EUR ancestry), the RIKEN/BioBank Japan Project and AGEN cohorts (15,252 individuals of EAS ancestry), and the COGENT Consortium (16,128 individuals of AFR ancestry). Phenotypic information on all participating

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cohorts is provided in Table S1 and has been reported previously.[8,11,12,14,15] We conducted replication analyses of the identified trait-loci associations in six independent studies: the Gutenberg Health Study (GHS cohorts 1 and 2, both EUR ancestry), the Genes and Blood-Clotting Study (GBC, EUR ancestry), the NEO study (EUR ancestry), the JUPITER trial (EUR ancestry), and the HANDLS study (AFR ancestry)[16–21] (total replication size N = 16,389).

Erythrocyte Phenotype Modeling

We analyzed six erythrocyte traits: hemoglobin concentration (Hb, g/dL), hematocrit (Hct, percentage), mean corpuscular hemoglobin (MCH, picograms), mean corpuscular hemoglobin concentration (MCHC, g/dL), mean corpuscular volume (MCV, femtoliters), and red blood cell count (RBC, 1M cells/cm^3). Trait units were harmonized across all studies. MCH, MCHC, MCV, and RBC were transformed to obtain normal distributions. We excluded samples deviating more than 3 SD from the ethnic- and trait-specific mean within each contributing study, because we focused on determinants of variation in the general population rather than on specific hematological diseases that are overrepresented at the extremes of the trait distribution (Table S2).

Genotyping

In brief, the cohorts comprise unrelated individuals, except for the Framingham Heart Study (related individuals of European ancestry) and GeneSTAR (related individuals of European or African ancestry). SNPs with a minor allele frequency < 1%, missingness > 5, or HWE $p < 10^{-7}$ were excluded. Genotypes were imputed to approximately 2.5 million SNPs using HapMap Phase II CEU. The RIKEN and the BioBank Japan Project and AGEN cohorts comprise unrelated individuals of East Asian ancestry (EAS). SNPs with a minor allele frequency < 0.01, missingness > 1%, or HWE $p < 10^{-7}$ were excluded. Individuals with a call rate < 98% were excluded as well. Genotypes were imputed to approximately 2.5 million SNPs using HapMap Phase II JPT and CHB. The COGENT consortium cohorts comprise individuals of African American ancestry (AFR). SNPs with a minor allele frequency < 1% or missingness > 10% were excluded. Genotypes were imputed to approximately 2.5 million SNPs using HapMap Phase II CEU and YRI.

Cohort-Specific GWASs

For the initial GWA analyses, each cohort used linear regression to assess the association of all SNPs meeting the quality control criteria with each of the six traits separately. An additive genetic model was used and the regressions were adjusted for age, sex, and study site (if applicable). The Framingham Heart Study and the GeneSTAR study used linear mixed effects models to account for relatedness, and these models included adjustment for principal components.

Ethnic-Specific GWAS Meta-analyses

GWAS results of SNPs with a minor allele frequency (MAF) ≥ 1% and an imputation quality > 30% were analyzed in a fixed-effect meta-analysis (METAL software[22]) within each ancestry group, with genomic control (GC) correction of the individual GWAS results of each contributing cohort and the final meta-analysis results.[23]

Trans-ethnic Meta-analyses

For the trans-ethnic meta-analyses, the three sets of the ethnic-specific meta-analysis summary statistics were then combined with three approaches. First, we performed for each trait a trans-ethnic fixed-effect inverse variance-weighted meta-analysis of the EUR, EAS, and AFR GWAS summary statistics using METAL. Second, the ethnic-specific GWAS summary statistics were also combined using the MANTRA (Meta-Analysis of Trans-ethnic Association Studies) package, a meta-analysis software tool allowing for heterogeneity in allelic effects due to differences in LD structure in different ancestry clusters.[24] MANTRA results are reported as log10 Bayes's factors ($\log_{10}$BF). Finally, the three sets of ethnic-specific results were analyzed by means of the Han and Eskin RE2 model, a meta-analysis method developed for higher statistical power under heterogeneity.[25] We used the METASOFT 3.0c tool as developed by the Buhm Han laboratories (Web Resources). For the fixed-effects and the RE2 models, we applied a genome-wide significance threshold adjusted for multiple testing, as we analyzed six traits in our study. Given that the traits under investigation are correlated (Table S10), we used eigenvalues to assess the effective number of independent traits according to Ji and Li,[26] and we estimated this number at 4.0549 using the Matrix Spectral Decomposition tool (Web Resources). We therefore considered p values smaller than 1.25×10^{-8} (i.e., 5×10^{-8} / 4.0549) as genome-wide significant. For the MANTRA discovery analyses, a $\log_{10}$BF > 6.1 was considered as a genome-wide significant threshold value.[27]

Replication in Human Cohorts

The six independent replication studies—the Gutenberg Health Study (GHS cohorts 1 and 2, both EUR ancestry), the Genes and Blood-Clotting Study (GBC, EUR ancestry), the NEO study (EUR ancestry), the JUPITER trial (EUR ancestry), and the HANDLS study (AFR ancestry)[16–21] (total replication size N = 16,389)—provided linear regression results for the nine trait-locus combinations. Their results were meta-analyzed with a fixed effects inverse variance weighted method (METAL) and the RE2 methodology. Additionally, we meta-analyzed replication results with the discovery data using fixed-effects, MANTRA, and RE2 methods. For the replication analyses of the nine individual trait-locus combinations, we applied a threshold of $p < 0.05/9$. Additional human replication findings are provided in Supplemental Data.

Fine-Mapping

We used the MANTRA results to fine-map the regions of trait-associated index SNPs. We defined regions by identifying variants within a 1 Mb window around each index SNP (500 kb upstream and 500 kb downstream). For each SNP in a region, the posterior probability that this SNP is driving the region's association signal was calculated by dividing the SNP's BF by the summation of the BFs of all SNPs in the region. Credible sets (CSs) were subsequently created by sorting the SNPs in each region in descending order based on their BF (starting with the index SNP since this SNP has the region's largest BF by definition). Going down the sorted list, the SNPs' posterior probabilities were summed until the cumulative value exceeded 99% of the total cumulative posterior probability for all SNPs in the region. The length of a CS was expressed in base pairs. We compared 99% CSs for the trans-ethnic results and the results of a EUR-only MANTRA analysis.[13,24,28] For the MANTRA fine-mapping analyses, a less stringent threshold value of $\log_{10}$BF > 5 was applied, because we wanted to include

previously identified regions that may not have showed up in the more stringent MANTRA discovery analyses.

Heterogeneity Analysis

Heterogeneity of the associations across the different ethnicities was assessed by the I^2 and Cochran's Q statistics as reported by METAL[22] and the posterior probability of heterogeneity as reported by MANTRA.[24]

ENCODE Annotation

We evaluated the SNPs identified in the discovery analyses against the ENCODE Project Consortium's database of functional elements in the K562 erythroleukemic line.[29]

Experiments in Zebrafish

To substantiate the fine mapping of the *RBPMS*/*GTF2E2* region biologically, we tested the effect of morpholino knockdown in zebrafish for both *RBPMS* and *GTF2E2* orthologous genes, followed by assays of erythrocyte development.

Zebrafish *rbpms*, *rbpms2*, and *gtf2e2* were identified and confirmed by peptide sequence homology study and gene synteny analysis. For *rbpms*, we relied solely on peptide homology comparison and domain structure since no syntenic region was previously annotated and found by this study.

For each morpholino (MO), its design incorporated information about gene structure and translational initiation sites (Gene-Tool Inc.). MOs targeting each transcript were injected into single-cell embryos at 1, 3, and 5 ng/embryo to find an optimal dose at which there was minimal non-specific toxicity. The stepwise doses also give a range of phenotypes from a hypomorph to a near complete knockdown for most transcripts, which were used to assess the additive model of genetic association. After injection, embryos were collected at specified time points, 16–18 ss, 22–26 hpf, and 48 hpf using both standard morphological features of the whole embryo and hours post-fertilization (hpf) to minimize differences in embryonic development staging caused by the MO injection.[30,31] The embryos were then assayed for hematopoietic development by whole-mount in situ hybridization and benzidine staining. We conducted two assays simultaneously for globin transcription and hemoglobin formation. For the globin transcription, developing erythrocytes in the intermediate cell mass of the embryos were assayed by embryonic β-globin 3 expression at the 16 somite stage, or 16–18 hpf.[31] Benzidine staining phenotype was categorized from subtle decrease to complete absence of staining, which was categorized as mild, intermediate, or strong effect. Morphologically normal morphants with decreased blood formation were scored for hematopoietic effect.

In zebrafish, *rbpms* was not annotated in the known EST and cDNA databases, although a genomic sequence in the telomeric region on chromosome 7 predicting a coding sequence (80% peptide sequence similarity) was identified. In addition, the synteny between human *RBPMS* and *GTF2E2* is not conserved in zebrafish where *rbpms* and *gtf2e2* are located on two separate chromosomes, chromosomes 7 and 1, respectively. *rbpms2* was annotated with two paralogs on chromosome 7 (26 Mb away from and centromeric to the true *rbpms*) and chromosome 25 of the zebrafish genome. This orthology mapping was confirmed again by this research based on gene synteny and 88% and 91% sequence similarity, respectively, for *rbpms2b* and *rbpms2a* to human *RBPMS2*. These two zebrafish *RBPMS2* orthologs have a higher overall sequence similarity to human *RBPMS* than the true zebrafish *rbpms*, but both have a *RBPMS2*-signature stretch of alanine in the C terminus of the protein. Therefore, to confirm our *rbpms* orthology study and to confirm functional conservation of *rbpms* in zebrafish, MO individual knockdown of both *rbpms2a* and *rbpms2b* was also performed in independent experiments, showing much less or no effect by *rbpms2a* knock-down and moderate effect by *rbpms2b* impact on erythropoiesis, suggesting functional compensation of the genes in the *rbpms* family in zebrafish during embryonic erythropoiesis.

Chromatin Immunoprecipitation and Assay for Transposase Accessible Chromatin in Human CD34$^+$ Cell Lines

For ChIP-seq experiments, the following antibodies were used: Gata1 (Santa Cruz cat# sc265X), Gata2 (Santa Cruz cat# sc9008X), and H3K27ac (Abcam cat# ab4729; RRID: AB_2118291). ChIP experiments were performed as previously described with slight modifications.[32,33] In brief, 20–30 million cells for each ChIP were crosslinked by the addition of 1/10 volume 11% fresh formaldehyde for 10 min at room temperature. The crosslinking was quenched by the addition of 1/20 volume 2.5 M glycine. Cells were washed twice with ice-cold PBS and the pellet was flash-frozen in liquid nitrogen. Cells were kept at −80°C until the experiments were performed. Cells were lysed in 10 mL of lysis buffer 1 (50 mM HEPES-KOH [pH 7.5], 140 mM NaCl, 1 mM EDTA, 10% glycerol, 0.5% NP-40, 0.25% Triton X-100, and protease inhibitors) for 10 min at 4°C. After centrifugation, cells were resuspended in 10 mL of lysis buffer 2 (10 mM Tris-HCl [pH 8.0], 200 mM NaCl, 1 mM EDTA, 0.5 mM EGTA, and protease inhibitors) for 10 min at room temperature. Cells were pelleted and resuspended in 3 mL of sonication buffer for K562 and U937 and 1 mL for other cells used (10 mM Tris-HCl [pH 8.0], 100 mM NaCl, 1 mM EDTA, 0.5 mM EGTA, 0.1% Na-Deoxycholate, 0.05% Nlauroylsarcosine, and protease inhibitors) and sonicated in a Bioruptor sonicator for 24–40 cycles of 30 s followed by 1 min resting intervals. Samples were centrifuged for 10 min at 18,000 × *g* and 1% of TritonX was added to the supernatant. Prior to the immunoprecipitation, 50 mL of protein G beads (Invitrogen 100-04D) for each reaction were washed twice with PBS, 0.5% BSA. Finally, the beads were resuspended in 250 mL of PBS, 0.5% BSA, and 5 mg of each antibody. Beads were rotated for at least 6 hr at 40°C and then washed twice with PBS, 0.5% BSA. Cell lysates were added to the beads and incubated at 40°C overnight. Beads were washed 1× with 20 mM Tris-HCl (pH 8), 150 mM NaCl, 2 mM EDTA, 0.1% SDS, 1% Triton X-100, 1× with 20 mM Tris-HCl (pH 8), 500 mM NaCl, 2 mM EDTA, 0.1% SDS, 1% Triton X-100, 1× with 10 mM Tris-HCl (pH 8), 250 nM LiCl, 2 mM EDTA, 1% NP40, and 1× with TE and finally resuspended in 200 mL elution buffer (50 mM Tris-HCl [pH 8.0], 10 mM EDTA, and 0.5%–1% SDS). 50 μL of cell lysates prior to addition to the beads was kept as input. Crosslinking was reversed by incubating samples at 65°C for at least 6 hr. Afterward the cells were treated with RNase and proteinase K and the DNA was extracted by phenol/chloroform extraction.

ChIP-seq libraries were prepared using the following protocol. End repair of immunoprecipitated DNA was performed using the End-It DNA End-Repair kit (Epicenter, ER81050) and incubating the samples at 25°C for 45 min. End-repaired DNA was purified using AMPure XP Beads (1.8× the reaction volume) (Agencourt AMPure XP – PCR purification Beads, BeckmanCoulter, A63881) and separating beads using DynaMag-96 Side Skirted Magnet

(Life Technologies, 12027). A tail was added to the end-repaired DNA using NEB Klenow Fragment Enzyme (3′-5′ exo, M0212L), 1× NEB buffer 2, and 0.2 mM dATP (Invitrogen, 18252-015) and incubating the reaction mix at 37°C for 30 min. A-tailed DNA was cleaned up using AMPure beads (1.8× reaction volume). Subsequently, cleaned-up dA-tailed DNA went through Adaptor ligation reaction using Quick Ligation Kit (NEB, M2200L) according to the manufacturer's protocol. Adaptor-ligated DNA was first cleaned up using AMPure beads (1.8× of reaction volume), eluted in 100 μL and then size-selected using AMPure beads (0.9× of the final supernatant volume, 90 μL). Adaptor ligated DNA fragments of proper size were enriched with PCR reaction using Fusion High-Fidelity PCR Master Mix kit (NEB, M0531S) and specific index primers supplied in NEBNext Multiplex Oligo Kit for Illumina (Index Primer Set 1, NEB, E7335L). Conditions for PCR used are as follows: 98°C, 30 s; (98°C, 10 s; 65°C, 30 s; 72°C, 30 s) × 15 to 18 cycles; 72°C, 5 min; hold at 4°C. PCR-enriched fragments were further size selected by running the PCR reaction mix in 2% low-molecular-weight agarose gel (Bio-Rad, 161-3107) and subsequently purifying them using QIAquick Gel Extraction Kit (28704). Libraries were eluted in 25 μL elution buffer. After measuring concentration in Qubit, all the libraries went through quality-control analysis using an Agilent Bioanalyzer. Samples with proper size (250–300 bp) were selected for next generation sequencing using Illumina Hiseq 2000 or 2500 platform.

Alignment and visualization ChIP-seq reads were aligned to the human reference genome (hg19) using bowtie with parameters -k 2 -m 2 -S.[34] WIG files for display were created using MACS[35] with parameters -w -S–space = 50–nomodel–shiftsize = 200 and were displayed in IGV.[36,37]

High-confidence peaks of ChIP-seq signal were identified using MACS with parameters–keepdup = auto -p 1e-9 and corresponding input control. Bound genes are RefSeq genes that contact a MACS-defined peak between −10,000 bp from the TSS and +5,000 bp from the TES.

For the assay for transposase accessible chromatin (ATAC-seq), $CD34^+$ cells were expanded and differentiated using the protocol mentioned above. Before collection, cells were treated with 25 ng/mL hrBMP4 for 2 hr. 5×10^4 cells per differentiation stage were harvested by spinning at 500 × *g* for 5 min, 4°C. Cells were washed once with 50 μL of cold 1× PBS and spun down at 500 × *g* for 5 min, 4°C. After discarding supernatant, cells were lysed using 50 μL cold lysis buffer (10 mM Tris-HCl [pH 7.4], 10 mM NaCl, 3 mM $MgCl_2$, 0.1% IGEPAL CA-360) and spun down immediately at 500 × *g* for 10 min, 4°C. The cells were then precipitated and kept on ice and subsequently resuspended in 25 μL 2X TD Buffer (Illumina Nextera kit), 2.5 μL transposase enzyme (Illumina Nextera kit, 15028252), and 22.5 μL nuclease-free water in a total of 50 μL reaction for 1 hr at 37°C. DNA was then purified using QIAGEN MinElute PCR purification kit (28004) in a final volume of 10 μL. Libraries were constructed according to Illumina protocol using the DNA treated with transposase, NEB PCR master mix, Sybr green, and universal and library-specific Nextera index primers. The first round of PCR was performed under the following conditions: 72°C, 5 min; 98°C, 30 s; (98°C, 10 s; 63°C, 30 s; 72°C, 1 min) × 5 cycles; hold at 4°C. Reactions were kept on ice and, using a 5 μL reaction aliquot, the appropriate number of additional cycles required for further amplification was determined in a side qPCR reaction: 98°C, 30 s; (98°C, 10 s; 63°C, 30 s; 72°C, 1 min) × 20 cycles; hold at 4°C. Upon determining the additional number of PCR cycles required further for each sample, library amplification was conducted using the following conditions: 98°C, 30 s; (98°C,10 s; 63°C, 30 s; 72°C, 1 min) × appropriate number of cycles; hold at 4°C. Libraries prepared went through quality-control analysis using an Agilent Bioanalyzer. Samples with appropriate nucleosomal laddering profiles were selected for next generation sequencing using Illumina Hiseq 2500 platform.

All human ChIP-seq datasets were aligned to build version NCBI37/HG19 of the human genome using Bowtie2 (v.2.2.1)[34] with the following parameters:–end-to-end, -N0, -L20. We used the MACS2 v.2.1.0[35] peak finding algorithm to identify regions of ATAC-seq peaks, with the following parameter: –nomodel–shift −100–extsize 200. A q-value threshold of enrichment of 0.05 was used for all datasets.

Evaluation in Mouse Crosses

To further affirm the trait loci we identified, and in an attempt to further fine-map the intervals identified in our discovery analyses through cross-species comparisons, we evaluated the new loci in syntenic regions in 12 inter-strain mouse QTL crosses.[38]

In brief, mice from 12 different strains were inter-crossed[38] and the same erythrocyte traits we have studied by GWAS were measured in peripheral blood. The Jackson Laboratory Animal Care and Use Committee approved all protocols. The number of markers genotyped per cross varied by the platform used, and the total number per cross is provided in Table S9. QTL analysis was performed for each erythrocyte trait using R/qtl v1.07-12 (Web Resources).[39] Genetic map positions of all markers used were updated to the new mouse genetic map using online mouse map converter tool (Web Resources).[40] All phenotypic data were ranked-Z transformed to approximate the normal distribution prior to analysis. The QTL analysis was performed as a genome-wide scan with sex as an additive covariate. Permutation testing (1,000 permutations) was used to determine significance, and LOD scores greater than the 95^{th} percentile ($p < 0.05$) were considered significant. QTL confidence intervals were determined by the posterior probability.[41,42] For each candidate region in the mouse, the coordinates were obtained from the Mouse Genome Database, which is part of Mouse Genome Informatics (MGI), using the "Genes and Markers" query (Web Resources). Protein coding genes, non-coding RNA genes, and unclassified genes were queried.

Results

In this study we analyzed the association of genetic variation in 71,638 individuals and 6 clinically relevant erythrocyte traits which are commonly measured, accounting for the diverse ethnic background of the participants.

We identified 44 previously reported loci[7–12,43–47] (Table S3) and 9 other significant trait-locus associations at 7 loci ($p < 5 \times 10^{-8}$ or $\log_{10}BF > 6.1$, Table 1). *SHROOM3* was simultaneously identified in an exome chip analysis by our group in overlapping samples.[48] Ethnic-specific results are presented in Table S4. Regional association plots are shown for each region in Figure S1, showing ethnic-specific results, the trans-ethnic meta-analysis, and plots of pairwise LD across the regions for EUR, EAS, and AFR ancestry.

Five of the discovered trait loci showed a significant association in the fixed-effects trans-ethnic METAL analyses, in

Table 1. Findings from the METAL and MANTRA Trans-ethnic Analyses

						METAL		MANTRA		RE2
Trait	**SNP**	**Chr**	**Gene**	**c/nc**	**N**	**Effect (SE)**	**p**	**$Log_{10}BF$**	**posthg**	**p**
Hb	rs2299433	7	*MET*	T/C	63,091	0.041 (0.008)	6.16×10^{-8}	6.195	0.027	1.20×10^{-7}
Hct	rs6430549	2	*TMEM163* / ACMSD	A/G	71,647	0.103 (0.018)	4.96×10^{-9}	7.408	0.120	8.46×10^{-9}
Hct	rs2299433	7	*MET*	T/C	63,532	0.102 (0.019)	5.66×10^{-8}	6.199	0.099	9.87×10^{-8}
MCH	rs2060597	3	*PLCL2*	T/C	38,836	0.006 (0.001)	4.18×10^{-10}	8.178	0.009	9.75×10^{-10}
MCH	rs2979489	8	*RBPMS*	A/G	37,531	−0.002 (0.001)	8.89×10^{-5}	9.723	1.000	1.19×10^{-12}
MCV	rs10929547	2	*ID2*	A/C	50,870	−0.002 (0.0003)	2.50×10^{-9}	7.977	0.007	2.14×10^{-9}
MCV	rs9821630	3	*PLCL2*	A/G	48,697	−0.002 (0.0004)	6.86×10^{-9}	7.864	0.004	2.44×10^{-9}
MCV	rs2979489	8	*RBPMS*	A/G	48,697	−0.002 (0.0004)	7.24×10^{-9}	7.961	0.003	1.65×10^{-9}
MCV	rs6121246	20	*FOXS1*	T/C	49,896	0.003 (0.001)	4.05×10^{-7}	6.296	0.003	8.31×10^{-8}

Abbreviations are as follows: chr, chromosome number; c/nc, coding/non-coding allele; n, number of participants; SE, standard error; p, p value; $log_{10}BF$, logarithm of Bayes Factor; posthg, posterior probability of heterogeneity.

the Bayesian MANTRA analyses, and in the RE2 analyses; these were *TMEM163*/*ACMSD* for Hct, *PLCL2:rs2060597* for MCH, and *ID2*, *PLCL2:rs9821630*, and *RBPMS* for MCV. Two loci (*MET* and *FOXS1*) showed a borderline significant effect in METAL and RE2 and a strong significant effect in MANTRA for HB and MCV, respectively. The association of rs2979489 (*RBPMS*) further showed a strong association with MCH in the multi-ethnic Bayesian meta-analysis and in the RE2 model but was not detected in the multi-ethnic fixed-effects meta-analysis, nor in any of the ethnic-specific meta-analyses for this trait. Interestingly, MCH and MCV are correlated traits, yet strong heterogeneity of effect was observed for this SNP's association with MCH only, as indicated by both METAL (I^2 statistic 94%, p value Cochran's Q statistic of heterogeneity 6.48×10^{-8}) and MANTRA (posterior probability of heterogeneity = 1) (Table 1). Inspection of the discovery datasets showed that one of the African American cohorts supplied data for MCV but not for MCH, which resulted in a stronger positive association of rs2979489 with MCH than with MCV in the AFR meta-analyses. This phenomenon was accompanied by greater evidence of heterogeneity for MCH in the trans-ethnic meta-analyses because the EUR and EAS associations were in the opposite direction to that observed in the AFR meta-analysis. The MANTRA and RE2 analyses were able to account for this heterogeneity and thus yield a stronger result as compared to METAL for this trait locus.

Replication Analyses

In the meta-analyses of the replication cohorts, the trait-SNP combinations HT-*TMEM163*/*ACMSD* and MCH-*RBPMS* achieved a Bonferroni-corrected significance threshold with both fixed effects and RE2 methods ($p < 0.05/9$). *ID2* was Bonferroni-significant in the fixed-effects model and nominally significant in the RE2 model. Furthermore, we found nominal significance for MCV-*RBPMS* (fixed-effects analyses) and *FOXS1* (fixed-effects and RE2) (Table S5).

When we compared the discovery and replication combined meta-analyses with the discovery analyses alone, we observed stronger associations for Hct-*TMEM163/ACMSD*, MCH-*PLCL2*, MCV-*ID2*, and MCV-*RBPMS* in all three models (fixed-effects, MANTRA, and RE2). For MCH-*RBPMS*, we found a stronger association in the fixed-effects analysis (Table S6).

Statistical Fine-Mapping

We found that 31 trait-specific trans-ethnic 99% CSs showed a decrease in length of at least 50% as compared to their EUR-only CS counterparts (26 unique loci across the 6 erythrocyte traits) (Table S7).

Among the loci identified in this study, the chromosome 8 *RBPMS* locus showed fine-mapping according to this criterion (Table 2, Figure 1). For MCH, the EUR credible set spanned 204,200 bp, encompassing *RBPMS* and *GTF2E2*. The multi-ethnic credible set comprised just one SNP, rs2979489, within the first intron of *RBPMS* (Figure 1). Remarkably, this associated SNP rs2979489 is located adjacent to a GATA-motif where a gradual switch of binding from GATA2 to GATA1 takes place during commitment of human CD34 progenitors toward erythroid lineage (Figure 2, bottom left). Moreover, an assay for chromatin accessibility sites (ATAC-seq) and H3K27a ChIP-seq clearly identify that the genomic region proximal to this SNP is actively regulated during human erythroid differentiation (Figure 2, bottom right).

Among the known loci, fine mapping narrowed signals as shown in Table S7.

Interestingly, trans-ethnic fine-mapping of the *XRN1* locus (MCH) led us to the rs6791816 polymorphism. Van der Harst et al. identified the same SNP in their exploration of nucleosome-depleted regions (NDRs, representing active regulatory elements for erythropoeisis) in a follow-up

Table 2. Fine Mapping of a Chromosome 8 Locus Identified in European Ancestry Meta-analysis by MANTRA Trans-ethnic Analysis

			EUR				Multi-ethnic			
Trait	**Chr**	**Gene**	**topSNP**	**log_{10}BF**	**n_SNPs**	**width (bp)**	**topSNP**	**log_{10}BF**	**n_SNPs**	**width (bp)**
MCH	8	*RBPMS*	rs2979502	6.32982	21	241480	rs2979489	9.72267	1	1
MCV	8	*RBPMS*	rs2979489	6.13733	11	241480	rs2979489	7.96132	1	1

Abbreviations are as follows: chr, chromosome number; log_{10}BF, logarithm of Bayes Factor; n_SNPs, number of SNPs in the region.

analysis of their GWAS results.[10] By means of subsequent formaldehyde-assisted isolation of regulatory elements followed by next-generation sequencing (FAIRE-seq), they pinpointed rs6791816 as an NDR SNP in LD with their initial index SNP for MCH and MCV.

Furthermore, fine-mapping of both the *MPND* locus (MCH) and *SH3GL1* locus (MCV) pointed to the rs8887 SNP within the 3′ UTR of *PLIN4*. The rs8887 SNP minor allele has been shown experimentally to create a novel seed site for miR-522, resulting in decreased *PLIN4* expression.[49] miR-522 is expressed in circulating blood,[50] and these data suggest that an allele-specific miR-522 regulation of *PLIN4* by rs8887 could serve as a functional mechanism underlying the identified association.

We additionally showed fine mapping in several other intervals (Table S7) with fine-mapped genes about which less is known about their potential biologic role in erythropoeisis or red blood cell function. These regions are of interest for further hypothesis generation based upon the GWAS findings.

ENCODE Analyses

We further evaluated the SNPs from the chromosome 8 *RBPMS* region against the ENCODE Project Consortium's database of numerous functional elements in the K562 erythroleukemic line.[29] The lone SNP that was fine mapped at the locus, rs2979489, was found in a strong enhancer element as defined by Segway, supporting a functional role for this SNP and *RBPMS*. The other SNPs in the *RBPMS* region, excluded by the statistical fine-mapping exercise, were not annotated as regulatory in the ENCODE data (Table S8).

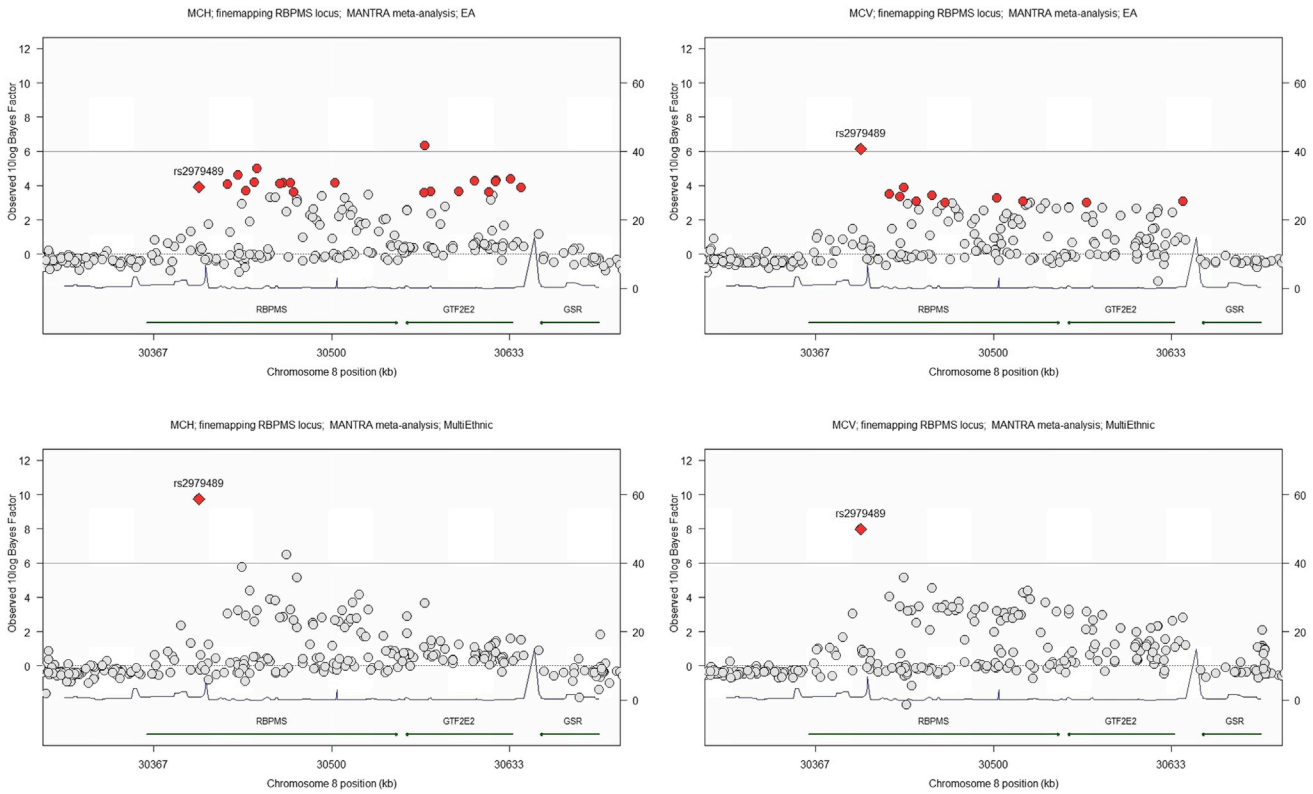

Figure 1. Fine Mapping of the Chromosome 8 *RBPMS/GTF2E2* Locus
99% credible sets (red dots) around the top hit rs2979489 (red diamond). European Ancestry MANTRA analyses (top) for MCH (left) and MCV (right) are shown, compared to 99% credible sets of the trans-ethnic MANTRA analyses (bottom, MCH on the left and MCV on the right).

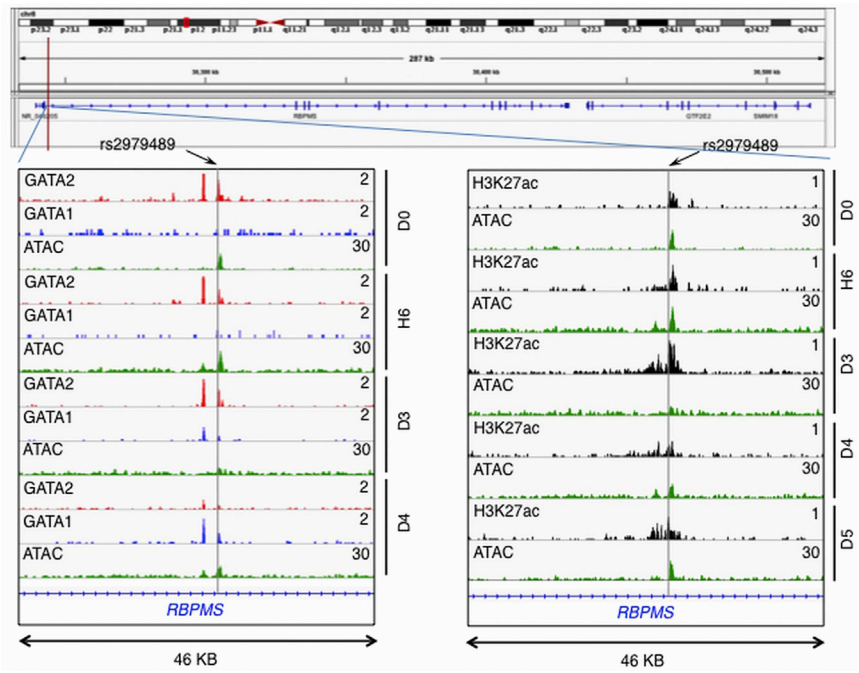

Figure 2. rs2979489 Is Localized to a Potential Regulatory Site that Involves Transition Binding of GATA2 to GATA1 during Erythrocyte Differentiation
Top shows gene-track view of rs2979489 location in the *RBPMS*/*GTF2E2* gene region. Bottom left: gene track of RBPMS gene showing overlap of GATA2, GATA1, and ATAC-seq peaks (red, blue, and green, respectively) during human erythroid differentiation. Bottom right: overlap of ATAC-seq (green) and H3K27ac ChIP-seq (black) during differentiation at the region proximal to the SNP rs2979489. The gray horizontal line indicates the position of SNP rs 2979489. D0, day 0; H6, hour 6; D3, day 3; D4, day 4; and D5, day 5 of erythroid differentiation time-course post-induction of differentiation.

Experiments in Zebrafish

We identified a erythropoietic effect for the zebrafish *rbpms*. Both embryonic globin expression at 16 ss and o-dianisidine/benzidine staining at 48 hpf significantly decreased in morphants, indicating a decrease in both globin transcription and Hb levels (Figure 3). This loss-of-function finding is consistent with a decreased mean erythrocyte Hb content observed in our human association results. In zebrafish, the *rbpms* orthology mapping included *rbpms2a*, *rbpms2b*, and *rbpms*, and loss-of-function phenotypes of all orthologs were tested experimentally. The results suggested a clear erythropoietic effect with limited functional compensation of the genes in the rbpms family in zebrafish during embryonic erythropoiesis. On the other hand, morpholino knockdown experiments with the zebrafish ortholog of *GTF2E2* did not show an apparent erythropoietic effect.

Review of the human association results showed no evidence of pleiotropy across the RBPMS family of genes and denote that the human association is specific to *RBPMS* (Supplemental Data). This review was conducted because the orthology in the fish led to inclusion of *rbpms2* in the zebrafish analyses as well. These findings indicate that the statistical fine-mapping was useful to home in on *RPBMS* as a causal gene influencing erythropoiesis.

Evaluation in Mouse Crosses

In the eight regions from our discovery analysis, six had evidence of cross-species validation by evidence of syntenic gene within the linkage peak in the mouse QTL results (Table 3). However, the human GWAS intervals were not narrowed by the mouse QTL results for any of these loci (Table S9).

Discussion

We conducted GWASs and meta-analyses of six erythrocyte traits (Hb, Hct, MCH, MCHC, MCV, and RBC) in 71,638 individuals from European, Asian, and African American ancestry. While prior genome-wide association studies have identified loci associated with erythrocyte traits through the analysis of ancestrally homogeneous cohorts and consortia, largely biased toward European ancestry studies, trans-ethnic analysis has not previously been performed while accounting for differences in genetic architecture in ethnically diverse groups.

We identified seven loci for erythrocyte traits (nine locus-trait combinations) and replicated 44 previously identified loci. We fine-mapped several known and new loci. One fine-mapped locus led us to a region on chromosome 8 associated with MCH and MCV.

In the chromosome 8 *RBPMS/GTF2E2* locus, the index variant rs2979489, which was associated with MCV and MCH and highlighted in the trans-ethnic fine-mapping analyses, is located within the first intron of *RBPMS* (RNA binding protein with multiple splicing), notably at an open chromatin site at which a switch of GATA1/2 binding occurs during erythroid differentiation. The *RBPMS* protein product regulates a variety of RNA processes, including pre-mRNA splicing, RNA transport, localization, translation, and stability.[51,52] *RBPMS* is expressed at relatively low levels in mammalian erythroblasts and the protein product has not been detected in mature human erythrocytes.[53,54]

The rs2979489 polymorphism showed remarkably high heterogeneity in effect on the MCH trait across the different ethnicities, with different directions of effect for the AFR meta-analysis results compared to the EUR and ASN findings. If the variant is causal, this pattern of association could reflect gene-environment interaction. In this case, different exposures in AFR compared to EUR/ASN

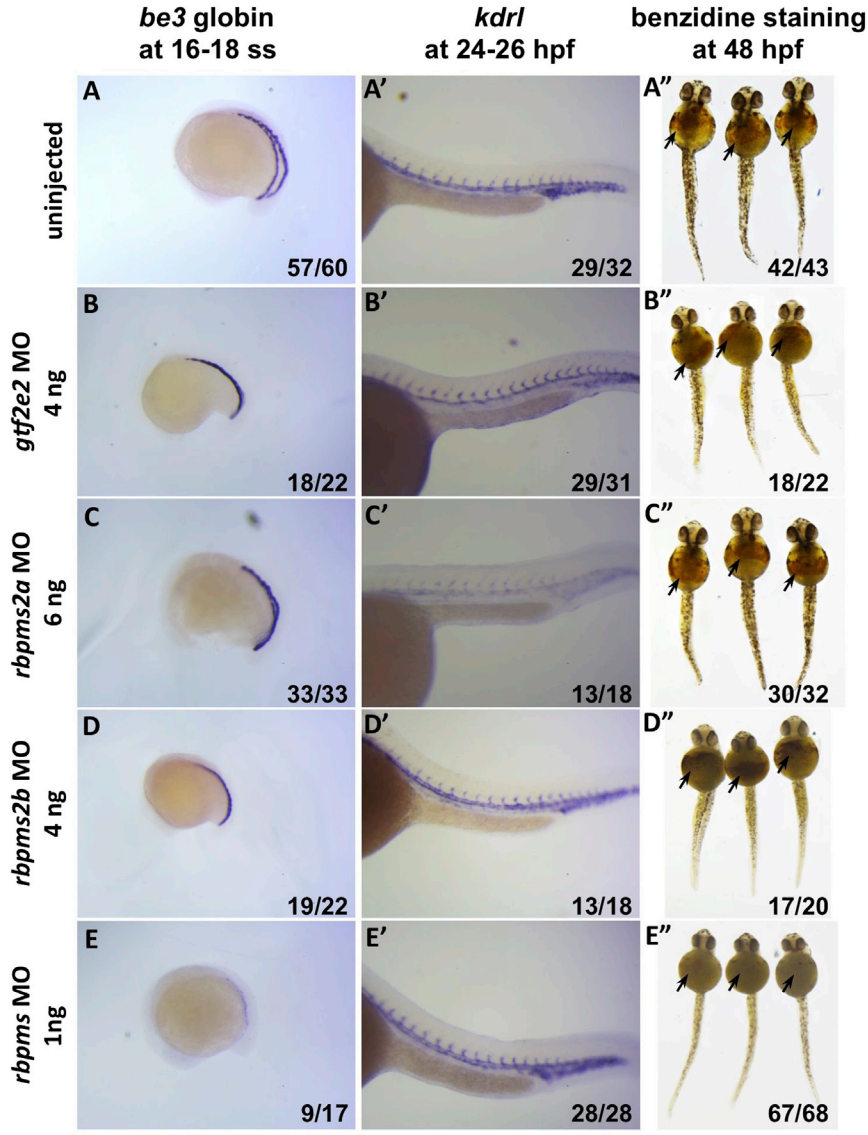

Figure 3. Loss-of-Function Analysis of the *RBPMS*, *RBPMS2*, and *GTF2E2* Orthologs in Zebrafish

After injection of 0–3 ng ATG and splicing morpholinos (MOs) against the RBPMS zebrafish ortholog (row E), both the o-dianisidine/benzidine staining (arrows) in embryos at 48 hpf (right) and the embryonic βe3 globin expression in embryos at 16–18 ss (left) are obviously decreased, indicating a dose-dependent disruption in erythropoiesis in the experimentally treated embryos as compared to uninjected and *gtf2e2*-, *rbpms2a*-, and *rbpms2b*-MO-injected controls (rows A–D). Representative results are shown for the embryos injected with MOs against the RBPMS ortholog in (E) as well as for the embryos injected with MOs against *rbpms2a* (C) and *rbpms2b* (D) at higher doses. Injections of MO against the zebrafish *GTF2E2* ortholog (B) also at a higher dose show no obvious effect on βe3 globin expression at 16–18 ss and o-dianisidine/benzidine staining at 48 hpf. Expression pattern of vascular marker gene *kdrl* (A–E, middle) is relatively normal in all MO-injected embryos at 24–26 hpf, suggesting grossly normal development of cells in other organs. The numbers on the lower right corner of each image indicate the number of embryos with phenotypes similar to the ones shown on each of the images over the total number of embryos examined in each of the experimental groups.

populations may lead to a marginal effect of the SNP in opposing directions by different selection pressures. If, however, rs2979489 is not causal, but rather a marker in LD with the causal variant, then the opposing direction of effects could reflect very different LD structures in the different populations, also indicating selection, or theoretically it could even reflect different causal variants in AFR and EUR/EAS—and rs2979489 being just in strong LD with both causal variants.

The SNP rs2979489 is located adjacent to a GATA-motif where a gradual switch of binding from GATA2 to GATA1 takes place during commitment of human CD34 progenitors toward erythroid lineage. These observations suggest that rs2979489 localizes at a potential regulatory site where a modulation of erythroid cell differentiation occurs and the presence of rs2979489 may lead to observed red cell trait alterations in human populations, possibly through regulation of *RBPMS* expression timing, level, and/or splicing variation. Although *RBPMS* previously had no known role in hematopoiesis or more specifically in erythropoiesis, *RBPMS* has been previously shown to be upregulated in transcriptional profiles of murine and human hematopoietic stem cells.[55–57] Its role may be at much earlier stages during the differentiation of erythrocytes from erythroblasts and/or hematopoietic stem cells. RBPMS is known to physically interact with Smad2, Smad3, and Smad4 and stimulate smad-mediated transactivation through enhanced Smad2 and Smad3 phosphorylation and associated promotion of nuclear accumulation of Smad proteins.[58] These Smad proteins are known to regulate the TGF-β-mediated regulation of hematopoietic cell fate and erythroid differentiation.[59] *RBPMS* has four annotated transcript isoforms, and further delineation of the tissue specificity, timing of expression, and function of these transcripts in the context of the genetic variant we identified warrants further study.

Among the additional six loci, we identified two loci in which the index SNP was located within annotated genes, rs6430549 in *ACMSD* (aminocarboxymuconate semi aldehyde decarboxylase, intronic) and rs2299433 in *MET* (mesenchymal epithelial transition factor, intronic). No previous hematologic role has been described for either region. Variants in the chromosome 2q21.3 *ACMSD* region

Table 3. Mouse QTL Validation of the Findings from MANTRA Trans-ethnic Analyses

Trait	Chr	Gene	Human (hg18/Build 36) (Chromosome:Position)	Mouse (37 mm9) (Chromosome:Position)	Significant and Suggestive Mouse QTL[a] Peak (95% CI) (Mb)	LOD
Hct	2	*TMEM163/ACMSD*	chr2: 135,196,450–135,438,613	chr1: 129,581,372–129,711,586[b]	141.0 (54.8–158.9)*	3.72*
Hct	4	*SHROOM3*	chr4: 77,586,311–77,629,342	chr5: 93,112,461–93,394,344	46.0 (19.6–106.5)	2.34
Hct	7	*MET*	chr7: 116,118,114–116,131,947	chr6: 17,432,318–17,447,418[b]	37.6 (6.6–127.9)	2.75
MCH	8	*RBPMS*	chr8: 30,400,375–30,400,375	chr8: 34,893,115–35,040,335	78.9 (28.0–96.1)*	3.98*
MCV	3	*PLCL2*	chr3: 16,860,239–16,945,942	chr17: 50,604,848–50,698,773[b]	46.0 (28.6–55.3)*	5.46*
MCV	20	*FOXS1*	chr20: 29,684,484–29,897,013	chr2: 152,576,419–152,758,874[b]	170.1 (147.6–179.3)*	4.69*

[a]Gene found in a significant (indicated with asterisk) or suggestive 95% CI mouse QTL, not corresponding to the human interval.
[b]Within the corresponding human interval (±250 kb).

have previously been associated with blood metabolite levels, obesity, and Parkinson disease.[60–62] A genetic variant in the first intron of *MET* was significantly associated with both Hb and Hct; however, association was not observed in replication samples, possibly due to lower power in the replication experiment. Three additional loci were intergenic but close to a coding gene (rs10929547 near *ID2* [inhibitor of DNA binding 2, dominant-negative helix-loop-helix protein], rs6121246 near *FOXS1* [forkhead box S1], and rs2060597 approximately 40 kbp upstream of *PLCL2* [phospholipase C-like 2]). The roles of variants in these regions in determining erythrocyte traits are unknown.[53,63]

In the statistical fine-mapping analyses, the trans-ethnic meta-analysis approach resulted in smaller 99% credible intervals in all of the loci identified in this study. Since these loci were identified in analyses that accounted for heterogeneity in allelic effects between ethnic groups, in which the heterogeneity may be due to variation in LD patterns, we examined the LD patterns in these loci. Not surprisingly, we noted that the consistent decrease in the size of 99% credible interval across all loci is likely due to the inclusion of cohorts of African ancestry, an ethnic group with generally smaller LD blocks throughout the genome. The loss-of-function screens in zebrafish for the chromosome 8 signal suggested that these analyses successfully identified a single gene (*RBPMS*) with erythropoietic effect within one of the fine-mapped intervals. We also fine-mapped previously known regions such as the chromosome 6p21.1 region associated with RBC count and highlighted *CCND3*, which has been experimentally shown to regulate RBC count experimentally in a knockout mouse model.[64] These examples suggest that attempts to refine association signals using these types of approaches in existing samples may yield functional candidates for further mechanistic hypothesis testing, which is a major goal of GWASs.

Trans-ethnic genome-wide meta-analyses of common variants have aided in the characterization of genetic loci for various complex traits.[13,65–67] Our data demonstrate the benefits of trans-ethnic genome-wide meta-analysis in identifying and fine-mapping genetic loci of erythrocyte traits. By exploiting the differences in genetic architecture of the associations within these loci in various ethnic groups, we may identify causal genes influencing clinically relevant hematologic traits. Use of a similar approach for other complex traits is likely to provide deeper insights into the biological mechanisms underlying human traits.

Accession Numbers

Summary data have been deposited in the database of Genotypes and Phenotypes (dbGaP) under CHARGE (Cohorts for Heart and Aging Research in Genomic Epidemiology) Consortium Summary Results from Genomic Studies. The dbGaP study accession number is phs000930.

Supplemental Data

Supplemental data include Supplemental Acknowledgments, individual study methods and cohort descriptions, pleiotropy analysis, 10 tables, and a figure with 123 panels.

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Web Resources

Center for Genome Dynamics, http://cgd.jax.org
dbGaP, http://www.ncbi.nlm.nih.gov/gap
Matrix Spectral Decomposition, http://neurogenetics.qimrberghofer.edu.au/matSpD/
METASOFT 3.0c, http://www.buhmhan.com/software
MGI Genes and Markers Query, http://www.informatics.jax.org/marker
R/qtl v1.07-12, http://www.rqtl.org

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Supplemental Data

Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for *RBPMS* in Erythropoiesis

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Acknowledgements

Individual Study Methods and Cohort Descriptions

The cohorts contributing to this study were general population samples. All participants provided written informed consent and studies were approved by their local Research Ethics Committees and/or Institutional Review Boards. Summary demographic characteristics are listed in **Table S2**. References for ascertainment methods and erythrocyte trait measurement for each participating study are given below.

European Ancestry Cohorts

- Age, Gene/Environment Susceptibility-Reykjavik Study (AGES)[1,2]
- Atherosclerosis Risk in Communities Study (ARIC)[2,3]
- Austrian Stroke Prevention Study (ASPS) [4]
- Baltimore Longitudinal Study of Aging (BLSA)[5]
- Coronary Artery Risk Development in Young Adults (CARDIA)[6]
- Cardiovascular Health Study (CHS)[2,7]
- Framingham Heart Study (FHS)[2,8]
- Johns Hopkins Genetic Study of Atherosclerosis Risk (GeneSTAR)[9–11]
- Health, Aging, and Body Composition (HealthABC)[9,12]
- Invecchiare in Chianti Study (InCHIANTI)[5]
- PROspective Study of Pravastatin in the Elderly at Risk (PROSPER/PHASE)[13]
- Rotterdam Study I (RS-I)[2,14]
- Rotterdam Study II (RS-II)[14]
- Rotterdam Study III (RS-III)[14]

East-Asian Ancestry Cohorts

- The BioBank Japan Project (RIKEN)[15,16]
- Asian Genetic Epidemiology Network (AGEN)[17,18]

African-American Ancestry Cohorts

- Atherosclerosis Risk in Communities Study (ARIC)[3,12,19]
- Jackson Heart Study (JHS)[12,19,20]
- Coronary Artery Risk Development in Young Adults (CARDIA)[6,12,19]
- Cardiovascular Health Study (CHS)[7]
- Johns Hopkins Genetic Study of Atherosclerosis Risk (GeneSTAR) [9–11]

Health, Aging, and Body Composition (HealthABC)[9,12]

Women's Health Initiative (WHI)[12,19,21]

Replication CohortsGutenberg Health Study (GHS)[22]

Genes and Blood-Clotting Study (GBC)[23]

Netherlands Epidemiology of Obesity Study (NEO)[24]

JUPITER Trial[25]

HealthyAging in Neighborhoods of Diversity across the Life Span (HANDLS)[9,12]

Supplemental Methods and Results

Additional Human Replication Findings

The discovery and replication results were meta-analysed separately for the EUR and AFR cohorts in METAL and with RE2, and as a further step, the combined METAL results were further meta-analysed with the EAS discovery data using METAL,MANTRA and RE2 methods. (**Table S5**).

In both the replication and discovery samples, we verified the allele directions in the original input files to address the question whether allele flipping could account for the *RBPMS* finding for MCH. In our results rs2979489 only became genome-wide significant in the trans-ethnic meta-analysis; the individual ethnic-specific results were not significant. We checked the allele frequencies in several 1000G panels. In all cases A was the most common allele and G the rarest, as is the case in our HapMap analyses.

Pleiotropy analysis

To further relate these findings in the rbpms gene family back to the human association data, we evaluated *RBPMS* in WBC traits and *RBPMS2* in our RBC analyses and WBC traits. The purpose of this analysis was to explore possible pleiotropy which might suggest effects on an earlier hematopoietic progenitor cell. Variants in the *RBPMS* and *RBPMS2* gene regions (+/- 50kb from exon borders) showed no association with WBC traits in a trans-ethnic analysis of the same cohorts.[26] Further, there was no evidence of association with erythrocyte traits in the *RBPMS2* region. Therefore, while there may be evidence of a functional class effect of the rbpms genes in the zebrafish experimental data, the human association data suggest that genetic variation in the *RBPMS* locus specifically influences erythrocyte traits in humans and that *RBPMS* is likely the true causal gene underlying this association.

Supplemental Figures

Figure S1

-log P value plots and varLD plots

Regional association plots for loci identified by our trans-ethnic analysis. For each trait-locus identified in the MANTRA analyses, including the novel and previously known loci, we have plotted the individual ethnicity-specific meta-analysis (METAL) results, the trans-ethnic fixed effects meta-analysis (METAL) and the Bayesian meta-analysis (MANTRA) results with SNPs colored according to the credible interval set for that region. Also shown for each region is the pair-wise LD correlation (varLD) and RNA expression of genes within the locus in erythroblast cell lines).[27]

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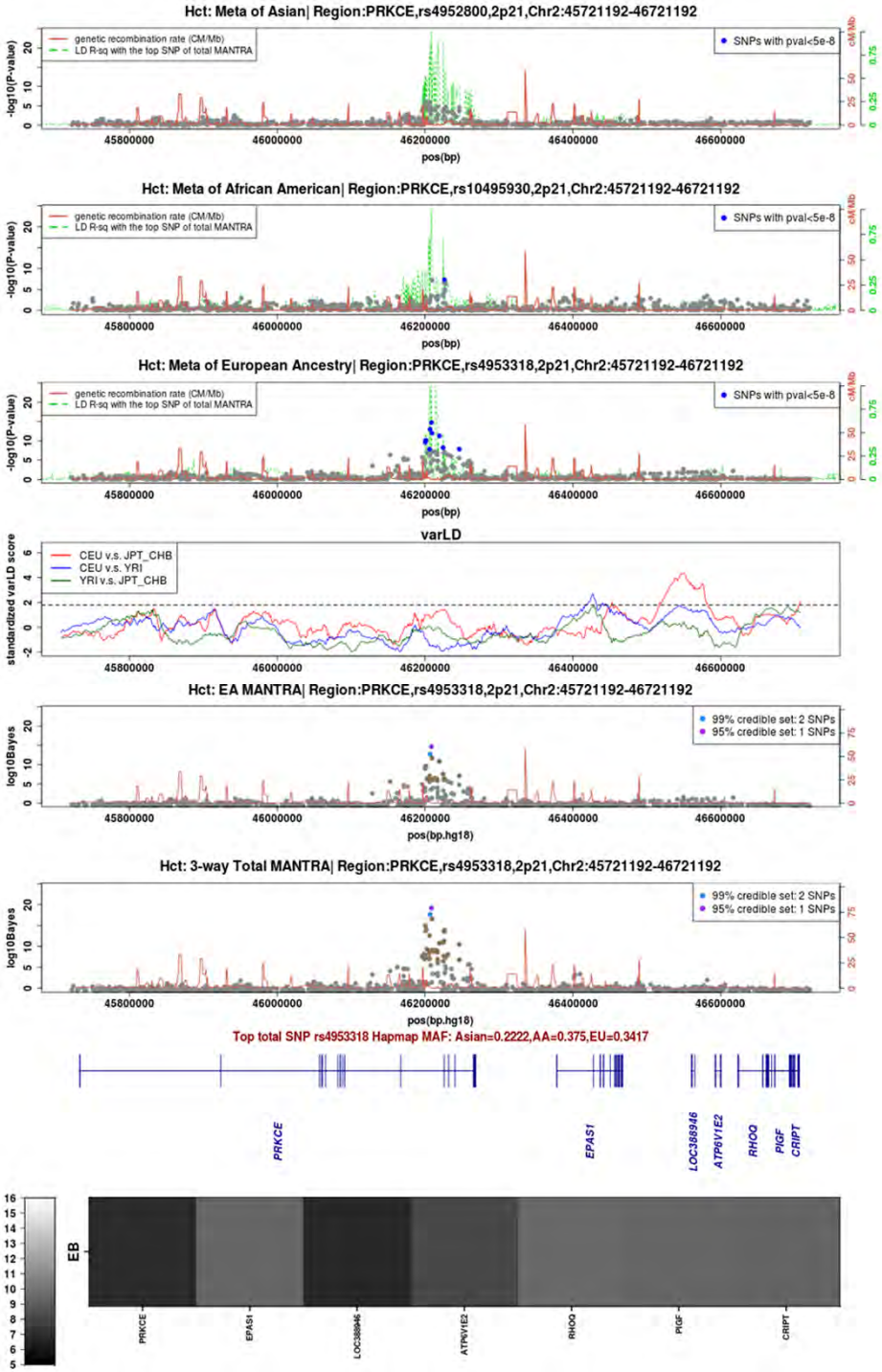
trait	Region	chr	cyto	Index SNP	Total_gene	Page
Hct	1	2	2p21	rs4953318	PRKCE	10
Hct	2	2	2q21	rs6430549	ACMSD	11
Hct	3	4	4q12	rs218237	KIT	12
Hct	4	4	4q21	rs1398018	SHROOM3	13
Hct	5	6	6p22	rs1800562	HFE	14
Hct	6	6	6q23	rs9399137	HBS1L	15
Hct	7	7	7q22	rs2075672	ACTL6B	16
Hct	8	7	7q31	rs2299433	MET	17
Hct	9	7	7q36	rs10224210	PRKAG2	18
Hct	10	9	9q34	rs495828	ABO	19
Hct	11	10	10q21	rs16926246	HK1	20
Hct	12	12	12q24	rs3184504	SH2B3	21
Hct	13	15	15q24	rs4886755	NRG4	22
Hct	14	17	17q21	rs241030	CRHR1	23
Hct	15	22	22q12	rs2413450	TMPRSS6	24
Hct	16	22	22q13	rs5765524	FBLN1	25
Hb	1	2	2p21	rs4953318	PRKCE	27
Hb	2	3	3q29	rs12632706	TFRC	28
Hb	3	4	4q12	rs170117	KIT	29
Hb	4	6	6p22	rs1800562	HFE	30
Hb	5	6	6p21	rs412657	NOTCH4	31
Hb	6	7	7q22	rs1617640	EPO	32
Hb	7	7	7q31	rs2299433	MET	33
Hb	8	7	7q36	rs10480299	PRKAG2	34
Hb	9	9	9q34	rs495828	ABO	35
Hb	10	10	10q21	rs16926246	HK1	36
Hb	11	12	12q24	rs11066301	PTPN11	37
Hb	12	15	15q24	rs4886755	NRG4	38
Hb	13	16	16p13	rs2562181	MPG	39
Hb	14	17	17q21	rs241030	CRHR1	40
Hb	15	22	22q12	rs4820268	TMPRSS6	41
MCHC	1	1	1q23	rs2479868	SPTA1	43
MCHC	2	6	6p22	rs198846	HIST1H1T	44
MCHC	3	6	6q23	rs9376090	HBS1L	45
MCHC	4	8	8p11	rs4737009	ANK1	46
MCHC	5	12	12q24	rs671	NA	47
MCHC	6	16	16p13	rs7197554	C16orf35	48
MCHC	7	16	16q24	rs2608604	CDT1	49
MCHC	8	22	22q12	rs2413450	TMPRSS6	50
MCH	1	1	1q31	rs12127588	PTPRC	52
MCH	2	2	2p16	rs13019832	BCL11A	53
MCH	3	3	3p24	rs2060597	PLCL2	54
MCH	4	3	3p24	rs1505307	THRB	55
MCH	5	3	3q23	rs6791816	ATR	56
MCH	6	3	3q29	rs9859401	TFRC	57

MCH	7	4	4q12	rs218237	KIT	58
MCH	8	5	5p15	rs2736100	TERT	59
MCH	9	6	6p22	rs1800562	HFE	60
MCH	10	6	6p21	rs9349205	CCND3	61
MCH	11	6	6q21	rs9400273	CCDC162P/CD164	62
MCH	12	6	6q23	rs7776054	HBS1L	63
MCH	13	6	6q24	rs592423	CITED2/LOC655434	64
MCH	14	7	7p12	rs12669559	IKZF1	65
MCH	15	7	7q22	rs12532878	MOSPD3	66
MCH	16	8	8p21	rs2076940	XPO7	67
MCH	17	8	8p12	rs2979489	RBPMS	68
MCH	18	9	9p24	rs10758656	RCL1/MIR101-2	69
MCH	19	10	10q11	rs11239550	08-mrt	70
MCH	20	10	10q11	rs17720193	NA	71
MCH	21	12	12p13	rs7309743	CCND2	72
MCH	22	12	12q24	rs2074356	NA	73
MCH	23	14	14q23	rs7155454	FNTB/MIR4706	74
MCH	24	15	15q22	rs7165102	C15orf44	75
MCH	25	16	16p13	rs1122794	ITFG3	76
MCH	26	17	17q11	rs9892942	ERAL1	77
MCH	27	19	19p13	rs8887	KIAA1881/PLIN4	78
MCH	28	19	19p13	rs2242517	GCDH	79
MCH	29	20	20q13	rs737092	RBM38	80
MCH	30	22	22q12	rs2413450	TMPRSS6	81
MCV	1	1	1q23	rs12041363	OR10R2	83
MCV	2	1	1q31	rs1036332	PTPRC/LOC100131234	84
MCV	3	1	1q44	rs3811444	TRIM58	85
MCV	4	2	2p25	rs10929547	ID2	86
MCV	5	2	2p16	rs13027161	BCL11A/MIR4432	87
MCV	6	3	3p24	rs9821630	PLCL2	88
MCV	7	3	3p24	rs1505307	THRB	89
MCV	8	3	3q23	rs6780250	ATR	90
MCV	9	3	3q29	rs3893275	ZDHHC19	91
MCV	10	4	4q12	rs218237	KIT	92
MCV	11	5	5p15	rs2736100	TERT	93
MCV	12	6	6p22	rs198833	HIST1H1T	94
MCV	13	6	6p21	rs9349205	CCND3	95
MCV	14	6	6q21	rs9374080	CD164/CCDC162P	96
MCV	15	6	6q23	rs7776054	HBS1L	97
MCV	16	6	6q24	rs592423	CITED2/LOC645434	98
MCV	17	6	6q26	rs381500	QKI	99
MCV	18	7	7p12	rs12718598	IKZF1	100
MCV	19	7	7q22	rs7385804	TFR2	101
MCV	20	8	8p21	rs10503716	XPO7	102
MCV	21	8	8p12	rs2979489	RBPMS	103
MCV	22	9	9p24	rs10758658	RCL1/MIR101-2	104
MCV	23	9	9q34	rs8176749	ABO	105
MCV	24	10	10q11	rs963029	08-mrt	106
MCV	25	12	12p13	rs11611647	CCND2	107
MCV	26	12	12q24	rs2074356	NA	108
MCV	27	14	14q23	rs726668	MAXMIR4706	109
MCV	28	15	15q22	rs7176565	DENND4A/MIR4511	110

MCV	29	16	16p13	rs13336641	NA	111
MCV	30	17	17q11	rs12325788	TRAF4	112
MCV	31	18	18q21	rs9949494	C18orf25	113
MCV	32	19	19p13	rs8887	KIAA1881/PLIN4	114
MCV	33	19	19p13	rs9384	GCDH	115
MCV	34	20	20q11	rs6121246	FKHL18/FOXS1	116
MCV	35	20	20q13	rs737092	RBM38	117
MCV	36	22	22q11	rs4820091	UBE2L3	118
MCV	37	22	22q12	rs5754115	FBXO7	119
MCV	38	22	22q12	rs2413450	TMPRSS6	120
MCV	39	22	22q13	rs140522	LOC440836/ODF3B	121
RBC	1	2	2p21	rs4952800	PRKCE	123
RBC	2	4	4p14	rs3860068	TMEM156	124
RBC	3	4	4q12	rs218237	KIT	125
RBC	4	6	6p21	rs9349205	CCND3	126
RBC	5	6	6q21	rs9400273	CD164/CCDC162P	127
RBC	6	6	6q23	rs9376090	HBS1L	128
RBC	7	6	6q24	rs592423	CITED2/LOC645434	129
RBC	8	7	7q22	rs2075672	ACTL6B	130
RBC	9	9	9p24	rs10758656	RCL1/MIR101-2	131
RBC	10	9	9q34	rs579459	ABO	132
RBC	11	12	12p13	rs7309743	CCND2	133
RBC	12	16	16p13	rs13339636	NA	134
RBC	13	17	17q21	rs2732706	LRRC37A	135
RBC	14	19	19p13	rs17706531	GCDH	136
RBC	15	22	22q13	rs12148	SCO2	137

HCT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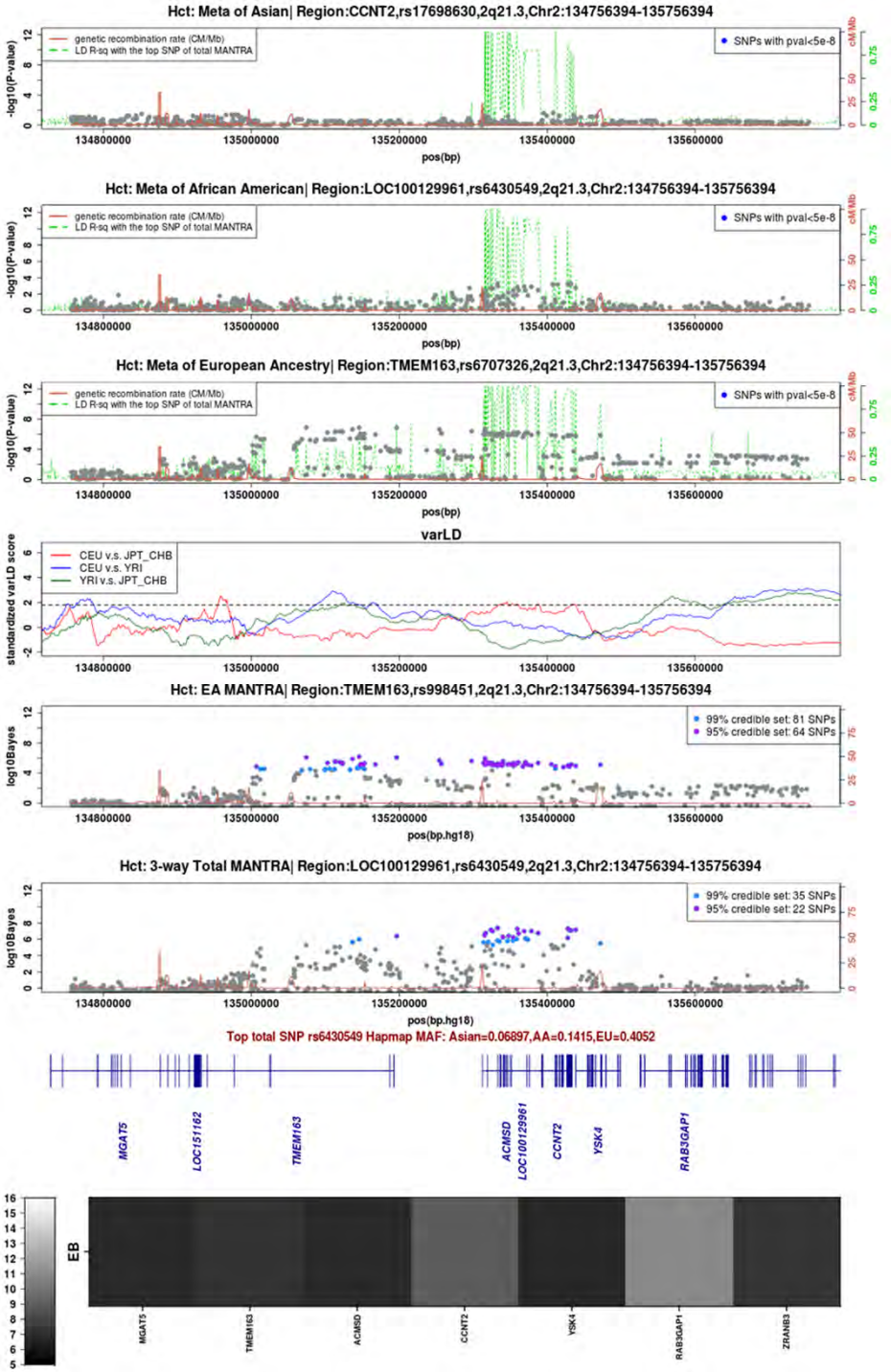
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:PRKCE,rs10495930,2p21,Chr2:45721192-46721192
Hct: Meta of European Ancestry| Region:PRKCE,rs4953318,2p21,Chr2:45721192-46721192
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:PRKCE,rs4953318,2p21,Chr2:45721192-46721192
99% credible set: 2 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:PRKCE,rs4953318,2p21,Chr2:45721192-46721192
Top total SNP rs4953318 Hapmap MAF: Asian=0.2222,AA=0.375,EU=0.3417
PRKCE
EPAS1
LOC388946
ATP6V1E2
RHOQ
PIGF
CRIPT
EB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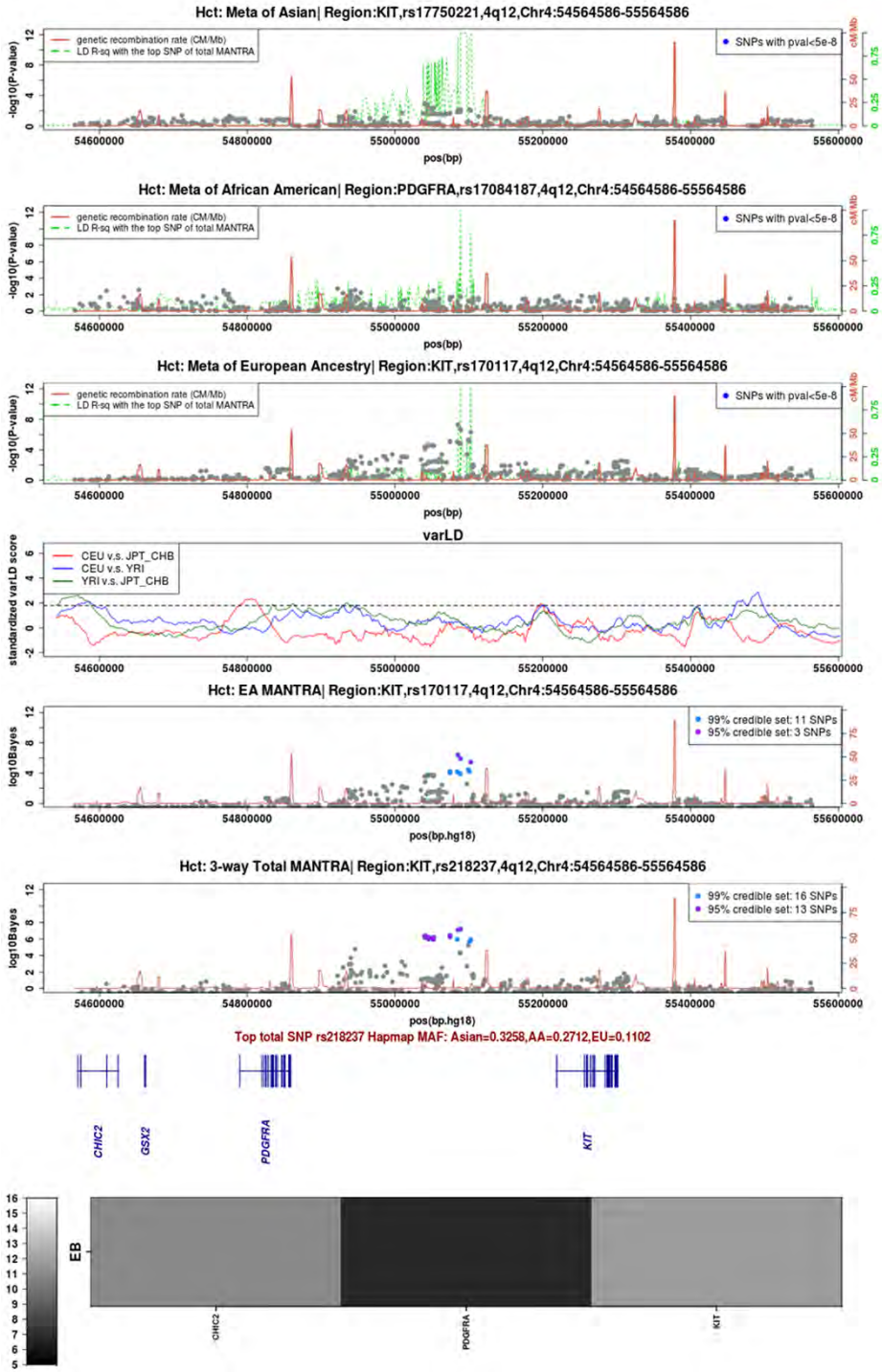
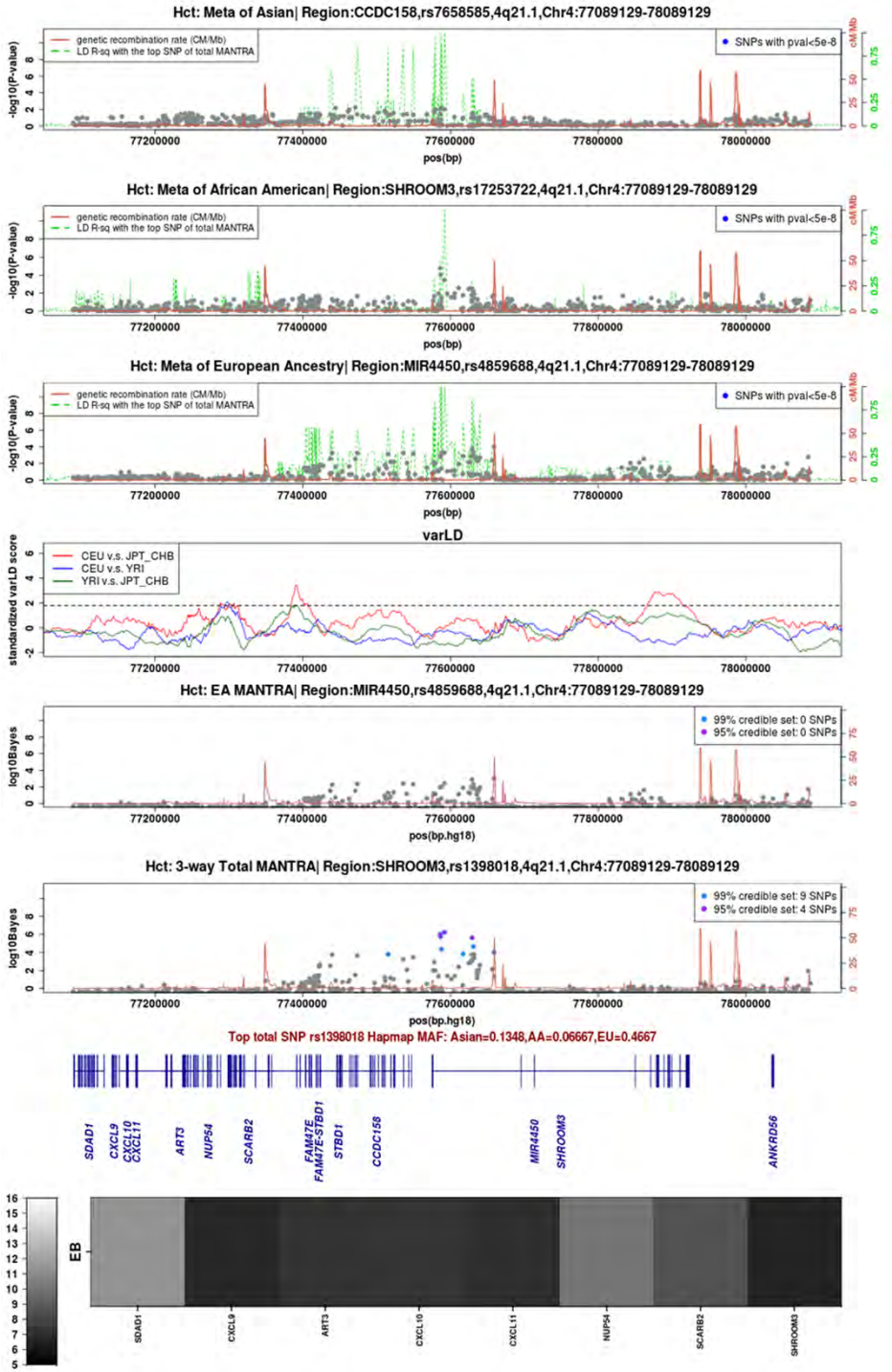
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:LOC100129961,rs6430549,2q21.3,Chr2:134756394-135756394
Hct: Meta of European Ancestry| Region:TMEM163,rs6707326,2q21.3,Chr2:134756394-135756394
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:TMEM163,rs998451,2q21.3,Chr2:134756394-135756394
99% credible set: 81 SNPs
95% credible set: 64 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:LOC100129961,rs6430549,2q21.3,Chr2:134756394-135756394
99% credible set: 35 SNPs
95% credible set: 22 SNPs
Top total SNP rs6430549 Hapmap MAF: Asian=0.06897,AA=0.1415,EU=0.4052
MGAT5
LOC151162
TMEM163
ACMSD
LOC100129961
CCNT2
YSK4
RAB3GAP1
EB
ZRANB3


