SUPPLEMENTARY ONLINE MATERIAL

New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism

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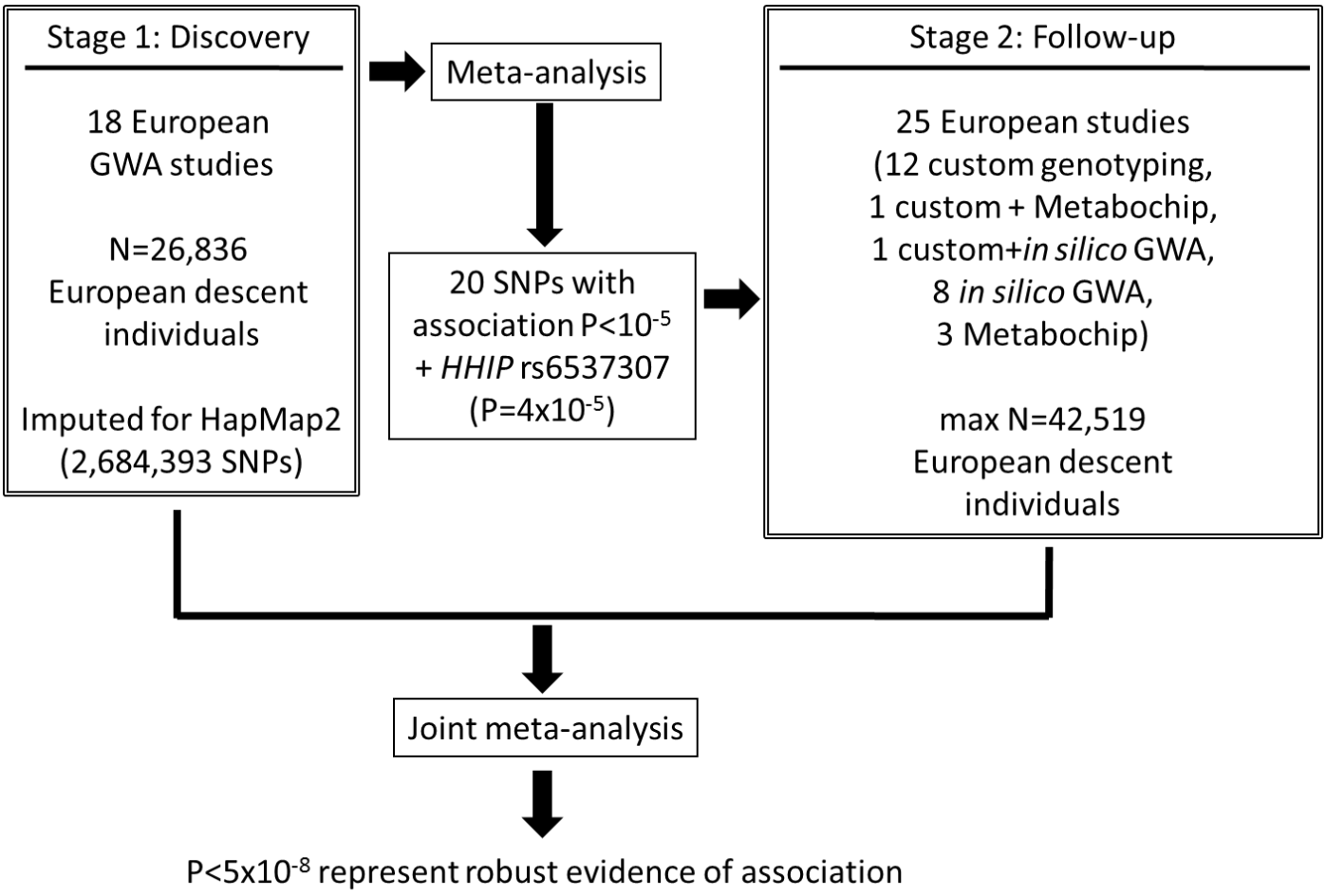
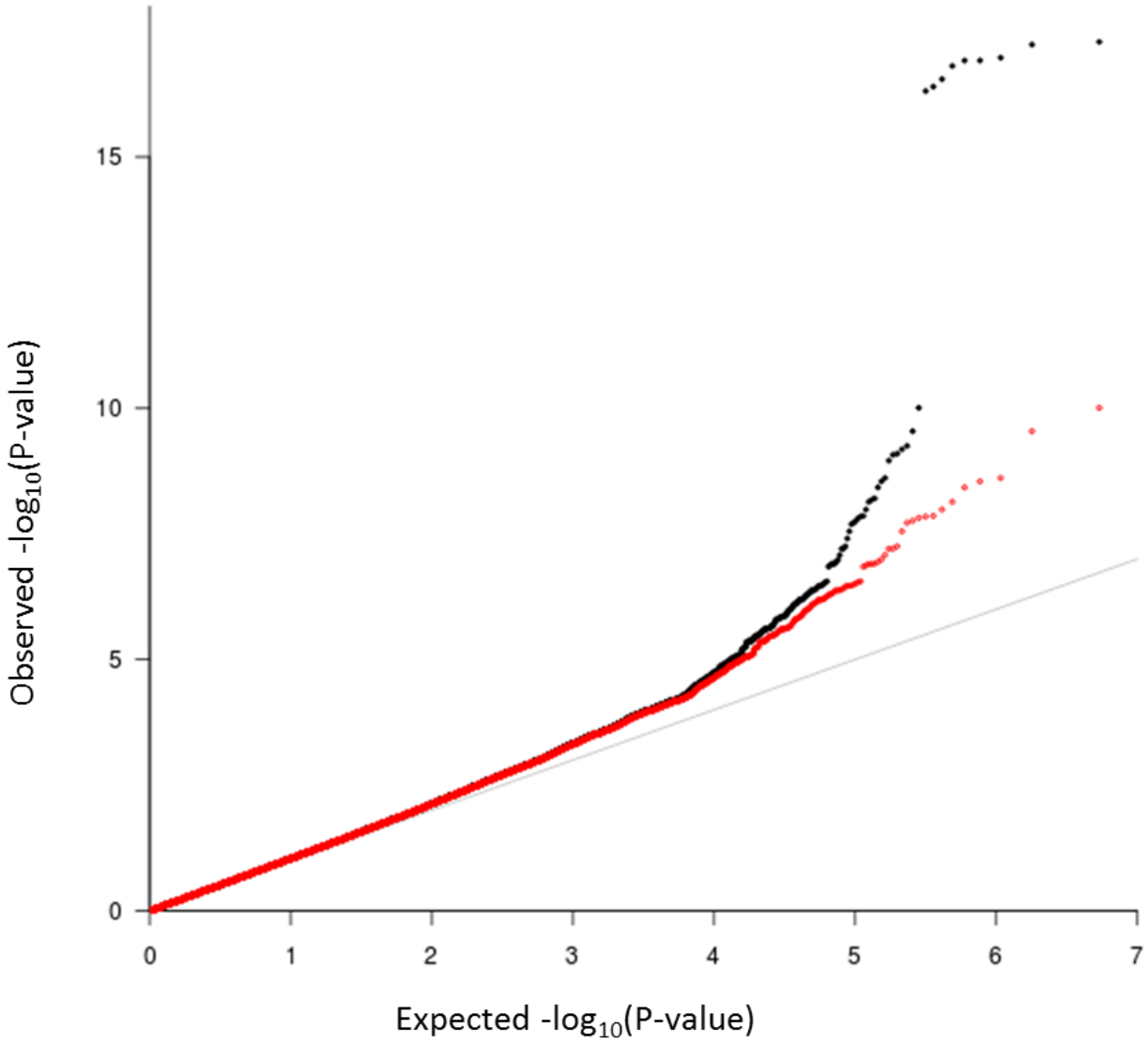
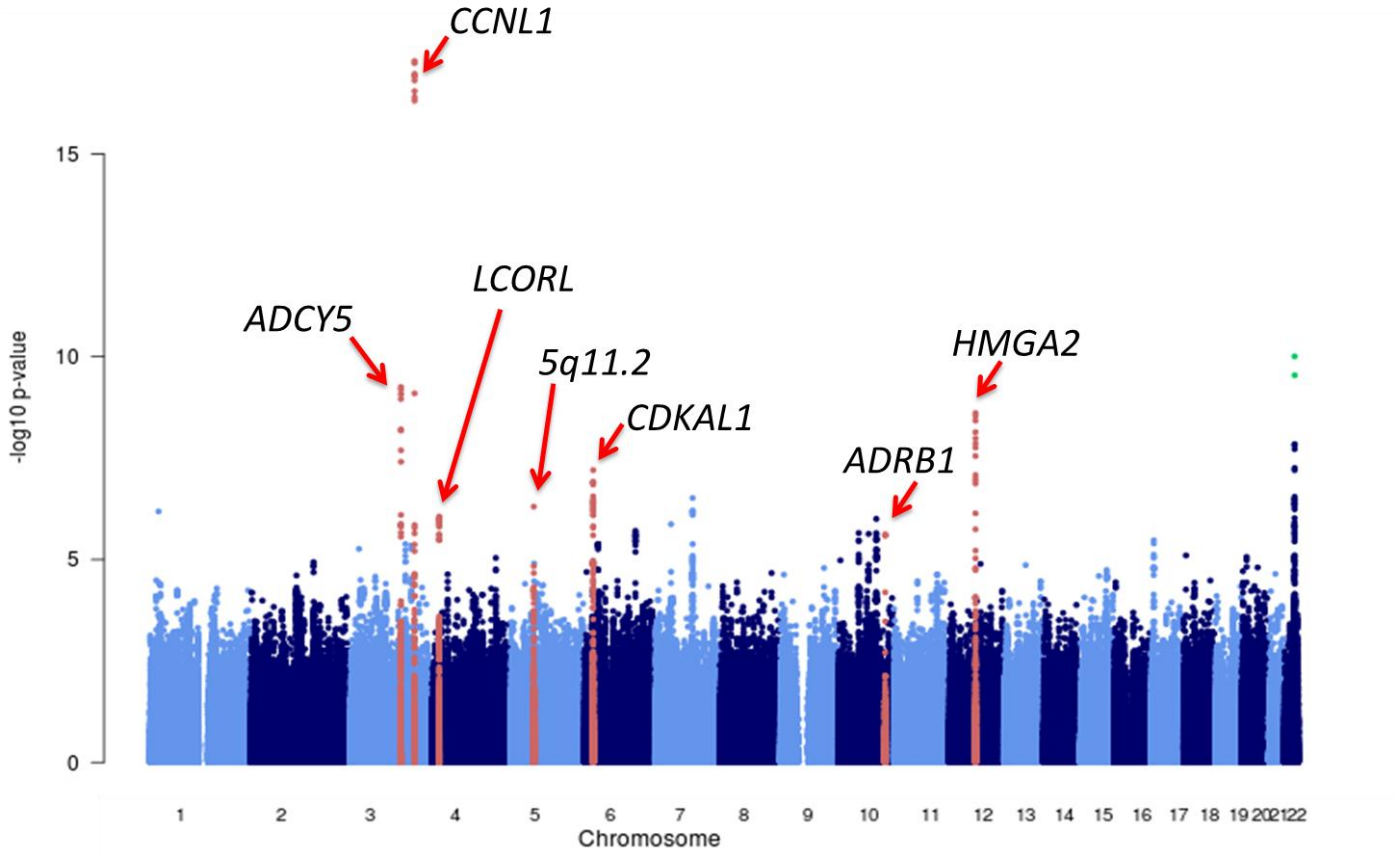
Supplementary Figure 1. Summary of study design.



