# DATA SUPPLEMENT

## A myocardial infarction-associated SNP at 6p24 interferes with MEF2 binding and associates with *PHACTR1* expression levels in human coronary arteries

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## Supplemental Methods

### Western blot

HUVEC treated or not with VEGF or with siRNA were washed twice with PBS and then incubated 30 min on ice with 200µL of lysis buffer (100mM Tris pH8, 300mM NaCl, 0.2% SDS, 2% NP-40 and 0.5% NaDeoxycholate). We centrifuged the lysate for 10 min at maximum speed at 4°C and we measured protein concentration using the Bradford assay. After separation by SDS-PAGE, we transferred proteins on nitrocellulose membranes (0.2µM from Biorad) and incubated them with the appropriate antibodies diluted in TBS-T + milk 5%: PHACTR1 1:1000 from Sigma-Aldrich, Phospho-p44/42 MAPK 1:4000 from Cell Signaling, MEF2 1:1000 from Santa Cruz, β-actin 1:3000 from Sigma-Aldrich and ECL anti-rabbit IgG-HRP 1:10,000 from Amersham. For detection, we used the Western Lightning Plus kit from Perkin Elmer.

**Supplemental Table I.** Characteristics of study participants selected from the Montreal Heart Institute (MHI) Biobank. See Materials and Methods for a description of the inclusion and exclusion criteria. Values with '±' are means and standard deviations. [1]Mean age at first myocardial infarction (MI) for cases and at baseline for controls. [2]Hypertension is defined as a previous diagnosis of hypertension, on antihypertensive therapy or with systolic blood pressure ≥140 mmHg or diastolic blood pressure ≥90 mmHg. [3]Diabetes mellitus is defined as a previous diagnosis of diabetes or treatment with antidiabetic drugs. [4]Hypercholesterolemia is defined as a previous diagnosis of hypercholesterolemia or treatment with lipid-lowering drugs.

| **Characteristics** | **MHI Biobank myocardial infarction (MI) DNA panel** | |
|---|---|---|
| | **Cases** | **Controls** |
| N | 1176 | 1996 |
| Mean age (years)[1] | 54.5 ± 10.7 | 60.5 ± 12.0 |
| Female gender (%) | 20.9 | 57.2 |
| Ever smoking (%) | 79.0 | 59.2 |
| Hypertension (%)[2] | 69.1 | 38.4 |
| Systolic blood pressure (mmHg) | 124 ± 17 | 127 ± 16 |
| Diastolic blood pressure (mmHg) | 71 ± 10 | 75 ± 9 |
| Type 2 diabetes (%)[3] | 26.9 | 9.2 |
| Hypercholesterolemia (%)[4] | 89.2 | 39.5 |
| LDL-cholesterol (mmol/L) | 2.86 ± 0.85 | 2.06 ± 0.70 |
| HDL-cholesterol (mmol/L) | 1.36 ± 0.36 | 1.10 ± 0.28 |
| Body mass index (kg/m$^2$) | 29.0 ± 6.1 | 27.7 ± 6.1 |

**Supplemental Table II.** Association results between 45 validated myocardial infarction (MI) and/or coronary artery disease (CAD) SNPs and MI status in 1176 MI cases and 1996 controls selected from the Montreal Heart Institute (MHI) Biobank. Genotyping was performed with the Sequenom iPLEX platform or the Illumina HumanExome Beadchip. Individuals with >10% missing genotypes and markers with >5% missing genotypes or a Hardy-Weinberg *P*<0.001 were removed from the analysis. Analysis was performed in PLINK[1] using logistic regression under an additive genetic model and adjusting for sex, age, age-squared, hypertension, diabetes and lipid-lowering drugs usage. [a]We provide the Bonferonni-corrected P-value for 45 SNPs tested. [b]The effect of a SNP is in the right direction if the odds ratio for the effect allele is in the same direction than the published literature. Under the null hypothesis, you expect 50% of the SNPs to be in the right direction, but we observe 78% (35/45). [c]A SNP scores “yes” in this column if the odds ratio for the effect allele is consistent with the published literature and if the uncorrected one-tailed P-value <0.05. Under the null, we expect 5% of the SNP to score yes (1.75/35 SNPs) and we found 34% (12/35 SNPs).

| **Locus** | **Chr** | **SNP** | **Pos (hg19)** | **Effect allele** | **Odds ratio** | **P-value** | **Adjusted P-value[a]** | **Right Direction[b]** | **One-tailed *P*<0.05[c]** |
|---|---|---|---|---|---|---|---|---|---|
| *PCSK9* | 1 | rs11206510 | 55496039 | G | 0.9781 | 0.8011 | 1 | yes | no |
| *PPAP2B* | 1 | rs17114036 | 56962821 | G | 1.058 | 0.6341 | 1 | no | no |
| *SORT1* | 1 | rs602633 | 109821511 | A | 0.8487 | 0.0589 | 1 | yes | yes |
| *IL6R* | 1 | rs4845625 | 154422067 | A | 1.012 | 0.8629 | 1 | yes | no |
| *MIA3* | 1 | rs17465637 | 222823529 | A | 0.9185 | 0.2627 | 1 | yes | no |
| *AK097927* | 2 | rs16986953 | 19942473 | A | 1.214 | 0.1451 | 1 | yes | no |
| *APOB* | 2 | rs515135 | 21286057 | A | 1.243 | 0.01069 | 0.48 | no | no |
| *ABCG5/ABCG8* | 2 | rs6544713 | 44073881 | A | 1.133 | 0.09291 | 1 | yes | yes |
| *GGCX/VAMP8* | 2 | rs1561198 | 85809989 | A | 1.093 | 0.1963 | 1 | yes | no |
| *ZEB2-AC074093.1* | 2 | rs2252641 | 145801461 | G | 1.126 | 0.0926 | 1 | yes | yes |
| *WDR12* | 2 | rs6725887 | 203454130 | C | 1.278 | 0.01128 | 0.51 | yes | yes |
| *MRAS* | 3 | rs9818870 | 139604812 | T | 0.9073 | 0.3055 | 1 | no | no |
| *GUCY1A3* | 4 | rs7692387 | 156635309 | A | 0.9573 | 0.6097 | 1 | yes | no |
| *SLC22A4/SLC22A5* | 5 | rs273909 | 131667353 | G | 1.236 | 0.05243 | 1 | yes | yes |
| *PHACTR1* | 6 | rs12526453 | 12927544 | G | 0.7882 | 8.4E-04 | 0.038 | yes | yes |
| *ANKS1A* | 6 | rs17609940 | 35034800 | C | 0.9541 | 0.5963 | 1 | yes | no |
| *KCNK5* | 6 | rs10947789 | 39174922 | G | 0.9384 | 0.4418 | 1 | yes | no |
| *TCF21* | 6 | rs12190287 | 134214525 | G | 0.83 | 0.01138 | 0.51 | yes | yes |
| *LPA* | 6 | rs3798220 | 160881127 | C | 0.8201 | 0.3523 | 1 | no | no |
| *PLG* | 6 | rs4252120 | 161143608 | G | 1.038 | 0.6344 | 1 | no | no |
| *HDAC9* | 7 | rs2023938 | 19036775 | G | 1.021 | 0.8524 | 1 | yes | no |
| *7q22* | 7 | rs10953541 | 107244545 | T | 0.8675 | 0.0808 | 1 | yes | yes |
| *ZC3HC1* | 7 | rs11556924 | 129663496 | T | 0.9015 | 0.1497 | 1 | yes | no |
| *LPL* | 8 | rs264 | 19813180 | A | 0.94 | 0.5238 | 1 | yes | no |
| *TRIB1* | 8 | rs2954029 | 126490972 | T | 0.9905 | 0.8893 | 1 | yes | no |
| *CDKN2A/CDKN2B* | 9 | rs4977574 | 22098574 | A | 0.9196 | 0.2308 | 1 | yes | no |
| *ABO* | 9 | rs579459 | 136154168 | C | 1.072 | 0.3748 | 1 | yes | no |
| *KIAA1462* | 10 | rs2505083 | 30335122 | C | 1.06 | 0.4068 | 1 | yes | no |
| *CXCL12* | 10 | rs1746048 | 44095830 | T | 0.9525 | 0.6236 | 1 | yes | no |
| *LIPA* | 10 | rs1412444 | 91002927 | T | 1.142 | 0.06824 | 1 | yes | yes |
| *CYP17A1* | 10 | rs12413409 | 104719096 | A | 0.8629 | 0.2748 | 1 | yes | no |
| *PDGFD* | 11 | rs974819 | 103660567 | T | 1.163 | 0.03535 | 1 | yes | yes |
| *APOA5* | 11 | rs964184 | 116648917 | G | 0.8446 | 0.088 | 1 | no | no |
| *SH2B3* | 12 | rs3184504 | 111884608 | T | 1.101 | 0.1588 | 1 | yes | no |
| *FLT1* | 13 | rs9319428 | 28973621 | A | 1.07 | 0.3676 | 1 | yes | no |
| *COL4A1* | 13 | rs4773144 | 110960712 | G | 1.109 | 0.1423 | 1 | yes | no |
| *HHIPL1* | 14 | rs2895811 | 100133942 | C | 0.9776 | 0.7418 | 1 | no | no |
| *ADAMTS7* | 15 | rs3825807 | 79089111 | G | 0.9213 | 0.2311 | 1 | yes | no |
| *FURIN/FES* | 15 | rs17514846 | 91416550 | A | 1.181 | 0.01746 | 0.79 | yes | yes |
| *SMG6* | 17 | rs216172 | 2126504 | C | 0.9468 | 0.4375 | 1 | no | no |
| *RASD1* | 17 | rs12936587 | 17543722 | A | 0.9011 | 0.1307 | 1 | yes | no |

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|---|---|---|---|---|---|---|---|---|---|
| *UBE2Z* | 17 | rs46522 | 46988597 | C | 0.8075 | 0.002056 | 0.093 | yes | yes |
| *LDLR* | 19 | rs1122608 | 11024601 | T | 1.003 | 0.9683 | 1 | no | no |
| *APOE/APOC1* | 19 | rs2075650 | 45395619 | G | 0.8508 | 0.1316 | 1 | no | no |
| Gene desert/*KCNE2* | 21 | rs9982601 | 35599128 | A | 1.17 | 0.108 | 1 | yes | no |

**Supplemental Table III.** *PHACTR1* markers genotyped in 1176 myocardial infarction (MI) cases and 1996 controls selected from the Montreal Heart Institute (MHI) Biobank. The seven rare *PHACTR1* variants were also genotyped in an additional independent subset of the MHI Biobank totaling 870 MI cases and 1494 controls.

| Marker | Rationale for genotyping |
|---|---|
| rs12526453 | Canonical *PHACTR1* MI SNP, tagSNP |
| rs2026457 | tagSNP |
| rs34944538 | tagSNP |
| rs66867947 | tagSNP |
| rs59402659 | tagSNP |
| rs6921974 | tagSNP |
| rs2026458 | tagSNP |
| rs9381462 | tagSNP |
| rs7454157 | tagSNP |
| rs8180628 | tagSNP |
| rs9349379 | tagSNP |
| rs9395224 | tagSNP |
| rs1412741 | tagSNP |
| rs1412744 | tagSNP |
| rs7738252 | top SNP at the *PHACTR1* locus for association with coronary heart disease in African Americans (Lettre et al., PLoS Genet. 2011) |
| rs11757278 | eQTL SNP for *PHACTR1* transcript level (Pickrell et al., Nature, 2010). This marker was added to the genotyping pool for completeness, although it is not associated with CAD/MI, nor in linkage disequilibrium with rs9349379 in the MHI Biobank ($r^2$=0, D'=0.014, physical distance=276 kb). |
| rs36000655 | Frameshift indel, 1000 Genomes Project |
| rs61746695 | Rare missense p.Arg94Pro (CGT=>CCT), 1000 Genomes Project |
| rs17602409 | Rare missense p.Ile247Met (ATC=>ATG), 1000 Genomes Project |
| ss836901033 | Rare missense p.Ser190Pro (TCT=>CCT), targeted re-sequencing |
| ss836901061 | Rare missense p.Glu196Lys (GAA=>AAA), targeted re-sequencing |
| ss836901074 | Rare, 3' splice site at exon 12, targeted re-sequencing |
| ss836901090 | Rare, 3'UTR, targeted re-sequencing |

**Supplemental Table IV.** Association results between myocardial infarction risk and imputed genotypes for DNA sequence polymorphisms at the *PHACTR1* locus. We performed the analysis using logistic regression and testing an additive genetic model, as implemented in the mach2dat software. We corrected for the following covariates: sex, age, age-squared, hypertension status, type 2 diabetes status and lipid-lowering drug usage.