Hct: Meta of Asian| Region:KIT,rs17750221,4q12,Chr4:54564586-55564586
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:PDGFRA,rs17084187,4q12,Chr4:54564586-55564586
Hct: Meta of European Ancestry| Region:KIT,rs170117,4q12,Chr4:54564586-55564586
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:KIT,rs170117,4q12,Chr4:54564586-55564586
99% credible set: 11 SNPs
95% credible set: 3 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:KIT,rs218237,4q12,Chr4:54564586-55564586
99% credible set: 16 SNPs
95% credible set: 13 SNPs
Top total SNP rs218237 Hapmap MAF: Asian=0.3258,AA=0.2712,EU=0.1102
CHIC2
GSX2
PDGFRA
KIT
EB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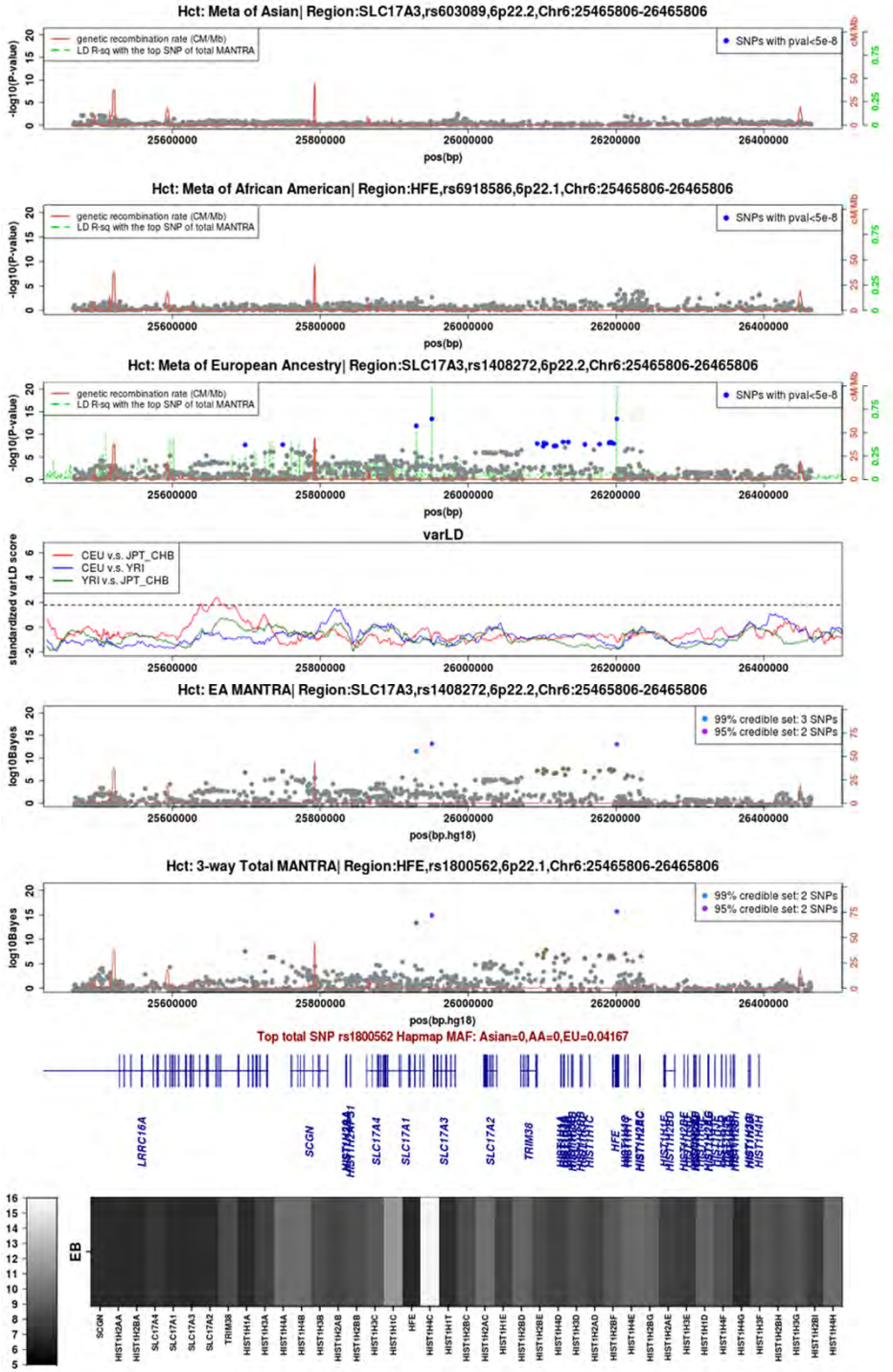
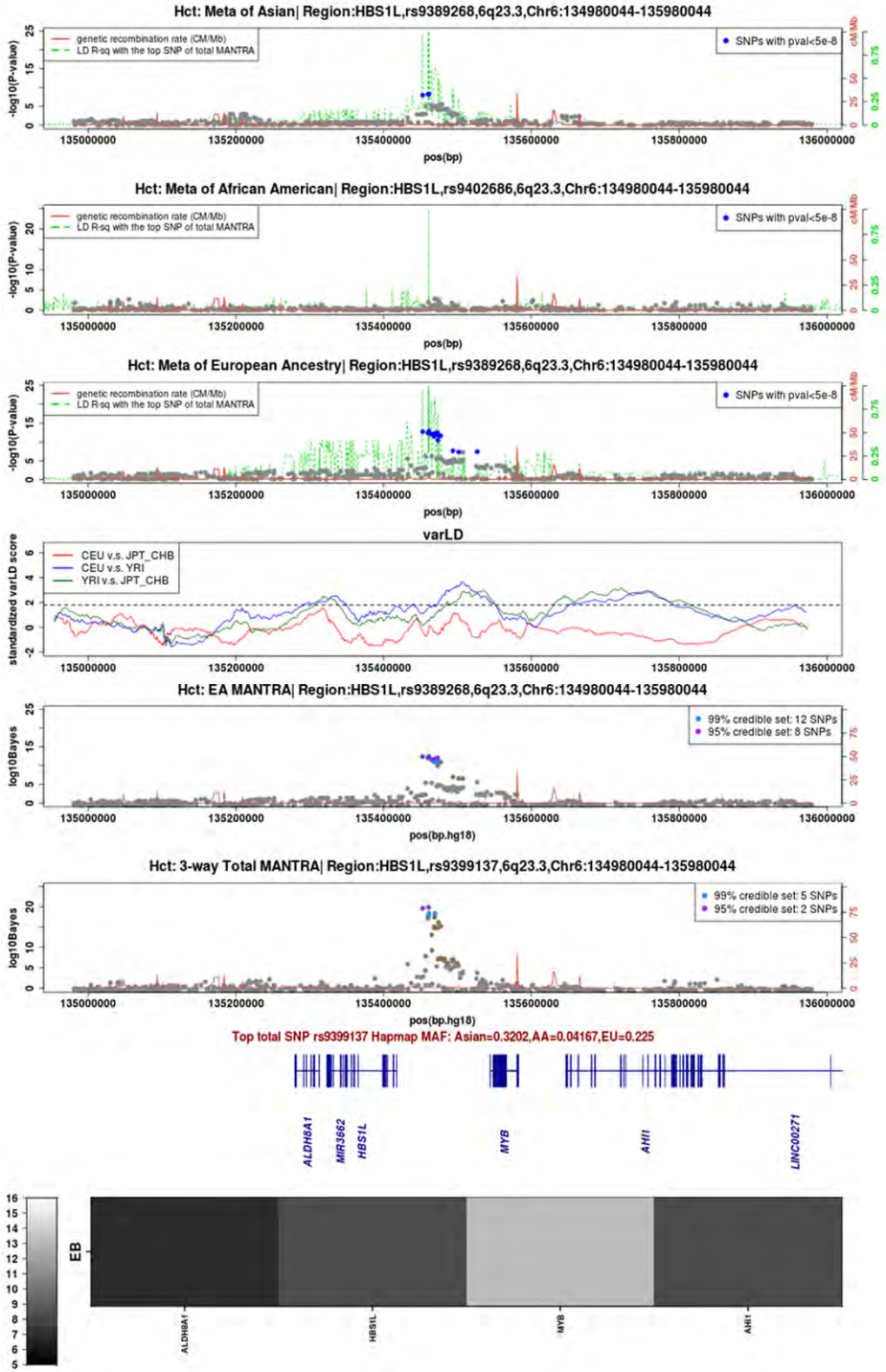
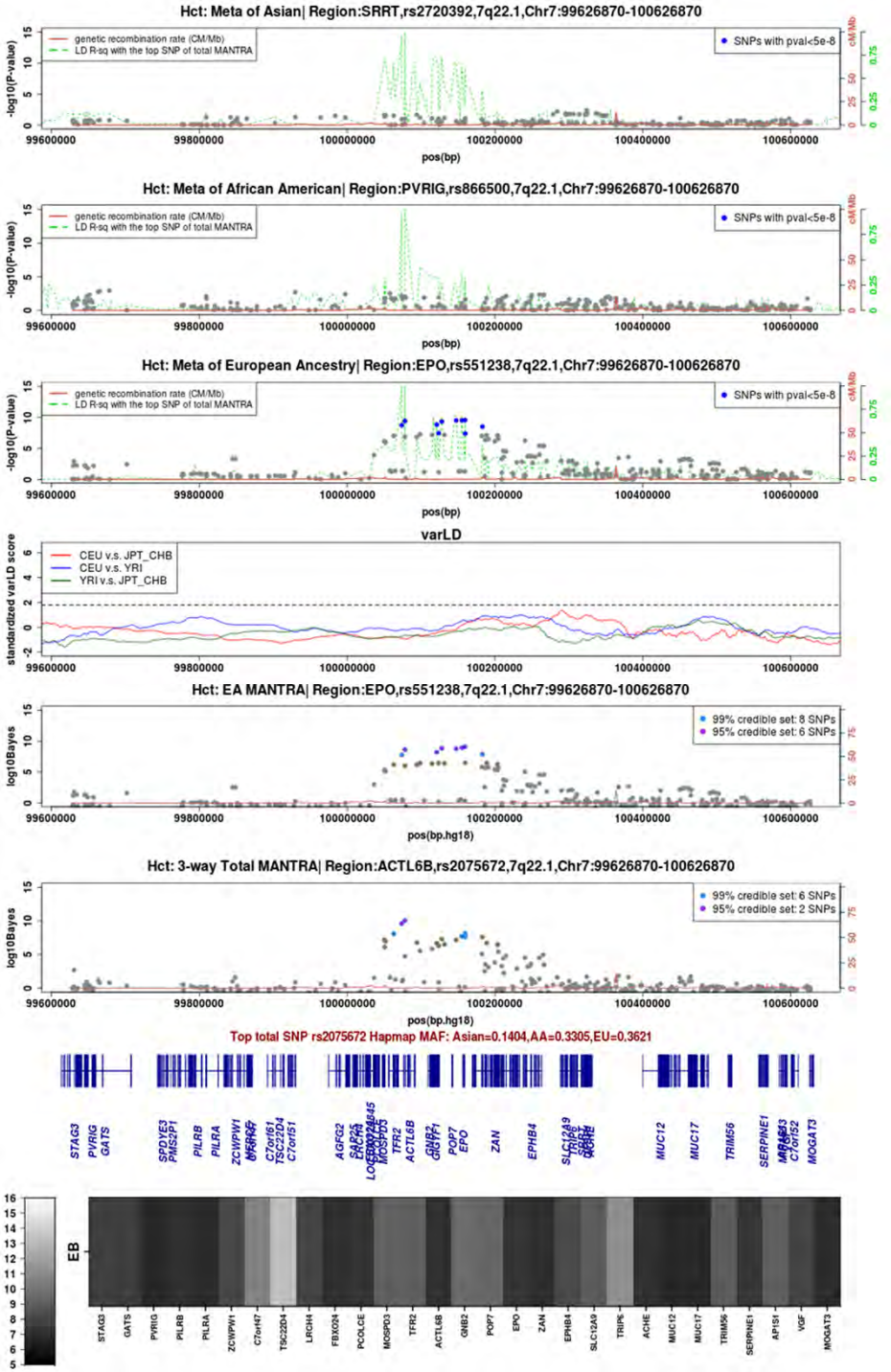
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
77200000
77400000
77600000
77800000
78000000
pos(bp)
Hct: Meta of African American| Region:SHROOM3,rs17253722,4q21.1,Chr4:77089129-78089129
Hct: Meta of European Ancestry| Region:MIR4450,rs4859688,4q21.1,Chr4:77089129-78089129
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:MIR4450,rs4859688,4q21.1,Chr4:77089129-78089129
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:SHROOM3,rs1398018,4q21.1,Chr4:77089129-78089129
99% credible set: 9 SNPs
95% credible set: 4 SNPs
Top total SNP rs1398018 Hapmap MAF: Asian=0.1348,AA=0.06667,EU=0.4667
SDAD1
CXCL9
CXCL10
CXCL11
ART3
NUP54
SCARB2
FAM47E
FAM47E-STBD1
STBD1
CCDC158
MIR4450
SHROOM3
ANKRD56
EB


Hct: Meta of Asian| Region:SLC17A3,rs603089,6p22.2,Chr6:25465806-26465806
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:HFE,rs6918586,6p22.1,Chr6:25465806-26465806
Hct: Meta of European Ancestry| Region:SLC17A3,rs1408272,6p22.2,Chr6:25465806-26465806
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:SLC17A3,rs1408272,6p22.2,Chr6:25465806-26465806
99% credible set: 3 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:HFE,rs1800562,6p22.1,Chr6:25465806-26465806
99% credible set: 2 SNPs
95% credible set: 2 SNPs
Top total SNP rs1800562 Hapmap MAF: Asian=0,AA=0,EU=0.04167
LRRC16A
SCGN
SLC17A4
SLC17A1
SLC17A3
SLC17A2
TRIM38
HFE
EB


Hct: Meta of Asian| Region:HBS1L,rs9389268,6q23.3,Chr6:134980044-135980044
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:HBS1L,rs9402686,6q23.3,Chr6:134980044-135980044
Hct: Meta of European Ancestry| Region:HBS1L,rs9389268,6q23.3,Chr6:134980044-135980044
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:HBS1L,rs9389268,6q23.3,Chr6:134980044-135980044
99% credible set: 12 SNPs
95% credible set: 8 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:HBS1L,rs9399137,6q23.3,Chr6:134980044-135980044
99% credible set: 5 SNPs
95% credible set: 2 SNPs
Top total SNP rs9399137 Hapmap MAF: Asian=0.3202,AA=0.04167,EU=0.225
ALDH6A1
MIR3662
HBS1L
MYB
AHI1
LINC00271
EB


Hct: Meta of Asian| Region:SRRT,rs2720392,7q22.1,Chr7:99626870-100626870
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:PVRIG,rs866500,7q22.1,Chr7:99626870-100626870
Hct: Meta of European Ancestry| Region:EPO,rs551238,7q22.1,Chr7:99626870-100626870
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:EPO,rs551238,7q22.1,Chr7:99626870-100626870
99% credible set: 8 SNPs
95% credible set: 6 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:ACTL6B,rs2075672,7q22.1,Chr7:99626870-100626870
99% credible set: 6 SNPs
95% credible set: 2 SNPs
Top total SNP rs2075672 Hapmap MAF: Asian=0.1404,AA=0.3305,EU=0.3621
STAG3
PVRIG
GATS
SPDYE3
PMS2P1
PILRB
PILRA
ZCWPW1
C7orf161
TSC22D4
C7orf51
AGFG2
TFR2
ACTL6B
POP7
EPO
ZAN
EPHB4
MUC12
MUC17
TRIM56
SERPINE1
C7orf52
MOGAT3
EB
STAG3
GATS
PVRIG
PILRB
PILRA
ZCWPW1
C7orf47
TSC22D4
LRGH4
FBXO24
PCOLCE
MOSPD3
TFR2
ACTL6B
GNB2
POP7
EPO
ZAN
EPHB4
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TRIPK
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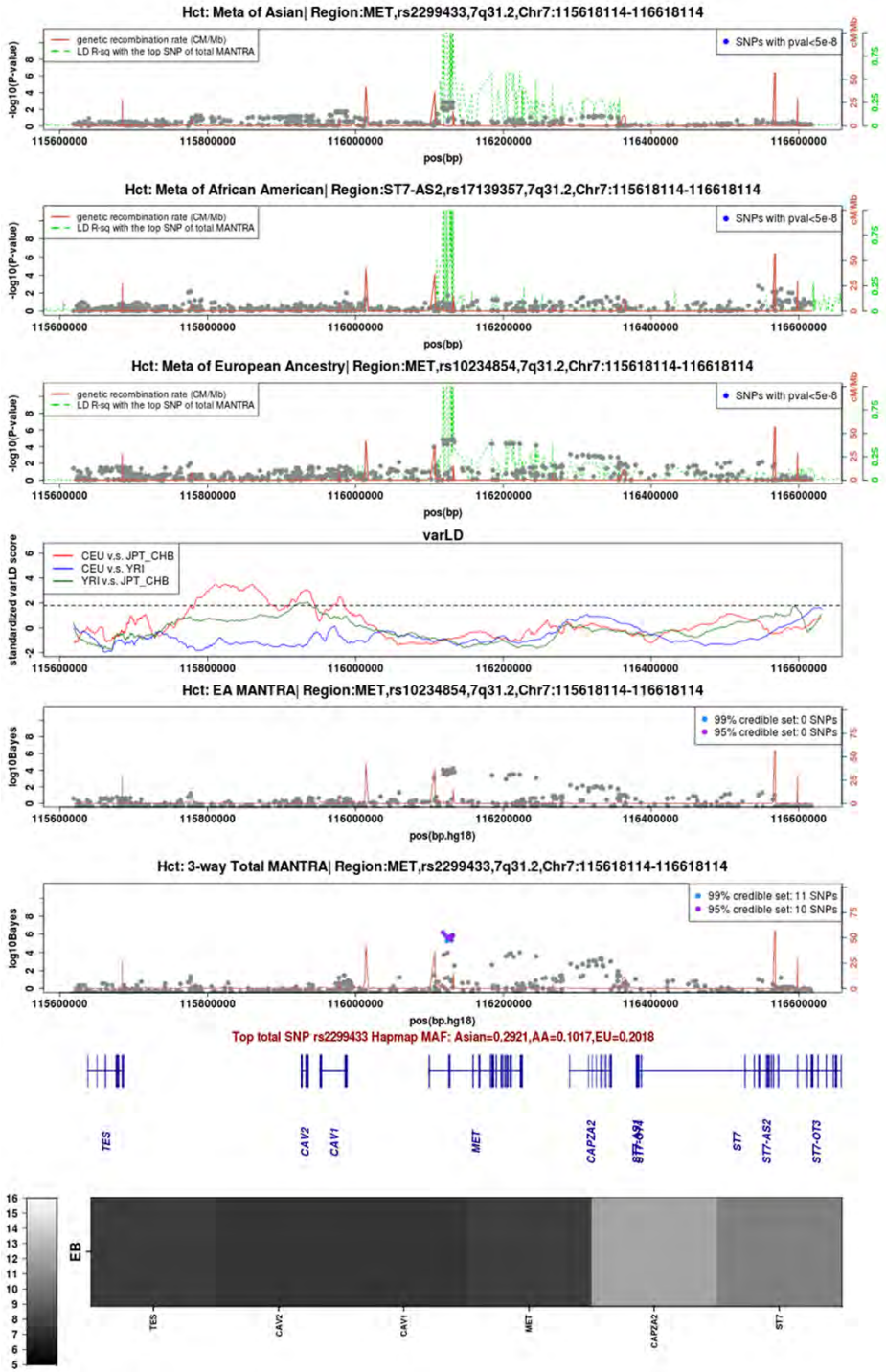
API5I
VGF
MOGAT3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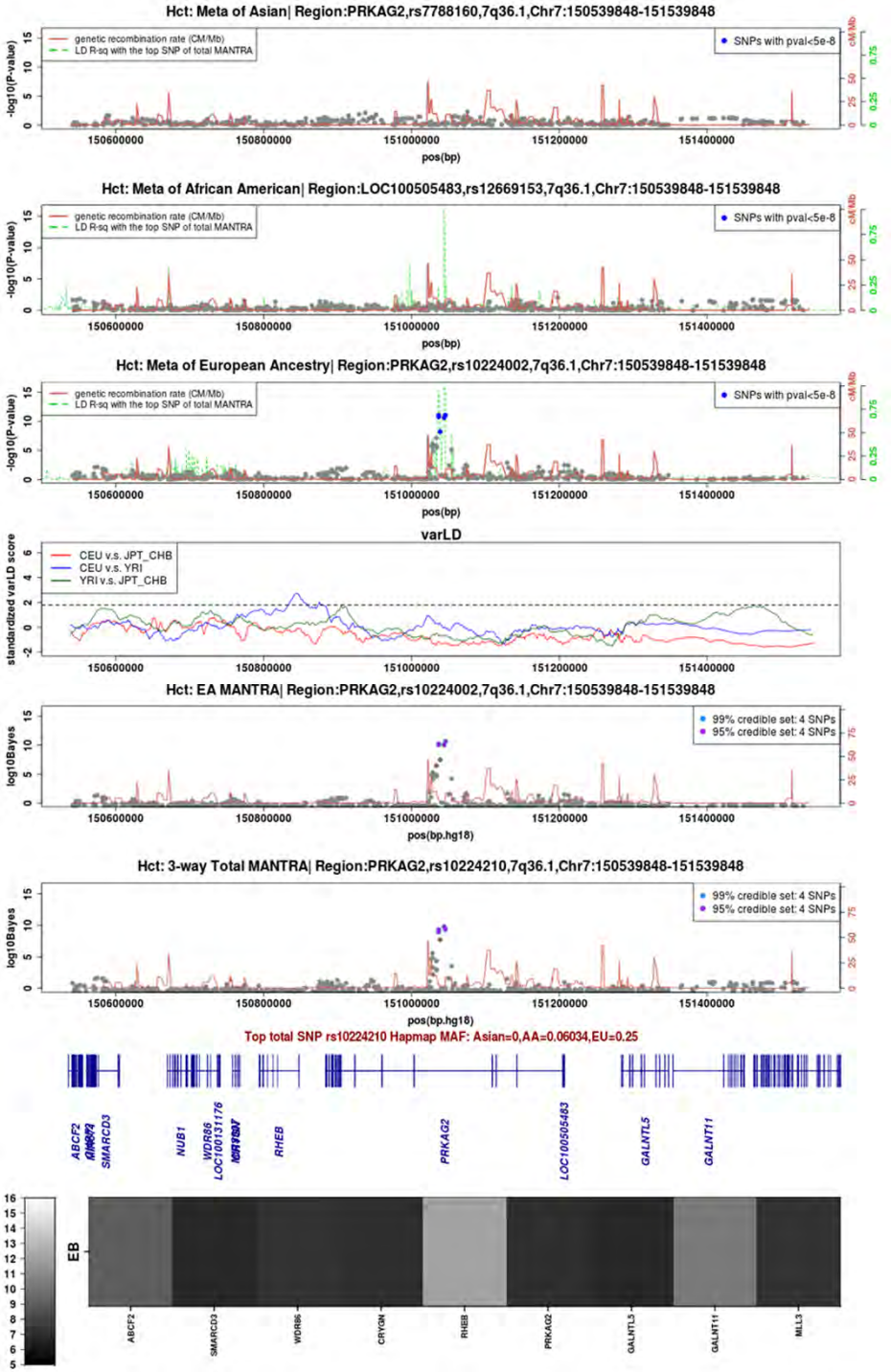
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:ST7-AS2,rs17139357,7q31.2,Chr7:115618114-116618114
Hct: Meta of European Ancestry| Region:MET,rs10234854,7q31.2,Chr7:115618114-116618114
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:MET,rs10234854,7q31.2,Chr7:115618114-116618114
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:MET,rs2299433,7q31.2,Chr7:115618114-116618114
99% credible set: 11 SNPs
95% credible set: 10 SNPs
Top total SNP rs2299433 Hapmap MAF: Asian=0.2921,AA=0.1017,EU=0.2018
TES
CAV2
CAV1
MET
CAPZA2
BTF-A94
ST7
ST7-AS2
ST7-OT3
EB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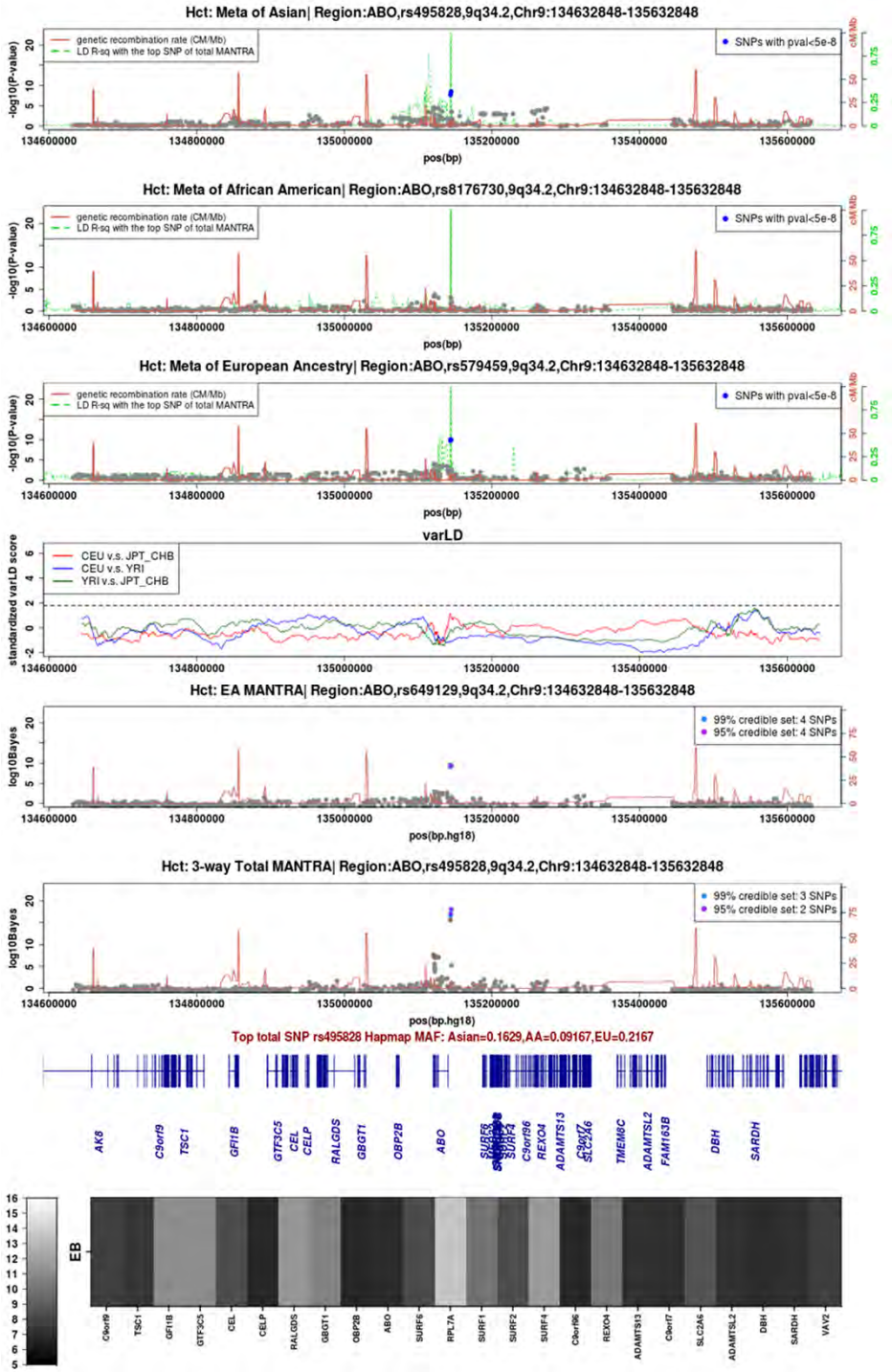
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:LOC100505483,rs12669153,7q36.1,Chr7:150539848-151539848
Hct: Meta of European Ancestry| Region:PRKAG2,rs10224002,7q36.1,Chr7:150539848-151539848
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:PRKAG2,rs10224002,7q36.1,Chr7:150539848-151539848
99% credible set: 4 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:PRKAG2,rs10224210,7q36.1,Chr7:150539848-151539848
Top total SNP rs10224210 Hapmap MAF: Asian=0,AA=0.06034,EU=0.25
ABCF2
SMARCD3
NUB1
WDR86
RHEB
PRKAG2
LOC100505483
GALNTL5
GALNT11
EB
CRYGN
MLL3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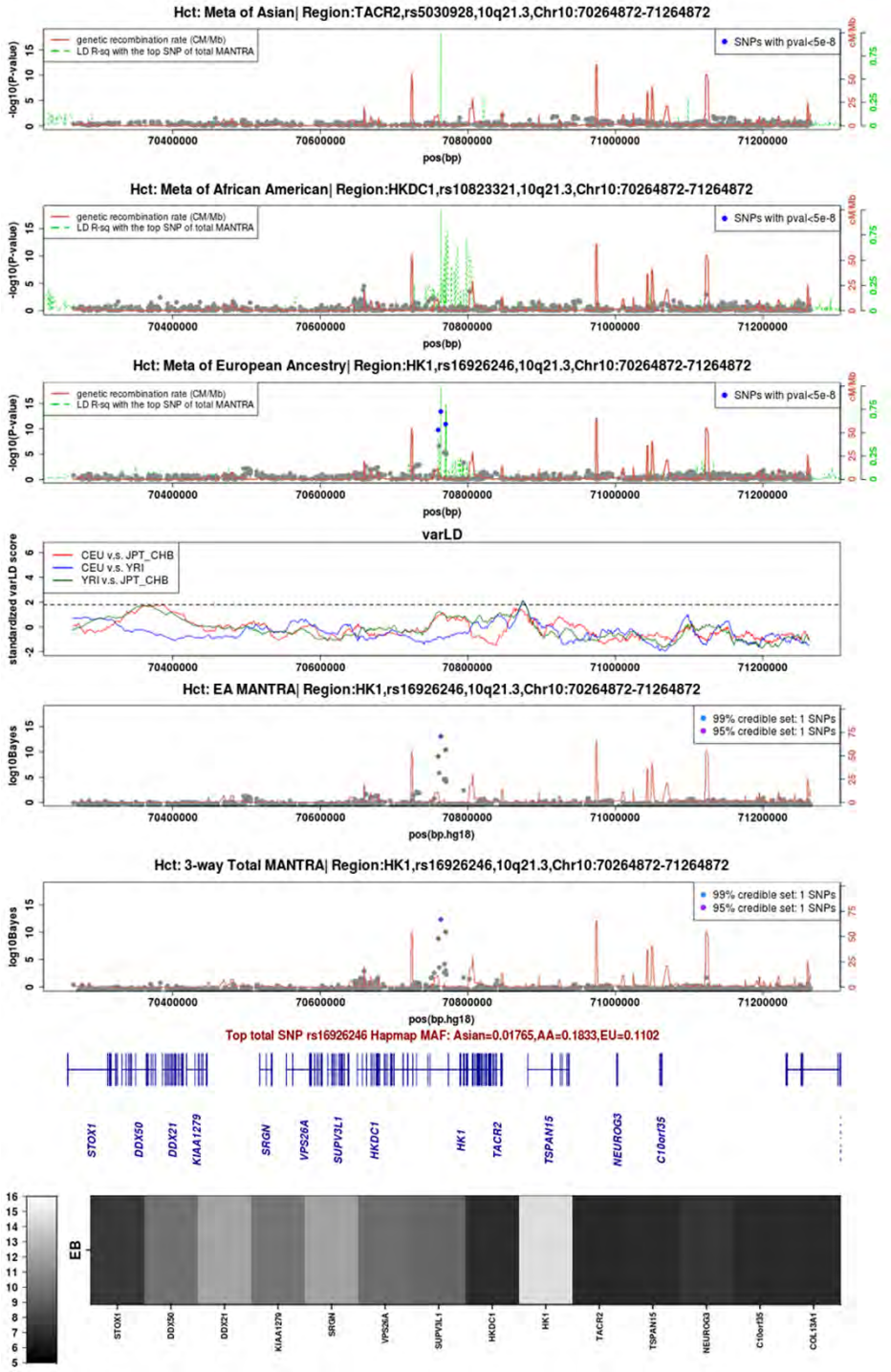
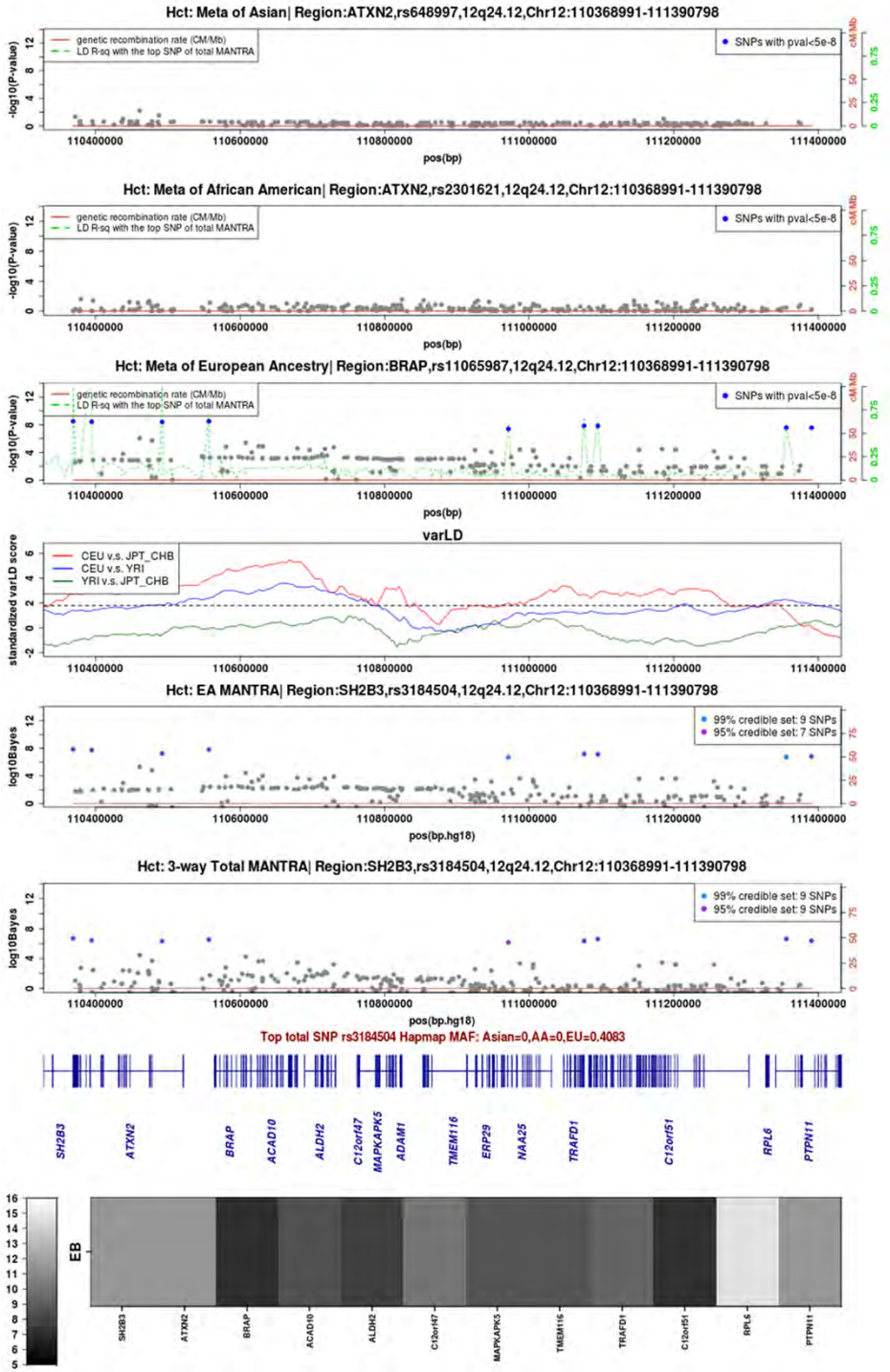
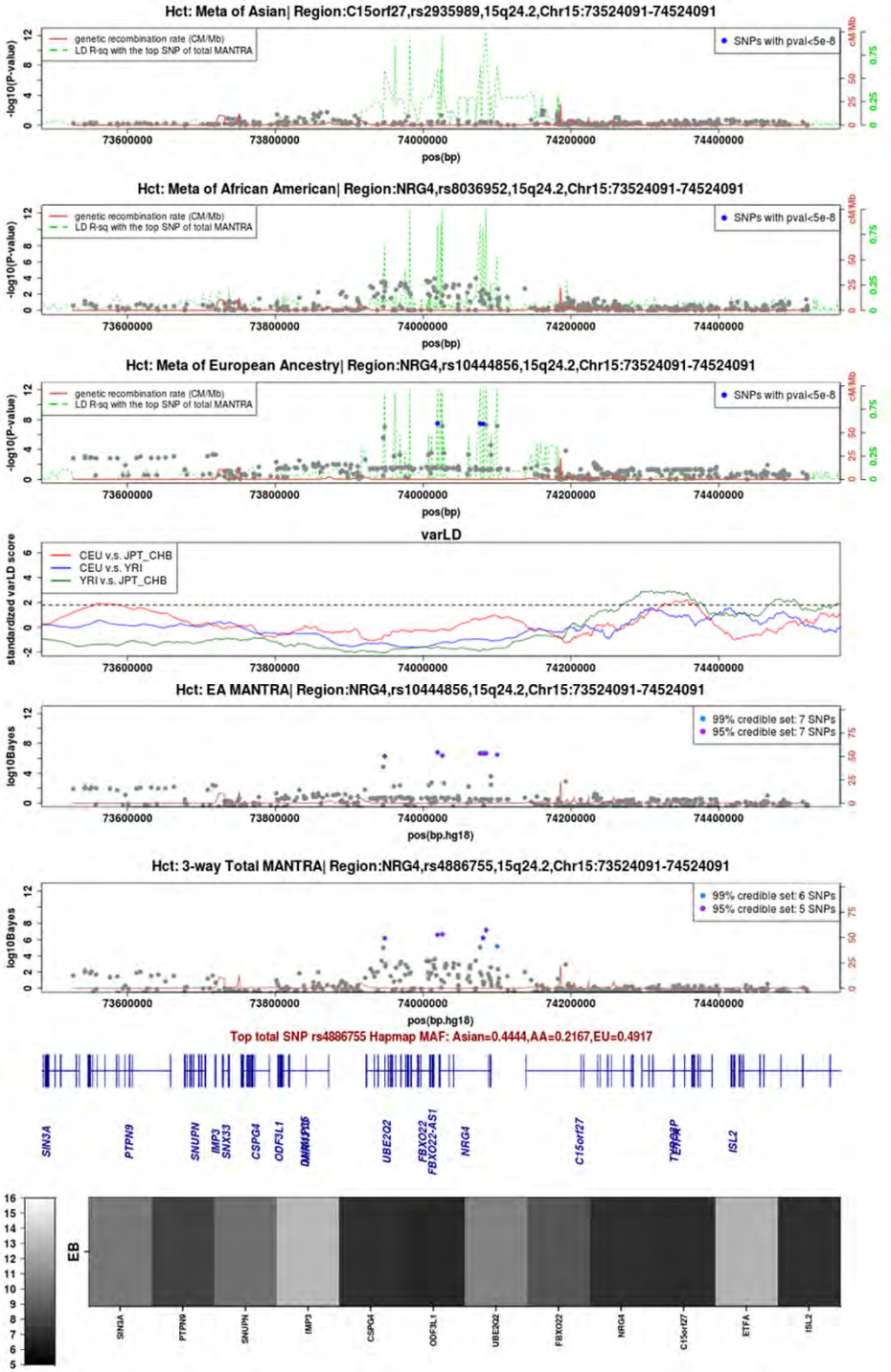
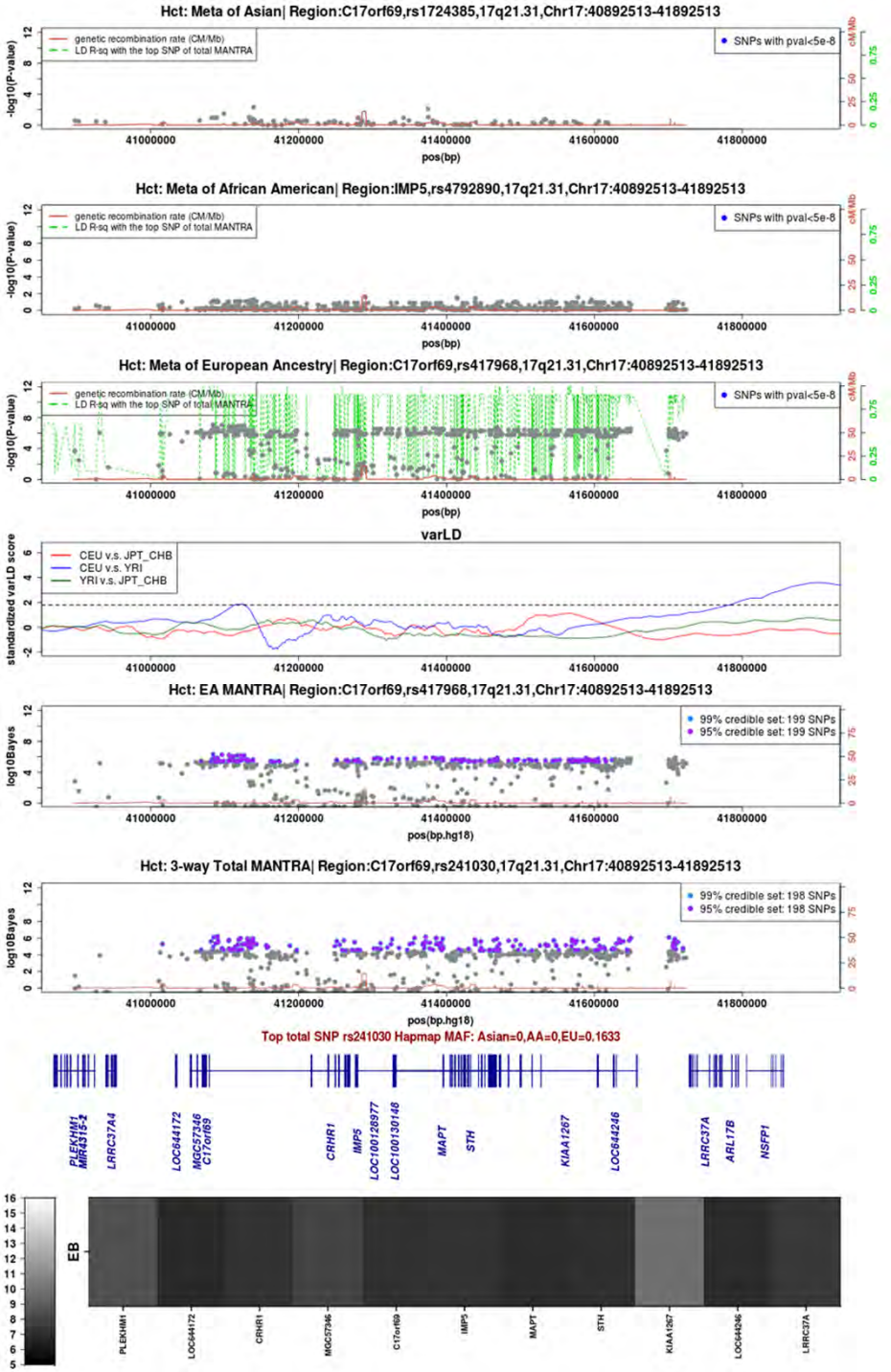
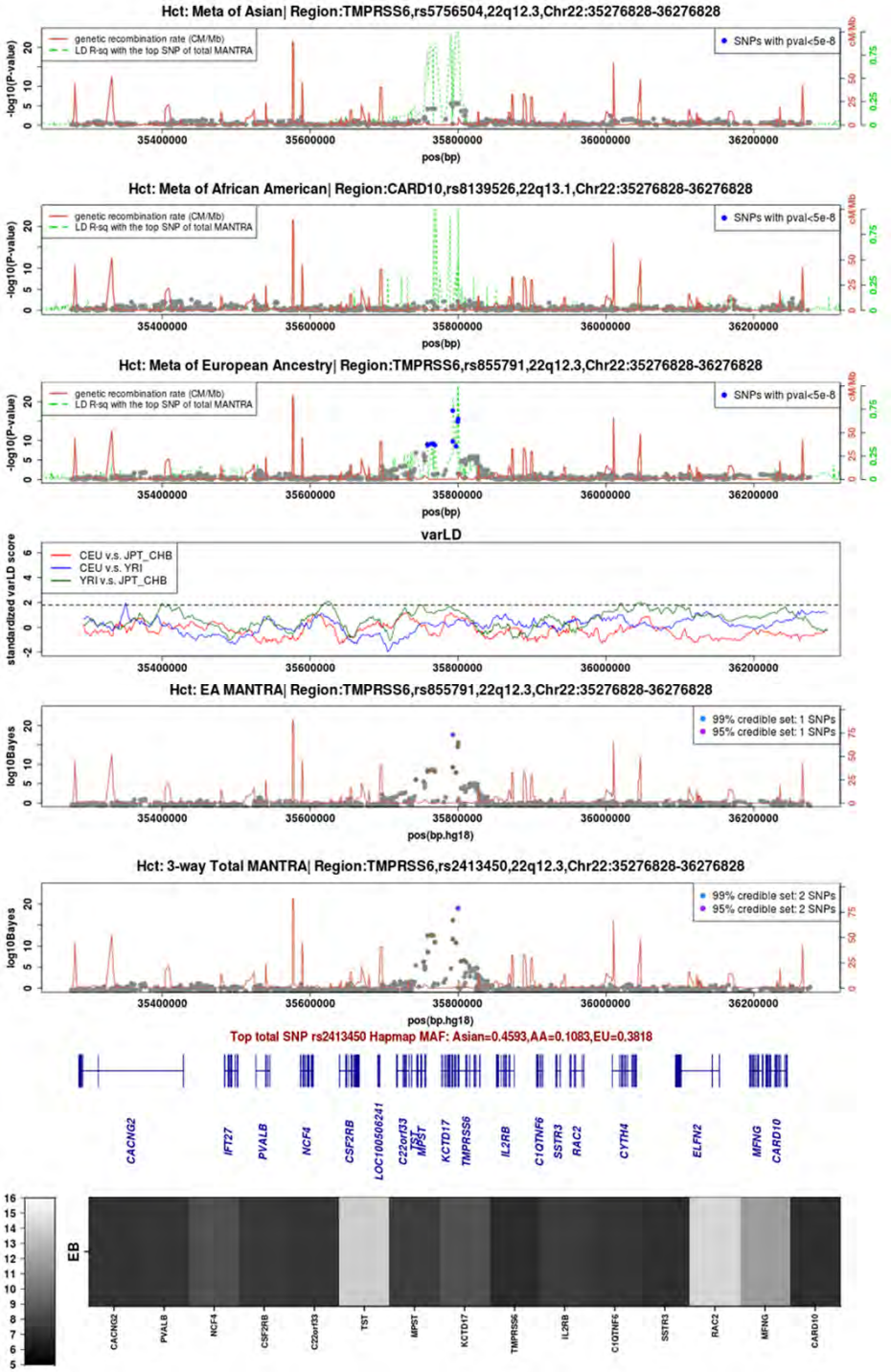
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:ABO,rs8176730,9q34.2,Chr9:134632848-135632848
Hct: Meta of European Ancestry| Region:ABO,rs579459,9q34.2,Chr9:134632848-135632848
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:ABO,rs649129,9q34.2,Chr9:134632848-135632848
99% credible set: 4 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:ABO,rs495828,9q34.2,Chr9:134632848-135632848
99% credible set: 3 SNPs
95% credible set: 2 SNPs
Top total SNP rs495828 Hapmap MAF: Asian=0.1629,AA=0.09167,EU=0.2167
AK8
C9orf9
TSC1
GFI1B
GTF3C5
CEL
CELP
RALGDS
GBGT1
OBP2B
ABO
SURF6
SURF1
SURF4
C9orf96
REXO4
ADAMTS13
C9orf7
SLC2A6
TMEM8C
ADAMTSL2
FAM163B
DBH
SARDH
EB
RPL7A
SURF2
SURF4
ADAMTS13
VAV2

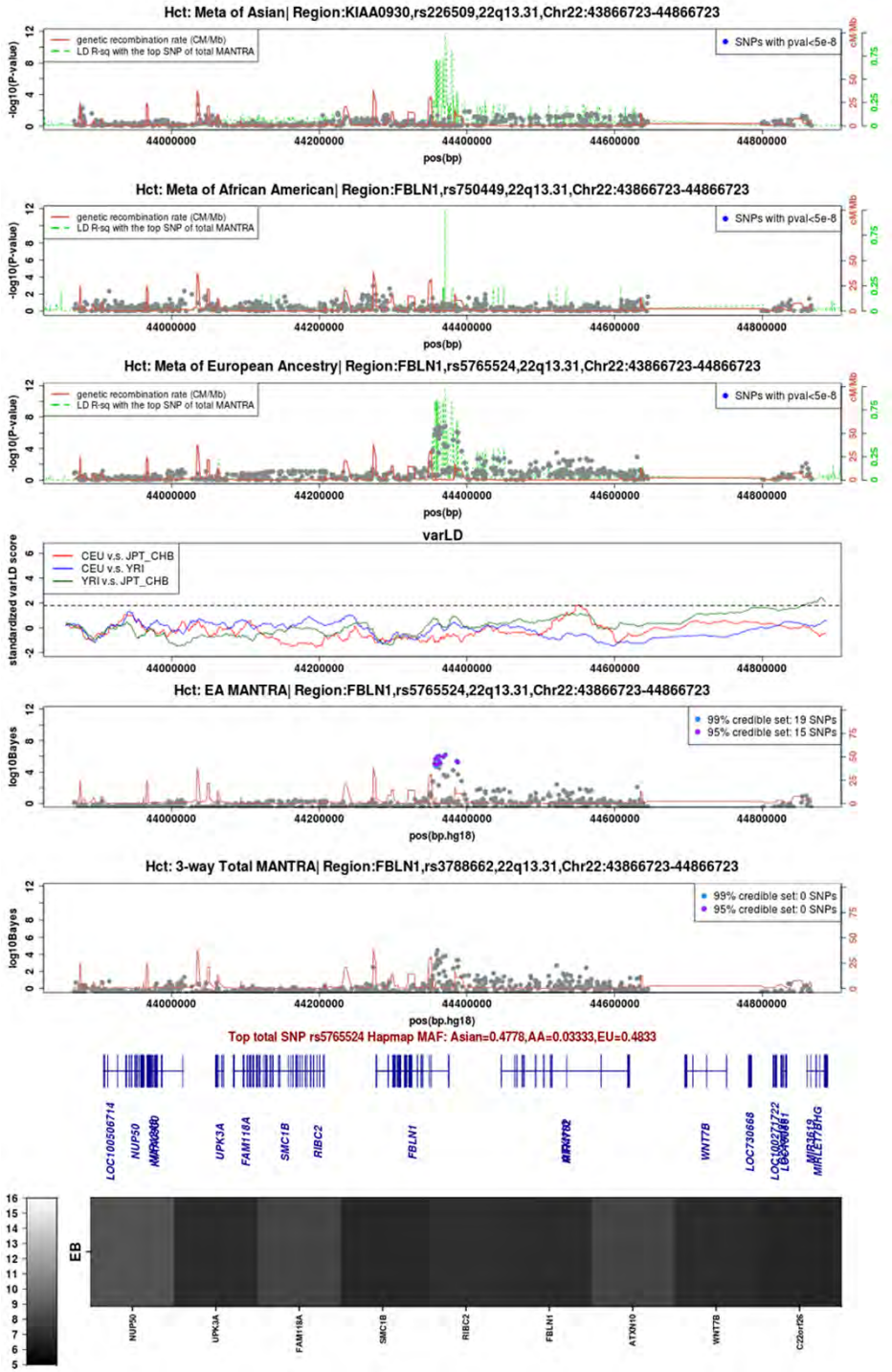

Hct: Meta of Asian| Region:TACR2,rs5030928,10q21.3,Chr10:70264872-71264872
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:HKDC1,rs10823321,10q21.3,Chr10:70264872-71264872
Hct: Meta of European Ancestry| Region:HK1,rs16926246,10q21.3,Chr10:70264872-71264872
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:HK1,rs16926246,10q21.3,Chr10:70264872-71264872
99% credible set: 1 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:HK1,rs16926246,10q21.3,Chr10:70264872-71264872
Top total SNP rs16926246 Hapmap MAF: Asian=0.01765,AA=0.1833,EU=0.1102
STOX1
DDX50
DDX21
KIAA1279
SRGN
VPS26A
SUPV3L1
HKDC1
HK1
TACR2
TSPAN15
NEUROG3
C10orf35
EB
COL13A1


Hct: Meta of Asian| Region:ATXN2,rs648997,12q24.12,Chr12:110368991-111390798
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:ATXN2,rs2301621,12q24.12,Chr12:110368991-111390798
Hct: Meta of European Ancestry| Region:BRAP,rs11065987,12q24.12,Chr12:110368991-111390798
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:SH2B3,rs3184504,12q24.12,Chr12:110368991-111390798
99% credible set: 9 SNPs
95% credible set: 7 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:SH2B3,rs3184504,12q24.12,Chr12:110368991-111390798
99% credible set: 9 SNPs
95% credible set: 9 SNPs
Top total SNP rs3184504 Hapmap MAF: Asian=0,AA=0,EU=0.4083
SH2B3
ATXN2
BRAP
ACAD10
ALDH2
C12orf47
MAPKAPK5
ADAM1
TMEM116
ERP29
NAA25
TRAFD1
C12orf51
RPL6
PTPN11
EB

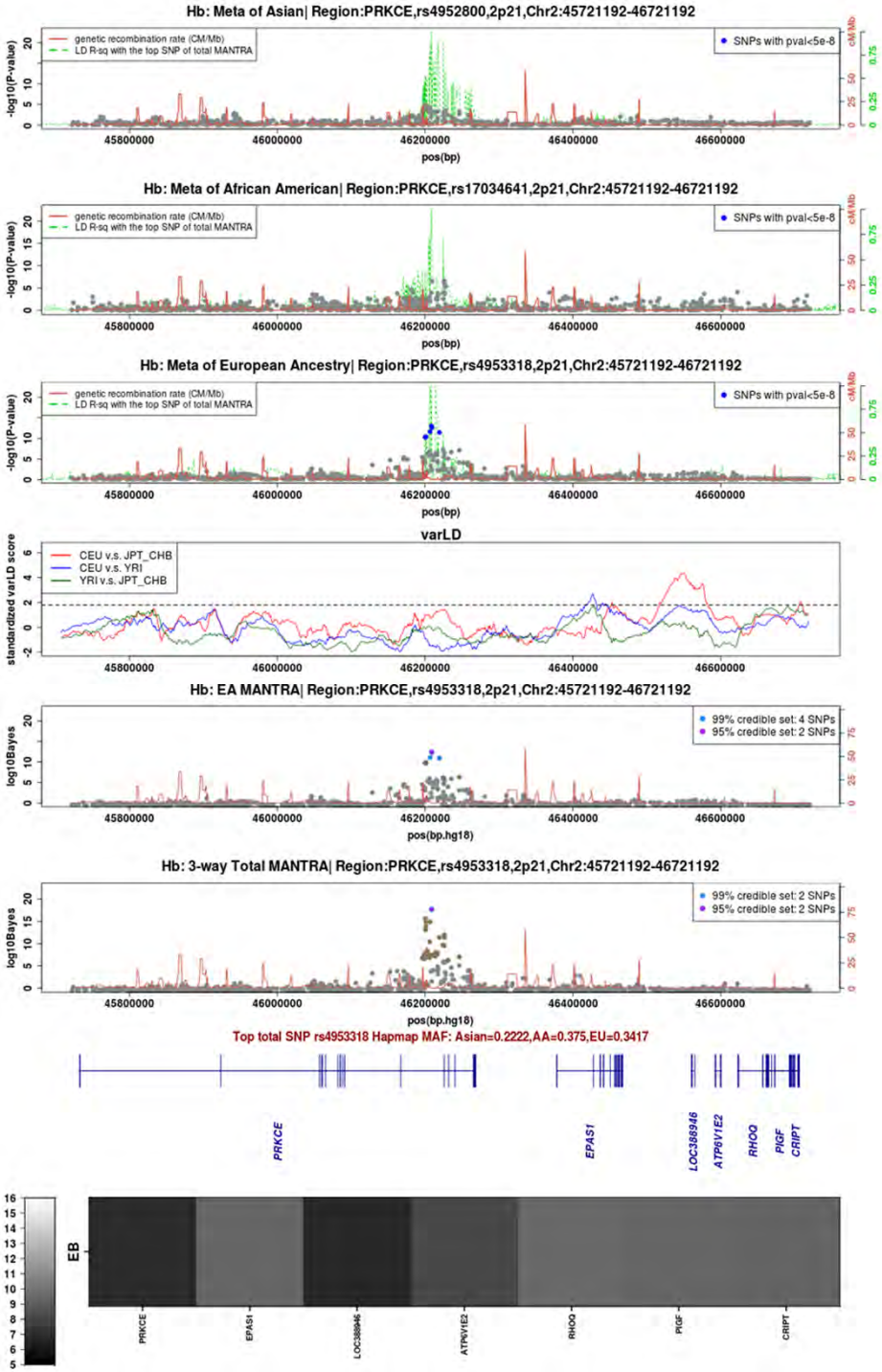

Hct: Meta of Asian| Region:C15orf27,rs2935989,15q24.2,Chr15:73524091-74524091
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:NRG4,rs8036952,15q24.2,Chr15:73524091-74524091
Hct: Meta of European Ancestry| Region:NRG4,rs10444856,15q24.2,Chr15:73524091-74524091
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:NRG4,rs10444856,15q24.2,Chr15:73524091-74524091
99% credible set: 7 SNPs
95% credible set: 7 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:NRG4,rs4886755,15q24.2,Chr15:73524091-74524091
99% credible set: 6 SNPs
95% credible set: 5 SNPs
Top total SNP rs4886755 Hapmap MAF: Asian=0.4444,AA=0.2167,EU=0.4917
SIN3A
PTPN9
SNUPN
IMP3
SNX33
CSPG4
ODF3L1
UBE2O2
FBXO22
FBXO22-AS1
NRG4
C15orf27
ISL2
EB
ETFA

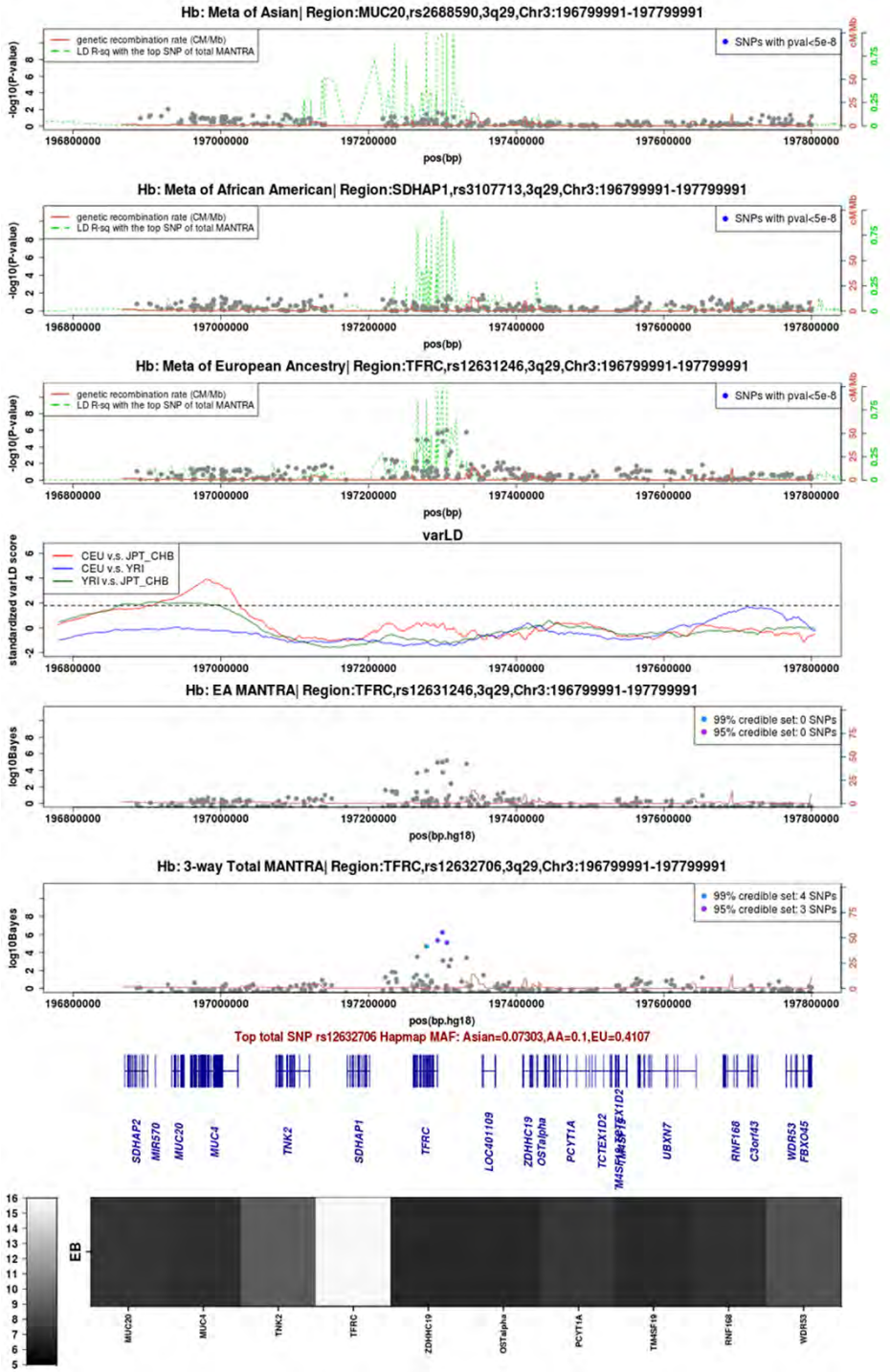

Hct: Meta of Asian| Region:C17orf69,rs1724385,17q21.31,Chr17:40892513-41892513
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:IMP5,rs4792890,17q21.31,Chr17:40892513-41892513
Hct: Meta of European Ancestry| Region:C17orf69,rs417968,17q21.31,Chr17:40892513-41892513
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:C17orf69,rs417968,17q21.31,Chr17:40892513-41892513
99% credible set: 199 SNPs
95% credible set: 199 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:C17orf69,rs241030,17q21.31,Chr17:40892513-41892513
99% credible set: 198 SNPs
95% credible set: 198 SNPs
Top total SNP rs241030 Hapmap MAF: Asian=0,AA=0,EU=0.1633
PLEKHM1
MIR4315-2
LRRC37A4
LOC644172
MGC57346
C17orf69
CRHR1
IMP5
LOC100128977
LOC100130148
MAPT
STH
KIAA1267
LOC644246
LRRC37A
ARL17B
NSFP1
EB

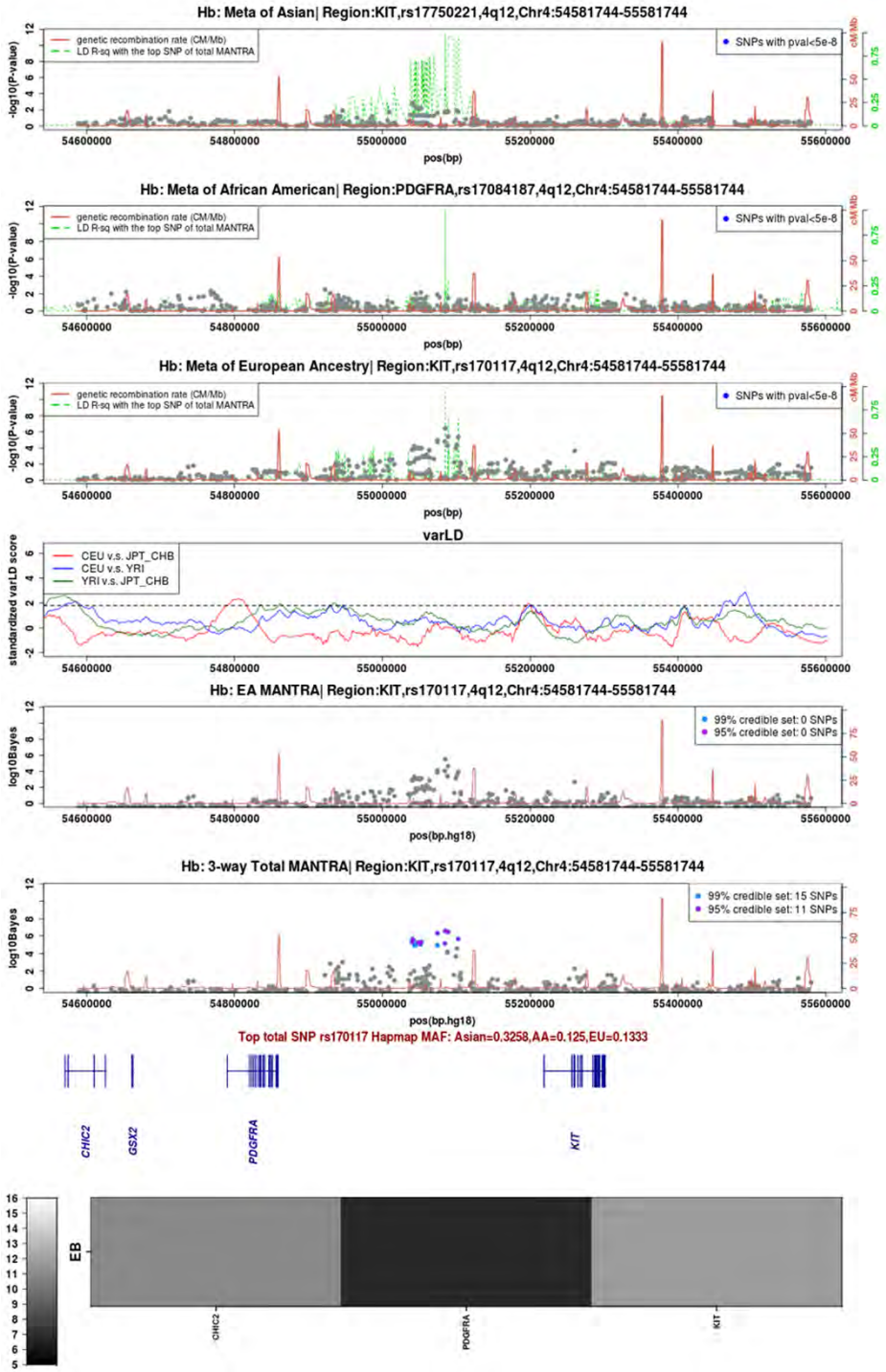

Hct: Meta of Asian| Region:TMPRSS6,rs5756504,22q12.3,Chr22:35276828-36276828
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:CARD10,rs8139526,22q13.1,Chr22:35276828-36276828
Hct: Meta of European Ancestry| Region:TMPRSS6,rs855791,22q12.3,Chr22:35276828-36276828
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:TMPRSS6,rs855791,22q12.3,Chr22:35276828-36276828
99% credible set: 1 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:TMPRSS6,rs2413450,22q12.3,Chr22:35276828-36276828
99% credible set: 2 SNPs
95% credible set: 2 SNPs
Top total SNP rs2413450 Hapmap MAF: Asian=0.4593,AA=0.1083,EU=0.3818
CACNG2
IFT27
PVALB
NCF4
CSF2RB
LOC100506241
C22orf33
TST
MPST
KCTD17
TMPRSS6
IL2RB
C1QTNF6
SSTR3
RAC2
CYTH4
ELFN2
MFNG
CARD10
EB

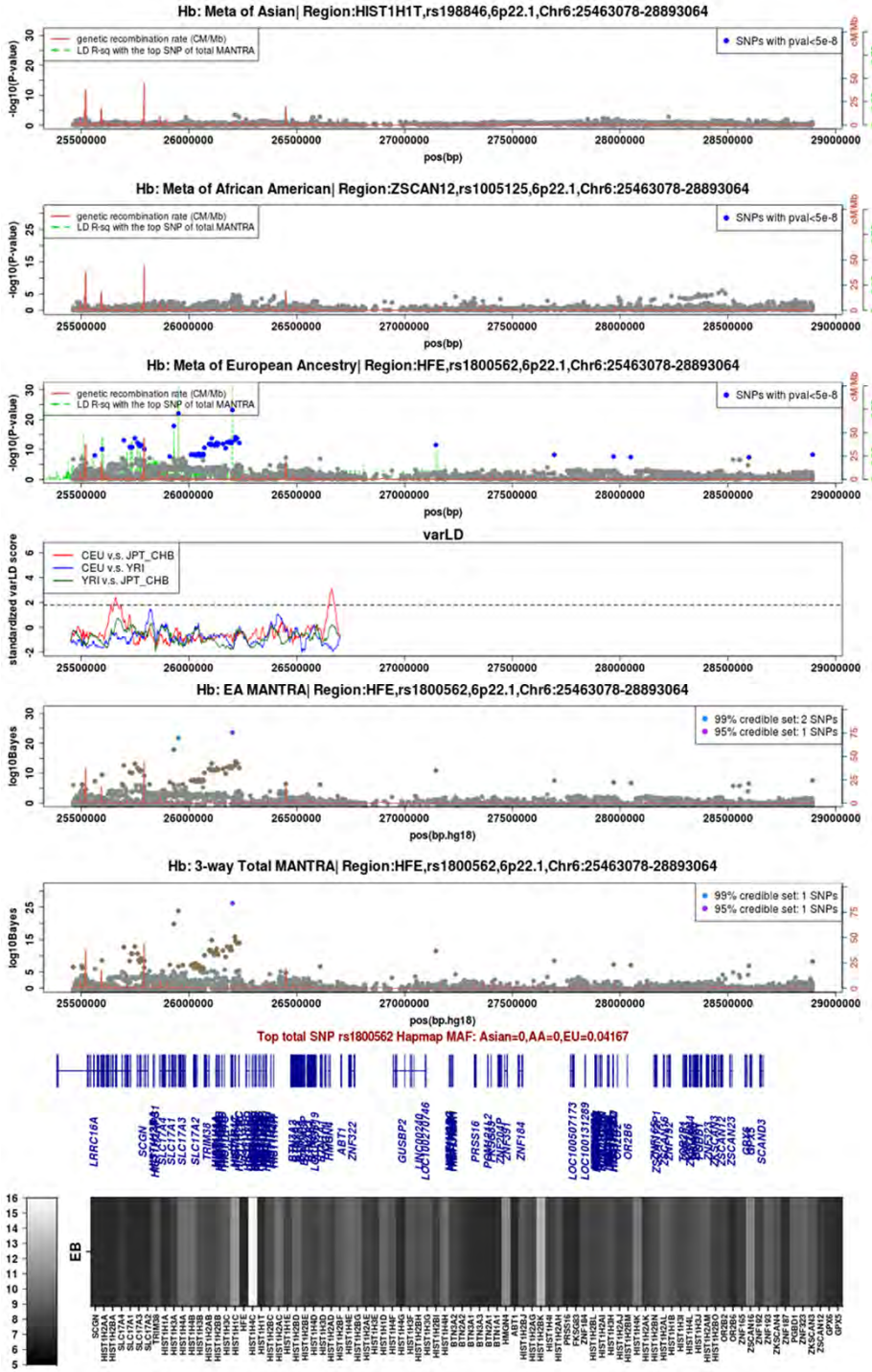

Hct: Meta of Asian| Region:KIAA0930,rs226509,22q13.31,Chr22:43866723-44866723
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hct: Meta of African American| Region:FBLN1,rs750449,22q13.31,Chr22:43866723-44866723
Hct: Meta of European Ancestry| Region:FBLN1,rs5765524,22q13.31,Chr22:43866723-44866723
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hct: EA MANTRA| Region:FBLN1,rs5765524,22q13.31,Chr22:43866723-44866723
99% credible set: 19 SNPs
95% credible set: 15 SNPs
log10Bayes
pos(bp.hg18)
Hct: 3-way Total MANTRA| Region:FBLN1,rs3788662,22q13.31,Chr22:43866723-44866723
99% credible set: 0 SNPs
95% credible set: 0 SNPs
Top total SNP rs5765524 Hapmap MAF: Asian=0.4778,AA=0.03333,EU=0.4833
LOC100506714
NUP50
UPK3A
FAM118A
SMC1B
RIBC2
FBLN1
WNT7B
LOC730668
EB
NUP50
UPK3A
FAM118A
SMC1B
RIBC2
FBLN1
ATXN10
WNT7B
C22orf25

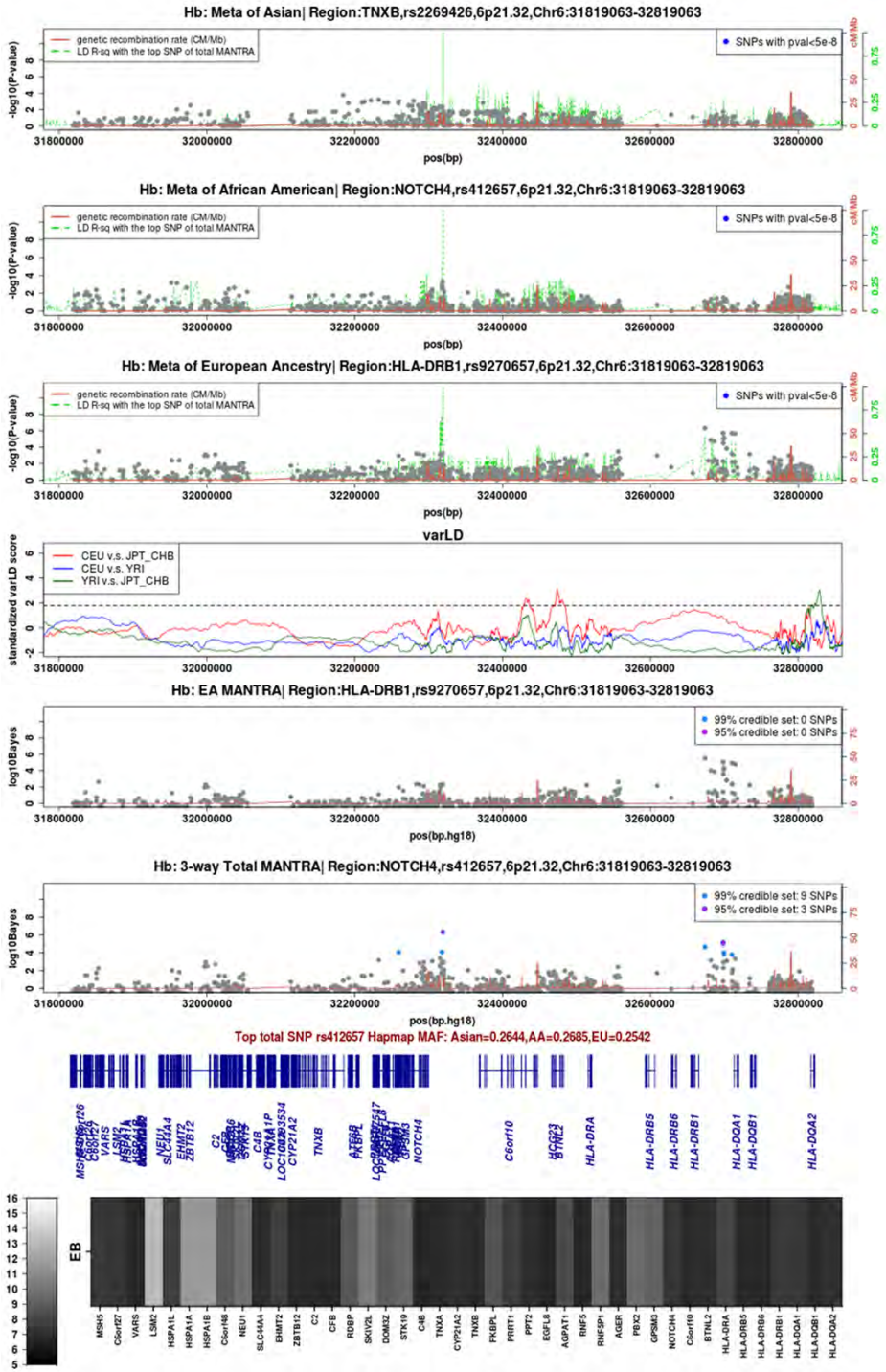
Hb

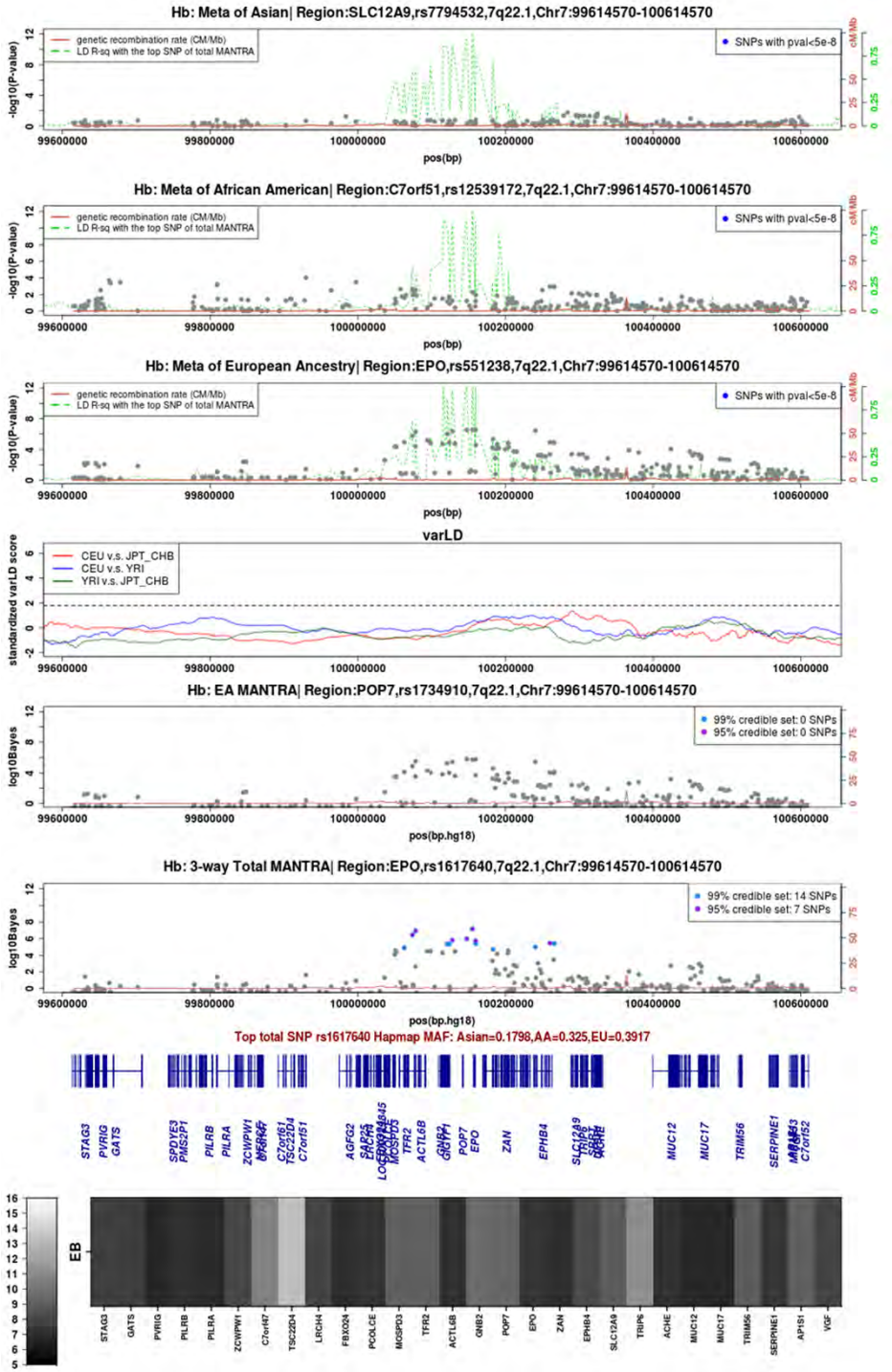

Hb: Meta of Asian| Region:PRKCE,rs4952800,2p21,Chr2:45721192-46721192
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:PRKCE,rs17034641,2p21,Chr2:45721192-46721192
Hb: Meta of European Ancestry| Region:PRKCE,rs4953318,2p21,Chr2:45721192-46721192
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:PRKCE,rs4953318,2p21,Chr2:45721192-46721192
99% credible set: 4 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:PRKCE,rs4953318,2p21,Chr2:45721192-46721192
99% credible set: 2 SNPs
95% credible set: 2 SNPs
Top total SNP rs4953318 Hapmap MAF: Asian=0.2222,AA=0.375,EU=0.3417
PRKCE
EPAS1
LOC388946
ATP6V1E2
RHOQ
PIGF
CRIPT
EB

