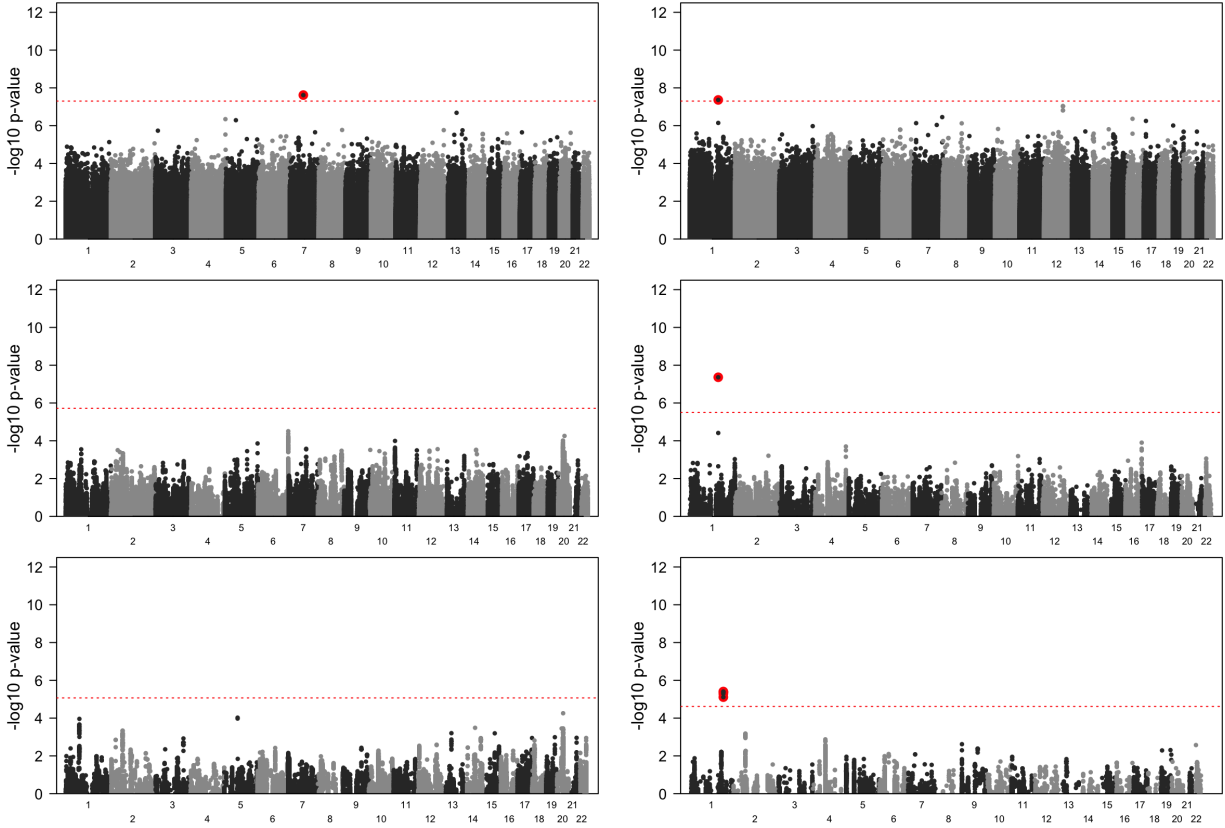
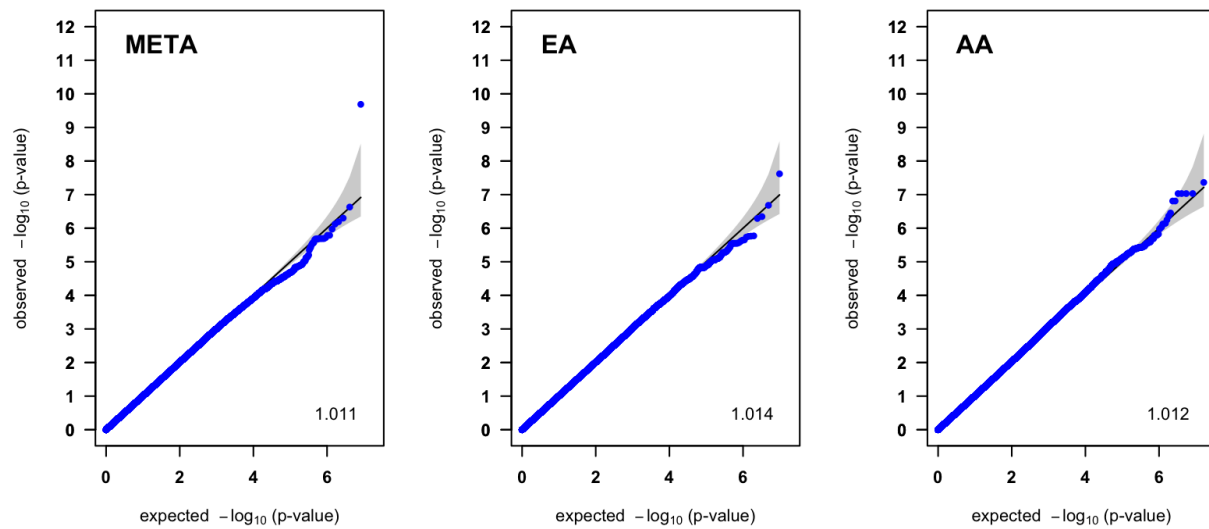


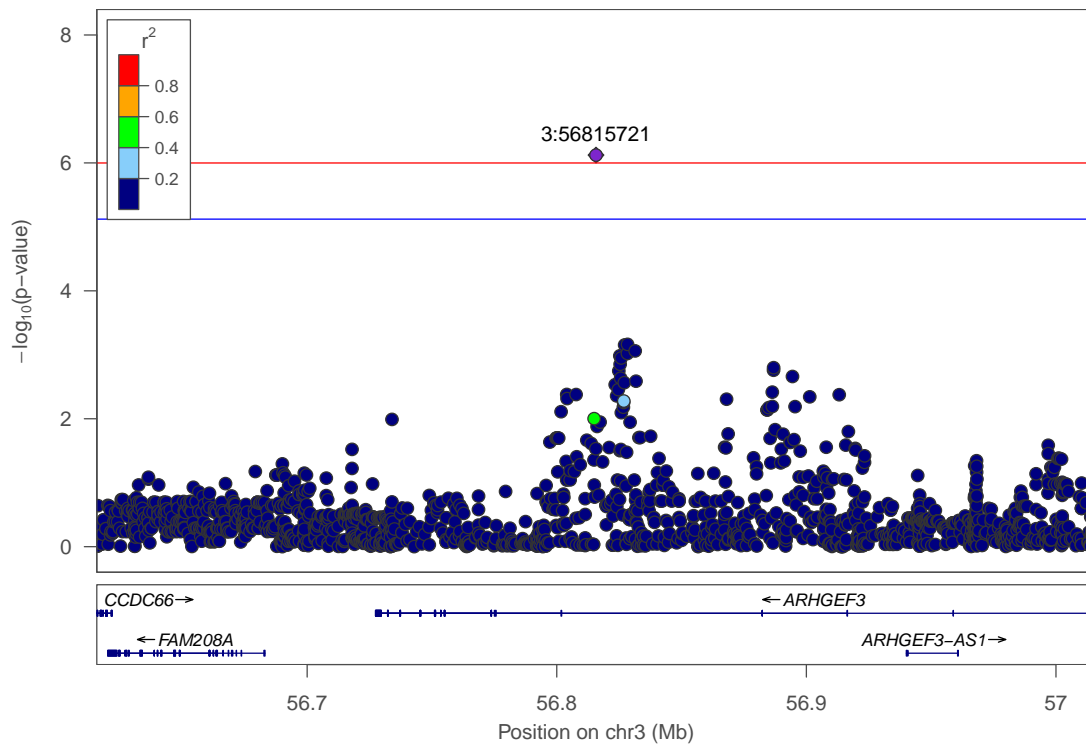
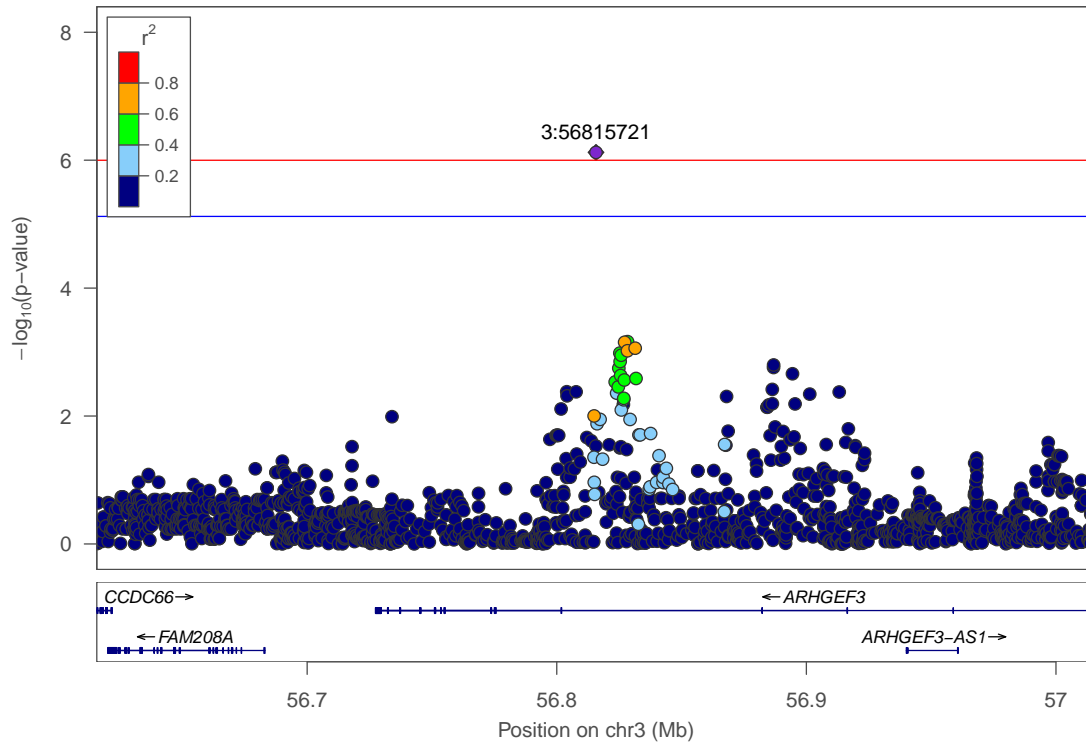
## Supplementary Materials



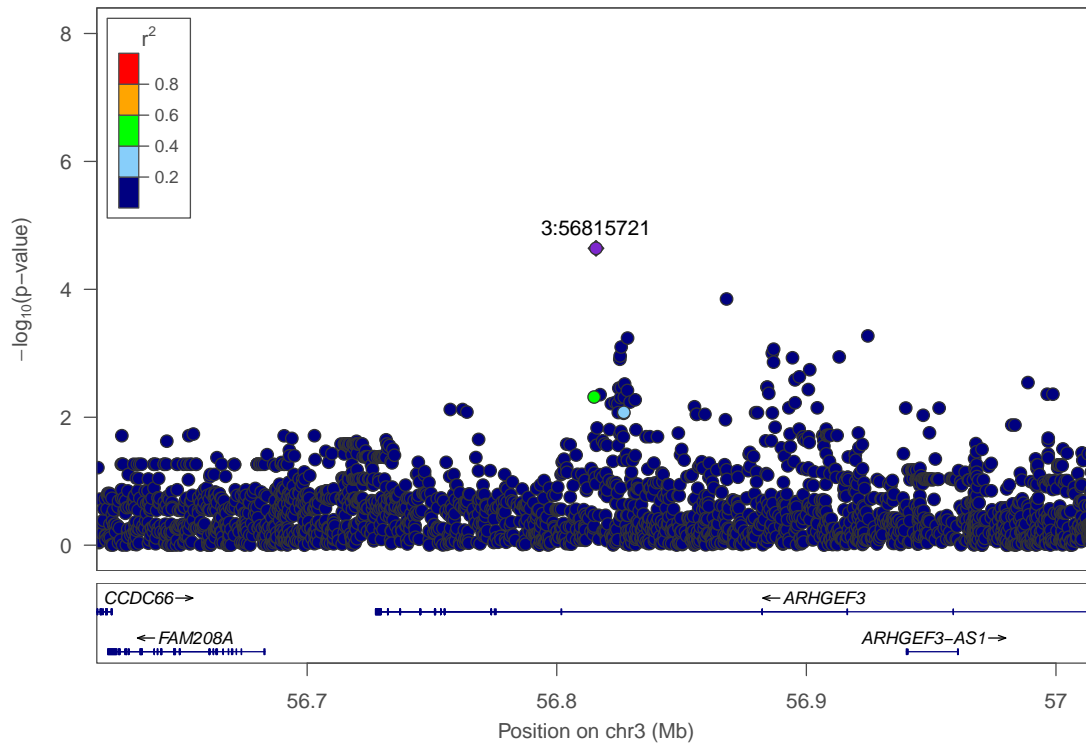
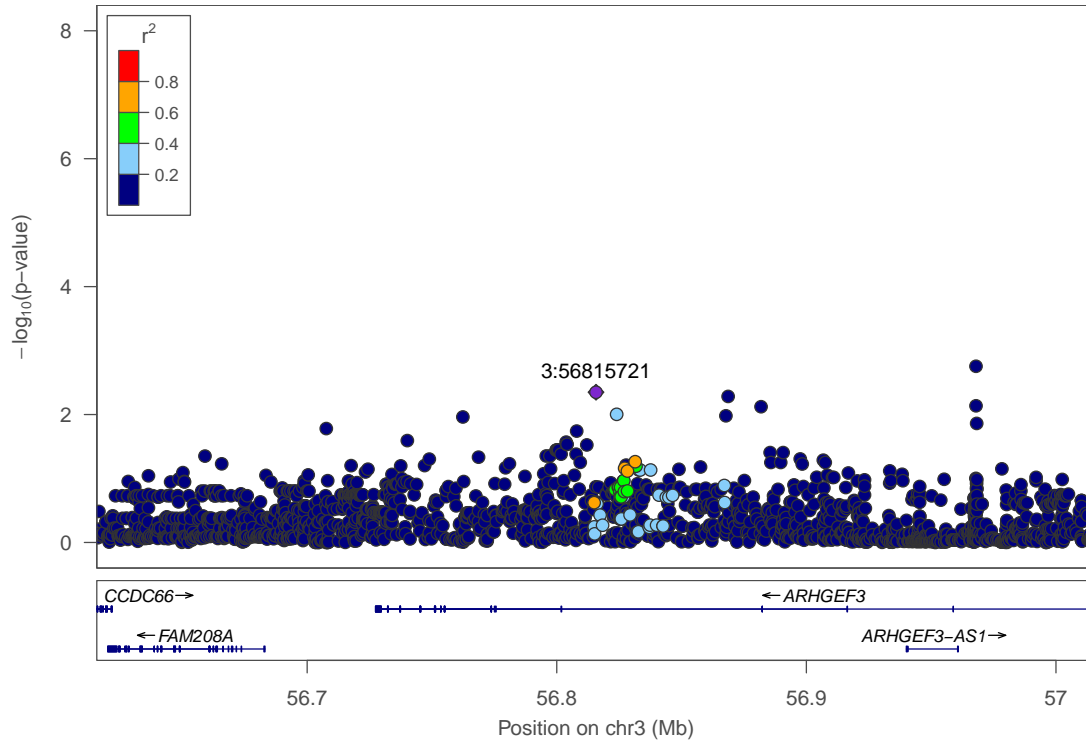
**Supplementary Figure 1:** Stratified GWAS results for the EA (**left**) and AA (**right**) families. **Top:** Manhattan plots of the GWAS for all 9,796,070 and 16,415,214 SNPs passing quality control, respectively. The dashed horizontal line is at  $p = 5 \times 10^{-8}$ , representing the standard GWAS cut-off for significance. **Middle:** Manhattan plots of the GWAS for the 208,230 and 54,085 eQTL in the PLTs. The dashed horizontal lines are at 5.72 ( $p = 1.91 \times 10^{-6}$ ) and 5.50 ( $p = 3.15 \times 10^{-6}$ ), representing the cut-off for a 5% FWER derived using permutations. **Bottom:** Manhattan plots of the GWAS for the 50,255 and 9,046 eQTL in the MKs. The dashed horizontal lines are at 5.07 ( $p = 8.54 \times 10^{-6}$ ) and 4.62 ( $p = 2.41 \times 10^{-5}$ ), representing the cut-off for a 5% FWER derived using permutations. SNPs passing the respective significance thresholds (highlighted with a red background) are listed in Table 1.