| Marker | Chromosome | Position (hg19) | Alleles | Frequency (Allele 1) | Imputation (rsq_hat) | Odds ratio (Allele 1) | P-value |
|---|---|---|---|---|---|---|---|
| rs1572000 | 6 | 12769487 | G,A | 0.5998 | 0.614 | 1.183 | 0.05643 |
| rs10948235 | 6 | 12770823 | T,C | 0.6602 | 0.6017 | 1.16 | 0.1094 |
| rs950720 | 6 | 12773990 | C,T | 0.6606 | 0.6177 | 1.158 | 0.1089 |
| rs1412749 | 6 | 12774363 | C,G | 0.5853 | 0.6548 | 1.179 | 0.05226 |
| 6:12775414:AT_A | 6 | 12775414 | R,D | 0.6592 | 0.6257 | 1.152 | 0.1183 |
| rs6941422 | 6 | 12775753 | T,C | 0.59 | 0.6573 | 1.177 | 0.05474 |
| rs9472511 | 6 | 12775922 | C,T | 0.9288 | 0.6023 | 1.171 | 0.3457 |
| rs6941624 | 6 | 12775930 | T,C | 0.659 | 0.6293 | 1.152 | 0.1181 |
| rs9472512 | 6 | 12776029 | A,G | 0.9286 | 0.602 | 1.171 | 0.3467 |
| rs9472513 | 6 | 12776067 | C,G | 0.9288 | 0.6034 | 1.171 | 0.346 |
| rs9472514 | 6 | 12776212 | G,A | 0.9288 | 0.6036 | 1.171 | 0.3462 |
| rs7757205 | 6 | 12777449 | G,A | 0.5901 | 0.6624 | 1.175 | 0.05555 |
| rs7758513 | 6 | 12777571 | C,T | 0.6609 | 0.6342 | 1.145 | 0.1338 |
| rs9472519 | 6 | 12777723 | A,G | 0.9299 | 0.606 | 1.181 | 0.321 |
| rs9463105 | 6 | 12777790 | C,A | 0.929 | 0.6237 | 1.17 | 0.3401 |
| rs9472520 | 6 | 12777828 | A,G | 0.9289 | 0.6243 | 1.17 | 0.3399 |
| rs11758650 | 6 | 12778109 | C,A | 0.6578 | 0.6488 | 1.144 | 0.1298 |
| rs11753864 | 6 | 12778218 | G,A | 0.6584 | 0.6494 | 1.146 | 0.1252 |
| rs9463106 | 6 | 12778864 | G,A | 0.5866 | 0.6856 | 1.17 | 0.05799 |
| rs6922969 | 6 | 12780032 | T,C | 0.5864 | 0.6895 | 1.169 | 0.05808 |
| rs6938417 | 6 | 12780185 | G,A | 0.5863 | 0.6909 | 1.169 | 0.05804 |
| rs1572002 | 6 | 12780990 | G,A | 0.5863 | 0.6933 | 1.169 | 0.05803 |
| rs9472528 | 6 | 12781353 | A,G | 0.9288 | 0.6362 | 1.168 | 0.3399 |
| rs9381391 | 6 | 12781416 | C,T | 0.5696 | 0.7016 | 1.165 | 0.06127 |
| rs12528721 | 6 | 12782518 | C,G | 0.9287 | 0.6407 | 1.166 | 0.3414 |
| rs9463110 | 6 | 12782602 | T,G | 0.5854 | 0.7014 | 1.168 | 0.05819 |
| rs12525210 | 6 | 12782675 | G,A | 0.9287 | 0.6412 | 1.166 | 0.3416 |
| rs7760140 | 6 | 12782968 | G,T | 0.6566 | 0.6682 | 1.142 | 0.1301 |
| rs9296464 | 6 | 12784293 | T,C | 0.6565 | 0.6717 | 1.141 | 0.1302 |
| rs9296465 | 6 | 12784464 | A,G | 0.5859 | 0.7068 | 1.168 | 0.05698 |
| rs12524974 | 6 | 12784785 | A,G | 0.6564 | 0.6745 | 1.141 | 0.1304 |
| rs55764622 | 6 | 12784847 | T,A | 0.9283 | 0.648 | 1.165 | 0.3411 |
| rs2327617 | 6 | 12785023 | C,T | 0.6664 | 0.6357 | 1.147 | 0.1294 |
| 6:12785347:AC_A | 6 | 12785347 | R,D | 0.6564 | 0.6773 | 1.141 | 0.1304 |
| rs10948244 | 6 | 12786085 | T,C | 0.6845 | 0.6734 | 1.155 | 0.1064 |
| rs9472549 | 6 | 12786237 | C,A | 0.9284 | 0.6538 | 1.164 | 0.3409 |
| rs9472551 | 6 | 12786272 | C,A | 0.5843 | 0.723 | 1.166 | 0.05701 |
| rs10948247 | 6 | 12786511 | C,A | 0.6559 | 0.6882 | 1.14 | 0.1277 |
| rs1412751 | 6 | 12787247 | G,A | 0.5842 | 0.7258 | 1.165 | 0.0571 |
| rs944766 | 6 | 12787449 | C,T | 0.584 | 0.7289 | 1.165 | 0.05709 |
| rs883947 | 6 | 12787714 | C,T | 0.6556 | 0.6944 | 1.14 | 0.1277 |
| rs944767 | 6 | 12788029 | C,G | 0.7411 | 0.7236 | 1.097 | 0.3106 |
| rs2015761 | 6 | 12788243 | A,C | 0.9283 | 0.6627 | 1.163 | 0.3407 |
| rs2015764 | 6 | 12788283 | G,A | 0.5841 | 0.7332 | 1.164 | 0.05704 |
| 6:12788487:TA_T | 6 | 12788487 | R,D | 0.5835 | 0.7368 | 1.162 | 0.05956 |
| rs1412752 | 6 | 12788776 | A,T | 0.6549 | 0.6991 | 1.139 | 0.1273 |

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|---|---|---|---|---|---|---|---|
| rs6458460 | 6 | 12789038 | C,A | 0.5816 | 0.7376 | 1.163 | 0.05749 |
| rs6458461 | 6 | 12789191 | C,T | 0.5836 | 0.7388 | 1.164 | 0.05704 |
| rs73722844 | 6 | 12789322 | T,C | 0.9334 | 0.6153 | 1.182 | 0.3254 |
| rs73722845 | 6 | 12789323 | G,A | 0.9334 | 0.6156 | 1.182 | 0.3257 |
| rs9472558 | 6 | 12789655 | C,T | 0.6552 | 0.7045 | 1.138 | 0.128 |
| rs2095123 | 6 | 12790079 | A,G | 0.6505 | 0.6965 | 1.141 | 0.1221 |
| rs2327619 | 6 | 12790353 | G,A | 0.6556 | 0.7068 | 1.14 | 0.1231 |
| rs7747656 | 6 | 12790872 | A,G | 0.6565 | 0.707 | 1.143 | 0.1157 |
| rs1412753 | 6 | 12791207 | G,C | 0.6555 | 0.7109 | 1.14 | 0.123 |
| rs4714866 | 6 | 12791802 | G,A | 0.583 | 0.7499 | 1.162 | 0.05704 |
| rs4714868 | 6 | 12791878 | T,C | 0.583 | 0.7502 | 1.162 | 0.05702 |
| rs9463114 | 6 | 12794542 | G,A | 0.9292 | 0.6657 | 1.164 | 0.3388 |
| rs73722849 | 6 | 12795009 | G,A | 0.9307 | 0.6812 | 1.154 | 0.3666 |
| rs10807323 | 6 | 12795031 | G,A | 0.5829 | 0.6792 | 0.743 | 0.0004155 |
| rs6924150 | 6 | 12795621 | C,T | 0.5826 | 0.7586 | 1.161 | 0.05696 |
| 6:12796108:AT_A | 6 | 12796108 | R,D | 0.5813 | 0.7567 | 1.161 | 0.05839 |
| rs9463117 | 6 | 12796984 | A,G | 0.928 | 0.6902 | 1.159 | 0.3409 |
| rs4714870 | 6 | 12797055 | T,G | 0.654 | 0.7352 | 1.135 | 0.1279 |
| rs9463119 | 6 | 12797496 | A,G | 0.9278 | 0.698 | 1.158 | 0.3399 |
| rs9472566 | 6 | 12797940 | C,T | 0.927 | 0.6928 | 1.154 | 0.353 |
| rs7757835 | 6 | 12798443 | A,G | 0.6543 | 0.7411 | 1.136 | 0.1232 |
| rs7757858 | 6 | 12798477 | A,C | 0.5814 | 0.7805 | 1.159 | 0.05633 |
| rs9472583 | 6 | 12799417 | C,A | 0.6538 | 0.759 | 1.132 | 0.1301 |
| rs17617207 | 6 | 12800332 | G,A | 0.5792 | 0.7994 | 1.155 | 0.05969 |
| rs16873383 | 6 | 12800443 | A,T | 0.6523 | 0.758 | 1.131 | 0.1334 |
| rs12530186 | 6 | 12800690 | T,C | 0.6537 | 0.7635 | 1.132 | 0.1305 |
| rs2876298 | 6 | 12800727 | C,A | 0.9135 | 0.6167 | 1.151 | 0.3524 |
| rs12523719 | 6 | 12800824 | T,G | 0.6537 | 0.7646 | 1.132 | 0.1301 |
| rs9472587 | 6 | 12800874 | A,T | 0.6536 | 0.766 | 1.131 | 0.1302 |
| rs9472590 | 6 | 12801104 | C,G | 0.6534 | 0.7669 | 1.131 | 0.1324 |
| 6:12801131:G_GA | 6 | 12801131 | R,I | 0.6738 | 0.6451 | 1.14 | 0.1473 |
| rs6917492 | 6 | 12801487 | C,T | 0.6664 | 0.7252 | 1.141 | 0.1182 |
| rs6917493 | 6 | 12801488 | C,G | 0.6673 | 0.722 | 1.142 | 0.1186 |
| rs6916334 | 6 | 12801594 | G,T | 0.653 | 0.7717 | 1.131 | 0.1292 |
| rs62389219 | 6 | 12801782 | C,T | 0.9457 | 0.6243 | 1.284 | 0.1828 |
| rs9381401 | 6 | 12801967 | A,C | 0.5824 | 0.7247 | 0.75 | 0.0004147 |
| rs28451666 | 6 | 12802374 | G,A | 0.6529 | 0.7735 | 1.131 | 0.129 |
| rs13214313 | 6 | 12802428 | G,A | 0.6528 | 0.7754 | 1.131 | 0.1291 |
| rs13203774 | 6 | 12802502 | T,C | 0.654 | 0.7728 | 1.132 | 0.1277 |
| rs13203883 | 6 | 12802560 | T,C | 0.6546 | 0.7696 | 1.131 | 0.1297 |
| rs9463134 | 6 | 12802815 | G,C | 0.6536 | 0.7746 | 1.132 | 0.1271 |
| rs9472594 | 6 | 12803223 | C,A | 0.6527 | 0.7802 | 1.131 | 0.1289 |
| rs12215445 | 6 | 12803314 | G,A | 0.8574 | 0.6003 | 1.329 | 0.02295 |
| rs6919327 | 6 | 12803410 | A,G | 0.5781 | 0.82 | 1.154 | 0.05766 |
| rs9463136 | 6 | 12803416 | T,C | 0.6527 | 0.782 | 1.13 | 0.1289 |
| rs9463137 | 6 | 12803582 | G,T | 0.6526 | 0.7828 | 1.13 | 0.1288 |
| rs9472595 | 6 | 12803718 | C,T | 0.6525 | 0.7839 | 1.13 | 0.1291 |
| rs9463138 | 6 | 12803792 | A,G | 0.6529 | 0.7837 | 1.13 | 0.1296 |
| rs1953089 | 6 | 12804619 | C,T | 0.6526 | 0.7895 | 1.13 | 0.1287 |
| rs9463140 | 6 | 12804870 | A,G | 0.9265 | 0.7341 | 1.153 | 0.3398 |
| rs13196135 | 6 | 12804875 | G,A | 0.6794 | 0.7638 | 1.141 | 0.1124 |
| rs6935309 | 6 | 12804882 | T,C | 0.6548 | 0.782 | 1.13 | 0.131 |
| rs6458473 | 6 | 12804934 | G,C | 0.6525 | 0.7917 | 1.13 | 0.1284 |
| rs6930873 | 6 | 12805039 | A,T | 0.6525 | 0.7921 | 1.13 | 0.1286 |
| rs6909834 | 6 | 12805582 | C,T | 0.6524 | 0.7953 | 1.129 | 0.1288 |
| rs6913075 | 6 | 12805821 | G,C | 0.6526 | 0.7968 | 1.13 | 0.1266 |
| rs6914513 | 6 | 12805843 | C,T | 0.6016 | 0.7552 | 1.159 | 0.06245 |
| rs1412738 | 6 | 12805995 | A,G | 0.653 | 0.7961 | 1.131 | 0.1229 |
| rs7762417 | 6 | 12807829 | C,T | 0.6513 | 0.8028 | 1.131 | 0.1225 |