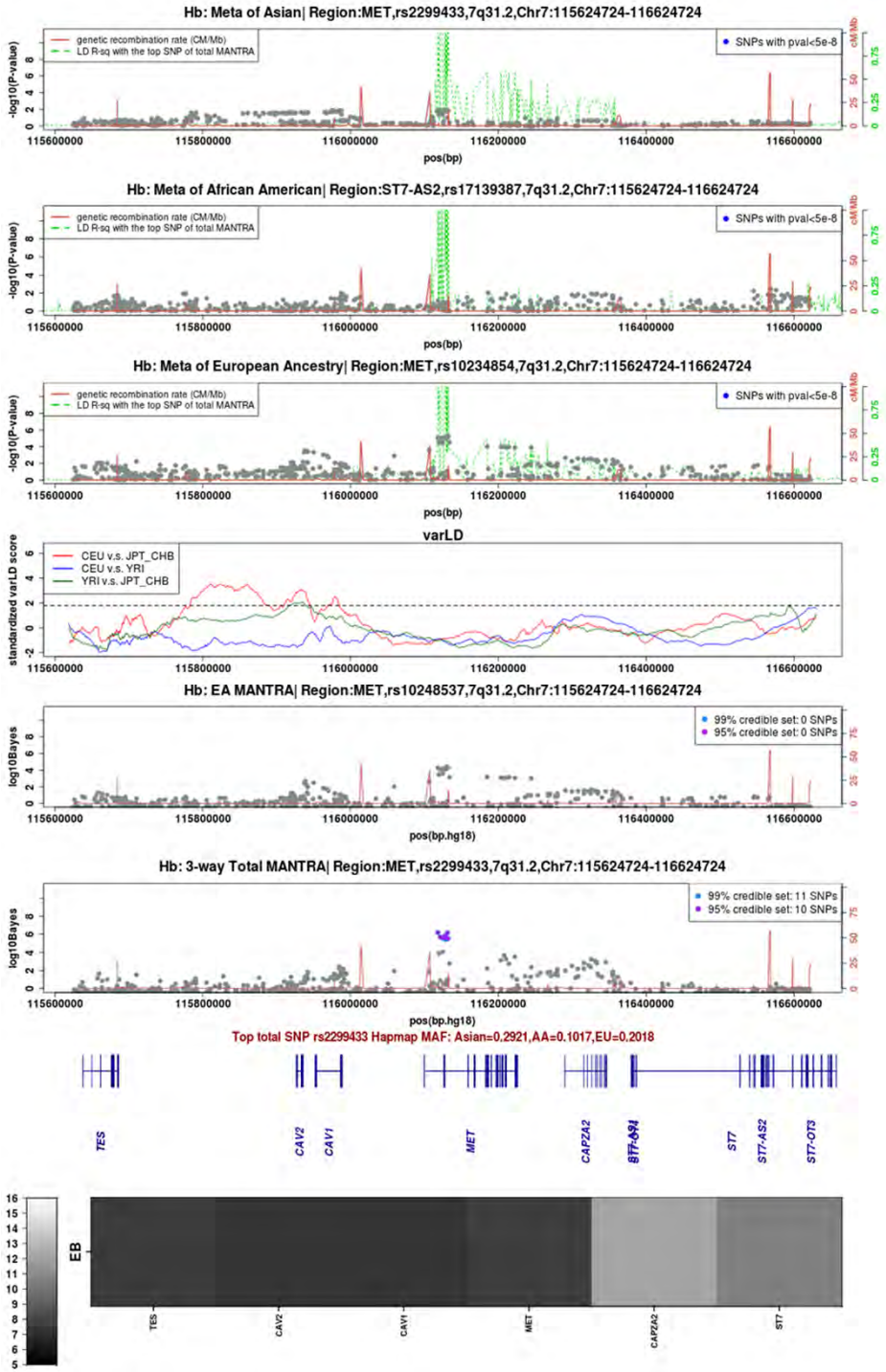

Hb: Meta of Asian| Region:MUC20,rs2688590,3q29,Chr3:196799991-197799991
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:SDHAP1,rs3107713,3q29,Chr3:196799991-197799991
Hb: Meta of European Ancestry| Region:TFRC,rs12631246,3q29,Chr3:196799991-197799991
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:TFRC,rs12631246,3q29,Chr3:196799991-197799991
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:TFRC,rs12632706,3q29,Chr3:196799991-197799991
99% credible set: 4 SNPs
95% credible set: 3 SNPs
Top total SNP rs12632706 Hapmap MAF: Asian=0.07303,AA=0.1,EU=0.4107
SDHAP2
MIR570
MUC20
MUC4
TNK2
SDHAP1
TFRC
LOC401109
ZDHHC19
OSTalpha
PCYT1A
TCTEX1D2
UBXN7
RNF168
C3orf43
WDR53
FBXO45
EB
MUC20
MUC4
TNK2
TFRC
ZDHHC19
OSTalpha
PCYT1A
TMEM189
RNF168
WDR53

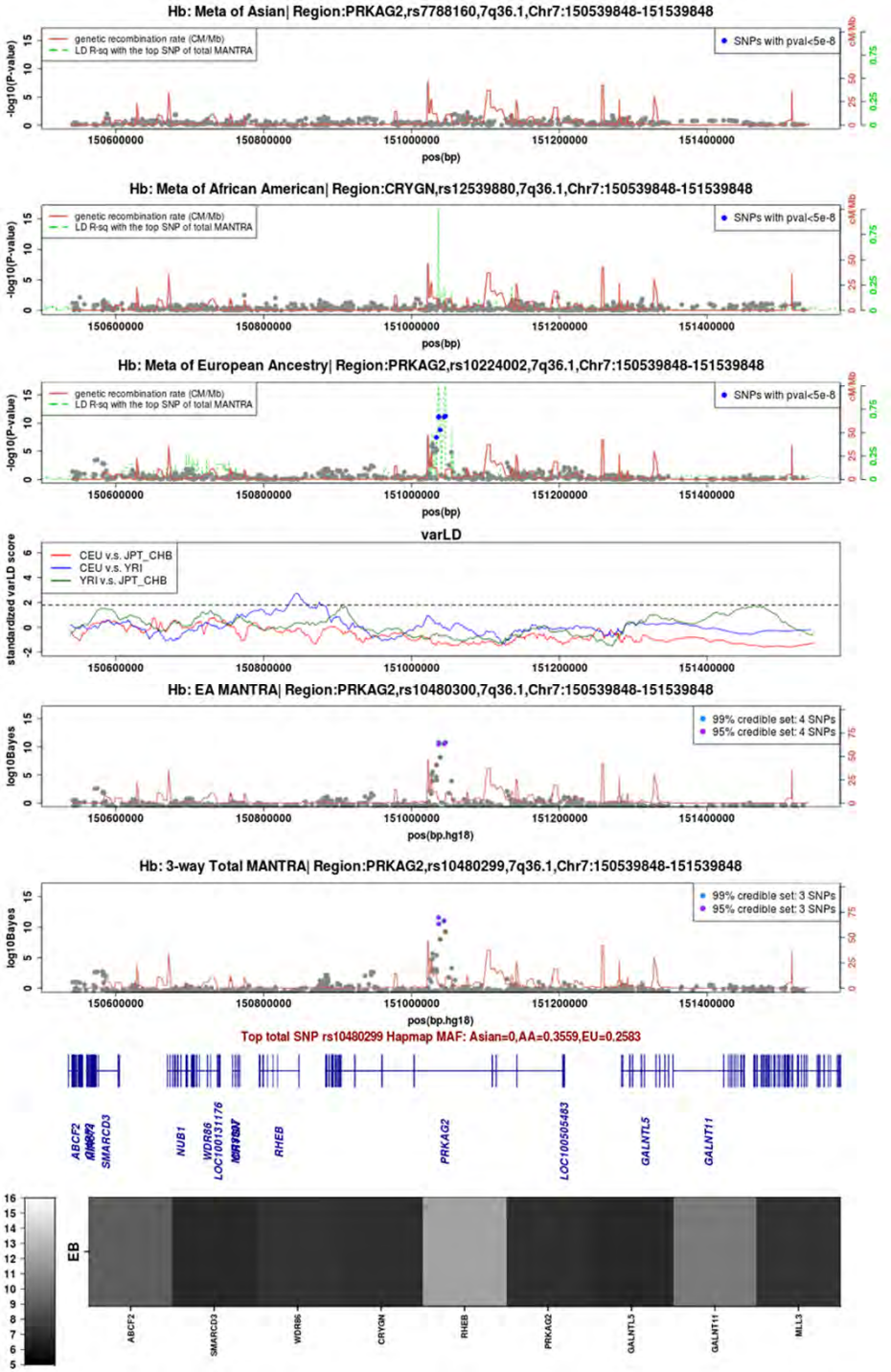

Hb: Meta of Asian| Region:KIT,rs17750221,4q12,Chr4:54581744-55581744
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:PDGFRA,rs17084187,4q12,Chr4:54581744-55581744
Hb: Meta of European Ancestry| Region:KIT,rs170117,4q12,Chr4:54581744-55581744
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:KIT,rs170117,4q12,Chr4:54581744-55581744
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:KIT,rs170117,4q12,Chr4:54581744-55581744
99% credible set: 15 SNPs
95% credible set: 11 SNPs
Top total SNP rs170117 Hapmap MAF: Asian=0.3258,AA=0.125,EU=0.1333
CHIC2
GSX2
PDGFRA
KIT
EB

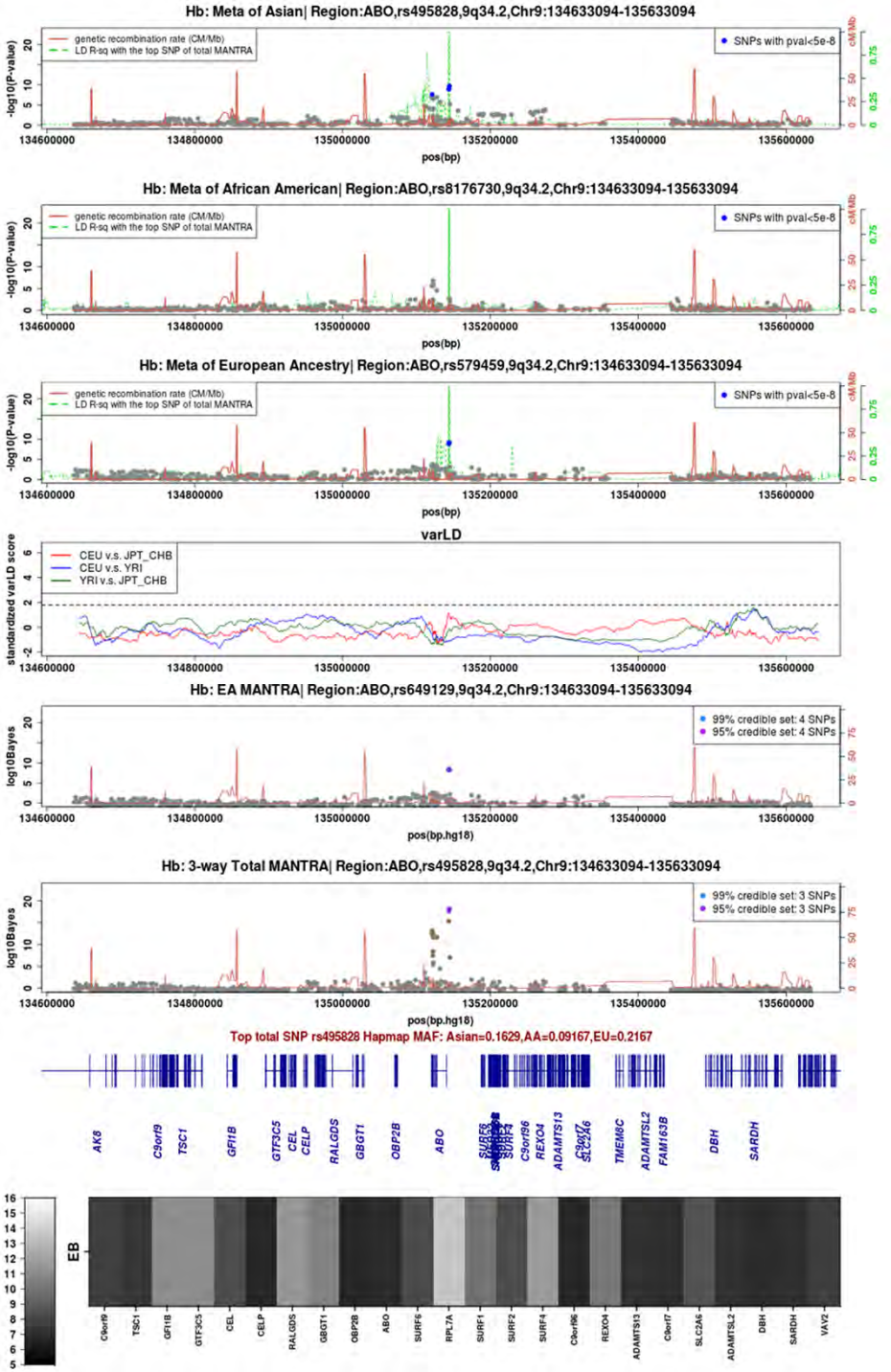

Hb: Meta of Asian| Region:HIST1H1T,rs198846,6p22.1,Chr6:25463078-28893064
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:ZSCAN12,rs1005125,6p22.1,Chr6:25463078-28893064
Hb: Meta of European Ancestry| Region:HFE,rs1800562,6p22.1,Chr6:25463078-28893064
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:HFE,rs1800562,6p22.1,Chr6:25463078-28893064
99% credible set: 2 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:HFE,rs1800562,6p22.1,Chr6:25463078-28893064
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs1800562 Hapmap MAF: Asian=0,AA=0,EU=0.04167
EB

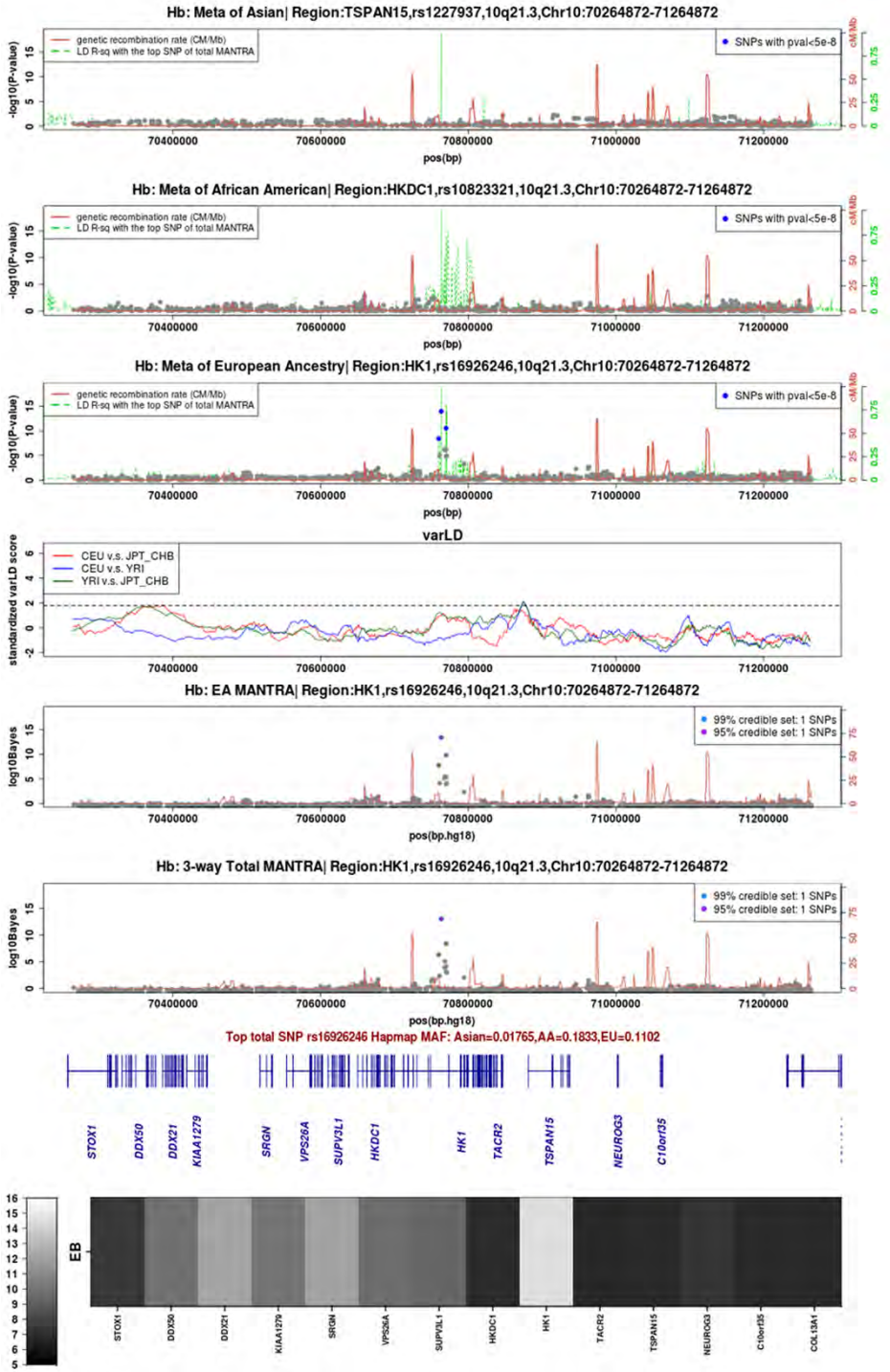

Hb: Meta of Asian| Region:TNXB,rs2269426,6p21.32,Chr6:31819063-32819063
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:NOTCH4,rs412657,6p21.32,Chr6:31819063-32819063
Hb: Meta of European Ancestry| Region:HLA-DRB1,rs9270657,6p21.32,Chr6:31819063-32819063
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:HLA-DRB1,rs9270657,6p21.32,Chr6:31819063-32819063
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:NOTCH4,rs412657,6p21.32,Chr6:31819063-32819063
99% credible set: 9 SNPs
95% credible set: 3 SNPs
Top total SNP rs412657 Hapmap MAF: Asian=0.2644,AA=0.2685,EU=0.2542
EB
MSH5
C6orf27
VARS
LSM2
HSPA1L
HSPA1A
HSPA1B
C6orf48
NEU1
SLC44A4
EHMT2
ZBTB12
C2
CFB
RDBP
SKIV2L
DOM3Z
STK19
C4B
TNXA
CYP21A2
TNXB
FKBPL
PRRT1
PPT2
EGFL8
AGPAT1
RNF5
RNF5P1
AGER
PBX2
GPSM3
NOTCH4
C6orf10
BTNL2
HLA-DRA
HLA-DRB5
HLA-DRB6
HLA-DRB1
HLA-DQA1
HLA-DQB1
HLA-DQA2

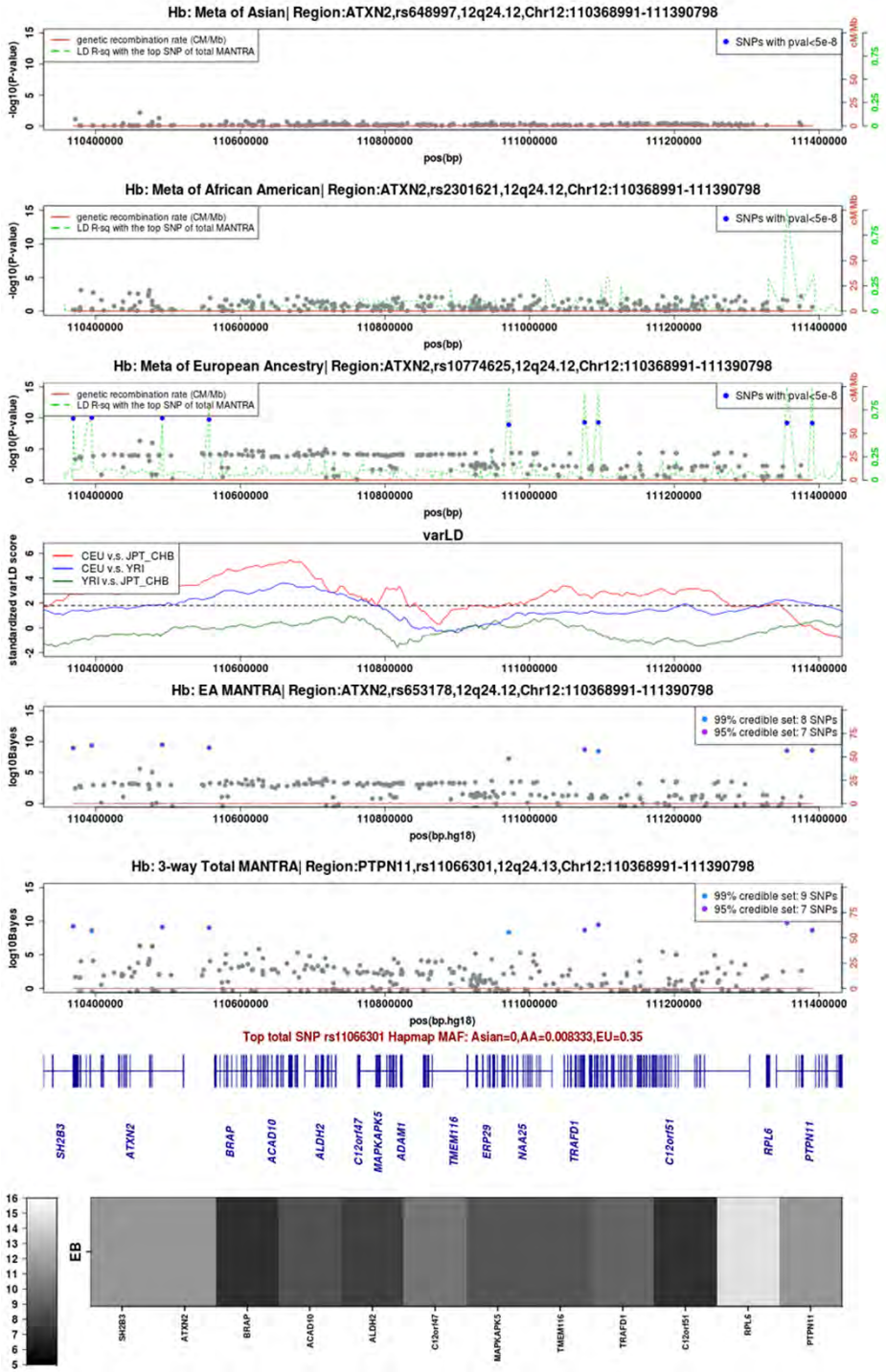

Hb: Meta of Asian| Region:SLC12A9,rs7794532,7q22.1,Chr7:99614570-100614570
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:C7orf51,rs12539172,7q22.1,Chr7:99614570-100614570
Hb: Meta of European Ancestry| Region:EPO,rs551238,7q22.1,Chr7:99614570-100614570
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:POP7,rs1734910,7q22.1,Chr7:99614570-100614570
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:EPO,rs1617640,7q22.1,Chr7:99614570-100614570
99% credible set: 14 SNPs
95% credible set: 7 SNPs
Top total SNP rs1617640 Hapmap MAF: Asian=0.1798,AA=0.325,EU=0.3917
STAG3
PVRIG
GATS
SPDYE3
PMS2P1
PILRB
PILRA
ZCWPW1
C7orf47
TSC22D4
C7orf51
AGFG2
TFR2
ACTL6B
GNB2
POP7
EPO
ZAN
EPHB4
SLC12A9
MUC12
MUC17
TRIM56
SERPINE1
C7orf52
EB
LRCH4
FBXO24
PCOLCE
MOSPD3
TRIP6
ACHE
AP1S1
VGF

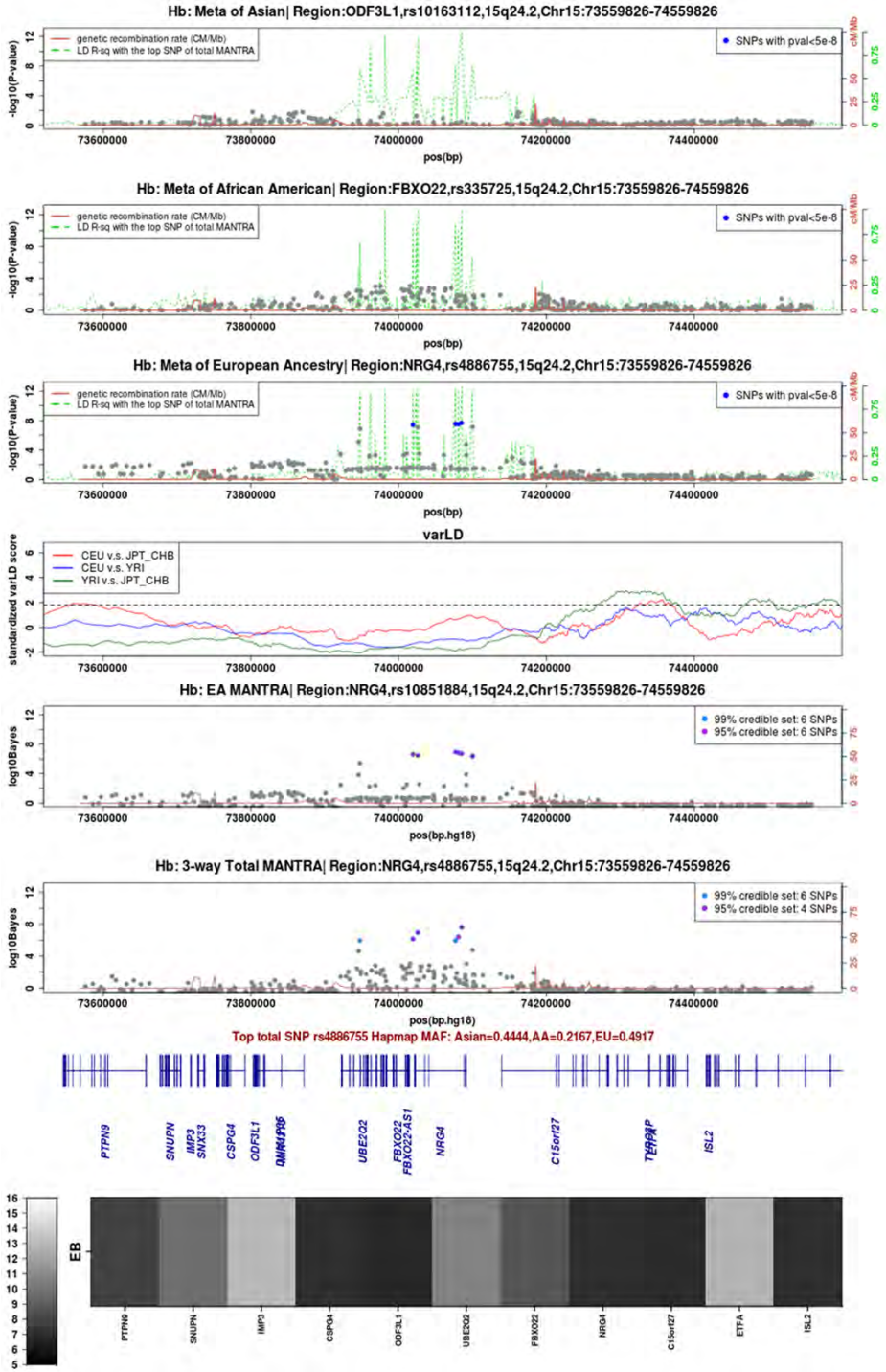

Hb: Meta of Asian| Region:MET,rs2299433,7q31.2,Chr7:115624724-116624724
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:ST7-AS2,rs17139387,7q31.2,Chr7:115624724-116624724
Hb: Meta of European Ancestry| Region:MET,rs10234854,7q31.2,Chr7:115624724-116624724
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:MET,rs10248537,7q31.2,Chr7:115624724-116624724
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:MET,rs2299433,7q31.2,Chr7:115624724-116624724
99% credible set: 11 SNPs
95% credible set: 10 SNPs
Top total SNP rs2299433 Hapmap MAF: Asian=0.2921,AA=0.1017,EU=0.2018
TES
CAV2
CAV1
MET
CAPZA2
ST7
ST7-AS2
ST7-OT3
EB

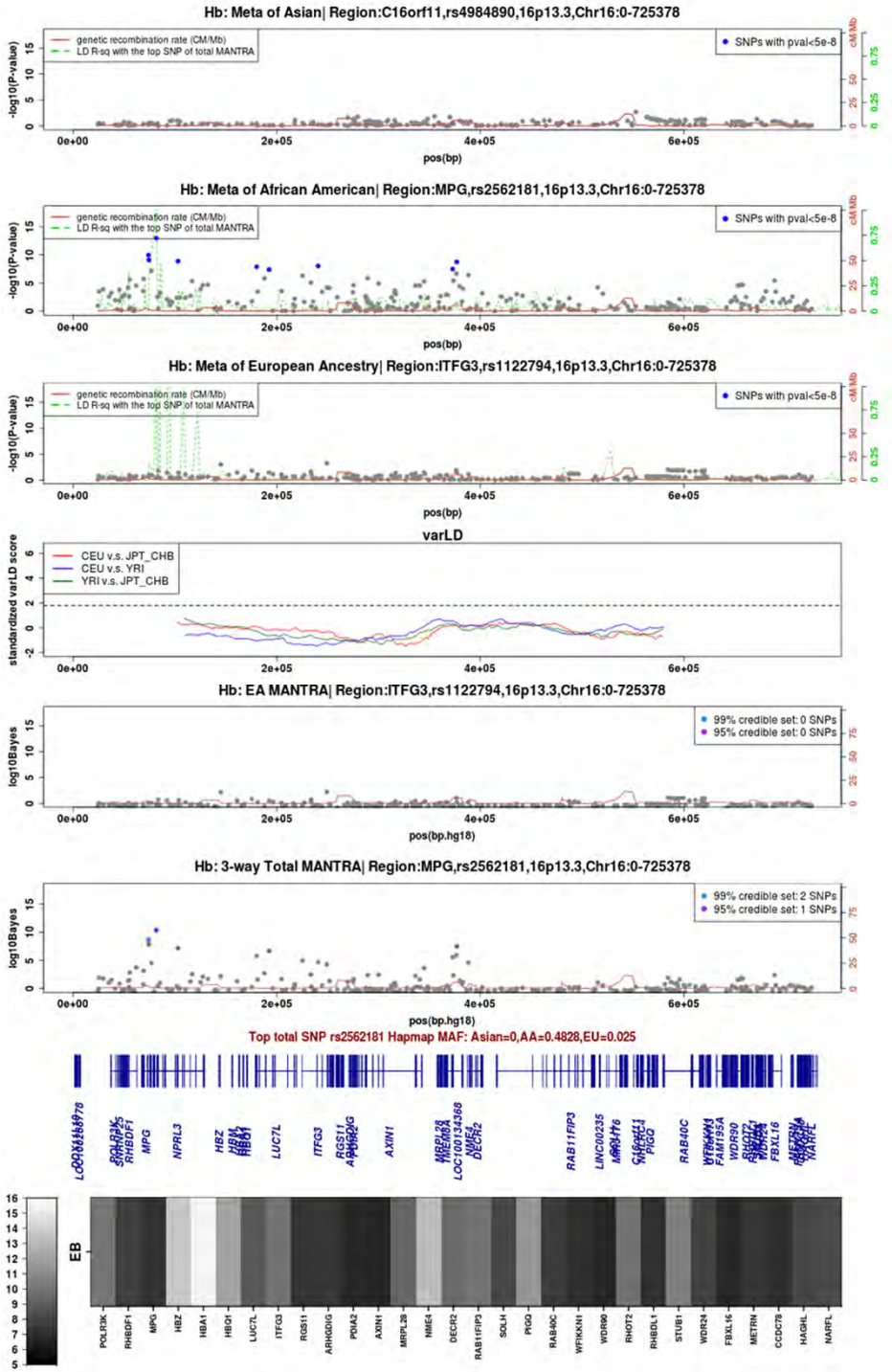

Hb: Meta of Asian| Region:PRKAG2,rs7788160,7q36.1,Chr7:150539848-151539848
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:CRYGN,rs12539880,7q36.1,Chr7:150539848-151539848
Hb: Meta of European Ancestry| Region:PRKAG2,rs10224002,7q36.1,Chr7:150539848-151539848
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:PRKAG2,rs10480300,7q36.1,Chr7:150539848-151539848
99% credible set: 4 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:PRKAG2,rs10480299,7q36.1,Chr7:150539848-151539848
99% credible set: 3 SNPs
95% credible set: 3 SNPs
Top total SNP rs10480299 Hapmap MAF: Asian=0,AA=0.3559,EU=0.2583
ABCF2
SMARCD3
NUB1
WDR86
LOC100131176
RHEB
PRKAG2
LOC100505483
GALNTL5
GALNT11
EB
ABCF2
SMARCD3
WDR86
CRYGN
RHEB
PRKAG2
GALNTL5
GALNT11
MLL3

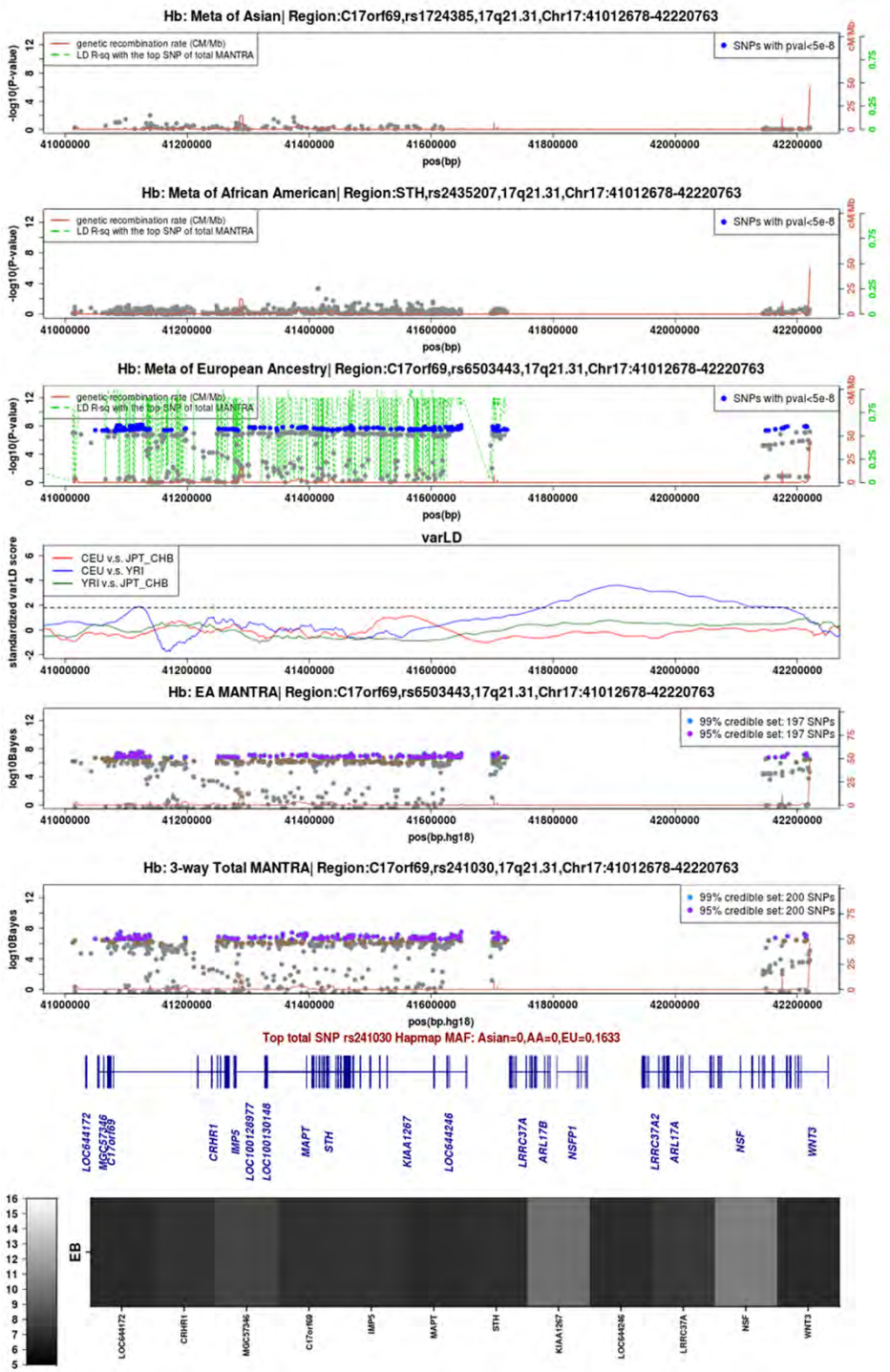

Hb: Meta of Asian| Region:ABO,rs495828,9q34.2,Chr9:134633094-135633094
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:ABO,rs8176730,9q34.2,Chr9:134633094-135633094
Hb: Meta of European Ancestry| Region:ABO,rs579459,9q34.2,Chr9:134633094-135633094
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:ABO,rs649129,9q34.2,Chr9:134633094-135633094
99% credible set: 4 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:ABO,rs495828,9q34.2,Chr9:134633094-135633094
99% credible set: 3 SNPs
95% credible set: 3 SNPs
Top total SNP rs495828 Hapmap MAF: Asian=0.1629,AA=0.09167,EU=0.2167
AK8
C9orf9
TSC1
GFI1B
GTF3C5
CEL
CELP
RALGDS
GBGT1
OBP2B
ABO
SURF6
RPL7A
SURF1
SURF2
SURF4
C9orf96
REXO4
ADAMTS13
C9orf7
SLC2A6
TMEM8C
ADAMTSL2
FAM163B
DBH
SARDH
EB
VAV2

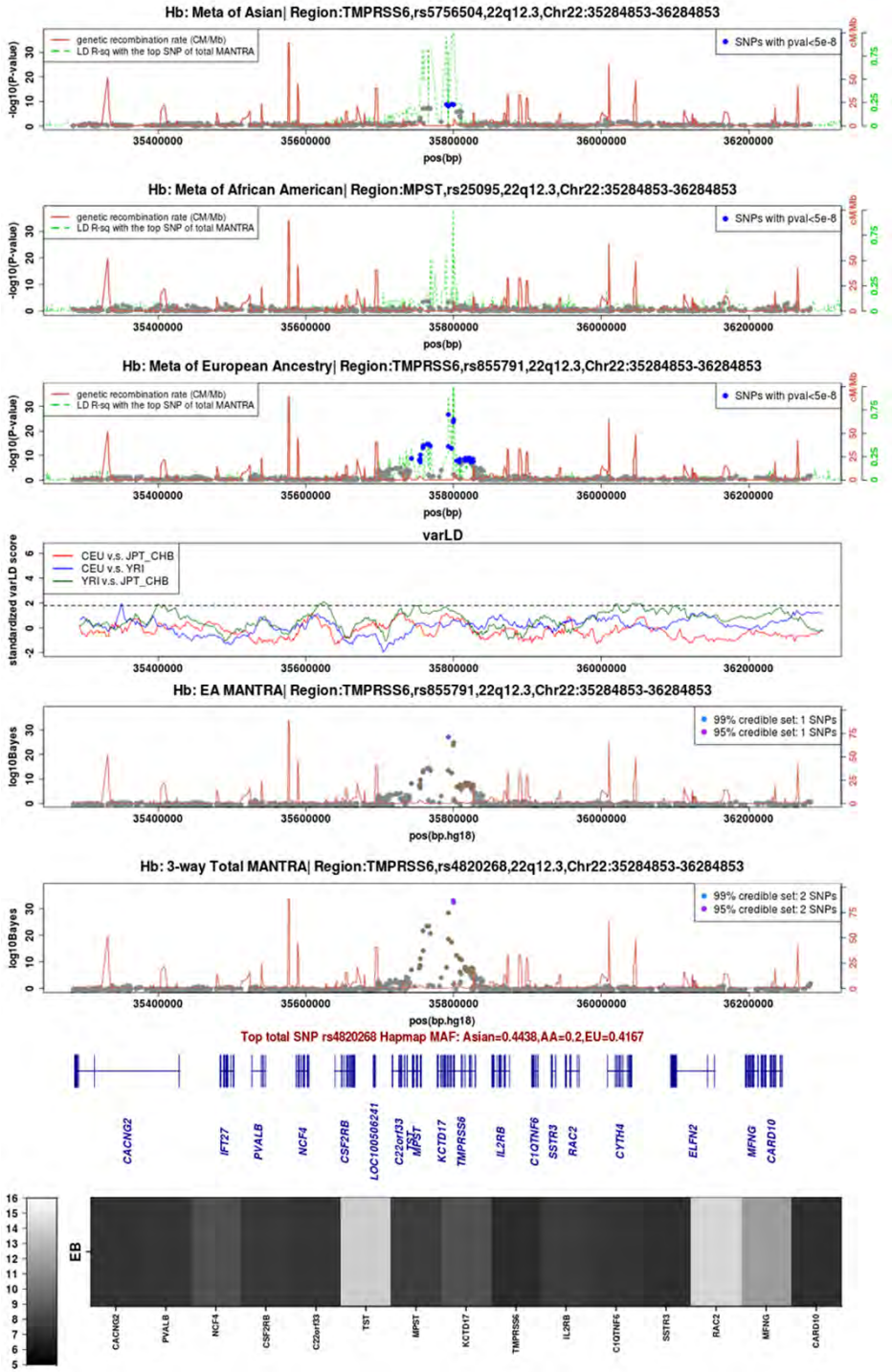

Hb: Meta of Asian| Region:TSPAN15,rs1227937,10q21.3,Chr10:70264872-71264872
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:HKDC1,rs10823321,10q21.3,Chr10:70264872-71264872
Hb: Meta of European Ancestry| Region:HK1,rs16926246,10q21.3,Chr10:70264872-71264872
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:HK1,rs16926246,10q21.3,Chr10:70264872-71264872
99% credible set: 1 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:HK1,rs16926246,10q21.3,Chr10:70264872-71264872
Top total SNP rs16926246 Hapmap MAF: Asian=0.01765,AA=0.1833,EU=0.1102
STOX1
DDX50
DDX21
KIAA1279
SRGN
VPS26A
SUPV3L1
HKDC1
HK1
TACR2
TSPAN15
NEUROG3
C10orf35
EB
COL13A1


Hb: Meta of Asian| Region:ATXN2,rs648997,12q24.12,Chr12:110368991-111390798
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:ATXN2,rs2301621,12q24.12,Chr12:110368991-111390798
Hb: Meta of European Ancestry| Region:ATXN2,rs10774625,12q24.12,Chr12:110368991-111390798
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:ATXN2,rs653178,12q24.12,Chr12:110368991-111390798
99% credible set: 8 SNPs
95% credible set: 7 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:PTPN11,rs11066301,12q24.13,Chr12:110368991-111390798
99% credible set: 9 SNPs
95% credible set: 7 SNPs
Top total SNP rs11066301 Hapmap MAF: Asian=0,AA=0.008333,EU=0.35
SH2B3
ATXN2
BRAP
ACAD10
ALDH2
C12orf47
MAPKAPK5
ADAM1
TMEM116
ERP29
NAA25
TRAFD1
C12orf51
RPL6
PTPN11
EB

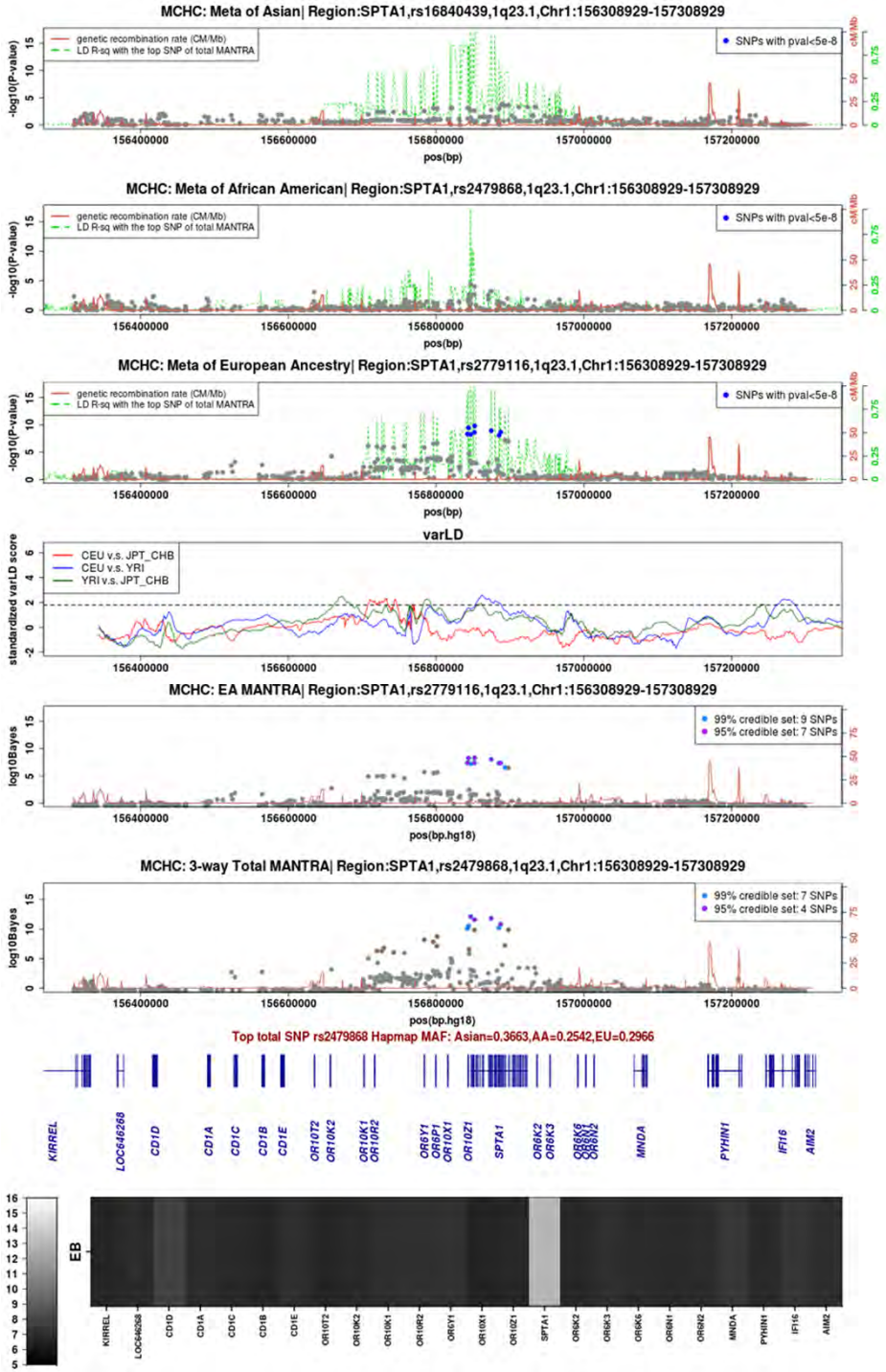

Hb: Meta of Asian| Region:ODF3L1,rs10163112,15q24.2,Chr15:73559826-74559826
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:FBXO22,rs335725,15q24.2,Chr15:73559826-74559826
Hb: Meta of European Ancestry| Region:NRG4,rs4886755,15q24.2,Chr15:73559826-74559826
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:NRG4,rs10851884,15q24.2,Chr15:73559826-74559826
99% credible set: 6 SNPs
95% credible set: 6 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:NRG4,rs4886755,15q24.2,Chr15:73559826-74559826
99% credible set: 6 SNPs
95% credible set: 4 SNPs
Top total SNP rs4886755 Hapmap MAF: Asian=0.4444,AA=0.2167,EU=0.4917
PTPN9
SNUPN
IMP3
SNX33
CSPG4
ODF3L1
UBE2Q2
FBXO22
FBXO22-AS1
NRG4
C15orf27
ISL2
EB
ETFA

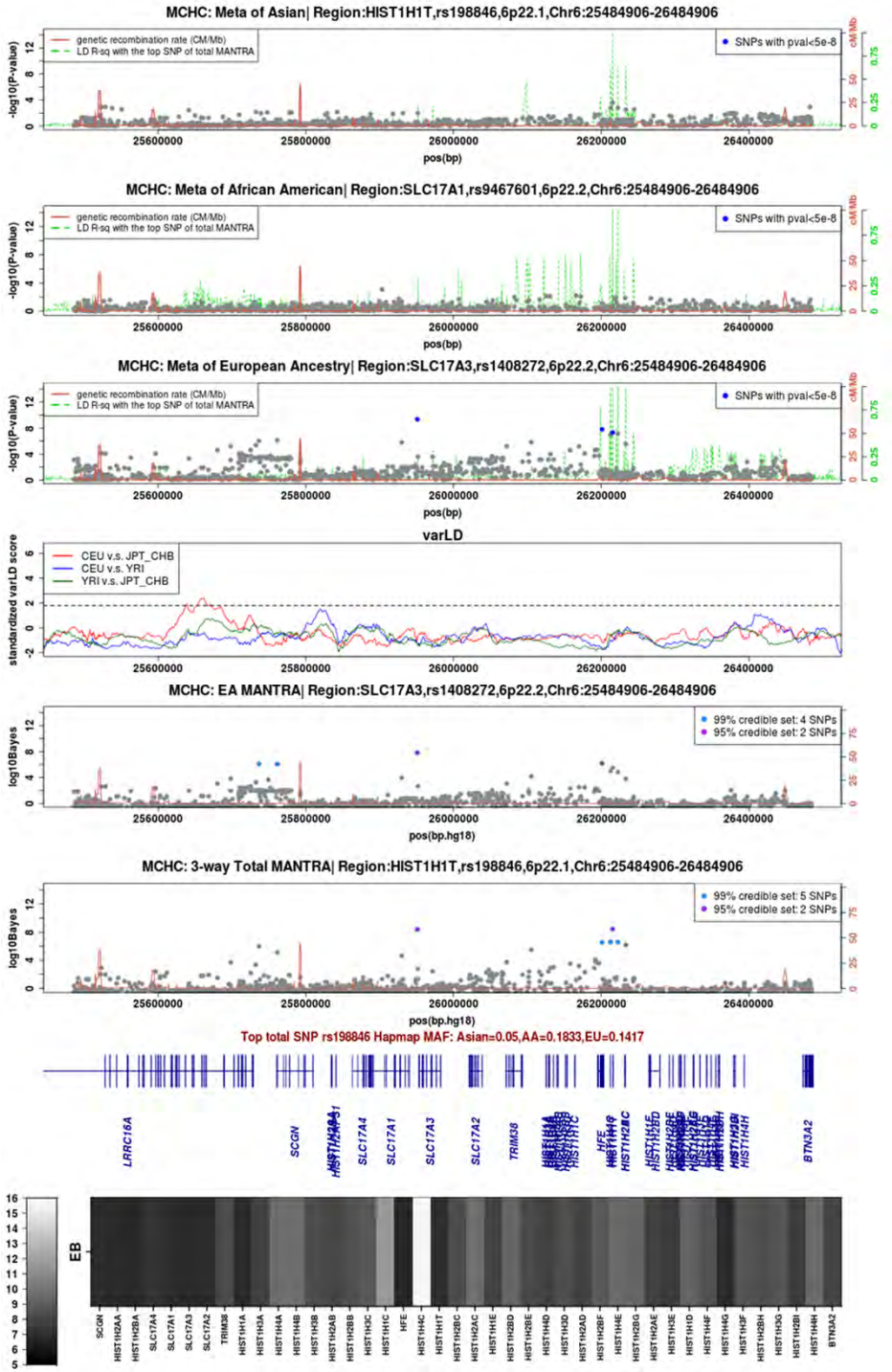

Hb: Meta of Asian| Region:C16orf11,rs4984890,16p13.3,Chr16:0-725378
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:MPG,rs2562181,16p13.3,Chr16:0-725378
Hb: Meta of European Ancestry| Region:ITFG3,rs1122794,16p13.3,Chr16:0-725378
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:ITFG3,rs1122794,16p13.3,Chr16:0-725378
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:MPG,rs2562181,16p13.3,Chr16:0-725378
99% credible set: 2 SNPs
95% credible set: 1 SNPs
Top total SNP rs2562181 Hapmap MAF: Asian=0,AA=0.4828,EU=0.025
EB
POLR3K
RHBDF1
MPG
HBZ
HBA1
HBD1
LUC7L
ITFG3
RGS11
ARHGDIG
PDIA2
AXIN1
MRPL28
NME4
DECR2
RAB11FIP3
SOLH
PIGO
RAB40C
WFIKKN1
WDR90
RHOT2
RHBDL1
STUB1
WDR24
FBXL16
METRN
CCDC78
HAGHL
NARFL

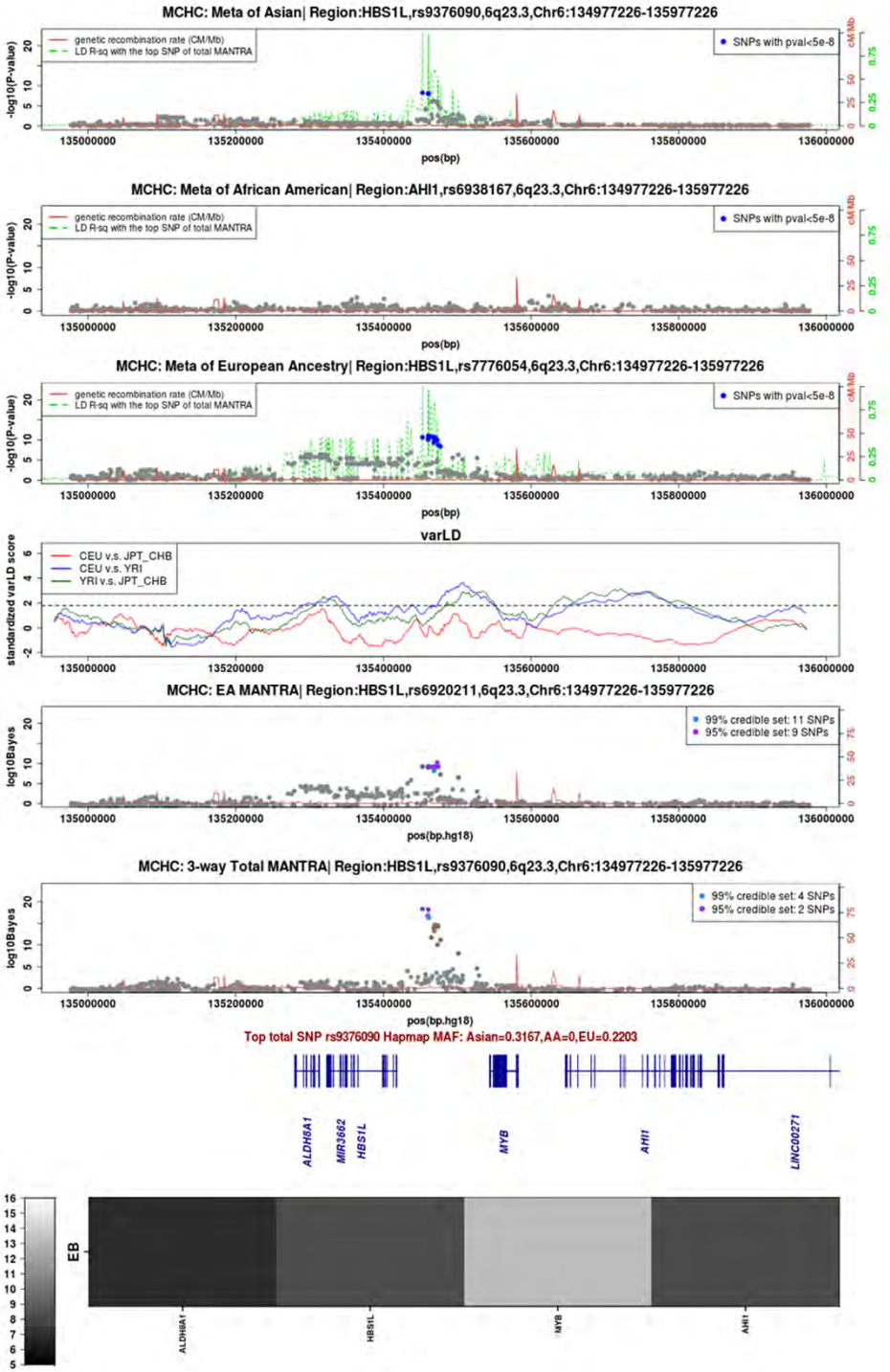

Hb: Meta of Asian| Region:C17orf69,rs1724385,17q21.31,Chr17:41012678-42220763
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:STH,rs2435207,17q21.31,Chr17:41012678-42220763
Hb: Meta of European Ancestry| Region:C17orf69,rs6503443,17q21.31,Chr17:41012678-42220763
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:C17orf69,rs6503443,17q21.31,Chr17:41012678-42220763
99% credible set: 197 SNPs
95% credible set: 197 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:C17orf69,rs241030,17q21.31,Chr17:41012678-42220763
99% credible set: 200 SNPs
95% credible set: 200 SNPs
Top total SNP rs241030 Hapmap MAF: Asian=0,AA=0,EU=0.1633
LOC644172
MGC57346
C17orf69
CRHR1
IMP5
LOC100128977
LOC100130148
MAPT
STH
KIAA1267
LOC644246
LRRC37A
ARL17B
NSFP1
LRRC37A2
ARL17A
NSF
WNT3
EB

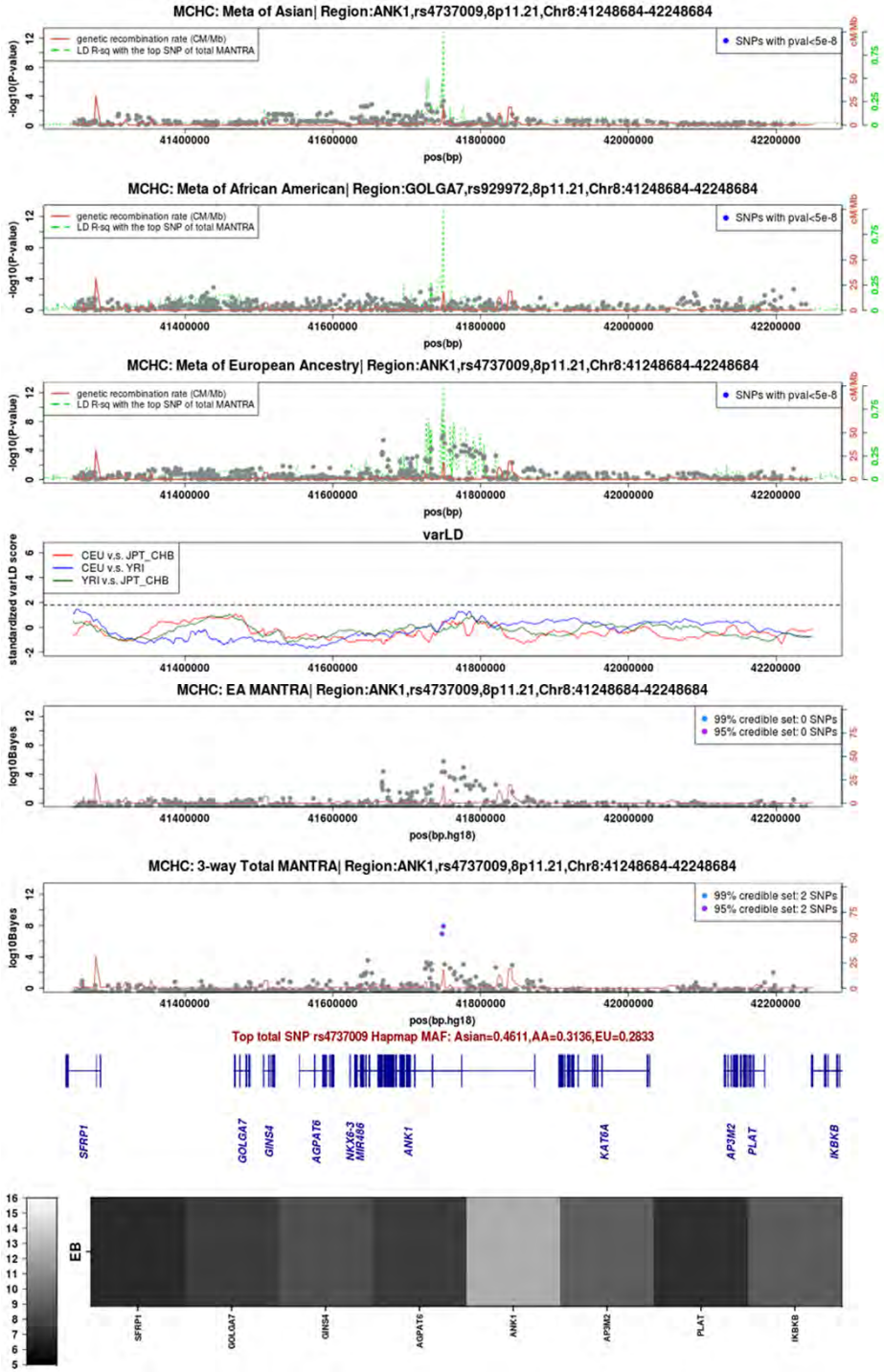

Hb: Meta of Asian| Region:TMPRSS6,rs5756504,22q12.3,Chr22:35284853-36284853
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
Hb: Meta of African American| Region:MPST,rs25095,22q12.3,Chr22:35284853-36284853
Hb: Meta of European Ancestry| Region:TMPRSS6,rs855791,22q12.3,Chr22:35284853-36284853
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
Hb: EA MANTRA| Region:TMPRSS6,rs855791,22q12.3,Chr22:35284853-36284853
99% credible set: 1 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
Hb: 3-way Total MANTRA| Region:TMPRSS6,rs4820268,22q12.3,Chr22:35284853-36284853
99% credible set: 2 SNPs
95% credible set: 2 SNPs
Top total SNP rs4820268 Hapmap MAF: Asian=0.4438,AA=0.2,EU=0.4167
CACNG2
IFT27
PVALB
NCF4
CSF2RB
LOC100506241
C22orf33
TST
MPST
KCTD17
TMPRSS6
IL2RB
C1QTNF6
SSTR3
RAC2
CYTH4
ELFN2
MFNG
CARD10
EB

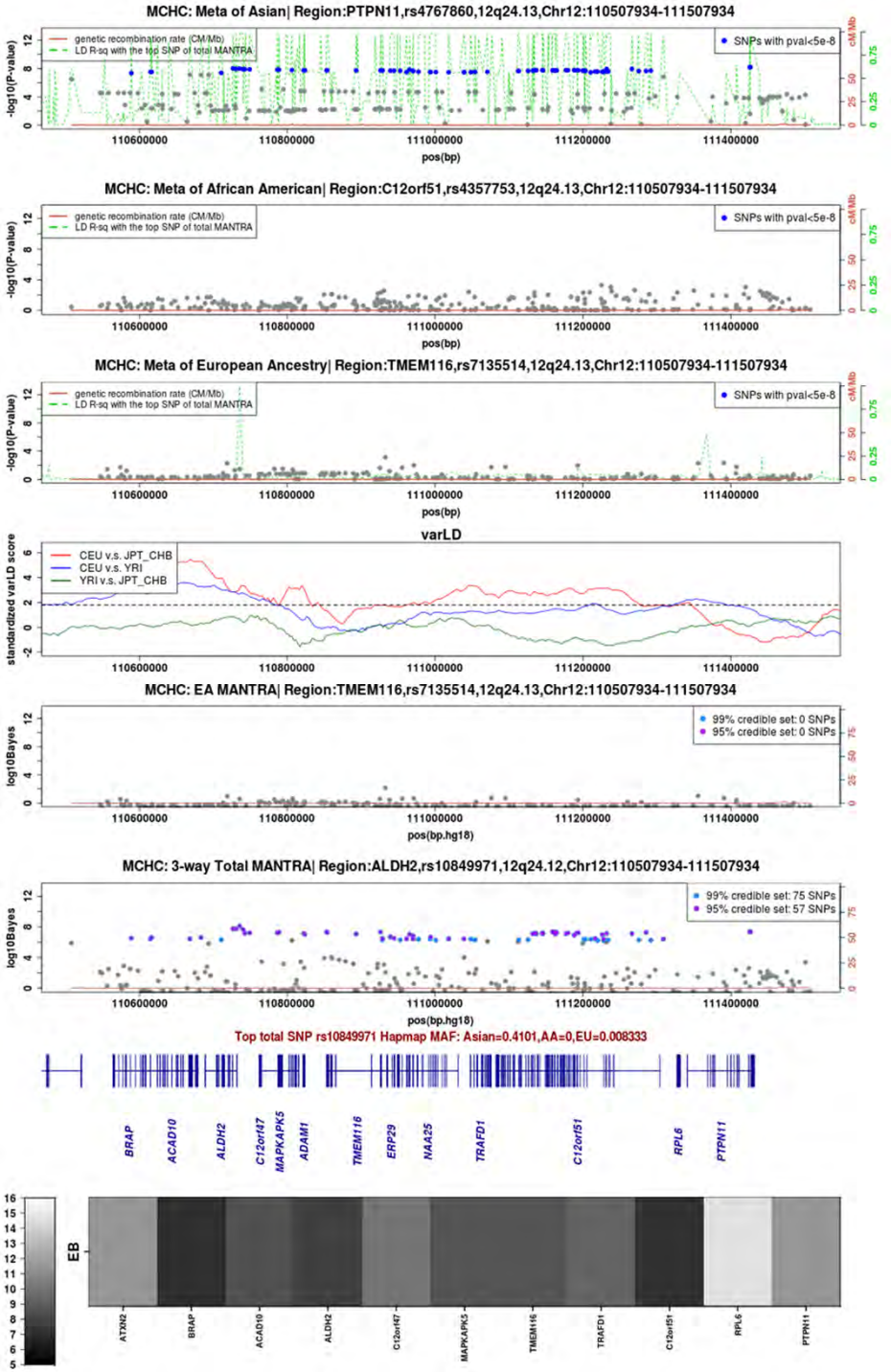
MCHC


MCHC: Meta of Asian| Region:SPTA1,rs16840439,1q23.1,Chr1:156308929-157308929
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCHC: Meta of African American| Region:SPTA1,rs2479868,1q23.1,Chr1:156308929-157308929
MCHC: Meta of European Ancestry| Region:SPTA1,rs2779116,1q23.1,Chr1:156308929-157308929
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCHC: EA MANTRA| Region:SPTA1,rs2779116,1q23.1,Chr1:156308929-157308929
99% credible set: 9 SNPs
95% credible set: 7 SNPs
log10Bayes
pos(bp.hg18)
MCHC: 3-way Total MANTRA| Region:SPTA1,rs2479868,1q23.1,Chr1:156308929-157308929
99% credible set: 7 SNPs
95% credible set: 4 SNPs
Top total SNP rs2479868 Hapmap MAF: Asian=0.3663,AA=0.2542,EU=0.2966
KIRREL
LOC646268
CD1D
CD1A
CD1C
CD1B
CD1E
OR10T2
OR10K2
OR10K1
OR10R2
OR6Y1
OR6P1
OR10X1
OR10Z1
SPTA1
OR6K2
OR6K3
OR6K6
OR6N1
OR6N2
MNDA
PYHIN1
IFI16
AIM2
EB


MCHC: Meta of Asian| Region:HIST1H1T,rs198846,6p22.1,Chr6:25484906-26484906
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCHC: Meta of African American| Region:SLC17A1,rs9467601,6p22.2,Chr6:25484906-26484906
MCHC: Meta of European Ancestry| Region:SLC17A3,rs1408272,6p22.2,Chr6:25484906-26484906
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCHC: EA MANTRA| Region:SLC17A3,rs1408272,6p22.2,Chr6:25484906-26484906
99% credible set: 4 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
MCHC: 3-way Total MANTRA| Region:HIST1H1T,rs198846,6p22.1,Chr6:25484906-26484906
99% credible set: 5 SNPs
95% credible set: 2 SNPs
Top total SNP rs198846 Hapmap MAF: Asian=0.05,AA=0.1833,EU=0.1417
LRRC16A
SCGN
SLC17A4
SLC17A1
SLC17A3
SLC17A2
TRIM38
HFE
BTN3A2
EB


MCHC: Meta of Asian| Region:HBS1L,rs9376090,6q23.3,Chr6:134977226-135977226
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCHC: Meta of African American| Region:AHI1,rs6938167,6q23.3,Chr6:134977226-135977226
MCHC: Meta of European Ancestry| Region:HBS1L,rs7776054,6q23.3,Chr6:134977226-135977226
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCHC: EA MANTRA| Region:HBS1L,rs6920211,6q23.3,Chr6:134977226-135977226
99% credible set: 11 SNPs
95% credible set: 9 SNPs
log10Bayes
pos(bp.hg18)
MCHC: 3-way Total MANTRA| Region:HBS1L,rs9376090,6q23.3,Chr6:134977226-135977226
99% credible set: 4 SNPs
95% credible set: 2 SNPs
Top total SNP rs9376090 Hapmap MAF: Asian=0.3167,AA=0,EU=0.2203
ALDH8A1
MIR3662
HBS1L
MYB
AHI1
LINC00271
EB


MCHC: Meta of Asian| Region:ANK1,rs4737009,8p11.21,Chr8:41248684-42248684
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCHC: Meta of African American| Region:GOLGA7,rs929972,8p11.21,Chr8:41248684-42248684
MCHC: Meta of European Ancestry| Region:ANK1,rs4737009,8p11.21,Chr8:41248684-42248684
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCHC: EA MANTRA| Region:ANK1,rs4737009,8p11.21,Chr8:41248684-42248684
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCHC: 3-way Total MANTRA| Region:ANK1,rs4737009,8p11.21,Chr8:41248684-42248684
99% credible set: 2 SNPs
95% credible set: 2 SNPs
Top total SNP rs4737009 Hapmap MAF: Asian=0.4611,AA=0.3136,EU=0.2833
SFRP1
GOLGA7
GINS4
AGPAT6
NKX6-3
MIR486
ANK1
KAT6A
AP3M2
PLAT
IKBKB
EB


MCHC: Meta of Asian| Region:PTPN11,rs4767860,12q24.13,Chr12:110507934-111507934
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCHC: Meta of African American| Region:C12orf51,rs4357753,12q24.13,Chr12:110507934-111507934
MCHC: Meta of European Ancestry| Region:TMEM116,rs7135514,12q24.13,Chr12:110507934-111507934
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCHC: EA MANTRA| Region:TMEM116,rs7135514,12q24.13,Chr12:110507934-111507934
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCHC: 3-way Total MANTRA| Region:ALDH2,rs10849971,12q24.12,Chr12:110507934-111507934
99% credible set: 75 SNPs
95% credible set: 57 SNPs
Top total SNP rs10849971 Hapmap MAF: Asian=0.4101,AA=0,EU=0.008333
BRAP
ACAD10
ALDH2
C12orf47
MAPKAPK5
ADAM1
TMEM116
ERP29
NAA25
TRAFD1
C12orf51
RPL6
PTPN11
EB
ATXN2
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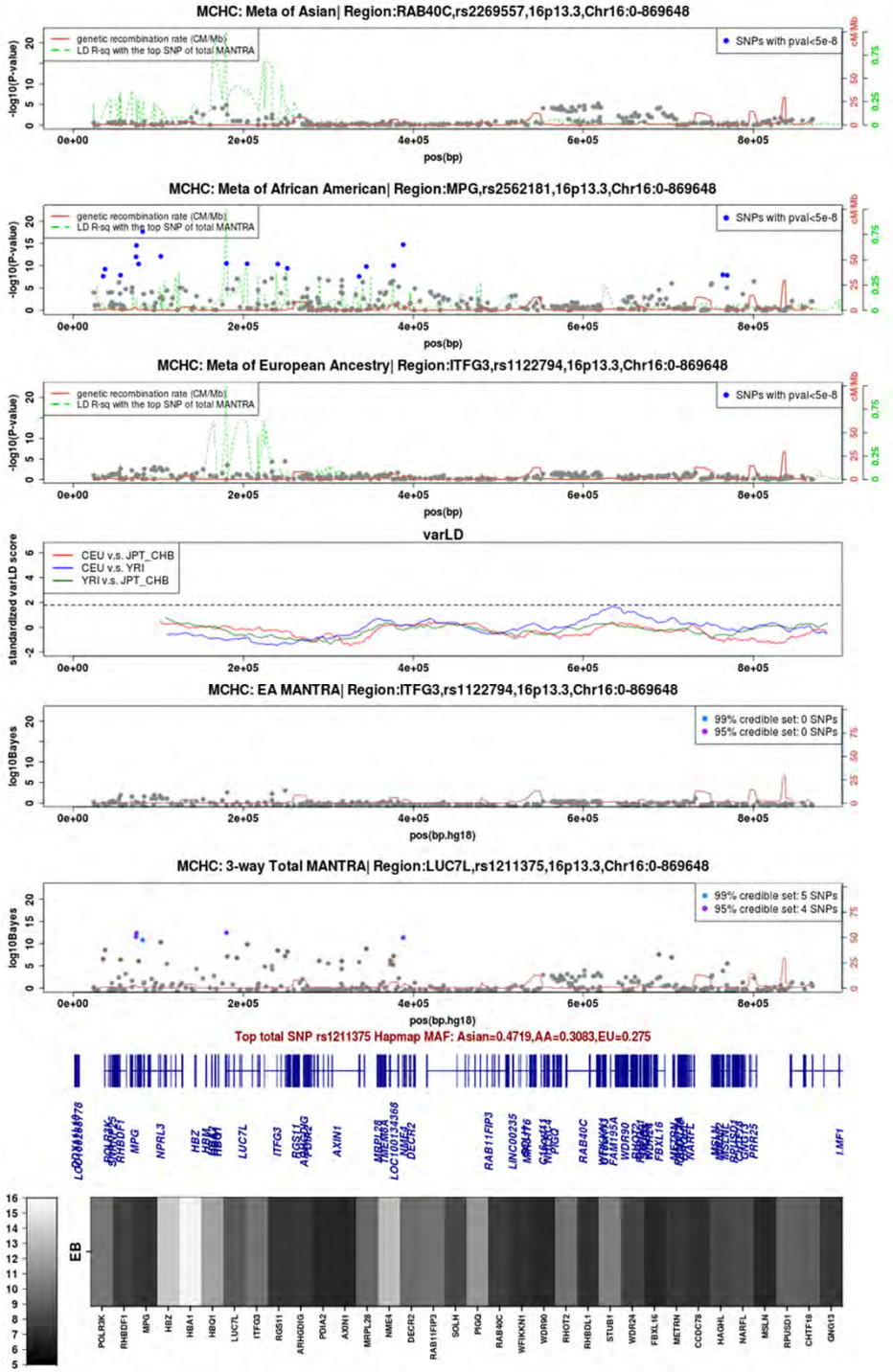
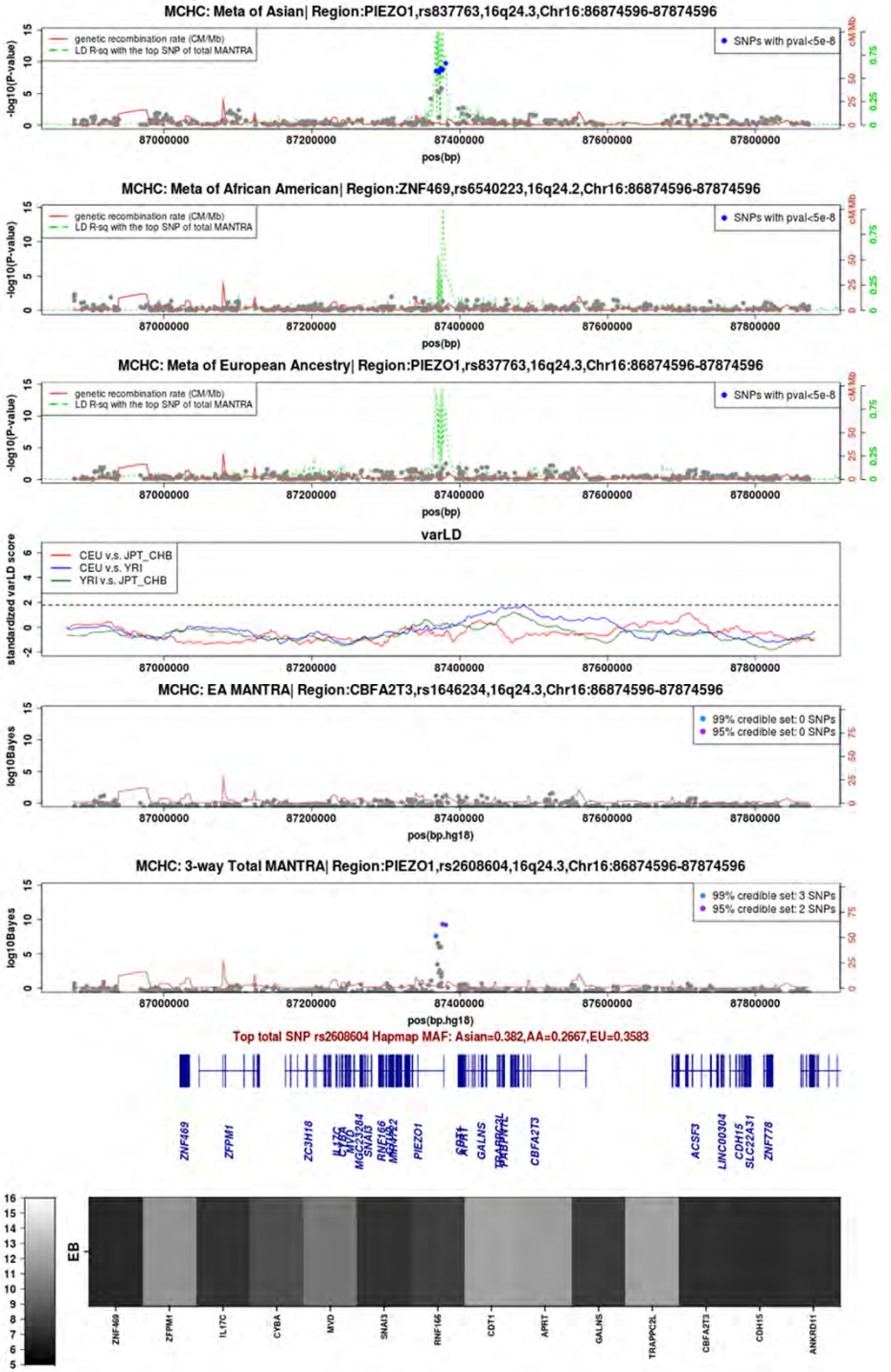
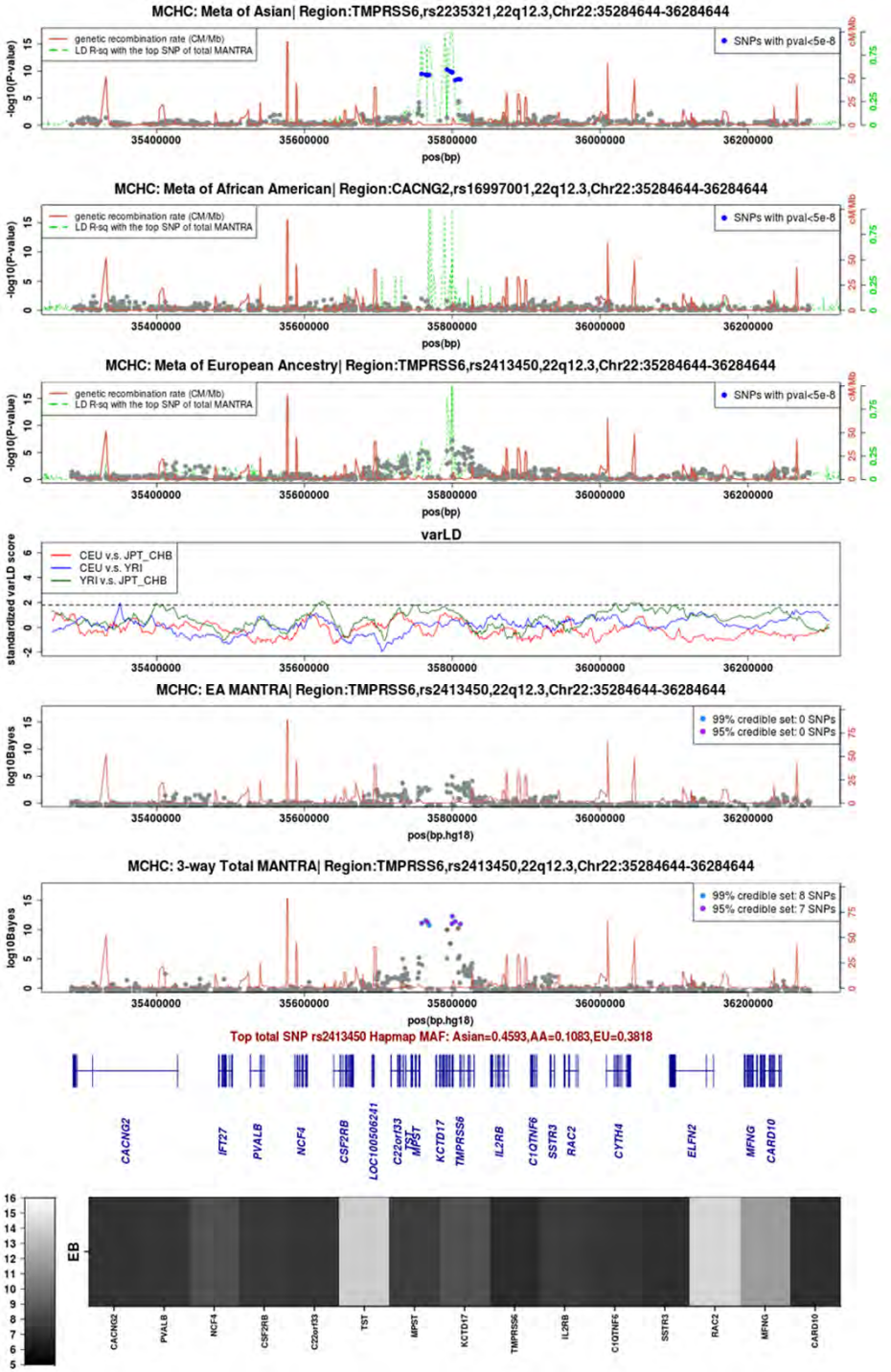
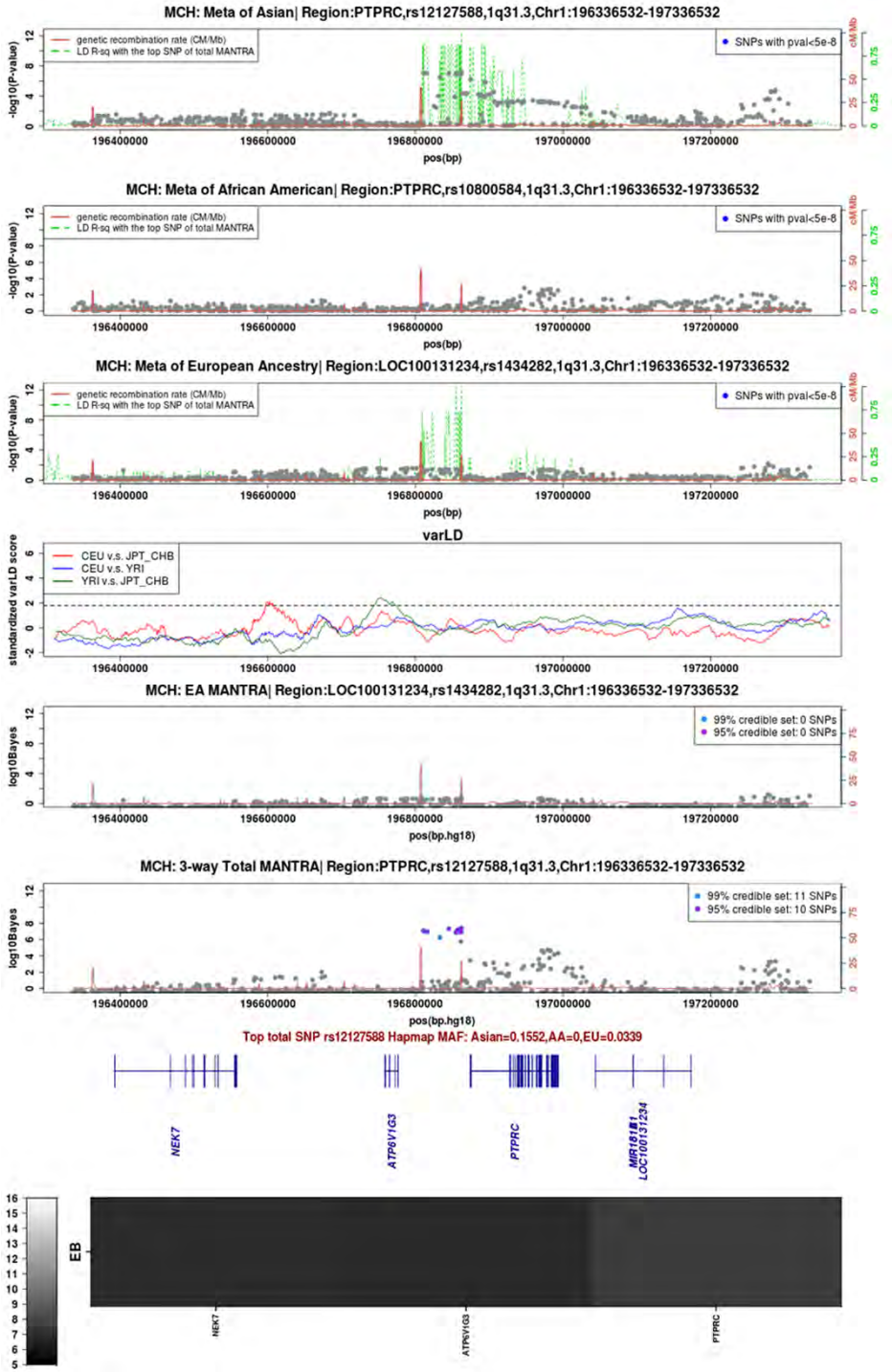
TMEM116
TRAFD1
C12orf51
RPL6
PTPN11