Supplementary Figure 2. Quantile-quantile plot of 2,684,393 single nucleotide polymorphisms (SNPs) from the meta-analysis of up to N=26,836 discovery samples. The black dots represent observed *P* values and the black line represents the expected *P* values under the null distribution. The red dots represent observed *P* values after excluding the previously identified *ADCY5* and *CCNL1* signals.

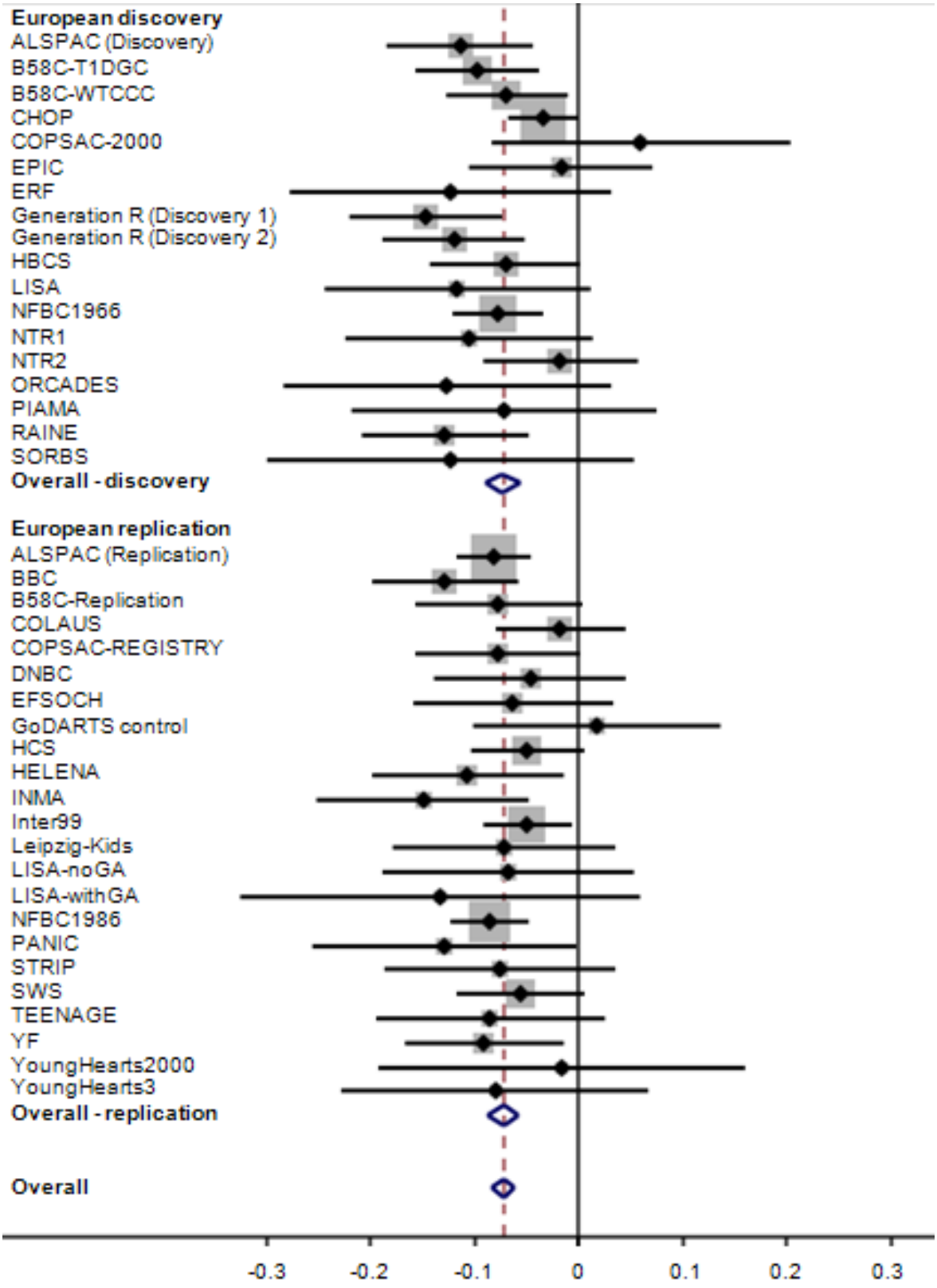


Supplementary Figure 3. Manhattan plot of the association *P* values for birth weight from the **discovery** meta-analysis (*n* = up to 26,836). The -$\log_{10}$ of the *P* value for each of 2,684,393 SNPs (y-axis) is plotted against the genomic position (NCBI Build 36; x-axis). Association signals that reached genome-wide significance ($P < 5x10^{-8}$) in the global meta-analysis of discovery and follow-up studies are shown in red.

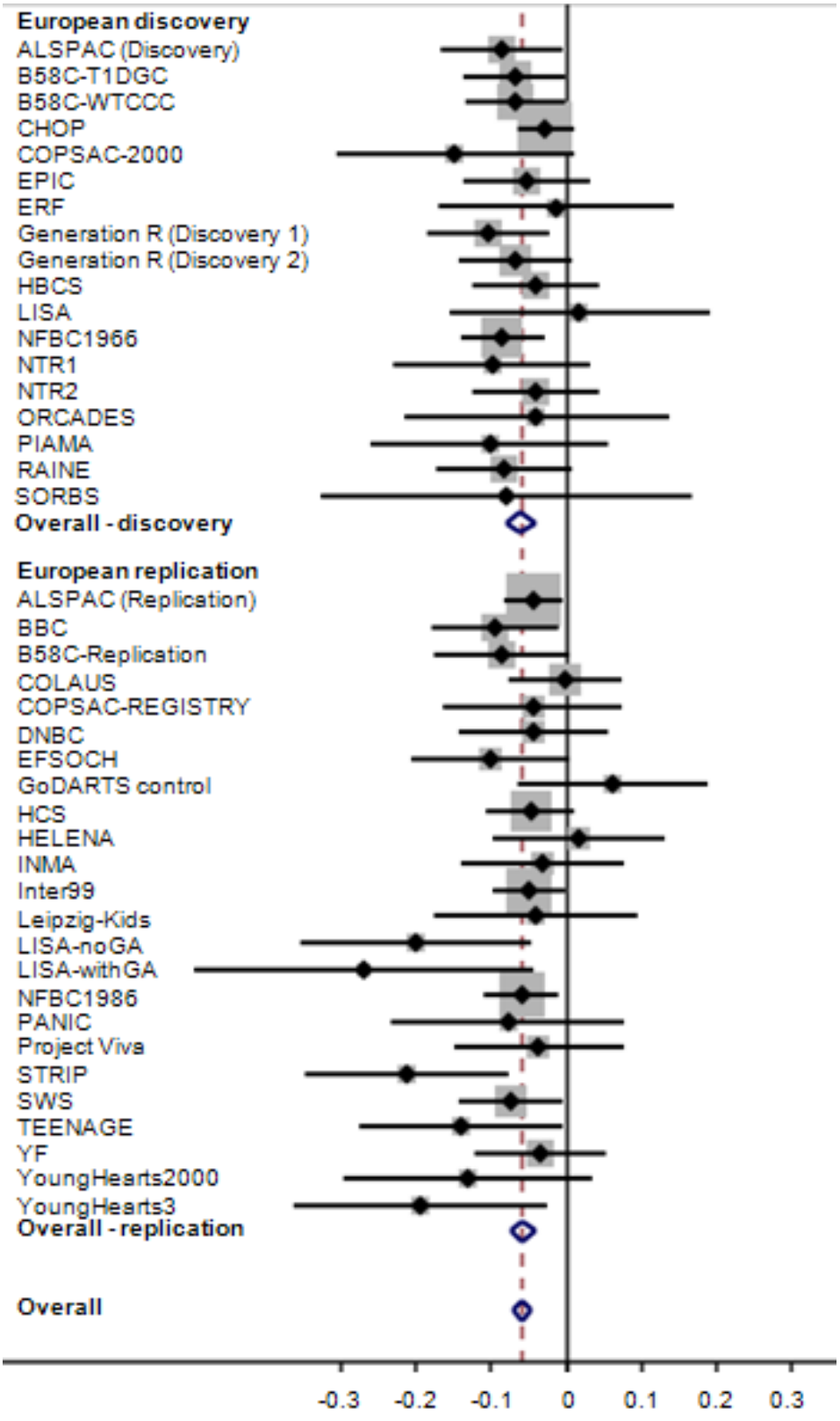


Supplementary Figure 4. Forest plots of the associations between birth weight and (a) *CCNL1*, (b) *ADCY5*, (c) *HMGA2*, (d) *CDKAL1*, (e) *5q11.2*, (f) *LCORL* and (g) *ADRB1* in Europeans. In each plot, the dashed red line indicates the effect size from the overall meta-analysis of discovery and follow-up samples.

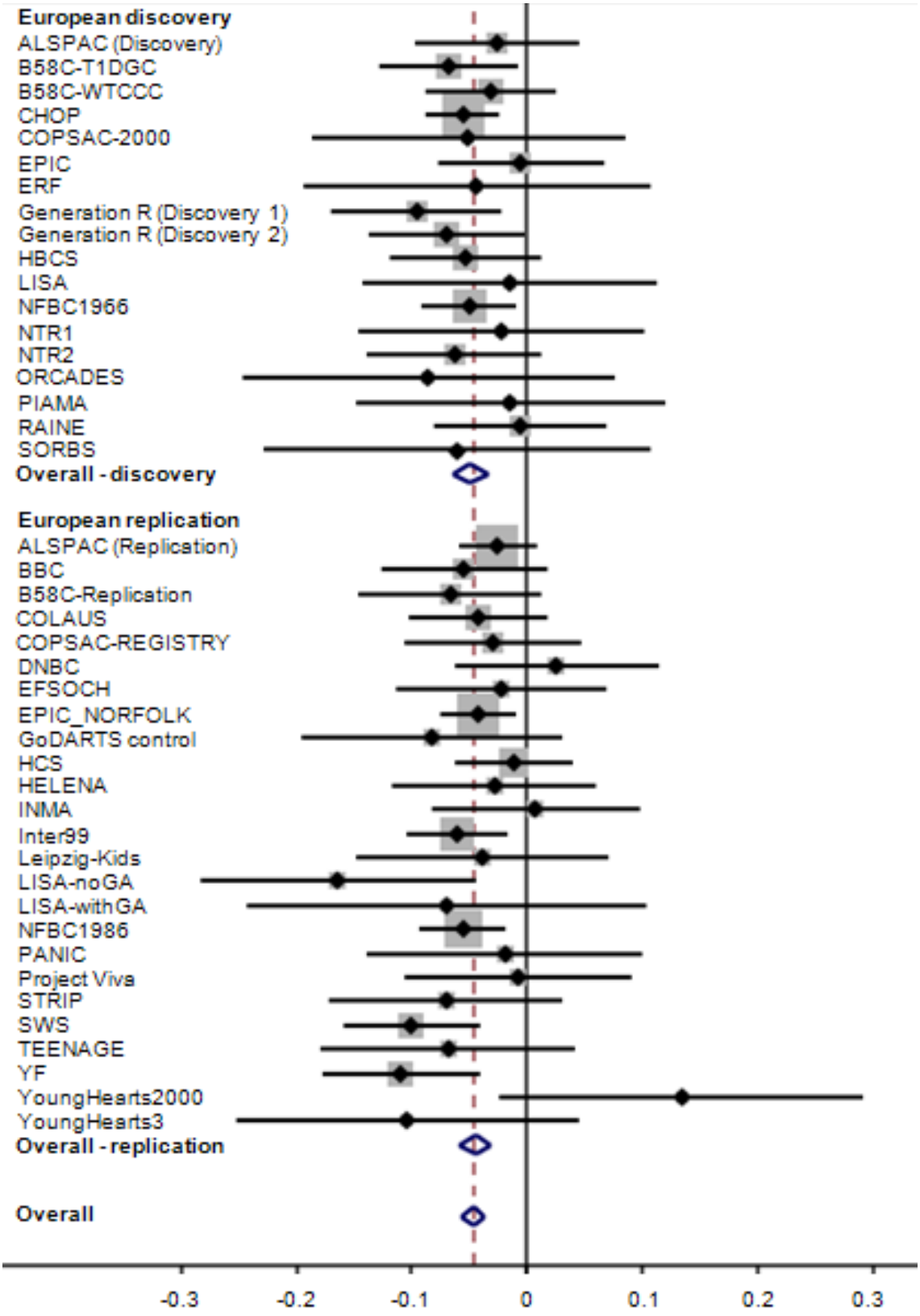
(a) *CCNL1* (overall n = 61,142; $P = 3.6 \times 10^{-38}$; heterogeneity P = 0.49)