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|---|---|---|---|---|---|---|---|
| rs7762547 | 6 | 12807877 | C,A | 0.5783 | 0.8491 | 1.151 | 0.05776 |
| rs10498681 | 6 | 12808284 | C,T | 0.9278 | 0.7772 | 1.138 | 0.3752 |
| rs12525116 | 6 | 12809740 | T,C | 0.9282 | 0.788 | 1.139 | 0.3717 |
| rs7760286 | 6 | 12810937 | A,G | 0.6527 | 0.8376 | 1.128 | 0.1233 |
| rs56270763 | 6 | 12810945 | C,T | 0.928 | 0.7951 | 1.139 | 0.3682 |
| rs1011188 | 6 | 12812948 | A,G | 0.9284 | 0.8098 | 1.138 | 0.3672 |
| rs62389220 | 6 | 12815105 | C,G | 0.942 | 0.7286 | 1.22 | 0.2386 |
| rs62389221 | 6 | 12815161 | A,G | 0.9385 | 0.7641 | 1.202 | 0.2499 |
| rs2151221 | 6 | 12816578 | C,G | 0.9281 | 0.824 | 1.136 | 0.3676 |
| rs7764490 | 6 | 12817237 | A,G | 0.5746 | 0.9381 | 1.139 | 0.06417 |
| rs1412740 | 6 | 12817590 | A,G | 0.5756 | 0.9402 | 1.138 | 0.06639 |
| rs13215300 | 6 | 12817608 | T,C | 0.9384 | 0.7818 | 1.2 | 0.2502 |
| rs1412741 | 6 | 12817667 | A,G | 0.6365 | 0.9969 | 1.097 | 0.1845 |
| rs13215271 | 6 | 12817748 | A,G | 0.9384 | 0.7828 | 1.199 | 0.2506 |
| rs4711841 | 6 | 12818142 | G,C | 0.6366 | 0.9958 | 1.097 | 0.1842 |
| rs35784087 | 6 | 12818204 | T,C | 0.9384 | 0.7842 | 1.199 | 0.25 |
| rs1332840 | 6 | 12818865 | G,C | 0.5736 | 0.9445 | 1.139 | 0.06469 |
| rs62389223 | 6 | 12819405 | C,T | 0.9394 | 0.7727 | 1.199 | 0.2567 |
| rs7776079 | 6 | 12819572 | A,G | 0.5678 | 0.9502 | 1.136 | 0.06935 |
| rs114389430 | 6 | 12820655 | G,A | 0.9799 | 0.734 | 0.72 | 0.23 |
| rs9472672 | 6 | 12821258 | A,G | 0.8381 | 0.8709 | 1.18 | 0.09176 |
| rs6915402 | 6 | 12821491 | A,T | 0.5655 | 0.9452 | 1.168 | 0.02776 |
| rs10434854 | 6 | 12822566 | C,T | 0.8478 | 0.8734 | 1.178 | 0.1046 |
| rs10434855 | 6 | 12822711 | C,A | 0.9143 | 0.7865 | 1.148 | 0.3022 |
| rs7768030 | 6 | 12822973 | A,C | 0.9134 | 0.7923 | 1.152 | 0.2876 |
| rs9381417 | 6 | 12823820 | G,A | 0.9134 | 0.7959 | 1.151 | 0.2883 |
| rs58666803 | 6 | 12824263 | T,C | 0.9193 | 0.737 | 1.169 | 0.2713 |
| rs60954427 | 6 | 12824264 | G,A | 0.9272 | 0.7653 | 1.194 | 0.2256 |
| rs56408440 | 6 | 12824700 | C,T | 0.848 | 0.8819 | 1.175 | 0.1072 |
| rs57387500 | 6 | 12824892 | A,G | 0.8477 | 0.8835 | 1.175 | 0.1076 |
| rs77664195 | 6 | 12824994 | A,G | 0.9185 | 0.8296 | 1.163 | 0.2592 |
| rs4142300 | 6 | 12825772 | A,G | 0.8478 | 0.8863 | 1.174 | 0.1081 |
| rs2026457 | 6 | 12825805 | G,A | 0.5685 | 0.9999 | 1.167 | 0.0249 |
| rs2026458 | 6 | 12825874 | C,T | 0.5692 | 0.9992 | 0.788 | 0.0005787 |
| rs9349344 | 6 | 12826479 | T,C | 0.568 | 0.9971 | 1.167 | 0.0249 |
| rs35278288 | 6 | 12826700 | A,G | 0.9138 | 0.8043 | 1.15 | 0.2904 |
| rs13215145 | 6 | 12827170 | G,A | 0.9344 | 0.8618 | 1.189 | 0.2376 |
| rs9349346 | 6 | 12827334 | A,T | 0.5628 | 0.9716 | 1.172 | 0.02223 |
| 6:12828114:AG_A | 6 | 12828114 | R,D | 0.8484 | 0.8848 | 1.175 | 0.1075 |
| rs17679286 | 6 | 12828434 | A,G | 0.933 | 0.8109 | 1.132 | 0.4053 |
| 6:12828992:T_TA | 6 | 12828992 | R,I | 0.8439 | 0.7393 | 1.203 | 0.08705 |
| rs9381427 | 6 | 12830144 | T,C | 0.8473 | 0.8763 | 1.171 | 0.1165 |
| rs6915585 | 6 | 12831273 | G,A | 0.9143 | 0.8051 | 1.151 | 0.2886 |
| rs62389228 | 6 | 12832840 | A,G | 0.9307 | 0.7941 | 1.092 | 0.5534 |
| rs12528956 | 6 | 12833077 | T,C | 0.736 | 0.933 | 1.12 | 0.1579 |
| rs7741088 | 6 | 12834122 | C,T | 0.9377 | 0.8302 | 1.2 | 0.2316 |
| rs1571996 | 6 | 12834714 | T,C | 0.9138 | 0.8003 | 1.151 | 0.2874 |
| 6:12835139:GT_G | 6 | 12835139 | R,D | 0.5715 | 0.9518 | 0.782 | 0.0005227 |
| 6:12835490:G_GA | 6 | 12835490 | R,I | 0.9208 | 0.8243 | 1.171 | 0.2454 |
| rs6458493 | 6 | 12835673 | G,A | 0.8469 | 0.8829 | 1.174 | 0.1085 |
| rs12528247 | 6 | 12835880 | C,A | 0.9282 | 0.8647 | 1.132 | 0.3721 |
| rs6458494 | 6 | 12836186 | T,C | 0.847 | 0.8825 | 1.175 | 0.1063 |
| rs28734939 | 6 | 12837663 | T,A | 0.867 | 0.7948 | 1.198 | 0.1079 |
| rs9395161 | 6 | 12838334 | C,T | 0.848 | 0.8815 | 1.177 | 0.104 |
| rs9381435 | 6 | 12838426 | C,T | 0.8477 | 0.883 | 1.176 | 0.1051 |
| rs9395162 | 6 | 12838532 | T,A | 0.848 | 0.8816 | 1.177 | 0.1043 |
| rs9463187 | 6 | 12839176 | A,C | 0.723 | 0.9422 | 1.118 | 0.1555 |
| rs1412742 | 6 | 12840104 | G,A | 0.8508 | 0.8887 | 1.175 | 0.11 |
| rs1412743 | 6 | 12840112 | C,G | 0.851 | 0.8883 | 1.174 | 0.1118 |

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|---|---|---|---|---|---|---|---|
| rs16873431 | 6 | 12840508 | T,C | 0.8554 | 0.867 | 1.18 | 0.1089 |
| 6:12840537:G_GA | 6 | 12840537 | R,I | 0.851 | 0.8886 | 1.174 | 0.1119 |
| rs13192509 | 6 | 12840877 | C,G | 0.8512 | 0.8873 | 1.175 | 0.1109 |
| rs16873436 | 6 | 12841033 | G,C | 0.851 | 0.8887 | 1.174 | 0.1121 |
| rs1537334 | 6 | 12841241 | C,G | 0.8517 | 0.8931 | 1.171 | 0.1167 |
| rs3945322 | 6 | 12841306 | G,A | 0.8517 | 0.8916 | 1.168 | 0.1239 |
| rs9357503 | 6 | 12841985 | T,A | 0.8519 | 0.8936 | 1.172 | 0.1151 |
| rs9349350 | 6 | 12842285 | A,G | 0.8522 | 0.8922 | 1.173 | 0.1143 |
| rs5017386 | 6 | 12842373 | G,T | 0.8519 | 0.8938 | 1.172 | 0.1154 |
| rs4711842 | 6 | 12842531 | G,A | 0.8522 | 0.8925 | 1.173 | 0.1144 |
| rs1537335 | 6 | 12842563 | G,A | 0.8519 | 0.8938 | 1.172 | 0.1155 |
| rs1537336 | 6 | 12842883 | C,A | 0.853 | 0.8778 | 1.176 | 0.1116 |
| rs1537337 | 6 | 12843006 | G,A | 0.8522 | 0.8927 | 1.173 | 0.1143 |
| rs1537338 | 6 | 12843203 | A,G | 0.8525 | 0.8865 | 1.176 | 0.1094 |
| rs9369605 | 6 | 12843219 | A,C | 0.852 | 0.8914 | 1.174 | 0.1119 |
| rs16873447 | 6 | 12844001 | A,T | 0.852 | 0.8937 | 1.173 | 0.1145 |
| rs16873449 | 6 | 12844141 | A,T | 0.852 | 0.8938 | 1.172 | 0.1147 |
| rs13192344 | 6 | 12844264 | C,A | 0.852 | 0.8938 | 1.172 | 0.1147 |
| rs9381436 | 6 | 12844405 | C,T | 0.852 | 0.894 | 1.172 | 0.1147 |
| rs9367239 | 6 | 12844465 | A,G | 0.852 | 0.8941 | 1.172 | 0.1147 |
| rs2184027 | 6 | 12844712 | A,G | 0.852 | 0.8952 | 1.172 | 0.1157 |
| rs13194950 | 6 | 12844775 | G,A | 0.9373 | 0.9077 | 1.166 | 0.2897 |
| rs4714913 | 6 | 12845085 | C,T | 0.8517 | 0.8962 | 1.171 | 0.1169 |
| rs4711845 | 6 | 12845156 | A,G | 0.852 | 0.8953 | 1.172 | 0.116 |
| rs4711848 | 6 | 12845240 | C,A | 0.8511 | 0.895 | 1.172 | 0.1151 |
| rs9349352 | 6 | 12846517 | C,T | 0.8518 | 0.8979 | 1.172 | 0.1139 |
| rs9369607 | 6 | 12846847 | T,A | 0.9192 | 0.8452 | 1.172 | 0.2321 |
| rs2065490 | 6 | 12847494 | T,C | 0.8522 | 0.8975 | 1.173 | 0.1129 |
| rs2065491 | 6 | 12847595 | A,T | 0.8522 | 0.8976 | 1.173 | 0.113 |
| rs9367240 | 6 | 12848685 | C,T | 0.8522 | 0.8977 | 1.173 | 0.1138 |
| rs9296486 | 6 | 12848969 | T,G | 0.8522 | 0.8982 | 1.173 | 0.1136 |
| rs9296487 | 6 | 12849031 | T,C | 0.5666 | 0.9553 | 1.19 | 0.01329 |
| rs9296488 | 6 | 12849304 | A,G | 0.8519 | 0.8998 | 1.172 | 0.1151 |
| rs62389889 | 6 | 12849622 | G,T | 0.9372 | 0.9123 | 1.164 | 0.2946 |
| rs9381439 | 6 | 12849678 | G,A | 0.8522 | 0.8987 | 1.173 | 0.1138 |
| rs12215208 | 6 | 12850294 | C,T | 0.5778 | 0.905 | 0.769 | 0.0003128 |
| rs9395172 | 6 | 12850534 | G,A | 0.571 | 0.9395 | 1.185 | 0.01699 |
| rs36043593 | 6 | 12850604 | C,T | 0.9372 | 0.9132 | 1.164 | 0.295 |
| rs6900427 | 6 | 12851560 | G,A | 0.933 | 0.9558 | 1.134 | 0.361 |
| rs13191496 | 6 | 12851625 | G,A | 0.9369 | 0.916 | 1.162 | 0.2994 |
| rs6917097 | 6 | 12851768 | T,C | 0.5709 | 0.9395 | 1.186 | 0.01645 |
| rs4714930 | 6 | 12852478 | T,G | 0.5737 | 0.9383 | 1.189 | 0.01491 |
| rs59402659 | 6 | 12853162 | A,G | 0.7247 | 0.9999 | 1.13 | 0.1093 |
| rs9369612 | 6 | 12853192 | T,C | 0.916 | 0.8254 | 1.158 | 0.2664 |
| rs34448141 | 6 | 12853265 | C,T | 0.9714 | 0.7876 | 1.565 | 0.04765 |
| rs62389892 | 6 | 12853979 | A,G | 0.9369 | 0.9179 | 1.16 | 0.3024 |
| rs6914233 | 6 | 12854443 | T,C | 0.933 | 0.9587 | 1.132 | 0.3666 |
| rs62389893 | 6 | 12854881 | G,T | 0.9406 | 0.8755 | 1.175 | 0.2867 |
| rs62389894 | 6 | 12854962 | A,T | 0.9369 | 0.9187 | 1.16 | 0.304 |
| rs35657920 | 6 | 12855243 | A,C | 0.8492 | 0.886 | 1.164 | 0.1317 |
| rs7454135 | 6 | 12855542 | T,G | 0.5709 | 0.9459 | 1.193 | 0.01256 |
| rs75506162 | 6 | 12855702 | C,T | 0.9165 | 0.8259 | 1.165 | 0.2484 |
| rs62389896 | 6 | 12855854 | A,G | 0.93 | 0.8426 | 1.093 | 0.5377 |
| rs13205779 | 6 | 12856004 | A,G | 0.933 | 0.9604 | 1.131 | 0.37 |
| 6:12856483:C_CT | 6 | 12856483 | R,I | 0.937 | 0.7109 | 1.218 | 0.2279 |
| rs9395185 | 6 | 12856827 | A,G | 0.8492 | 0.8853 | 1.164 | 0.132 |
| rs35395772 | 6 | 12857393 | G,A | 0.9372 | 0.9182 | 1.161 | 0.3017 |
| rs4714931 | 6 | 12857408 | A,G | 0.9165 | 0.8255 | 1.166 | 0.2473 |
| 6:12857625:CG_C | 6 | 12857625 | R,D | 0.9407 | 0.8763 | 1.175 | 0.2886 |