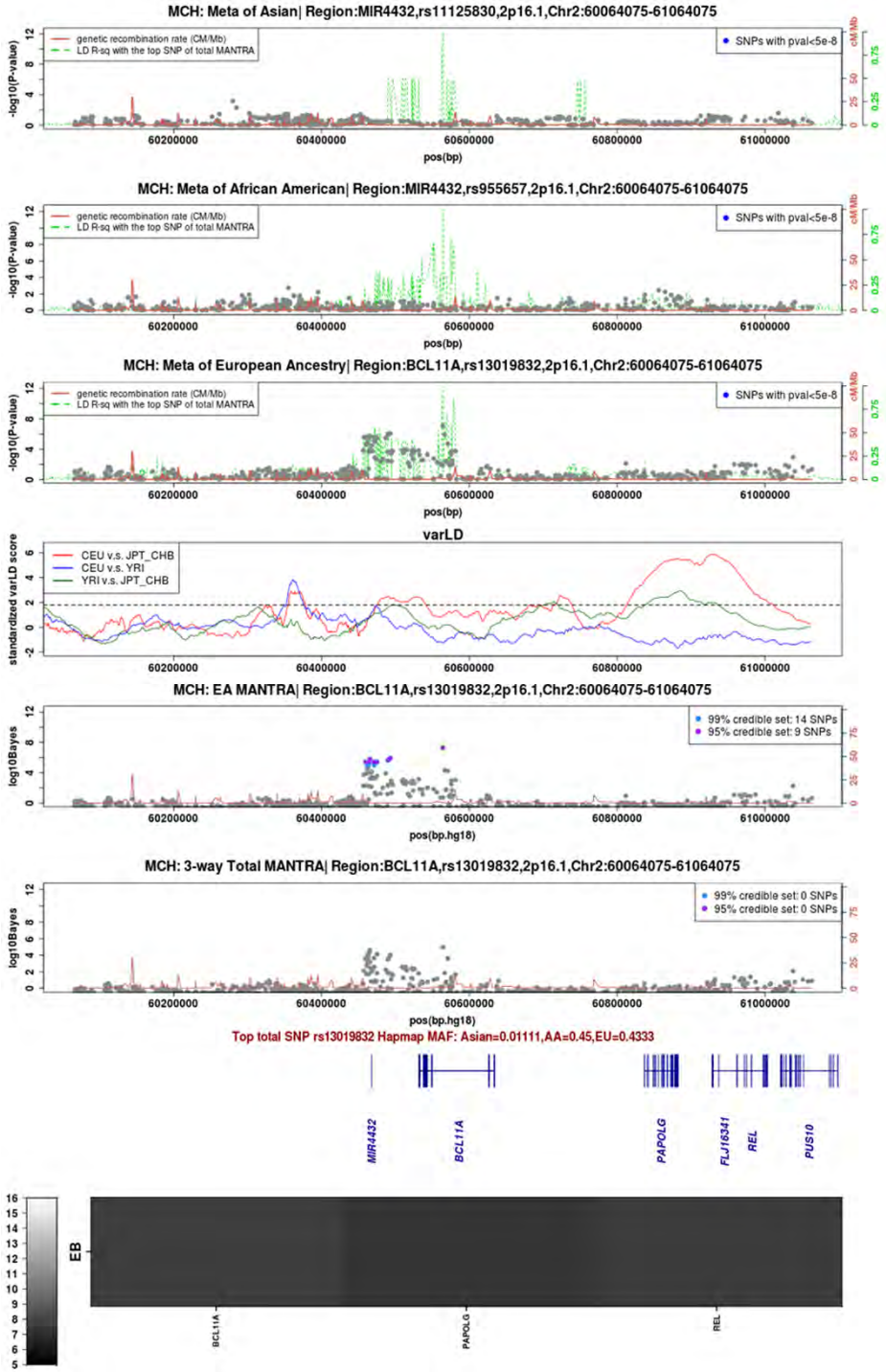

MCHC: Meta of Asian| Region:RAB40C,rs2269557,16p13.3,Chr16:0-869648
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCHC: Meta of African American| Region:MPG,rs2562181,16p13.3,Chr16:0-869648
MCHC: Meta of European Ancestry| Region:ITFG3,rs1122794,16p13.3,Chr16:0-869648
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCHC: EA MANTRA| Region:ITFG3,rs1122794,16p13.3,Chr16:0-869648
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCHC: 3-way Total MANTRA| Region:LUC7L,rs1211375,16p13.3,Chr16:0-869648
99% credible set: 5 SNPs
95% credible set: 4 SNPs
Top total SNP rs1211375 Hapmap MAF: Asian=0.4719,AA=0.3083,EU=0.275
EB
POLR3K
RHBDF1
MPG
HBZ
HBA1
HBQ1
LUC7L
ITFG3
RGS11
ARHGDIG
PDIA2
AXIN1
MRPL28
NME4
DECR2
RAB11FIP3
SOLH
PIGQ
RAB40C
WFIKKN1
WDR90
RHOT2
RHBDL1
STUB1
WDR24
FBXL16
METRN
CCDC78
HAGHL
NARFL
MSLN
RPUSD1
CHTF18
GNG13

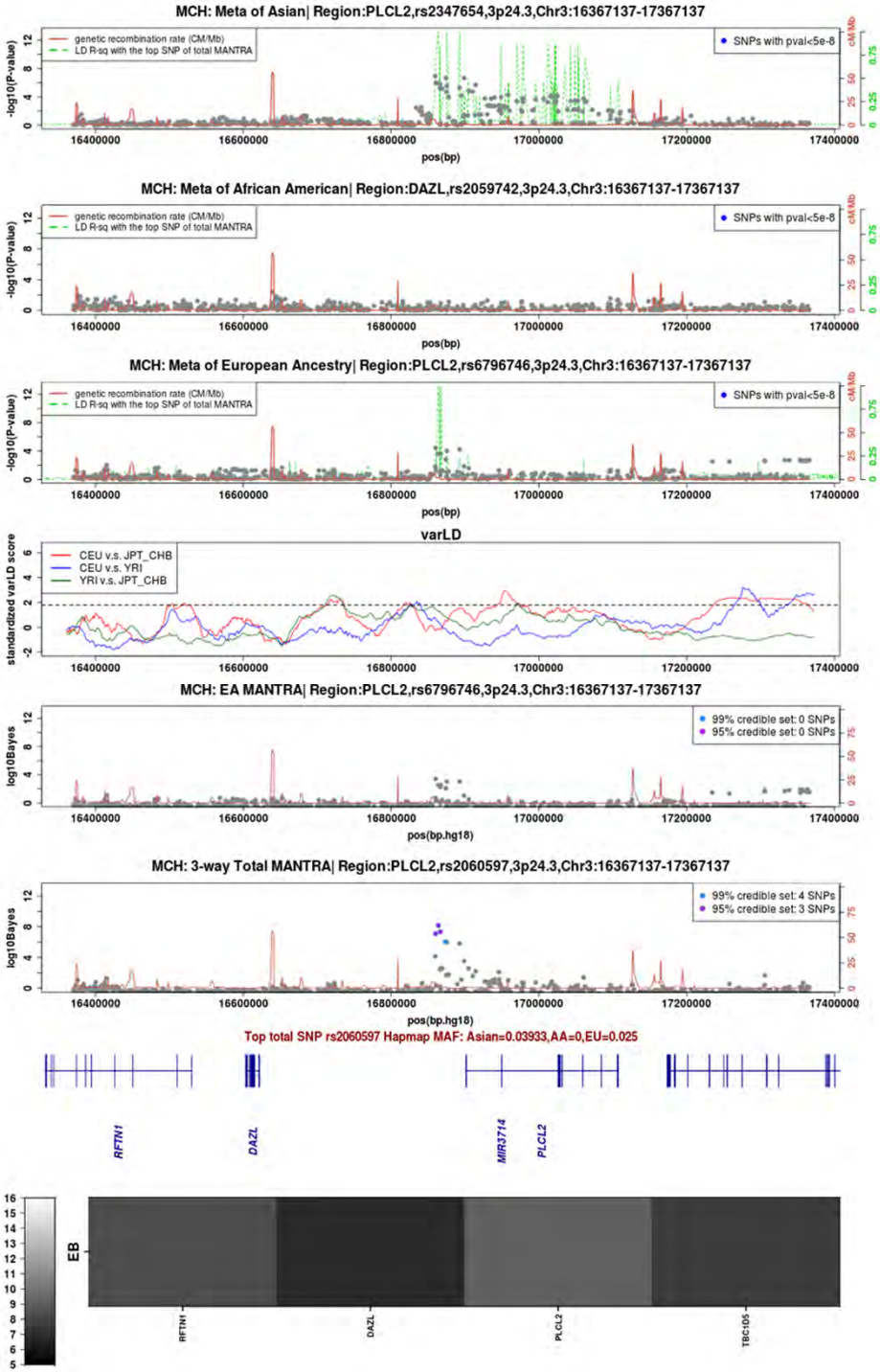

MCHC: Meta of Asian| Region:PIEZO1,rs837763,16q24.3,Chr16:86874596-87874596
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCHC: Meta of African American| Region:ZNF469,rs6540223,16q24.2,Chr16:86874596-87874596
MCHC: Meta of European Ancestry| Region:PIEZO1,rs837763,16q24.3,Chr16:86874596-87874596
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCHC: EA MANTRA| Region:CBFA2T3,rs1646234,16q24.3,Chr16:86874596-87874596
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCHC: 3-way Total MANTRA| Region:PIEZO1,rs2608604,16q24.3,Chr16:86874596-87874596
99% credible set: 3 SNPs
95% credible set: 2 SNPs
Top total SNP rs2608604 Hapmap MAF: Asian=0.382,AA=0.2667,EU=0.3583
ZNF469
ZFPM1
ZC3H18
PIEZO1
GALNS
CBFA2T3
ACSF3
LINC00304
CDH15
SLC22A31
ZNF778
EB
ZNF469
ZFPM1
IL17C
CYBA
MYD
SNAI3
RNF166
CDT1
APRT
GALNS
TRAPPC2L
CBFA2T3
CDH15
ANKRD11

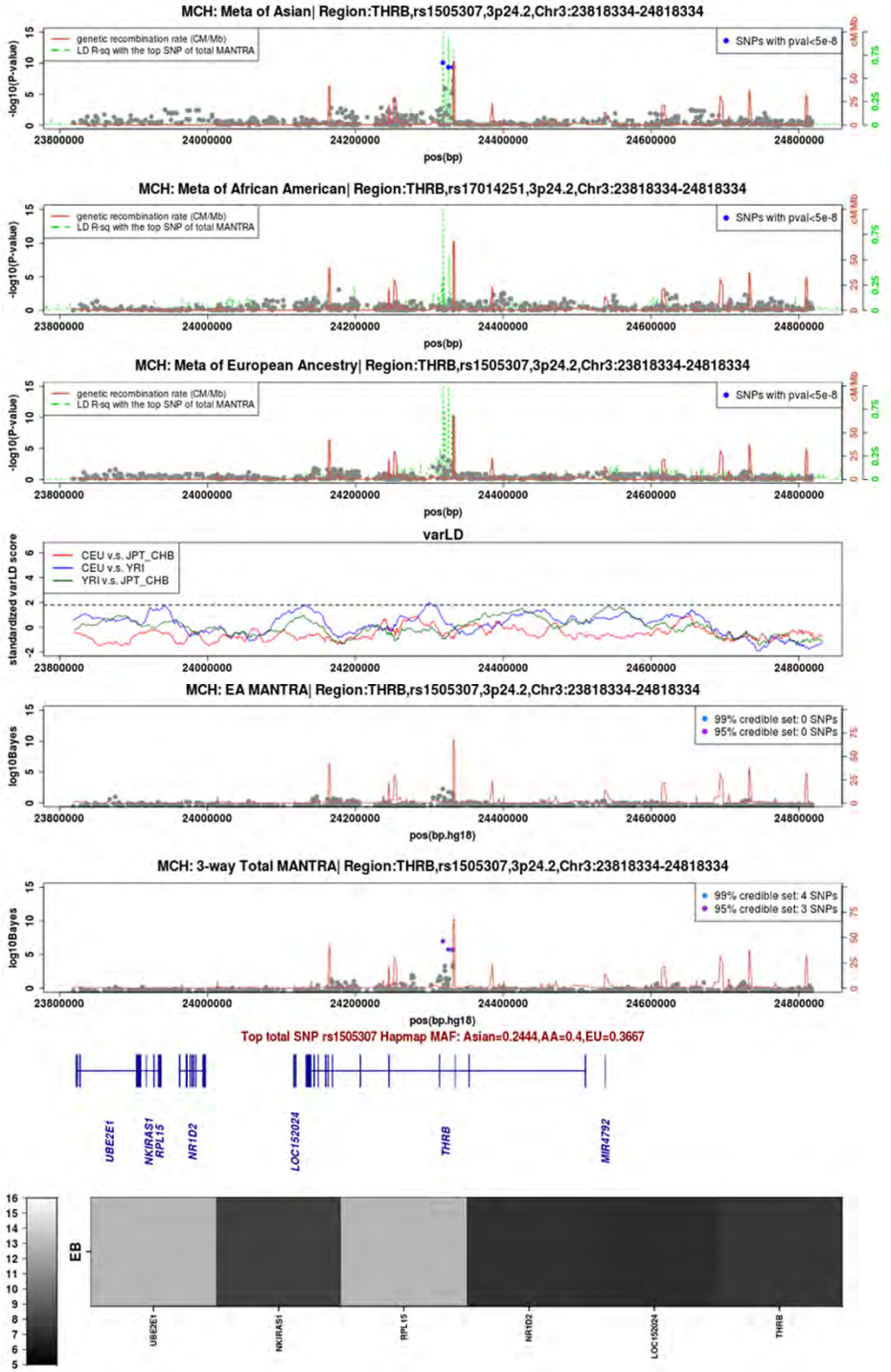

MCHC: Meta of Asian| Region:TMPRSS6,rs2235321,22q12.3,Chr22:35284644-36284644
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCHC: Meta of African American| Region:CACNG2,rs16997001,22q12.3,Chr22:35284644-36284644
MCHC: Meta of European Ancestry| Region:TMPRSS6,rs2413450,22q12.3,Chr22:35284644-36284644
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCHC: EA MANTRA| Region:TMPRSS6,rs2413450,22q12.3,Chr22:35284644-36284644
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCHC: 3-way Total MANTRA| Region:TMPRSS6,rs2413450,22q12.3,Chr22:35284644-36284644
99% credible set: 8 SNPs
95% credible set: 7 SNPs
Top total SNP rs2413450 Hapmap MAF: Asian=0.4593,AA=0.1083,EU=0.3818
CACNG2
IFT27
PVALB
NCF4
CSF2RB
LOC100506241
C22orf33
TST
MPST
KCTD17
TMPRSS6
IL2RB
C1QTNF6
SSTR3
RAC2
CYTH4
ELFN2
MFNG
CARD10
EB

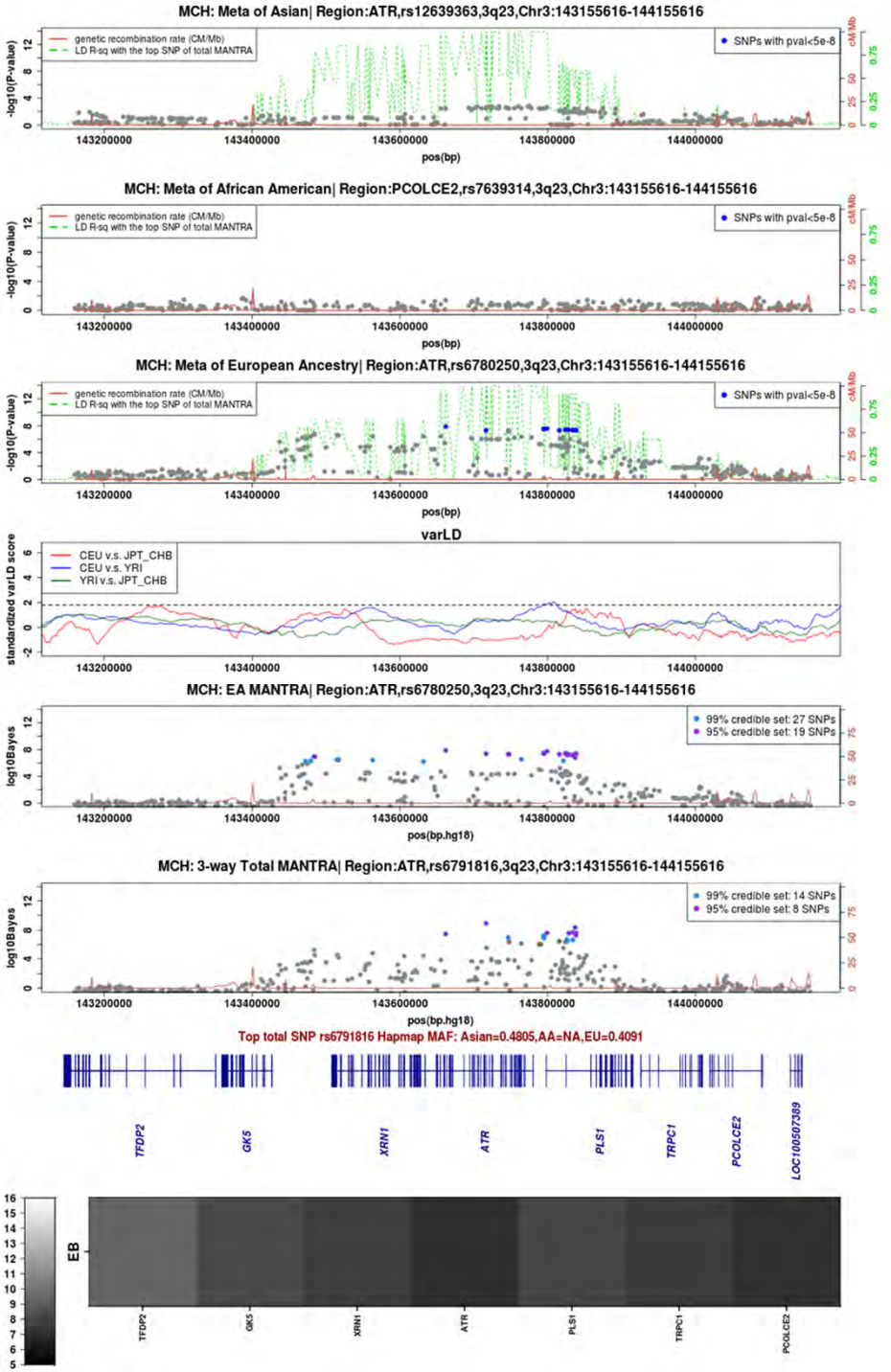
MCH

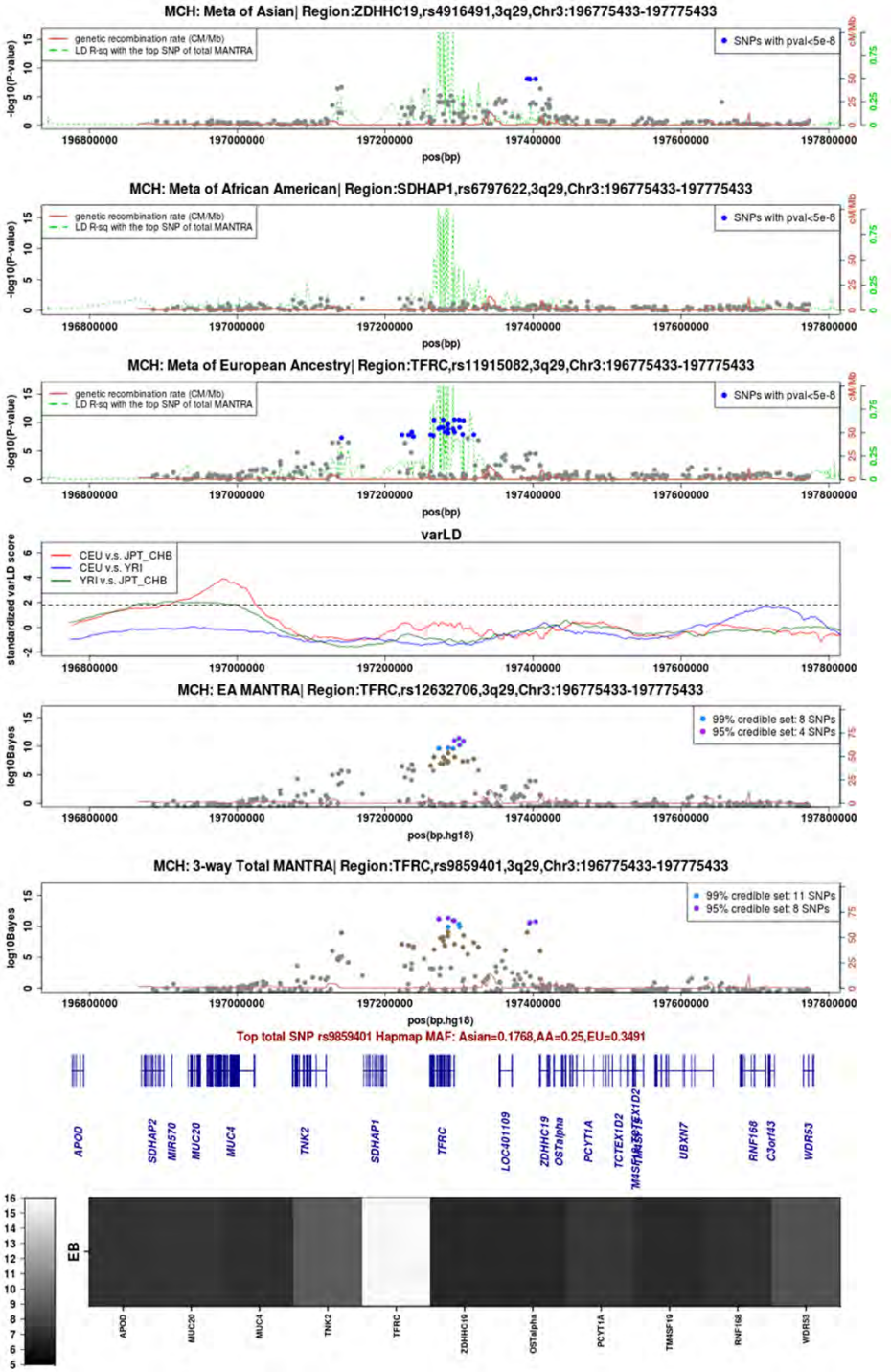

MCH: Meta of Asian| Region:PTPRC,rs12127588,1q31.3,Chr1:196336532-197336532
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
196400000
196600000
196800000
197000000
197200000
pos(bp)
MCH: Meta of African American| Region:PTPRC,rs10800584,1q31.3,Chr1:196336532-197336532
MCH: Meta of European Ancestry| Region:LOC100131234,rs1434282,1q31.3,Chr1:196336532-197336532
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:LOC100131234,rs1434282,1q31.3,Chr1:196336532-197336532
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:PTPRC,rs12127588,1q31.3,Chr1:196336532-197336532
99% credible set: 11 SNPs
95% credible set: 10 SNPs
Top total SNP rs12127588 Hapmap MAF: Asian=0.1552,AA=0,EU=0.0339
NEK7
ATP6V1G3
PTPRC
MIR1281
LOC100131234
EB

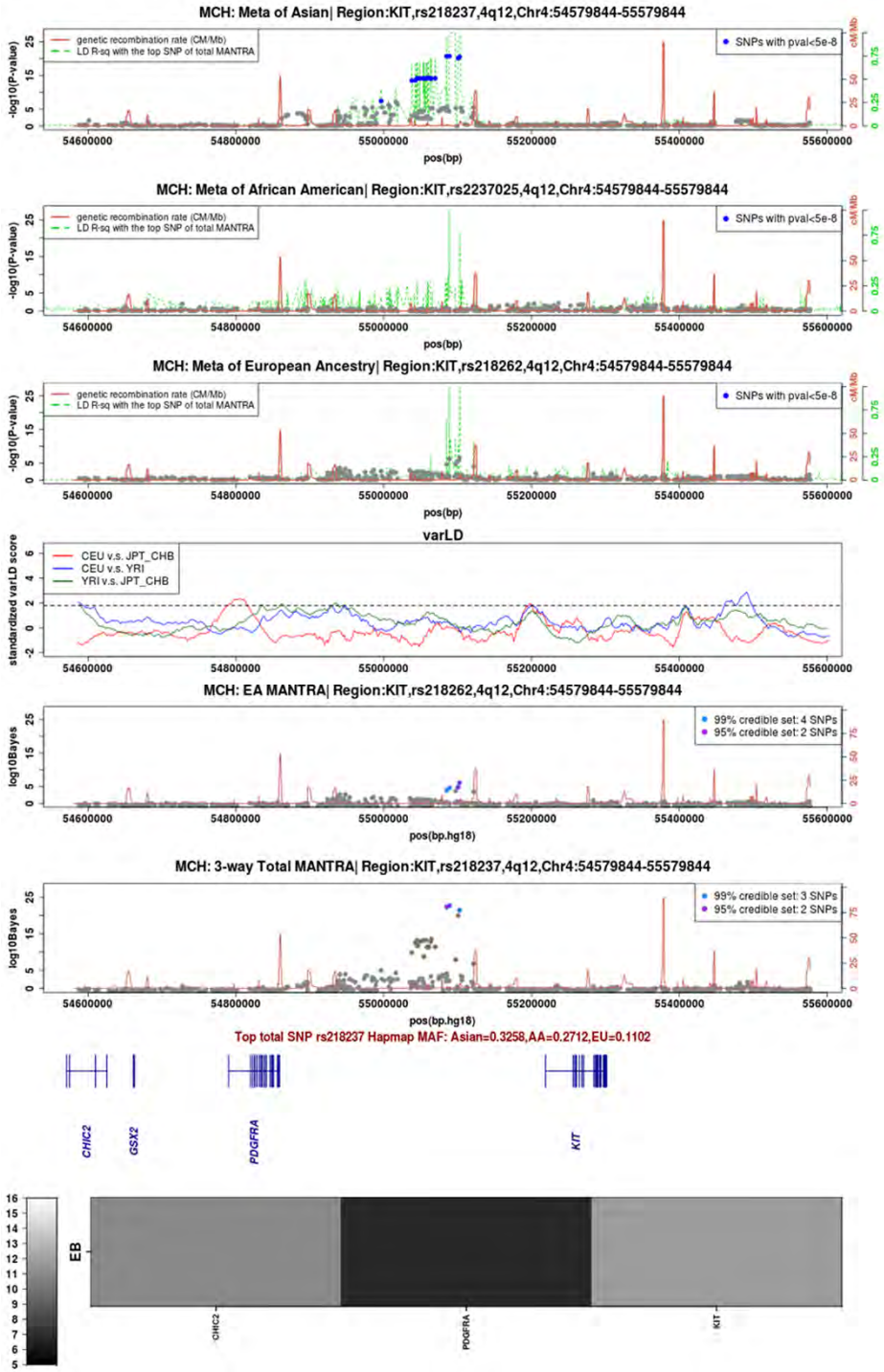

MCH: Meta of Asian| Region:MIR4432,rs11125830,2p16.1,Chr2:60064075-61064075
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:MIR4432,rs955657,2p16.1,Chr2:60064075-61064075
MCH: Meta of European Ancestry| Region:BCL11A,rs13019832,2p16.1,Chr2:60064075-61064075
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:BCL11A,rs13019832,2p16.1,Chr2:60064075-61064075
99% credible set: 14 SNPs
95% credible set: 9 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:BCL11A,rs13019832,2p16.1,Chr2:60064075-61064075
99% credible set: 0 SNPs
95% credible set: 0 SNPs
Top total SNP rs13019832 Hapmap MAF: Asian=0.01111,AA=0.45,EU=0.4333
MIR4432
BCL11A
PAPOLG
FLJ16341
REL
PUS10
EB

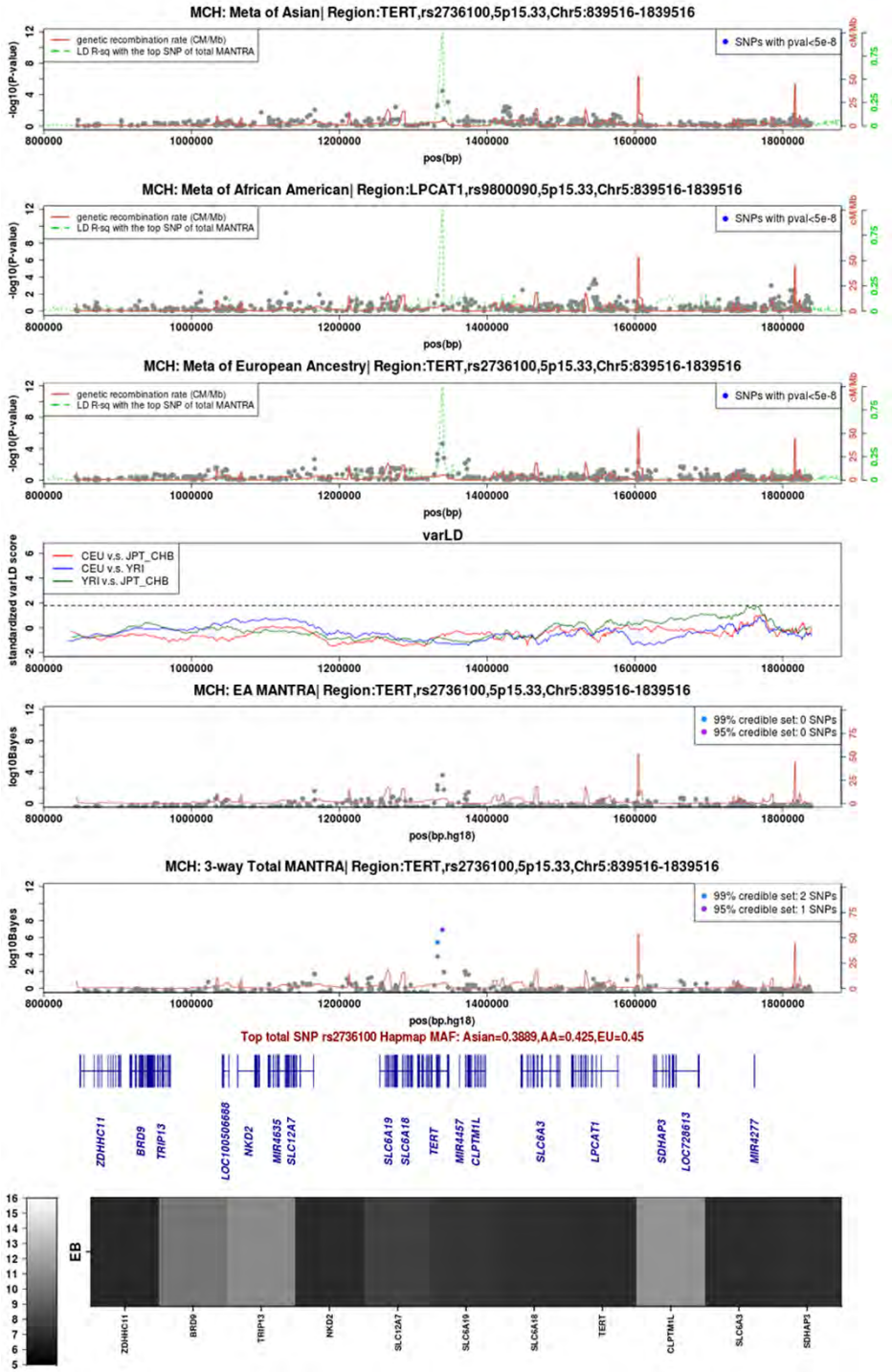

MCH: Meta of Asian| Region:PLCL2,rs2347654,3p24.3,Chr3:16367137-17367137
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:DAZL,rs2059742,3p24.3,Chr3:16367137-17367137
MCH: Meta of European Ancestry| Region:PLCL2,rs6796746,3p24.3,Chr3:16367137-17367137
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:PLCL2,rs6796746,3p24.3,Chr3:16367137-17367137
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:PLCL2,rs2060597,3p24.3,Chr3:16367137-17367137
99% credible set: 4 SNPs
95% credible set: 3 SNPs
Top total SNP rs2060597 Hapmap MAF: Asian=0.03933,AA=0,EU=0.025
RFTN1
DAZL
MIR3714
PLCL2
EB
TBC1D5

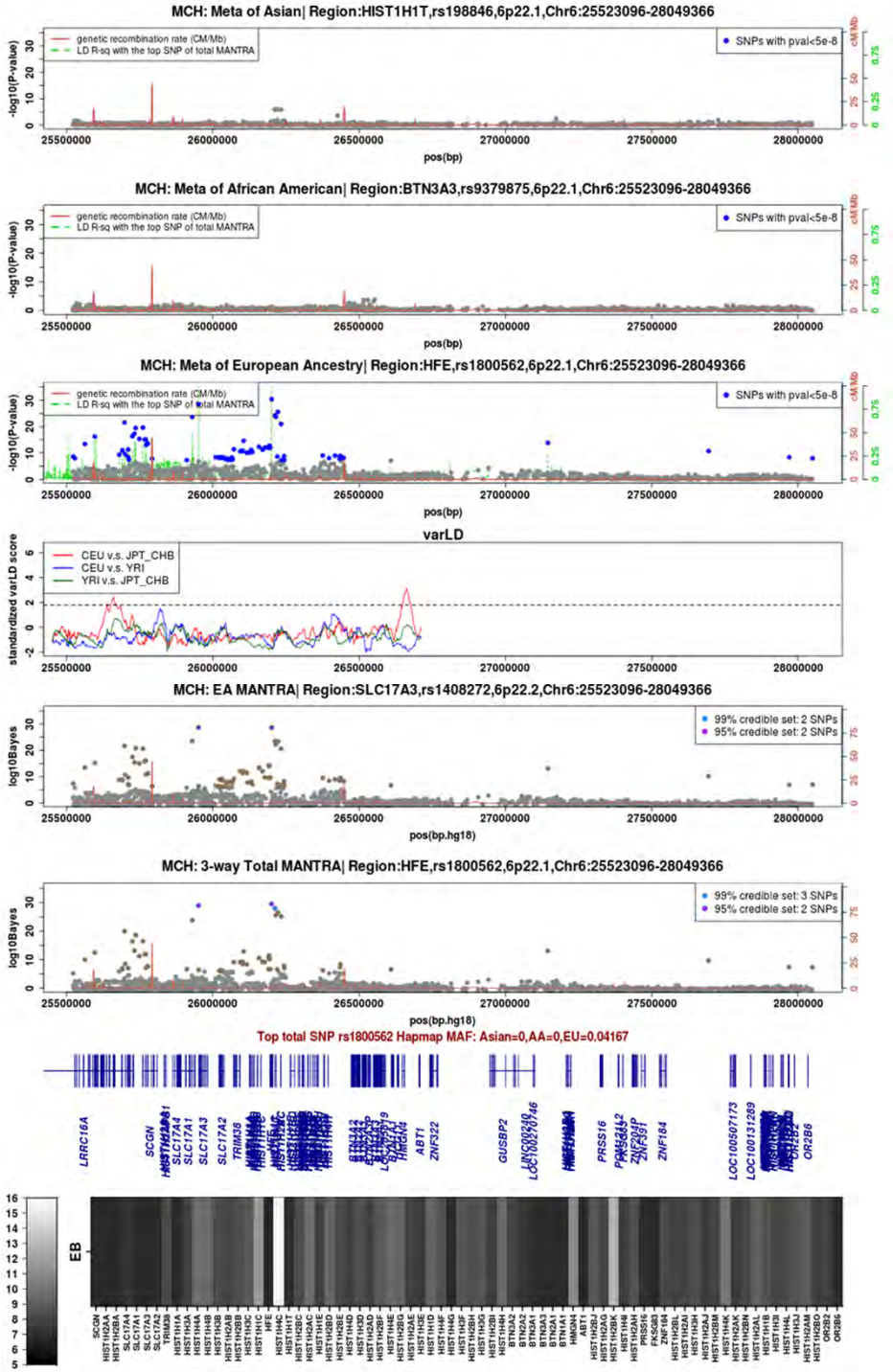

MCH: Meta of Asian| Region:THRB,rs1505307,3p24.2,Chr3:23818334-24818334
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:THRB,rs17014251,3p24.2,Chr3:23818334-24818334
MCH: Meta of European Ancestry| Region:THRB,rs1505307,3p24.2,Chr3:23818334-24818334
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:THRB,rs1505307,3p24.2,Chr3:23818334-24818334
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:THRB,rs1505307,3p24.2,Chr3:23818334-24818334
99% credible set: 4 SNPs
95% credible set: 3 SNPs
Top total SNP rs1505307 Hapmap MAF: Asian=0.2444,AA=0.4,EU=0.3667
UBE2E1
NKIRAS1
RPL15
NR1D2
LOC152024
THRB
MIR4792
EB

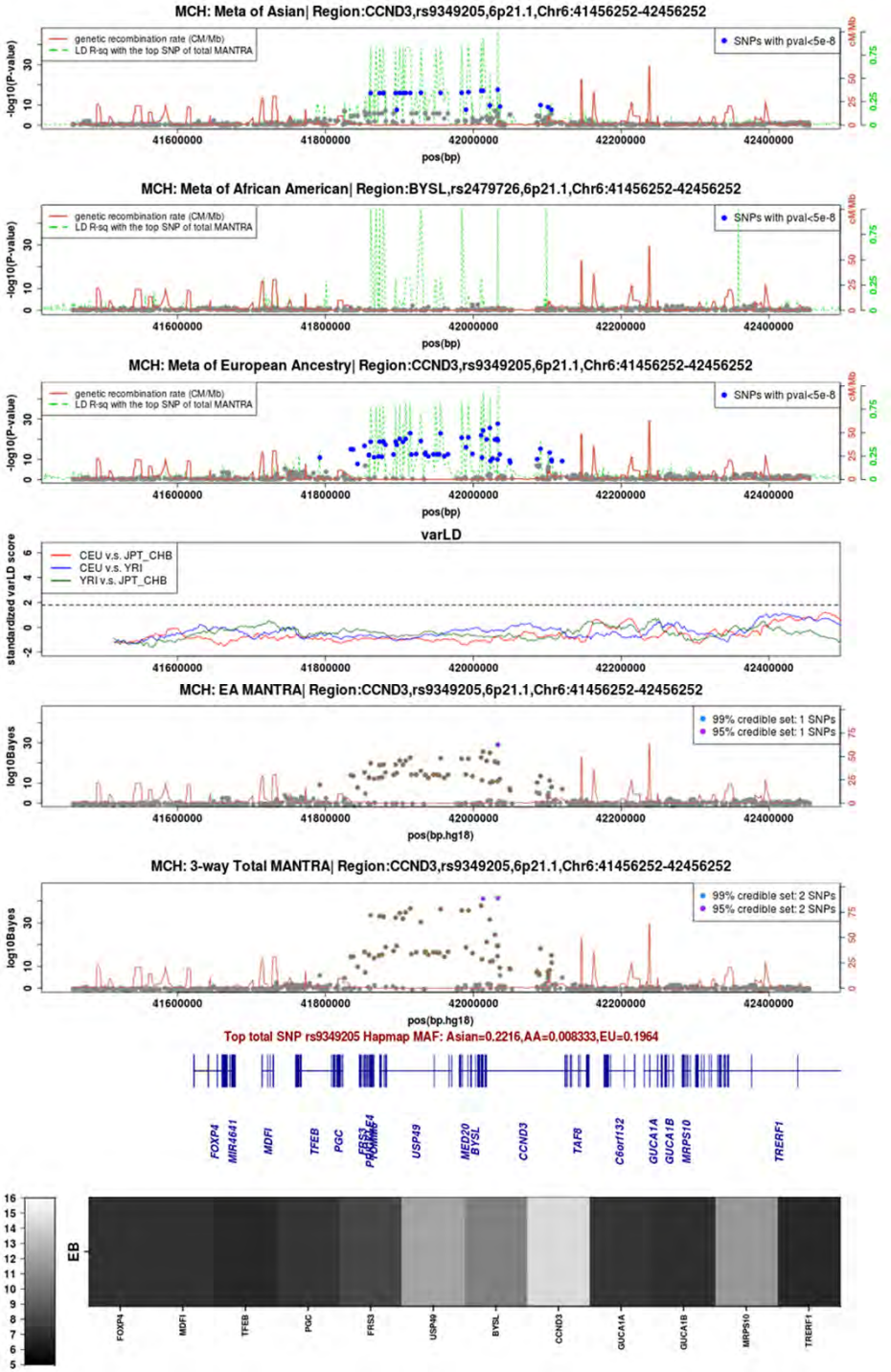

MCH: Meta of Asian| Region:ATR,rs12639363,3q23,Chr3:143155616-144155616
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:PCOLCE2,rs7639314,3q23,Chr3:143155616-144155616
MCH: Meta of European Ancestry| Region:ATR,rs6780250,3q23,Chr3:143155616-144155616
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:ATR,rs6780250,3q23,Chr3:143155616-144155616
99% credible set: 27 SNPs
95% credible set: 19 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:ATR,rs6791816,3q23,Chr3:143155616-144155616
99% credible set: 14 SNPs
95% credible set: 8 SNPs
Top total SNP rs6791816 Hapmap MAF: Asian=0.4805,AA=NA,EU=0.4091
TFDP2
GK5
XRN1
ATR
PLS1
TRPC1
PCOLCE2
LOC100507389
EB

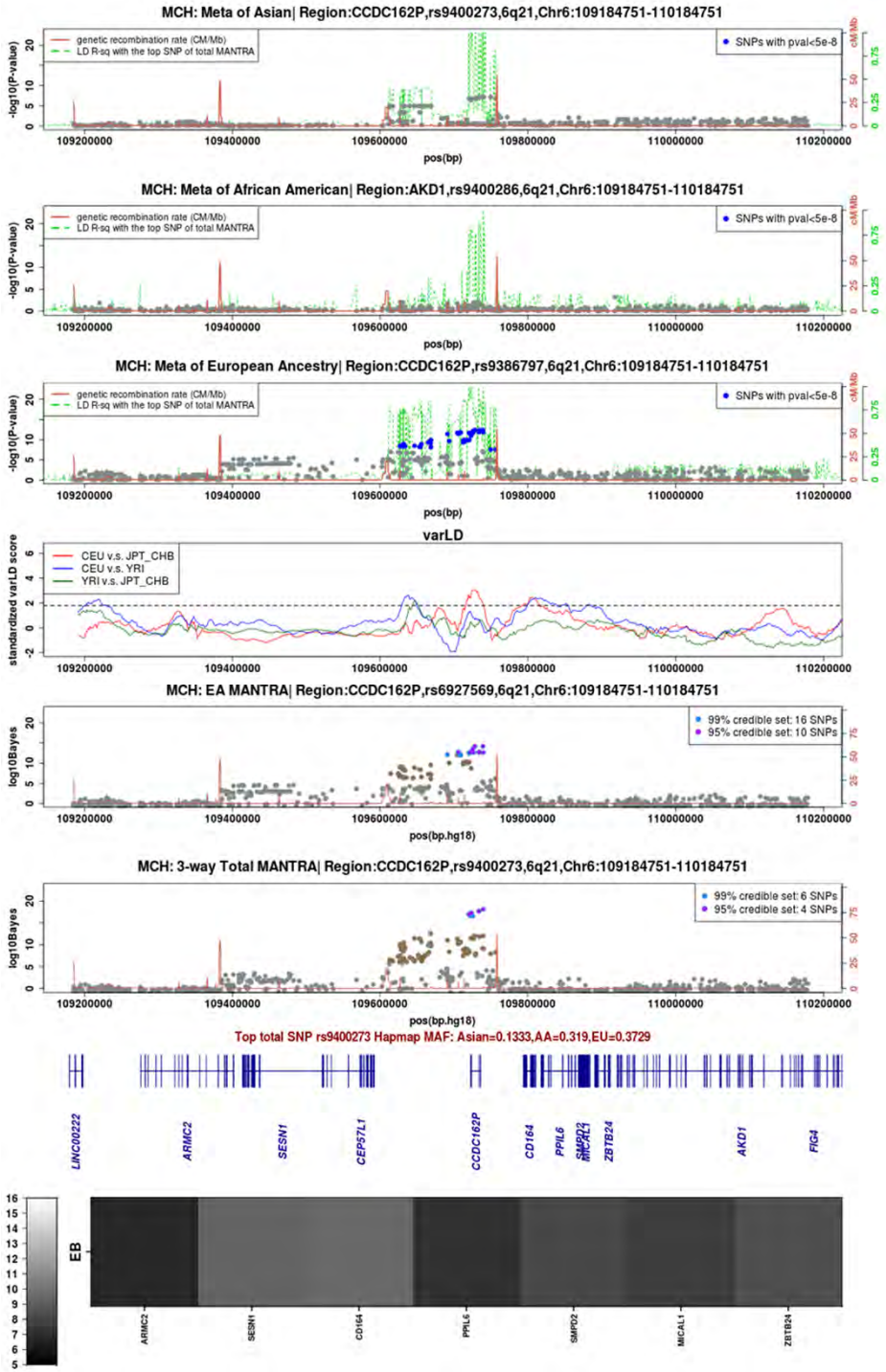

MCH: Meta of Asian| Region:ZDHHC19,rs4916491,3q29,Chr3:196775433-197775433
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:SDHAP1,rs6797622,3q29,Chr3:196775433-197775433
MCH: Meta of European Ancestry| Region:TFRC,rs11915082,3q29,Chr3:196775433-197775433
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:TFRC,rs12632706,3q29,Chr3:196775433-197775433
99% credible set: 8 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:TFRC,rs9859401,3q29,Chr3:196775433-197775433
99% credible set: 11 SNPs
95% credible set: 8 SNPs
Top total SNP rs9859401 Hapmap MAF: Asian=0.1768,AA=0.25,EU=0.3491
APOD
SDHAP2
MIR570
MUC20
MUC4
TNK2
SDHAP1
TFRC
LOC401109
ZDHHC19
OSTalpha
PCYT1A
TCTEX1D2
UBXN7
RNF168
C3orf43
WDR53
EB

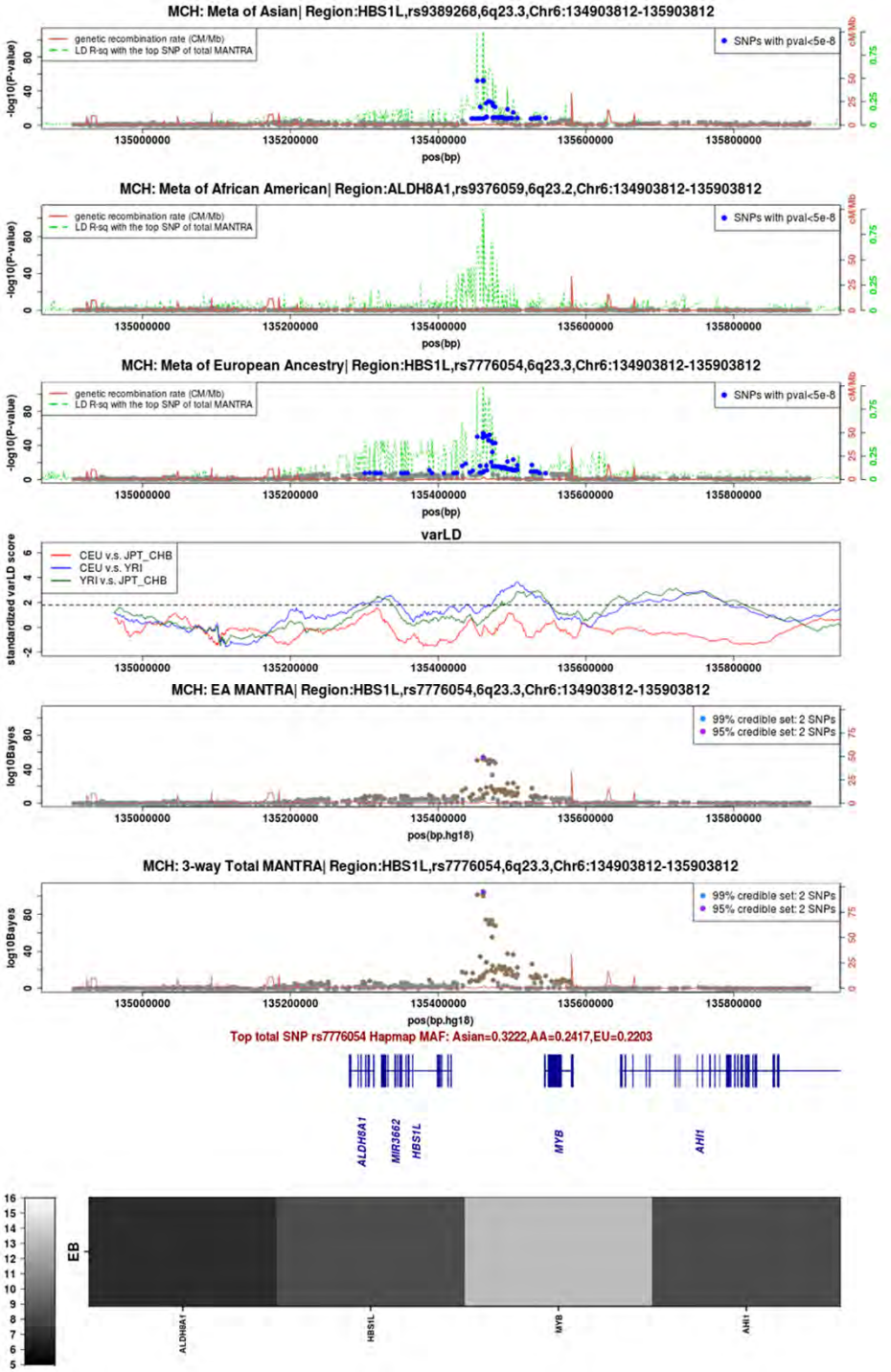

MCH: Meta of Asian| Region:KIT,rs218237,4q12,Chr4:54579844-55579844
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:KIT,rs2237025,4q12,Chr4:54579844-55579844
MCH: Meta of European Ancestry| Region:KIT,rs218262,4q12,Chr4:54579844-55579844
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:KIT,rs218262,4q12,Chr4:54579844-55579844
99% credible set: 4 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:KIT,rs218237,4q12,Chr4:54579844-55579844
99% credible set: 3 SNPs
95% credible set: 2 SNPs
Top total SNP rs218237 Hapmap MAF: Asian=0.3258,AA=0.2712,EU=0.1102
CHIC2
GSX2
PDGFRA
KIT
EB

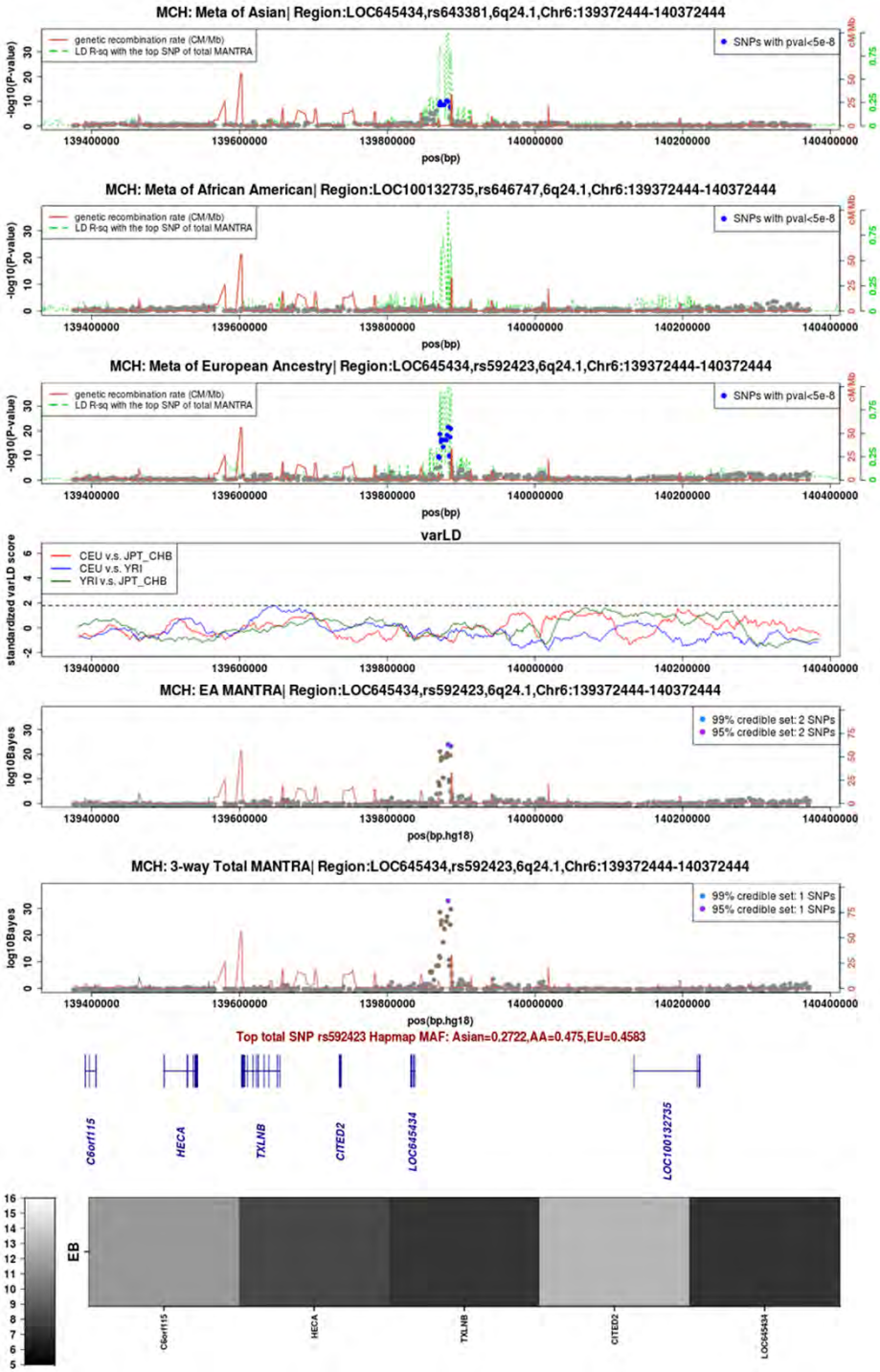

MCH: Meta of Asian| Region:TERT,rs2736100,5p15.33,Chr5:839516-1839516
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:LPCAT1,rs9800090,5p15.33,Chr5:839516-1839516
MCH: Meta of European Ancestry| Region:TERT,rs2736100,5p15.33,Chr5:839516-1839516
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:TERT,rs2736100,5p15.33,Chr5:839516-1839516
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:TERT,rs2736100,5p15.33,Chr5:839516-1839516
99% credible set: 2 SNPs
95% credible set: 1 SNPs
Top total SNP rs2736100 Hapmap MAF: Asian=0.3889,AA=0.425,EU=0.45
ZDHHC11
BRD9
TRIP13
LOC100506668
NKD2
MIR4635
SLC12A7
SLC6A19
SLC6A18
TERT
MIR4457
CLPTM1L
SLC6A3
LPCAT1
SDHAP3
LOC728613
MIR4277
EB

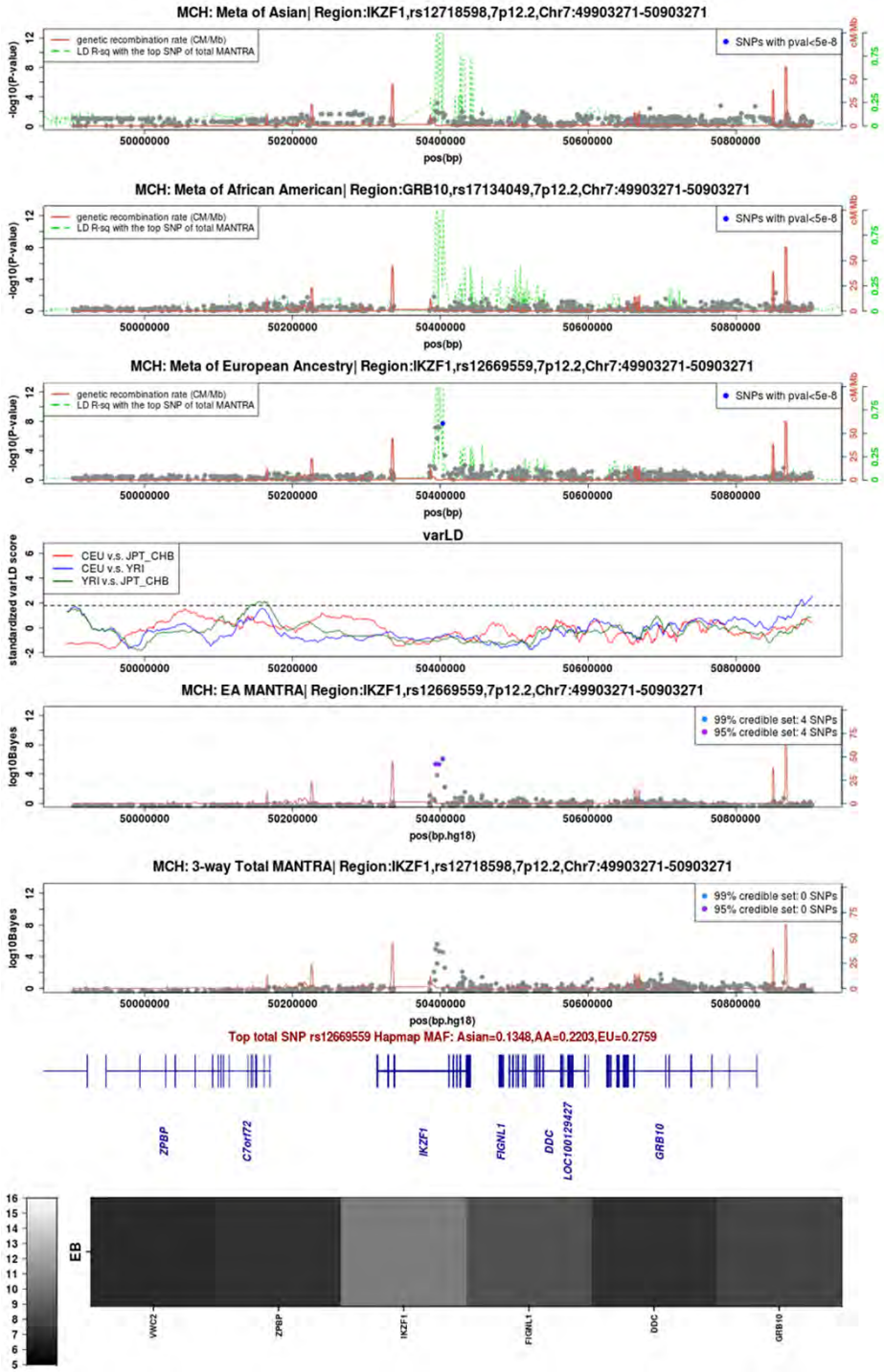

MCH: Meta of Asian| Region:HIST1H1T,rs198846,6p22.1,Chr6:25523096-28049366
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:BTN3A3,rs9379875,6p22.1,Chr6:25523096-28049366
MCH: Meta of European Ancestry| Region:HFE,rs1800562,6p22.1,Chr6:25523096-28049366
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:SLC17A3,rs1408272,6p22.2,Chr6:25523096-28049366
99% credible set: 2 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:HFE,rs1800562,6p22.1,Chr6:25523096-28049366
99% credible set: 3 SNPs
95% credible set: 2 SNPs
Top total SNP rs1800562 Hapmap MAF: Asian=0,AA=0,EU=0.04167
LRRC16A
SCGN
SLC17A4
SLC17A1
SLC17A2
SLC17A3
TRIM38
ABT1
ZNF322
GUSBP2
PRSS16
ZNF184
LOC100507173
LOC100131289
OR2B2
OR2B6
EB

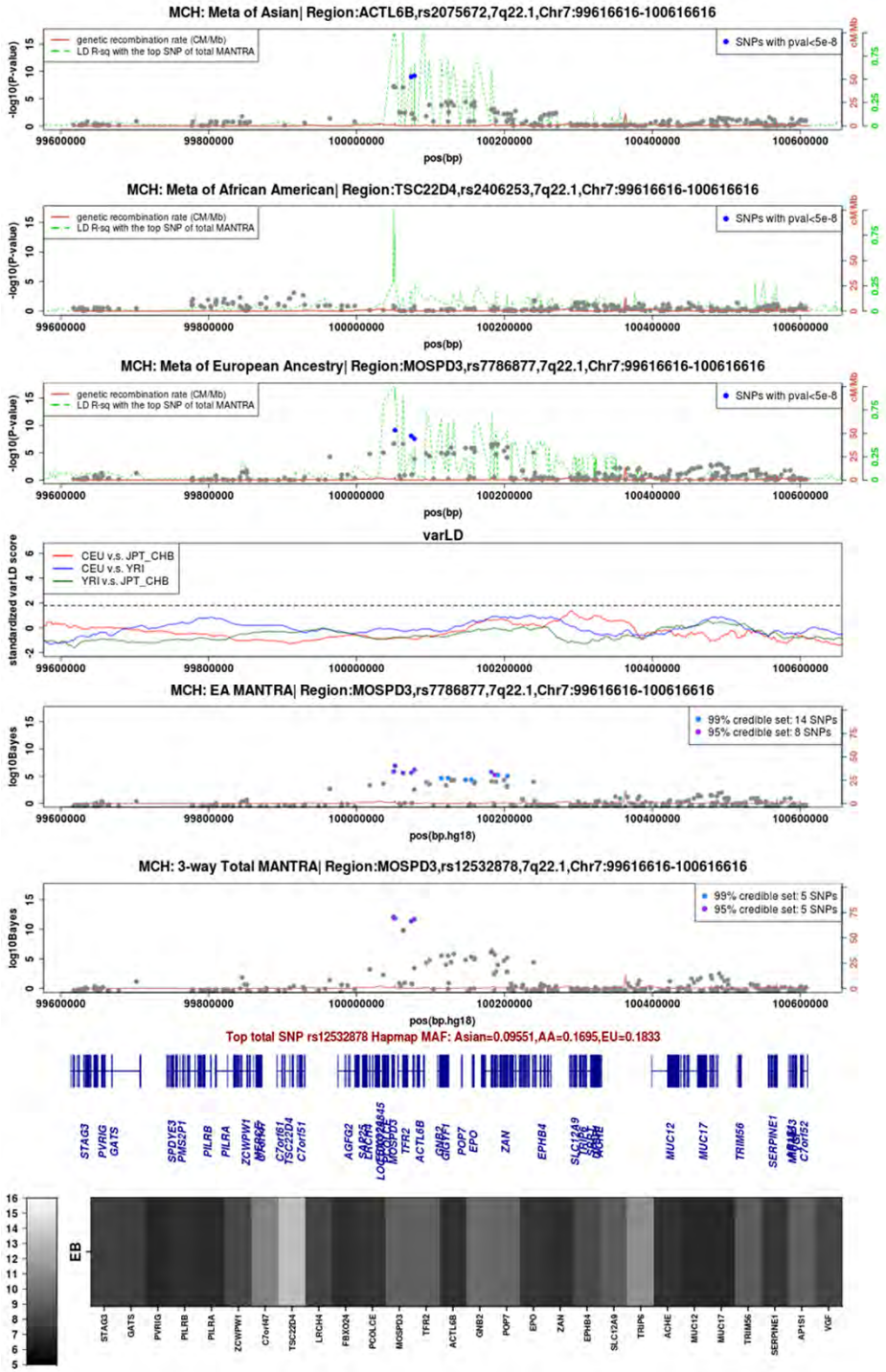

MCH: Meta of Asian| Region:CCND3,rs9349205,6p21.1,Chr6:41456252-42456252
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:BYSL,rs2479726,6p21.1,Chr6:41456252-42456252
MCH: Meta of European Ancestry| Region:CCND3,rs9349205,6p21.1,Chr6:41456252-42456252
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:CCND3,rs9349205,6p21.1,Chr6:41456252-42456252
99% credible set: 1 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:CCND3,rs9349205,6p21.1,Chr6:41456252-42456252
99% credible set: 2 SNPs
95% credible set: 2 SNPs
Top total SNP rs9349205 Hapmap MAF: Asian=0.2216,AA=0.008333,EU=0.1964
FOXP4
MIR4641
MDFI
TFEB
PGC
FRS3
PDIMM64
USP49
MED20
BYSL
CCND3
TAF8
C6orf132
GUCA1A
GUCA1B
MRPS10
TRERF1
EB

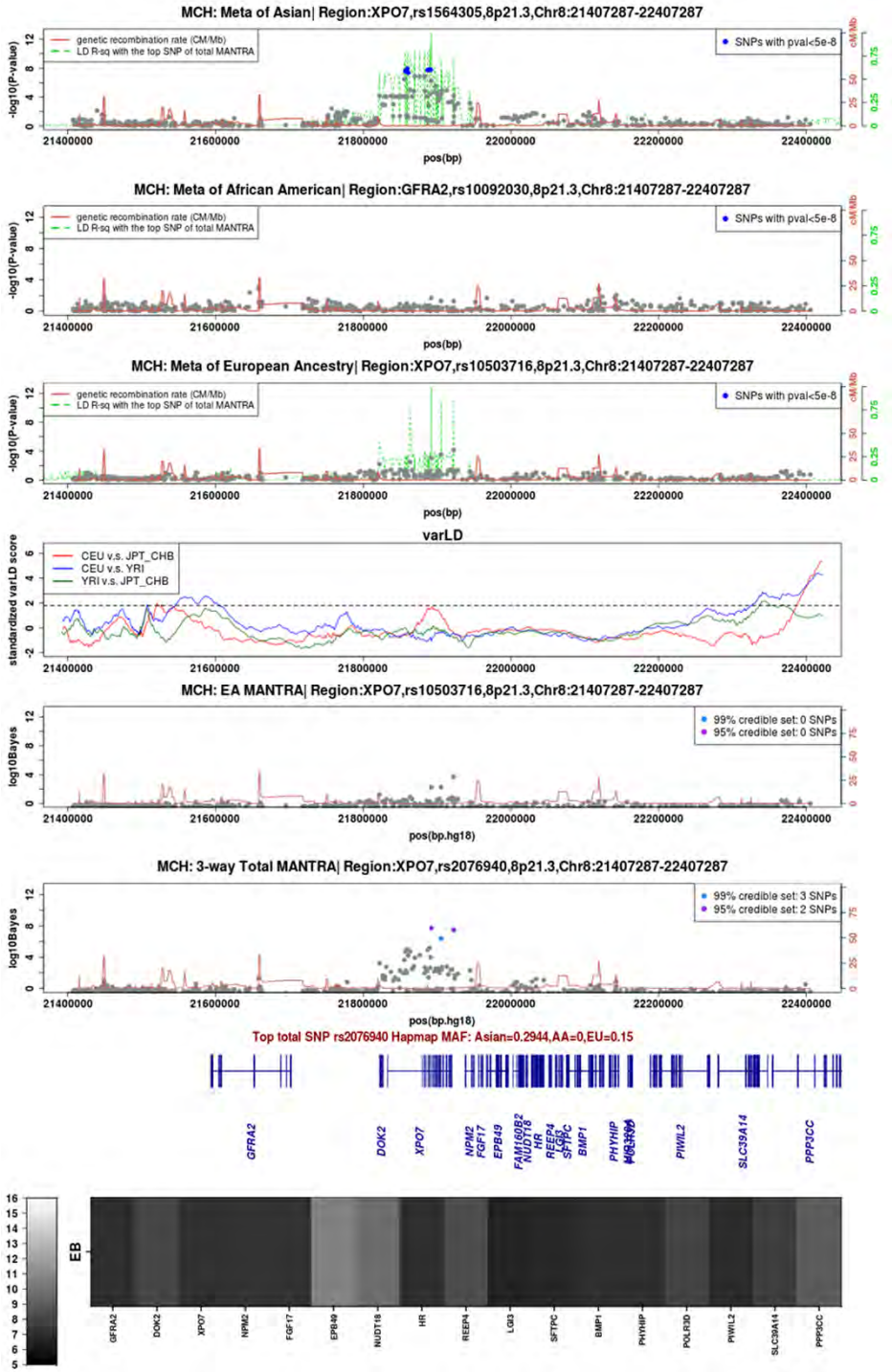

MCH: Meta of Asian| Region:CCDC162P,rs9400273,6q21,Chr6:109184751-110184751
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:AKD1,rs9400286,6q21,Chr6:109184751-110184751
MCH: Meta of European Ancestry| Region:CCDC162P,rs9386797,6q21,Chr6:109184751-110184751
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:CCDC162P,rs6927569,6q21,Chr6:109184751-110184751
99% credible set: 16 SNPs
95% credible set: 10 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:CCDC162P,rs9400273,6q21,Chr6:109184751-110184751
99% credible set: 6 SNPs
95% credible set: 4 SNPs
Top total SNP rs9400273 Hapmap MAF: Asian=0.1333,AA=0.319,EU=0.3729
LINC00222
ARMC2
SESN1
CEP57L1
CCDC162P
CD164
PPIL6
SMPD2
MICAL1
ZBTB24
AKD1
FIG4
EB

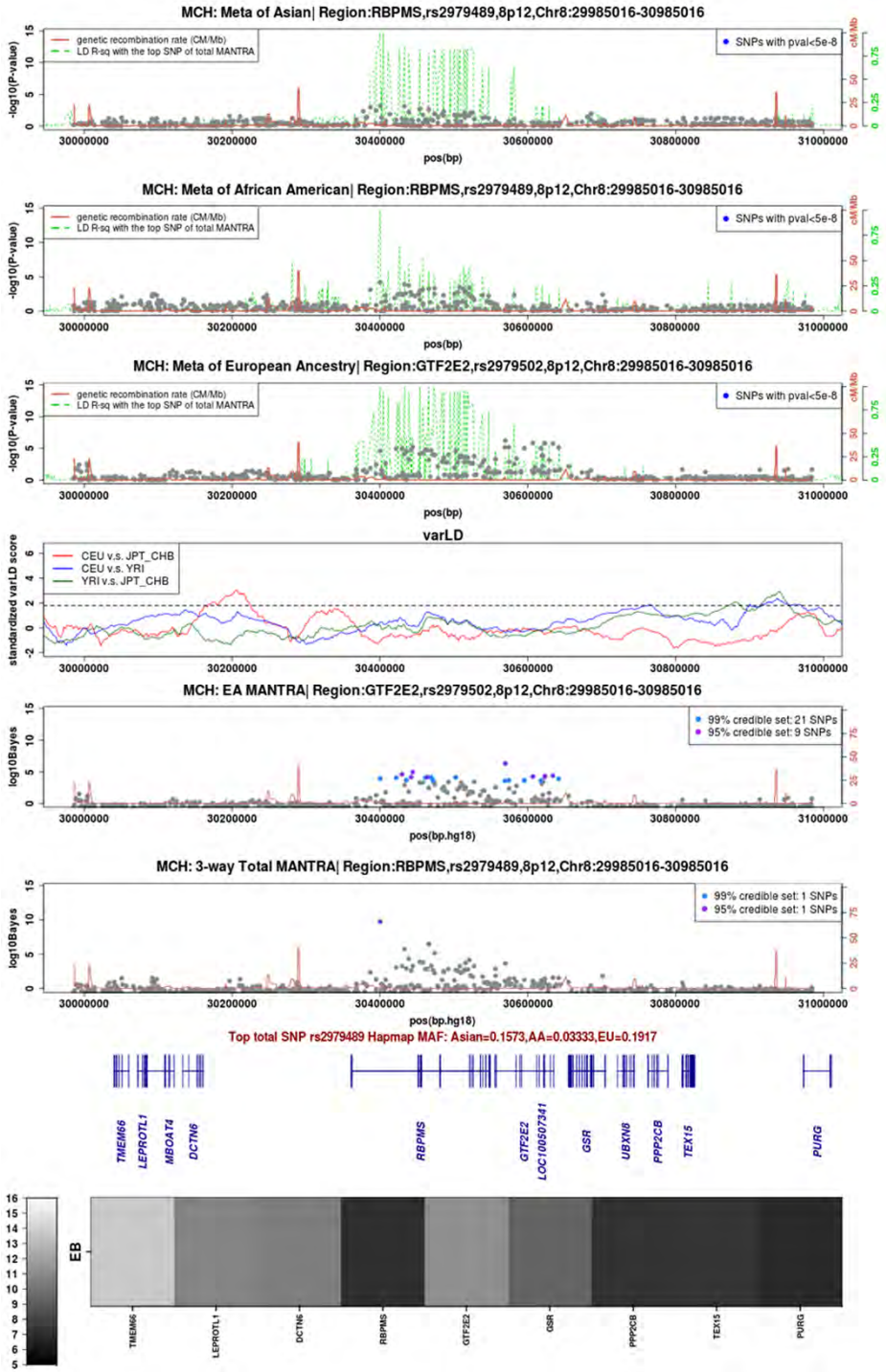

MCH: Meta of Asian| Region:HBS1L,rs9389268,6q23.3,Chr6:134903812-135903812
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
135000000
135200000
135400000
135600000
135800000
pos(bp)
MCH: Meta of African American| Region:ALDH8A1,rs9376059,6q23.2,Chr6:134903812-135903812
MCH: Meta of European Ancestry| Region:HBS1L,rs7776054,6q23.3,Chr6:134903812-135903812
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:HBS1L,rs7776054,6q23.3,Chr6:134903812-135903812
99% credible set: 2 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:HBS1L,rs7776054,6q23.3,Chr6:134903812-135903812
Top total SNP rs7776054 Hapmap MAF: Asian=0.3222,AA=0.2417,EU=0.2203
ALDH8A1
MIR3662
HBS1L
MYB
AHI1
EB