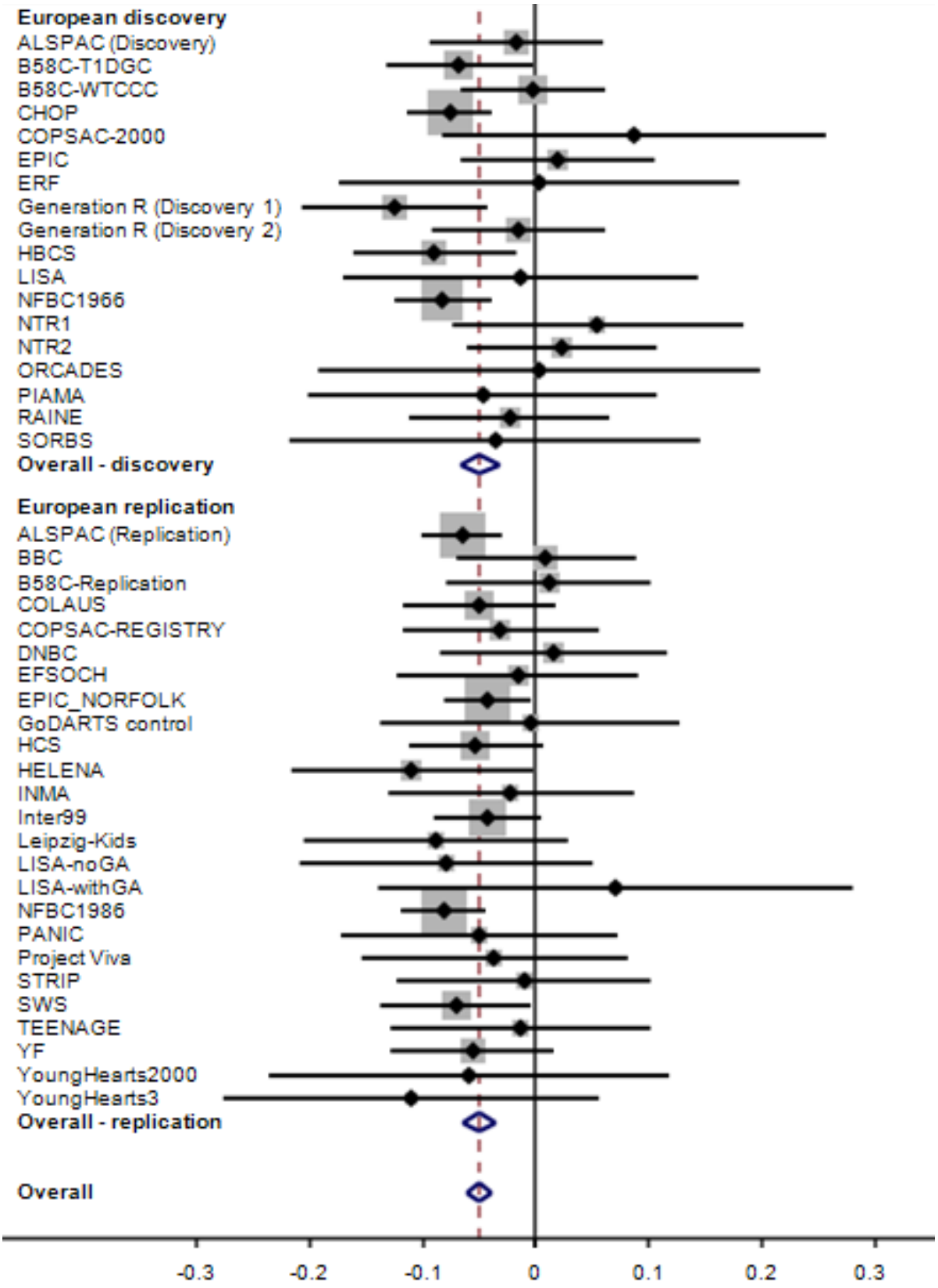
(b) *ADCY5* (overall *n* = 61,509; $P = 5.5 \times 10^{-20}$; heterogeneity *P* = 0.69)



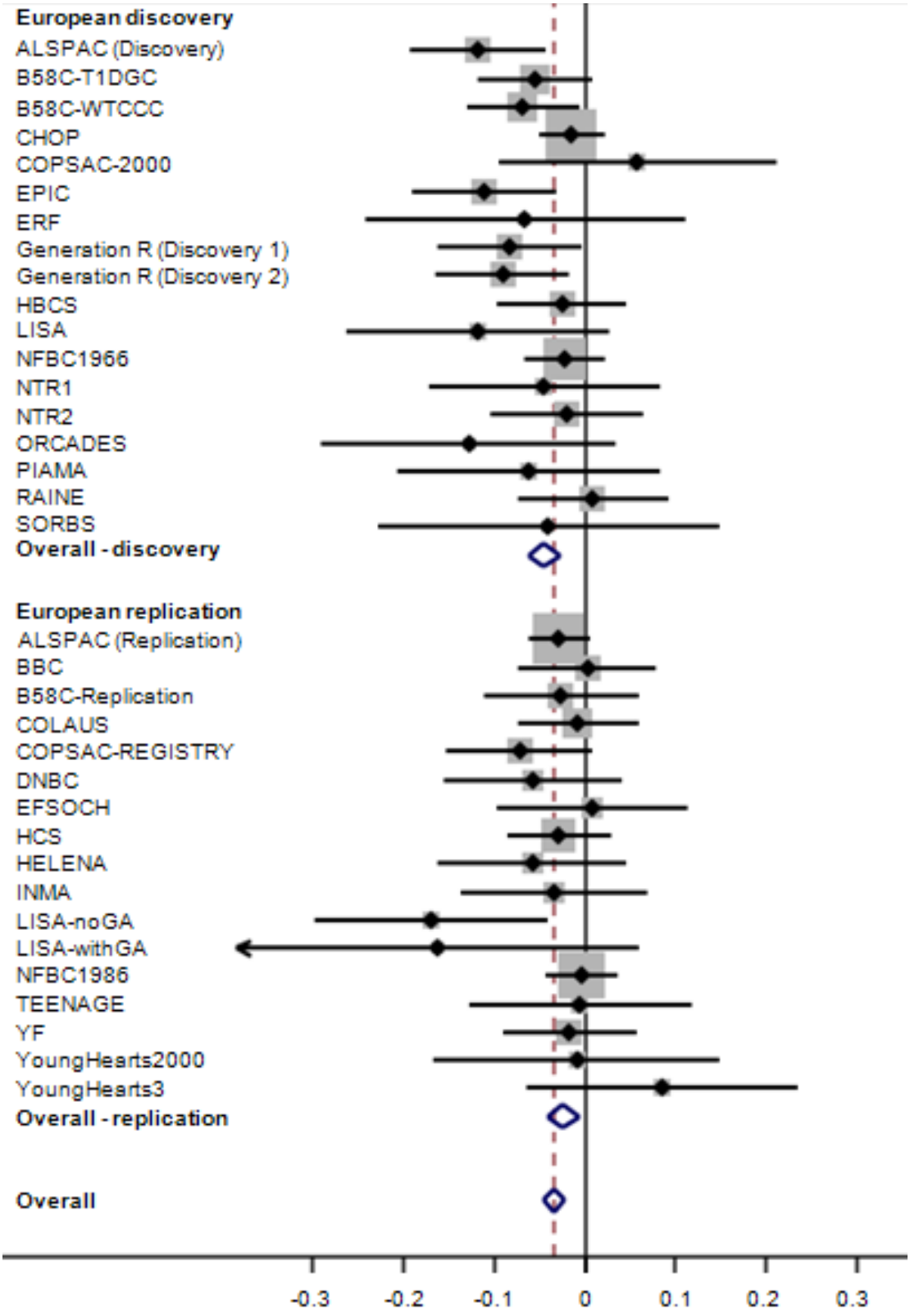
(c) *HMGA2* (overall *n* = 68,655; *P* = 1.4x10^{-19}; heterogeneity *P* = 0.82)