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|---|---|---|---|---|---|---|---|
| rs7748950 | 6 | 12858223 | T,C | 0.7218 | 0.9889 | 1.126 | 0.1208 |
| rs13198167 | 6 | 12858242 | G,A | 0.9371 | 0.9185 | 1.161 | 0.3021 |
| rs72835698 | 6 | 12858776 | G,A | 0.9296 | 0.8436 | 1.089 | 0.5506 |
| rs35621699 | 6 | 12858904 | T,C | 0.9371 | 0.9191 | 1.16 | 0.3038 |
| rs6458503 | 6 | 12859556 | C,T | 0.7219 | 0.989 | 1.126 | 0.121 |
| rs55879442 | 6 | 12859873 | T,C | 0.9284 | 0.8903 | 1.141 | 0.3347 |
| rs9296494 | 6 | 12859886 | A,G | 0.6549 | 0.9932 | 1.149 | 0.05422 |
| rs9395190 | 6 | 12860080 | T,C | 0.6549 | 0.9933 | 1.149 | 0.05428 |
| rs144273252 | 6 | 12860491 | T,C | 0.9845 | 0.6917 | 0.751 | 0.3693 |
| rs6924353 | 6 | 12860700 | C,T | 0.9531 | 0.7441 | 1.342 | 0.1082 |
| rs6912532 | 6 | 12860762 | T,C | 0.9332 | 0.9656 | 1.129 | 0.3768 |
| rs6927781 | 6 | 12860987 | G,C | 0.937 | 0.9227 | 1.157 | 0.3095 |
| rs62389900 | 6 | 12862200 | G,T | 0.937 | 0.9245 | 1.156 | 0.3125 |
| rs16873462 | 6 | 12862244 | G,A | 0.937 | 0.9246 | 1.156 | 0.3128 |
| rs17617491 | 6 | 12862562 | C,T | 0.9263 | 0.8834 | 1.159 | 0.2776 |
| rs7770745 | 6 | 12862978 | A,T | 0.7247 | 0.9795 | 1.126 | 0.1254 |
| rs17679417 | 6 | 12863108 | A,T | 0.7298 | 0.9747 | 1.145 | 0.08181 |
| rs34348949 | 6 | 12863250 | A,G | 0.937 | 0.9254 | 1.156 | 0.3136 |
| rs9381451 | 6 | 12863621 | T,C | 0.9157 | 0.8257 | 1.178 | 0.2155 |
| rs7771962 | 6 | 12863738 | T,C | 0.7249 | 0.9959 | 1.13 | 0.1092 |
| rs9472752 | 6 | 12864134 | T,C | 0.5709 | 0.927 | 1.198 | 0.01142 |
| rs6914467 | 6 | 12864309 | G,A | 0.9369 | 0.9265 | 1.155 | 0.3152 |
| rs9381455 | 6 | 12864898 | C,T | 0.7052 | 0.9144 | 1.137 | 0.1006 |
| rs9381456 | 6 | 12865148 | A,G | 0.6555 | 0.9996 | 1.147 | 0.05717 |
| rs6901070 | 6 | 12865243 | G,A | 0.6545 | 0.9935 | 1.146 | 0.05815 |
| rs6921974 | 6 | 12865376 | T,C | 0.6555 | 0.9997 | 1.147 | 0.05724 |
| rs60844130 | 6 | 12865503 | C,G | 0.8591 | 0.7718 | 1.177 | 0.1437 |
| rs9296495 | 6 | 12865649 | G,A | 0.5706 | 0.9438 | 1.196 | 0.0114 |
| rs35227817 | 6 | 12866528 | G,A | 0.9403 | 0.8824 | 1.17 | 0.2983 |
| rs55803153 | 6 | 12866927 | G,A | 0.9362 | 0.9115 | 1.142 | 0.3569 |
| rs35954478 | 6 | 12867215 | A,G | 0.9376 | 0.8836 | 1.158 | 0.3213 |
| rs1412744 | 6 | 12867696 | A,G | 0.7261 | 0.9969 | 1.177 | 0.03282 |
| rs113606396 | 6 | 12868263 | G,A | 0.841 | 0.6887 | 1.167 | 0.1681 |
| rs55637633 | 6 | 12868320 | C,A | 0.9397 | 0.8752 | 1.176 | 0.2822 |
| rs62389950 | 6 | 12868726 | C,T | 0.8539 | 0.8807 | 1.076 | 0.474 |
| rs1360579 | 6 | 12871736 | G,A | 0.713 | 0.9603 | 1.154 | 0.06176 |
| rs9472777 | 6 | 12872092 | G,A | 0.7109 | 0.9699 | 1.153 | 0.06135 |
| rs4714946 | 6 | 12872220 | G,A | 0.723 | 0.9602 | 1.169 | 0.04348 |
| rs4711856 | 6 | 12872477 | G,A | 0.943 | 0.9196 | 1.16 | 0.327 |
| rs78881531 | 6 | 12872817 | C,T | 0.944 | 0.9308 | 1.158 | 0.3329 |
| rs9381462 | 6 | 12873775 | G,A | 0.4902 | 0.9993 | 1.195 | 0.008286 |
| rs1571997 | 6 | 12874309 | A,G | 0.4822 | 0.9693 | 1.204 | 0.006721 |
| rs66867947 | 6 | 12874672 | T,G | 0.7118 | 0.9986 | 1.136 | 0.08712 |
| rs1332841 | 6 | 12875054 | G,T | 0.7097 | 0.9838 | 1.139 | 0.08342 |
| rs9472786 | 6 | 12877597 | G,T | 0.7152 | 0.9622 | 1.156 | 0.05828 |
| rs9472790 | 6 | 12879101 | T,A | 0.4851 | 0.9522 | 1.213 | 0.005116 |
| rs1332842 | 6 | 12879851 | C,T | 0.9444 | 0.9376 | 1.157 | 0.3368 |
| rs17679501 | 6 | 12879996 | T,A | 0.7128 | 0.9614 | 1.158 | 0.05392 |
| rs4711857 | 6 | 12880109 | C,T | 0.7133 | 0.9629 | 1.158 | 0.05395 |
| rs4711858 | 6 | 12880131 | T,C | 0.7216 | 0.9637 | 1.163 | 0.05022 |
| rs8180628 | 6 | 12881163 | G,A | 0.6624 | 0.9947 | 1.2 | 0.01061 |
| rs1537340 | 6 | 12881855 | G,A | 0.6926 | 0.9181 | 1.321 | 0.000321 |
| rs17617584 | 6 | 12882064 | A,G | 0.9411 | 0.8632 | 1.13 | 0.4274 |
| rs59802022 | 6 | 12882105 | C,A | 0.9408 | 0.8559 | 1.128 | 0.435 |
| rs55908560 | 6 | 12882732 | C,T | 0.9419 | 0.8705 | 1.128 | 0.4362 |
| rs13208248 | 6 | 12883524 | C,A | 0.6741 | 0.9187 | 1.316 | 0.0002878 |
| rs9349371 | 6 | 12886313 | C,T | 0.9181 | 0.7322 | 1.089 | 0.5557 |
| rs9367253 | 6 | 12888047 | A,T | 0.8871 | 0.6661 | 1.06 | 0.6528 |
| rs9357513 | 6 | 12888105 | A,G | 0.9226 | 0.7819 | 1.096 | 0.521 |

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|---|---|---|---|---|---|---|---|
| rs146401688 | 6 | 12888498 | C,T | 0.985 | 0.7133 | 1.184 | 0.5946 |
| rs71562459 | 6 | 12888602 | G,C | 0.6917 | 0.9916 | 1.304 | 0.0003331 |
| rs1332844 | 6 | 12889004 | T,C | 0.6158 | 0.9375 | 1.315 | 0.0001361 |
| rs34944538 | 6 | 12889145 | A,G | 0.6915 | 0.9978 | 1.302 | 0.0003432 |
| 6:12889973:CT_C | 6 | 12889973 | R,D | 0.9486 | 0.892 | 1.125 | 0.4693 |
| rs9349372 | 6 | 12890676 | T,C | 0.9202 | 0.751 | 1.107 | 0.4805 |
| rs35355695 | 6 | 12891103 | G,T | 0.6959 | 0.9796 | 1.299 | 0.0004641 |
| rs7750679 | 6 | 12891301 | C,T | 0.6171 | 0.9333 | 1.312 | 0.0001619 |
| rs6902050 | 6 | 12892236 | A,G | 0.9202 | 0.7482 | 1.105 | 0.4862 |
| rs1332845 | 6 | 12892456 | A,G | 0.699 | 0.9673 | 1.306 | 0.0004021 |
| rs6925904 | 6 | 12892486 | G,A | 0.6171 | 0.9335 | 1.31 | 0.0001719 |
| rs1332846 | 6 | 12892523 | T,A | 0.6976 | 0.9718 | 1.305 | 0.0003968 |
| rs1332847 | 6 | 12892754 | C,T | 0.6977 | 0.9716 | 1.305 | 0.0003985 |
| rs2876300 | 6 | 12894103 | A,G | 0.6965 | 0.9651 | 1.308 | 0.0003746 |
| rs2095122 | 6 | 12894858 | T,C | 0.9212 | 0.7539 | 1.103 | 0.4972 |
| rs9296512 | 6 | 12894904 | C,G | 0.6085 | 0.9049 | 1.324 | 0.0001153 |
| rs2104908 | 6 | 12895056 | G,A | 0.9183 | 0.7318 | 1.109 | 0.4714 |
| rs62389954 | 6 | 12896740 | G,A | 0.6964 | 0.9617 | 1.308 | 0.0003766 |
| rs4714951 | 6 | 12897307 | C,T | 0.6978 | 0.967 | 1.306 | 0.0004011 |
| rs73362169 | 6 | 12897549 | C,T | 0.9425 | 0.8474 | 1.129 | 0.441 |
| rs1831705 | 6 | 12898162 | G,A | 0.95 | 0.8975 | 1.125 | 0.4713 |
| rs1831706 | 6 | 12898178 | T,C | 0.9435 | 0.8051 | 1.135 | 0.4367 |
| rs13219256 | 6 | 12898292 | C,T | 0.698 | 0.9661 | 1.306 | 0.0004085 |
| rs9395214 | 6 | 12898884 | G,C | 0.5983 | 0.936 | 1.297 | 0.0002556 |
| rs7751826 | 6 | 12900977 | T,C | 0.6092 | 0.9477 | 1.298 | 0.000236 |
| rs9369640 | 6 | 12901441 | A,C | 0.6095 | 0.9501 | 1.298 | 0.0002403 |
| rs62389955 | 6 | 12902248 | A,G | 0.6432 | 0.9715 | 1.3 | 0.000247 |
| rs6911226 | 6 | 12902290 | G,A | 0.6093 | 0.9542 | 1.297 | 0.000243 |
| rs6915983 | 6 | 12902441 | G,T | 0.6086 | 0.9431 | 1.298 | 0.0002474 |
| rs4714955 | 6 | 12903435 | C,T | 0.6449 | 0.9719 | 1.299 | 0.0002641 |
| rs1537341 | 6 | 12903900 | T,C | 0.9684 | 0.6472 | 1.043 | 0.8598 |
| rs9349379 | 6 | 12903957 | A,G | 0.6257 | 0.9827 | 0.727 | 5.88E-06 |
| rs7759918 | 6 | 12904536 | T,A | 0.9689 | 0.6565 | 1.039 | 0.8709 |
| rs9472888 | 6 | 12904903 | A,G | 0.9725 | 0.732 | 1.048 | 0.844 |
| rs6912234 | 6 | 12906346 | G,C | 0.9726 | 0.7374 | 1.05 | 0.8388 |
| rs2876301 | 6 | 12907411 | T,C | 0.5815 | 0.8658 | 1.305 | 0.0002876 |
| rs2876302 | 6 | 12907412 | A,G | 0.5863 | 0.8826 | 1.303 | 0.0002759 |
| rs2327620 | 6 | 12907591 | G,A | 0.6082 | 0.9696 | 1.289 | 0.0002904 |
| rs7760016 | 6 | 12908077 | A,G | 0.6012 | 0.9524 | 1.291 | 0.0002864 |
| rs7760527 | 6 | 12908408 | A,G | 0.6033 | 0.959 | 1.293 | 0.0002573 |
| rs13197912 | 6 | 12908747 | A,T | 0.6446 | 0.9708 | 1.294 | 0.0003239 |
| rs1571999 | 6 | 12909467 | A,G | 0.9637 | 0.6181 | 1.072 | 0.7627 |
| rs6916096 | 6 | 12909738 | T,C | 0.9687 | 0.6894 | 1.07 | 0.7714 |
| rs7454157 | 6 | 12909874 | G,A | 0.6159 | 0.9995 | 1.28 | 0.0003685 |
| rs6917613 | 6 | 12910698 | A,C | 0.9738 | 0.769 | 1.053 | 0.8283 |
| rs12530250 | 6 | 12911965 | A,G | 0.644 | 0.9748 | 1.292 | 0.0003432 |
| rs9381494 | 6 | 12913152 | T,C | 0.6017 | 0.9432 | 1.291 | 0.0003092 |
| rs11752630 | 6 | 12914967 | A,T | 0.9744 | 0.6895 | 1.073 | 0.7835 |
| rs4711863 | 6 | 12915417 | G,C | 0.6412 | 0.9555 | 1.292 | 0.0003758 |
| rs6915761 | 6 | 12915699 | A,G | 0.9672 | 0.6163 | 1.097 | 0.7002 |
| rs17679590 | 6 | 12919148 | G,A | 0.906 | 0.7744 | 1.023 | 0.8633 |
| rs2876303 | 6 | 12919867 | A,G | 0.6011 | 0.9187 | 1.298 | 0.0002815 |
| rs8180558 | 6 | 12919989 | C,T | 0.637 | 0.9364 | 1.295 | 0.0003738 |
| rs111395058 | 6 | 12921714 | A,T | 0.6395 | 0.9444 | 1.295 | 0.0003686 |
| rs9381500 | 6 | 12922535 | A,G | 0.6301 | 0.9194 | 1.287 | 0.0005756 |
| rs9369650 | 6 | 12922652 | A,C | 0.5815 | 0.8305 | 1.304 | 0.0004081 |
| rs2327621 | 6 | 12922689 | A,G | 0.6271 | 0.9093 | 1.287 | 0.0005913 |
| 6:12922721:CA_C | 6 | 12922721 | R,D | 0.6368 | 0.9431 | 1.278 | 0.0007076 |
| rs34343839 | 6 | 12922734 | C,T | 0.6366 | 0.9437 | 1.278 | 0.0007067 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| rs1014342 | 6 | 12923157 | C,T | 0.5775 | 0.8198 | 1.302 | 0.0004781 |
| rs62386818 | 6 | 12923767 | C,A | 0.6314 | 0.9285 | 1.283 | 0.0006197 |
| rs9369652 | 6 | 12924744 | T,C | 0.5789 | 0.8241 | 1.303 | 0.0004442 |
| rs1953088 | 6 | 12925936 | A,C | 0.5785 | 0.8232 | 1.303 | 0.000452 |
| rs12526453 | 6 | 12927544 | C,G | 0.6469 | 0.9995 | 1.27 | 0.0007372 |
| rs4714990 | 6 | 12927845 | T,C | 0.5382 | 0.6953 | 1.314 | 0.0007636 |
| rs6458545 | 6 | 12934302 | G,C | 0.5458 | 0.6533 | 1.323 | 0.0008546 |
| rs7739181 | 6 | 12934687 | G,A | 0.655 | 0.91 | 1.287 | 0.00076 |
| rs13201878 | 6 | 12943066 | A,G | 0.7141 | 0.6899 | 1.347 | 0.001064 |
| rs36119782 | 6 | 13054433 | G,A | 0.821 | 0.6514 | 0.812 | 0.053 |
| rs7762827 | 6 | 13054732 | C,G | 0.7992 | 0.6485 | 0.822 | 0.0564 |
| rs9296592 | 6 | 13055406 | T,C | 0.8007 | 0.6472 | 0.82 | 0.05523 |
| rs9473354 | 6 | 13059035 | C,A | 0.7812 | 0.975 | 0.863 | 0.06867 |
| rs4711908 | 6 | 13060208 | A,G | 0.7796 | 0.9911 | 0.864 | 0.06911 |
| rs4711909 | 6 | 13060214 | C,A | 0.7796 | 0.9915 | 0.864 | 0.06917 |
| rs7738252 | 6 | 13060568 | A,G | 0.7796 | 0.9941 | 0.865 | 0.06907 |
| rs6932757 | 6 | 13063361 | T,G | 0.8085 | 0.8148 | 0.838 | 0.05859 |
| rs9463408 | 6 | 13063824 | A,G | 0.78 | 0.9609 | 0.863 | 0.07091 |
| rs9463410 | 6 | 13064274 | A,G | 0.7797 | 0.9479 | 0.863 | 0.07135 |
| rs9473370 | 6 | 13065071 | A,C | 0.813 | 0.7513 | 0.831 | 0.05943 |
| rs4711910 | 6 | 13066375 | T,C | 0.8303 | 0.6875 | 0.814 | 0.05463 |
| rs35305875 | 6 | 13067511 | A,G | 0.8291 | 0.6768 | 0.813 | 0.05474 |
| rs34952336 | 6 | 13067820 | A,T | 0.8309 | 0.6675 | 0.811 | 0.05383 |
| rs4715082 | 6 | 13068291 | A,G | 0.816 | 0.7067 | 0.826 | 0.06149 |
| rs9463423 | 6 | 13069359 | T,C | 0.7328 | 0.7033 | 0.85 | 0.06954 |
| rs34381599 | 6 | 13071265 | T,G | 0.7441 | 0.6087 | 0.837 | 0.06789 |
| rs35229766 | 6 | 13072206 | T,C | 0.8306 | 0.6032 | 0.803 | 0.05555 |
| rs6458616 | 6 | 13072498 | A,G | 0.7443 | 0.6054 | 0.836 | 0.0683 |
| rs7750120 | 6 | 13072633 | T,C | 0.7329 | 0.6564 | 0.846 | 0.07087 |
| rs9349494 | 6 | 13173147 | G,A | 0.7698 | 0.6137 | 0.924 | 0.4423 |
| rs12528399 | 6 | 13177901 | G,T | 0.7703 | 0.6893 | 0.924 | 0.4178 |
| rs12527257 | 6 | 13178069 | T,C | 0.7715 | 0.6859 | 0.925 | 0.4209 |
| rs9463511 | 6 | 13178259 | G,A | 0.6907 | 0.6203 | 0.917 | 0.3507 |
| rs16873682 | 6 | 13178390 | A,G | 0.7734 | 0.68 | 0.924 | 0.418 |
| rs4097413 | 6 | 13178610 | A,G | 0.7705 | 0.6936 | 0.925 | 0.4173 |
| rs9381807 | 6 | 13179394 | G,A | 0.7703 | 0.6992 | 0.925 | 0.4167 |
| rs11757278 | 6 | 13180454 | T,C | 0.7042 | 0.9932 | 0.933 | 0.3507 |
| rs9381809 | 6 | 13182117 | G,C | 0.7719 | 0.6694 | 0.923 | 0.4191 |
| rs3778646 | 6 | 13182685 | G,T | 0.7724 | 0.6606 | 0.923 | 0.4189 |
| rs3823445 | 6 | 13182995 | G,A | 0.7409 | 0.7795 | 0.924 | 0.3699 |
| rs9381810 | 6 | 13183121 | T,C | 0.7402 | 0.7808 | 0.924 | 0.369 |
| rs9395520 | 6 | 13183523 | C,T | 0.7038 | 0.9226 | 0.931 | 0.355 |
| rs9381812 | 6 | 13183998 | A,G | 0.7399 | 0.768 | 0.924 | 0.3675 |
| rs10948524 | 6 | 13188493 | A,G | 0.7382 | 0.6813 | 0.919 | 0.3658 |
| rs9367368 | 6 | 13189275 | T,C | 0.7354 | 0.6592 | 0.918 | 0.3647 |
| rs9367369 | 6 | 13189941 | A,G | 0.7374 | 0.6641 | 0.918 | 0.3655 |