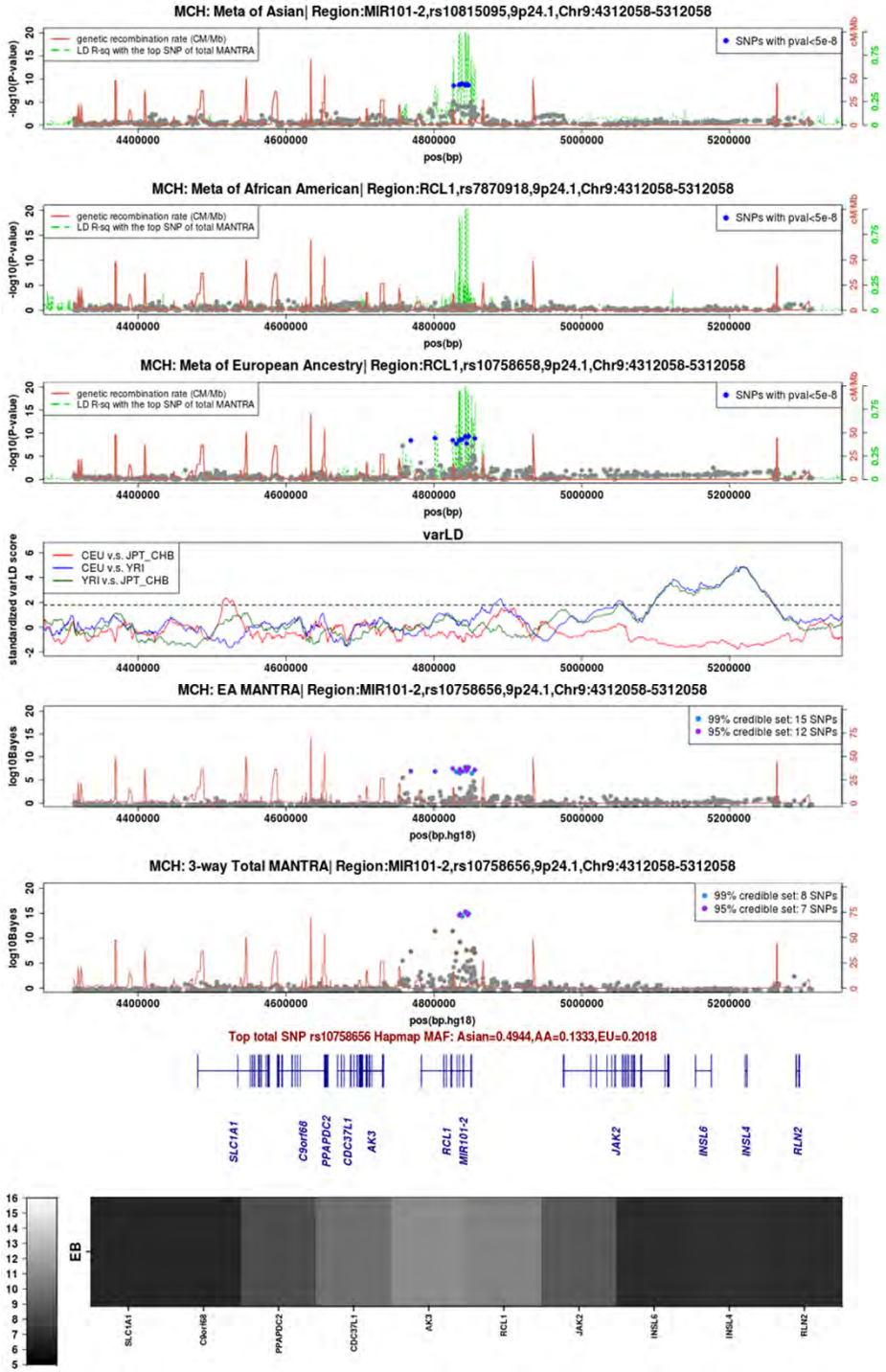

MCH: Meta of Asian| Region:LOC645434,rs643381,6q24.1,Chr6:139372444-140372444
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:LOC100132735,rs646747,6q24.1,Chr6:139372444-140372444
MCH: Meta of European Ancestry| Region:LOC645434,rs592423,6q24.1,Chr6:139372444-140372444
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:LOC645434,rs592423,6q24.1,Chr6:139372444-140372444
99% credible set: 2 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:LOC645434,rs592423,6q24.1,Chr6:139372444-140372444
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs592423 Hapmap MAF: Asian=0.2722,AA=0.475,EU=0.4583
C6orf115
HECA
TXLNB
CITED2
LOC645434
LOC100132735
EB

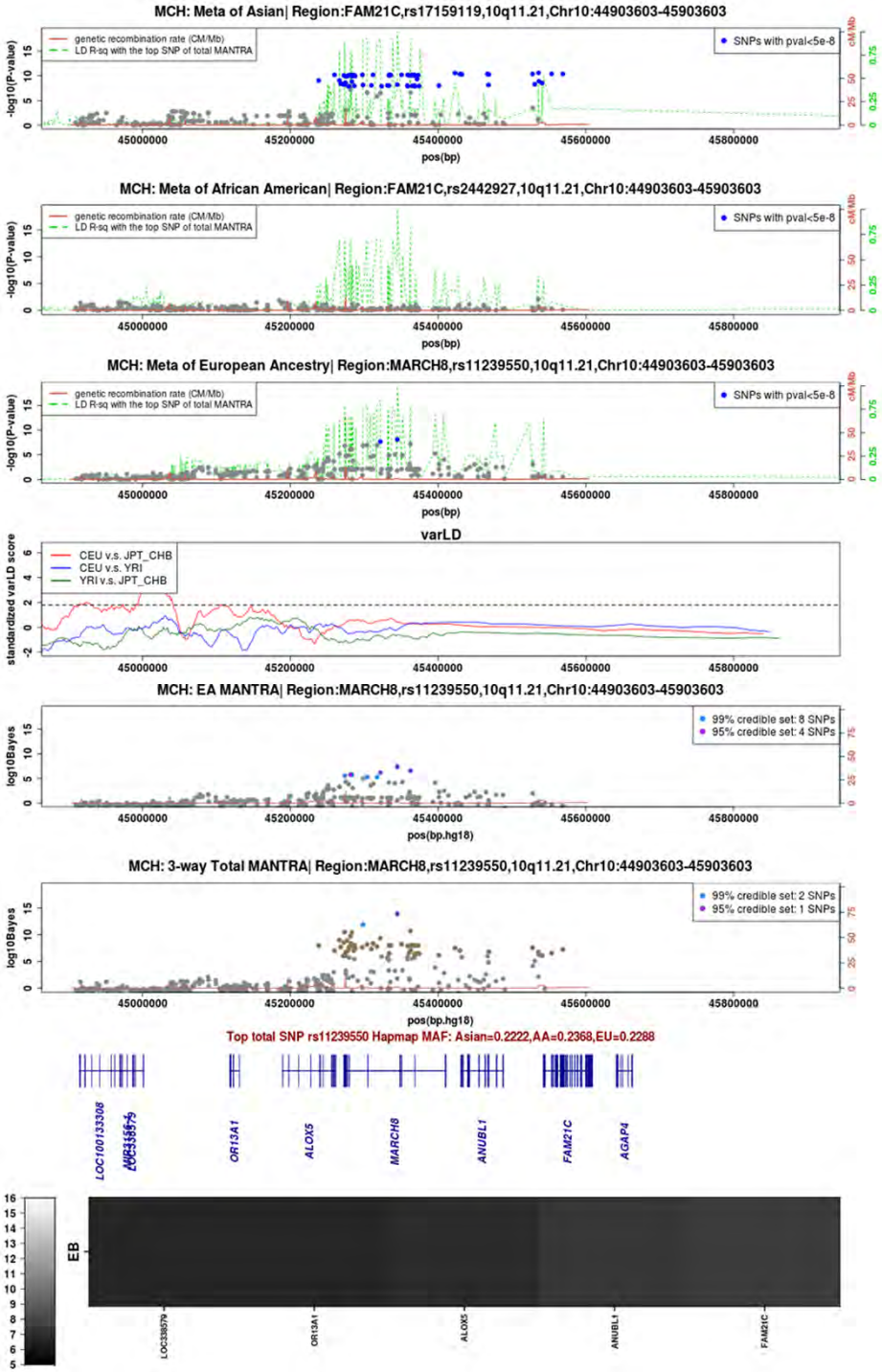

MCH: Meta of Asian| Region:IKZF1,rs12718598,7p12.2,Chr7:49903271-50903271
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:GRB10,rs17134049,7p12.2,Chr7:49903271-50903271
MCH: Meta of European Ancestry| Region:IKZF1,rs12669559,7p12.2,Chr7:49903271-50903271
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:IKZF1,rs12669559,7p12.2,Chr7:49903271-50903271
99% credible set: 4 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:IKZF1,rs12718598,7p12.2,Chr7:49903271-50903271
99% credible set: 0 SNPs
95% credible set: 0 SNPs
Top total SNP rs12669559 Hapmap MAF: Asian=0.1348,AA=0.2203,EU=0.2759
ZPBP
C7orf72
IKZF1
FIGNL1
DDC
LOC100129427
GRB10
EB
VWC2
ZPBP
IKZF1
FIGNL1
DDC
GRB10

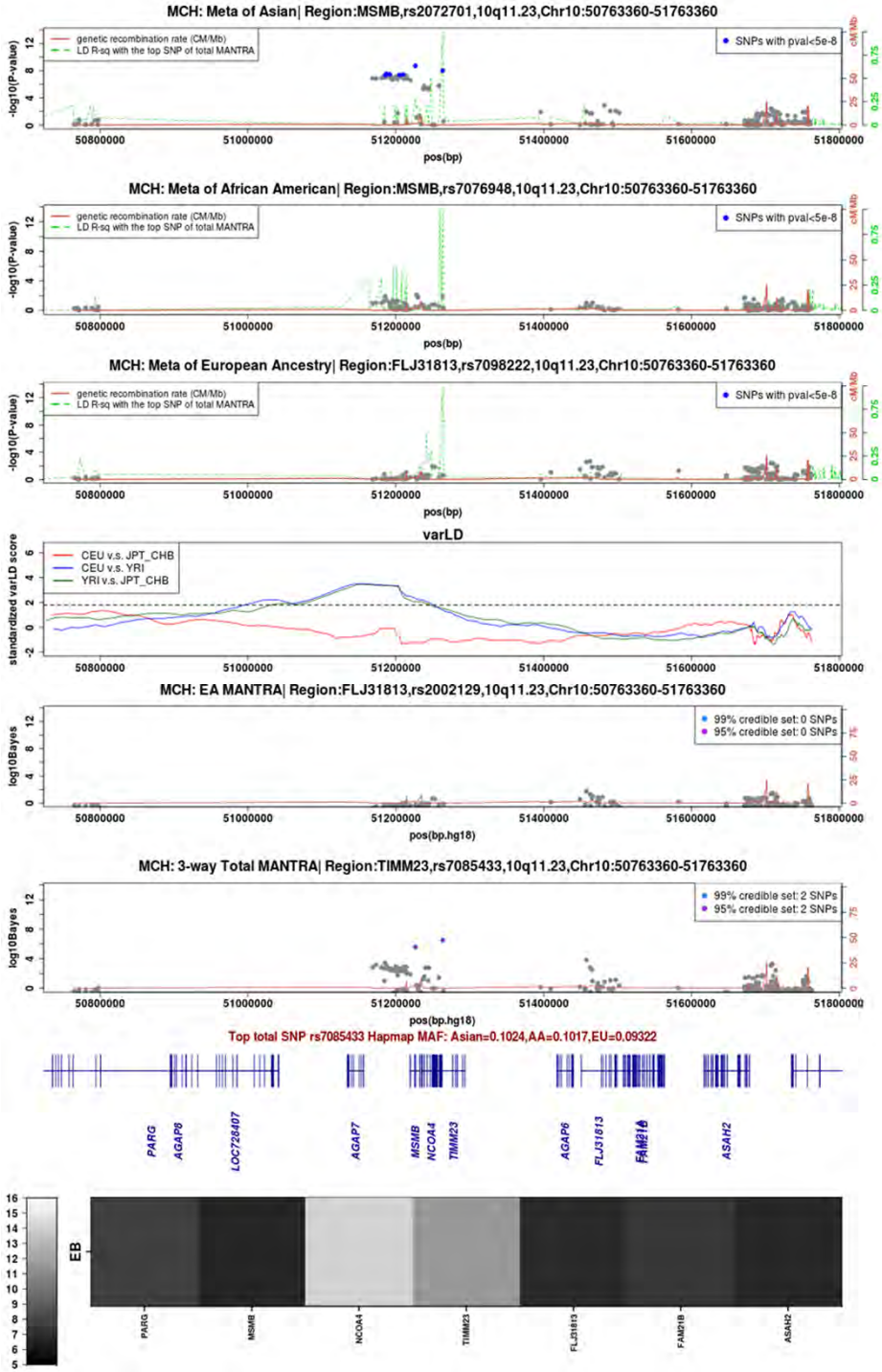

MCH: Meta of Asian| Region:ACTL6B,rs2075672,7q22.1,Chr7:99616616-100616616
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:TSC22D4,rs2406253,7q22.1,Chr7:99616616-100616616
MCH: Meta of European Ancestry| Region:MOSPD3,rs7786877,7q22.1,Chr7:99616616-100616616
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:MOSPD3,rs7786877,7q22.1,Chr7:99616616-100616616
99% credible set: 14 SNPs
95% credible set: 8 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:MOSPD3,rs12532878,7q22.1,Chr7:99616616-100616616
99% credible set: 5 SNPs
95% credible set: 5 SNPs
Top total SNP rs12532878 Hapmap MAF: Asian=0.09551,AA=0.1695,EU=0.1833
STAG3
PVRIG
GATS
SPDYE3
PWSIP1
PILRB
PILRA
ZCWPW1
C7orf51
TSC22D4
AGFG2
TFR2
ACTL6B
GNB2
POP7
EPO
ZAN
EPHB4
MUC12
MUC17
TRIM56
SERPINE1
EB

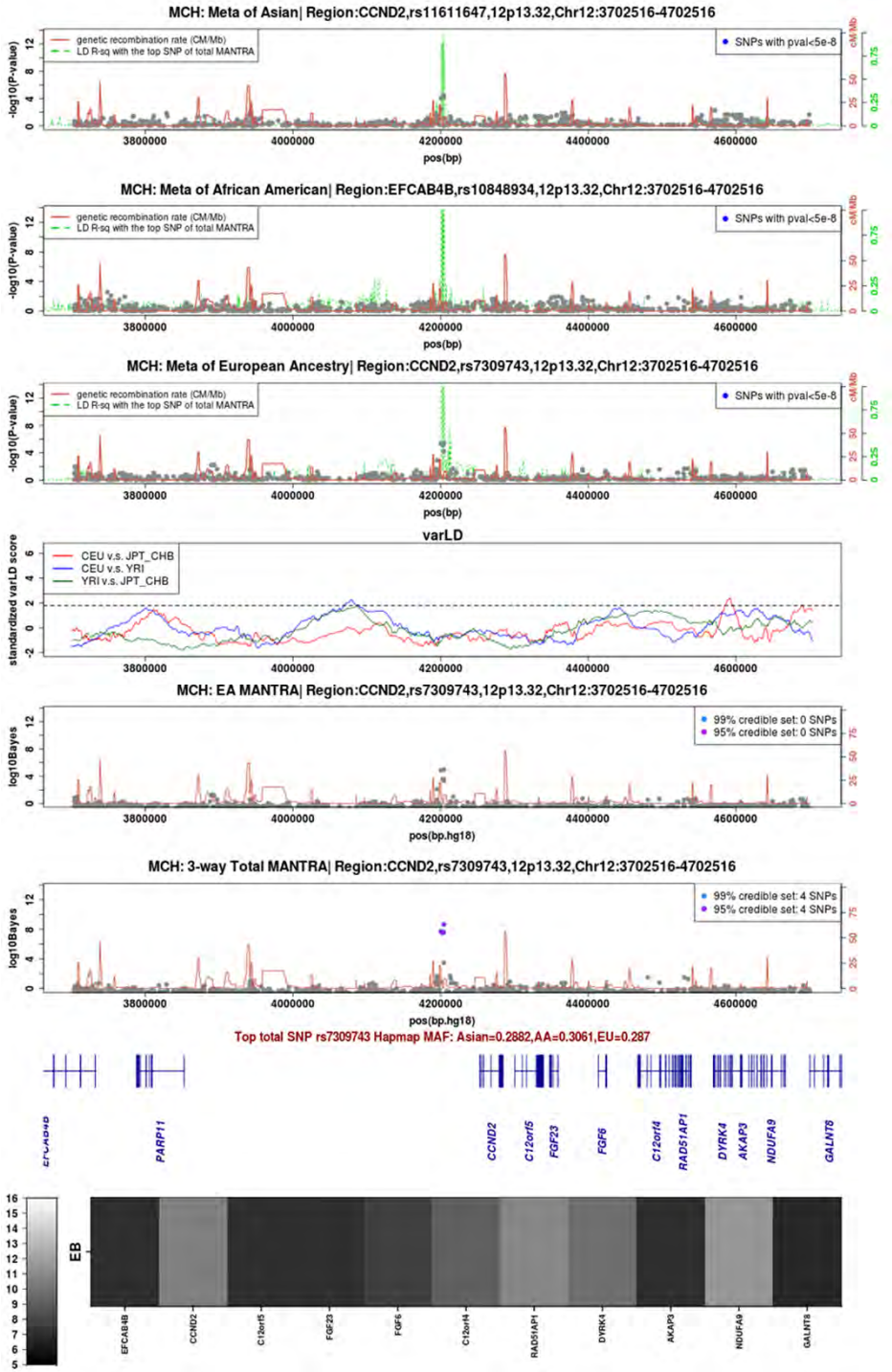

MCH: Meta of Asian| Region:XPO7,rs1564305,8p21.3,Chr8:21407287-22407287
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:GFRA2,rs10092030,8p21.3,Chr8:21407287-22407287
MCH: Meta of European Ancestry| Region:XPO7,rs10503716,8p21.3,Chr8:21407287-22407287
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:XPO7,rs10503716,8p21.3,Chr8:21407287-22407287
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:XPO7,rs2076940,8p21.3,Chr8:21407287-22407287
99% credible set: 3 SNPs
95% credible set: 2 SNPs
Top total SNP rs2076940 Hapmap MAF: Asian=0.2944,AA=0,EU=0.15
GFRA2
DOK2
XPO7
NPM2
FGF17
EPB49
NUDT18
HR
REEP4
LGI3
SFTPC
BMP1
PHYHIP
PWIL2
SLC39A14
PPP3CC
EB

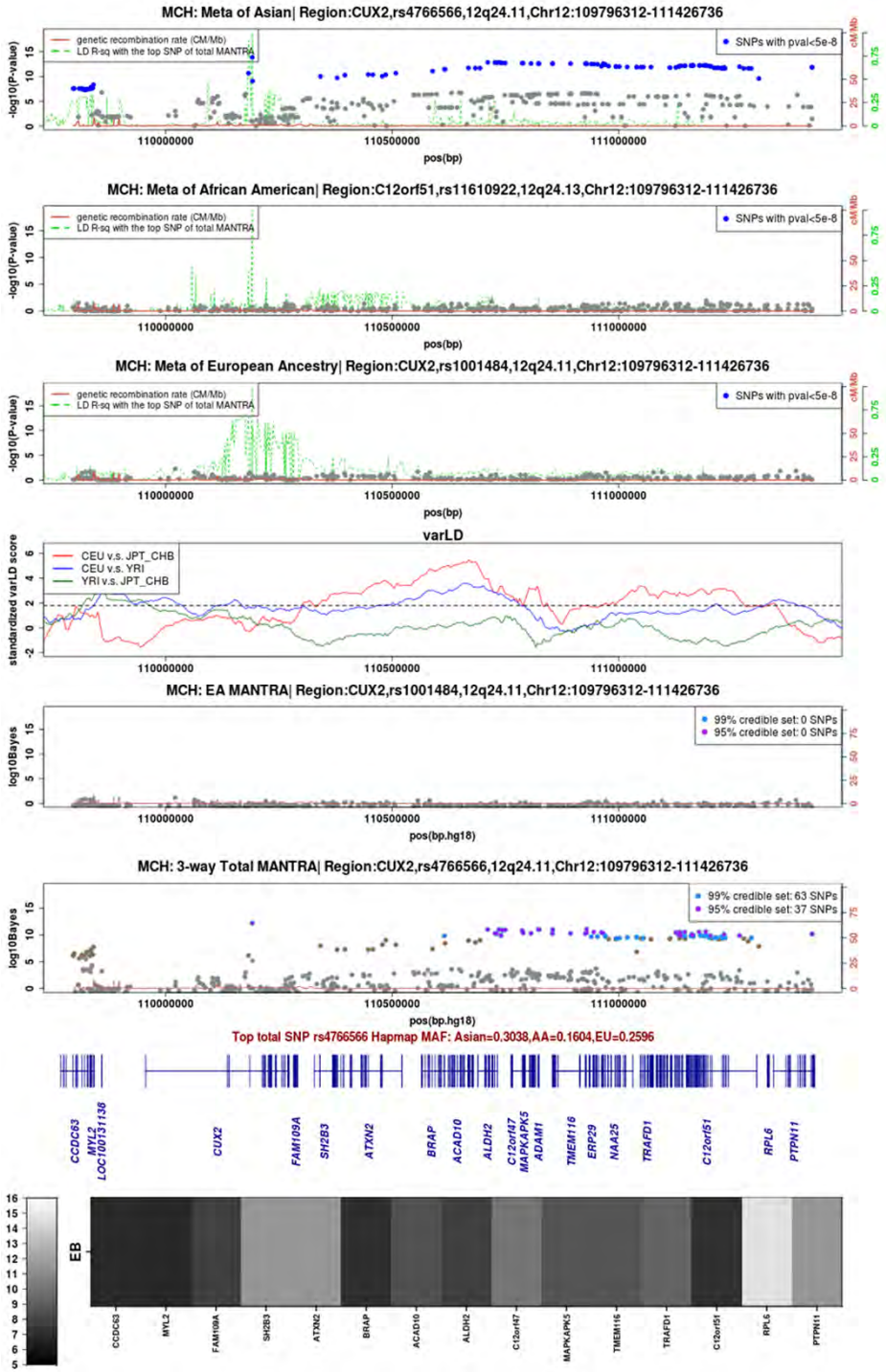

MCH: Meta of Asian| Region:RBPMS,rs2979489,8p12,Chr8:29985016-30985016
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:RBPMS,rs2979489,8p12,Chr8:29985016-30985016
MCH: Meta of European Ancestry| Region:GTF2E2,rs2979502,8p12,Chr8:29985016-30985016
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:GTF2E2,rs2979502,8p12,Chr8:29985016-30985016
99% credible set: 21 SNPs
95% credible set: 9 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:RBPMS,rs2979489,8p12,Chr8:29985016-30985016
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs2979489 Hapmap MAF: Asian=0.1573,AA=0.03333,EU=0.1917
TMEM66
LEPROTL1
MBOAT4
DCTN6
RBPMS
GTF2E2
LOC100507341
GSR
UBXN8
PPP2CB
TEX15
PURG
EB

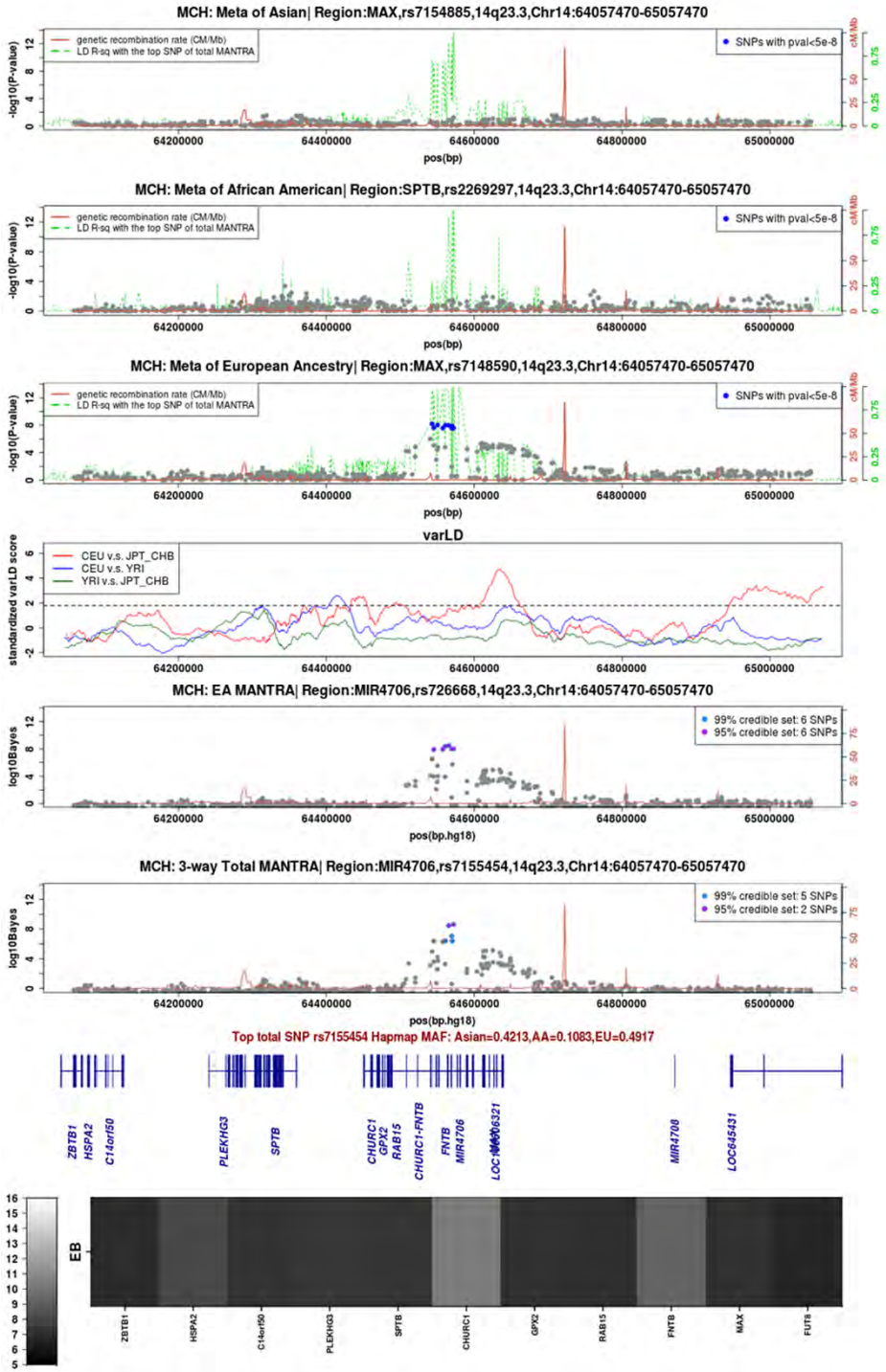

MCH: Meta of Asian| Region:MIR101-2,rs10815095,9p24.1,Chr9:4312058-5312058
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:RCL1,rs7870918,9p24.1,Chr9:4312058-5312058
MCH: Meta of European Ancestry| Region:RCL1,rs10758658,9p24.1,Chr9:4312058-5312058
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:MIR101-2,rs10758656,9p24.1,Chr9:4312058-5312058
99% credible set: 15 SNPs
95% credible set: 12 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:MIR101-2,rs10758656,9p24.1,Chr9:4312058-5312058
99% credible set: 8 SNPs
95% credible set: 7 SNPs
Top total SNP rs10758656 Hapmap MAF: Asian=0.4944,AA=0.1333,EU=0.2018
SLC1A1
C9orf68
PPAPDC2
CDC37L1
AK3
RCL1
MIR101-2
JAK2
INSL6
INSL4
RLN2
EB

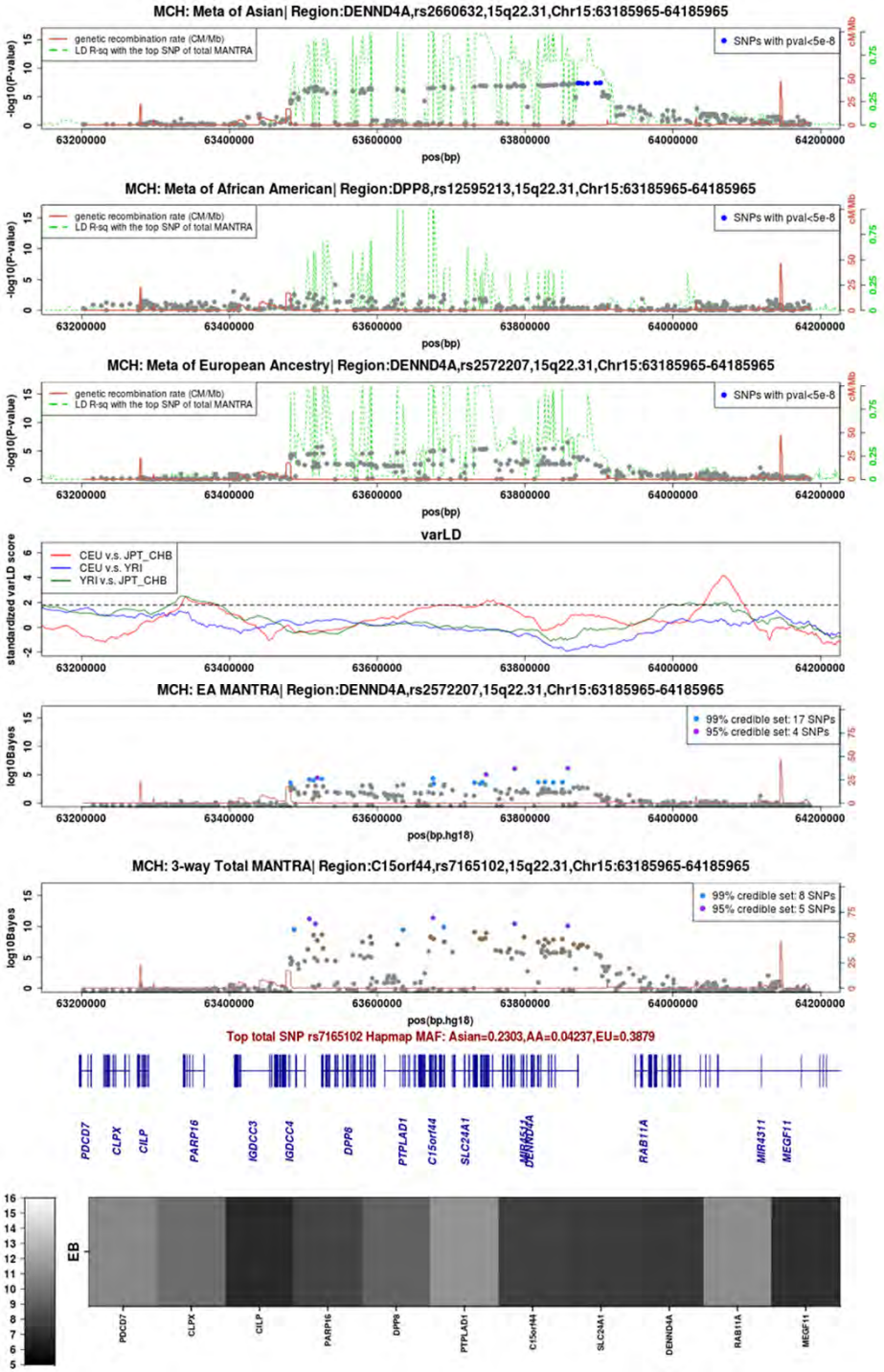

MCH: Meta of Asian| Region:FAM21C,rs17159119,10q11.21,Chr10:44903603-45903603
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:FAM21C,rs2442927,10q11.21,Chr10:44903603-45903603
MCH: Meta of European Ancestry| Region:MARCH8,rs11239550,10q11.21,Chr10:44903603-45903603
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:MARCH8,rs11239550,10q11.21,Chr10:44903603-45903603
99% credible set: 8 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:MARCH8,rs11239550,10q11.21,Chr10:44903603-45903603
99% credible set: 2 SNPs
95% credible set: 1 SNPs
Top total SNP rs11239550 Hapmap MAF: Asian=0.2222,AA=0.2368,EU=0.2288
LOC100133308
OR13A1
ALOX5
MARCH8
ANUBL1
FAM21C
AGAP4
EB
LOC338579

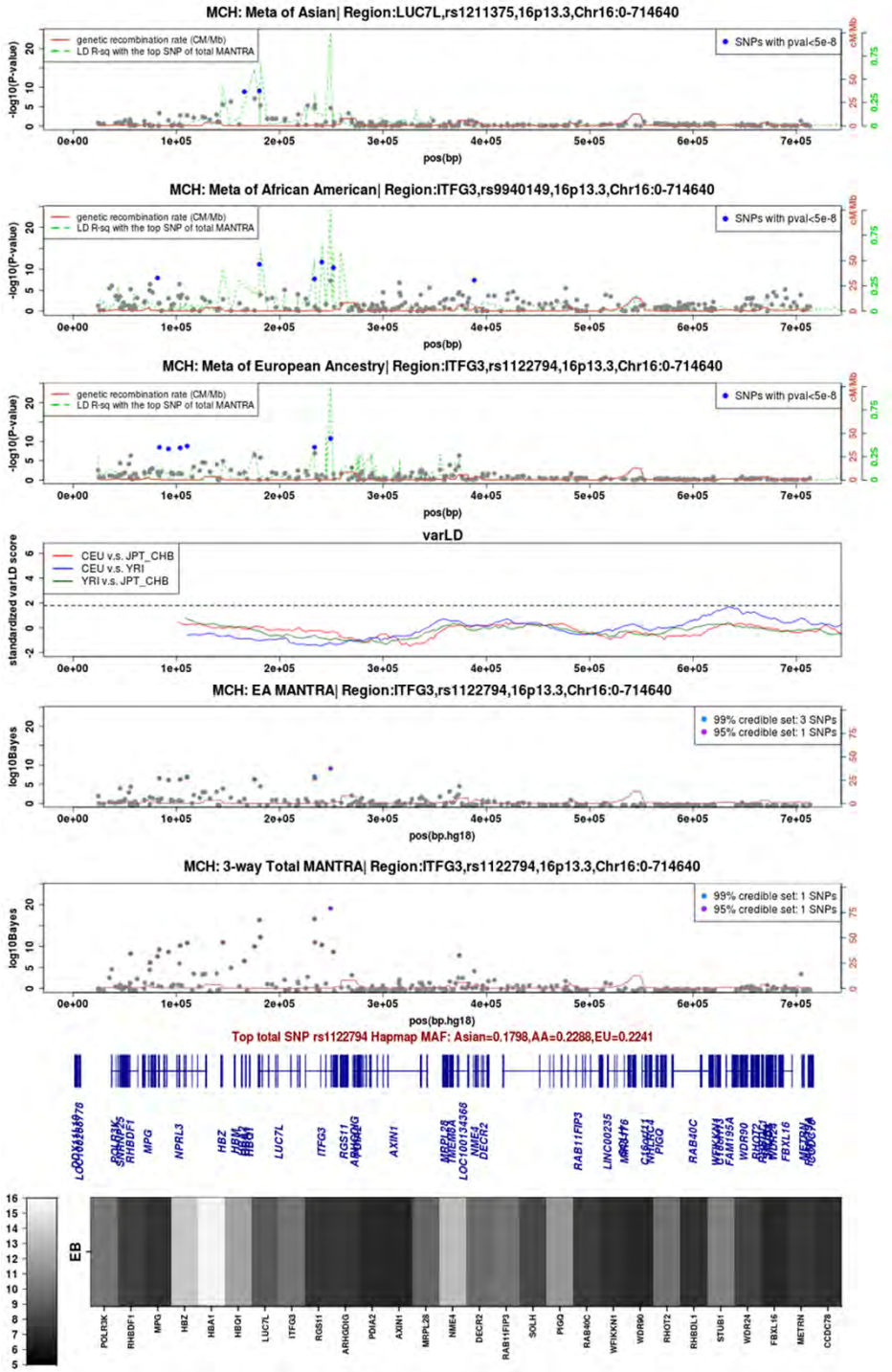

MCH: Meta of Asian| Region:MSMB,rs2072701,10q11.23,Chr10:50763360-51763360
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:MSMB,rs7076948,10q11.23,Chr10:50763360-51763360
MCH: Meta of European Ancestry| Region:FLJ31813,rs7098222,10q11.23,Chr10:50763360-51763360
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:FLJ31813,rs2002129,10q11.23,Chr10:50763360-51763360
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:TIMM23,rs7085433,10q11.23,Chr10:50763360-51763360
99% credible set: 2 SNPs
95% credible set: 2 SNPs
Top total SNP rs7085433 Hapmap MAF: Asian=0.1024,AA=0.1017,EU=0.09322
PARG
AGAP8
LOC728407
AGAP7
MSMB
NCOA4
TIMM23
AGAP6
FLJ31813
FAM21B
ASAH2
EB

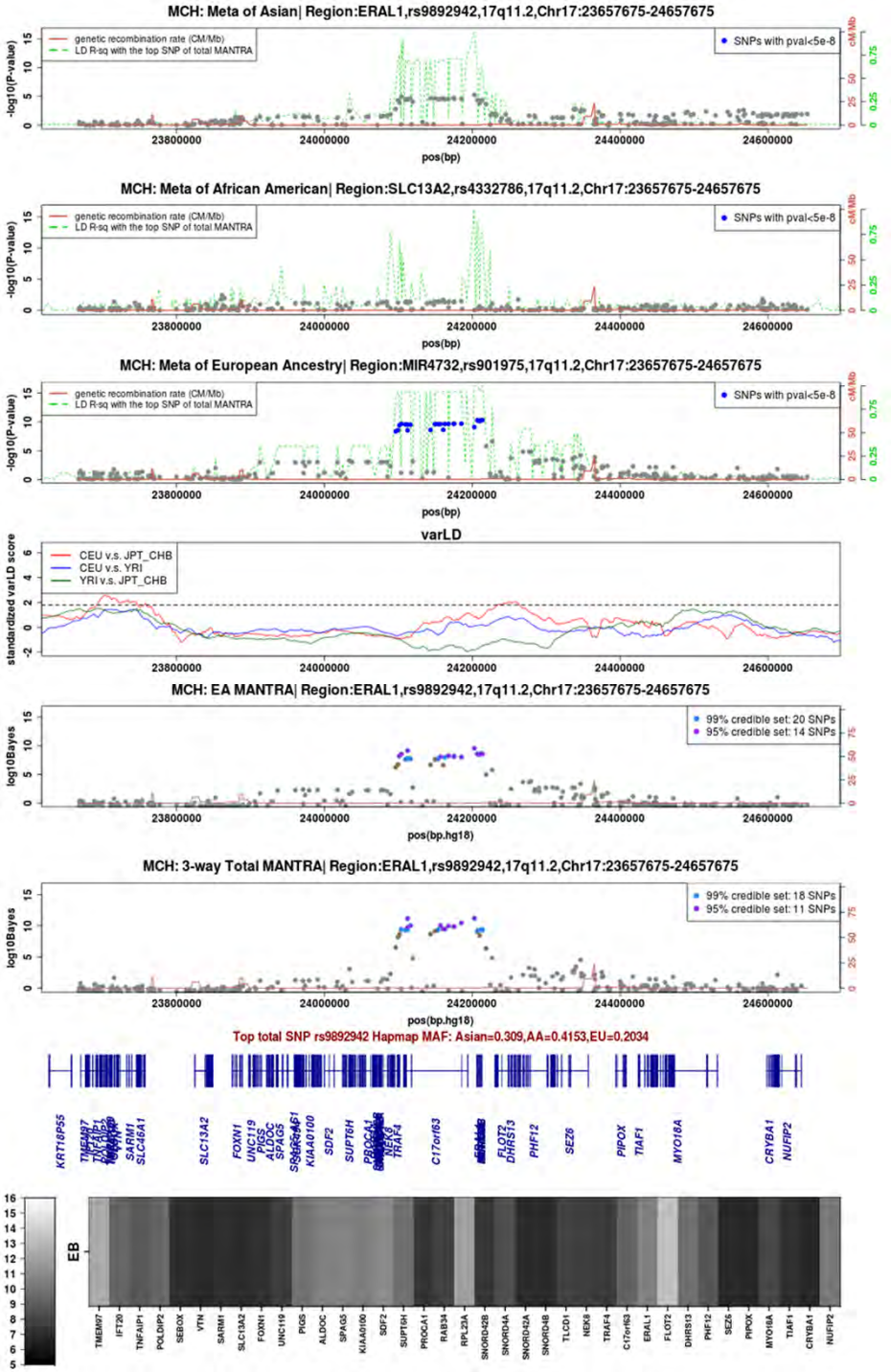

MCH: Meta of Asian| Region:CCND2,rs11611647,12p13.32,Chr12:3702516-4702516
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:EFCAB4B,rs10848934,12p13.32,Chr12:3702516-4702516
MCH: Meta of European Ancestry| Region:CCND2,rs7309743,12p13.32,Chr12:3702516-4702516
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:CCND2,rs7309743,12p13.32,Chr12:3702516-4702516
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:CCND2,rs7309743,12p13.32,Chr12:3702516-4702516
99% credible set: 4 SNPs
95% credible set: 4 SNPs
Top total SNP rs7309743 Hapmap MAF: Asian=0.2882,AA=0.3061,EU=0.287
EFCAB4B
PARP11
CCND2
C12orf5
FGF23
FGF6
C12orf4
RAD51AP1
DYRK4
AKAP3
NDUFA9
GALNT8
EB

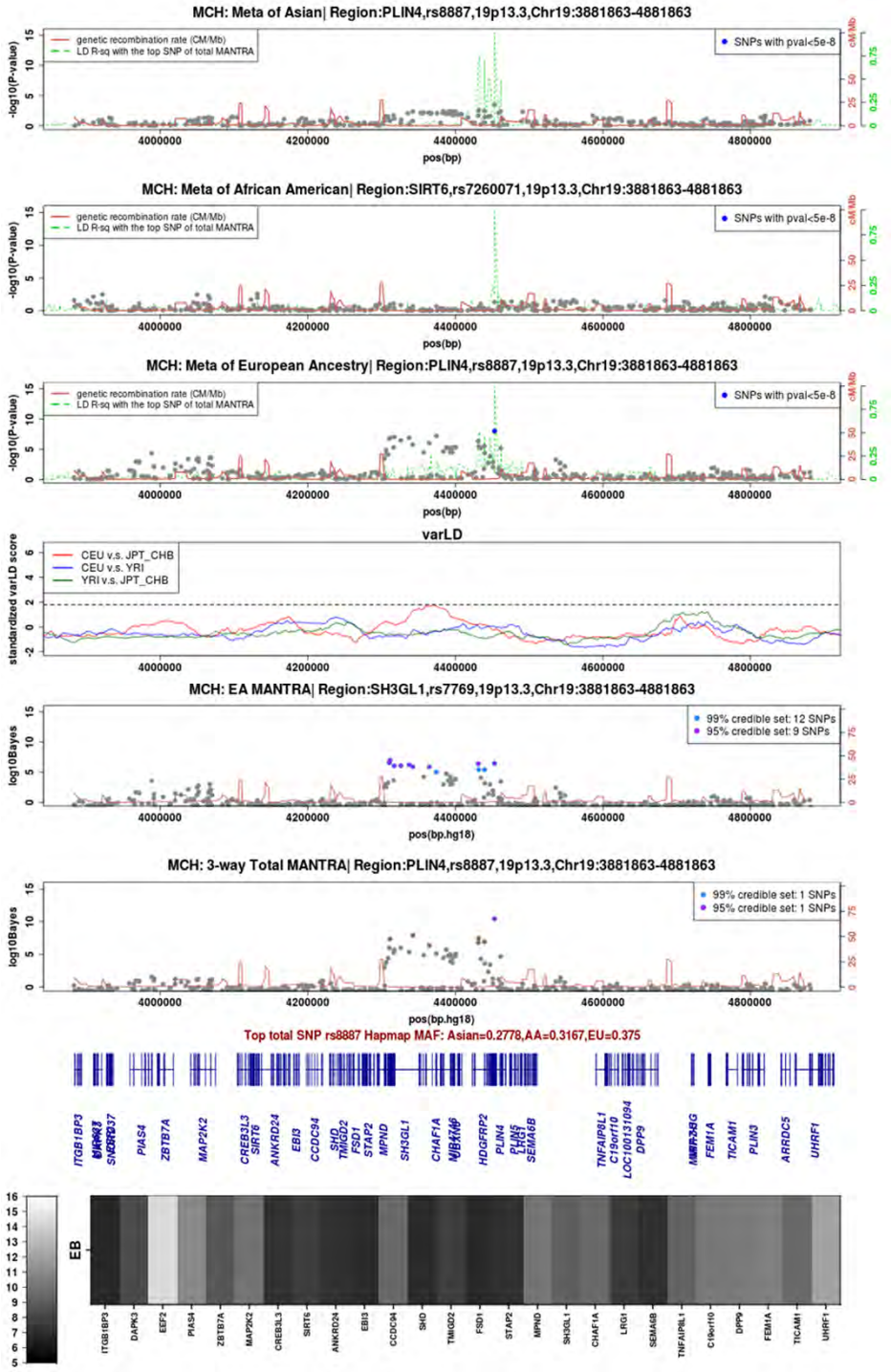

MCH: Meta of Asian| Region:CUX2,rs4766566,12q24.11,Chr12:109796312-111426736
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:C12orf51,rs11610922,12q24.13,Chr12:109796312-111426736
MCH: Meta of European Ancestry| Region:CUX2,rs1001484,12q24.11,Chr12:109796312-111426736
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:CUX2,rs1001484,12q24.11,Chr12:109796312-111426736
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:CUX2,rs4766566,12q24.11,Chr12:109796312-111426736
99% credible set: 63 SNPs
95% credible set: 37 SNPs
Top total SNP rs4766566 Hapmap MAF: Asian=0.3038,AA=0.1604,EU=0.2596
CCDC63
MYL2
LOC100131136
CUX2
FAM109A
SH2B3
ATXN2
BRAP
ACAD10
ALDH2
C12orf47
MAPKAPK5
ADAM1
TMEM116
ERP29
NAA25
TRAFD1
C12orf51
RPL6
PTPN11
EB

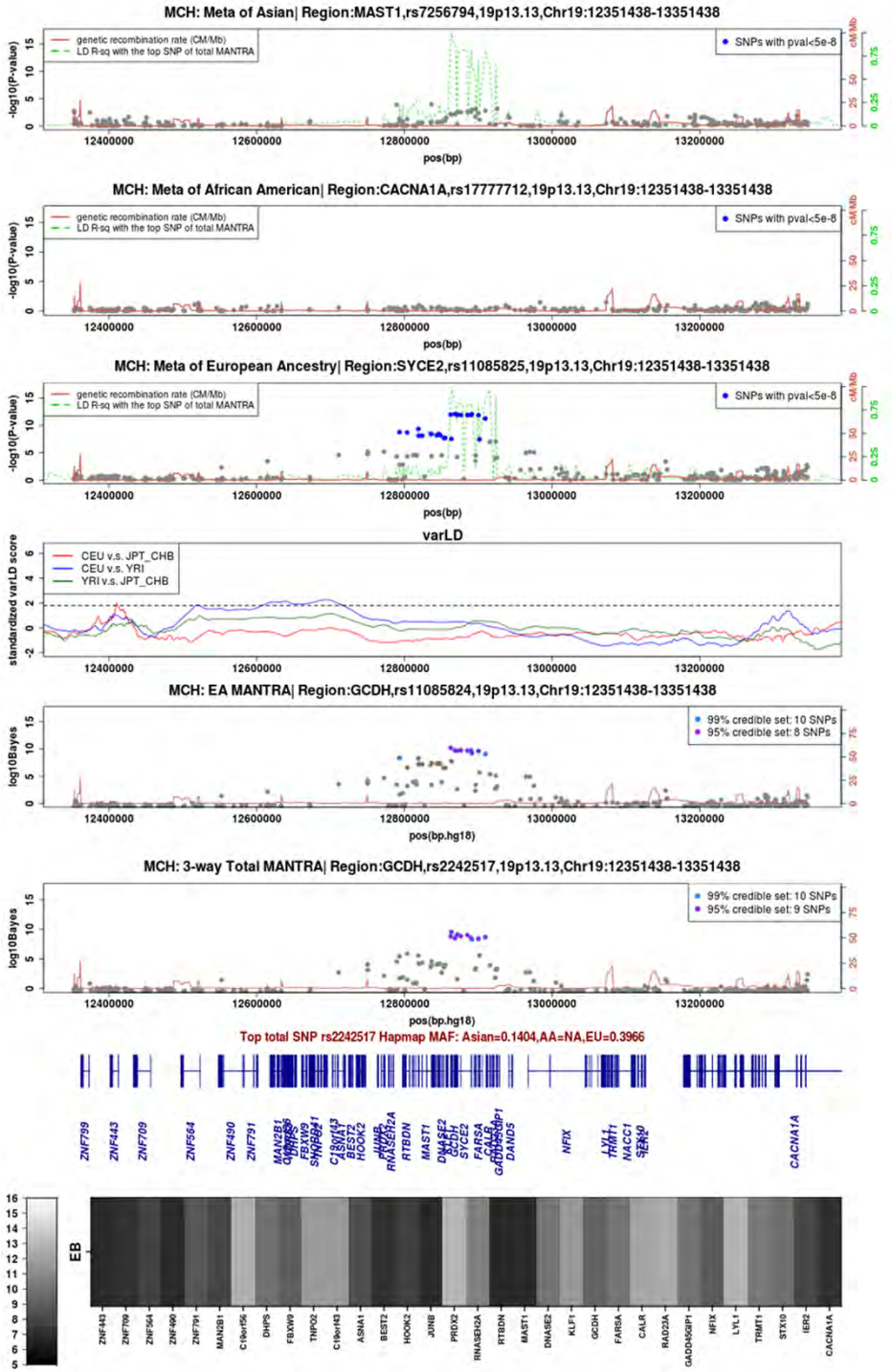

MCH: Meta of Asian| Region:MAX,rs7154885,14q23.3,Chr14:64057470-65057470
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:SPTB,rs2269297,14q23.3,Chr14:64057470-65057470
MCH: Meta of European Ancestry| Region:MAX,rs7148590,14q23.3,Chr14:64057470-65057470
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:MIR4706,rs726668,14q23.3,Chr14:64057470-65057470
99% credible set: 6 SNPs
95% credible set: 6 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:MIR4706,rs7155454,14q23.3,Chr14:64057470-65057470
99% credible set: 5 SNPs
95% credible set: 2 SNPs
Top total SNP rs7155454 Hapmap MAF: Asian=0.4213,AA=0.1083,EU=0.4917
ZBTB1
HSPA2
C14orf50
PLEKHG3
SPTB
CHURC1
GPX2
RAB15
CHURC1-FNTB
FNTB
MIR4706
MIR4708
LOC645431
EB
ZBTB1
HSPA2
C14orf50
PLEKHG3
SPTB
CHURC1
GPX2
RAB15
FNTB
MAX
FUT8

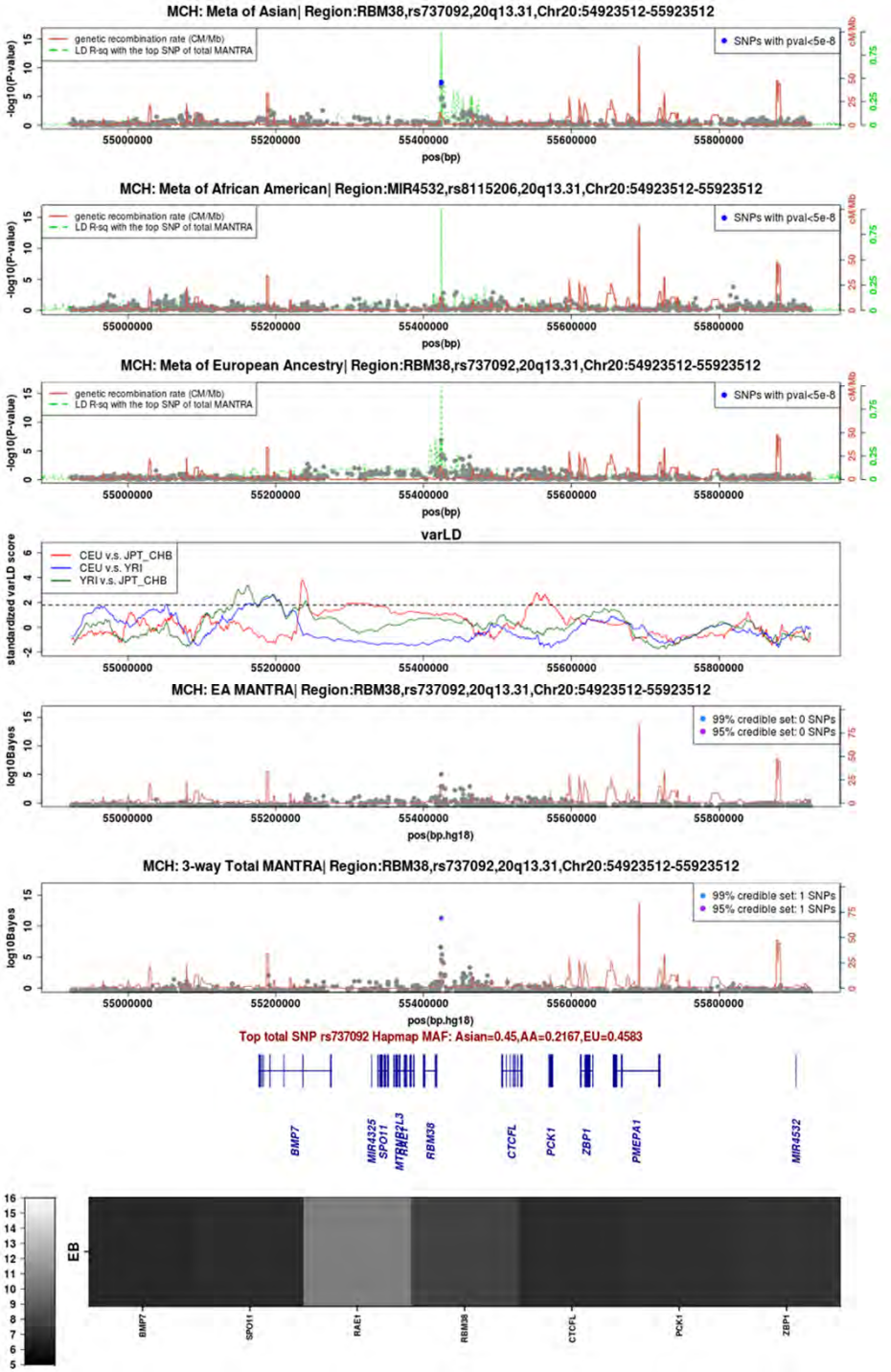

MCH: Meta of Asian| Region:DENND4A,rs2660632,15q22.31,Chr15:63185965-64185965
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:DPP8,rs12595213,15q22.31,Chr15:63185965-64185965
MCH: Meta of European Ancestry| Region:DENND4A,rs2572207,15q22.31,Chr15:63185965-64185965
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:DENND4A,rs2572207,15q22.31,Chr15:63185965-64185965
99% credible set: 17 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:C15orf44,rs7165102,15q22.31,Chr15:63185965-64185965
99% credible set: 8 SNPs
95% credible set: 5 SNPs
Top total SNP rs7165102 Hapmap MAF: Asian=0.2303,AA=0.04237,EU=0.3879
PDCD7
CLPX
CILP
PARP16
IQDCC3
IQDCC4
DPP8
PTPLAD1
C15orf44
SLC24A1
DENND4A
RAB11A
MIR4311
MEGF11
EB

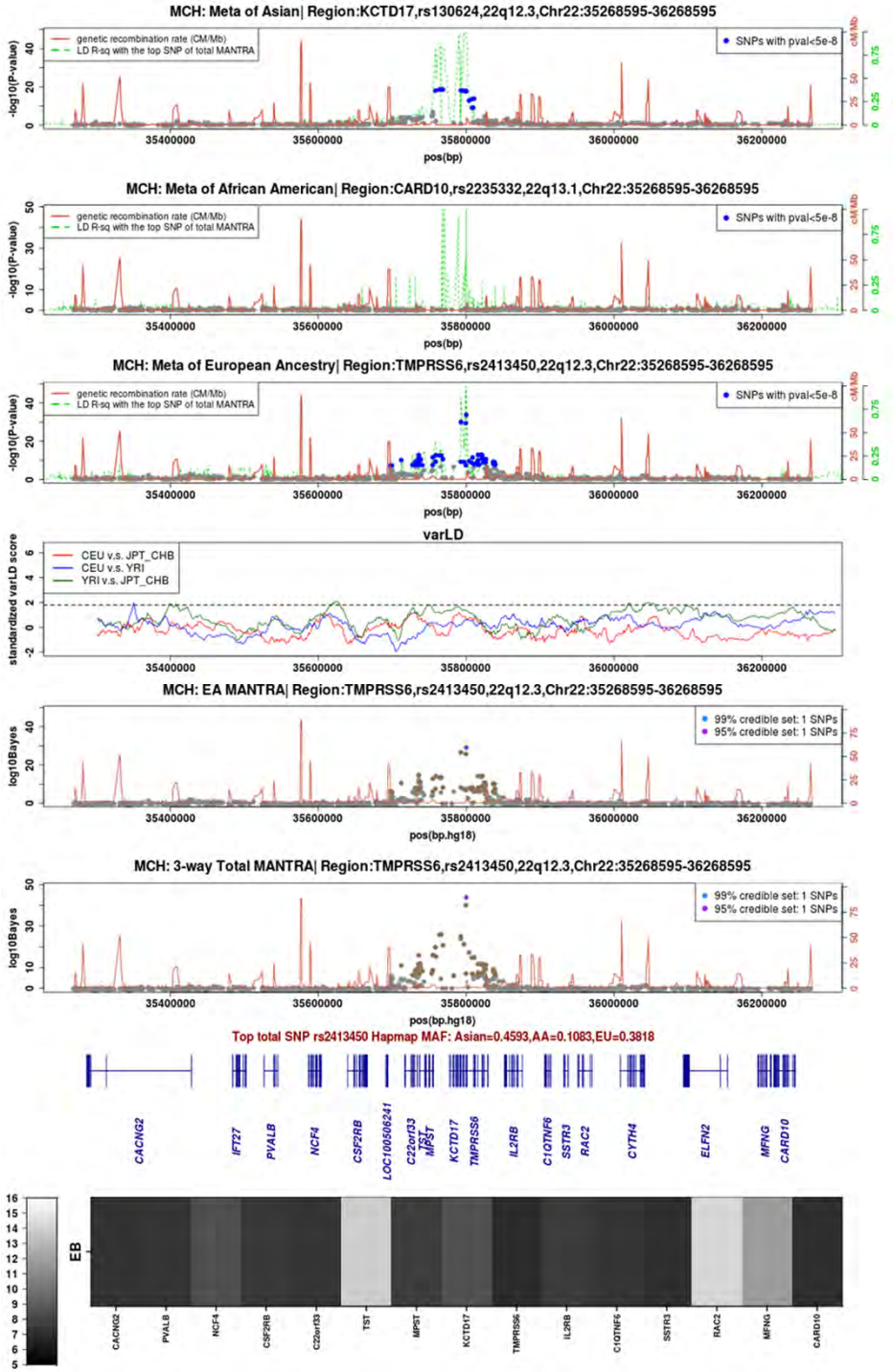

MCH: Meta of Asian| Region:LUC7L,rs1211375,16p13.3,Chr16:0-714640
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:ITFG3,rs9940149,16p13.3,Chr16:0-714640
MCH: Meta of European Ancestry| Region:ITFG3,rs1122794,16p13.3,Chr16:0-714640
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:ITFG3,rs1122794,16p13.3,Chr16:0-714640
99% credible set: 3 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:ITFG3,rs1122794,16p13.3,Chr16:0-714640
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs1122794 Hapmap MAF: Asian=0.1798,AA=0.2288,EU=0.2241
EB
PQLR3K
RHBDF1
MPG
HBZ
HBA1
HBQ1
LUC7L
ITFG3
RGS11
ARHGDIG
PDIA2
AXIN1
MRPL28
NME4
DECR2
RAB11FIP3
SOLH
PIGQ
RAB40C
WFIKKN1
WDR90
RHOT2
RHBDL1
STUB1
WDR24
FBXL16
METRN
CCDC78


MCH: Meta of Asian| Region:ERAL1,rs9892942,17q11.2,Chr17:23657675-24657675
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:SLC13A2,rs4332786,17q11.2,Chr17:23657675-24657675
MCH: Meta of European Ancestry| Region:MIR4732,rs901975,17q11.2,Chr17:23657675-24657675
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:ERAL1,rs9892942,17q11.2,Chr17:23657675-24657675
99% credible set: 20 SNPs
95% credible set: 14 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:ERAL1,rs9892942,17q11.2,Chr17:23657675-24657675
99% credible set: 18 SNPs
95% credible set: 11 SNPs
Top total SNP rs9892942 Hapmap MAF: Asian=0.309,AA=0.4153,EU=0.2034
KRT18P55
SLC13A2
FOXN1
UNC119
PIGS
ALDOC
SPAG5
KIAA0100
SDF2
SUPT6H
C17orf63
FLOT2
DHRS13
PHF12
SEZ6
PIPOX
TIAF1
MYO18A
CRYBA1
NUFIP2
EB
TMEM97
IFT20
TNFAIP1
POLDIP2
SEBOX
VTN
SARM1
SLC13A2
FOXN1
UNC119
PIGS
ALDOC
SPAG5
KIAA0100
SDF2
SUPT6H
PROCA1
RAB34
RPL23A
SNORD42B
SNORD4A
SNORD42A
SNORD4B
TLCD1
HEK8
TRAF4
C17orf63
ERAL1
FLOT2
DHRS13
PNF12
SEZ6
PIPOX
MYO18A
TIAF1
CRYBA1
NUFIP2

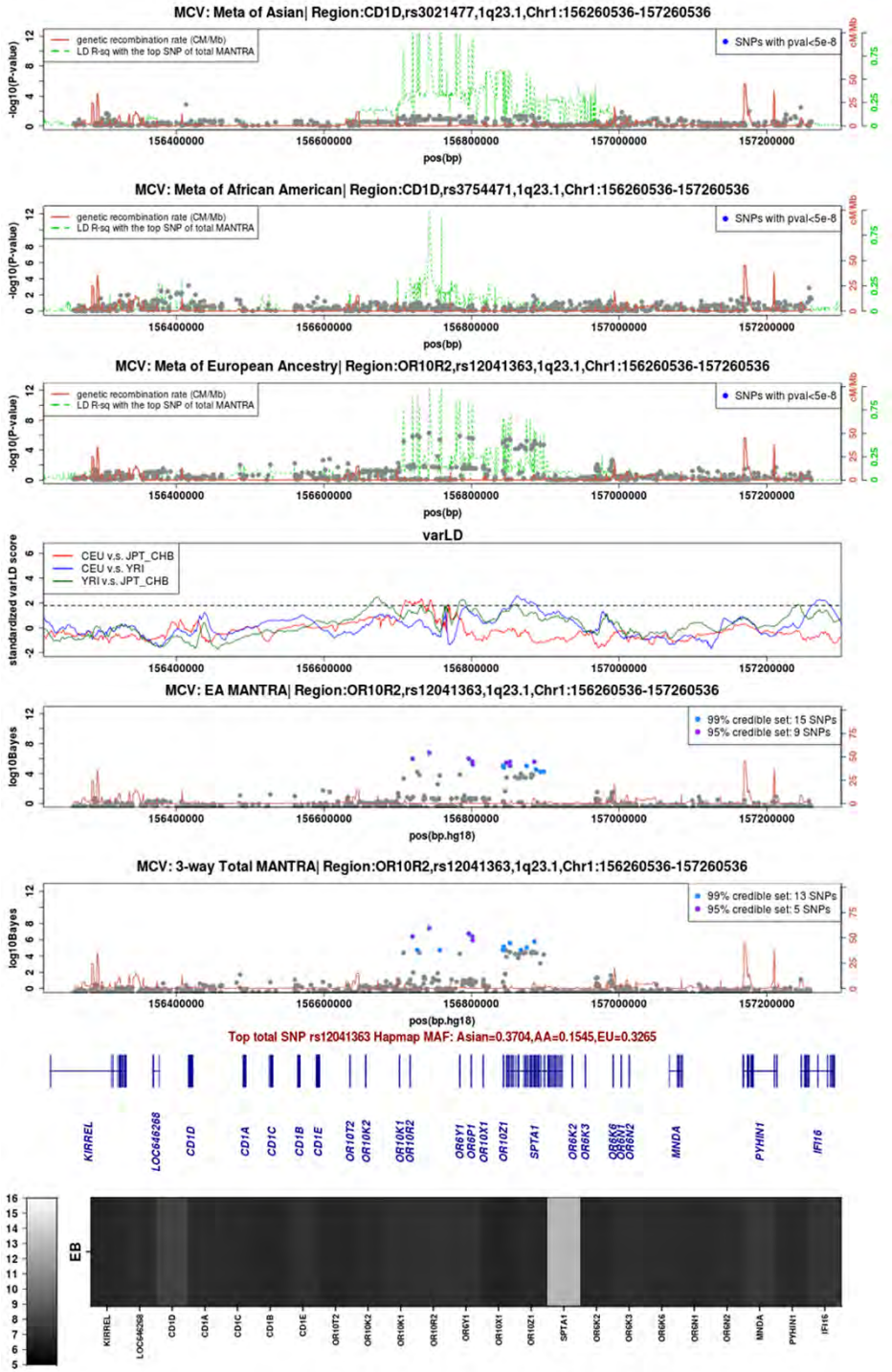

MCH: Meta of Asian| Region:PLIN4,rs8887,19p13.3,Chr19:3881863-4881863
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:SIRT6,rs7260071,19p13.3,Chr19:3881863-4881863
MCH: Meta of European Ancestry| Region:PLIN4,rs8887,19p13.3,Chr19:3881863-4881863
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:SH3GL1,rs7769,19p13.3,Chr19:3881863-4881863
99% credible set: 12 SNPs
95% credible set: 9 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:PLIN4,rs8887,19p13.3,Chr19:3881863-4881863
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs8887 Hapmap MAF: Asian=0.2778,AA=0.3167,EU=0.375
ITGB1BP3
PIAS4
ZBTB7A
MAP2K2
CREB3L3
SIRT6
ANKRD24
EBI3
CCDC94
SH0
TMIGD2
FSD1
STAP2
MPND
SH3GL1
CHAF1A
HDGFRP2
PLIN4
SEMA6B
TNFAIP8L1
C19orf10
LOC100131094
DPP9
FEM1A
TICAM1
PLIN3
ARRDC5
UHRF1
EB
DAPK3
EEF2
LRG1

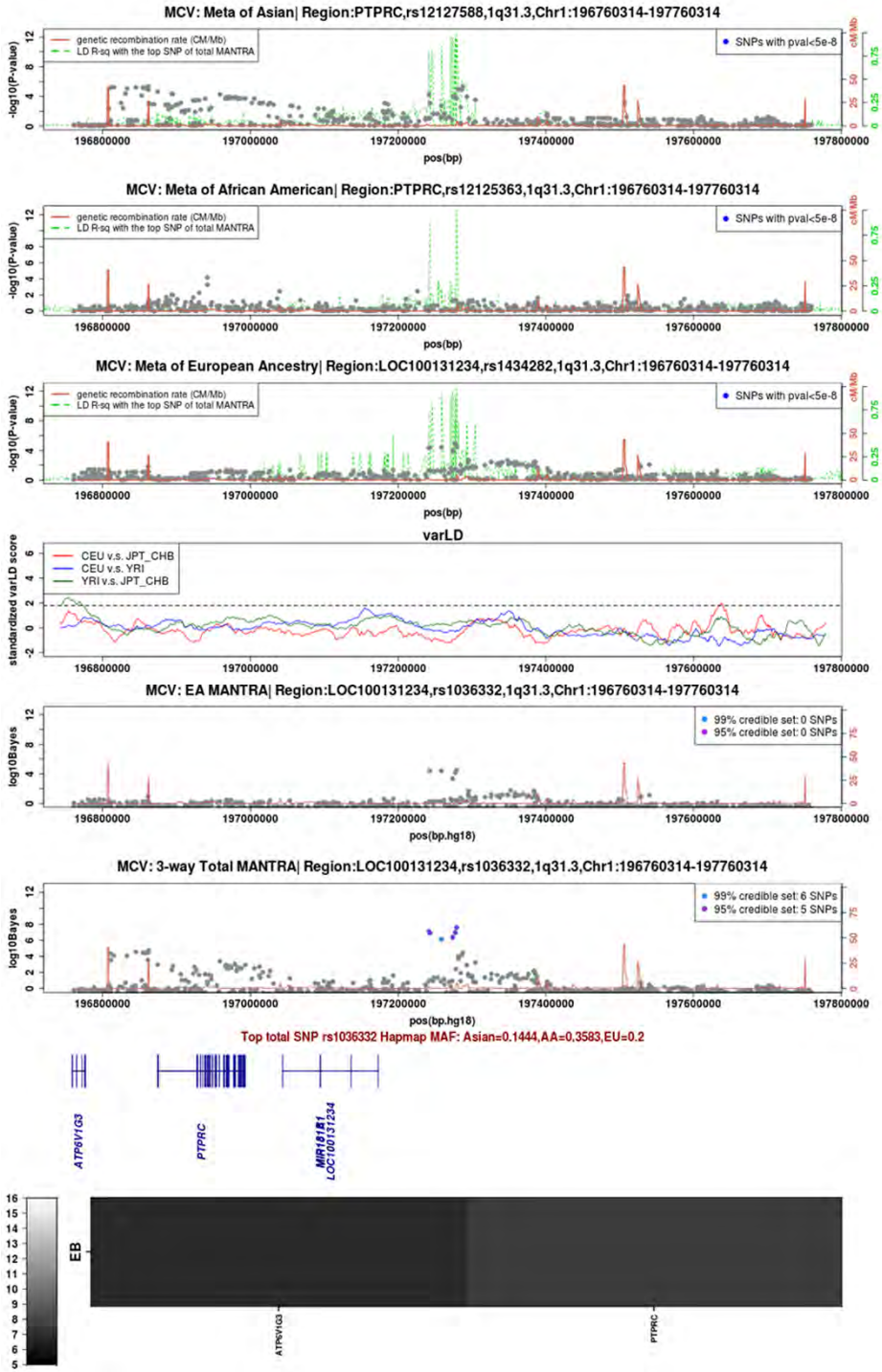

MCH: Meta of Asian| Region:MAST1,rs7256794,19p13.13,Chr19:12351438-13351438
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:CACNA1A,rs17777712,19p13.13,Chr19:12351438-13351438
MCH: Meta of European Ancestry| Region:SYCE2,rs11085825,19p13.13,Chr19:12351438-13351438
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:GCDH,rs11085824,19p13.13,Chr19:12351438-13351438
99% credible set: 10 SNPs
95% credible set: 8 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:GCDH,rs2242517,19p13.13,Chr19:12351438-13351438
99% credible set: 10 SNPs
95% credible set: 9 SNPs
Top total SNP rs2242517 Hapmap MAF: Asian=0.1404,AA=NA,EU=0.3966
ZNF799
ZNF443
ZNF709
ZNF564
ZNF490
ZNF791
MAN2B1
C19orf56
DHPS
FBXW9
TNPO2
C19orf43
ASNA1
BEST2
HOOK2
PRDX2
RNASEH2A
RTBDN
MAST1
DMAC2
KLF1
SYCE2
GCDH
FARSA
CALR
GADD45GIP1
DAND5
NFIX
LYL1
TRMT1
NACC1
STX10
SEX10
IER2
CACNA1A
EB

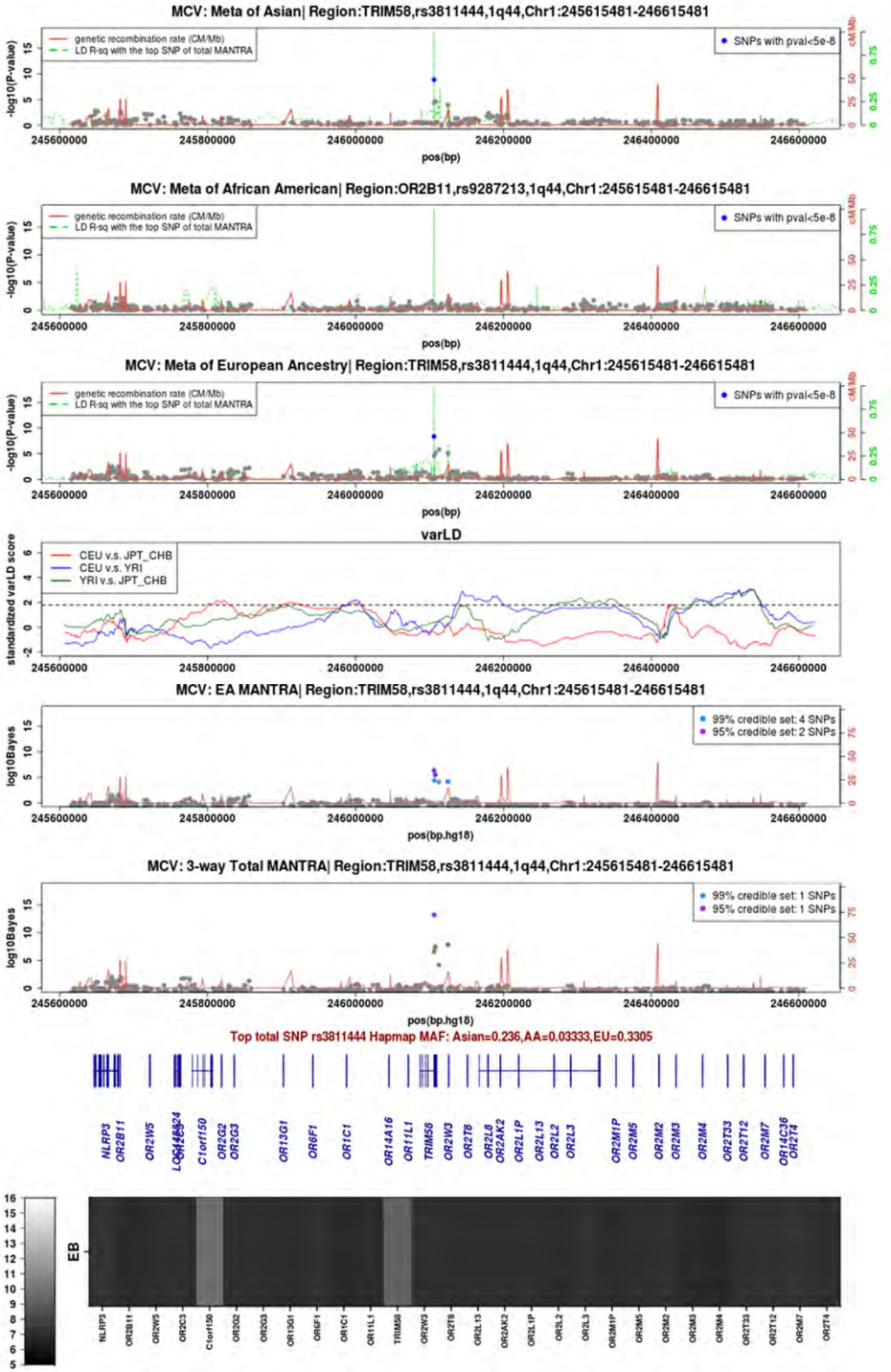

MCH: Meta of Asian| Region:RBM38,rs737092,20q13.31,Chr20:54923512-55923512
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:MIR4532,rs8115206,20q13.31,Chr20:54923512-55923512
MCH: Meta of European Ancestry| Region:RBM38,rs737092,20q13.31,Chr20:54923512-55923512
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:RBM38,rs737092,20q13.31,Chr20:54923512-55923512
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:RBM38,rs737092,20q13.31,Chr20:54923512-55923512
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs737092 Hapmap MAF: Asian=0.45,AA=0.2167,EU=0.4583
BMP7
MIR4325
SPO11
MTRNR2L3
RBM38
CTCFL
PCK1
ZBP1
PMEPA1
MIR4532
EB
BMP7
SPO11
RAE1
RBM38
CTCFL
PCK1
ZBP1

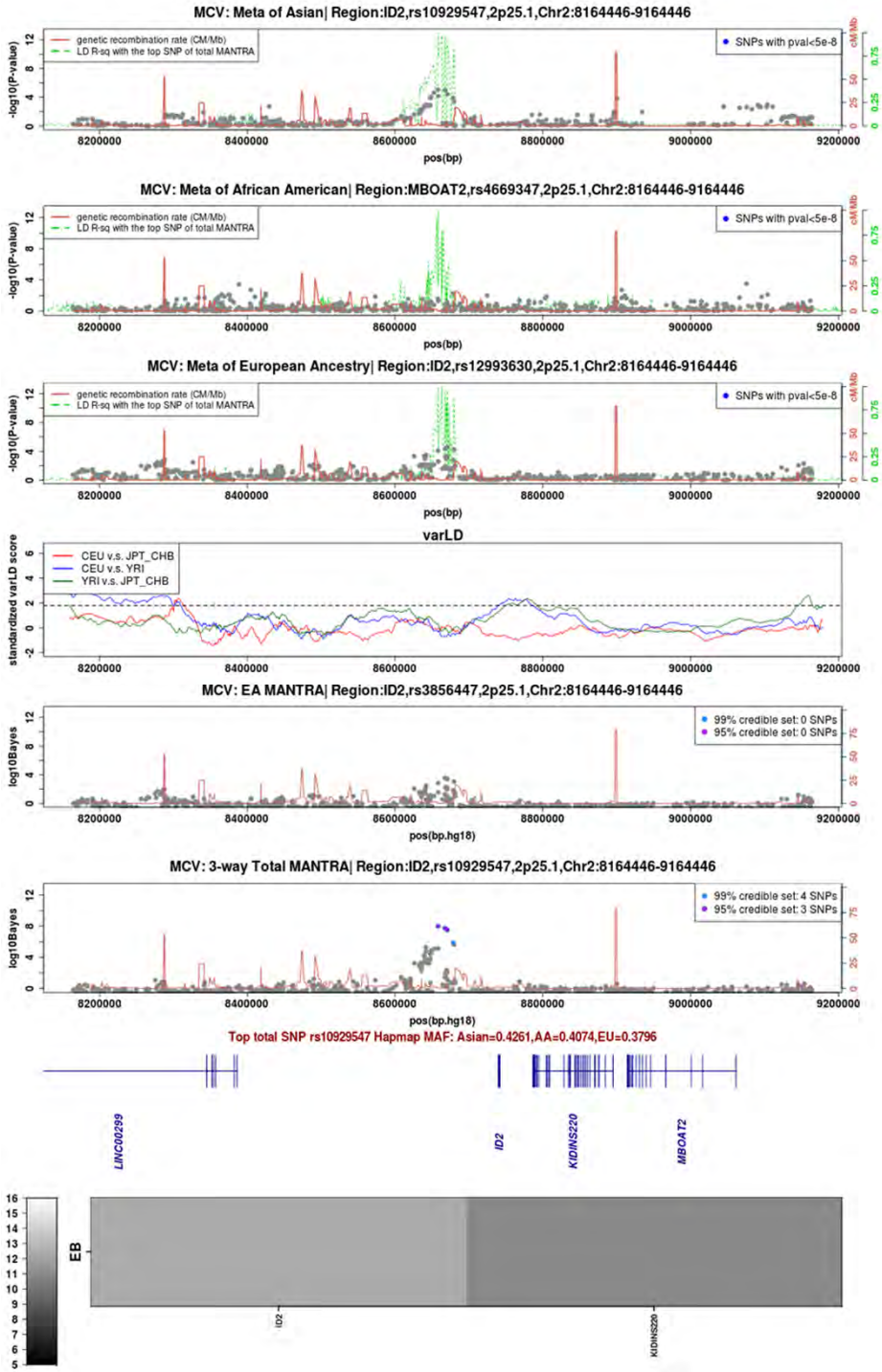

MCH: Meta of Asian| Region:KCTD17,rs130624,22q12.3,Chr22:35268595-36268595
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCH: Meta of African American| Region:CARD10,rs2235332,22q13.1,Chr22:35268595-36268595
MCH: Meta of European Ancestry| Region:TMPRSS6,rs2413450,22q12.3,Chr22:35268595-36268595
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCH: EA MANTRA| Region:TMPRSS6,rs2413450,22q12.3,Chr22:35268595-36268595
99% credible set: 1 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
MCH: 3-way Total MANTRA| Region:TMPRSS6,rs2413450,22q12.3,Chr22:35268595-36268595
Top total SNP rs2413450 Hapmap MAF: Asian=0.4593,AA=0.1083,EU=0.3818
CACNG2
IFT27
PVALB
NCF4
CSF2RB
LOC100506241
C22orf33
TST
MPST
KCTD17
TMPRSS6
IL2RB
C1QTNF6
SSTR3
RAC2
CYTH4
ELFN2
MFNG
CARD10
EB