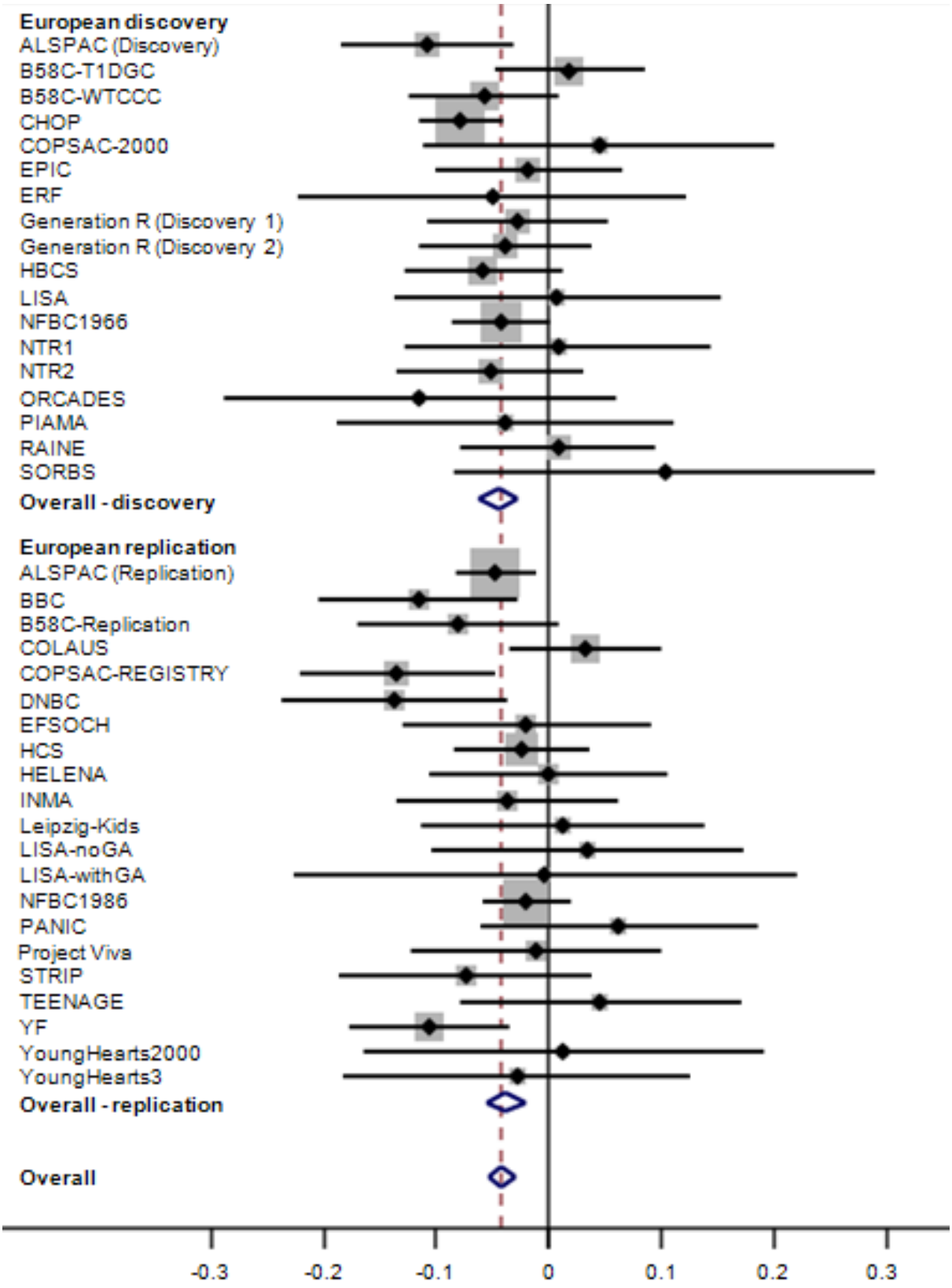
(d) *CDKAL1* (overall *n* = 68,822; *P* = 1.5x10^{-18}; heterogeneity *P* = 0.57)



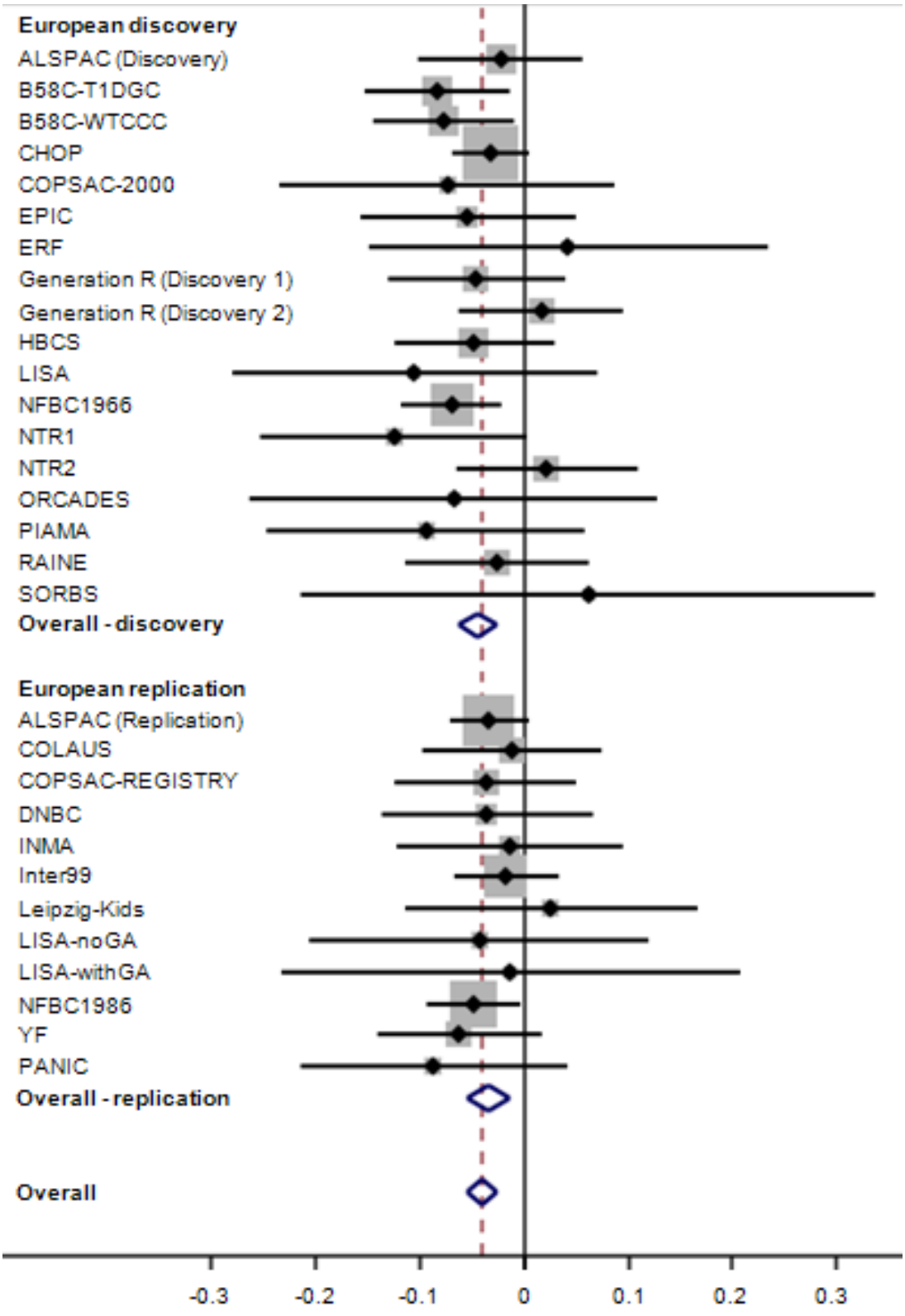
(e) *5q11.2* (overall *n* = 53,619; *P* = 4.6x10^{-8}; heterogeneity *P* = 0.40)



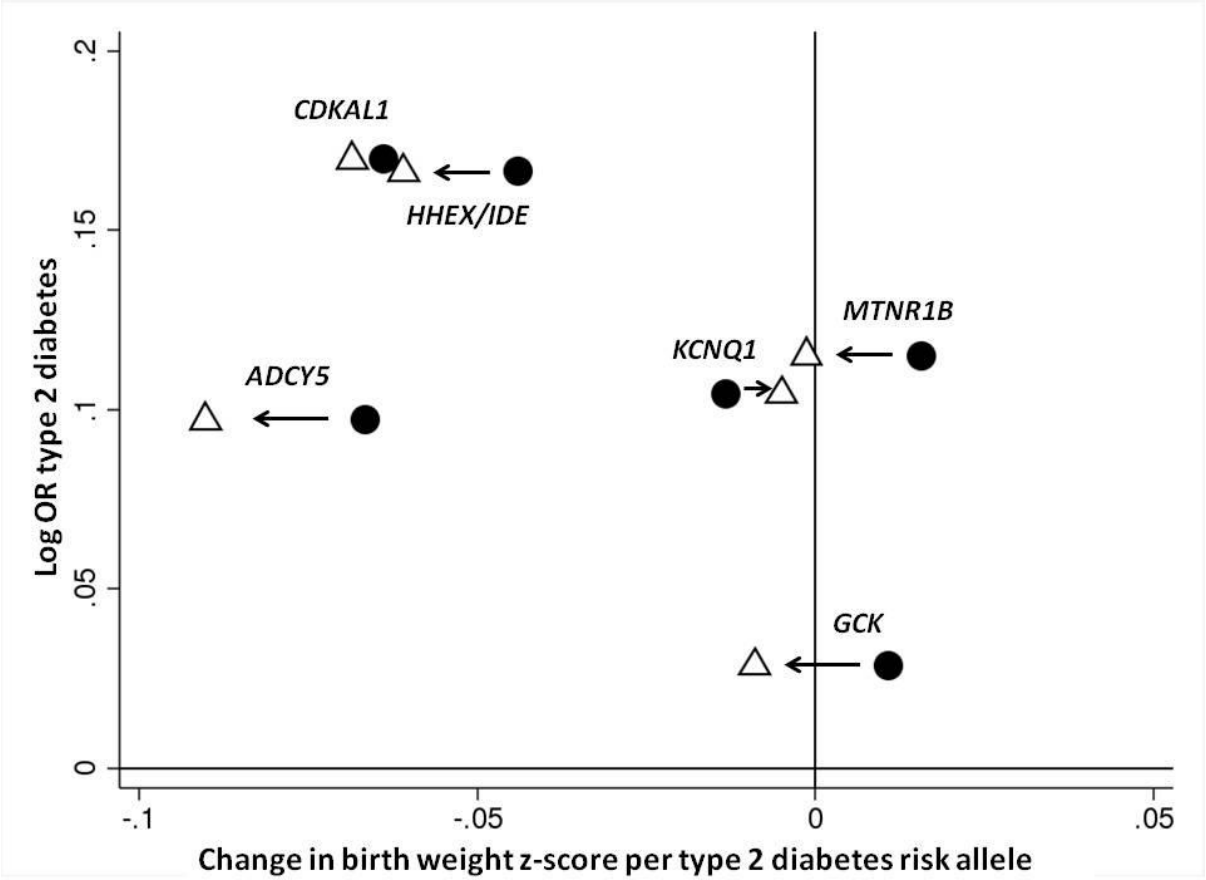
(f) *LCORL* (overall *n* = 55,877; $P = 4.6 \times 10^{-11}$; heterogeneity *P* = 0.16)