**Supplemental Table V.** Coordinates of the *PHACTR1* exons that were re-sequenced in 500 early-onset MI cases and 500 controls. We used a custom-made Agilent's SureSelect library for exon capture and non-indexed pooled sequencing to discover variants. We applied the Syzygy software to analyze the sequence data[2]. Results for this re-sequencing experiment are presented in reference [3].

| Feature name | Coordinates (hg19) |
|---|---|
| Exon1 | chr6:12825279-12825999 |
| Exon2 | chr6:12826870-12827110 |
| Exon3 | chr6:12857874-12857994 |
| Exon4 | chr6:13161544-13161784 |
| Exon5 | chr6:13268380-13268541 |
| Exon6 | chr6:13290692-13290932 |
| Exon7 | chr6:13314005-13314365 |
| Exon8 | chr6:13335969-13336269 |
| Exon9 | chr6:13338205-13338445 |
| Exon10 | chr6:13381023-13381171 |
| Exon11 | chr6:13386433-13386584 |
| Exon12 | chr6:13391582-13391822 |
| Exon13 | chr6:13394314-13394473 |
| Exon14 | chr6:13395219-13396059 |

**Supplemental Table VI.** List of non-synonymous *PHACTR1* variants identified by whole-exome sequencing of 4,703 myocardial infarction cases and 5,090 controls.

| Variant | Category | AminoAcid | MAF (case) | MAF (control) |
|---|---|---|---|---|
| 6:12749931_T/A | NON_SYNONYMOUS_CODING | D53E | 0 | 0.000196464 |
| 6:12749983_T/C | NON_SYNONYMOUS_CODING | Y71H | 0.000106315 | 0 |
| 6:12749994_G/T | NON_SYNONYMOUS_CODING | E74D | 0 | 0.000196464 |
| 6:12750019_G/A | NON_SYNONYMOUS_CODING | A83T | 0 | 9.82318E-05 |
| 6:12933867_G/A | NON_SYNONYMOUS_CODING | V85I | 0.001807357 | 0.006385069 |
| 6:12933894_G/A | NON_SYNONYMOUS_CODING | A94T | 0.000106315 | 9.82318E-05 |
| 6:12933907_C/T | NON_SYNONYMOUS_CODING | P98L | 0.000106315 | 9.82318E-05 |
| 6:12933912_G/A | NON_SYNONYMOUS_CODING | V100M | 0.004252605 | 0.003143418 |
| 6:12933928_G/A | NON_SYNONYMOUS_CODING | R105H | 0 | 9.82318E-05 |
| 6:12933942_G/A | NON_SYNONYMOUS_CODING | E110K | 0.000106315 | 0 |
| 6:12933945_C/A | NON_SYNONYMOUS_CODING | L111M | 0 | 9.82318E-05 |
| 6:12933966_G/A | NON_SYNONYMOUS_CODING | G118S | 0 | 9.82318E-05 |
| 6:12933969_C/A | NON_SYNONYMOUS_CODING | L119I | 0.001063151 | 0.002652259 |
| 6:12934002_G/A | NON_SYNONYMOUS_CODING | A130T | 0.00021263 | 0.000491159 |
| 6:12934033_G/A | NON_SYNONYMOUS_CODING | G140E | 0.000106315 | 0 |
| 6:12934044_A/G | NON_SYNONYMOUS_CODING | T144A | 0 | 9.82318E-05 |
| 6:12934045_C/T | NON_SYNONYMOUS_CODING | T144I | 0.00414629 | 0.004715128 |
| 6:12934055_G/A | NON_SYNONYMOUS_CODING | M147I | 0.000106315 | 0 |
| 6:12934059_C/G | NON_SYNONYMOUS_CODING | P149A | 0 | 0 |
| 6:12934071_G/C | NON_SYNONYMOUS_CODING | A153P | 0.000106315 | 0 |
| 6:12934098_C/A | NON_SYNONYMOUS_CODING | P162T | 0 | 9.82318E-05 |
| 6:12934106_G/C | NON_SYNONYMOUS_CODING | E164D | 0.000106315 | 9.82318E-05 |
| 6:13053627_G/A | NON_SYNONYMOUS_CODING | R94H | 0.000106315 | 0 |
| 6:13053655_C/G | NON_SYNONYMOUS_CODING | H103Q | 0 | 9.82318E-05 |
| 6:13182822_T/C | NON_SYNONYMOUS_CODING | S190P | 0.000106315 | 0 |
| 6:13182832_C/T | NON_SYNONYMOUS_CODING | A193V | 0.000106315 | 0 |
| 6:13182840_G/A | NON_SYNONYMOUS_CODING | E196K | 0.000106315 | 0 |
| 6:13182846_G/C | NON_SYNONYMOUS_CODING | E198Q | 0.000106315 | 9.82318E-05 |
| 6:13182850_C/G | NON_SYNONYMOUS_CODING | P199R | 0.000106315 | 0 |
| 6:13182895_C/T | NON_SYNONYMOUS_CODING | P100L | 0 | 9.82318E-05 |
| 6:13182916_C/CAGGT | FRAME_SHIFT | . | 0.000106315 | 0 |
| 6:13185044_T/A | NON_SYNONYMOUS_CODING | S112R | 0 | 9.82318E-05 |
| 6:13185051_G/A | NON_SYNONYMOUS_CODING | A115T | 0.000106315 | 0 |
| 6:13185190_C/T | NON_SYNONYMOUS_CODING | P130L | 0 | 9.82318E-05 |
| 6:13185211_C/T | NON_SYNONYMOUS_CODING | T137I | 0.000106315 | 0 |
| 6:13185216_A/G | NON_SYNONYMOUS_CODING | R139G | 0.000106315 | 0 |
| 6:13185238_G/T | SPLICE_SITE_DONOR | . | 0.000106315 | 0 |
| 6:13206058_C/T | NON_SYNONYMOUS_CODING | P226S | 0 | 9.82318E-05 |
| 6:13206074_G/T | NON_SYNONYMOUS_CODING | C231F | 0.00021263 | 0 |
| 6:13206089_T/G | NON_SYNONYMOUS_CODING | L236R | 0 | 9.82318E-05 |
| 6:13206137_G/C | NON_SYNONYMOUS_CODING | G107A | 0 | 0.000196464 |
| 6:13206174_G/C | NON_SYNONYMOUS_CODING | Q119H | 0.000106315 | 0 |
| 6:13206259_G/A | NON_SYNONYMOUS_CODING | G148S | 0 | 9.82318E-05 |
| 6:13206262_C/A | NON_SYNONYMOUS_CODING | Q149K | 0 | 9.82318E-05 |
| 6:13206283_G/A | NON_SYNONYMOUS_CODING | G156S | 0.00021263 | 9.82318E-05 |
| 6:13206302_C/T | NON_SYNONYMOUS_CODING | P162L | 0.00021263 | 0 |
| 6:13228059_G/A | NON_SYNONYMOUS_CODING | R188Q | 0 | 9.82318E-05 |
| 6:13228112_G/T | NON_SYNONYMOUS_CODING | V206F | 0 | 9.82318E-05 |
| 6:13228125_G/A | NON_SYNONYMOUS_CODING | G210E | 0 | 9.82318E-05 |
| 6:13228130_A/G | NON_SYNONYMOUS_CODING | M212V | 0 | 0.000196464 |
| 6:13228170_T/C | NON_SYNONYMOUS_CODING | I225T | 0 | 9.82318E-05 |
| 6:13228256_G/A | NON_SYNONYMOUS_CODING | E254K | 0 | 9.82318E-05 |
| 6:13230271_T/A | NON_SYNONYMOUS_CODING | S268T | 0.00021263 | 9.82318E-05 |
| 6:13230385_C/T | NON_SYNONYMOUS_CODING | R306W | 0 | 0.000589391 |

| | | | | |
|---|---|---|---|---|
| 6:13230430_G/C | NON_SYNONYMOUS_CODING | G154A | 0 | 9.82318E-05 |
| 6:13230435_C/T | NON_SYNONYMOUS_CODING | R156W | 0.000531576 | 0.000589391 |
| 6:13273058_T/C | NON_SYNONYMOUS_CODING | M17T | 0 | 9.82318E-05 |
| 6:13273059_G/C | NON_SYNONYMOUS_CODING | M17I | 0 | 0 |
| 6:13273069_C/T | NON_SYNONYMOUS_CODING | L21F | 0.000106315 | 0 |
| 6:13273087_C/T | NON_SYNONYMOUS_CODING | R27C | 0.000106315 | 0 |
| 6:13273088_G/A | NON_SYNONYMOUS_CODING | R27H | 0.005315756 | 0.002946955 |
| 6:13273094_G/A | NON_SYNONYMOUS_CODING | R29Q | 0.000106315 | 0 |
| 6:13283684_C/T | NON_SYNONYMOUS_CODING | R369W | 0.000106315 | 0 |
| 6:13283705_C/T | NON_SYNONYMOUS_CODING | R376C | 0.000106315 | 0 |
| 6:13283756_G/A | NON_SYNONYMOUS_CODING | A102T | 0 | 0 |
| 6:13283774_C/T | NON_SYNONYMOUS_CODING | R108C | 0 | 9.82318E-05 |
| 6:13283804_G/A | NON_SYNONYMOUS_CODING | G118R | 0.00021263 | 0.000589391 |
| 6:13283807_G/T | STOP_GAINED | E119* | 0 | 9.82318E-05 |
| 6:13283826_G/T | NON_SYNONYMOUS_CODING | G125V | 0.000106315 | 0 |
| 6:13286415_C/G | NON_SYNONYMOUS_CODING | T127S | 0.000106315 | 0 |
| 6:13288638_G/T | NON_SYNONYMOUS_CODING | R433L | 0 | 9.82318E-05 |