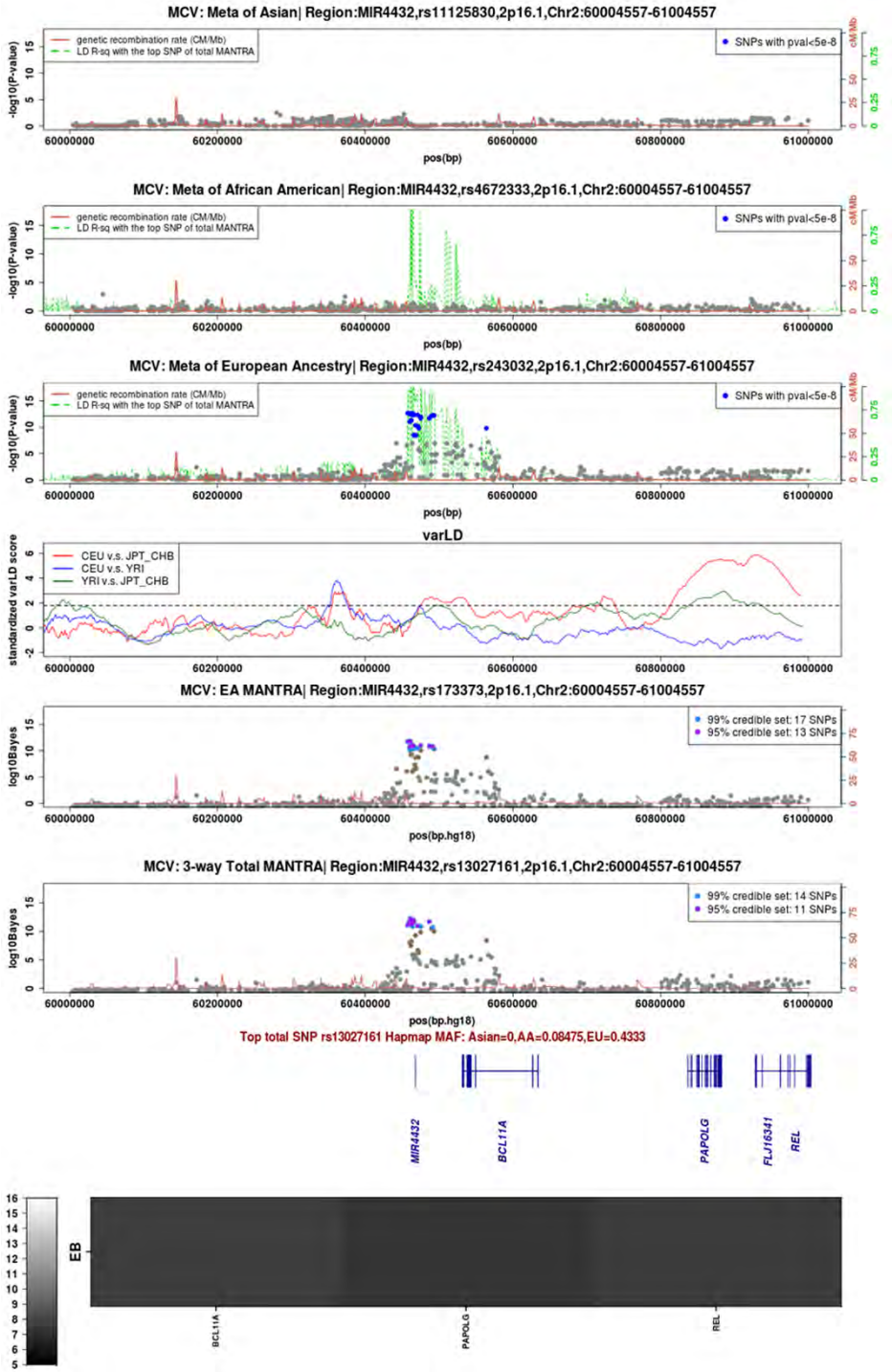
MCV

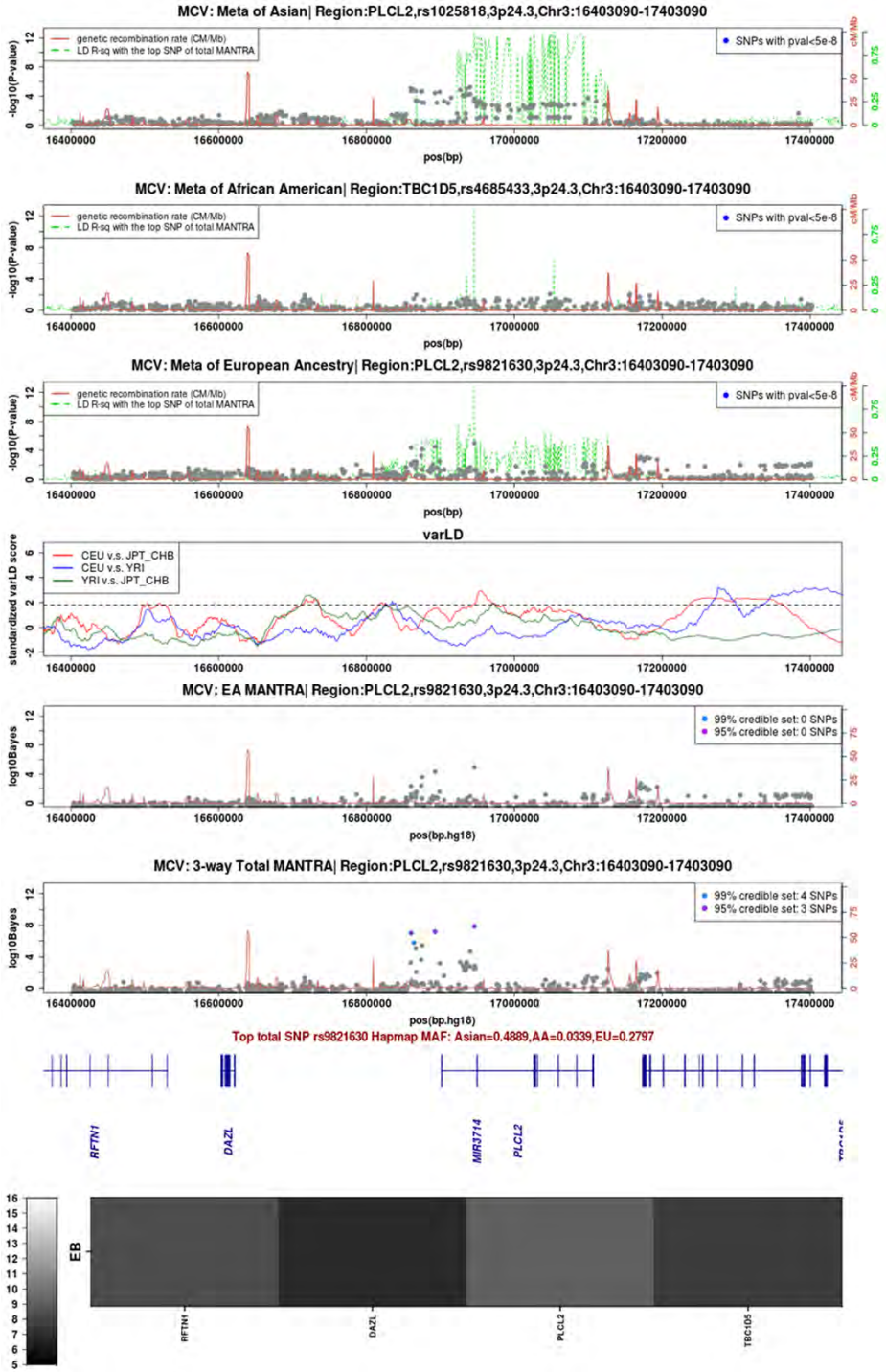

MCV: Meta of Asian| Region:CD1D,rs3021477,1q23.1,Chr1:156260536-157260536
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:CD1D,rs3754471,1q23.1,Chr1:156260536-157260536
MCV: Meta of European Ancestry| Region:OR10R2,rs12041363,1q23.1,Chr1:156260536-157260536
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:OR10R2,rs12041363,1q23.1,Chr1:156260536-157260536
99% credible set: 15 SNPs
95% credible set: 9 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:OR10R2,rs12041363,1q23.1,Chr1:156260536-157260536
99% credible set: 13 SNPs
95% credible set: 5 SNPs
Top total SNP rs12041363 Hapmap MAF: Asian=0.3704,AA=0.1545,EU=0.3265
KIRREL
LOC646268
CD1D
CD1A
CD1C
CD1B
CD1E
OR10T2
OR10K2
OR10K1
OR10R2
OR6Y1
OR6P1
OR10X1
OR10Z1
SPTA1
OR6K2
OR6K3
OR6K6
OR6N1
OR6N2
MNDA
PYHIN1
IFI16
EB

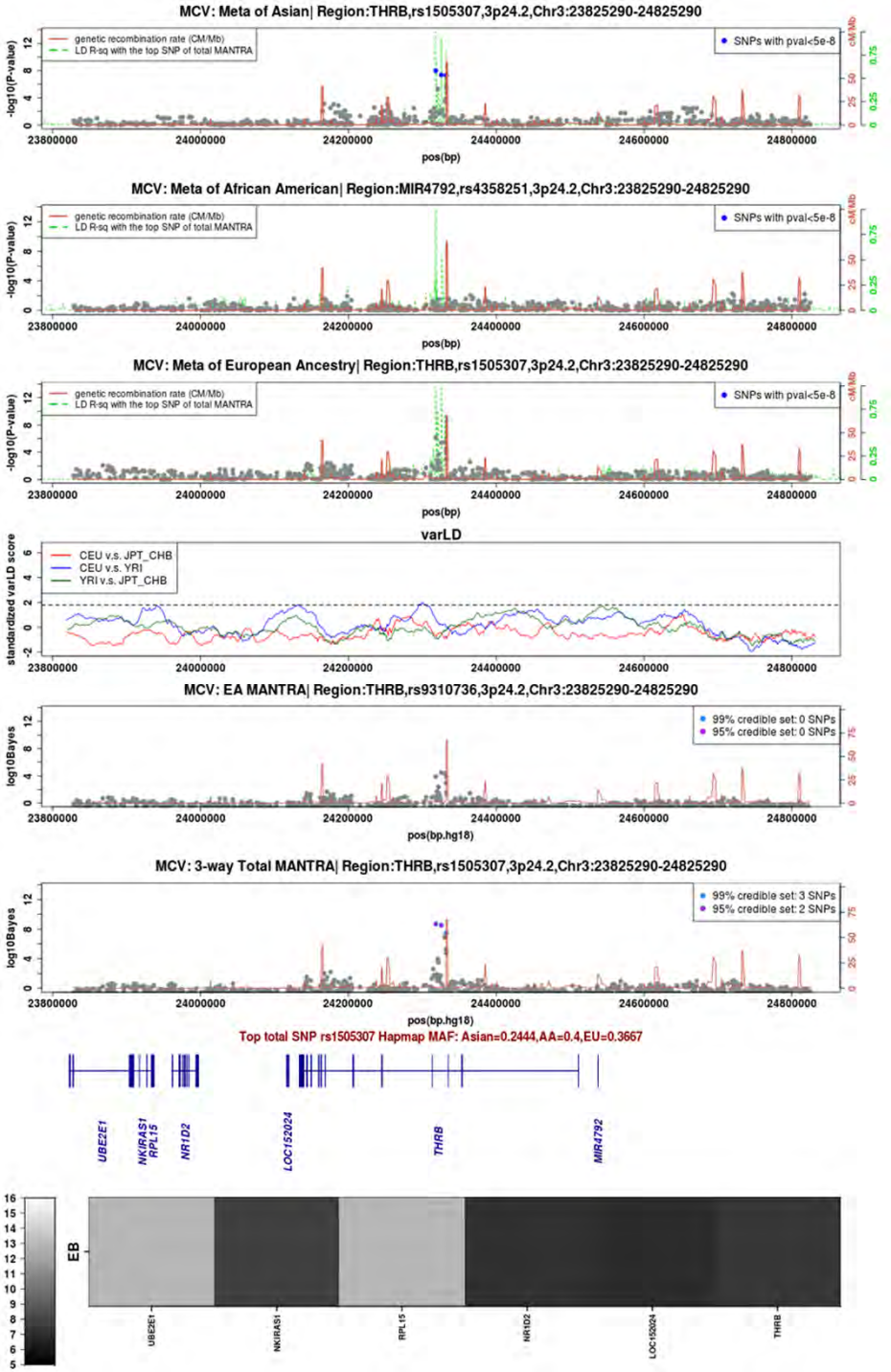

MCV: Meta of Asian| Region:PTPRC,rs12127588,1q31.3,Chr1:196760314-197760314
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:PTPRC,rs12125363,1q31.3,Chr1:196760314-197760314
MCV: Meta of European Ancestry| Region:LOC100131234,rs1434282,1q31.3,Chr1:196760314-197760314
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:LOC100131234,rs1036332,1q31.3,Chr1:196760314-197760314
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:LOC100131234,rs1036332,1q31.3,Chr1:196760314-197760314
99% credible set: 6 SNPs
95% credible set: 5 SNPs
Top total SNP rs1036332 Hapmap MAF: Asian=0.1444,AA=0.3583,EU=0.2
ATP6V1G3
PTPRC
MIR181A1
LOC100131234
EB

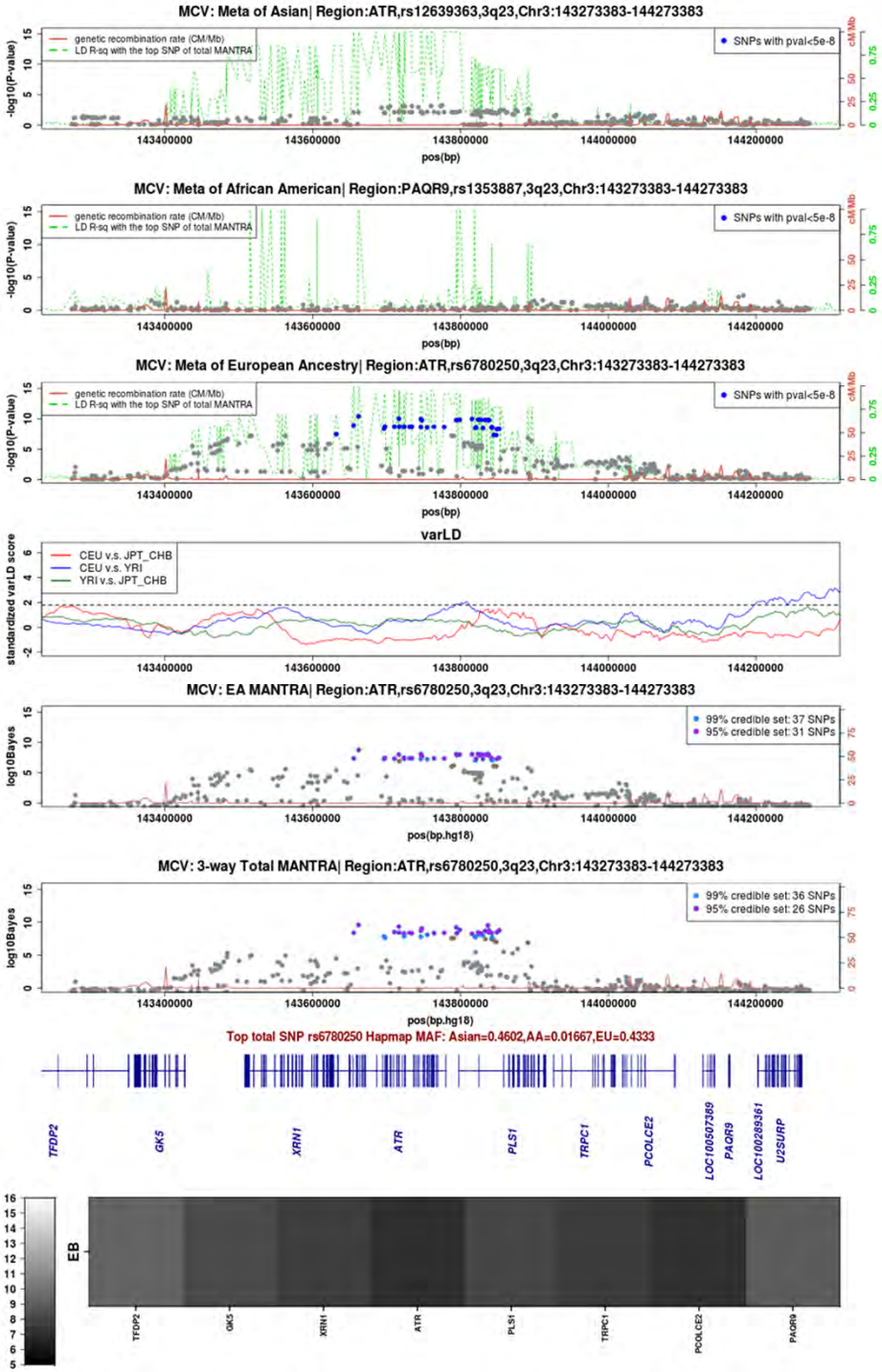

MCV: Meta of Asian| Region:TRIM58,rs3811444,1q44,Chr1:245615481-246615481
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:OR2B11,rs9287213,1q44,Chr1:245615481-246615481
MCV: Meta of European Ancestry| Region:TRIM58,rs3811444,1q44,Chr1:245615481-246615481
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:TRIM58,rs3811444,1q44,Chr1:245615481-246615481
99% credible set: 4 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:TRIM58,rs3811444,1q44,Chr1:245615481-246615481
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs3811444 Hapmap MAF: Asian=0.236,AA=0.03333,EU=0.3305
NLRP3
OR2B11
OR2W5
OR2C3
C1orf150
OR2G2
OR2G3
OR13G1
OR6F1
OR1C1
OR14A16
OR11L1
TRIM58
OR2W3
OR2T8
OR2L8
OR2AK2
OR2L1P
OR2L13
OR2L2
OR2L3
OR2M1P
OR2M5
OR2M2
OR2M3
OR2M4
OR2T33
OR2T12
OR2M7
OR14C36
OR2T4
EB

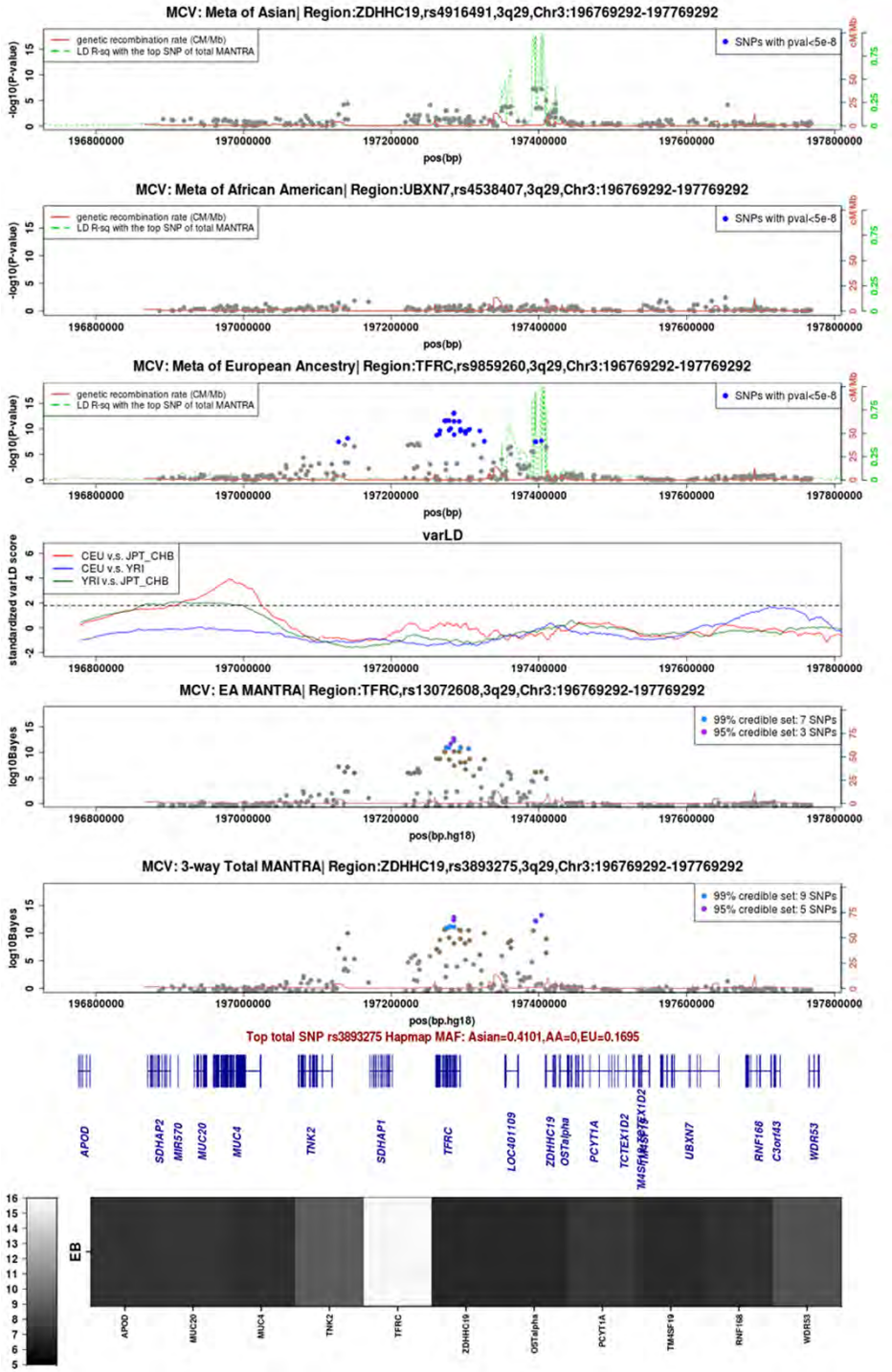

MCV: Meta of Asian| Region:ID2,rs10929547,2p25.1,Chr2:8164446-9164446
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:MBOAT2,rs4669347,2p25.1,Chr2:8164446-9164446
MCV: Meta of European Ancestry| Region:ID2,rs12993630,2p25.1,Chr2:8164446-9164446
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:ID2,rs3856447,2p25.1,Chr2:8164446-9164446
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:ID2,rs10929547,2p25.1,Chr2:8164446-9164446
99% credible set: 4 SNPs
95% credible set: 3 SNPs
Top total SNP rs10929547 Hapmap MAF: Asian=0.4261,AA=0.4074,EU=0.3796
LINC00299
ID2
KIDINS220
MBOAT2
EB

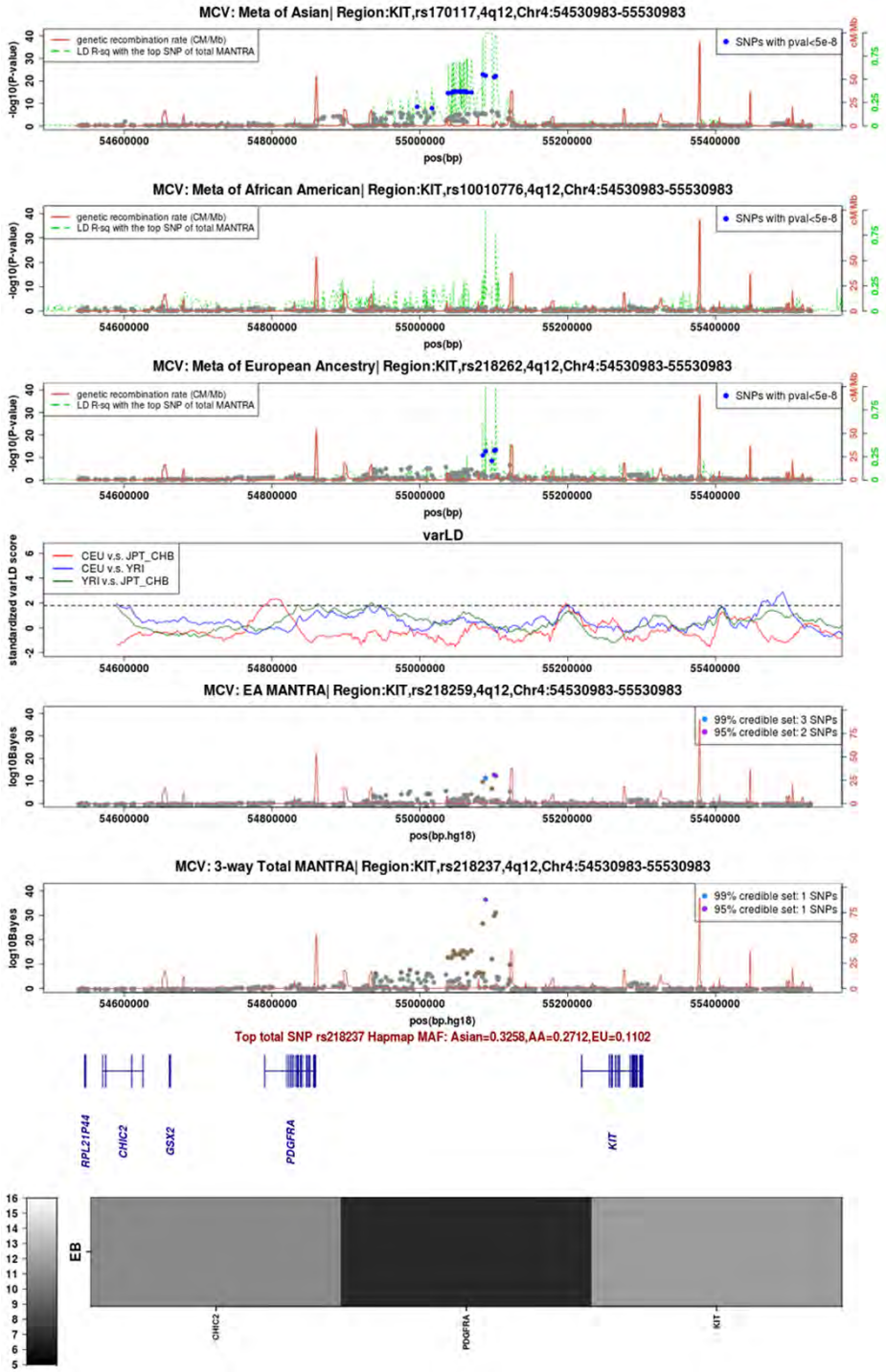

MCV: Meta of Asian| Region:MIR4432,rs11125830,2p16.1,Chr2:60004557-61004557
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:MIR4432,rs4672333,2p16.1,Chr2:60004557-61004557
MCV: Meta of European Ancestry| Region:MIR4432,rs243032,2p16.1,Chr2:60004557-61004557
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:MIR4432,rs173373,2p16.1,Chr2:60004557-61004557
99% credible set: 17 SNPs
95% credible set: 13 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:MIR4432,rs13027161,2p16.1,Chr2:60004557-61004557
99% credible set: 14 SNPs
95% credible set: 11 SNPs
Top total SNP rs13027161 Hapmap MAF: Asian=0,AA=0.08475,EU=0.4333
MIR4432
BCL11A
PAPOLG
FLJ16341
REL
EB

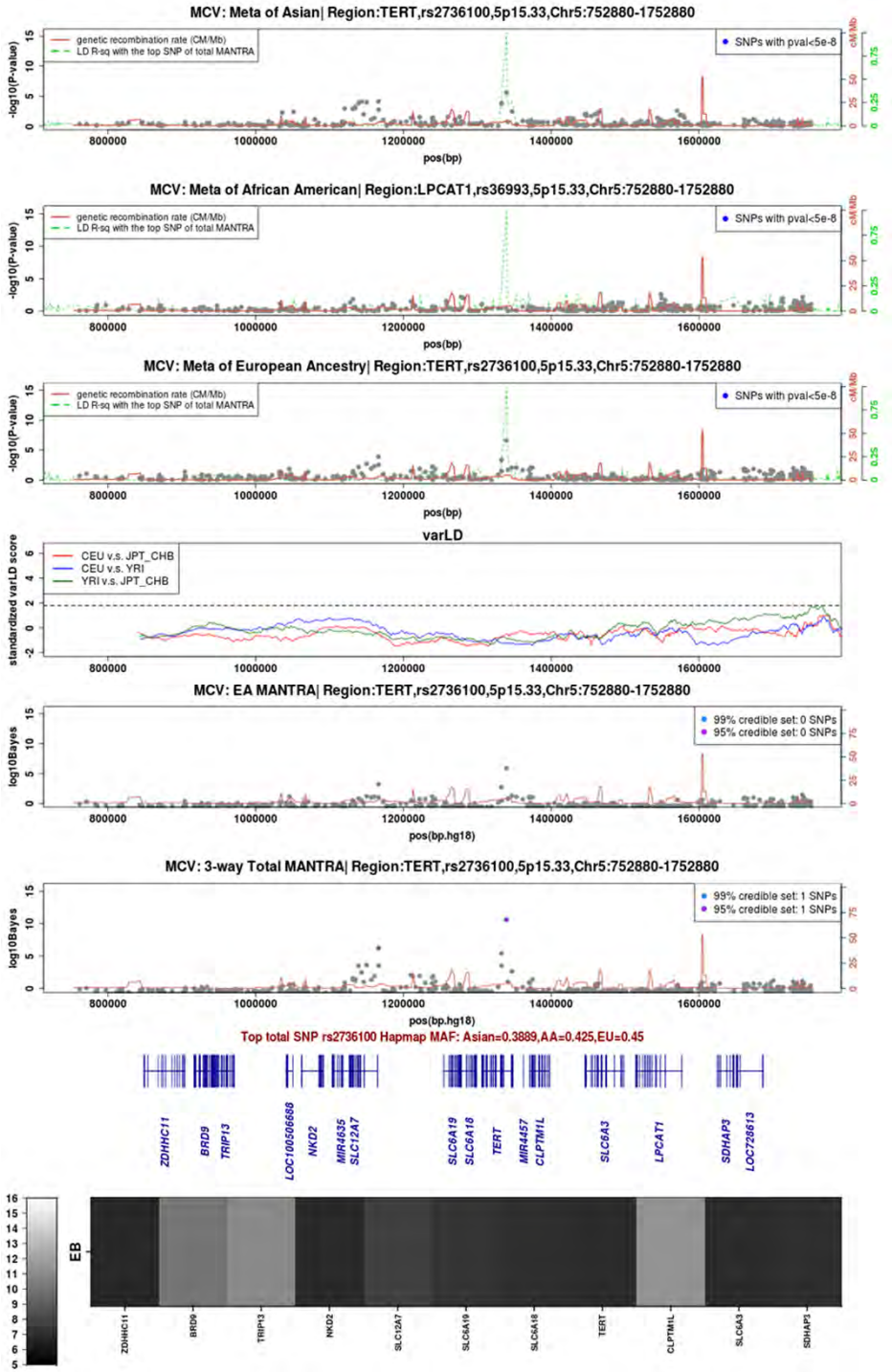

MCV: Meta of Asian| Region:PLCL2,rs1025818,3p24.3,Chr3:16403090-17403090
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:TBC1D5,rs4685433,3p24.3,Chr3:16403090-17403090
MCV: Meta of European Ancestry| Region:PLCL2,rs9821630,3p24.3,Chr3:16403090-17403090
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:PLCL2,rs9821630,3p24.3,Chr3:16403090-17403090
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:PLCL2,rs9821630,3p24.3,Chr3:16403090-17403090
99% credible set: 4 SNPs
95% credible set: 3 SNPs
Top total SNP rs9821630 Hapmap MAF: Asian=0.4889,AA=0.0339,EU=0.2797
RFTN1
DAZL
MIR3714
PLCL2
EB
RFTN1
DAZL
PLCL2
TBC1D5

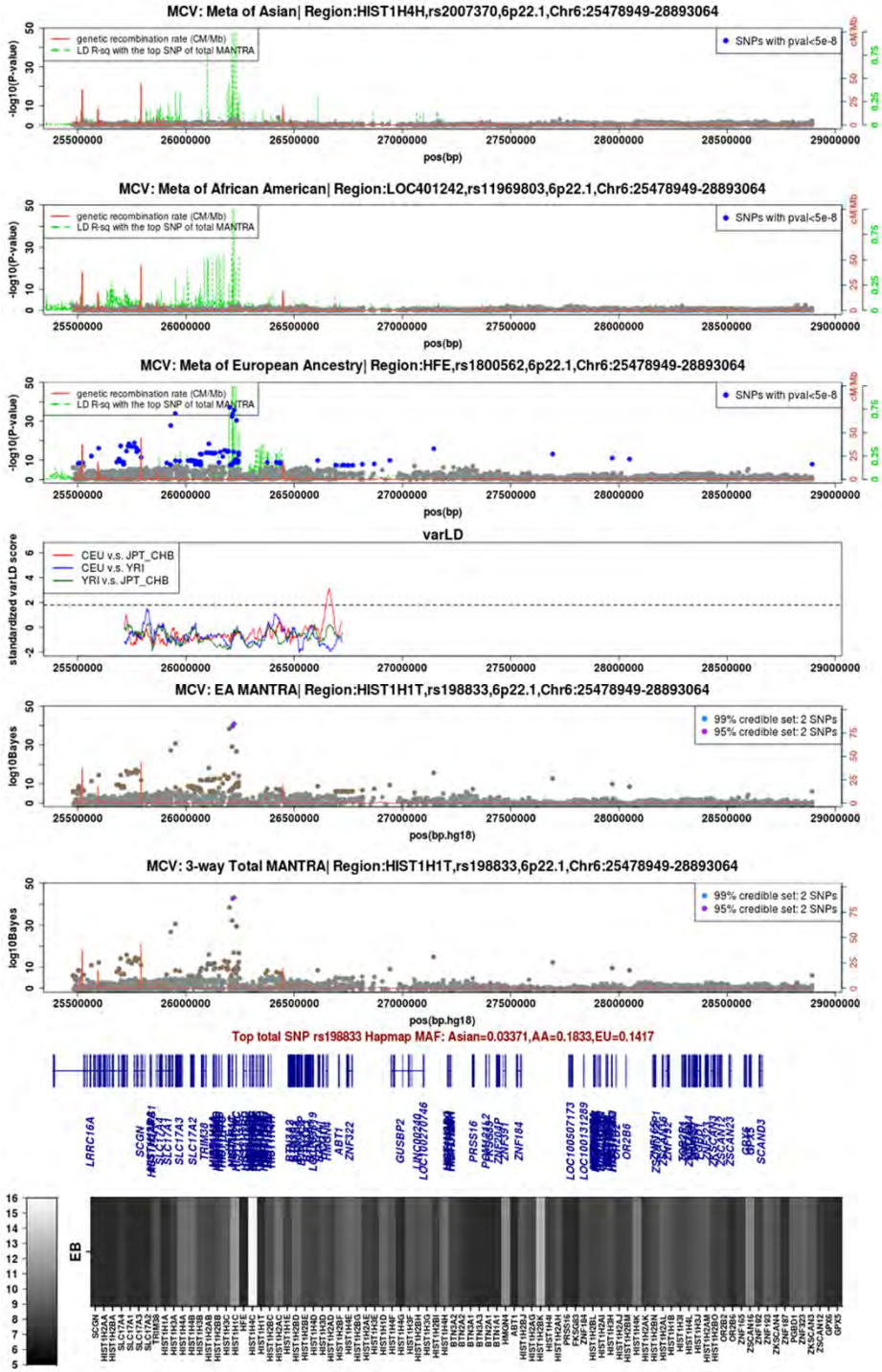

MCV: Meta of Asian| Region:THRB,rs1505307,3p24.2,Chr3:23825290-24825290
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:MIR4792,rs4358251,3p24.2,Chr3:23825290-24825290
MCV: Meta of European Ancestry| Region:THRB,rs1505307,3p24.2,Chr3:23825290-24825290
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:THRB,rs9310736,3p24.2,Chr3:23825290-24825290
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:THRB,rs1505307,3p24.2,Chr3:23825290-24825290
99% credible set: 3 SNPs
95% credible set: 2 SNPs
Top total SNP rs1505307 Hapmap MAF: Asian=0.2444,AA=0.4,EU=0.3667
UBE2E1
NKIRAS1
RPL15
NR1D2
LOC152024
THRB
MIR4792
EB

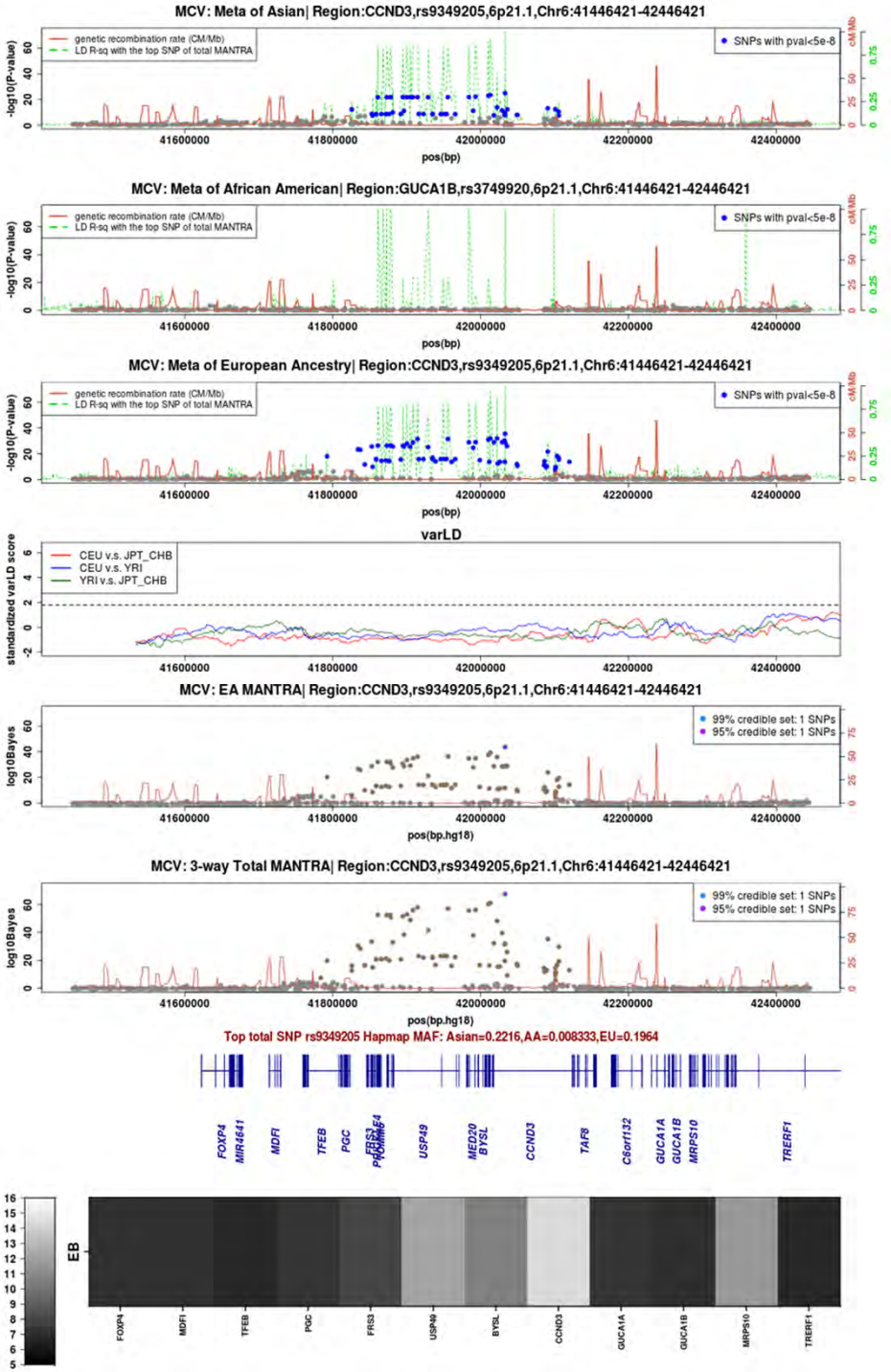

MCV: Meta of Asian| Region:ATR,rs12639363,3q23,Chr3:143273383-144273383
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
143400000
143600000
143800000
144000000
144200000
pos(bp)
MCV: Meta of African American| Region:PAQR9,rs1353887,3q23,Chr3:143273383-144273383
MCV: Meta of European Ancestry| Region:ATR,rs6780250,3q23,Chr3:143273383-144273383
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:ATR,rs6780250,3q23,Chr3:143273383-144273383
99% credible set: 37 SNPs
95% credible set: 31 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:ATR,rs6780250,3q23,Chr3:143273383-144273383
99% credible set: 36 SNPs
95% credible set: 26 SNPs
Top total SNP rs6780250 Hapmap MAF: Asian=0.4602,AA=0.01667,EU=0.4333
TFDP2
GK5
XRN1
ATR
PLS1
TRPC1
PCOLCE2
LOC100507369
PAQR9
LOC100289361
U2SURP
EB

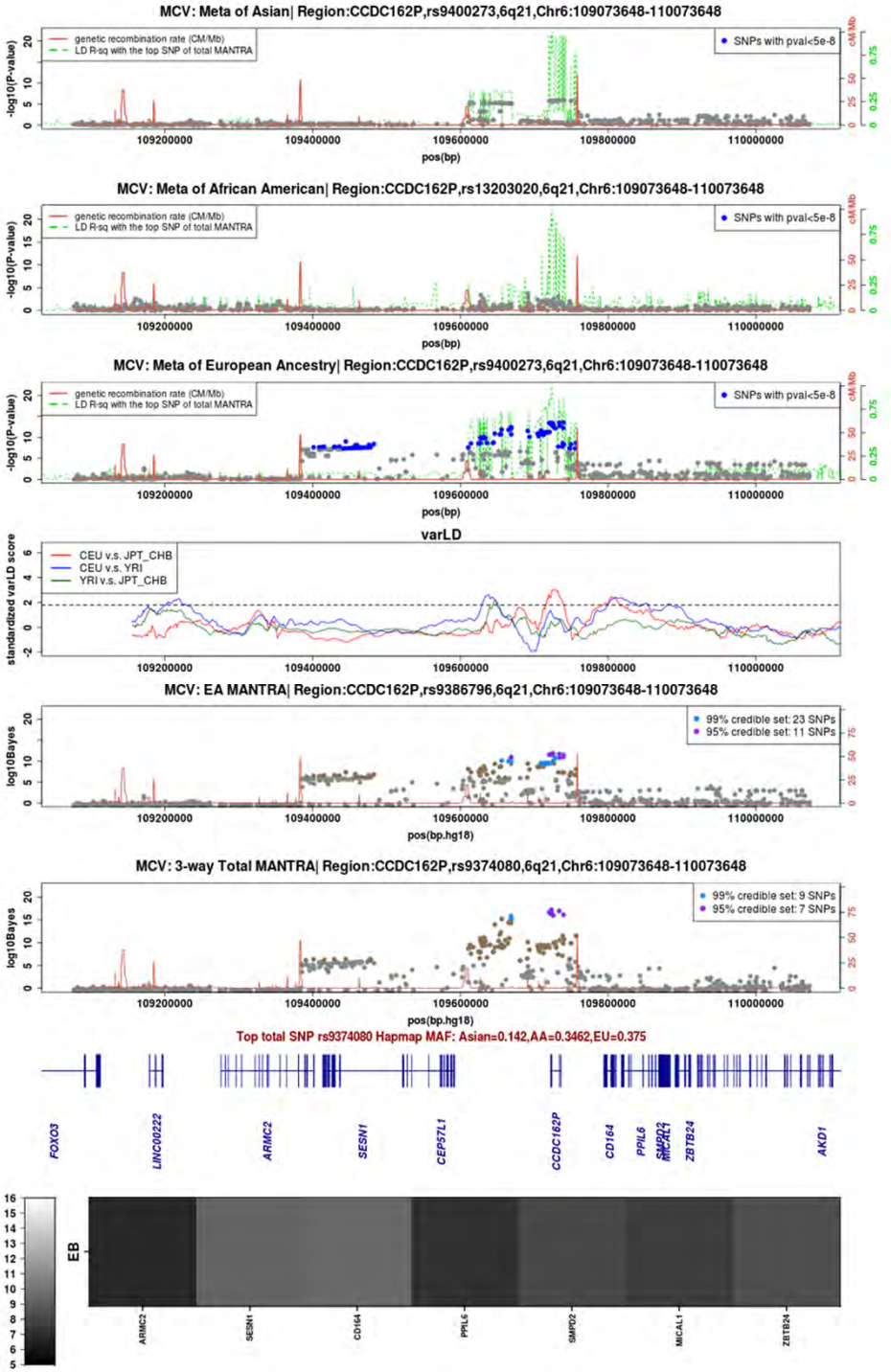

MCV: Meta of Asian| Region:ZDHHC19,rs4916491,3q29,Chr3:196769292-197769292
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:UBXN7,rs4538407,3q29,Chr3:196769292-197769292
MCV: Meta of European Ancestry| Region:TFRC,rs9859260,3q29,Chr3:196769292-197769292
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:TFRC,rs13072608,3q29,Chr3:196769292-197769292
99% credible set: 7 SNPs
95% credible set: 3 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:ZDHHC19,rs3893275,3q29,Chr3:196769292-197769292
99% credible set: 9 SNPs
95% credible set: 5 SNPs
Top total SNP rs3893275 Hapmap MAF: Asian=0.4101,AA=0,EU=0.1695
APOD
SDHAP2
MIR570
MUC20
MUC4
TNK2
SDHAP1
TFRC
LOC401109
ZDHHC19
OSTalpha
PCYT1A
TCTEX1D2
TMSF19
UBXN7
RNF168
C3orf43
WDR53
EB

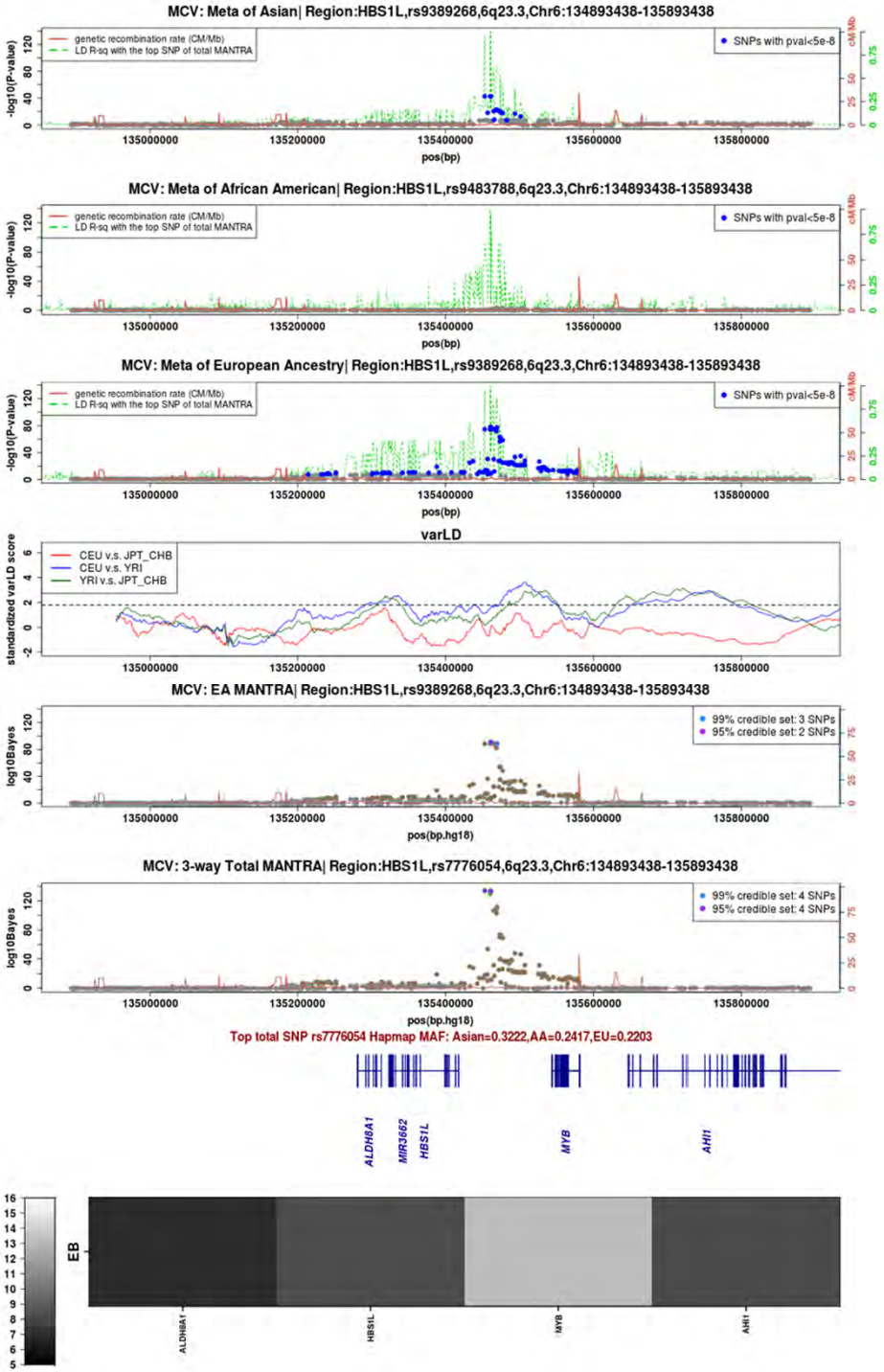

MCV: Meta of Asian| Region:KIT,rs170117,4q12,Chr4:54530983-55530983
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:KIT,rs10010776,4q12,Chr4:54530983-55530983
MCV: Meta of European Ancestry| Region:KIT,rs218262,4q12,Chr4:54530983-55530983
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:KIT,rs218259,4q12,Chr4:54530983-55530983
99% credible set: 3 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:KIT,rs218237,4q12,Chr4:54530983-55530983
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs218237 Hapmap MAF: Asian=0.3258,AA=0.2712,EU=0.1102
RPL21P44
CHIC2
GSX2
PDGFRA
KIT
EB

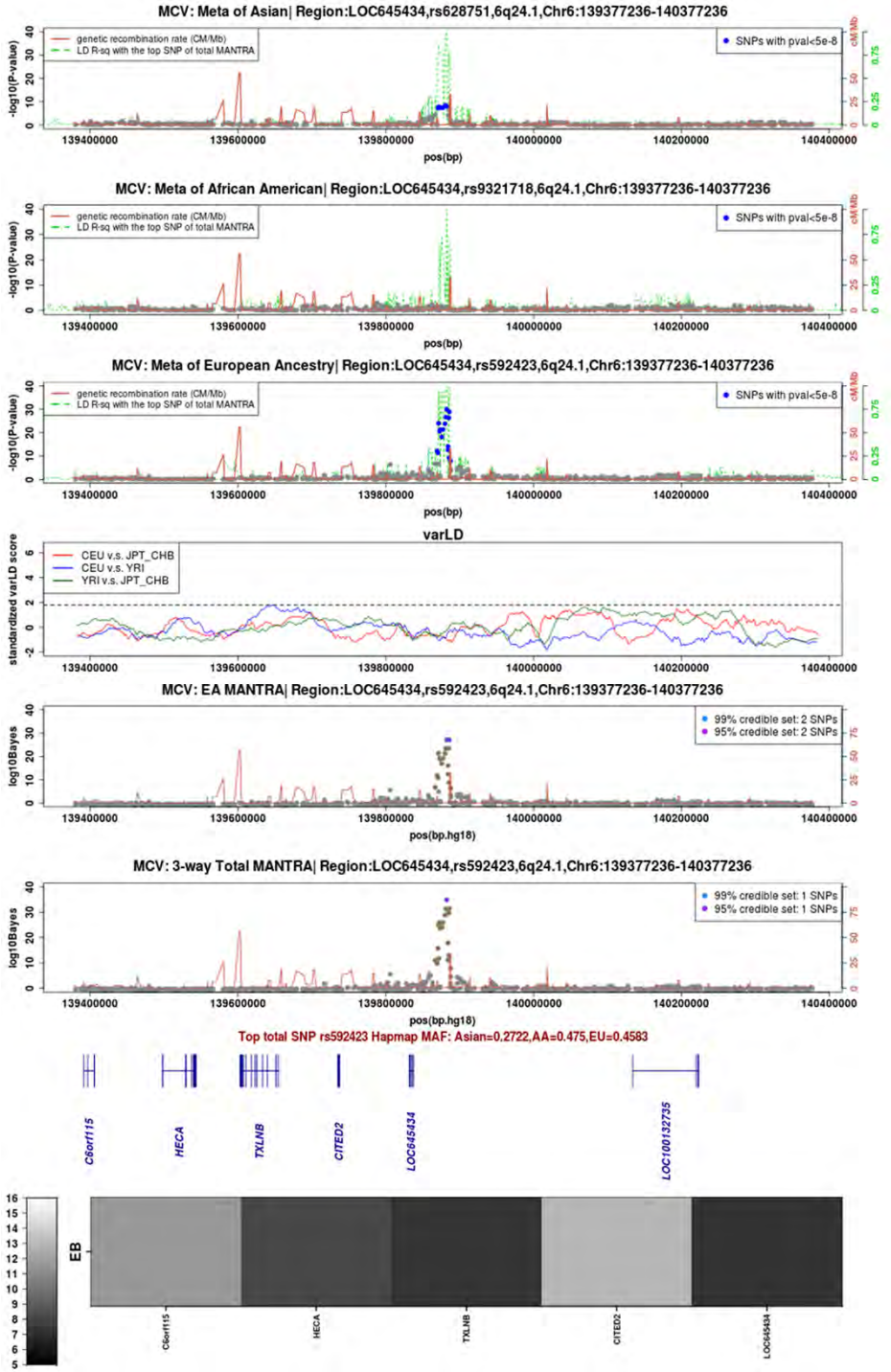

MCV: Meta of Asian| Region:TERT,rs2736100,5p15.33,Chr5:752880-1752880
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:LPCAT1,rs36993,5p15.33,Chr5:752880-1752880
MCV: Meta of European Ancestry| Region:TERT,rs2736100,5p15.33,Chr5:752880-1752880
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:TERT,rs2736100,5p15.33,Chr5:752880-1752880
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:TERT,rs2736100,5p15.33,Chr5:752880-1752880
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs2736100 Hapmap MAF: Asian=0.3889,AA=0.425,EU=0.45
ZDHHC11
BRD9
TRIP13
LOC100506688
NKD2
MIR4635
SLC12A7
SLC6A19
SLC6A18
TERT
MIR4457
CLPTM1L
SLC6A3
LPCAT1
SDHAP3
LOC728613
EB

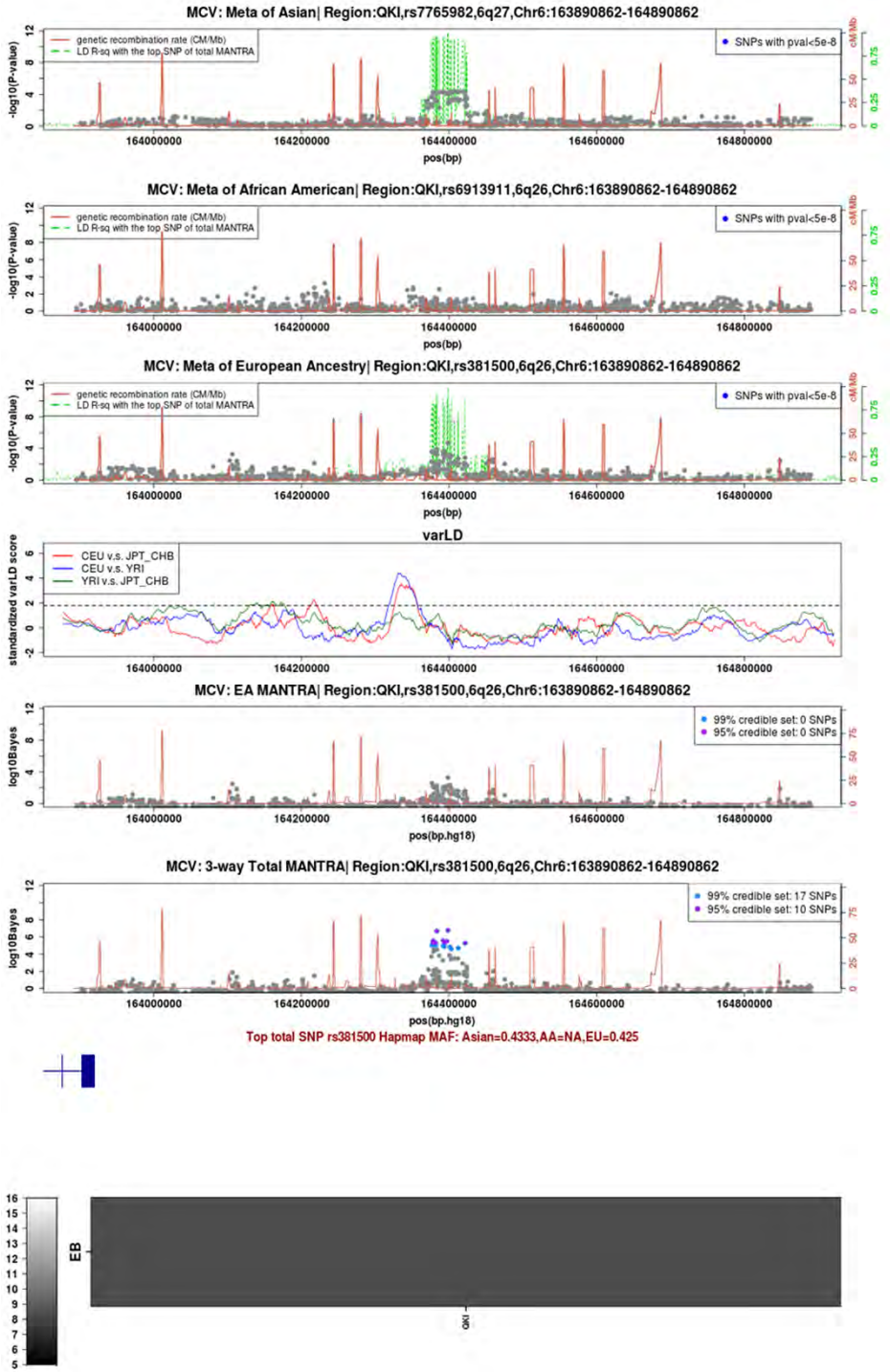

MCV: Meta of Asian| Region:HIST1H4H,rs2007370,6p22.1,Chr6:25478949-28893064
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:LOC401242,rs11969803,6p22.1,Chr6:25478949-28893064
MCV: Meta of European Ancestry| Region:HFE,rs1800562,6p22.1,Chr6:25478949-28893064
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:HIST1H1T,rs198833,6p22.1,Chr6:25478949-28893064
99% credible set: 2 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:HIST1H1T,rs198833,6p22.1,Chr6:25478949-28893064
Top total SNP rs198833 Hapmap MAF: Asian=0.03371,AA=0.1833,EU=0.1417
EB

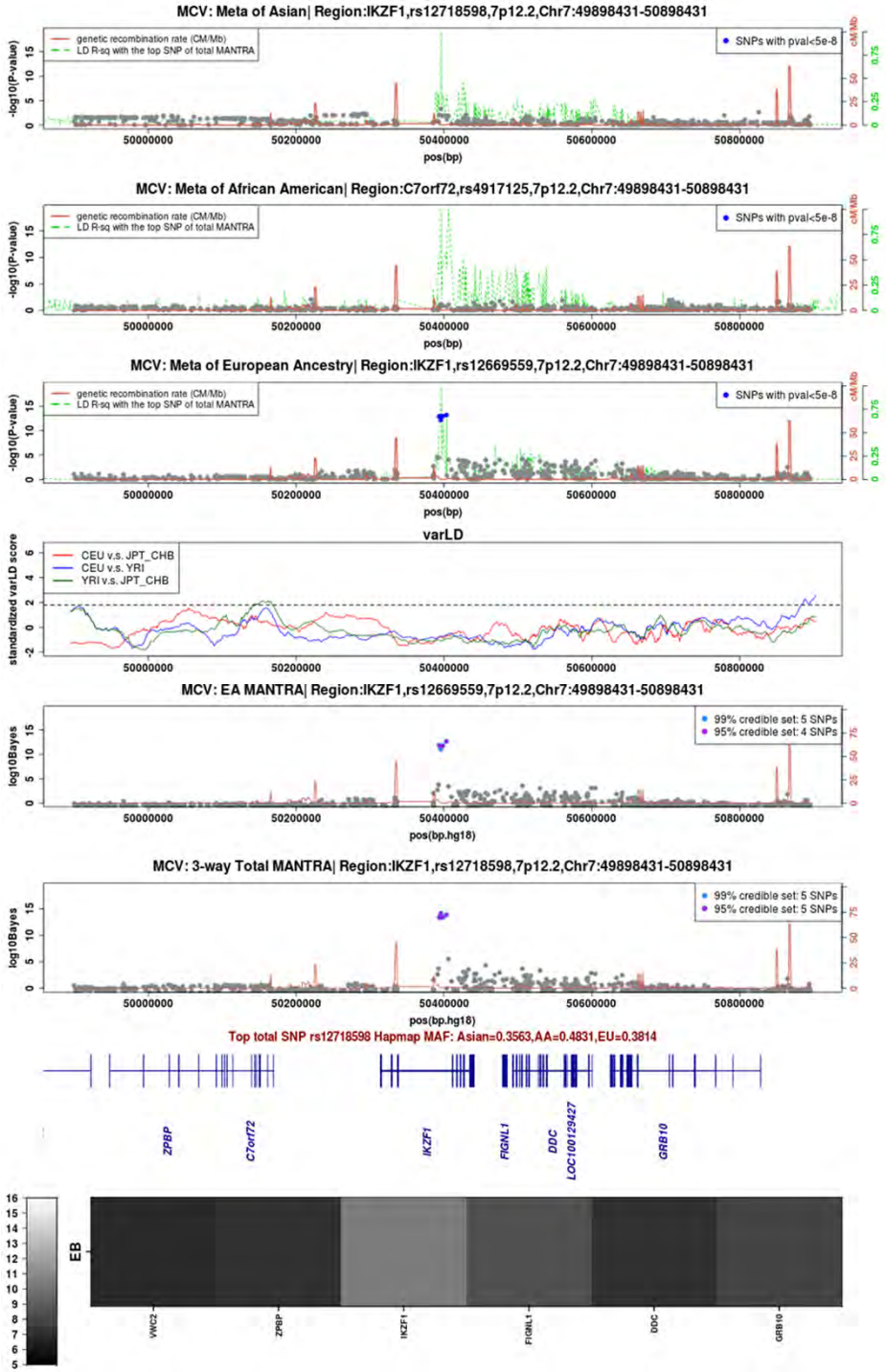

MCV: Meta of Asian| Region:CCND3,rs9349205,6p21.1,Chr6:41446421-42446421
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:GUCA1B,rs3749920,6p21.1,Chr6:41446421-42446421
MCV: Meta of European Ancestry| Region:CCND3,rs9349205,6p21.1,Chr6:41446421-42446421
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:CCND3,rs9349205,6p21.1,Chr6:41446421-42446421
99% credible set: 1 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:CCND3,rs9349205,6p21.1,Chr6:41446421-42446421
Top total SNP rs9349205 Hapmap MAF: Asian=0.2216,AA=0.008333,EU=0.1964
FOXP4
MIR4641
MDFI
TFEB
PGC
FRS3
PRDM14
USP49
MED20
BYSL
CCND3
TAF8
C6orf132
GUCA1A
GUCA1B
MRPS10
TRERF1
EB

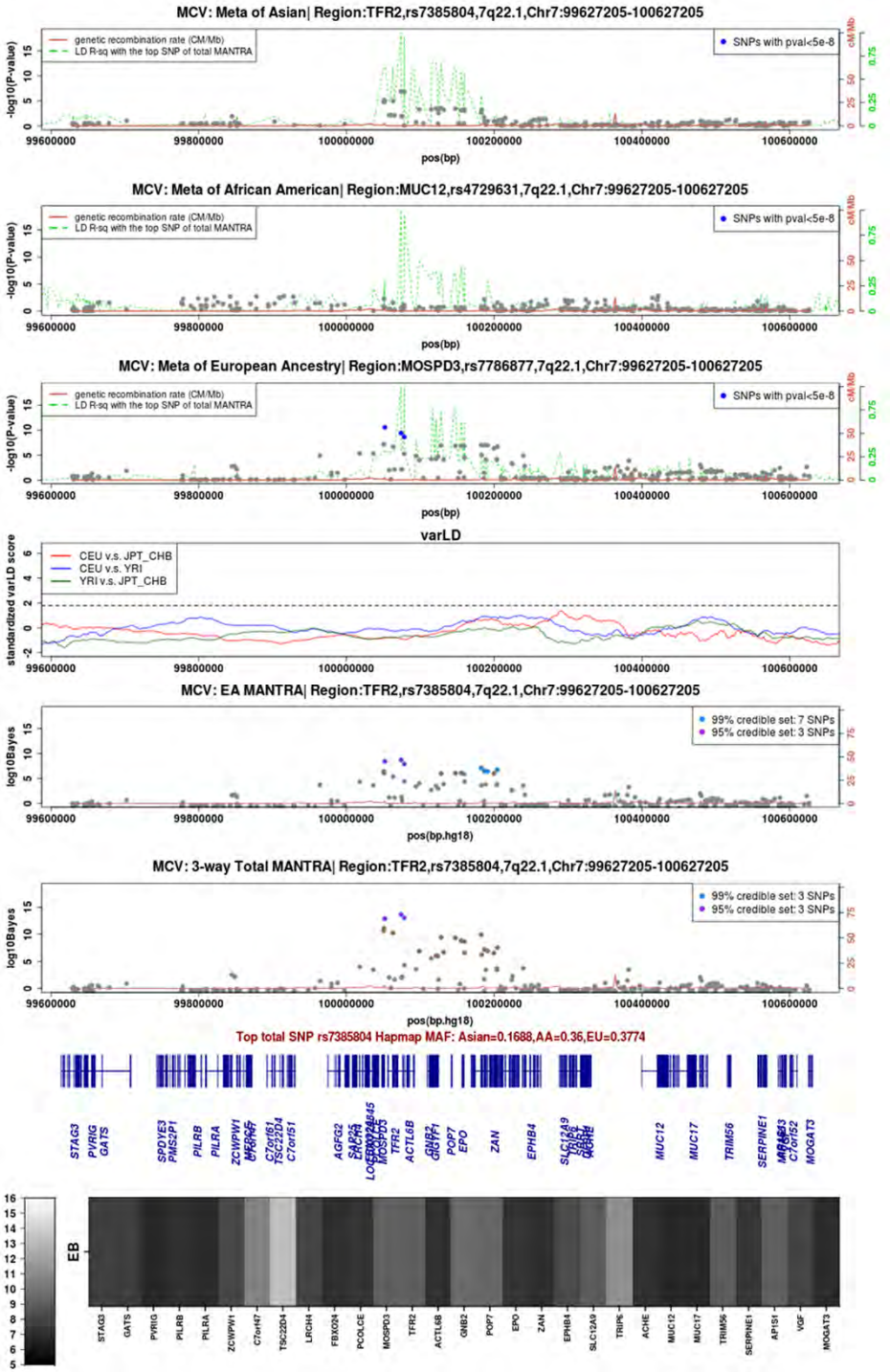

MCV: Meta of Asian| Region:CCDC162P,rs9400273,6q21,Chr6:109073648-110073648
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:CCDC162P,rs13203020,6q21,Chr6:109073648-110073648
MCV: Meta of European Ancestry| Region:CCDC162P,rs9400273,6q21,Chr6:109073648-110073648
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:CCDC162P,rs9386796,6q21,Chr6:109073648-110073648
99% credible set: 23 SNPs
95% credible set: 11 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:CCDC162P,rs9374080,6q21,Chr6:109073648-110073648
99% credible set: 9 SNPs
95% credible set: 7 SNPs
Top total SNP rs9374080 Hapmap MAF: Asian=0.142,AA=0.3462,EU=0.375
FOXO3
LINC00222
ARMC2
SESN1
CEP57L1
CCDC162P
CD164
PPIL6
SMPD2
MICAL1
ZBTB24
AKD1
EB

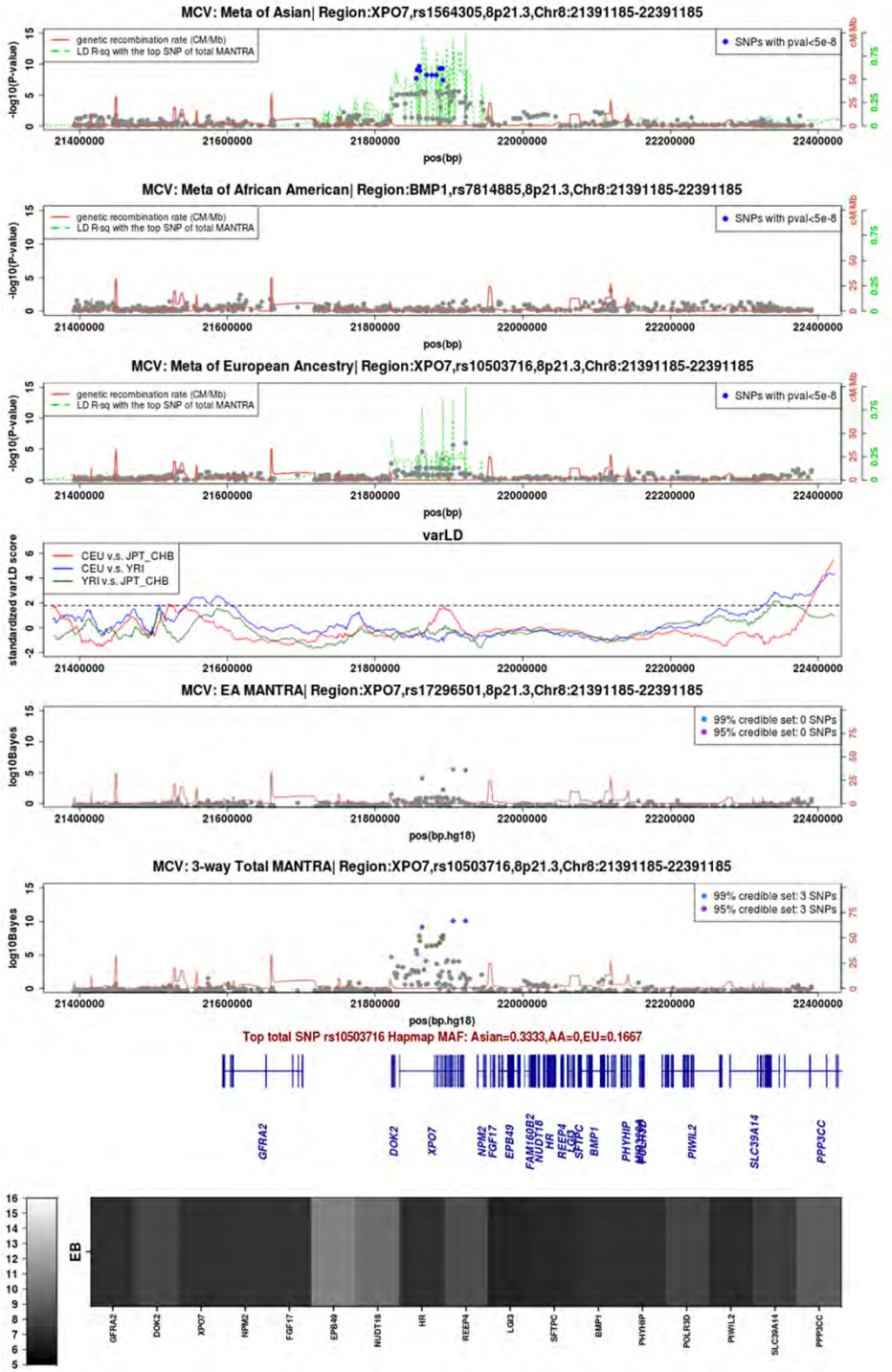

MCV: Meta of Asian| Region:HBS1L,rs9389268,6q23.3,Chr6:134893438-135893438
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:HBS1L,rs9483788,6q23.3,Chr6:134893438-135893438
MCV: Meta of European Ancestry| Region:HBS1L,rs9389268,6q23.3,Chr6:134893438-135893438
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:HBS1L,rs9389268,6q23.3,Chr6:134893438-135893438
99% credible set: 3 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:HBS1L,rs7776054,6q23.3,Chr6:134893438-135893438
99% credible set: 4 SNPs
95% credible set: 4 SNPs
Top total SNP rs7776054 Hapmap MAF: Asian=0.3222,AA=0.2417,EU=0.2203
ALDH8A1
MIR3662
HBS1L
MYB
AHI1
EB

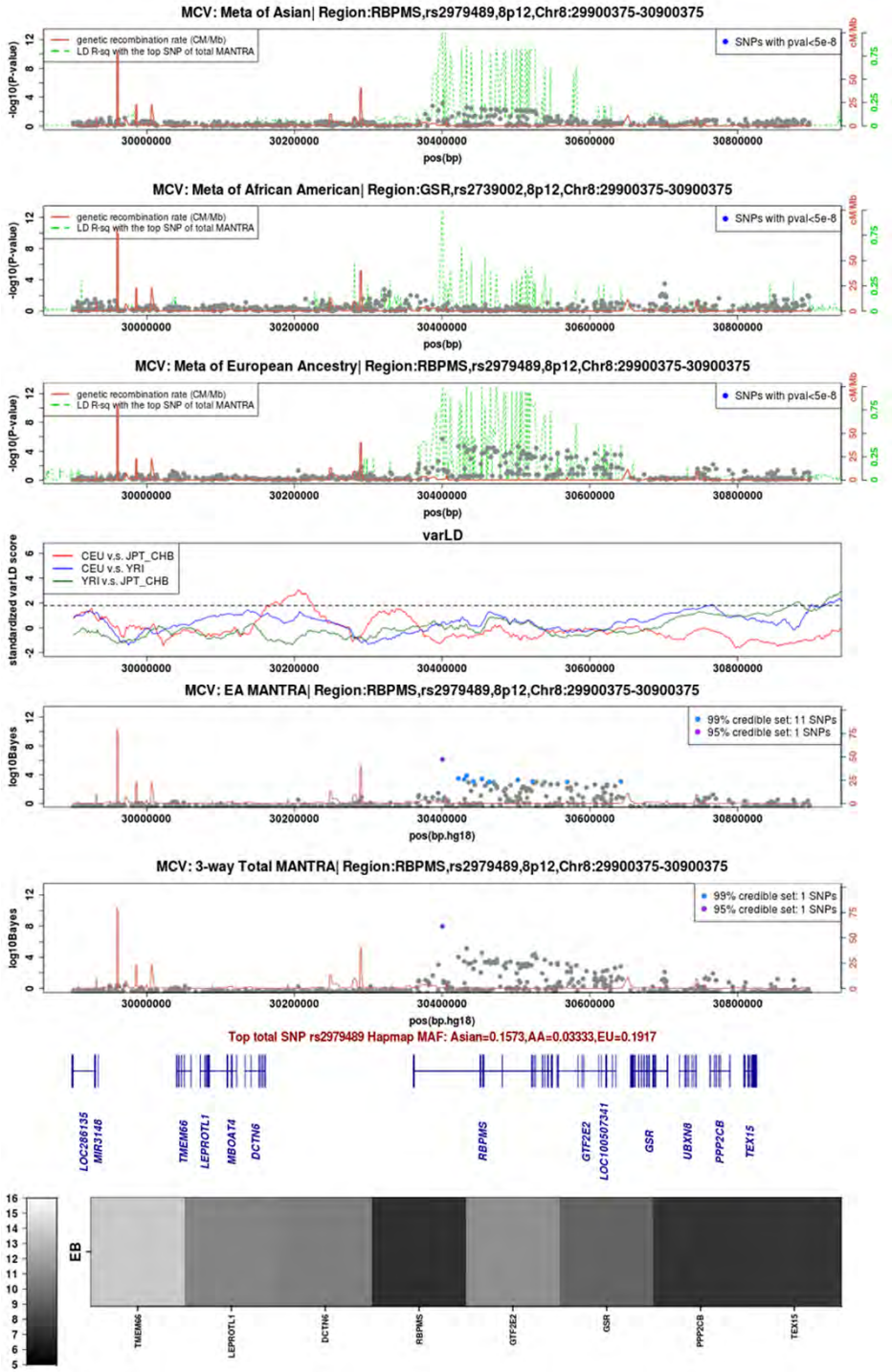

MCV: Meta of Asian| Region:LOC645434,rs628751,6q24.1,Chr6:139377236-140377236
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:LOC645434,rs9321718,6q24.1,Chr6:139377236-140377236
MCV: Meta of European Ancestry| Region:LOC645434,rs592423,6q24.1,Chr6:139377236-140377236
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:LOC645434,rs592423,6q24.1,Chr6:139377236-140377236
99% credible set: 2 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:LOC645434,rs592423,6q24.1,Chr6:139377236-140377236
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs592423 Hapmap MAF: Asian=0.2722,AA=0.475,EU=0.4583
C6orf115
HECA
TXLNB
CITED2
LOC645434
LOC100132735
EB