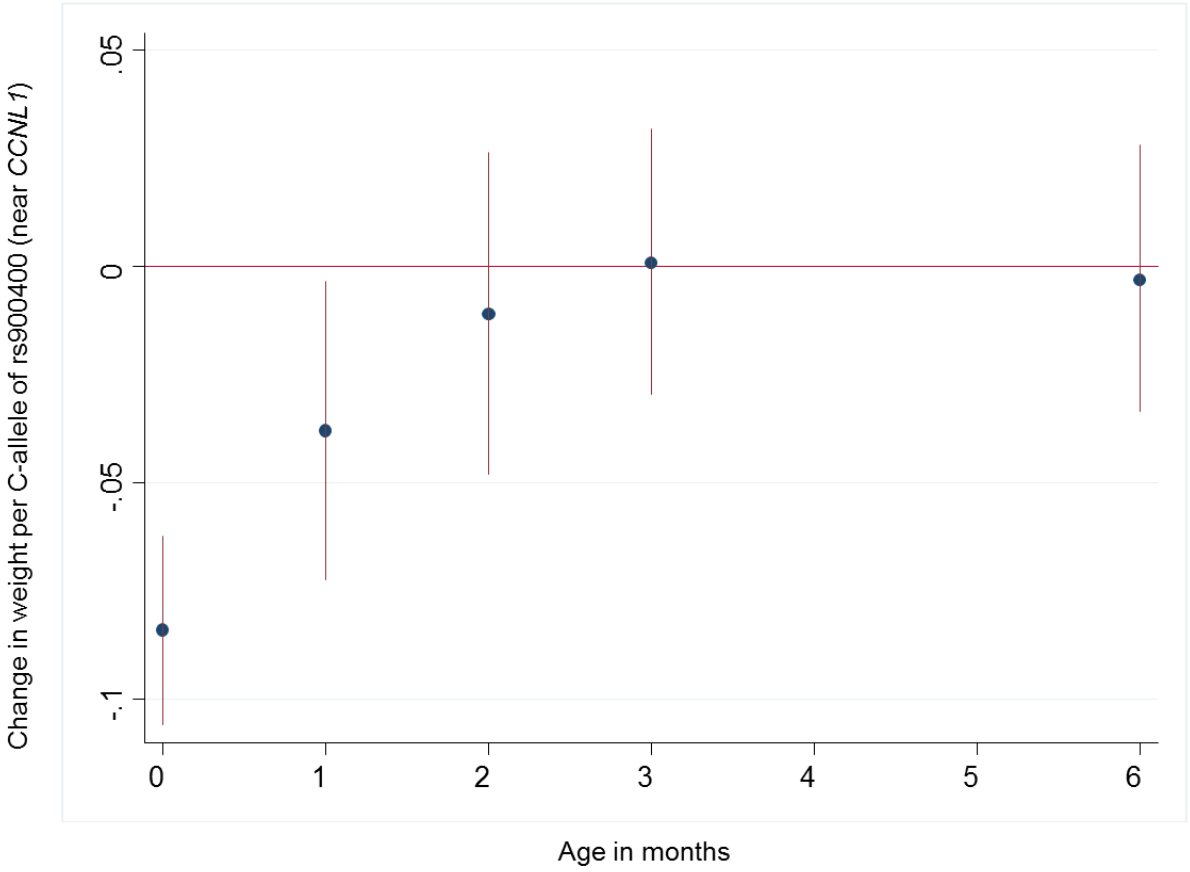
(g) *ADRB1* (overall *n* = 49,660; *P* = 3.6x10^{-9}; heterogeneity *P* = 0.97)



Supplementary Figure 5. Plot of type 2 diabetes effect size against birth weight effect size (n=5,327 ALSPAC mother-child pairs) for loci achieving $P < 0.01$ in the discovery meta-analysis. Circles are unadjusted for maternal genotype; triangles are adjusted for maternal genotype.

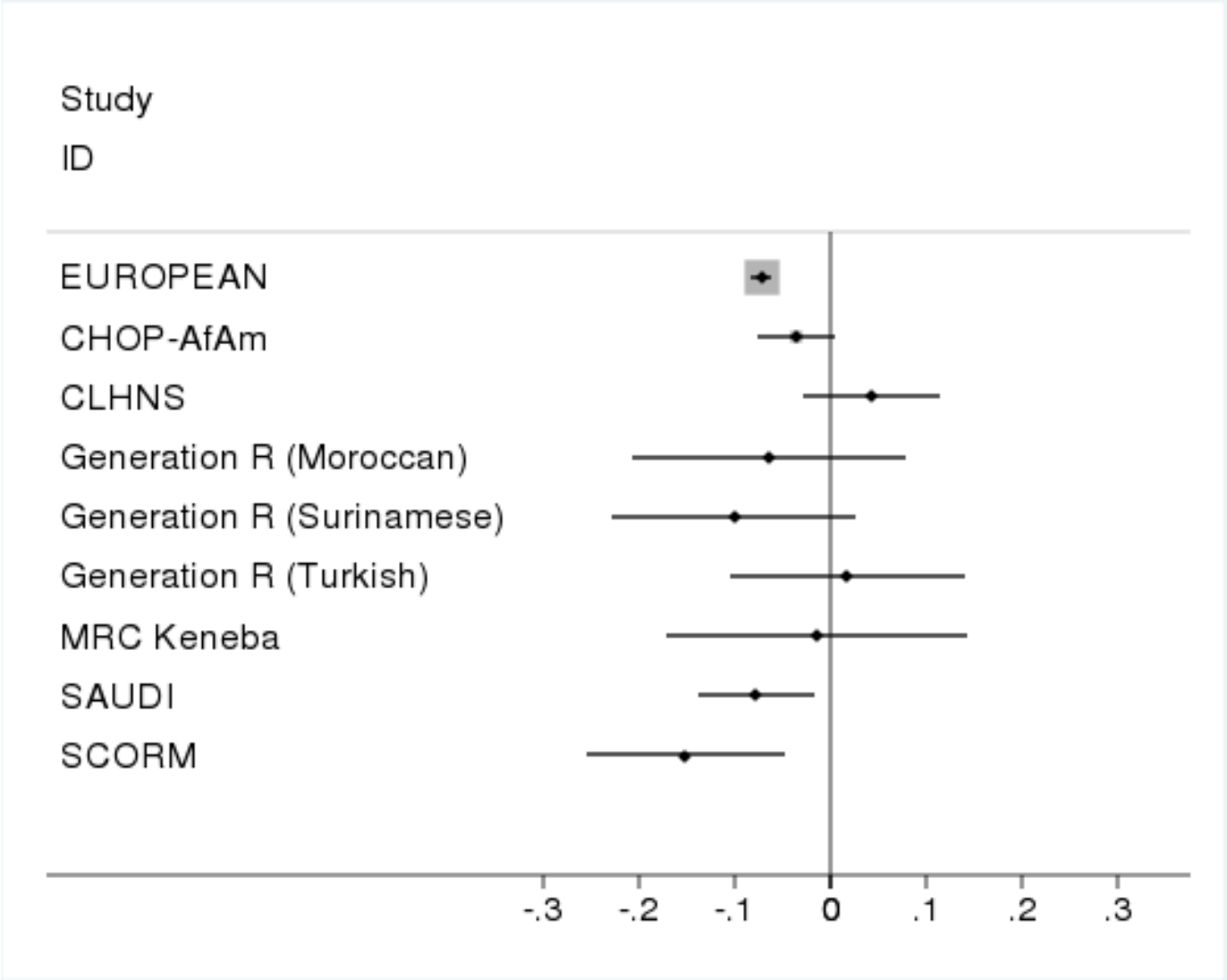


Supplementary Figure 6. Associations between SNP rs900400 near *CCNL1* and weight from birth to 6 months in seven studies with available postnatal data. The vertical lines show 95% confidence intervals around the effect size estimates. Total sample sizes: *n* = 15,090 (0 months); *n* = 6,952 (1 month); *n* = 5,720 (2 months); *n* = 7,857 (3 months); *n* = 7,535 (6 months).

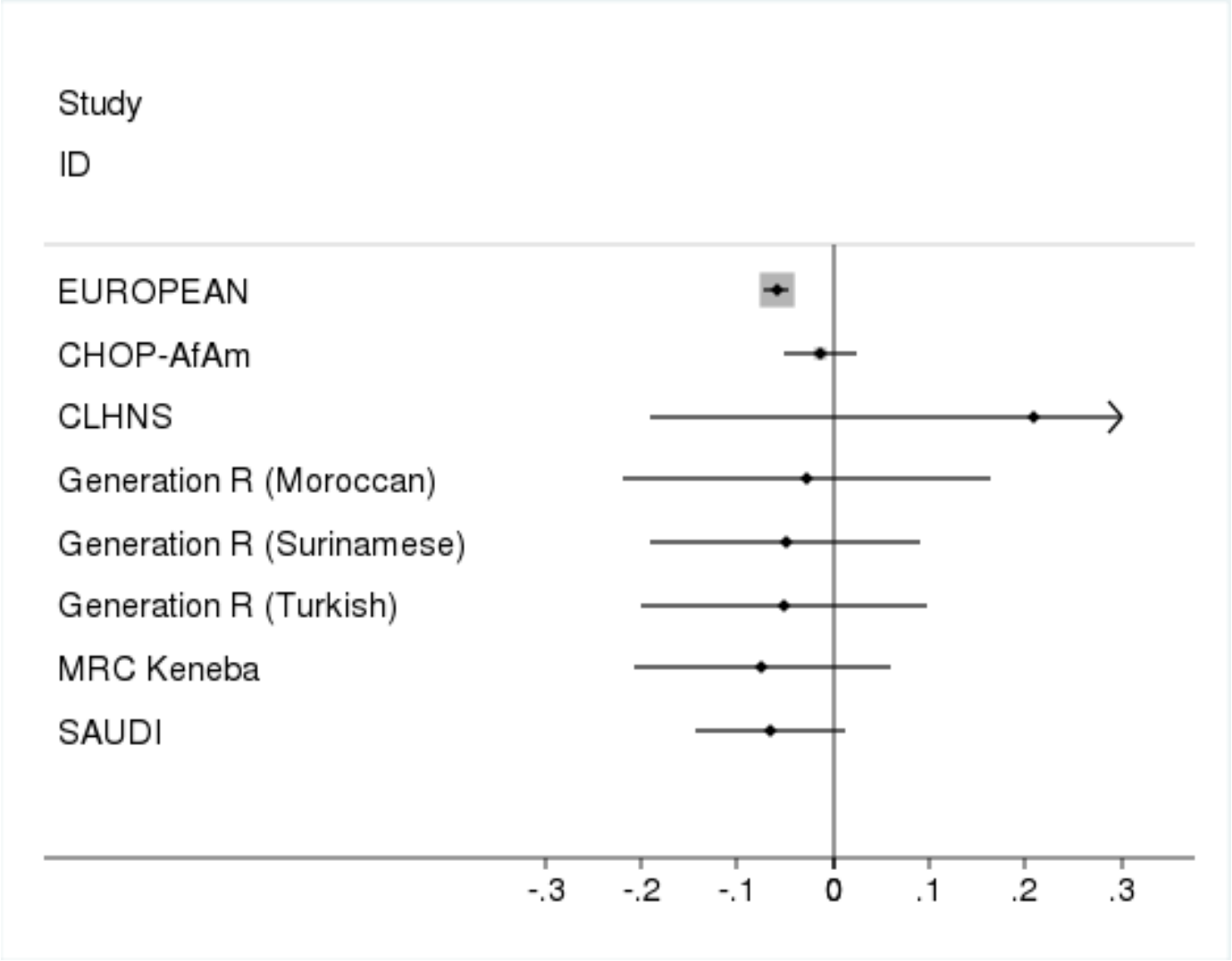


Supplementary Figure 7. Forest plots of the associations between birth weight and (a) *CCNL1*, (b) *ADCY5*, (c) *HMGA2*, (d) *CDKAL1*, (e) *5q11.2*, (f) *LCORL* and (g) *ADRB1* in non-Europeans. The overall European result is shown for comparison. The non-European studies are from East/Southeast Asia (Chinese [SCORM] and Filipino [CLHNS]), Africa (African-American [CHOP-AfAm], Mandinka [MRC Keneba] and Moroccan [Generation R]), Middle East (Arab [SAUDI], Turkish [Generation R]), and South America (Surinamese [Generation R]).