**Supplemental Table VII.** Clinical description of the 25 patients that underwent heart transplant at the Montreal Heart Institute. We used the right coronary arteries from these patients in our expression quantitative trait locus (eQTL) experiment. Sex and clinical diagnostic are not associated with *PHACTR1* expression levels (*P*>0.12). Histological characterization corresponds to the state (healthy or diseased) of the coronary artery when it was harvested. *PHACTR1* expression levels are higher in diseased coronaries (*P*=0.0092). In a predictive model (linear regression) of *PHACTR1* expression levels, when we adjust for coronary artery disease status, the association at rs9349379 remains significant (*P*=0.0016).

| **Patient ID** | **Sex** | **Clinical diagnostic** | **Histological characterization** |
|---|---|---|---|
| 1 | Female | Post radio-/chemotherapy cardiomyopathy | Diseased |
| 2 | Female | Viral cardiomyopathy | Healthy |
| 3 | Male | Dilated cardiomyopathy | Healthy |
| 4 | Male | Ischemic cardiomyopathy | Diseased |
| 5 | Male | Dilated cardiomyopathy | Diseased |
| 6 | Female | Ischemic cardiomyopathy | Diseased |
| 7 | Female | Idiopathic cardiomyopathy | Diseased |
| 8 | Male | Dilated cardiomyopathy | Diseased |
| 9 | Male | Hypertrophic cardiomyopathy | Diseased |
| 10 | Male | Ischemic cardiomyopathy | Diseased |
| 11 | Female | Ischemic cardiomyopathy | Diseased |
| 12 | Male | Ischemic cardiomyopathy | Diseased |
| 13 | Male | Dilated cardiomyopathy | Healthy |
| 14 | Female | Hypertrophic cardiomyopathy | Healthy |
| 15 | Male | Ischemic cardiomyopathy | Healthy |
| 16 | Male | Ischemic cardiomyopathy | Healthy |
| 17 | Male | Dilated cardiomyopathy | Healthy |
| 18 | Male | Ischemic cardiomyopathy | Diseased |
| 19 | Female | Dilated cardiomyopathy | Healthy |
| 20 | Male | Myocarditis | Diseased |
| 21 | Male | Dilated cardiomyopathy | Healthy |
| 22 | Male | Dilated cardiomyopathy | Healthy |
| 23 | Female | Hypertrophic cardiomyopathy | Healthy |
| 24 | Female | Post radio-/chemotherapy cardiomyopathy | Healthy |
| 25 | Female | Dilated cardiomyopathy | Healthy |

**Supplemental Table VIII.** Association results between *PHACTR1* expression levels in 25 human right coronary artery samples and *PHACTR1* SNPs. For analysis, we only kept markers with an imputation quality >0.6. We sorted results based on their association P-value with *PHACTR1* expression levels. Three variants (rs60844130, rs12215445, rs113606396) are marginally more significant than rs9349379, but they become non-significant after conditioning on genotypes at rs9349379. Given the very small sample size (n=25), these marginal differences could be due to statistical fluctuations. Moreover, these three markers are not associated with MI in the MHI Biobank.

| Marker | Chromosome | Position (hg19) | ALLELES | Frequency (allele 1) | Imputation (rsq_hat) | Effect | P-value | P-value (conditional on rs9349379) |
|---|---|---|---|---|---|---|---|---|
| rs60844130 | 6 | 12865503 | C,G | 0.8155 | 0.8494 | 1.185 | 0.01011 | 0.1419 |
| rs12215445 | 6 | 12803314 | G,A | 0.8185 | 0.6514 | 1.241 | 0.01022 | 0.0966 |
| rs113606396 | 6 | 12868263 | G,A | 0.8111 | 0.7827 | 1.157 | 0.01609 | 0.165 |
| rs9349379 | 6 | 12903957 | A,G | 0.5998 | 0.9911 | -0.581 | 0.01831 | NA |
| rs10807323 | 6 | 12795031 | G,A | 0.6644 | 0.7128 | -0.649 | 0.06512 | 0.8933 |
| rs9381401 | 6 | 12801967 | A,C | 0.6665 | 0.763 | -0.626 | 0.0663 | 0.8977 |
| rs2026458 | 6 | 12825874 | C,T | 0.6599 | 1 | -0.525 | 0.07456 | 0.8498 |
| 6:12835139:GT_G | 6 | 12835139 | R,D | 0.6604 | 0.9839 | -0.531 | 0.07667 | 0.8521 |
| rs12215208 | 6 | 12850294 | C,T | 0.6617 | 0.9525 | -0.523 | 0.08557 | 0.882 |
| rs7454157 | 6 | 12909874 | G,A | 0.6398 | 1 | 0.463 | 0.09324 | 1 |
| rs9296512 | 6 | 12894904 | C,G | 0.6343 | 0.8887 | 0.475 | 0.1044 | 0.9362 |
| rs1332844 | 6 | 12889004 | T,C | 0.6462 | 0.9202 | 0.458 | 0.1154 | 0.9779 |
| rs9369640 | 6 | 12901441 | A,C | 0.6365 | 0.9277 | 0.449 | 0.1163 | 0.8974 |
| rs2876302 | 6 | 12907412 | A,G | 0.6017 | 0.8599 | 0.455 | 0.1166 | 0.8455 |
| rs7751826 | 6 | 12900977 | T,C | 0.6361 | 0.9252 | 0.449 | 0.1168 | 0.8976 |
| rs2876301 | 6 | 12907411 | T,C | 0.5957 | 0.8399 | 0.459 | 0.1183 | 0.8451 |
| rs7750679 | 6 | 12891301 | C,T | 0.642 | 0.9131 | 0.454 | 0.1197 | 0.9231 |
| rs6911226 | 6 | 12902290 | G,A | 0.6329 | 0.9296 | 0.442 | 0.1207 | 0.8642 |
| rs13208248 | 6 | 12883524 | C,A | 0.6696 | 0.9159 | 0.483 | 0.1227 | 0.9432 |
| rs6925904 | 6 | 12892486 | G,A | 0.6441 | 0.9223 | 0.449 | 0.1227 | 0.8995 |
| rs2876303 | 6 | 12919867 | A,G | 0.6227 | 0.9143 | 0.436 | 0.1236 | 0.8206 |
| rs6915983 | 6 | 12902441 | G,T | 0.6325 | 0.9232 | 0.439 | 0.1247 | 0.8511 |
| rs35355695 | 6 | 12891103 | G,T | 0.6986 | 1 | 0.48 | 0.129 | 0.9797 |
| rs2327620 | 6 | 12907591 | G,A | 0.6222 | 0.9657 | 0.419 | 0.1297 | 0.8063 |
| rs13197912 | 6 | 12908747 | A,T | 0.6782 | 0.9852 | 0.442 | 0.131 | 0.9778 |
| rs4711863 | 6 | 12915417 | G,C | 0.6765 | 0.964 | 0.444 | 0.131 | 0.9652 |
| rs1332846 | 6 | 12892523 | T,A | 0.703 | 1 | 0.479 | 0.132 | 0.9736 |
| rs1332847 | 6 | 12892754 | C,T | 0.7031 | 1 | 0.479 | 0.1321 | 0.9738 |
| rs13219256 | 6 | 12898292 | C,T | 0.7033 | 0.9987 | 0.48 | 0.1322 | 0.9757 |
| rs4714951 | 6 | 12897307 | C,T | 0.7032 | 0.9992 | 0.48 | 0.1322 | 0.9754 |
| rs12530250 | 6 | 12911965 | A,G | 0.6782 | 0.9914 | 0.439 | 0.1323 | 0.9801 |
| rs1332845 | 6 | 12892456 | A,G | 0.7034 | 1 | 0.48 | 0.1323 | 0.9739 |
| rs34944538 | 6 | 12889145 | A,G | 0.7 | 1 | 0.47 | 0.1349 | 0.9809 |
| rs62389954 | 6 | 12896740 | G,A | 0.6979 | 0.9781 | 0.48 | 0.1365 | 0.964 |
| rs2876300 | 6 | 12894103 | A,G | 0.698 | 0.9804 | 0.479 | 0.1366 | 0.9669 |
| rs111395058 | 6 | 12921714 | A,T | 0.6731 | 0.9407 | 0.44 | 0.1388 | 0.8994 |
| rs71562459 | 6 | 12888602 | G,C | 0.6986 | 1 | 0.465 | 0.1398 | 0.9918 |
| rs4714955 | 6 | 12903435 | C,T | 0.6811 | 1 | 0.427 | 0.1432 | 0.9632 |
| rs62389955 | 6 | 12902248 | A,G | 0.6798 | 1 | 0.428 | 0.1436 | 0.9547 |
| rs7760527 | 6 | 12908408 | A,G | 0.6176 | 0.9614 | 0.402 | 0.1436 | 0.7543 |

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|---|---|---|---|---|---|---|---|---|
| rs9381494 | 6 | 12913152 | T,C | 0.6154 | 0.9445 | 0.397 | 0.1504 | 0.7296 |
| rs7760016 | 6 | 12908077 | A,G | 0.615 | 0.9606 | 0.393 | 0.1518 | 0.727 |
| rs8180558 | 6 | 12919989 | C,T | 0.6679 | 0.9247 | 0.429 | 0.1525 | 0.8466 |
| rs9395214 | 6 | 12898884 | G,C | 0.6125 | 0.9496 | 0.388 | 0.1594 | 0.7098 |
| rs9369650 | 6 | 12922652 | A,C | 0.611 | 0.8013 | 0.402 | 0.1764 | 0.6555 |
| rs6917613 | 6 | 12910698 | A,C | 0.975 | 0.6361 | 1.567 | 0.1779 | 0.4188 |
| rs9369652 | 6 | 12924744 | T,C | 0.611 | 0.7998 | 0.401 | 0.1779 | 0.6527 |
| rs1953088 | 6 | 12925936 | A,C | 0.611 | 0.7988 | 0.4 | 0.1789 | 0.6512 |
| rs1014342 | 6 | 12923157 | C,T | 0.6082 | 0.7977 | 0.395 | 0.1832 | 0.6359 |
| 6:12922721:CA_C | 6 | 12922721 | R,D | 0.6855 | 0.9496 | 0.389 | 0.1887 | 0.7815 |
| rs34343839 | 6 | 12922734 | C,T | 0.6854 | 0.9502 | 0.388 | 0.1889 | 0.7811 |
| rs12526453 | 6 | 12927544 | C,G | 0.6998 | 1 | 0.374 | 0.1926 | 0.813 |
| rs9381500 | 6 | 12922535 | A,G | 0.6711 | 0.903 | 0.389 | 0.1926 | 0.7075 |
| rs7739181 | 6 | 12934687 | G,A | 0.7024 | 0.9579 | 0.382 | 0.1971 | 0.8072 |
| rs2327621 | 6 | 12922689 | A,G | 0.6652 | 0.89 | 0.385 | 0.1993 | 0.6729 |
| rs62389950 | 6 | 12868726 | C,T | 0.8952 | 0.8702 | 0.687 | 0.1998 | 0.2064 |
| rs62386818 | 6 | 12923767 | C,A | 0.6801 | 0.928 | 0.382 | 0.2008 | 0.7303 |
| rs4714990 | 6 | 12927845 | T,C | 0.5764 | 0.6851 | 0.408 | 0.2059 | 0.6434 |
| rs6458545 | 6 | 12934302 | G,C | 0.5826 | 0.6602 | 0.408 | 0.2152 | 0.6405 |
| rs13201878 | 6 | 12943066 | A,G | 0.7276 | 0.7716 | 0.442 | 0.2197 | 0.7118 |
| rs6912532 | 6 | 12860762 | T,C | 0.938 | 0.9292 | 0.746 | 0.2398 | 0.1375 |
| rs16873462 | 6 | 12862244 | G,A | 0.9454 | 0.9001 | 0.775 | 0.2563 | 0.1189 |
| rs62389900 | 6 | 12862200 | G,T | 0.9454 | 0.9001 | 0.775 | 0.2563 | 0.1189 |
| rs6914467 | 6 | 12864309 | G,A | 0.9454 | 0.9013 | 0.774 | 0.2564 | 0.1188 |
| rs34348949 | 6 | 12863250 | A,G | 0.9454 | 0.9006 | 0.774 | 0.2565 | 0.119 |
| rs6927781 | 6 | 12860987 | G,C | 0.9455 | 0.8994 | 0.775 | 0.2566 | 0.119 |
| rs13198167 | 6 | 12858242 | G,A | 0.9455 | 0.8976 | 0.775 | 0.2567 | 0.1192 |
| rs35621699 | 6 | 12858904 | T,C | 0.9455 | 0.8981 | 0.775 | 0.2567 | 0.1192 |
| rs35395772 | 6 | 12857393 | G,A | 0.9455 | 0.8974 | 0.775 | 0.2569 | 0.1194 |
| rs36043593 | 6 | 12850604 | C,T | 0.9449 | 0.886 | 0.77 | 0.2613 | 0.1246 |
| rs62389889 | 6 | 12849622 | G,T | 0.945 | 0.8855 | 0.77 | 0.2615 | 0.1248 |
| rs13194950 | 6 | 12844775 | G,A | 0.9451 | 0.8824 | 0.771 | 0.262 | 0.1251 |
| rs55803153 | 6 | 12866927 | G,A | 0.9417 | 0.8687 | 0.736 | 0.276 | 0.1492 |
| rs13215145 | 6 | 12827170 | G,A | 0.9455 | 0.8579 | 0.762 | 0.2761 | 0.1308 |
| rs9463423 | 6 | 13069359 | T,C | 0.779 | 0.6377 | -0.444 | 0.2779 | 0.6959 |
| rs9473354 | 6 | 13059035 | C,A | 0.8408 | 0.998 | -0.401 | 0.2781 | 0.7544 |
| rs7738252 | 6 | 13060568 | A,G | 0.84 | 1 | -0.395 | 0.2793 | 0.7545 |
| rs4711908 | 6 | 13060208 | A,G | 0.8399 | 1 | -0.395 | 0.2799 | 0.7554 |
| rs4711909 | 6 | 13060214 | C,A | 0.8399 | 1 | -0.395 | 0.2799 | 0.7554 |
| rs6932757 | 6 | 13063361 | T,G | 0.8591 | 0.8503 | -0.459 | 0.2804 | 0.7873 |
| rs9473370 | 6 | 13065071 | A,C | 0.8622 | 0.766 | -0.489 | 0.2813 | 0.8025 |
| rs9463410 | 6 | 13064274 | A,G | 0.8381 | 0.941 | -0.408 | 0.2814 | 0.7617 |
| rs9463408 | 6 | 13063824 | A,G | 0.8386 | 0.9471 | -0.407 | 0.2815 | 0.7616 |
| rs36119782 | 6 | 13054433 | G,A | 0.8646 | 0.6631 | -0.527 | 0.283 | 0.8084 |
| rs7762827 | 6 | 13054732 | C,G | 0.8449 | 0.6352 | -0.506 | 0.2838 | 0.7841 |
| rs35229766 | 6 | 13072206 | T,C | 0.8709 | 0.6329 | -0.553 | 0.2857 | 0.8384 |
| rs9296592 | 6 | 13055406 | T,C | 0.846 | 0.6504 | -0.5 | 0.2859 | 0.7827 |
| rs13205779 | 6 | 12856004 | A,G | 0.9326 | 0.9094 | 0.661 | 0.2861 | 0.2007 |
| rs6914233 | 6 | 12854443 | T,C | 0.9326 | 0.9089 | 0.661 | 0.2862 | 0.2008 |
| rs34952336 | 6 | 13067820 | A,T | 0.8731 | 0.6878 | -0.534 | 0.2863 | 0.8379 |
| rs35305875 | 6 | 13067511 | A,G | 0.8719 | 0.696 | -0.527 | 0.2876 | 0.8378 |
| rs4711910 | 6 | 13066375 | T,C | 0.8734 | 0.7093 | -0.524 | 0.2887 | 0.8369 |
| rs6900427 | 6 | 12851560 | G,A | 0.9321 | 0.908 | 0.652 | 0.2915 | 0.2089 |
| rs4715082 | 6 | 13068291 | A,G | 0.8609 | 0.7147 | -0.493 | 0.293 | 0.83 |
| rs13215300 | 6 | 12817608 | T,C | 0.9482 | 0.8102 | 0.765 | 0.2996 | 0.1365 |
| rs13215271 | 6 | 12817748 | A,G | 0.9482 | 0.8113 | 0.765 | 0.2998 | 0.1364 |