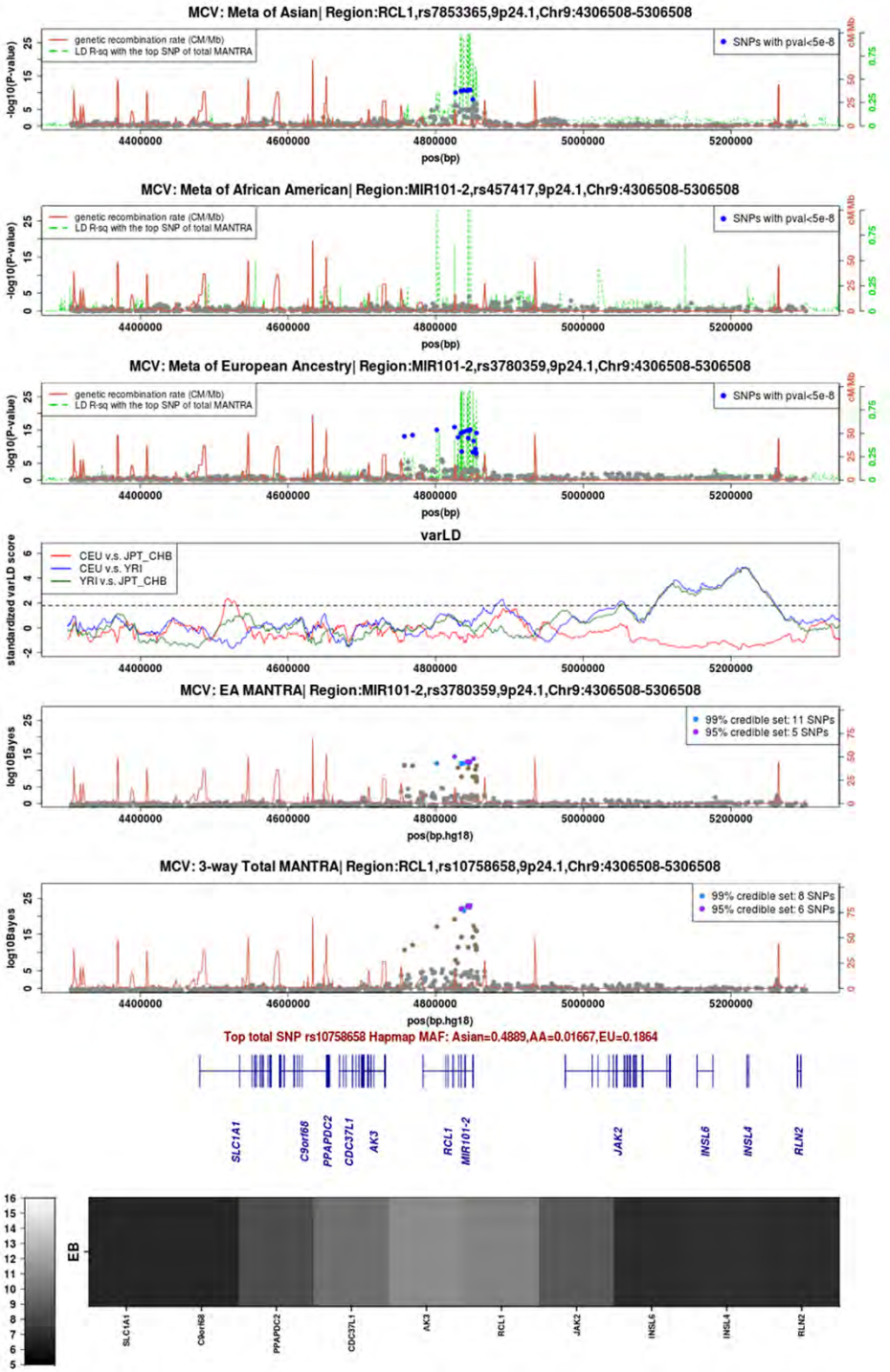

MCV: Meta of Asian| Region:QKI,rs7765982,6q27,Chr6:163890862-164890862
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:QKI,rs6913911,6q26,Chr6:163890862-164890862
MCV: Meta of European Ancestry| Region:QKI,rs381500,6q26,Chr6:163890862-164890862
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:QKI,rs381500,6q26,Chr6:163890862-164890862
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:QKI,rs381500,6q26,Chr6:163890862-164890862
99% credible set: 17 SNPs
95% credible set: 10 SNPs
Top total SNP rs381500 Hapmap MAF: Asian=0.4333,AA=NA,EU=0.425
EB
QKI

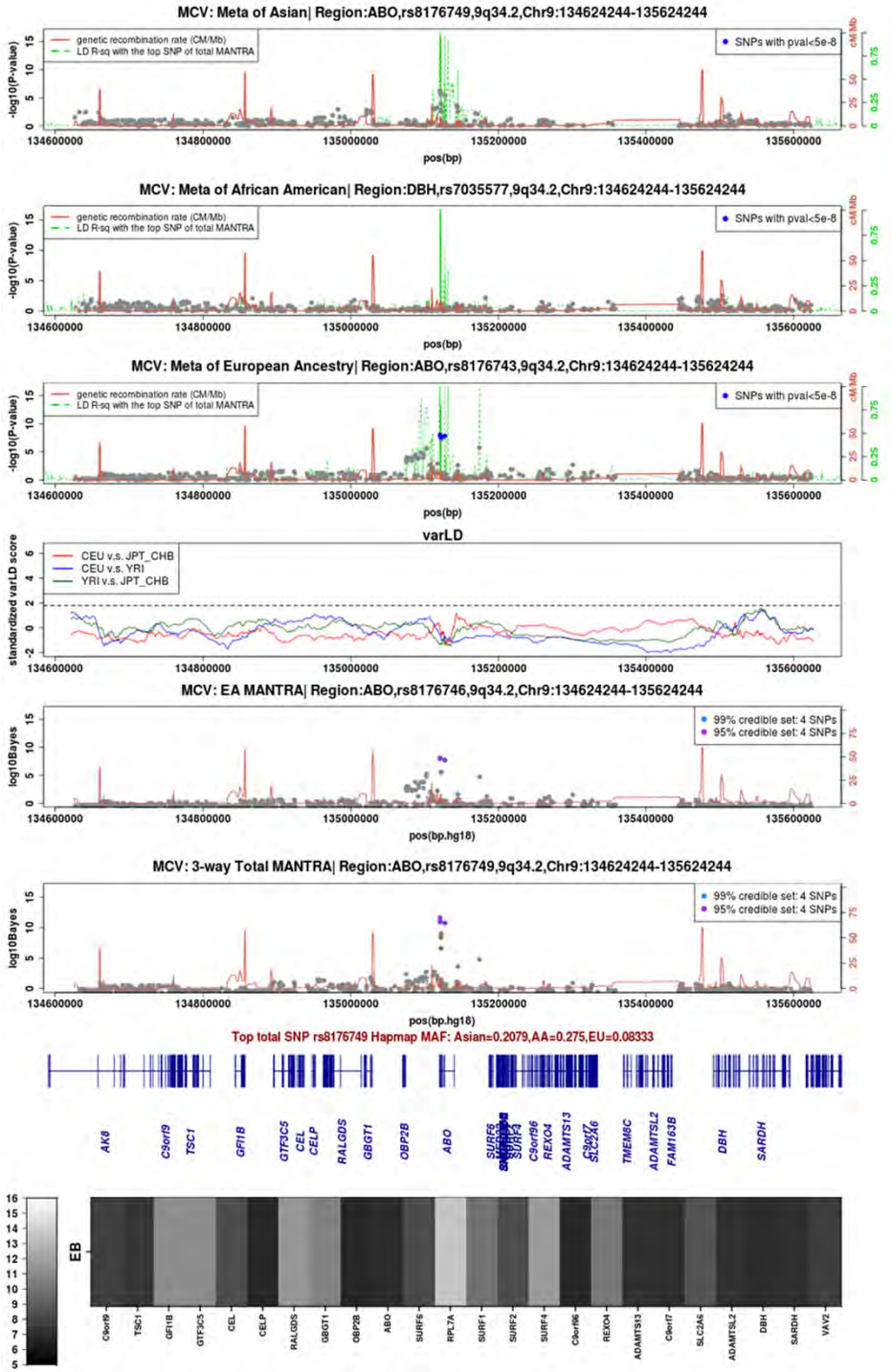

MCV: Meta of Asian| Region:IKZF1,rs12718598,7p12.2,Chr7:49898431-50898431
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:C7orf72,rs4917125,7p12.2,Chr7:49898431-50898431
MCV: Meta of European Ancestry| Region:IKZF1,rs12669559,7p12.2,Chr7:49898431-50898431
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:IKZF1,rs12669559,7p12.2,Chr7:49898431-50898431
99% credible set: 5 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:IKZF1,rs12718598,7p12.2,Chr7:49898431-50898431
99% credible set: 5 SNPs
95% credible set: 5 SNPs
Top total SNP rs12718598 Hapmap MAF: Asian=0.3563,AA=0.4831,EU=0.3814
ZPBP
C7orf72
IKZF1
FIGNL1
DDC
LOC100129427
GRB10
EB
VWC2
ZPBP
IKZF1
FIGNL1
DDC
GRB10

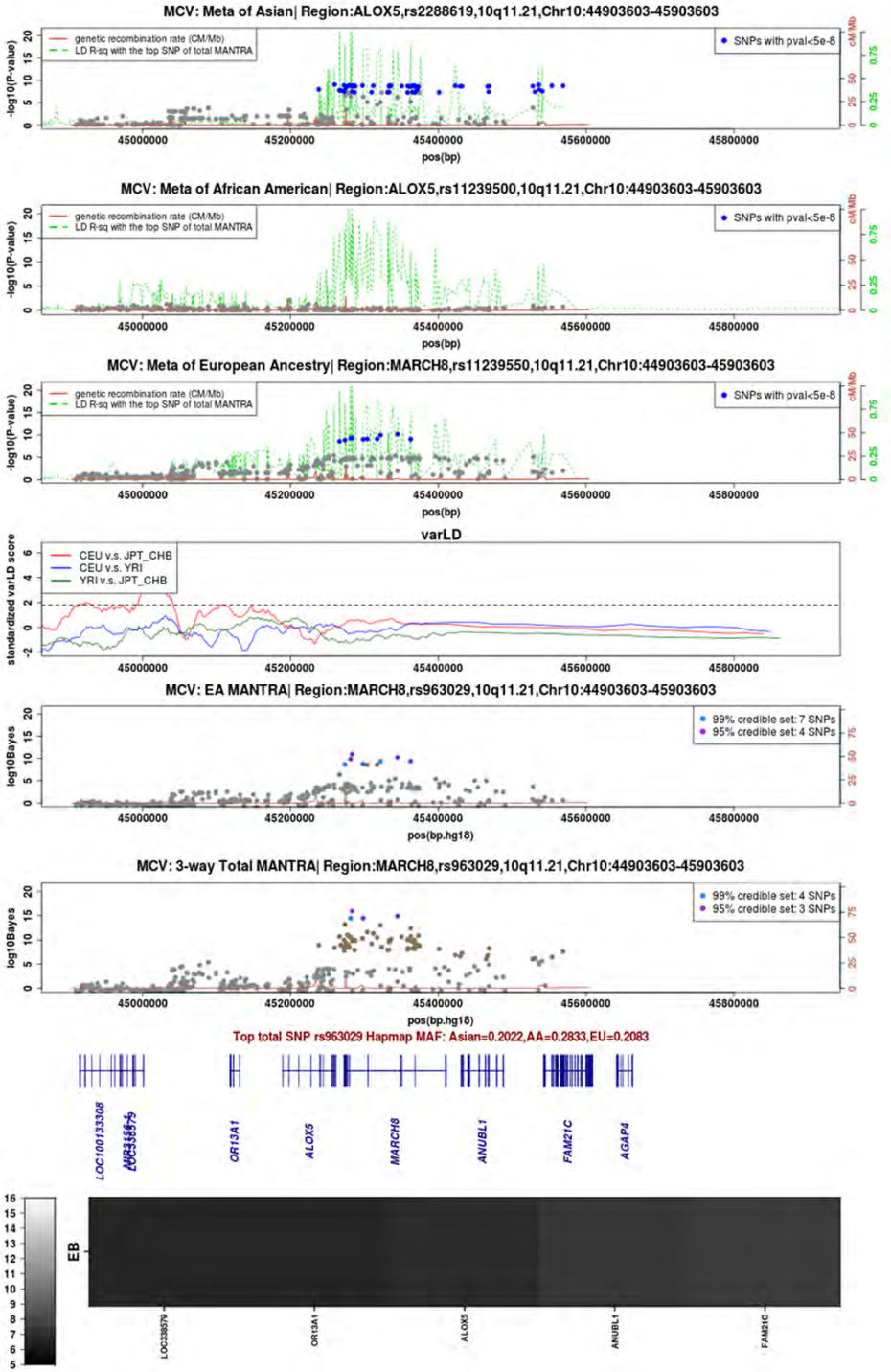

MCV: Meta of Asian| Region:TFR2,rs7385804,7q22.1,Chr7:99627205-100627205
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:MUC12,rs4729631,7q22.1,Chr7:99627205-100627205
MCV: Meta of European Ancestry| Region:MOSPD3,rs7786877,7q22.1,Chr7:99627205-100627205
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:TFR2,rs7385804,7q22.1,Chr7:99627205-100627205
99% credible set: 7 SNPs
95% credible set: 3 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:TFR2,rs7385804,7q22.1,Chr7:99627205-100627205
Top total SNP rs7385804 Hapmap MAF: Asian=0.1688,AA=0.36,EU=0.3774
STAG3
PVRIG
GATS
SPDYE3
PMS2P1
PILRB
PILRA
ZCWPW1
C7orf47
TSC22D4
C7orf51
AGFG2
FBXO24
PCOLCE
MOSPD3
TFR2
ACTL6B
GNB2
POP7
EPO
ZAN
EPHB4
MUC12
MUC17
TRIM56
SERPINE1
C7orf52
MOGAT3
EB

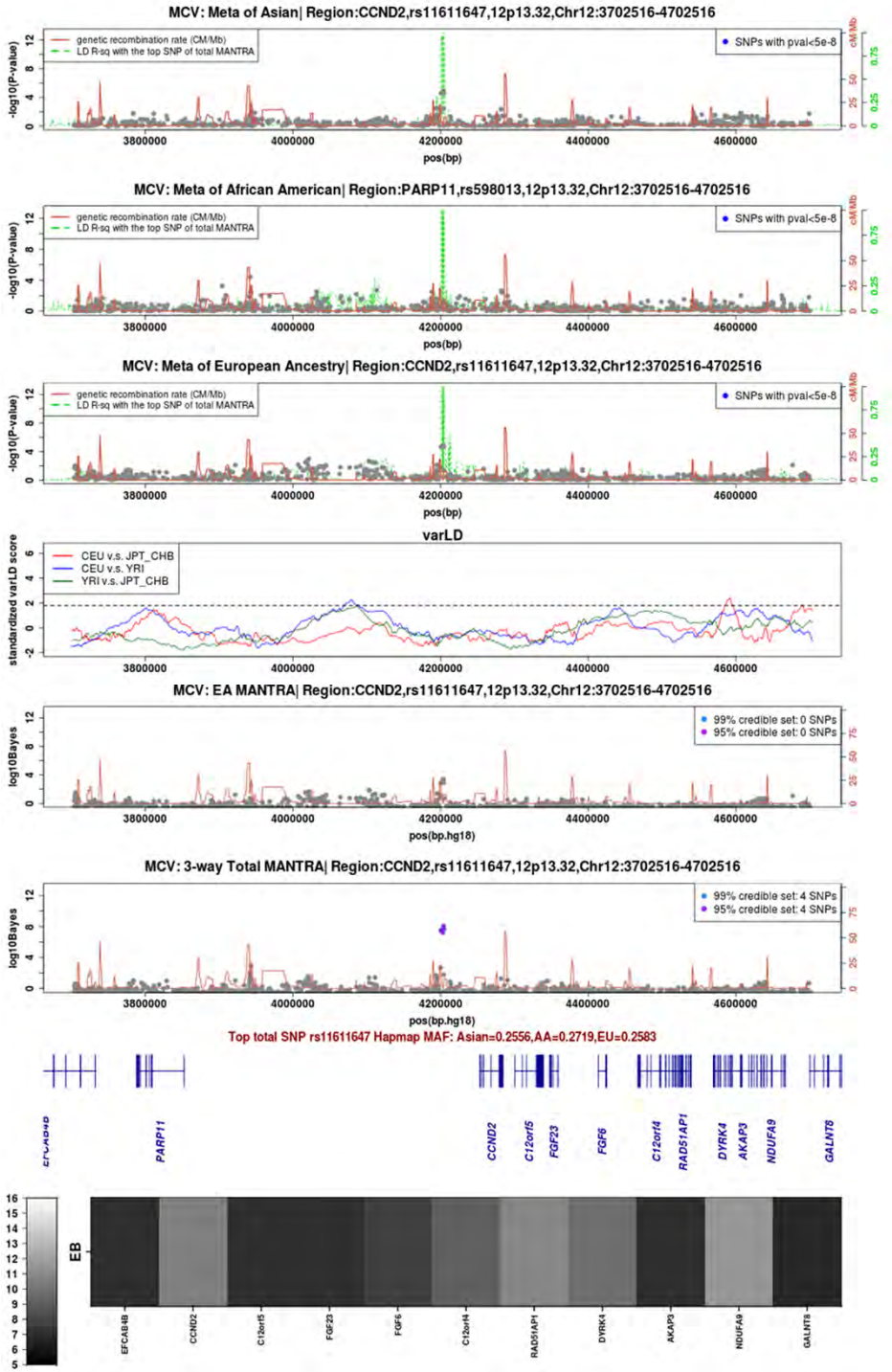

MCV: Meta of Asian| Region:XPO7,rs1564305,8p21.3,Chr8:21391185-22391185
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:BMP1,rs7814885,8p21.3,Chr8:21391185-22391185
MCV: Meta of European Ancestry| Region:XPO7,rs10503716,8p21.3,Chr8:21391185-22391185
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:XPO7,rs17296501,8p21.3,Chr8:21391185-22391185
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:XPO7,rs10503716,8p21.3,Chr8:21391185-22391185
99% credible set: 3 SNPs
95% credible set: 3 SNPs
Top total SNP rs10503716 Hapmap MAF: Asian=0.3333,AA=0,EU=0.1667
GFRA2
DOK2
XPO7
NPM2
FGF17
EPB49
FAM160B2
NUDT18
HR
REEP4
LG93
SFTPC
BMP1
PHYHIP
MGC33926
PIWIL2
SLC39A14
PPP3CC
EB
POLR3D

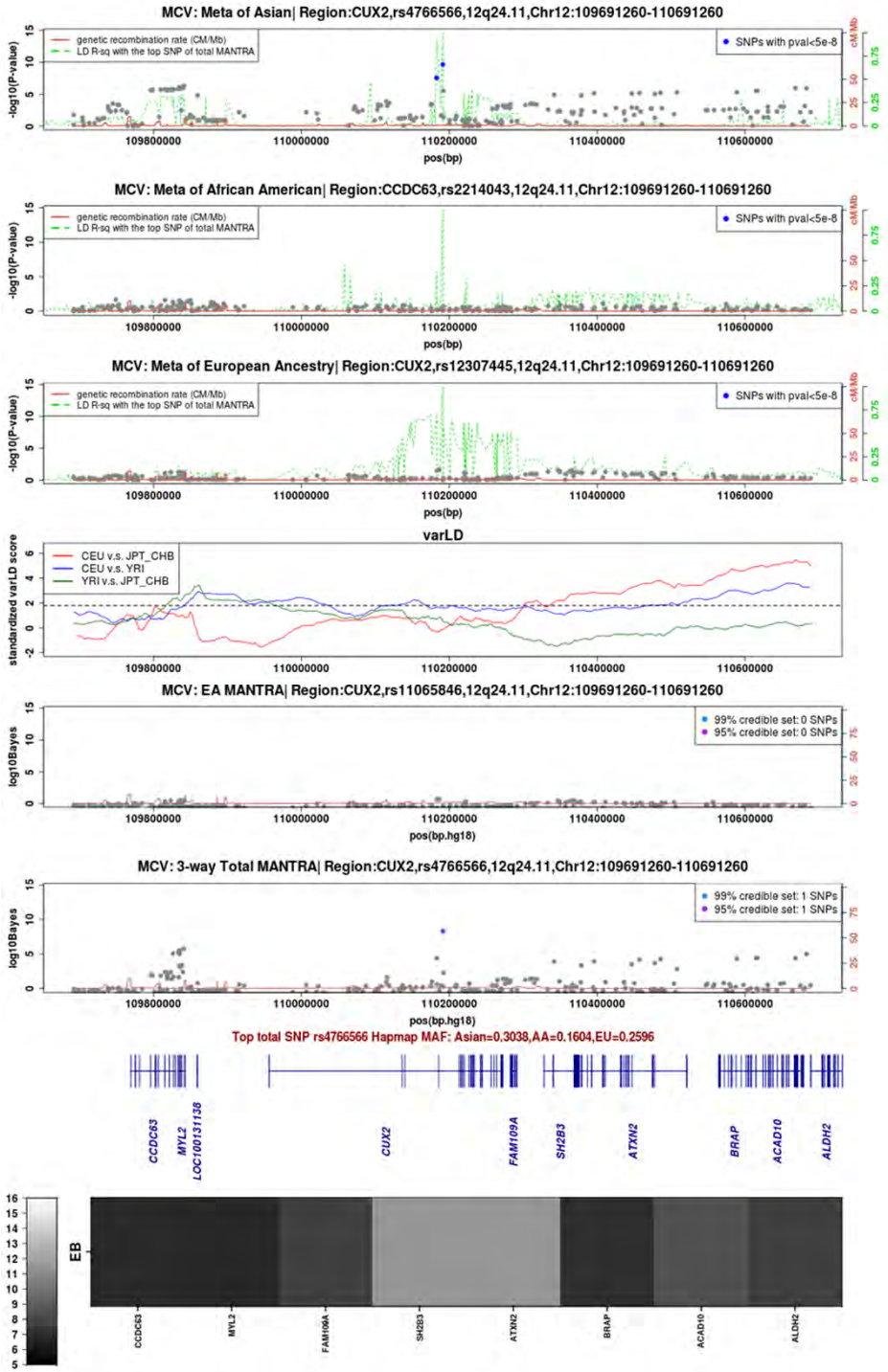

MCV: Meta of Asian| Region:RBPMS,rs2979489,8p12,Chr8:29900375-30900375
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:GSR,rs2739002,8p12,Chr8:29900375-30900375
MCV: Meta of European Ancestry| Region:RBPMS,rs2979489,8p12,Chr8:29900375-30900375
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:RBPMS,rs2979489,8p12,Chr8:29900375-30900375
99% credible set: 11 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:RBPMS,rs2979489,8p12,Chr8:29900375-30900375
Top total SNP rs2979489 Hapmap MAF: Asian=0.1573,AA=0.03333,EU=0.1917
LOC286135
MIR3148
TMEM66
LEPROTL1
MBOAT4
DCTN6
RBPMS
GTF2E2
LOC100507341
GSR
UBXN8
PPP2CB
TEX15
EB

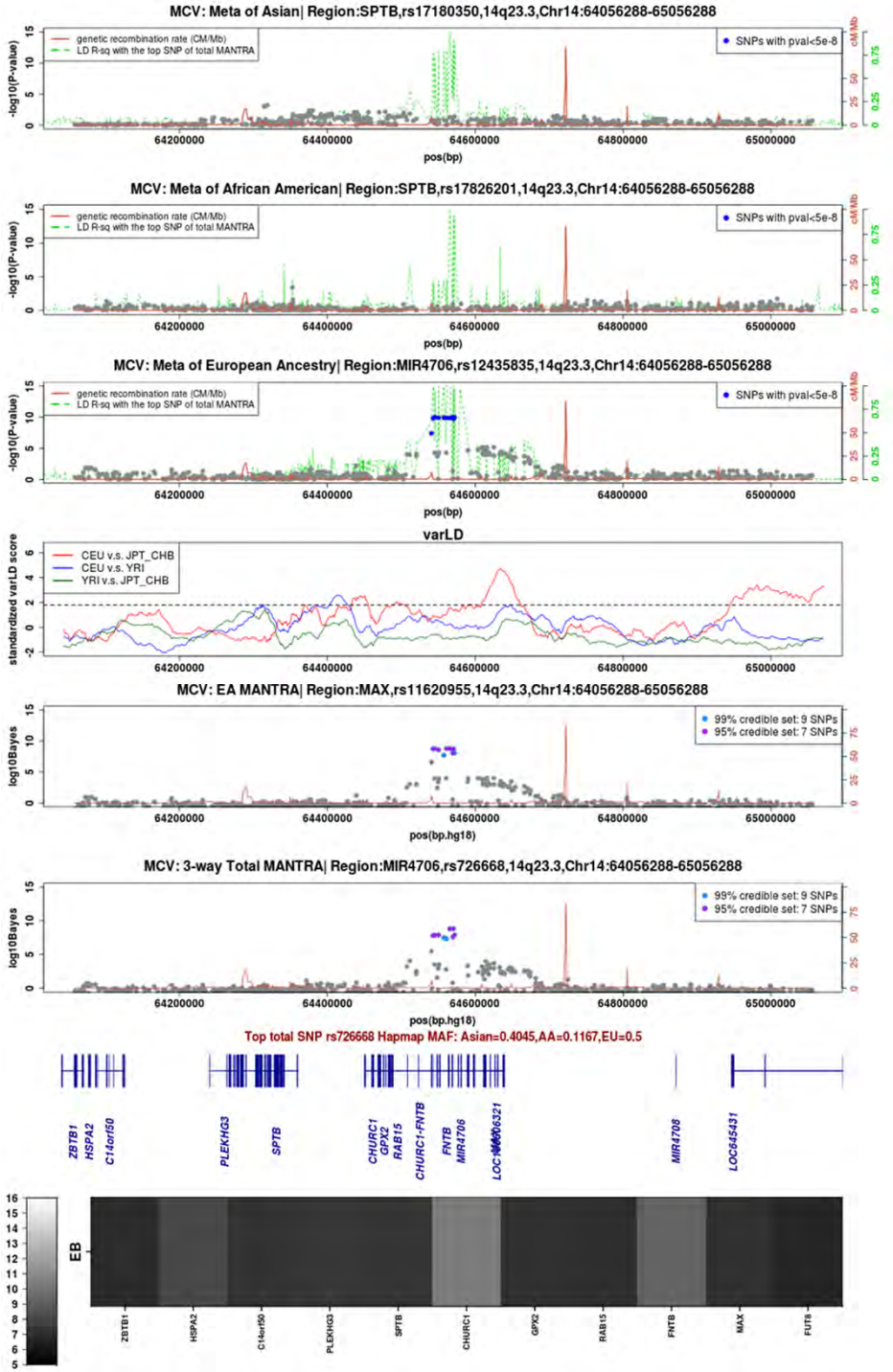

MCV: Meta of Asian| Region:RCL1,rs7853365,9p24.1,Chr9:4306508-5306508
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:MIR101-2,rs457417,9p24.1,Chr9:4306508-5306508
MCV: Meta of European Ancestry| Region:MIR101-2,rs3780359,9p24.1,Chr9:4306508-5306508
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:MIR101-2,rs3780359,9p24.1,Chr9:4306508-5306508
99% credible set: 11 SNPs
95% credible set: 5 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:RCL1,rs10758658,9p24.1,Chr9:4306508-5306508
99% credible set: 8 SNPs
95% credible set: 6 SNPs
Top total SNP rs10758658 Hapmap MAF: Asian=0.4889,AA=0.01667,EU=0.1864
SLC1A1
C9orf68
PPAPDC2
CDC37L1
AK3
RCL1
MIR101-2
JAK2
INSL6
INSL4
RLN2
EB

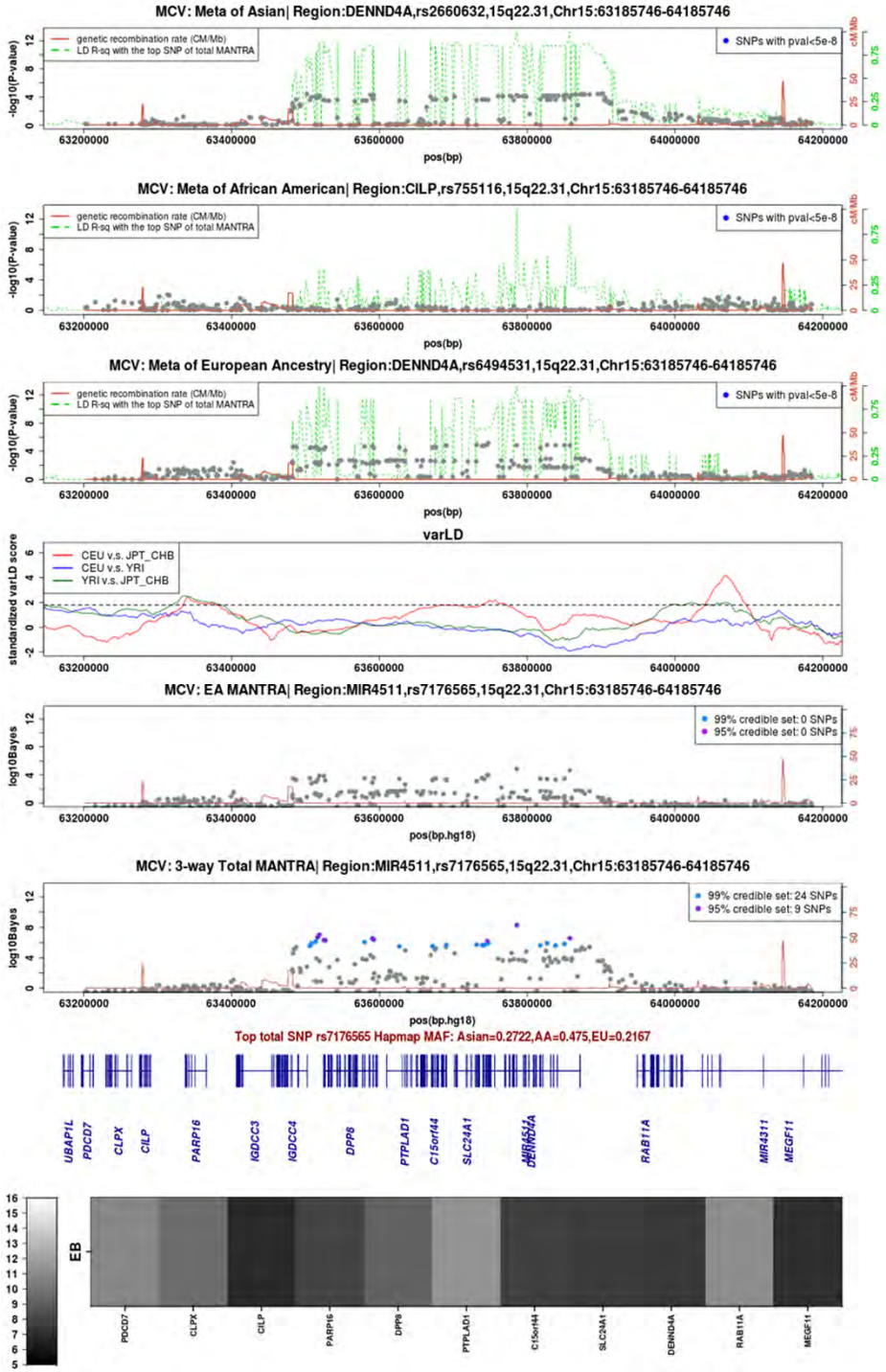

MCV: Meta of Asian| Region:ABO,rs8176749,9q34.2,Chr9:134624244-135624244
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:DBH,rs7035577,9q34.2,Chr9:134624244-135624244
MCV: Meta of European Ancestry| Region:ABO,rs8176743,9q34.2,Chr9:134624244-135624244
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:ABO,rs8176746,9q34.2,Chr9:134624244-135624244
99% credible set: 4 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:ABO,rs8176749,9q34.2,Chr9:134624244-135624244
Top total SNP rs8176749 Hapmap MAF: Asian=0.2079,AA=0.275,EU=0.08333
AK8
C9orf9
TSC1
GFI1B
GTF3C5
CEL
CELP
RALGDS
GBGT1
OBP2B
ABO
SURF6
SURF1
SURF2
SURF4
C9orf96
REXO4
ADAMTS13
C9orf7
SLC2A6
TMEM8C
ADAMTSL2
FAM163B
DBH
SARDH
EB
RPL7A
VAV2

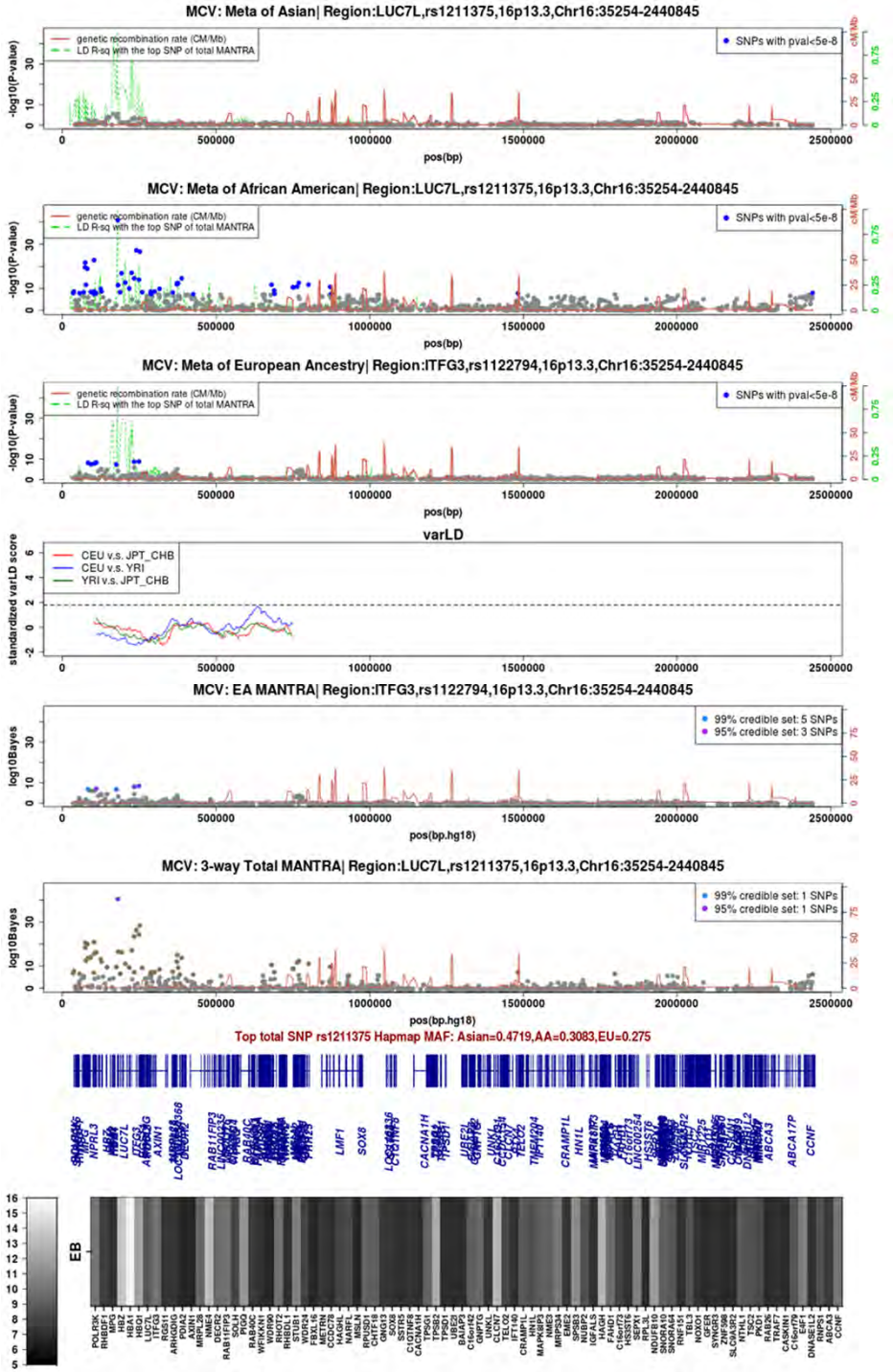

MCV: Meta of Asian| Region:ALOX5,rs2288619,10q11.21,Chr10:44903603-45903603
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:ALOX5,rs11239500,10q11.21,Chr10:44903603-45903603
MCV: Meta of European Ancestry| Region:MARCH8,rs11239550,10q11.21,Chr10:44903603-45903603
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:MARCH8,rs963029,10q11.21,Chr10:44903603-45903603
99% credible set: 7 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:MARCH8,rs963029,10q11.21,Chr10:44903603-45903603
99% credible set: 4 SNPs
95% credible set: 3 SNPs
Top total SNP rs963029 Hapmap MAF: Asian=0.2022,AA=0.2833,EU=0.2083
LOC100133308
OR13A1
ALOX5
MARCH8
ANUBL1
FAM21C
AGAP4
EB
LOC338579

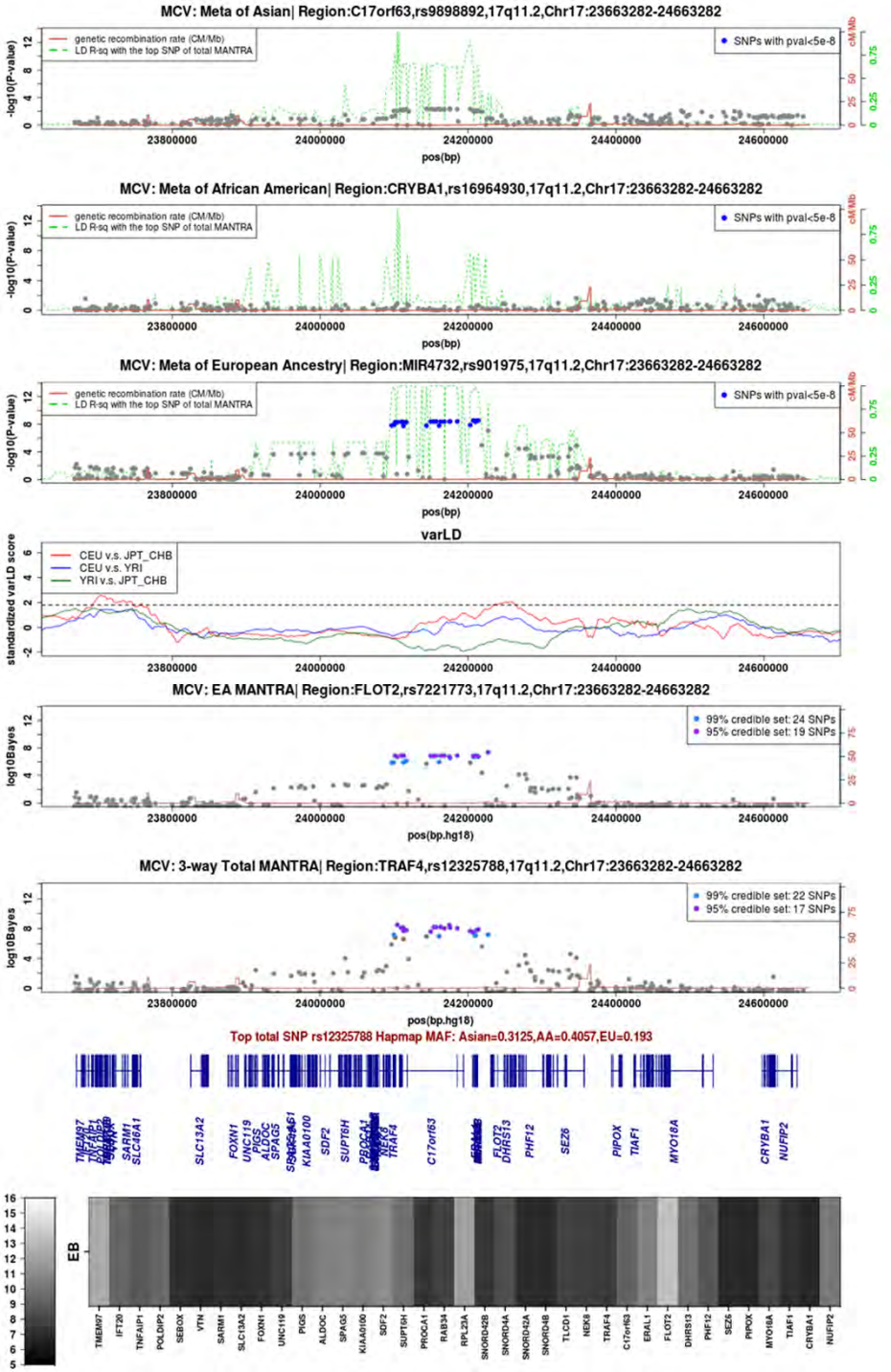

MCV: Meta of Asian| Region:CCND2,rs11611647,12p13.32,Chr12:3702516-4702516
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:PARP11,rs598013,12p13.32,Chr12:3702516-4702516
MCV: Meta of European Ancestry| Region:CCND2,rs11611647,12p13.32,Chr12:3702516-4702516
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:CCND2,rs11611647,12p13.32,Chr12:3702516-4702516
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:CCND2,rs11611647,12p13.32,Chr12:3702516-4702516
99% credible set: 4 SNPs
95% credible set: 4 SNPs
Top total SNP rs11611647 Hapmap MAF: Asian=0.2556,AA=0.2719,EU=0.2583
PARP11
CCND2
C12orf5
FGF23
FGF6
C12orf4
RAD51AP1
DYRK4
AKAP3
NDUFA9
GALNT8
EB

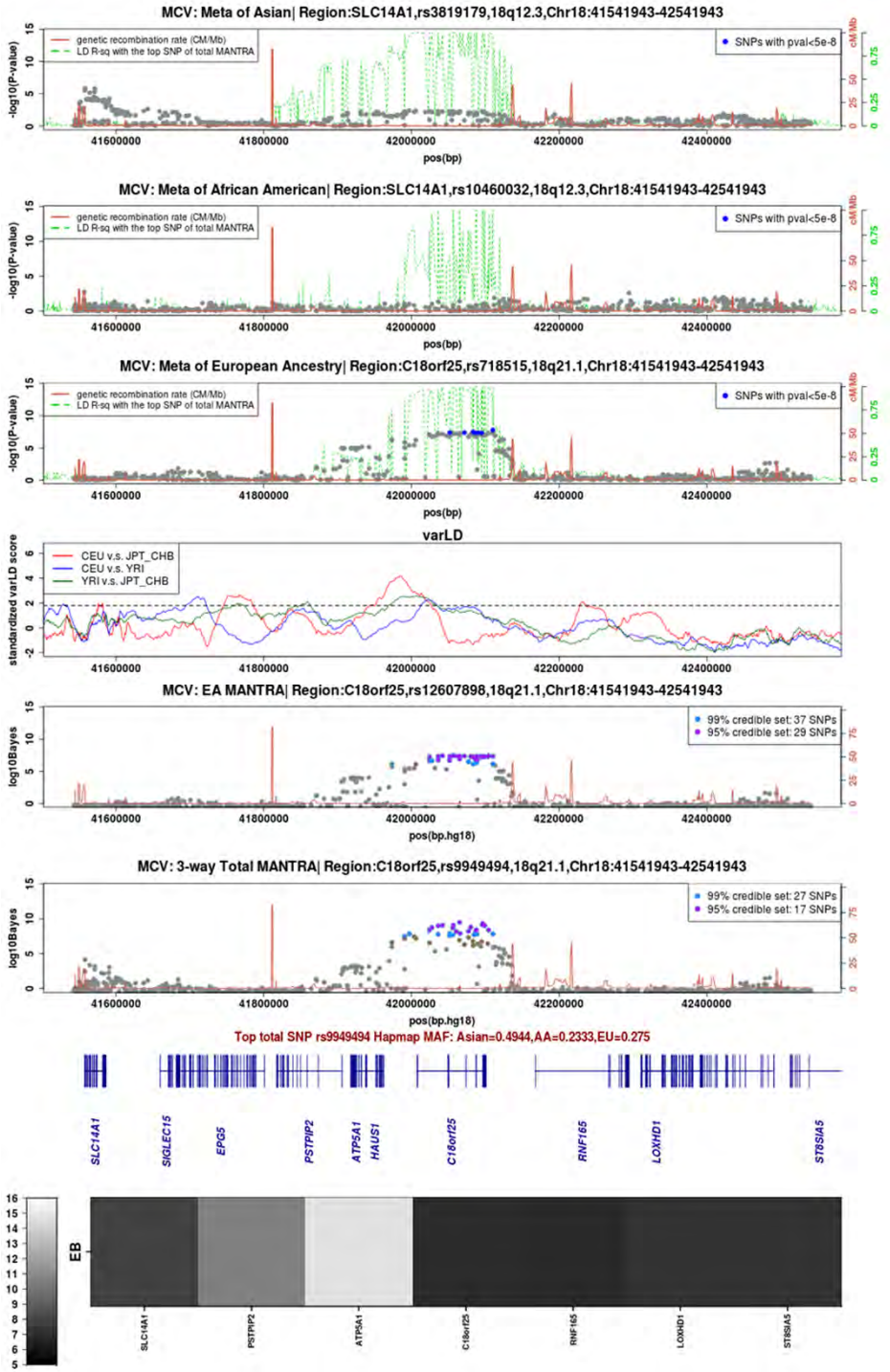

MCV: Meta of Asian| Region:CUX2,rs4766566,12q24.11,Chr12:109691260-110691260
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:CCDC63,rs2214043,12q24.11,Chr12:109691260-110691260
MCV: Meta of European Ancestry| Region:CUX2,rs12307445,12q24.11,Chr12:109691260-110691260
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:CUX2,rs11065846,12q24.11,Chr12:109691260-110691260
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:CUX2,rs4766566,12q24.11,Chr12:109691260-110691260
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs4766566 Hapmap MAF: Asian=0.3038,AA=0.1604,EU=0.2596
CCDC63
MYL2
LOC100131138
CUX2
FAM109A
SH2B3
ATXN2
BRAP
ACAD10
ALDH2
EB

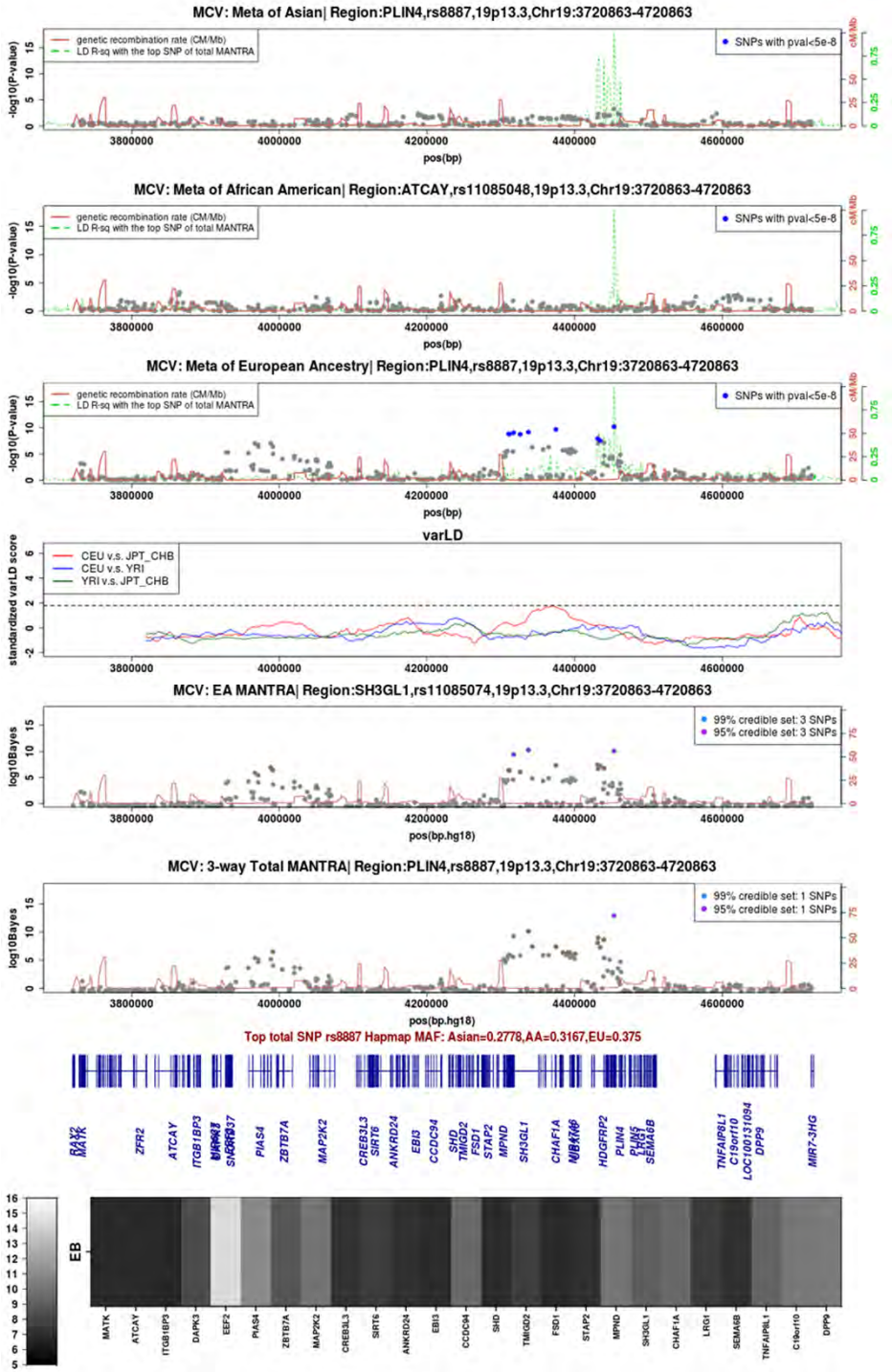

MCV: Meta of Asian| Region:SPTB,rs17180350,14q23.3,Chr14:64056288-65056288
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:SPTB,rs17826201,14q23.3,Chr14:64056288-65056288
MCV: Meta of European Ancestry| Region:MIR4706,rs12435835,14q23.3,Chr14:64056288-65056288
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:MAX,rs11620955,14q23.3,Chr14:64056288-65056288
99% credible set: 9 SNPs
95% credible set: 7 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:MIR4706,rs726668,14q23.3,Chr14:64056288-65056288
Top total SNP rs726668 Hapmap MAF: Asian=0.4045,AA=0.1167,EU=0.5
ZBTB1
HSPA2
C14orf50
PLEKHG3
SPTB
CHURC1
GPX2
RAB15
CHURC1-FNTB
FNTB
MIR4706
MIR4708
LOC645431
EB
ZBTB1
HSPA2
C14orf50
PLEKHG3
SPTB
CHURC1
GPX2
RAB15
FNTB
MAX
FUT8

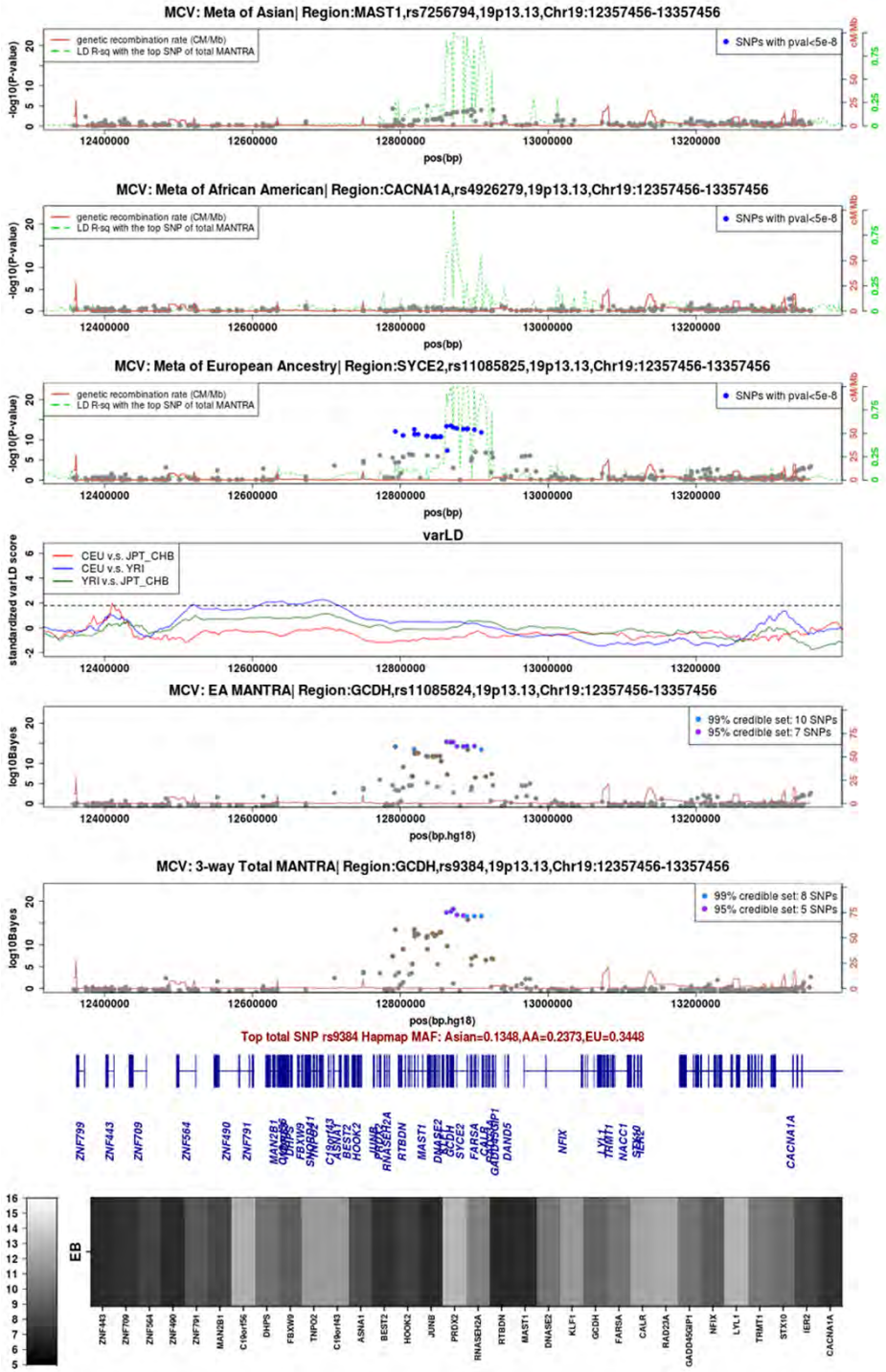

MCV: Meta of Asian| Region:DENND4A,rs2660632,15q22.31,Chr15:63185746-64185746
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:CILP,rs755116,15q22.31,Chr15:63185746-64185746
MCV: Meta of European Ancestry| Region:DENND4A,rs6494531,15q22.31,Chr15:63185746-64185746
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:MIR4511,rs7176565,15q22.31,Chr15:63185746-64185746
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:MIR4511,rs7176565,15q22.31,Chr15:63185746-64185746
99% credible set: 24 SNPs
95% credible set: 9 SNPs
Top total SNP rs7176565 Hapmap MAF: Asian=0.2722,AA=0.475,EU=0.2167
UBAP1L
PDCD7
CLPX
CILP
PARP16
IQDCC3
IQDCC4
DPP8
PTPLAD1
C15orf44
SLC24A1
DENND4A
RAB11A
MIR4311
MEGF11
EB

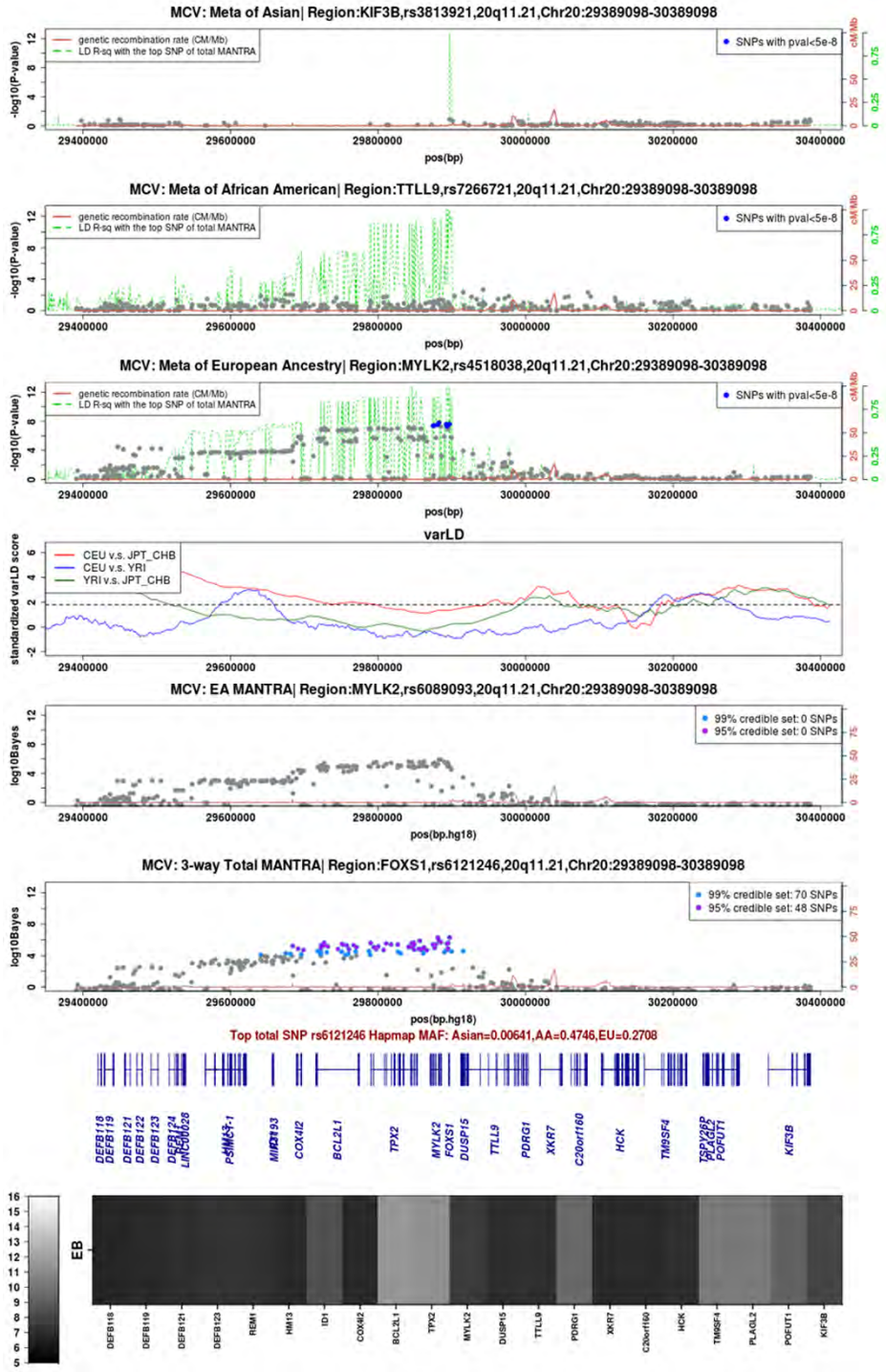

MCV: Meta of Asian| Region:LUC7L,rs1211375,16p13.3,Chr16:35254-2440845
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:LUC7L,rs1211375,16p13.3,Chr16:35254-2440845
MCV: Meta of European Ancestry| Region:ITFG3,rs1122794,16p13.3,Chr16:35254-2440845
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:ITFG3,rs1122794,16p13.3,Chr16:35254-2440845
99% credible set: 5 SNPs
95% credible set: 3 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:LUC7L,rs1211375,16p13.3,Chr16:35254-2440845
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs1211375 Hapmap MAF: Asian=0.4719,AA=0.3083,EU=0.275
EB


MCV: Meta of Asian| Region:C17orf63,rs9898892,17q11.2,Chr17:23663282-24663282
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:CRYBA1,rs16964930,17q11.2,Chr17:23663282-24663282
MCV: Meta of European Ancestry| Region:MIR4732,rs901975,17q11.2,Chr17:23663282-24663282
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:FLOT2,rs7221773,17q11.2,Chr17:23663282-24663282
99% credible set: 24 SNPs
95% credible set: 19 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:TRAF4,rs12325788,17q11.2,Chr17:23663282-24663282
99% credible set: 22 SNPs
95% credible set: 17 SNPs
Top total SNP rs12325788 Hapmap MAF: Asian=0.3125,AA=0.4057,EU=0.193
TMEM97 IFT20 TNFAIP1 POLDIP2 SEBOX VTN SARM1 SLC13A2 FOXN1 UNC119 PIGS ALDOC SPAG5 KIAA0100 SDF2 SUPT6H PROCA1 RAB34 RPL23A SNORD42B SNORD4A SNORD42A SNORD4B TLCD1 HEK8 TRAF4 C17orf63 ERAL1 FLOT2 DHRS13 PHF12 SEZ6 PIPOX MYO16A TIAF1 CRYBA1 NUFIP2
EB


MCV: Meta of Asian| Region:SLC14A1,rs3819179,18q12.3,Chr18:41541943-42541943
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:SLC14A1,rs10460032,18q12.3,Chr18:41541943-42541943
MCV: Meta of European Ancestry| Region:C18orf25,rs718515,18q21.1,Chr18:41541943-42541943
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:C18orf25,rs12607898,18q21.1,Chr18:41541943-42541943
99% credible set: 37 SNPs
95% credible set: 29 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:C18orf25,rs9949494,18q21.1,Chr18:41541943-42541943
99% credible set: 27 SNPs
95% credible set: 17 SNPs
Top total SNP rs9949494 Hapmap MAF: Asian=0.4944,AA=0.2333,EU=0.275
SLC14A1
SIGLEC15
EPG5
PSTPIP2
ATP5A1
HAUS1
C18orf25
RNF165
LOXHD1
ST8SIA5
EB


MCV: Meta of Asian| Region:PLIN4,rs8887,19p13.3,Chr19:3720863-4720863
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:ATCAY,rs11085048,19p13.3,Chr19:3720863-4720863
MCV: Meta of European Ancestry| Region:PLIN4,rs8887,19p13.3,Chr19:3720863-4720863
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:SH3GL1,rs11085074,19p13.3,Chr19:3720863-4720863
99% credible set: 3 SNPs
95% credible set: 3 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:PLIN4,rs8887,19p13.3,Chr19:3720863-4720863
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs8887 Hapmap MAF: Asian=0.2778,AA=0.3167,EU=0.375
EB
MATK
ATCAY
ITGB1BP3
DAPK3
EEF2
PIAS4
ZBTB7A
MAP2K2
CREB3L3
SIRT6
ANKRD24
EBI3
CCDC94
SHD
TMIGD2
FSD1
STAP2
MPND
SH3GL1
CHAF1A
LRG1
SEMA4B
TNFAIP8L1
C19orf10
DPP9


MCV: Meta of Asian| Region:MAST1,rs7256794,19p13.13,Chr19:12357456-13357456
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:CACNA1A,rs4926279,19p13.13,Chr19:12357456-13357456
MCV: Meta of European Ancestry| Region:SYCE2,rs11085825,19p13.13,Chr19:12357456-13357456
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:GCDH,rs11085824,19p13.13,Chr19:12357456-13357456
99% credible set: 10 SNPs
95% credible set: 7 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:GCDH,rs9384,19p13.13,Chr19:12357456-13357456
99% credible set: 8 SNPs
95% credible set: 5 SNPs
Top total SNP rs9384 Hapmap MAF: Asian=0.1348,AA=0.2373,EU=0.3448
ZNF799
ZNF443
ZNF709
ZNF564
ZNF490
ZNF791
MAN2B1
C19orf56
DHPS
FBXW9
TNPO2
C19orf43
ASNA1
BEST2
HOOK2
JUNB
PRDX2
RNASEH2A
RTBDN
MAST1
DNASE2
GCDH
SYCE2
FARSA
CALR
RAD23A
GADD45GIP1
DAND5
NFIX
LYL1
TRMT1
NACC1
STX10
IER2
CACNA1A
EB


MCV: Meta of Asian| Region:KIF3B,rs3813921,20q11.21,Chr20:29389098-30389098
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:TTLL9,rs7266721,20q11.21,Chr20:29389098-30389098
MCV: Meta of European Ancestry| Region:MYLK2,rs4518038,20q11.21,Chr20:29389098-30389098
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:MYLK2,rs6089093,20q11.21,Chr20:29389098-30389098
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:FOXS1,rs6121246,20q11.21,Chr20:29389098-30389098
99% credible set: 70 SNPs
95% credible set: 48 SNPs
Top total SNP rs6121246 Hapmap MAF: Asian=0.00641,AA=0.4746,EU=0.2708
DEFB118
DEFB119
DEFB121
DEFB122
DEFB123
DEFB124
LINC00028
PSMA3-AS1
MIR2193
COX4I2
BCL2L1
TPX2
MYLK2
FOXS1
DUSP15
TTLL9
PDRG1
XKR7
C20orf160
HCK
TM9SF4
TSPEAR
TSPEAR-AS2
POFUT1
KIF3B
EB
DEFB118
DEFB119
DEFB121
DEFB123
REM1
HM13
ID1
COX4I2
BCL2L1
TPX2
MYLK2
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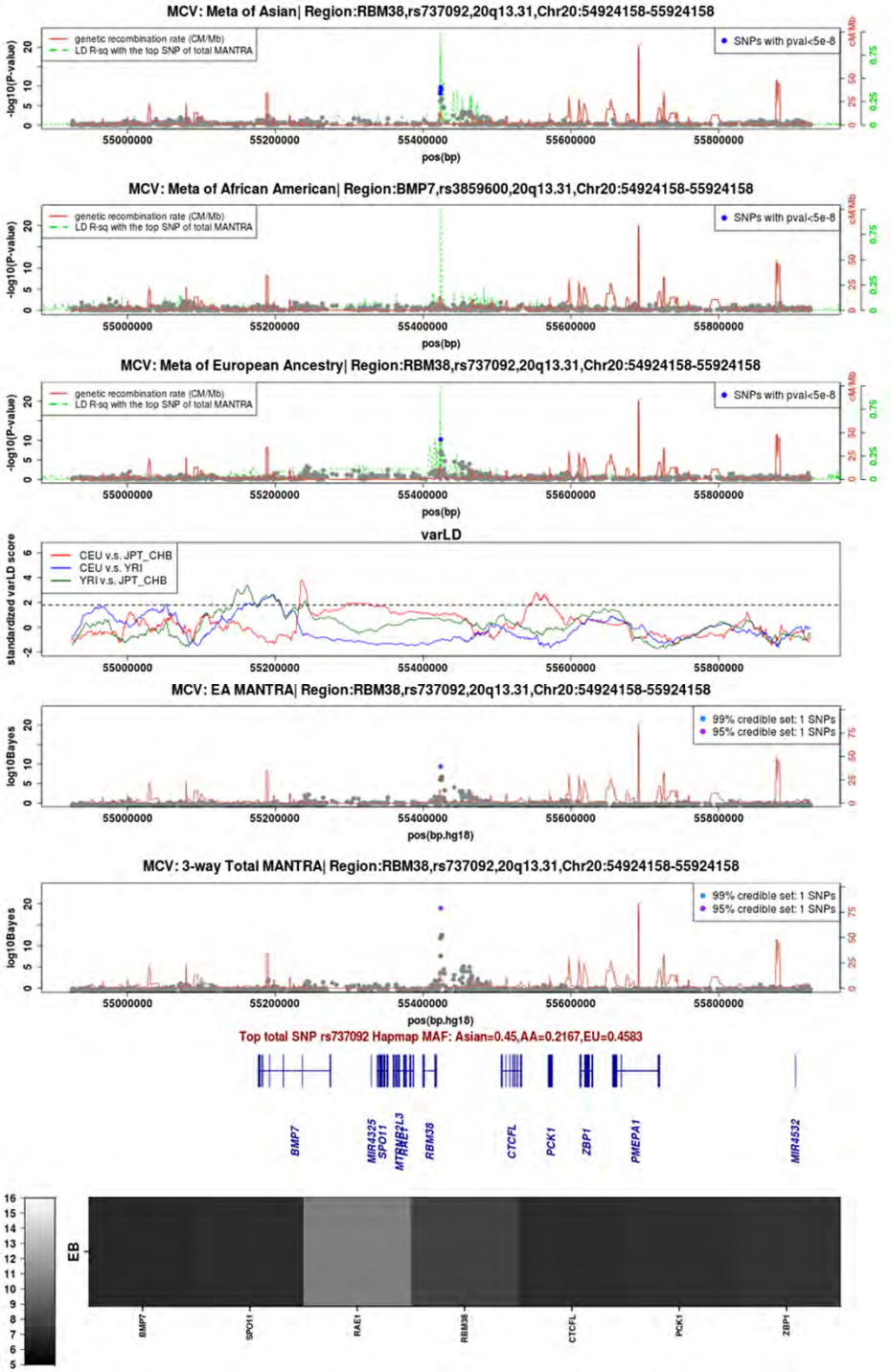
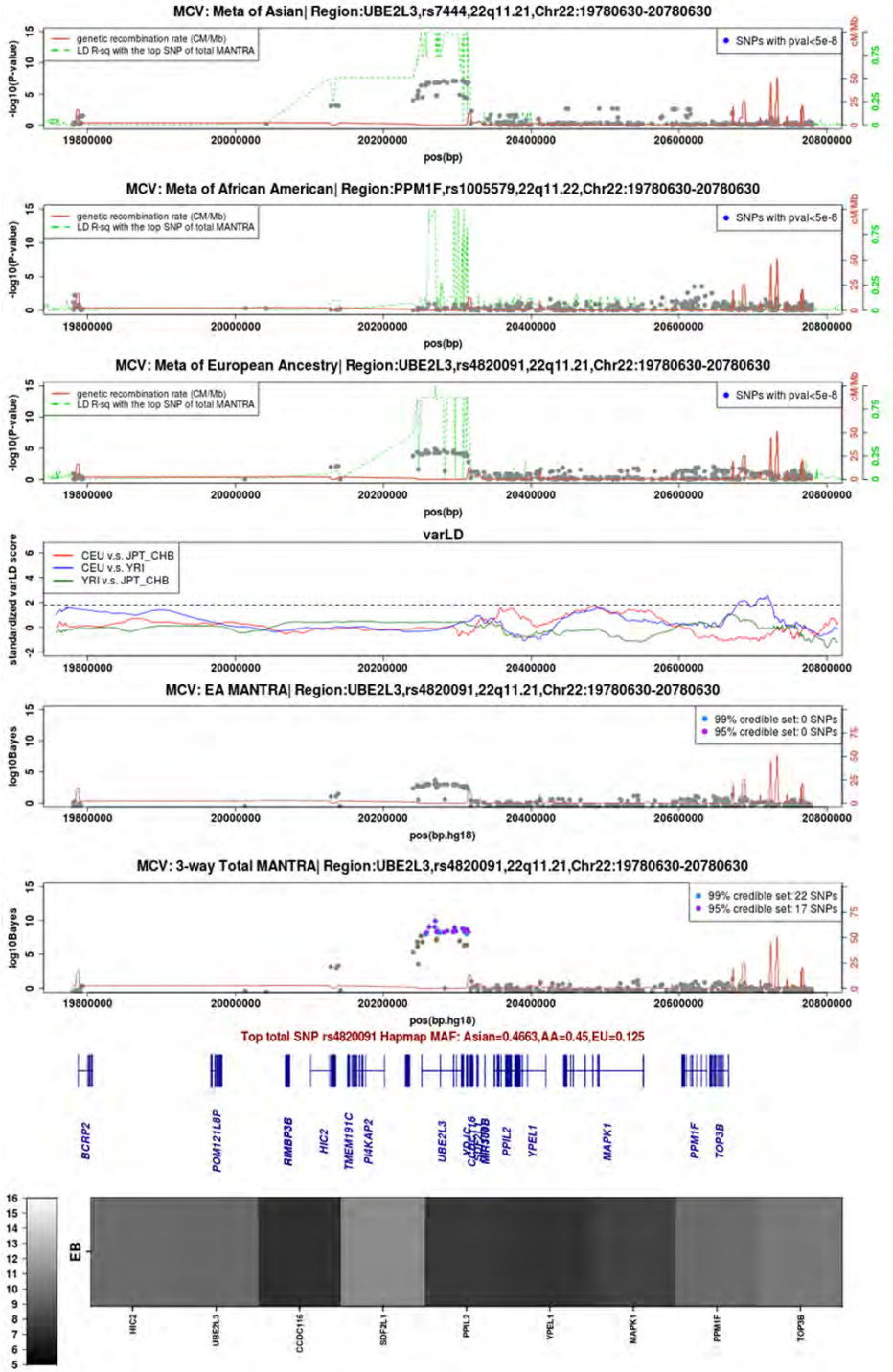
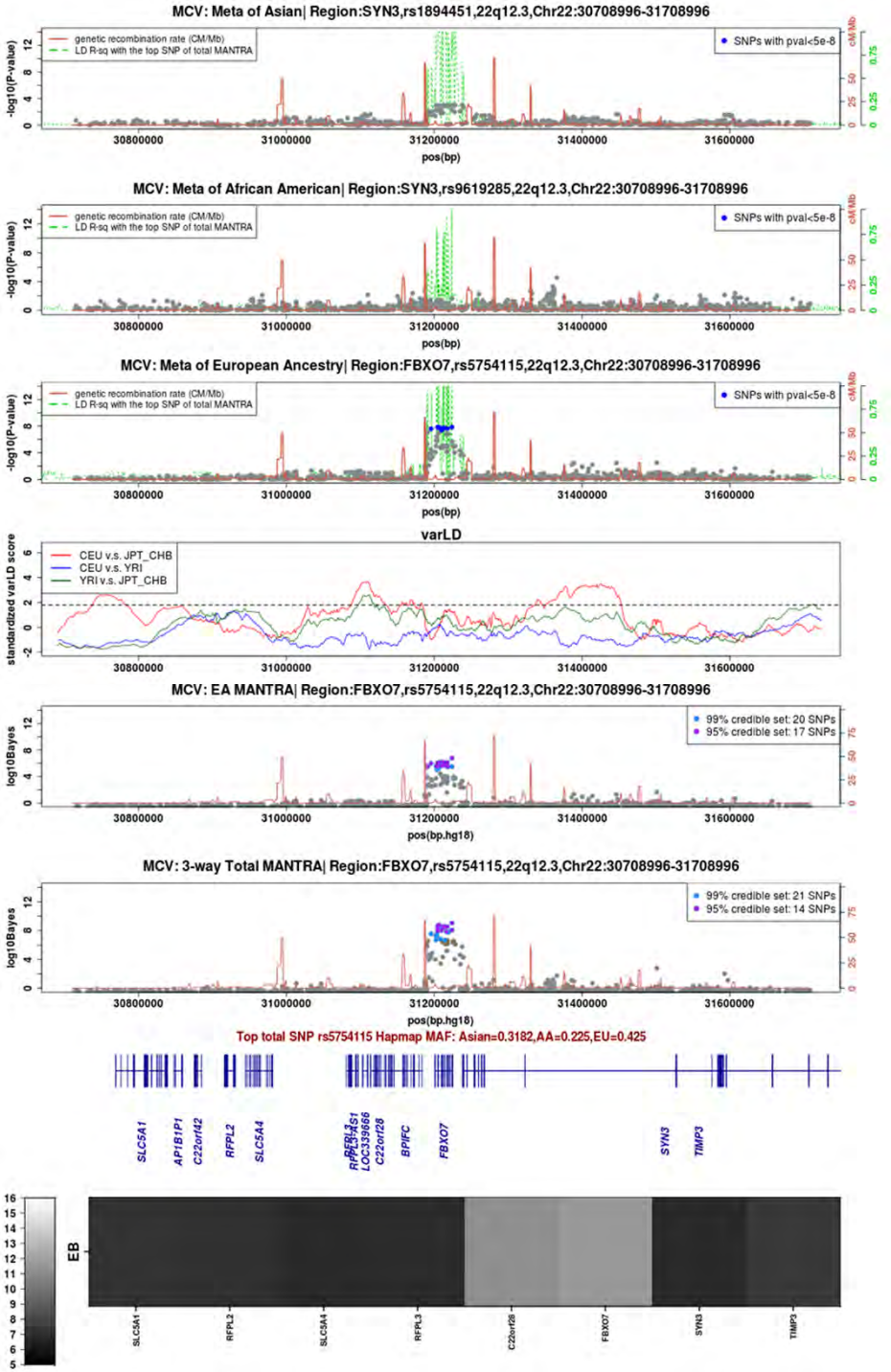
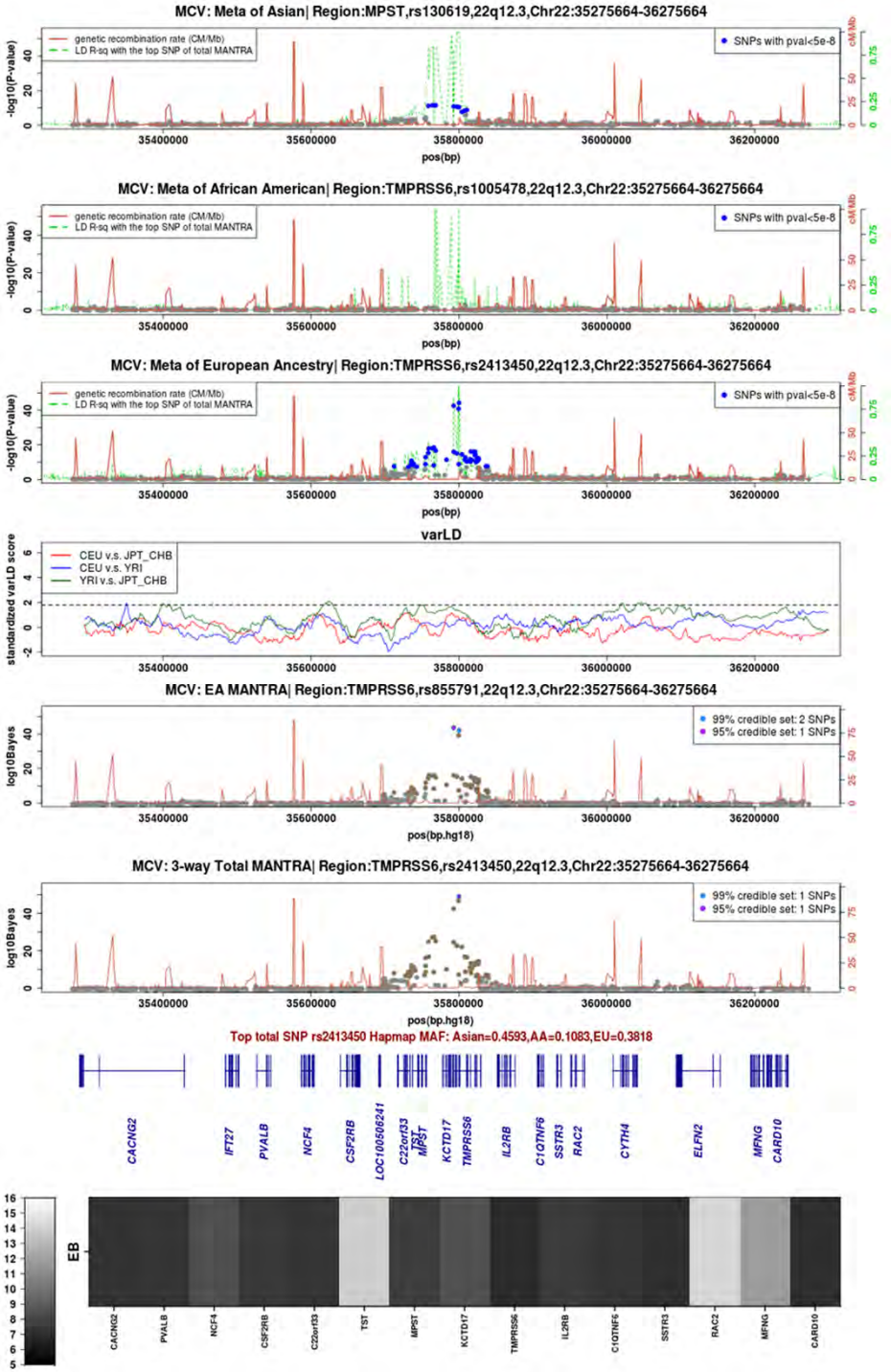
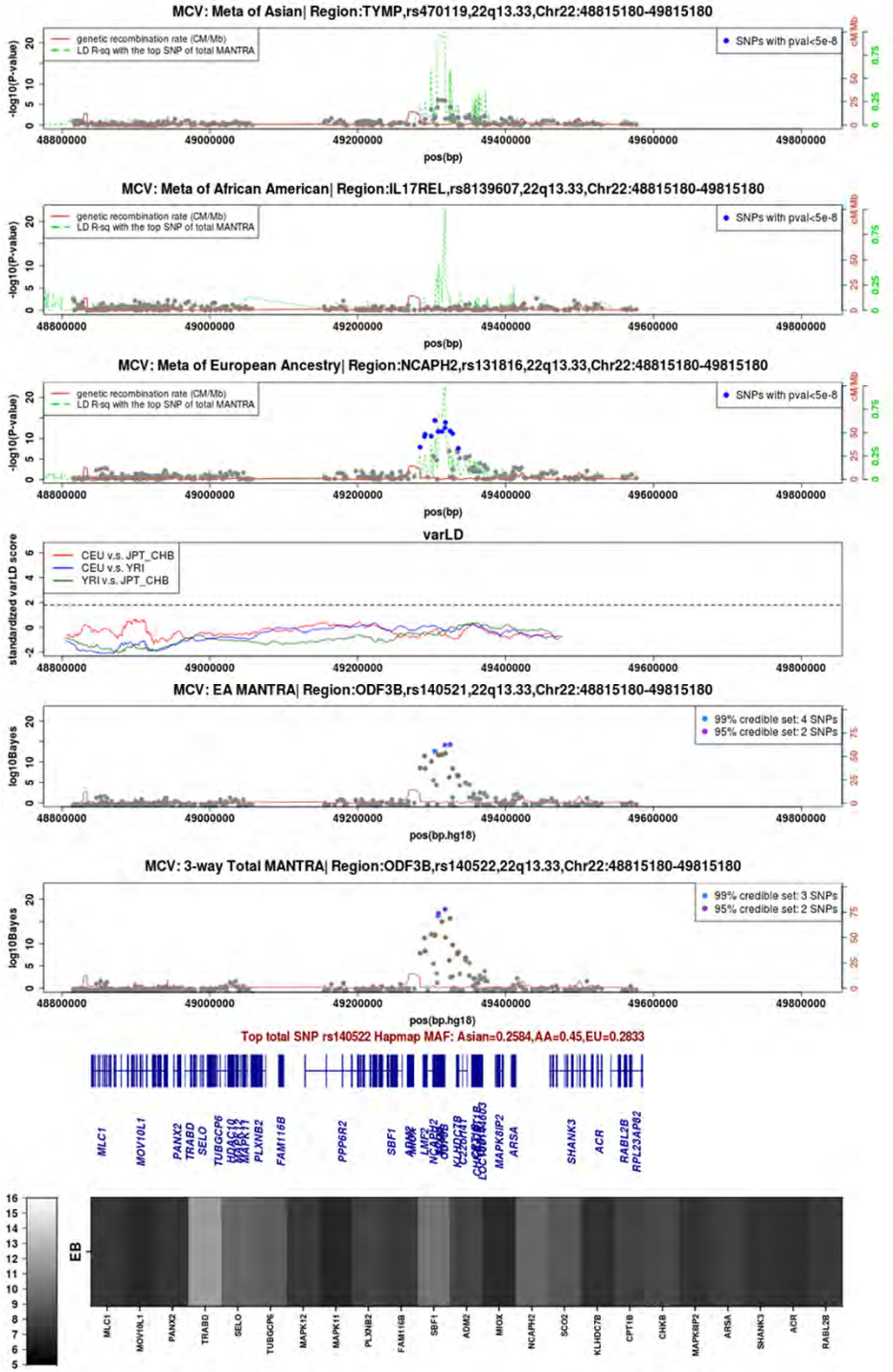
HCK
TM9SF4
PLAGL2
POFUT1
KIF3B