(a) *CCNL1*



(b) *ADCY5*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CHOP-AfAm
CLHNS
Generation R (Moroccan)
Generation R (Surinamese)
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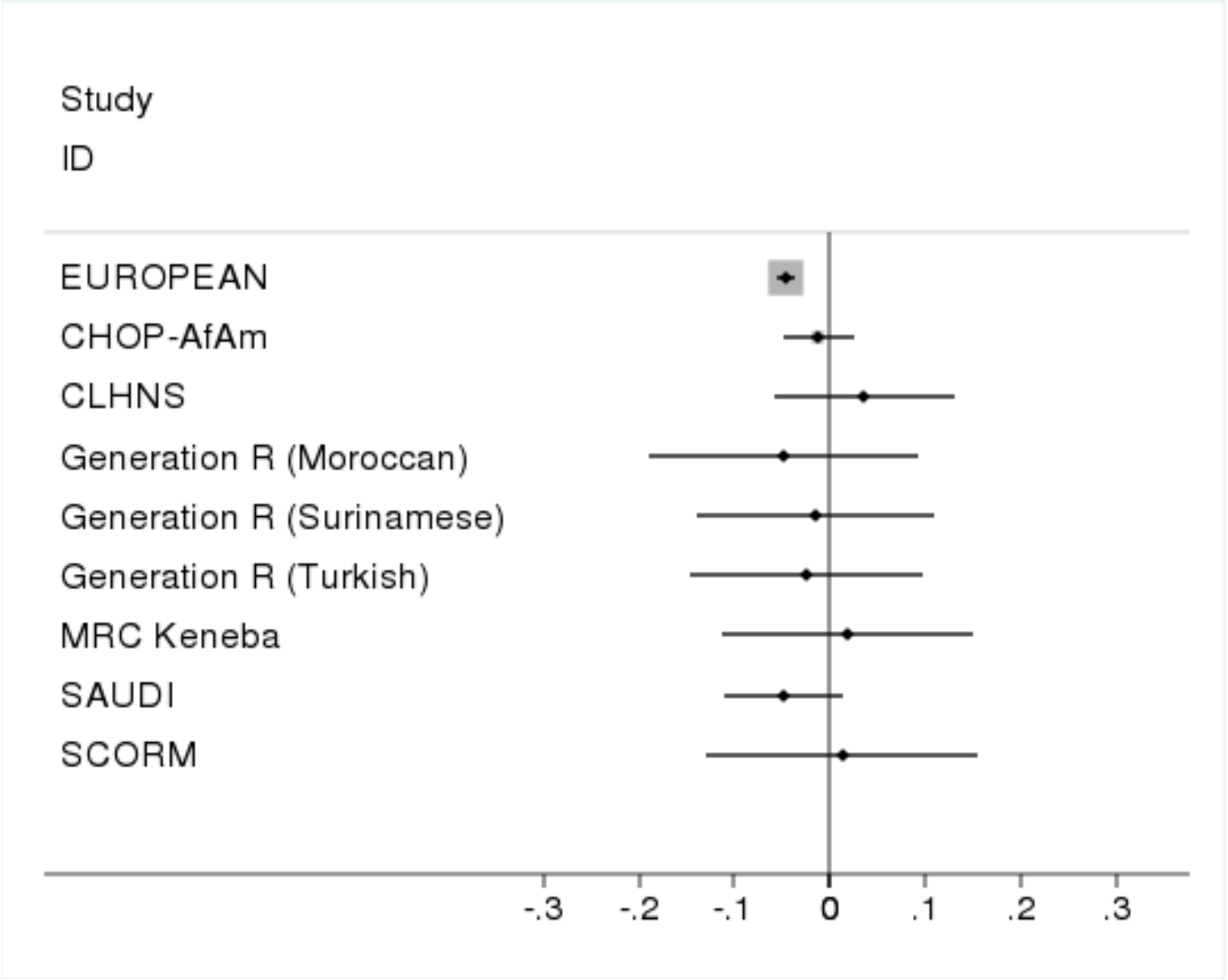
(c) *HMGA2*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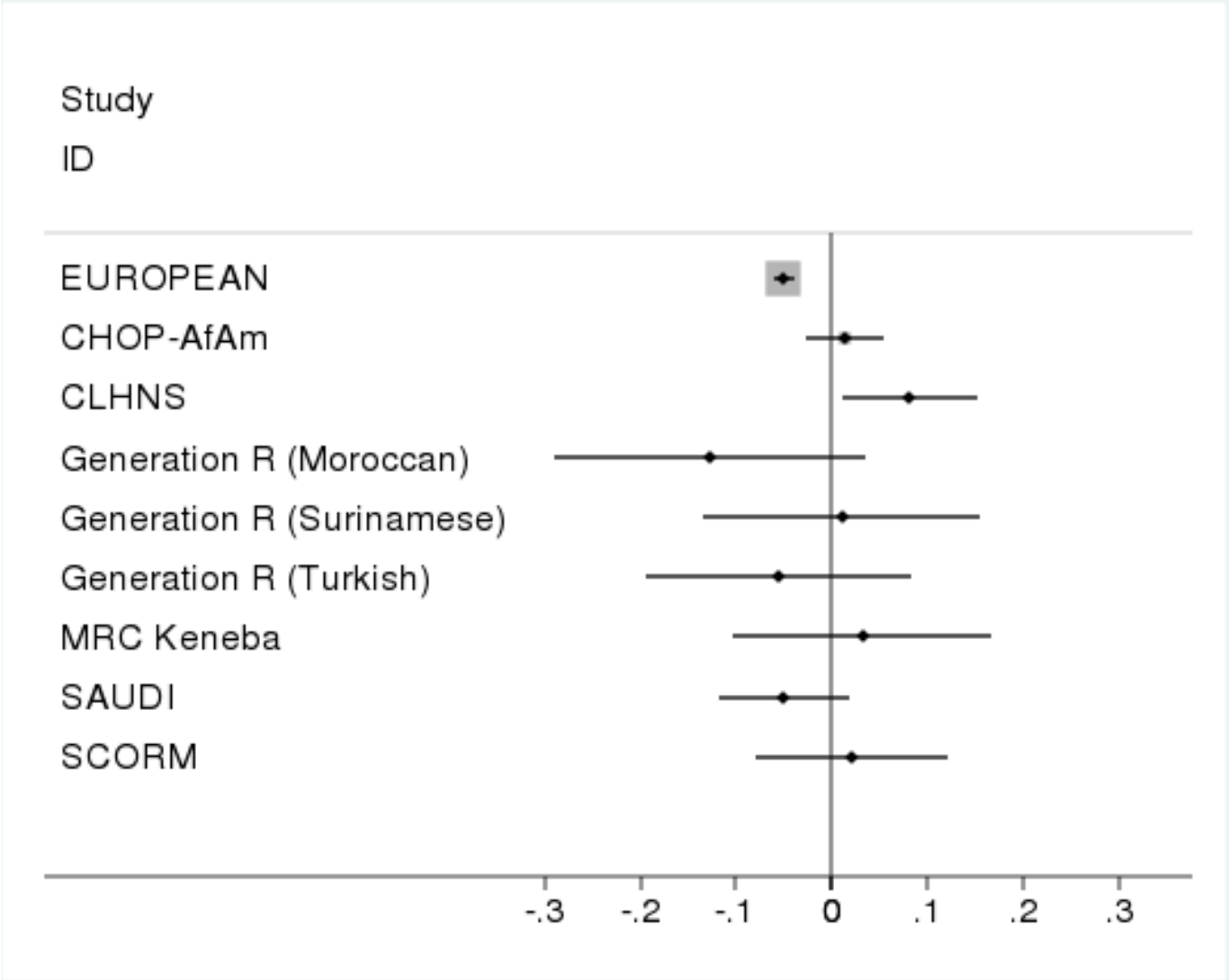
(d) *CDKAL1*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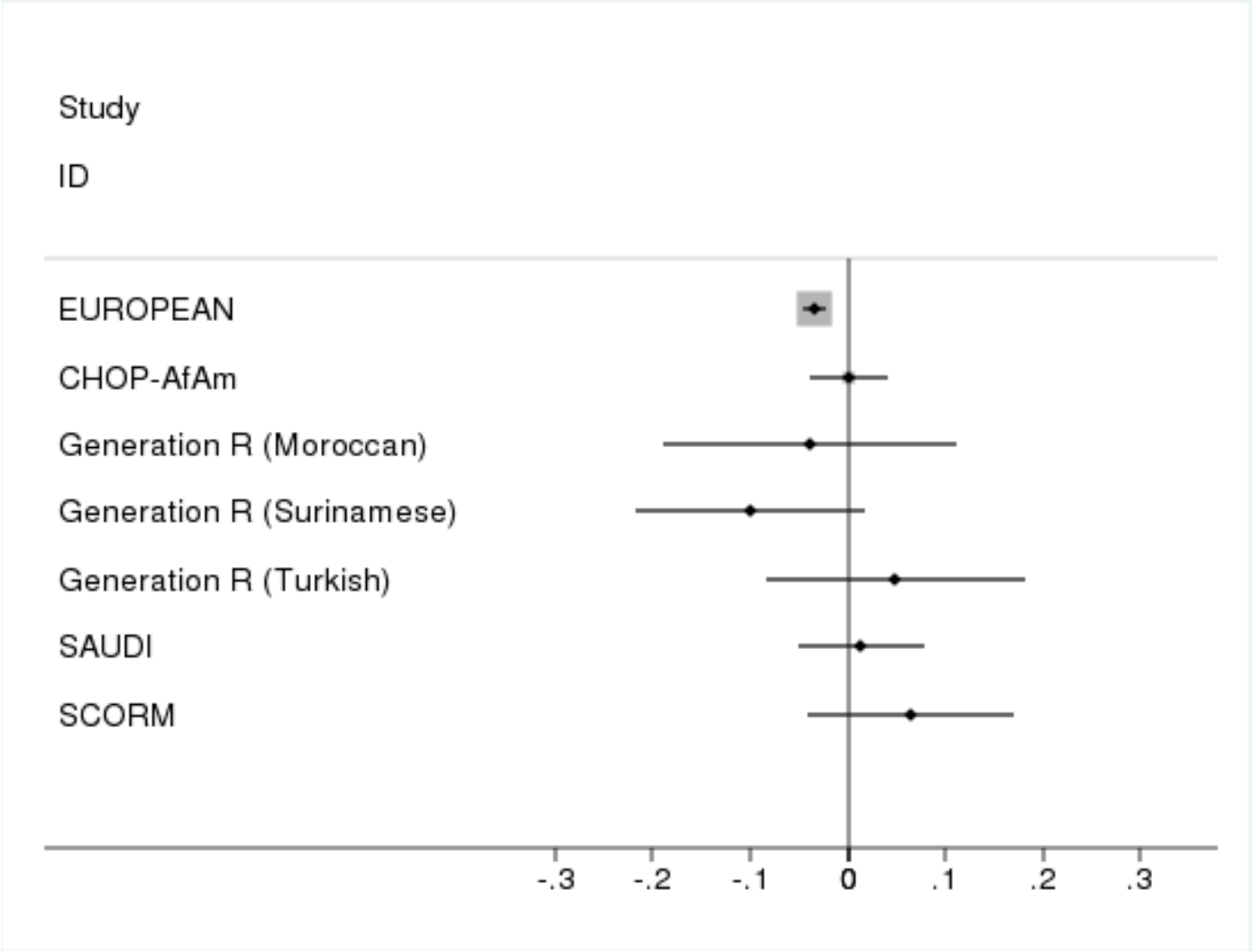
(e) *5q11.2*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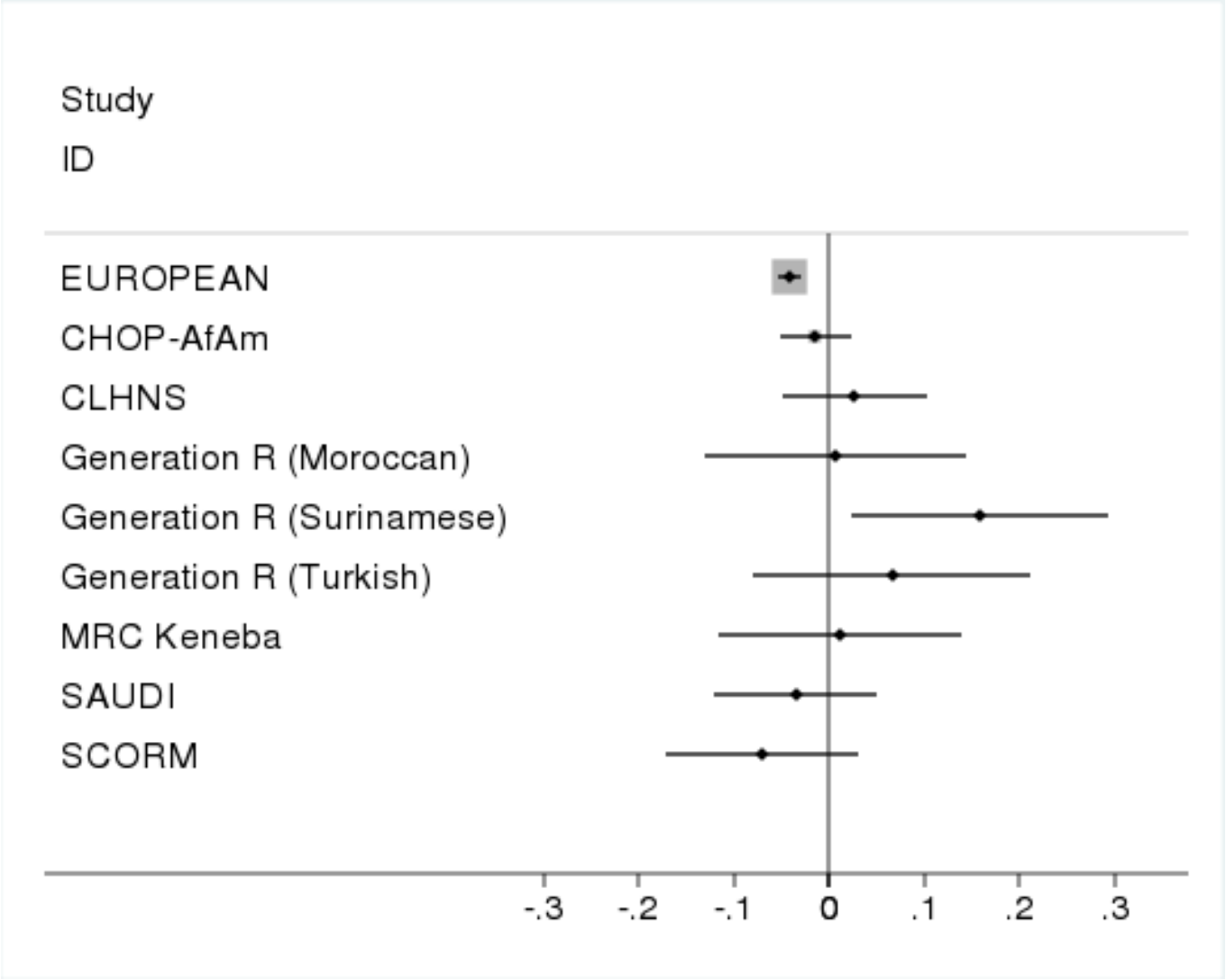
(f) *LCORL*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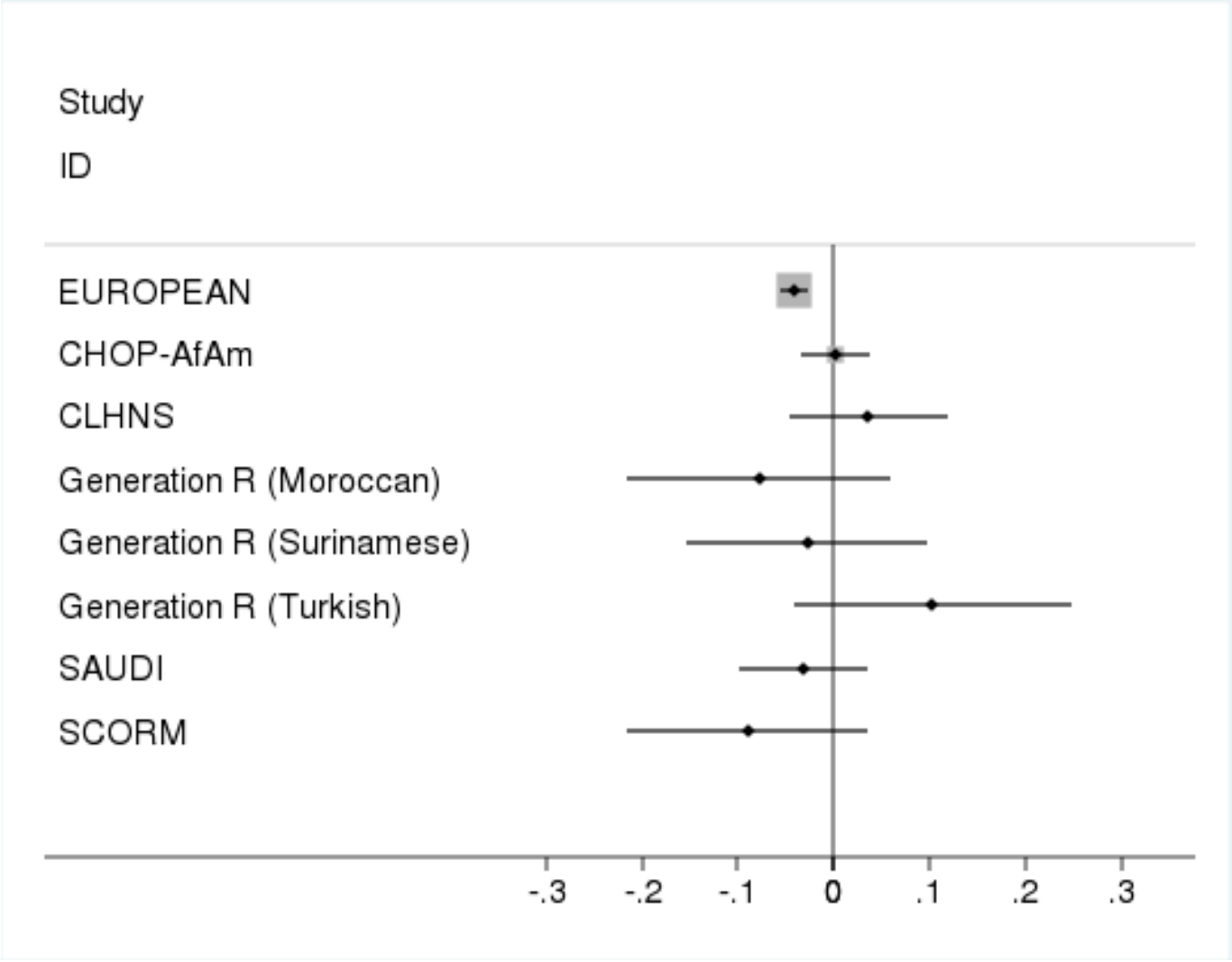
(g) *ADRB1*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Generation R (Moroccan)
Generation R (Surinamese)