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|---|---|---|---|---|---|---|---|---|
| rs35784087 | 6 | 12818204 | T,C | 0.9482 | 0.8124 | 0.764 | 0.3002 | 0.1365 |
| rs62389894 | 6 | 12854962 | A,T | 0.9401 | 0.8506 | 0.7 | 0.3002 | 0.175 |
| rs13191496 | 6 | 12851625 | G,A | 0.9401 | 0.8492 | 0.7 | 0.3005 | 0.1753 |
| rs62389221 | 6 | 12815161 | A,G | 0.9482 | 0.8019 | 0.768 | 0.3006 | 0.1369 |
| rs62389892 | 6 | 12853979 | A,G | 0.9401 | 0.8501 | 0.7 | 0.3008 | 0.1754 |
| rs35227817 | 6 | 12866528 | G,A | 0.9492 | 0.8512 | 0.748 | 0.3025 | 0.1316 |
| rs55637633 | 6 | 12868320 | C,A | 0.949 | 0.8492 | 0.747 | 0.3029 | 0.1324 |
| 6:12857625:CG_C | 6 | 12857625 | R,D | 0.9493 | 0.8472 | 0.749 | 0.303 | 0.1321 |
| rs62389893 | 6 | 12854881 | G,T | 0.9485 | 0.8355 | 0.741 | 0.309 | 0.1396 |
| rs7741088 | 6 | 12834122 | C,T | 0.9485 | 0.8235 | 0.744 | 0.3104 | 0.1403 |
| rs62389223 | 6 | 12819405 | C,T | 0.949 | 0.8037 | 0.754 | 0.312 | 0.1408 |
| rs35954478 | 6 | 12867215 | A,G | 0.9373 | 0.8379 | 0.657 | 0.3257 | 0.2208 |
| rs146401688 | 6 | 12888498 | C,T | 0.9634 | 0.8865 | 0.794 | 0.3342 | 0.4268 |
| rs28734939 | 6 | 12837663 | T,A | 0.8932 | 0.7447 | 0.509 | 0.3425 | 0.3082 |
| rs9395161 | 6 | 12838334 | C,T | 0.8592 | 0.9085 | 0.376 | 0.345 | 0.2874 |
| rs9395162 | 6 | 12838532 | T,A | 0.8592 | 0.9086 | 0.376 | 0.3453 | 0.2875 |
| rs13192509 | 6 | 12840877 | C,G | 0.8594 | 0.9126 | 0.375 | 0.3458 | 0.2876 |
| rs1537337 | 6 | 12843006 | G,A | 0.8605 | 0.9204 | 0.37 | 0.3511 | 0.2899 |
| rs9369605 | 6 | 12843219 | A,C | 0.8605 | 0.9203 | 0.37 | 0.3511 | 0.2899 |
| rs9367239 | 6 | 12844465 | A,G | 0.8603 | 0.9212 | 0.369 | 0.3519 | 0.2906 |
| rs9381436 | 6 | 12844405 | C,T | 0.8603 | 0.9212 | 0.369 | 0.3519 | 0.2906 |
| rs13192344 | 6 | 12844264 | C,A | 0.8603 | 0.921 | 0.369 | 0.3523 | 0.291 |
| rs16873449 | 6 | 12844141 | A,T | 0.8603 | 0.921 | 0.369 | 0.3523 | 0.291 |
| rs16873447 | 6 | 12844001 | A,T | 0.8603 | 0.9209 | 0.369 | 0.3524 | 0.2912 |
| rs2184027 | 6 | 12844712 | A,G | 0.8603 | 0.9214 | 0.369 | 0.3525 | 0.291 |
| rs2065490 | 6 | 12847494 | T,C | 0.8602 | 0.924 | 0.368 | 0.3526 | 0.2906 |
| rs4711845 | 6 | 12845156 | A,G | 0.8603 | 0.9215 | 0.369 | 0.3527 | 0.2912 |
| rs9296486 | 6 | 12848969 | T,G | 0.8602 | 0.9245 | 0.368 | 0.3527 | 0.2904 |
| rs9367240 | 6 | 12848685 | C,T | 0.8602 | 0.9243 | 0.368 | 0.3527 | 0.2904 |
| rs2065491 | 6 | 12847595 | A,T | 0.8602 | 0.9241 | 0.368 | 0.353 | 0.2907 |
| rs9381439 | 6 | 12849678 | G,A | 0.8602 | 0.9249 | 0.368 | 0.3532 | 0.2908 |
| rs4711842 | 6 | 12842531 | G,A | 0.8598 | 0.9178 | 0.367 | 0.3552 | 0.2973 |
| rs1537334 | 6 | 12841241 | C,G | 0.8595 | 0.9179 | 0.366 | 0.3559 | 0.2983 |
| rs1537336 | 6 | 12842883 | C,A | 0.8614 | 0.9118 | 0.366 | 0.3601 | 0.296 |
| rs62389220 | 6 | 12815105 | C,G | 0.952 | 0.7639 | 0.718 | 0.3613 | 0.1562 |
| rs9349350 | 6 | 12842285 | A,G | 0.8576 | 0.9032 | 0.359 | 0.3663 | 0.3195 |
| rs1412742 | 6 | 12840104 | G,A | 0.8548 | 0.906 | 0.355 | 0.3692 | 0.3326 |
| rs9381435 | 6 | 12838426 | C,T | 0.8546 | 0.9026 | 0.356 | 0.3694 | 0.3328 |
| rs1412743 | 6 | 12840112 | C,G | 0.8548 | 0.9062 | 0.355 | 0.3695 | 0.3327 |
| 6:12840537:G_GA | 6 | 12840537 | R,I | 0.8548 | 0.9064 | 0.355 | 0.3702 | 0.3331 |
| rs16873436 | 6 | 12841033 | G,C | 0.8548 | 0.9065 | 0.355 | 0.3702 | 0.3331 |
| rs1537338 | 6 | 12843203 | A,G | 0.8619 | 0.9076 | 0.358 | 0.3711 | 0.3036 |
| rs6458493 | 6 | 12835673 | G,A | 0.8541 | 0.9012 | 0.354 | 0.3714 | 0.3347 |
| rs6458494 | 6 | 12836186 | T,C | 0.8542 | 0.9008 | 0.354 | 0.3717 | 0.3349 |
| rs4714913 | 6 | 12845085 | C,T | 0.856 | 0.9149 | 0.35 | 0.3749 | 0.3333 |
| rs4711848 | 6 | 12845240 | C,A | 0.8555 | 0.9146 | 0.348 | 0.3776 | 0.337 |
| rs3945322 | 6 | 12841306 | G,A | 0.8552 | 0.9133 | 0.347 | 0.3795 | 0.3437 |
| rs9357503 | 6 | 12841985 | T,A | 0.8552 | 0.9138 | 0.347 | 0.3797 | 0.3439 |
| rs1537335 | 6 | 12842563 | G,A | 0.8552 | 0.914 | 0.347 | 0.38 | 0.3442 |
| rs5017386 | 6 | 12842373 | G,T | 0.8552 | 0.9139 | 0.347 | 0.3802 | 0.3443 |
| 6:12828114:AG_A | 6 | 12828114 | R,D | 0.8572 | 0.8986 | 0.35 | 0.3816 | 0.3355 |
| rs9349352 | 6 | 12846517 | C,T | 0.8549 | 0.9172 | 0.344 | 0.3821 | 0.3452 |
| rs9296488 | 6 | 12849304 | A,G | 0.8548 | 0.9183 | 0.344 | 0.3823 | 0.3454 |
| rs35657920 | 6 | 12855243 | A,C | 0.8535 | 0.9073 | 0.341 | 0.3863 | 0.3381 |
| rs9395185 | 6 | 12856827 | A,G | 0.8534 | 0.9067 | 0.341 | 0.3863 | 0.3382 |
| rs10434854 | 6 | 12822566 | C,T | 0.8558 | 0.8892 | 0.346 | 0.3884 | 0.3495 |