MCV: Meta of Asian| Region:RBM38,rs737092,20q13.31,Chr20:54924158-55924158
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:BMP7,rs3859600,20q13.31,Chr20:54924158-55924158
MCV: Meta of European Ancestry| Region:RBM38,rs737092,20q13.31,Chr20:54924158-55924158
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:RBM38,rs737092,20q13.31,Chr20:54924158-55924158
99% credible set: 1 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:RBM38,rs737092,20q13.31,Chr20:54924158-55924158
Top total SNP rs737092 Hapmap MAF: Asian=0.45,AA=0.2167,EU=0.4583
BMP7
MIR4325
SPO11
MTRNR2L3
RBM38
CTCFL
PCK1
ZBP1
PMEPA1
MIR4532
EB
BMP7
SPO11
RAE1
RBM38
CTCFL
PCK1
ZBP1

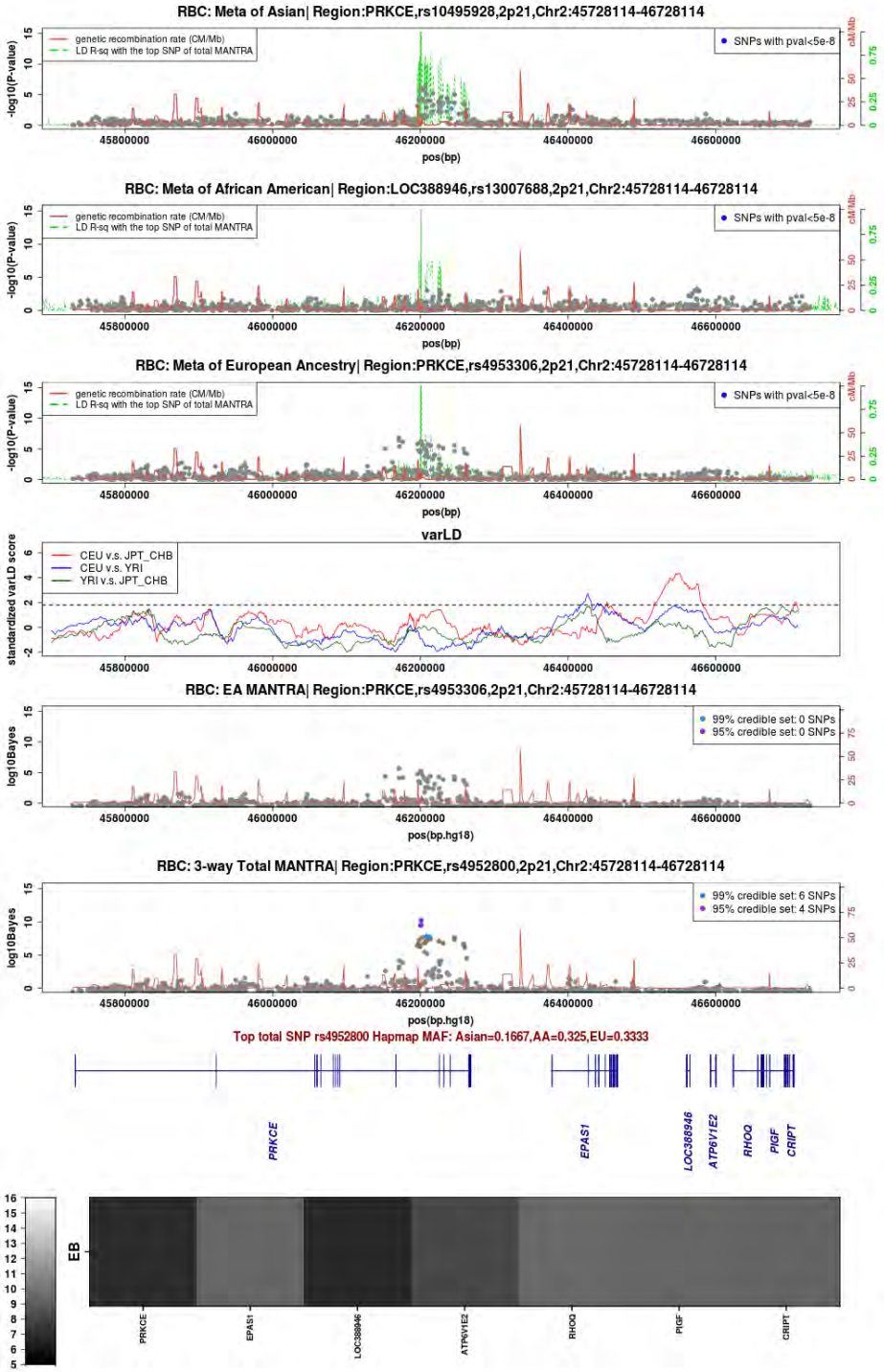

MCV: Meta of Asian| Region:UBE2L3,rs7444,22q11.21,Chr22:19780630-20780630
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:PPM1F,rs1005579,22q11.22,Chr22:19780630-20780630
MCV: Meta of European Ancestry| Region:UBE2L3,rs4820091,22q11.21,Chr22:19780630-20780630
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:UBE2L3,rs4820091,22q11.21,Chr22:19780630-20780630
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:UBE2L3,rs4820091,22q11.21,Chr22:19780630-20780630
99% credible set: 22 SNPs
95% credible set: 17 SNPs
Top total SNP rs4820091 Hapmap MAF: Asian=0.4663,AA=0.45,EU=0.125
BCRP2
POM121L8P
RIMBP3B
HIC2
TMEM191C
PI4KAP2
UBE2L3
YDJC
CCDC116
MIR5008
PPIL2
YPEL1
MAPK1
PPM1F
TOP3B
EB
HIC2
UBE2L3
CCDC116
SDF2L1
PPIL2
YPEL1
MAPK1
PPM1F
TOP3B

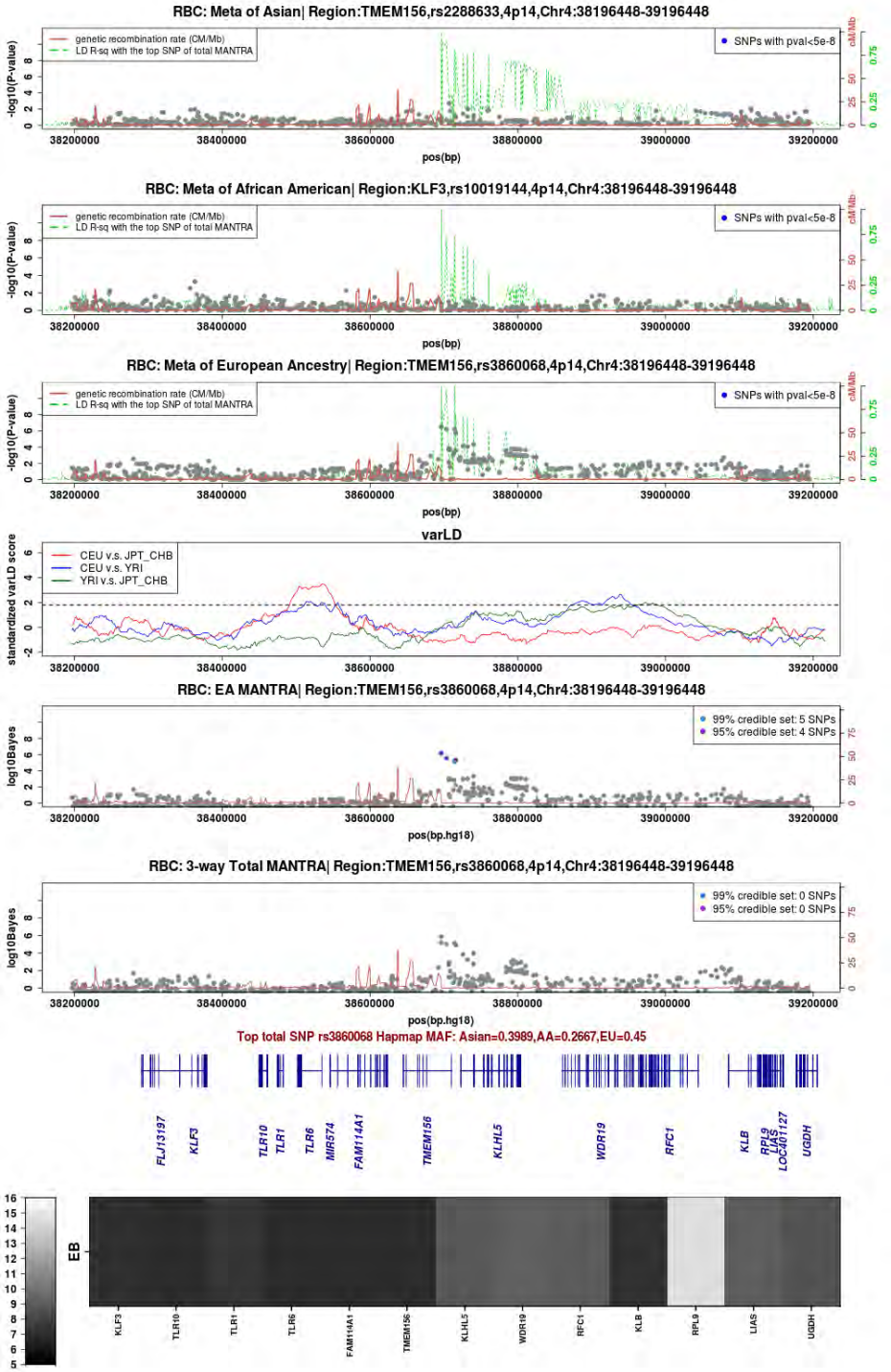

MCV: Meta of Asian| Region:SYN3,rs1894451,22q12.3,Chr22:30708996-31708996
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:SYN3,rs9619285,22q12.3,Chr22:30708996-31708996
MCV: Meta of European Ancestry| Region:FBXO7,rs5754115,22q12.3,Chr22:30708996-31708996
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:FBXO7,rs5754115,22q12.3,Chr22:30708996-31708996
99% credible set: 20 SNPs
95% credible set: 17 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:FBXO7,rs5754115,22q12.3,Chr22:30708996-31708996
99% credible set: 21 SNPs
95% credible set: 14 SNPs
Top total SNP rs5754115 Hapmap MAF: Asian=0.3182,AA=0.225,EU=0.425
SLC5A1
AP1B1P1
C22orf42
RFPL2
SLC5A4
RFPL3
RFPL3S1
LOC339666
C22orf28
BPIFC
FBXO7
SYN3
TIMP3
EB

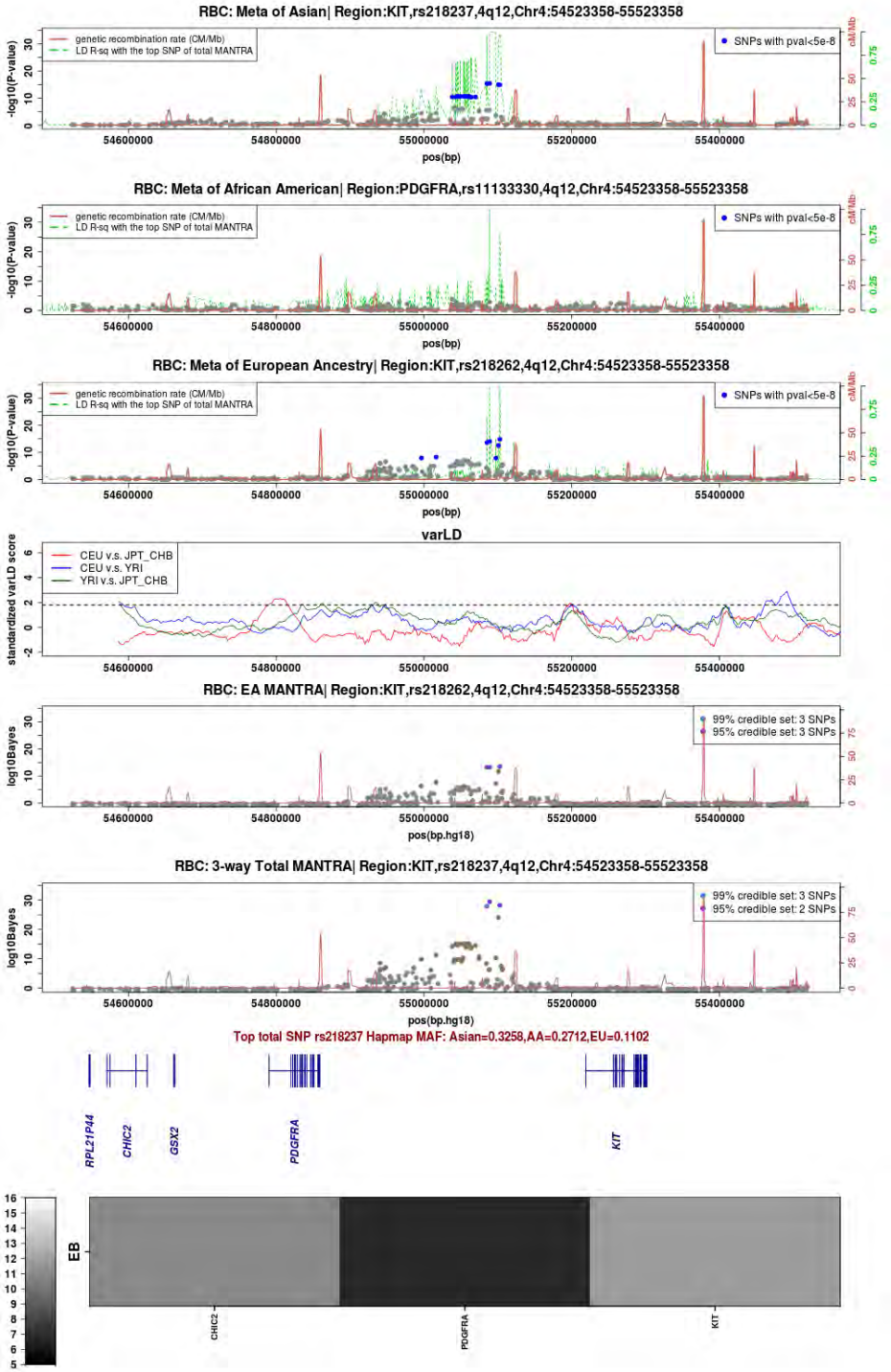

MCV: Meta of Asian| Region:MPST,rs130619,22q12.3,Chr22:35275664-36275664
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:TMPRSS6,rs1005478,22q12.3,Chr22:35275664-36275664
MCV: Meta of European Ancestry| Region:TMPRSS6,rs2413450,22q12.3,Chr22:35275664-36275664
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:TMPRSS6,rs855791,22q12.3,Chr22:35275664-36275664
99% credible set: 2 SNPs
95% credible set: 1 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:TMPRSS6,rs2413450,22q12.3,Chr22:35275664-36275664
99% credible set: 1 SNPs
95% credible set: 1 SNPs
Top total SNP rs2413450 Hapmap MAF: Asian=0.4593,AA=0.1083,EU=0.3818
CACNG2
IFT27
PVALB
NCF4
CSF2RB
LOC100506241
C22orf33
TST
MPST
KCTD17
TMPRSS6
IL2RB
C1QTNF6
SSTR3
RAC2
CYTH4
ELFN2
MFNG
CARD10
EB

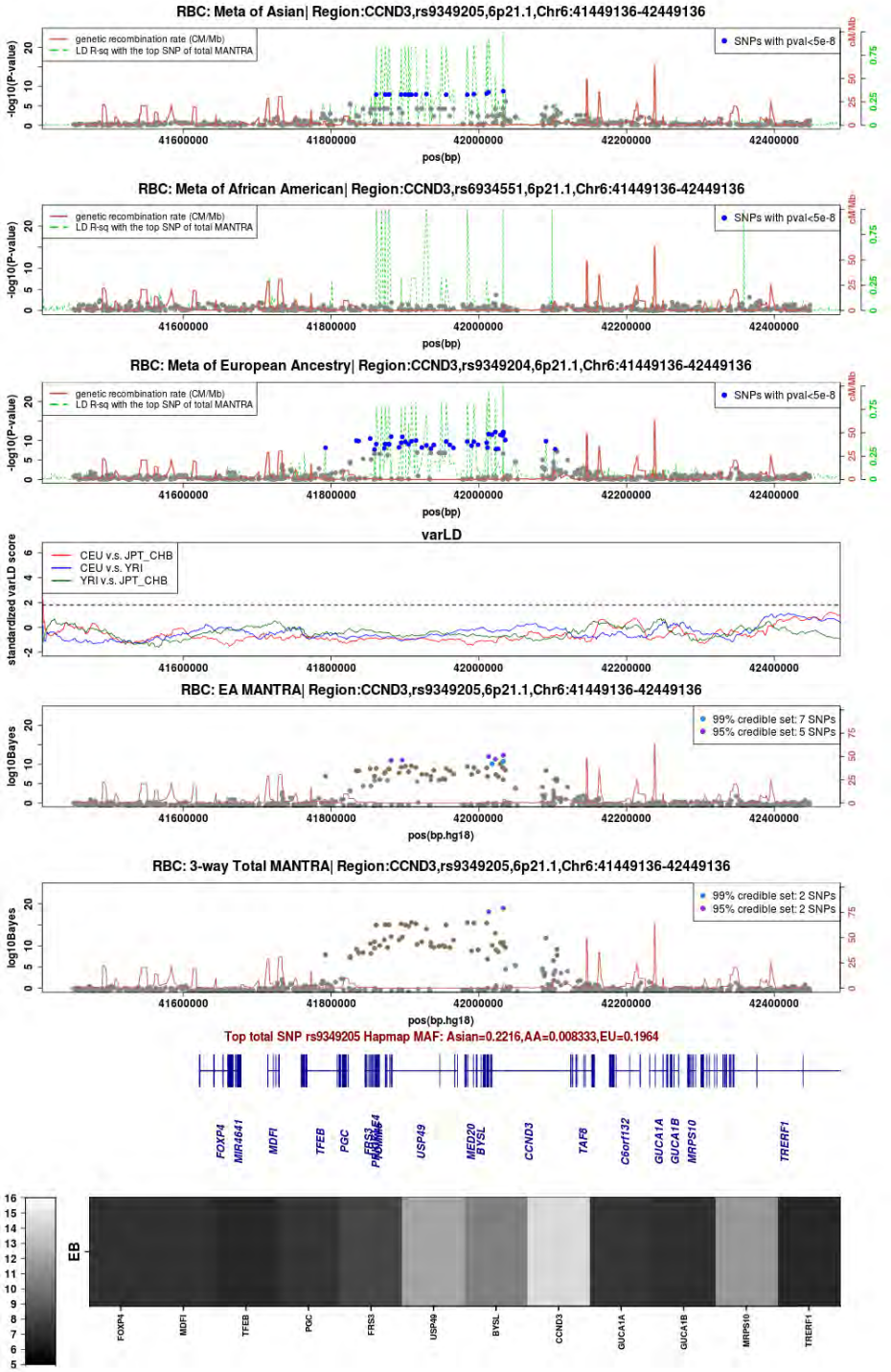

MCV: Meta of Asian| Region:TYMP,rs470119,22q13.33,Chr22:48815180-49815180
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
MCV: Meta of African American| Region:IL17REL,rs8139607,22q13.33,Chr22:48815180-49815180
MCV: Meta of European Ancestry| Region:NCAPH2,rs131816,22q13.33,Chr22:48815180-49815180
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
MCV: EA MANTRA| Region:ODF3B,rs140521,22q13.33,Chr22:48815180-49815180
99% credible set: 4 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
MCV: 3-way Total MANTRA| Region:ODF3B,rs140522,22q13.33,Chr22:48815180-49815180
99% credible set: 3 SNPs
95% credible set: 2 SNPs
Top total SNP rs140522 Hapmap MAF: Asian=0.2584,AA=0.45,EU=0.2833
MLC1
MOV10L1
PANX2
TRABD
SELO
TUBGCP6
PLXNB2
FAM116B
PPP6R2
SBF1
MAPK8IP2
ARSA
SHANK3
ACR
RABL2B
RPL23AP92
EB
MLC1
MOV10L1
PANX2
TRABD
SELO
TUBGCP6
MAPK12
MAPK11
PLXNB2
FAM116B
SBF1
ADM2
MIOX
NCAPH2
SCO2
KLHDC7B
CPT1B
CHKB
MAPK8IP2
ARSA
SHANK3
ACR
RABL2B

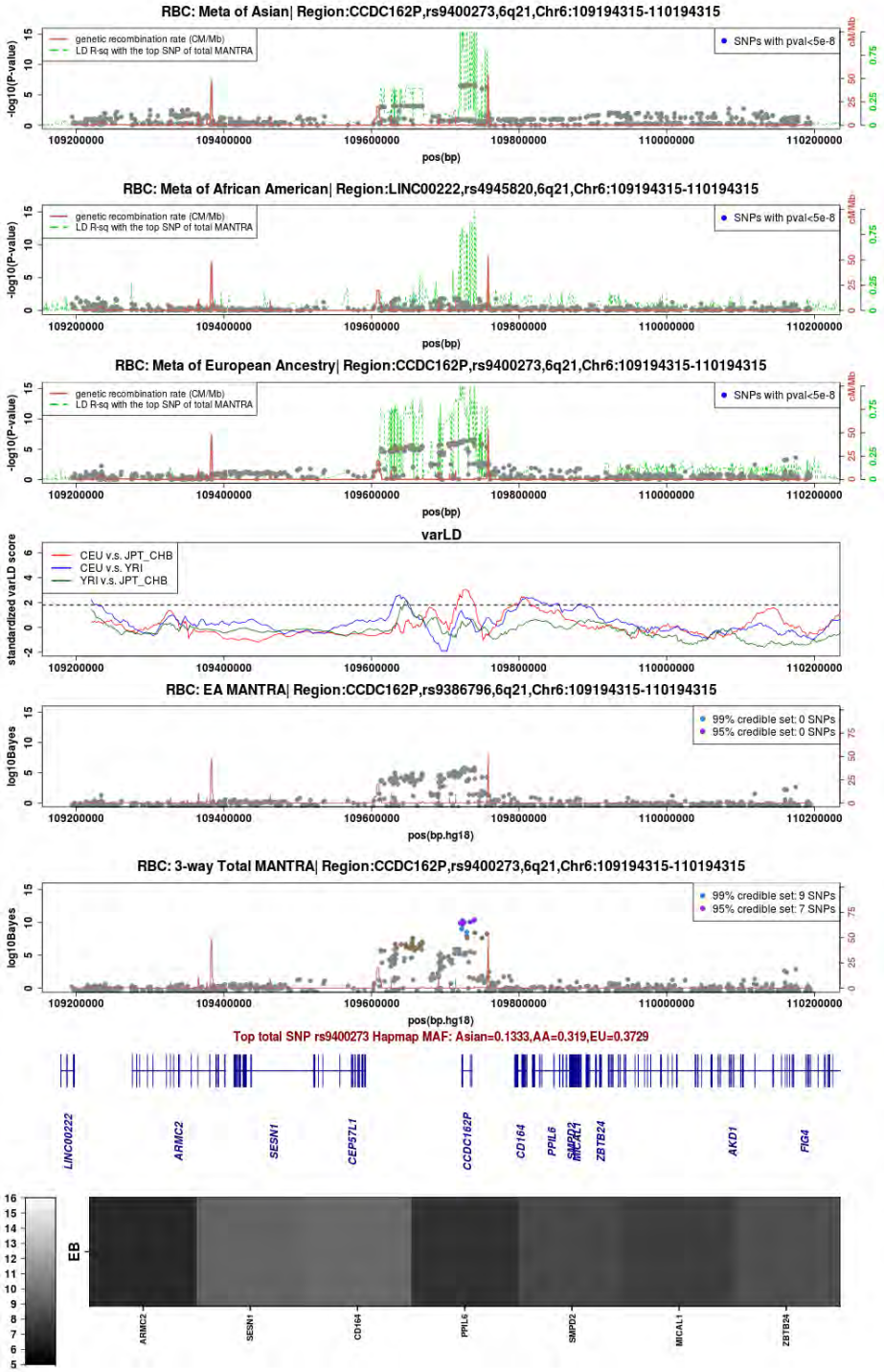
RBC

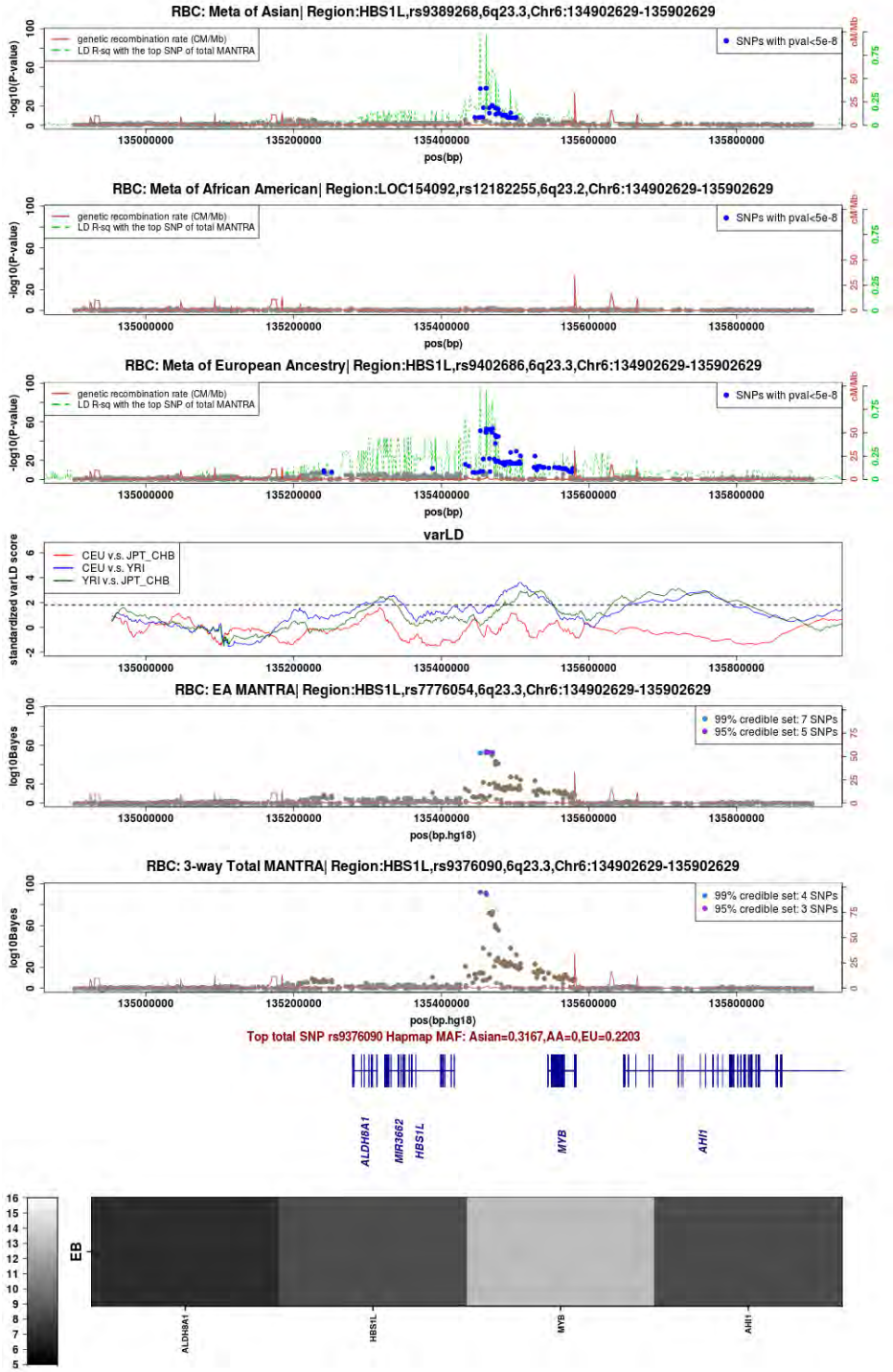

RBC: Meta of Asian| Region:PRKCE,rs10495928,2p21,Chr2:45728114-46728114
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:LOC388946,rs13007688,2p21,Chr2:45728114-46728114
RBC: Meta of European Ancestry| Region:PRKCE,rs4953306,2p21,Chr2:45728114-46728114
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:PRKCE,rs4953306,2p21,Chr2:45728114-46728114
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:PRKCE,rs4952800,2p21,Chr2:45728114-46728114
99% credible set: 6 SNPs
95% credible set: 4 SNPs
Top total SNP rs4952800 Hapmap MAF: Asian=0.1667,AA=0.325,EU=0.3333
PRKCE
EPAS1
LOC388946
ATP6V1E2
RHOQ
PIGF
CRIPT
EB

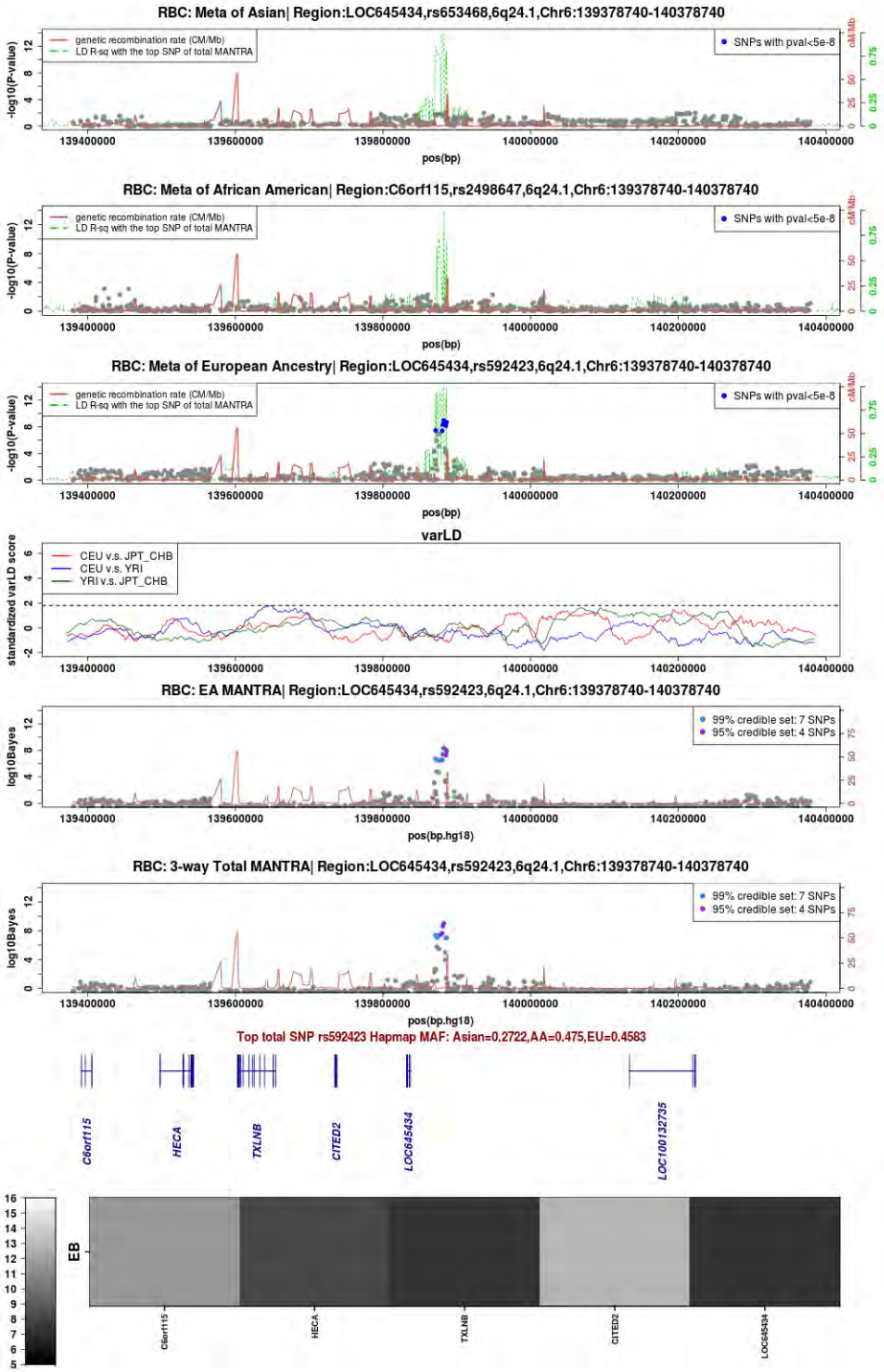

RBC: Meta of Asian| Region:TMEM156,rs2288633,4p14,Chr4:38196448-39196448
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:KLF3,rs10019144,4p14,Chr4:38196448-39196448
RBC: Meta of European Ancestry| Region:TMEM156,rs3860068,4p14,Chr4:38196448-39196448
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:TMEM156,rs3860068,4p14,Chr4:38196448-39196448
99% credible set: 5 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:TMEM156,rs3860068,4p14,Chr4:38196448-39196448
99% credible set: 0 SNPs
95% credible set: 0 SNPs
Top total SNP rs3860068 Hapmap MAF: Asian=0.3989,AA=0.2667,EU=0.45
FLJ13197
KLF3
TLR10
TLR1
TLR6
MIR574
FAM114A1
TMEM156
KLHL5
WDR19
RFC1
KLB
RPL9
LIAS
LOC401127
UGDH
EB

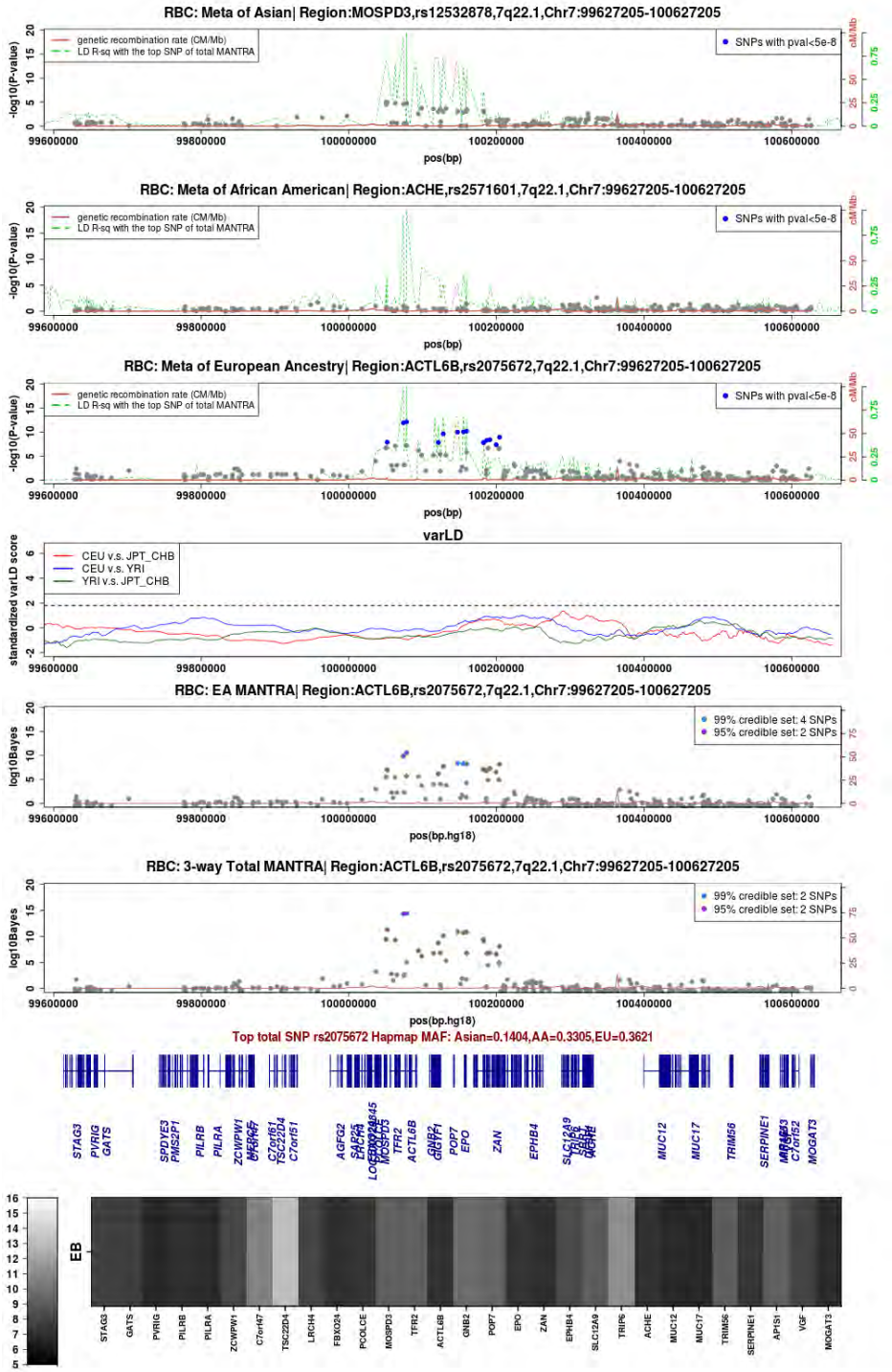

RBC: Meta of Asian| Region:KIT,rs218237,4q12,Chr4:54523358-55523358
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:PDGFRA,rs11133330,4q12,Chr4:54523358-55523358
RBC: Meta of European Ancestry| Region:KIT,rs218262,4q12,Chr4:54523358-55523358
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:KIT,rs218262,4q12,Chr4:54523358-55523358
99% credible set: 3 SNPs
95% credible set: 3 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:KIT,rs218237,4q12,Chr4:54523358-55523358
99% credible set: 3 SNPs
95% credible set: 2 SNPs
Top total SNP rs218237 Hapmap MAF: Asian=0.3258,AA=0.2712,EU=0.1102
RPL21P44
CHIC2
GSX2
PDGFRA
KIT
EB

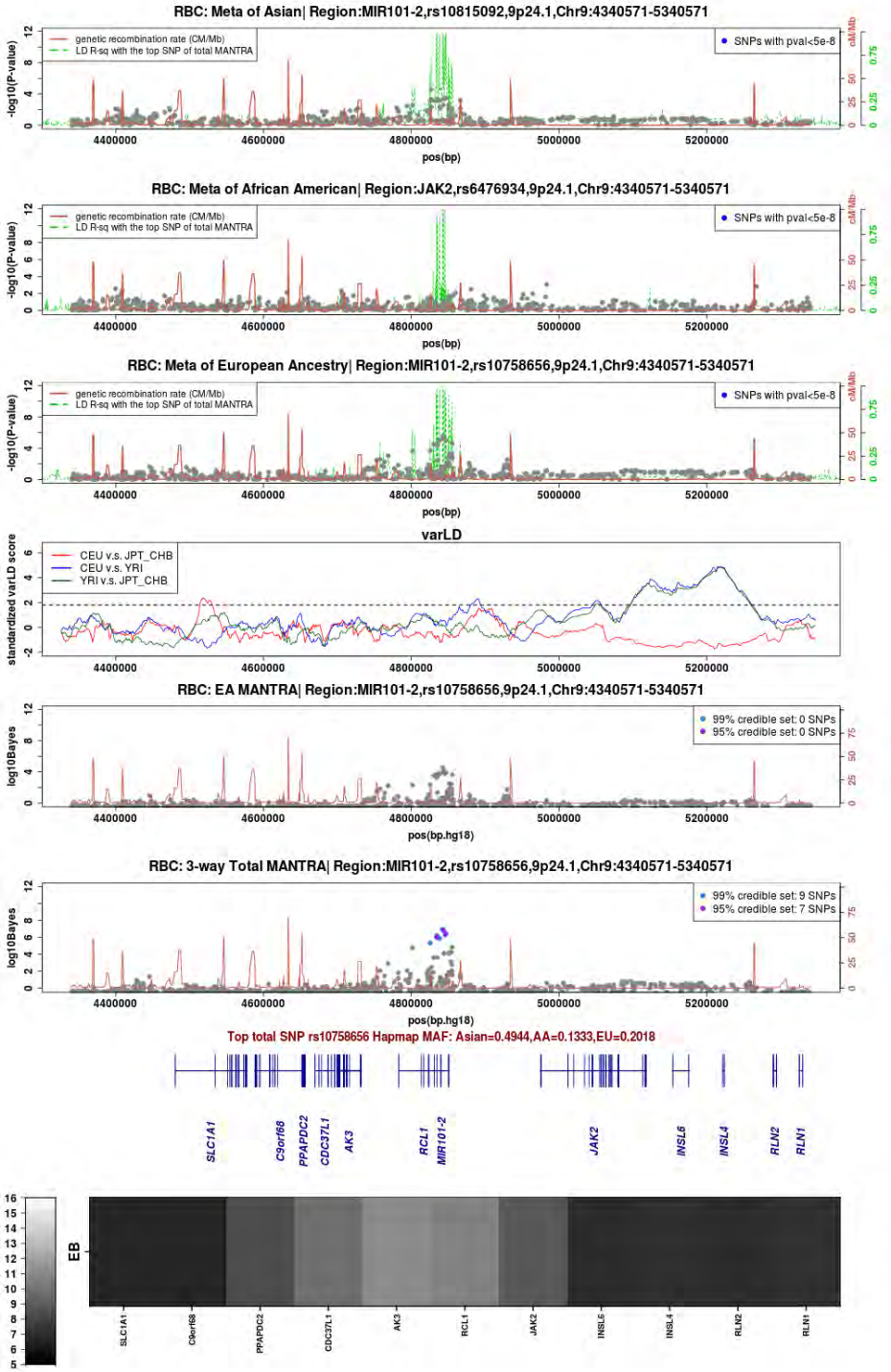

RBC: Meta of Asian| Region:CCND3,rs9349205,6p21.1,Chr6:41449136-42449136
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:CCND3,rs6934551,6p21.1,Chr6:41449136-42449136
RBC: Meta of European Ancestry| Region:CCND3,rs9349204,6p21.1,Chr6:41449136-42449136
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:CCND3,rs9349205,6p21.1,Chr6:41449136-42449136
99% credible set: 7 SNPs
95% credible set: 5 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:CCND3,rs9349205,6p21.1,Chr6:41449136-42449136
99% credible set: 2 SNPs
95% credible set: 2 SNPs
Top total SNP rs9349205 Hapmap MAF: Asian=0.2216,AA=0.008333,EU=0.1964
FOXP4
MIR4641
MDFI
TFEB
PGC
FRS3
PKIB
C6orf64
USP49
MED20
BYSL
CCND3
TAF8
C6orf132
GUCA1A
GUCA1B
MRPS10
TRERF1
EB

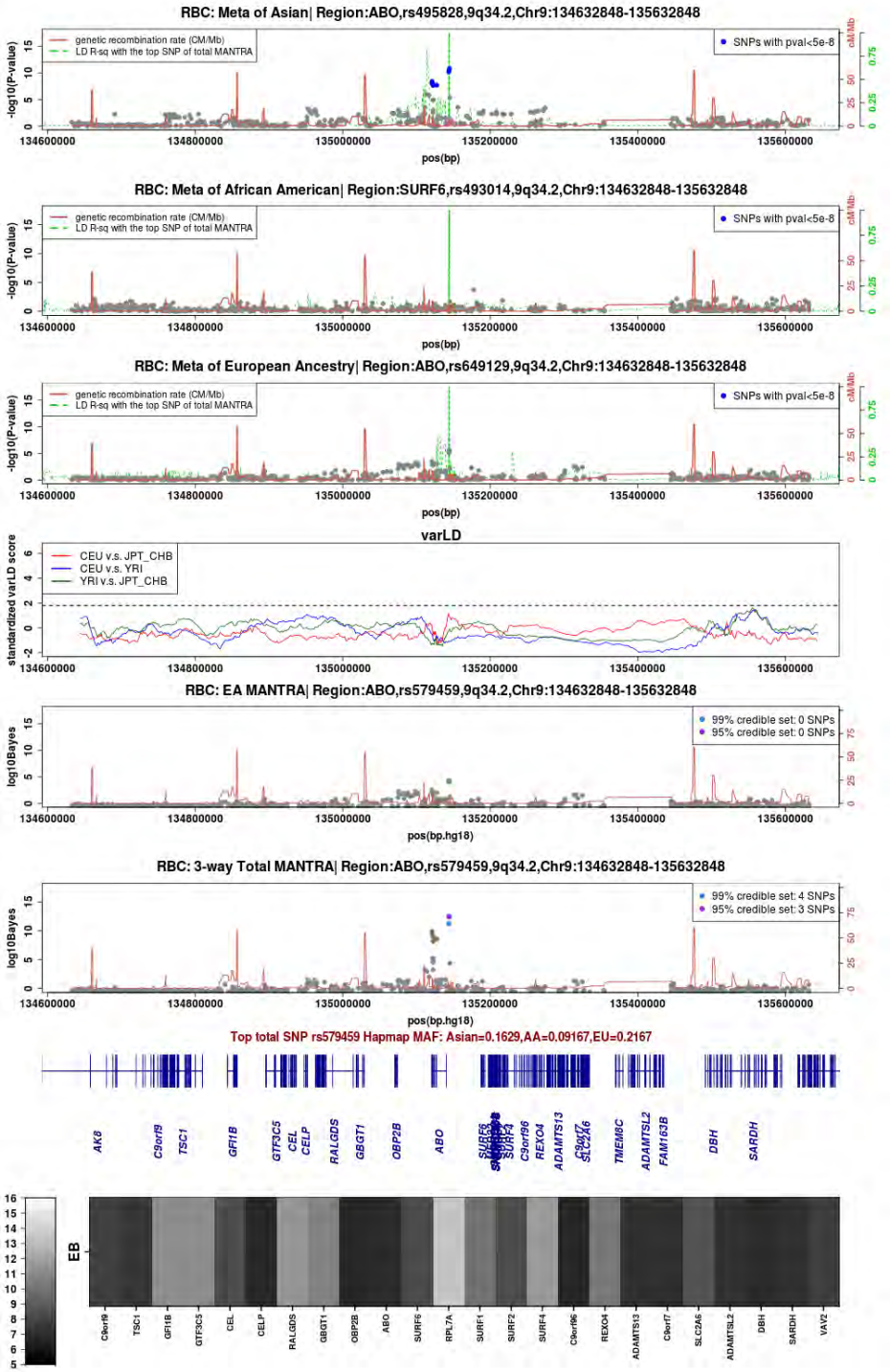

RBC: Meta of Asian| Region:CCDC162P,rs9400273,6q21,Chr6:109194315-110194315
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:LINC00222,rs4945820,6q21,Chr6:109194315-110194315
RBC: Meta of European Ancestry| Region:CCDC162P,rs9400273,6q21,Chr6:109194315-110194315
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:CCDC162P,rs9386796,6q21,Chr6:109194315-110194315
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:CCDC162P,rs9400273,6q21,Chr6:109194315-110194315
99% credible set: 9 SNPs
95% credible set: 7 SNPs
Top total SNP rs9400273 Hapmap MAF: Asian=0.1333,AA=0.319,EU=0.3729
LINC00222
ARMC2
SESN1
CEP57L1
CCDC162P
CD164
PPIL6
SMPD2
MICAL1
ZBTB24
AKD1
FIG4
EB

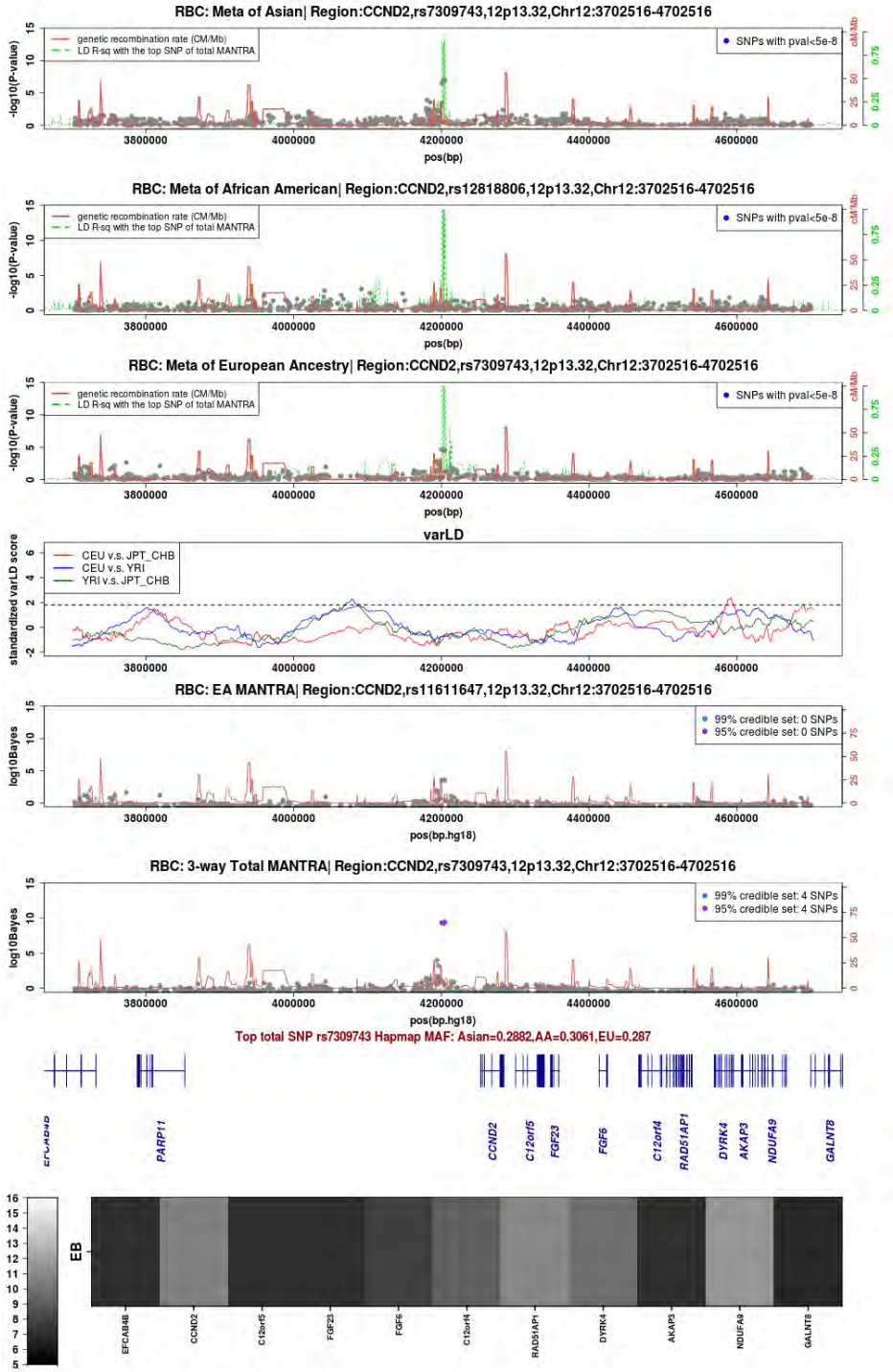

RBC: Meta of Asian| Region:HBS1L,rs9389268,6q23.3,Chr6:134902629-135902629
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:LOC154092,rs12182255,6q23.2,Chr6:134902629-135902629
RBC: Meta of European Ancestry| Region:HBS1L,rs9402686,6q23.3,Chr6:134902629-135902629
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:HBS1L,rs7776054,6q23.3,Chr6:134902629-135902629
99% credible set: 7 SNPs
95% credible set: 5 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:HBS1L,rs9376090,6q23.3,Chr6:134902629-135902629
99% credible set: 4 SNPs
95% credible set: 3 SNPs
Top total SNP rs9376090 Hapmap MAF: Asian=0.3167,AA=0,EU=0.2203
ALDH8A1
MIR3662
HBS1L
MYB
AHI1
EB

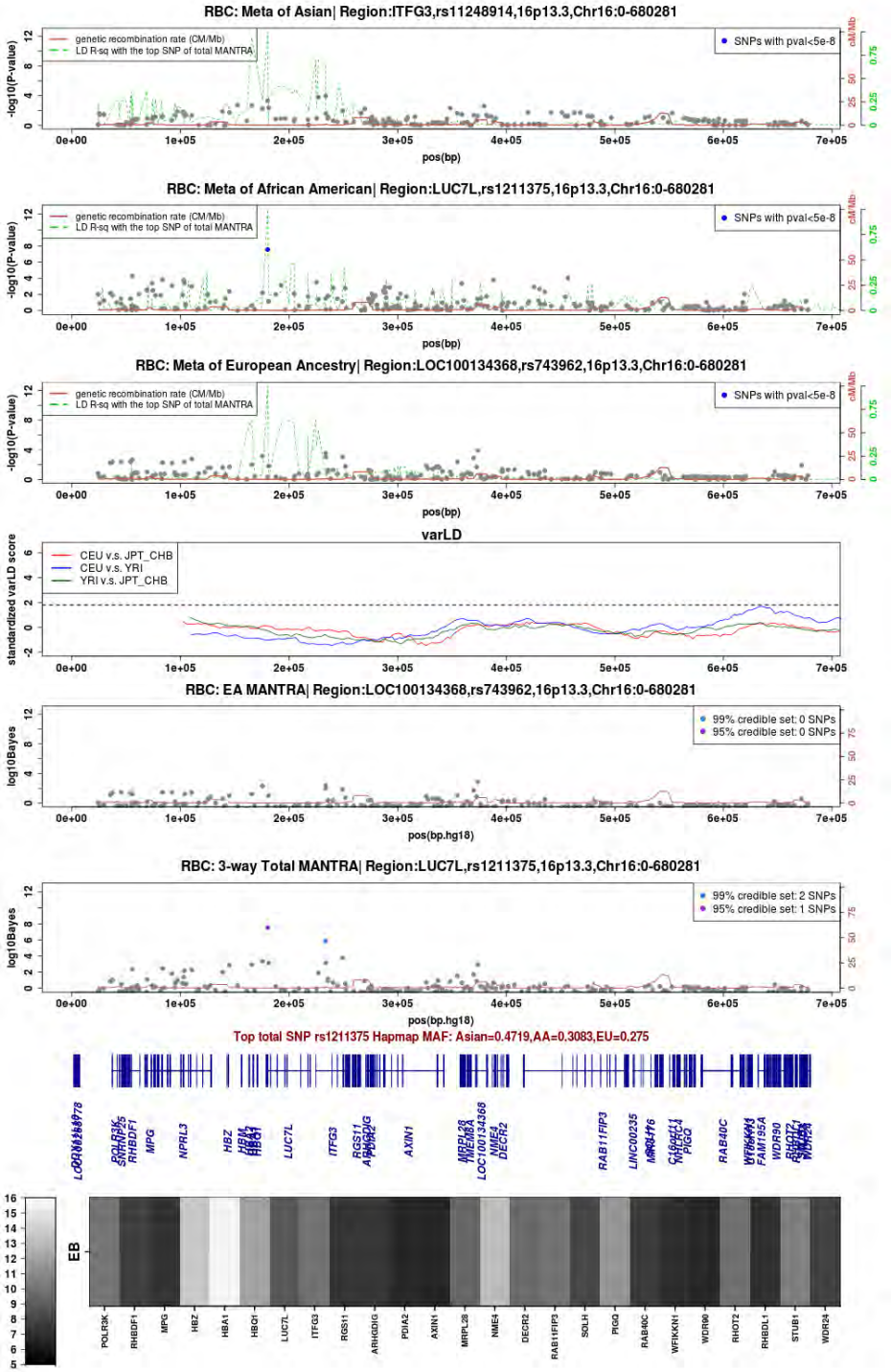

RBC: Meta of Asian| Region:LOC645434,rs653468,6q24.1,Chr6:139378740-140378740
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:C6orf115,rs2498647,6q24.1,Chr6:139378740-140378740
RBC: Meta of European Ancestry| Region:LOC645434,rs592423,6q24.1,Chr6:139378740-140378740
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:LOC645434,rs592423,6q24.1,Chr6:139378740-140378740
99% credible set: 7 SNPs
95% credible set: 4 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:LOC645434,rs592423,6q24.1,Chr6:139378740-140378740
Top total SNP rs592423 Hapmap MAF: Asian=0.2722,AA=0.475,EU=0.4583
C6orf115
HECA
TXLNB
CITED2
LOC645434
LOC100132735
EB

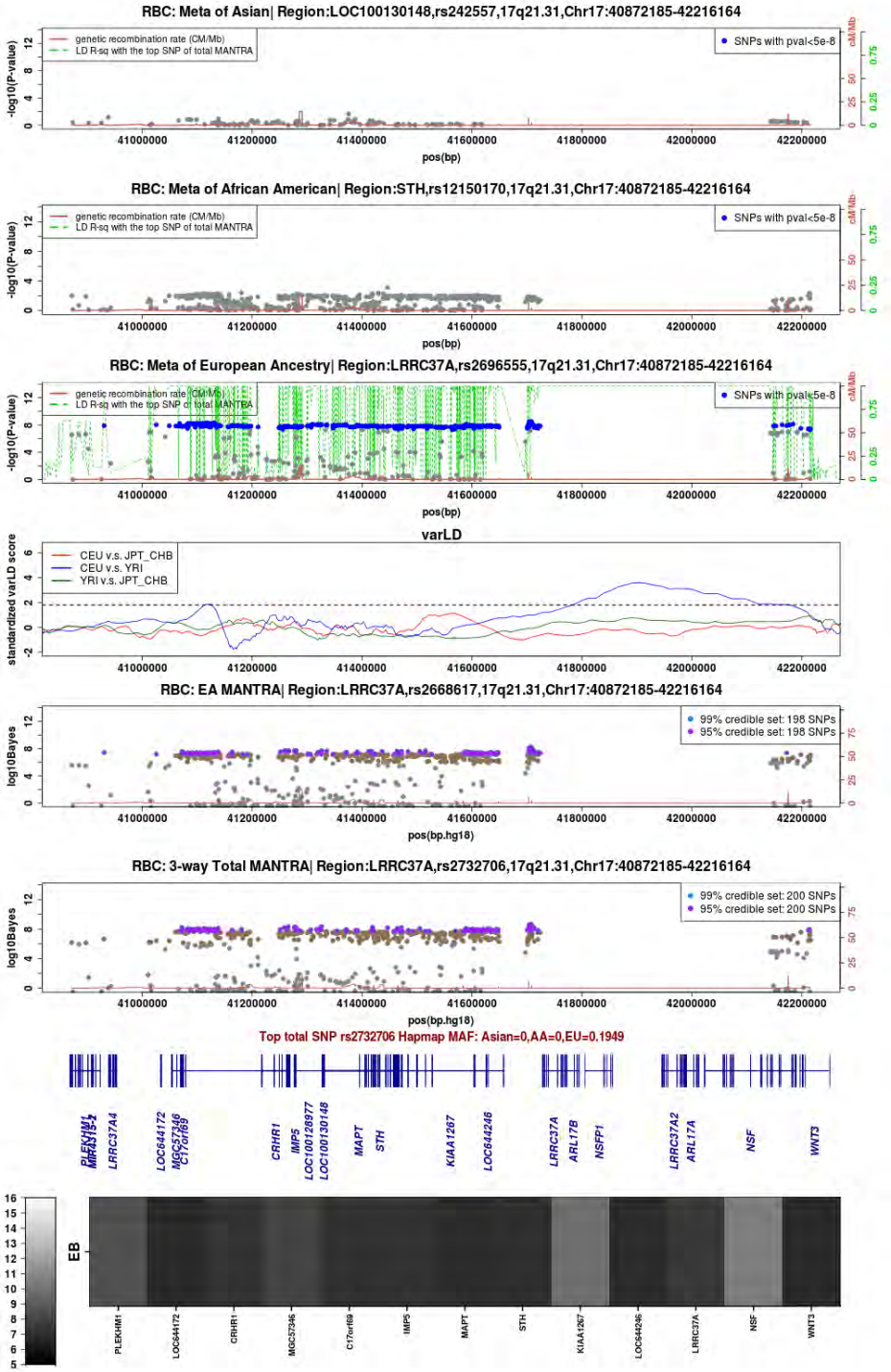

RBC: Meta of Asian| Region:MOSPD3,rs12532878,7q22.1,Chr7:99627205-100627205
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:ACHE,rs2571601,7q22.1,Chr7:99627205-100627205
RBC: Meta of European Ancestry| Region:ACTL6B,rs2075672,7q22.1,Chr7:99627205-100627205
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:ACTL6B,rs2075672,7q22.1,Chr7:99627205-100627205
99% credible set: 4 SNPs
95% credible set: 2 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:ACTL6B,rs2075672,7q22.1,Chr7:99627205-100627205
99% credible set: 2 SNPs
95% credible set: 2 SNPs
Top total SNP rs2075672 Hapmap MAF: Asian=0.1404,AA=0.3305,EU=0.3621
STAG3
PVRIG
GATS
SPDYE3
PMS2P1
PILRB
PILRA
ZCWPW1
C7orf61
TSC22D4
C7orf51
AGFG2
FBXO24
PCOLCE
MOSPD3
TFR2
ACTL6B
GNB2
POP7
EPO
ZAN
EPHB4
SLC12A9
TRIP6
ACHE
MUC12
MUC17
TRIM56
SERPINE1
APOL3
C7orf52
MOGAT3
EB

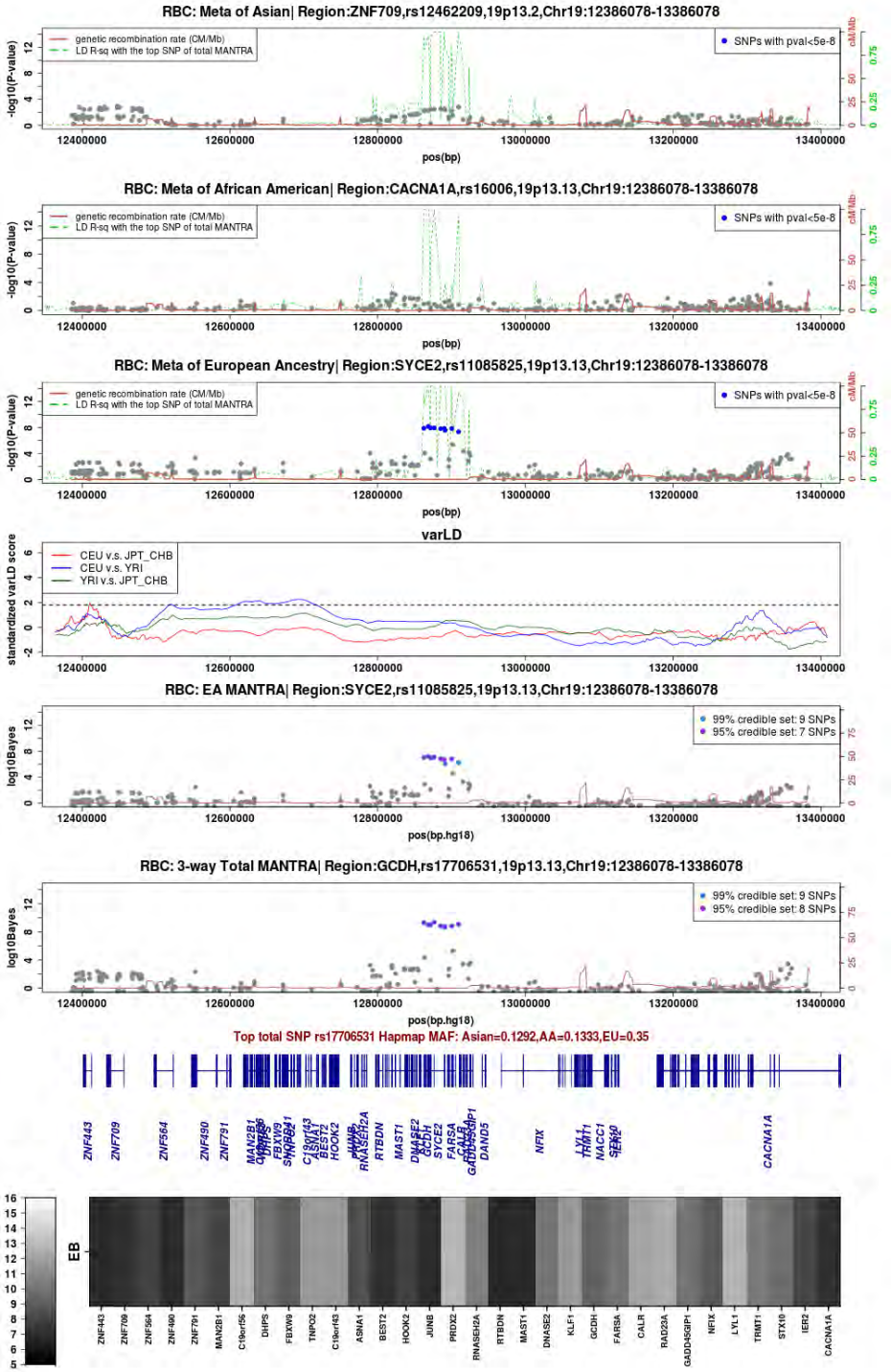

RBC: Meta of Asian| Region:MIR101-2,rs10815092,9p24.1,Chr9:4340571-5340571
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:JAK2,rs6476934,9p24.1,Chr9:4340571-5340571
RBC: Meta of European Ancestry| Region:MIR101-2,rs10758656,9p24.1,Chr9:4340571-5340571
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:MIR101-2,rs10758656,9p24.1,Chr9:4340571-5340571
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:MIR101-2,rs10758656,9p24.1,Chr9:4340571-5340571
99% credible set: 9 SNPs
95% credible set: 7 SNPs
Top total SNP rs10758656 Hapmap MAF: Asian=0.4944,AA=0.1333,EU=0.2018
SLC1A1
C9orf68
PPAPDC2
CDC37L1
AK3
RCL1
MIR101-2
JAK2
INSL6
INSL4
RLN2
RLN1
EB

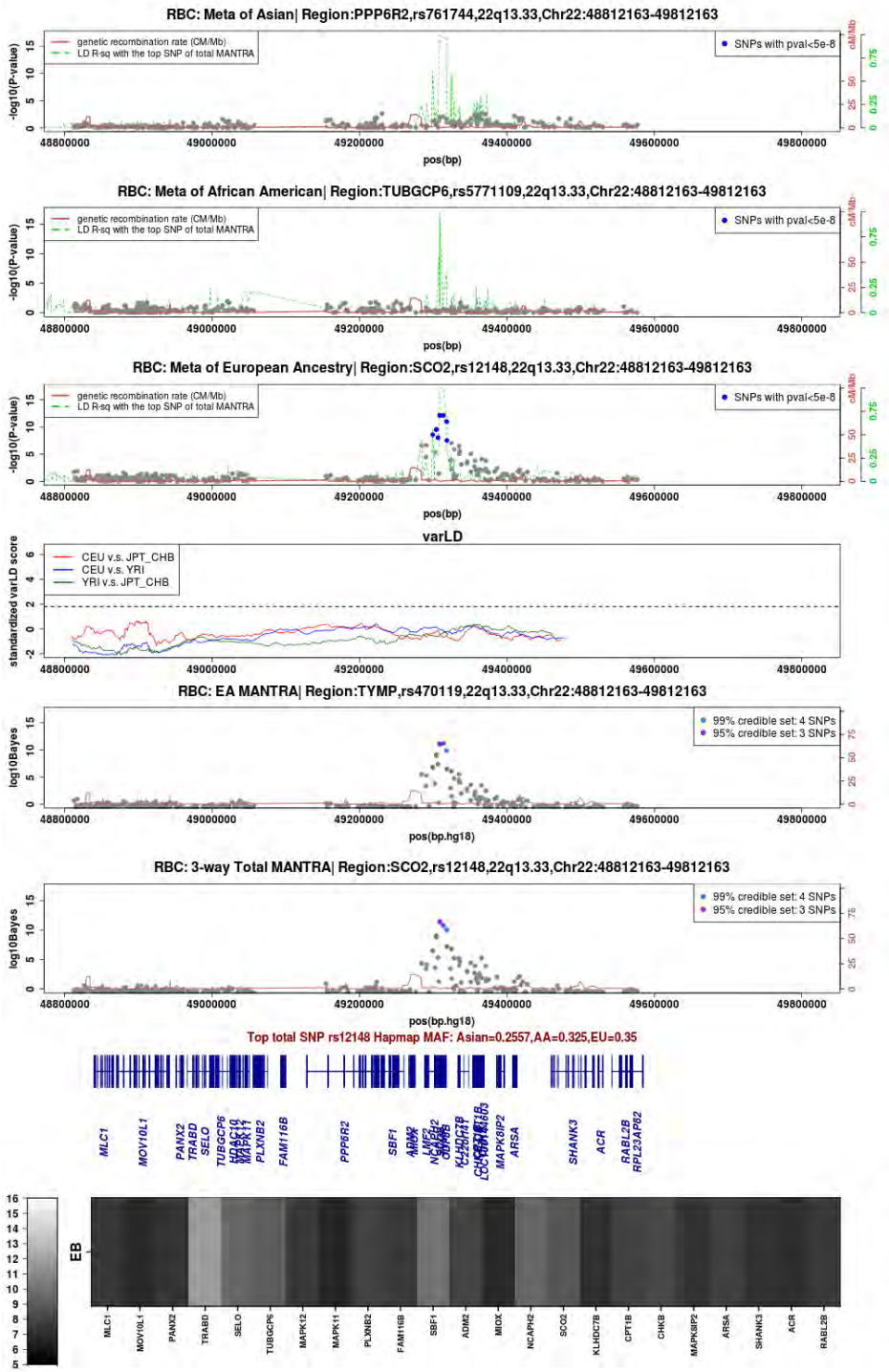

RBC: Meta of Asian| Region:ABO,rs495828,9q34.2,Chr9:134632848-135632848
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:SURF6,rs493014,9q34.2,Chr9:134632848-135632848
RBC: Meta of European Ancestry| Region:ABO,rs649129,9q34.2,Chr9:134632848-135632848
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:ABO,rs579459,9q34.2,Chr9:134632848-135632848
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:ABO,rs579459,9q34.2,Chr9:134632848-135632848
99% credible set: 4 SNPs
95% credible set: 3 SNPs
Top total SNP rs579459 Hapmap MAF: Asian=0.1629,AA=0.09167,EU=0.2167
AK8
C9orf9
TSC1
GFI1B
GTF3C5
CEL
CELP
RALGDS
GBGT1
OBP2B
ABO
SURF6
SURF1
SURF2
SURF4
C9orf96
REXO4
ADAMTS13
C9orf7
SLC2A6
TMEM8C
ADAMTSL2
FAM163B
DBH
SARDH
EB
VAV2


RBC: Meta of Asian| Region:CCND2,rs7309743,12p13.32,Chr12:3702516-4702516
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:CCND2,rs12818806,12p13.32,Chr12:3702516-4702516
RBC: Meta of European Ancestry| Region:CCND2,rs7309743,12p13.32,Chr12:3702516-4702516
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:CCND2,rs11611647,12p13.32,Chr12:3702516-4702516
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:CCND2,rs7309743,12p13.32,Chr12:3702516-4702516
99% credible set: 4 SNPs
95% credible set: 4 SNPs
Top total SNP rs7309743 Hapmap MAF: Asian=0.2882,AA=0.3061,EU=0.287
EFCAB4B
PARP11
CCND2
C12orf5
FGF23
FGF6
C12orf4
RAD51AP1
DYRK4
AKAP3
NDUFA9
GALNT8
EB


RBC: Meta of Asian| Region:ITFG3,rs11248914,16p13.3,Chr16:0-680281
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:LUC7L,rs1211375,16p13.3,Chr16:0-680281
RBC: Meta of European Ancestry| Region:LOC100134368,rs743962,16p13.3,Chr16:0-680281
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:LOC100134368,rs743962,16p13.3,Chr16:0-680281
99% credible set: 0 SNPs
95% credible set: 0 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:LUC7L,rs1211375,16p13.3,Chr16:0-680281
99% credible set: 2 SNPs
95% credible set: 1 SNPs
Top total SNP rs1211375 Hapmap MAF: Asian=0.4719,AA=0.3083,EU=0.275
EB
POLR3K
RHBDF1
MPG
HBZ
HBA1
HBQ1
LUC7L
ITFG3
RGS11
ARHGDIG
PDIA2
AXIN1
MRPL28
NME4
DECR2
RAB11FIP3
SDLH
PIGQ
RAB40C
WFIKKN1
WDR90
RHOT2
RHBDL1
STUB1
WDR24


RBC: Meta of Asian| Region:LOC100130148,rs242557,17q21.31,Chr17:40872185-42216164
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:STH,rs12150170,17q21.31,Chr17:40872185-42216164
RBC: Meta of European Ancestry| Region:LRRC37A,rs2696555,17q21.31,Chr17:40872185-42216164
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:LRRC37A,rs2668617,17q21.31,Chr17:40872185-42216164
99% credible set: 198 SNPs
95% credible set: 198 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:LRRC37A,rs2732706,17q21.31,Chr17:40872185-42216164
99% credible set: 200 SNPs
95% credible set: 200 SNPs
Top total SNP rs2732706 Hapmap MAF: Asian=0,AA=0,EU=0.1949
PLEKHM1
LRRC37A4
LOC644172
MGC57346
C17orf69
CRHR1
IMP5
LOC100128977
LOC100130148
MAPT
STH
KIAA1267
LOC644246
LRRC37A
ARL17B
NSFP1
LRRC37A2
ARL17A
NSF
WNT3
EB


RBC: Meta of Asian| Region:ZNF709,rs12462209,19p13.2,Chr19:12386078-13386078
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:CACNA1A,rs16006,19p13.13,Chr19:12386078-13386078
RBC: Meta of European Ancestry| Region:SYCE2,rs11085825,19p13.13,Chr19:12386078-13386078
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:SYCE2,rs11085825,19p13.13,Chr19:12386078-13386078
99% credible set: 9 SNPs
95% credible set: 7 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:GCDH,rs17706531,19p13.13,Chr19:12386078-13386078
99% credible set: 9 SNPs
95% credible set: 8 SNPs
Top total SNP rs17706531 Hapmap MAF: Asian=0.1292,AA=0.1333,EU=0.35
ZNF443
ZNF709
ZNF564
ZNF490
ZNF791
MAN2B1
RTBDN
MAST1
SYCE2
FARSA
DAND5
NFIX
CACNA1A
EB
ZNF443
ZNF709
ZNF564
ZNF490
ZNF791
MAN2B1
C19orf55
DHPS
FBXW9
TNPO2
C19orf43
ASNA1
BEST2
HOOK2
JUNB
PRDX2
RNASEH2A
RTBDN
MAST1
DNASE2
KLF1
GCDH
FARSA
CALR
RAD23A
GADD45GIP1
NFIX
LYL1
TRMT1
STX10
IER2
CACNA1A


RBC: Meta of Asian| Region:PPP6R2,rs761744,22q13.33,Chr22:48812163-49812163
genetic recombination rate (CM/Mb)
LD R-sq with the top SNP of total MANTRA
SNPs with pval<5e-8
-log10(P-value)
cM/Mb
pos(bp)
RBC: Meta of African American| Region:TUBGCP6,rs5771109,22q13.33,Chr22:48812163-49812163
RBC: Meta of European Ancestry| Region:SCO2,rs12148,22q13.33,Chr22:48812163-49812163
varLD
CEU v.s. JPT_CHB
CEU v.s. YRI
YRI v.s. JPT_CHB
standardized varLD score
RBC: EA MANTRA| Region:TYMP,rs470119,22q13.33,Chr22:48812163-49812163
99% credible set: 4 SNPs
95% credible set: 3 SNPs
log10Bayes
pos(bp.hg18)
RBC: 3-way Total MANTRA| Region:SCO2,rs12148,22q13.33,Chr22:48812163-49812163
Top total SNP rs12148 Hapmap MAF: Asian=0.2557,AA=0.325,EU=0.35
MLC1
MOV10L1
PANX2
TRABD
SELO
TUBGCP6
PLXNB2
FAM116B
PPP6R2
SBF1
MIOX
MAPK8IP2
ARSA
SHANK3
ACR
RABL2B
RPL23AP82
EB
MAPK12
MAPK11
ADM2
NCAPH2
SCO2
KLHDC7B
CPT1B
CHKB

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