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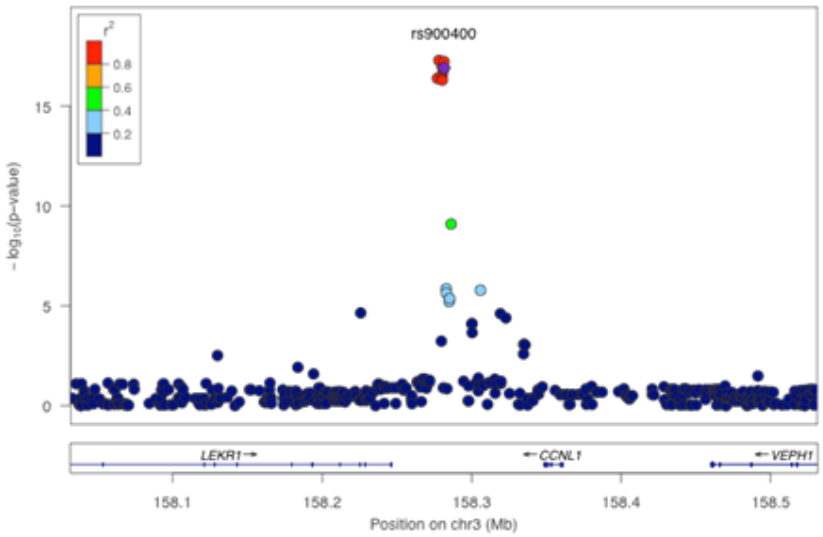
Supplementary Figure 8. Ethnicity-specific regional plots for (a) *CCNL1* and (b) *ADCY5* in European (n=26,813), East/Southeast Asian (n=2,135) and African American (n=6,315). Directly genotyped or imputed SNPs are plotted as a function of genomic position (NCBI Build 36). In each panel, the European discovery stage SNP taken forward for follow-up, i.e. rs900400 in *CCNL1* and rs9883204 in *ADCY5*, is represented by a purple diamond. Estimated recombination rates are plotted to reflect the local LD structure around these SNPs (according to a blue to red scale from r^2 = 0 to 1, based on pairwise r^2 values from HapMap CEU, JPT+CHB, and YRI, respectively).