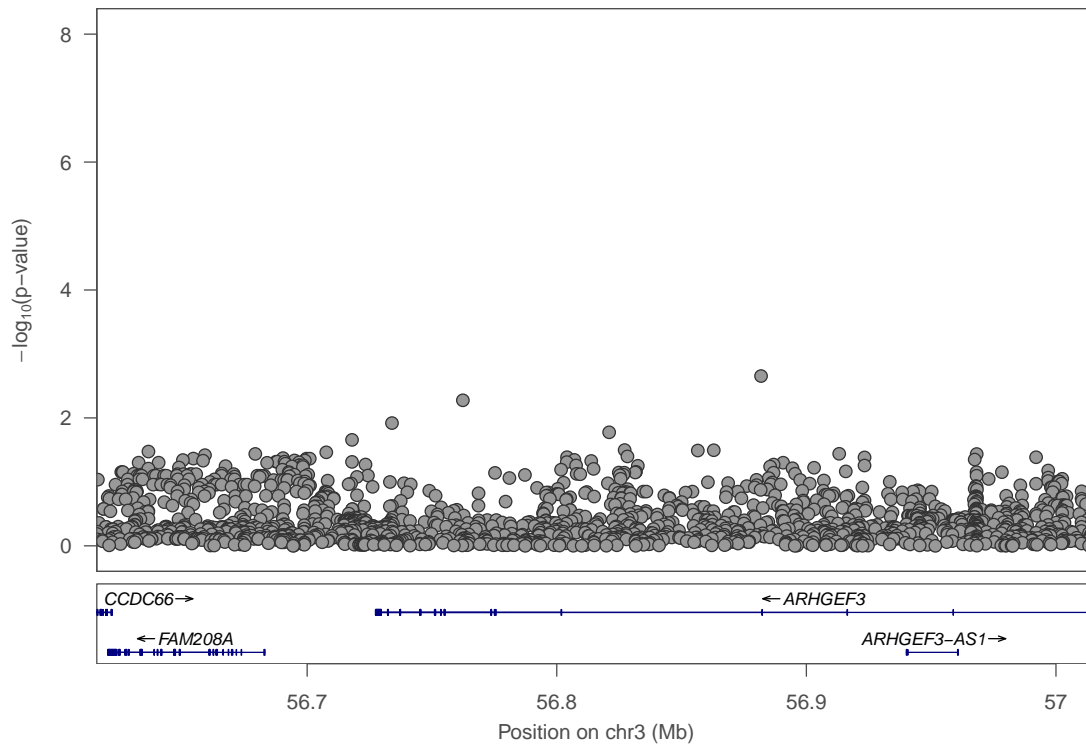
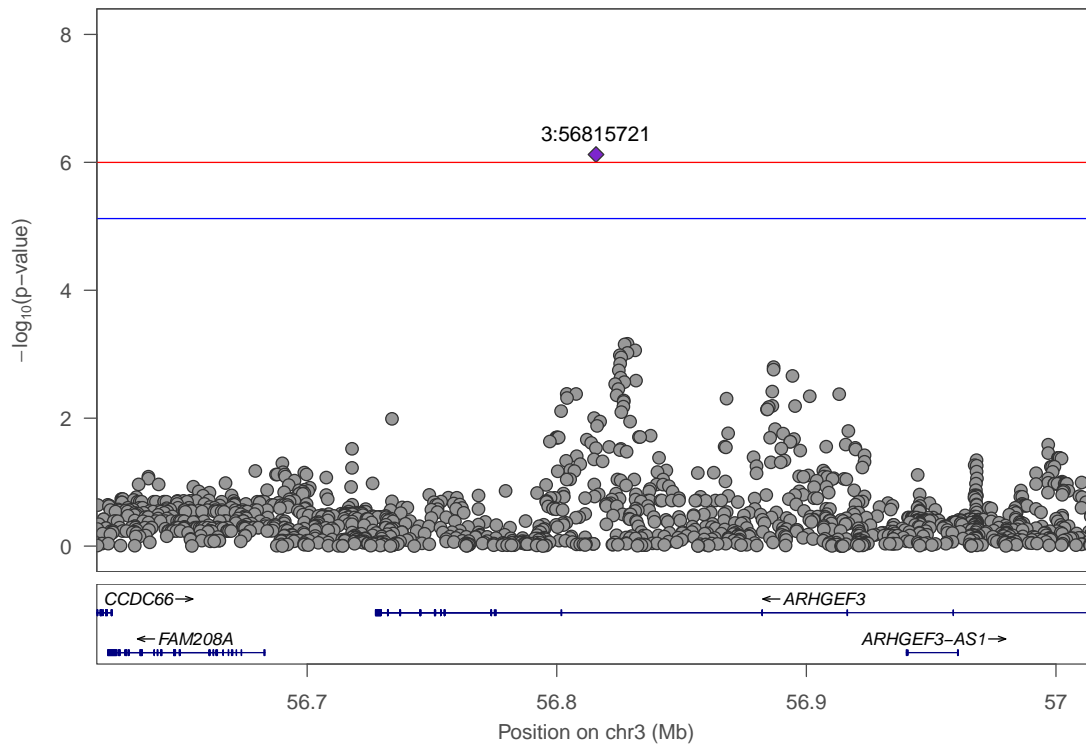
**Supplementary Figure 2:** Quantile-quantile plots of the expected versus observed  $-\log_{10}$  p-values from the post-aspirin trait meta-analysis (**left**), and the stratified EA (**middle**) and AA (**right**) analyses. The genomic control parameters, defined as median observed  $\chi^2$  test statistic divided by the median of a  $\chi^2_1$  null distribution [40], are shown in the lower right of each panel.



**Supplementary Figure 3:** LocusZoom plots (<http://locuszoom.org>) of the meta-analysis p-values around SNP rs1354034 (position 56,815,721 in chromosome 3) in the ARHGEF3 gene, associated with the post-aspirin platelet aggregation trait in the PLT and MK eQTL permutation analyses. Colors filling the circles indicate the linkage disequilibrium in the EA (**top**) and AA (**bottom**) families, respectively. The horizontal lines at values 6.00 and 5.12 represent the PLT (red,  $p = 1.00 \times 10^{-6}$ ) and MK (blue,  $p = 7.55 \times 10^{-6}$ ) FWER cut-offs derived from the permutation tests.



**Supplementary Figure 4:** LocusZoom plot of the stratified p-values (EA families **top**, AA families **bottom**) around SNP rs1354034 in the ARHGEF3 gene.



**Supplementary Figure 5: Top:** LocusZoom plot of the meta-analysis p-values around SNP rs1354034 in the ARHGEF3 gene. The horizontal lines represent the PLT (red) and MK (blue) FWER cut-offs, derived from the permutation tests. **Bottom:** Association p-values in this region after conditioning on SNP rs1354034.