(a) *CCNL1*

European



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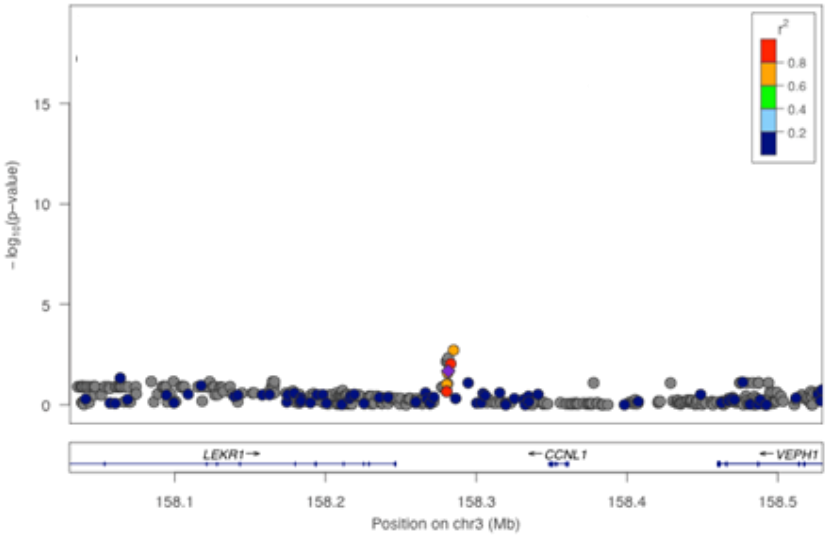
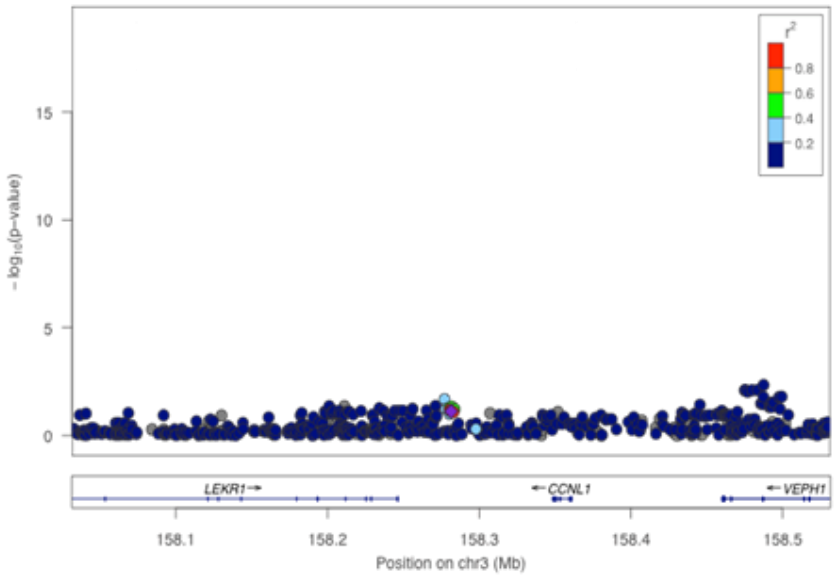
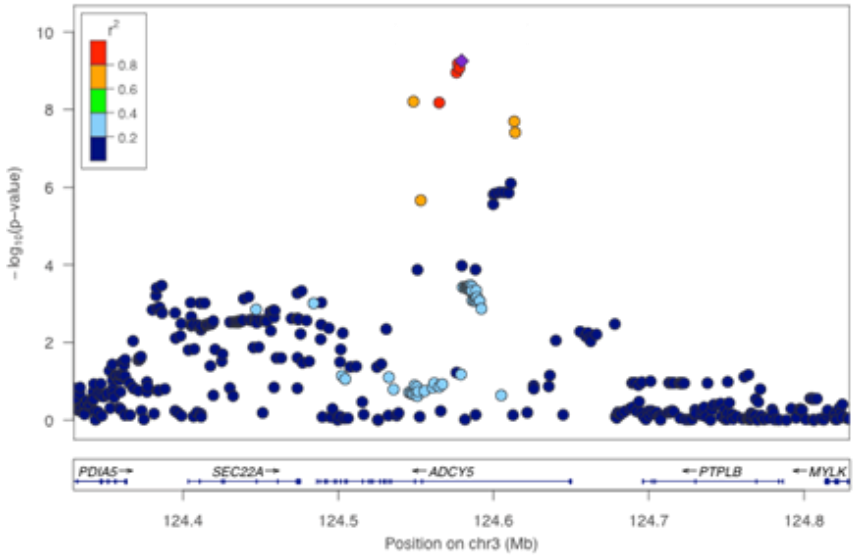


African American

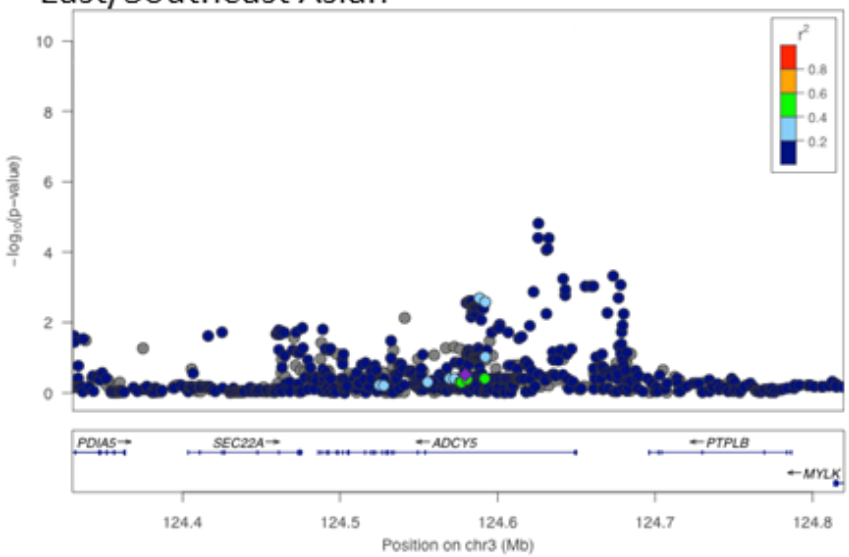


(b) *ADCY5*

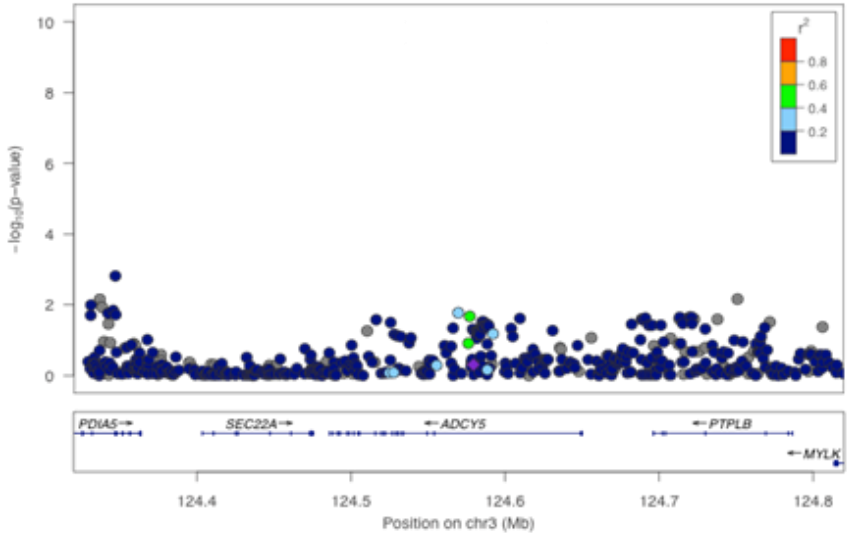
European



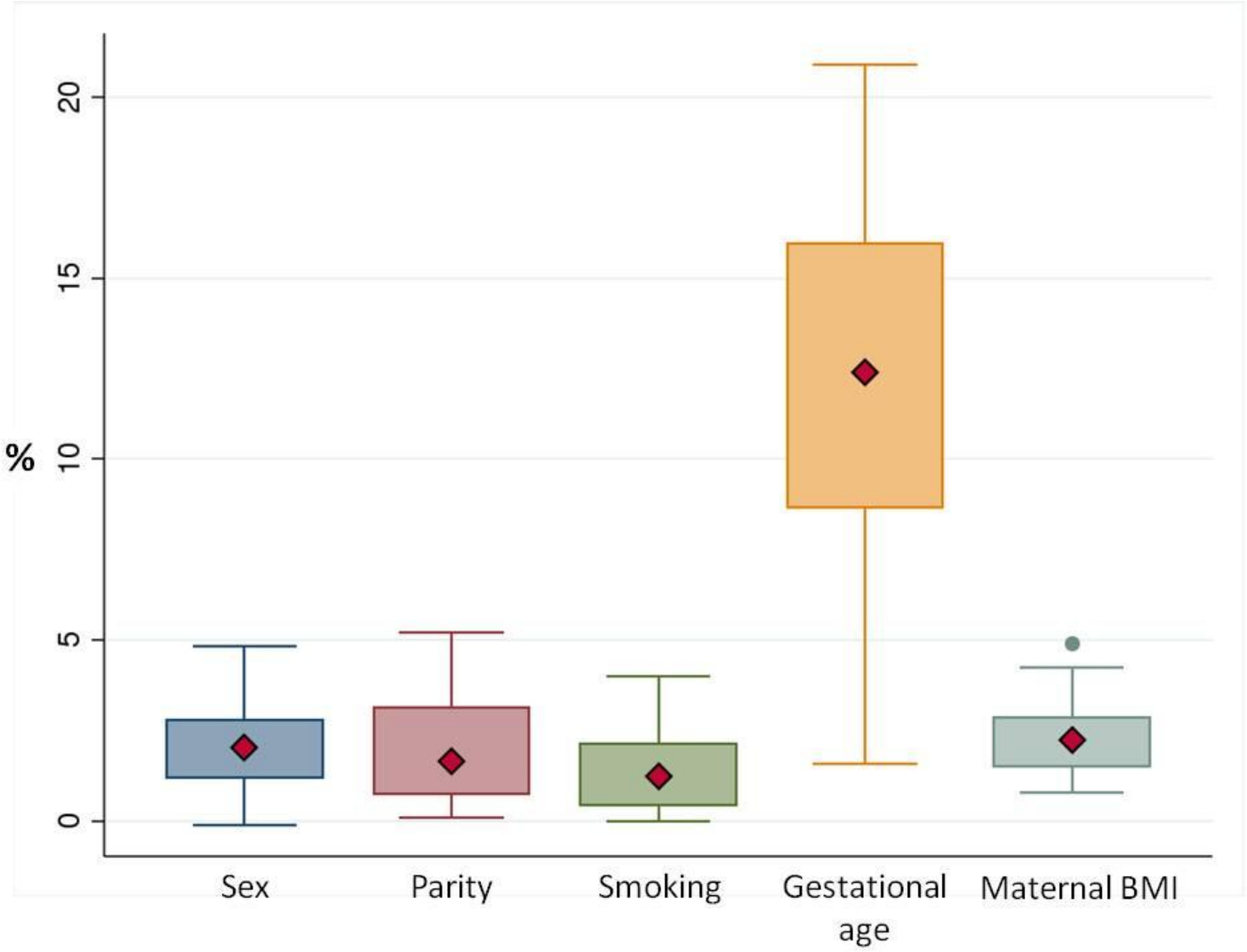
East/Southeast Asian



African American



Supplementary Figure 9. Box plot showing the percentage variance in birth weight explained by five related characteristics (x-axis) in all 43 European studies. Diamond = median; box = interquartile range; whiskers = median +/- 2*interquartile range; circle = outlier.



SUPPLEMENTARY NOTE

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SUPPLEMENTARY NOTE

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SUPPLEMENTARY NOTE

Early Growth Genetics Consortium (EGG) Membership and Affiliations

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