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|---|---|---|---|---|---|---|---|---|
| rs9472672 | 6 | 12821258 | A,G | 0.8517 | 0.88 | 0.343 | 0.3893 | 0.3471 |
| rs6924353 | 6 | 12860700 | C,T | 0.9576 | 0.7457 | 0.725 | 0.3894 | 0.1583 |
| rs1537340 | 6 | 12881855 | G,A | 0.6686 | 0.9196 | 0.283 | 0.3919 | 0.6407 |
| rs56408440 | 6 | 12824700 | C,T | 0.8553 | 0.8951 | 0.341 | 0.3923 | 0.3564 |
| rs57387500 | 6 | 12824892 | A,G | 0.8551 | 0.8968 | 0.341 | 0.3927 | 0.3565 |
| rs4142300 | 6 | 12825772 | A,G | 0.8551 | 0.8993 | 0.34 | 0.3929 | 0.3571 |
| rs16873431 | 6 | 12840508 | T,C | 0.8641 | 0.8912 | 0.347 | 0.3932 | 0.3195 |
| rs9381427 | 6 | 12830144 | T,C | 0.8543 | 0.8944 | 0.337 | 0.3967 | 0.3553 |
| 6:12828992:T_TA | 6 | 12828992 | R,I | 0.8479 | 0.758 | 0.299 | 0.4757 | 0.4197 |
| rs7770745 | 6 | 12862978 | A,T | 0.6897 | 0.9754 | -0.23 | 0.4792 | 0.1313 |
| rs6458503 | 6 | 12859556 | C,T | 0.687 | 0.9874 | -0.226 | 0.4826 | 0.1315 |
| rs7748950 | 6 | 12858223 | T,C | 0.687 | 0.9872 | -0.226 | 0.4829 | 0.1316 |
| rs72835698 | 6 | 12858776 | G,A | 0.9422 | 0.9429 | 0.427 | 0.5097 | 0.8468 |
| rs62389896 | 6 | 12855854 | A,G | 0.9425 | 0.9422 | 0.427 | 0.5114 | 0.8457 |
| rs9381455 | 6 | 12864898 | C,T | 0.6717 | 0.9226 | -0.218 | 0.5125 | 0.1287 |
| rs62389228 | 6 | 12832840 | A,G | 0.9432 | 0.9011 | 0.428 | 0.522 | 0.8485 |
| rs9463187 | 6 | 12839176 | A,C | 0.698 | 0.9955 | -0.194 | 0.5428 | 0.1917 |
| rs59402659 | 6 | 12853162 | A,G | 0.7 | 1 | -0.189 | 0.5479 | 0.1948 |
| rs7771962 | 6 | 12863738 | T,C | 0.7002 | 1 | -0.188 | 0.551 | 0.1963 |
| rs1360579 | 6 | 12871736 | G,A | 0.6417 | 1 | -0.188 | 0.5729 | 0.2409 |
| rs1412744 | 6 | 12867696 | A,G | 0.6399 | 1 | -0.186 | 0.5743 | 0.2401 |
| rs66867947 | 6 | 12874672 | T,G | 0.64 | 1 | -0.185 | 0.5756 | 0.2417 |
| rs9472777 | 6 | 12872092 | G,A | 0.6398 | 1 | -0.185 | 0.5762 | 0.2415 |
| rs1332841 | 6 | 12875054 | G,T | 0.6405 | 1 | -0.183 | 0.5809 | 0.2405 |
| rs12528956 | 6 | 12833077 | T,C | 0.7079 | 0.9621 | -0.173 | 0.5963 | 0.1976 |
| rs17679286 | 6 | 12828434 | A,G | 0.9434 | 0.7255 | 0.397 | 0.5984 | 0.8037 |
| rs17679417 | 6 | 12863108 | A,T | 0.7076 | 0.9858 | -0.168 | 0.6011 | 0.2003 |
| rs17679501 | 6 | 12879996 | T,A | 0.6507 | 0.9741 | -0.155 | 0.6459 | 0.2307 |
| rs4711857 | 6 | 12880109 | C,T | 0.6511 | 0.9742 | -0.155 | 0.6459 | 0.2299 |
| rs17679590 | 6 | 12919148 | G,A | 0.9328 | 0.7735 | 0.305 | 0.6481 | 0.9786 |
| rs9472786 | 6 | 12877597 | G,T | 0.6494 | 0.9807 | -0.153 | 0.6496 | 0.2459 |
| rs4714946 | 6 | 12872220 | G,A | 0.65 | 0.9794 | -0.15 | 0.6561 | 0.2559 |
| rs9472790 | 6 | 12879101 | T,A | 0.4823 | 0.9748 | 0.145 | 0.6653 | 0.5074 |
| rs9381417 | 6 | 12823820 | G,A | 0.9153 | 0.8452 | 0.246 | 0.6731 | 0.7923 |
| rs58666803 | 6 | 12824263 | T,C | 0.9167 | 0.8207 | 0.248 | 0.6778 | 0.7942 |
| rs35278288 | 6 | 12826700 | A,G | 0.915 | 0.8471 | 0.241 | 0.6782 | 0.8055 |
| rs6915585 | 6 | 12831273 | G,A | 0.9152 | 0.8478 | 0.241 | 0.6788 | 0.8056 |
| rs4711858 | 6 | 12880131 | T,C | 0.655 | 0.9626 | -0.139 | 0.6807 | 0.2425 |
| rs1571996 | 6 | 12834714 | T,C | 0.915 | 0.8468 | 0.239 | 0.6813 | 0.8055 |
| rs9381462 | 6 | 12873775 | G,A | 0.48 | 1 | 0.13 | 0.6959 | 0.5299 |
| rs1571997 | 6 | 12874309 | A,G | 0.4767 | 1 | 0.128 | 0.7023 | 0.5246 |
| rs944767 | 6 | 12788029 | C,G | 0.7091 | 0.7481 | -0.128 | 0.7113 | 0.2112 |
| rs7768030 | 6 | 12822973 | A,C | 0.9102 | 0.8184 | 0.203 | 0.7259 | 0.9134 |
| rs10434855 | 6 | 12822711 | C,A | 0.9102 | 0.8162 | 0.201 | 0.7288 | 0.9168 |
| rs4711841 | 6 | 12818142 | G,C | 0.6001 | 1 | -0.098 | 0.734 | 0.2478 |
| rs1412741 | 6 | 12817667 | A,G | 0.6001 | 1 | -0.098 | 0.7344 | 0.248 |
| rs8180628 | 6 | 12881163 | G,A | 0.6217 | 1 | -0.096 | 0.7378 | 0.08591 |
| rs9349494 | 6 | 13173147 | G,A | 0.7905 | 0.6554 | 0.175 | 0.7428 | 0.4822 |
| rs17617491 | 6 | 12862562 | C,T | 0.9239 | 0.9536 | 0.185 | 0.7471 | 0.8228 |
| rs55879442 | 6 | 12859873 | T,C | 0.9254 | 0.9408 | 0.185 | 0.7511 | 0.8237 |
| rs1011188 | 6 | 12812948 | A,G | 0.926 | 0.8645 | 0.193 | 0.7519 | 0.834 |
| rs12528247 | 6 | 12835880 | C,A | 0.9254 | 0.923 | 0.186 | 0.7529 | 0.8284 |
| rs2151221 | 6 | 12816578 | C,G | 0.9253 | 0.8984 | 0.188 | 0.7529 | 0.8344 |
| rs78881531 | 6 | 12872817 | C,T | 0.9801 | 1 | 0.322 | 0.7536 | 0.852 |
| rs60954427 | 6 | 12824264 | G,A | 0.9263 | 0.8834 | 0.189 | 0.7547 | 0.8205 |
| rs56270763 | 6 | 12810945 | C,T | 0.9256 | 0.8519 | 0.191 | 0.7556 | 0.8377 |

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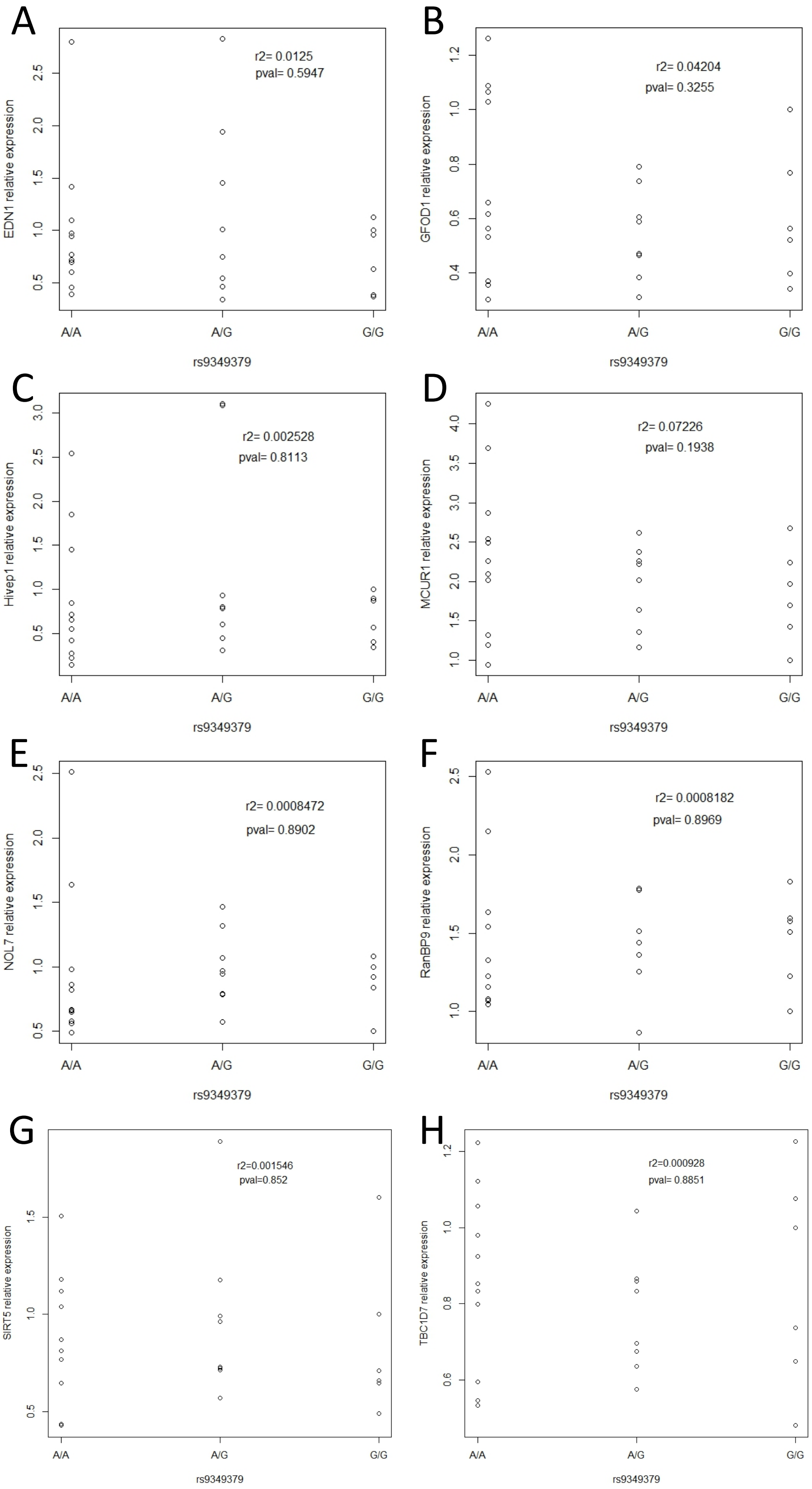
|---|---|---|---|---|---|---|---|---|
| rs73722849 | 6 | 12795009 | G,A | 0.9278 | 0.7548 | 0.205 | 0.7566 | 0.8338 |
| rs12525116 | 6 | 12809740 | T,C | 0.9258 | 0.8463 | 0.191 | 0.7573 | 0.835 |
| 6:12835490:G_GA | 6 | 12835490 | R,I | 0.9239 | 0.906 | 0.182 | 0.7575 | 0.8289 |
| rs1831706 | 6 | 12898178 | T,C | 0.975 | 0.7486 | 0.325 | 0.7579 | 0.7875 |
| rs1831705 | 6 | 12898162 | G,A | 0.9801 | 0.9398 | 0.326 | 0.7586 | 0.8424 |
| rs77664195 | 6 | 12824994 | A,G | 0.9227 | 0.9129 | 0.179 | 0.7591 | 0.8341 |
| rs1332842 | 6 | 12879851 | C,T | 0.9798 | 0.994 | 0.313 | 0.7602 | 0.8431 |
| rs9369607 | 6 | 12846847 | T,A | 0.923 | 0.9326 | 0.175 | 0.7615 | 0.8279 |
| rs10498681 | 6 | 12808284 | C,T | 0.9254 | 0.8369 | 0.188 | 0.7616 | 0.8389 |
| rs3778646 | 6 | 13182685 | G,T | 0.7957 | 0.7299 | 0.155 | 0.7618 | 0.493 |
| rs16873682 | 6 | 13178390 | A,G | 0.7959 | 0.7268 | 0.155 | 0.7623 | 0.4936 |
| rs12527257 | 6 | 13178069 | T,C | 0.7944 | 0.7322 | 0.153 | 0.7642 | 0.4945 |
| rs9381809 | 6 | 13182117 | G,C | 0.7954 | 0.7386 | 0.152 | 0.7653 | 0.4961 |
| rs73362169 | 6 | 12897549 | C,T | 0.9756 | 0.8111 | 0.298 | 0.7708 | 0.7876 |
| rs9381451 | 6 | 12863621 | T,C | 0.9198 | 0.9256 | 0.164 | 0.7743 | 0.8298 |
| rs4711856 | 6 | 12872477 | G,A | 0.9765 | 0.8663 | 0.29 | 0.7769 | 0.7625 |
| rs9463117 | 6 | 12796984 | A,G | 0.9224 | 0.7246 | 0.186 | 0.777 | 0.9179 |
| rs12528399 | 6 | 13177901 | G,T | 0.7932 | 0.7355 | 0.143 | 0.7773 | 0.5059 |
| rs4097413 | 6 | 13178610 | A,G | 0.7935 | 0.7398 | 0.143 | 0.7774 | 0.5058 |
| rs9463119 | 6 | 12797496 | A,G | 0.9224 | 0.7262 | 0.185 | 0.7777 | 0.9184 |
| rs12525210 | 6 | 12782675 | G,A | 0.9231 | 0.6851 | 0.191 | 0.7781 | 0.9176 |
| rs9463105 | 6 | 12777790 | C,A | 0.9239 | 0.6479 | 0.197 | 0.7784 | 0.9194 |
| rs55764622 | 6 | 12784847 | T,A | 0.9229 | 0.6901 | 0.19 | 0.7785 | 0.9194 |
| rs9369612 | 6 | 12853192 | T,C | 0.9208 | 0.9152 | 0.162 | 0.7785 | 0.8292 |
| rs12528721 | 6 | 12782518 | C,G | 0.9232 | 0.6845 | 0.191 | 0.7786 | 0.9184 |
| rs9472549 | 6 | 12786237 | C,A | 0.9229 | 0.6955 | 0.189 | 0.7788 | 0.9198 |
| rs9472520 | 6 | 12777828 | A,G | 0.9239 | 0.6485 | 0.197 | 0.7789 | 0.9199 |
| rs2015761 | 6 | 12788243 | A,C | 0.9228 | 0.7017 | 0.188 | 0.779 | 0.9195 |
| rs9381807 | 6 | 13179394 | G,A | 0.7935 | 0.7458 | 0.141 | 0.779 | 0.5071 |
| rs9472528 | 6 | 12781353 | A,G | 0.9232 | 0.6818 | 0.191 | 0.779 | 0.92 |
| rs9472519 | 6 | 12777723 | A,G | 0.9246 | 0.641 | 0.197 | 0.7805 | 0.9165 |
| rs9463114 | 6 | 12794542 | G,A | 0.9231 | 0.7106 | 0.185 | 0.7811 | 0.9167 |
| rs75506162 | 6 | 12855702 | C,T | 0.921 | 0.9152 | 0.16 | 0.7819 | 0.8314 |
| rs4714931 | 6 | 12857408 | A,G | 0.9209 | 0.9146 | 0.159 | 0.7827 | 0.8323 |
| rs73722845 | 6 | 12789323 | G,A | 0.9246 | 0.6917 | 0.187 | 0.7834 | 0.9114 |
| rs73722844 | 6 | 12789322 | T,C | 0.9246 | 0.6914 | 0.187 | 0.7835 | 0.9113 |
| rs9463140 | 6 | 12804870 | A,G | 0.9208 | 0.7728 | 0.172 | 0.7849 | 0.9211 |
| rs9472566 | 6 | 12797940 | C,T | 0.9216 | 0.7202 | 0.179 | 0.7852 | 0.924 |
| 6:12889973:CT_C | 6 | 12889973 | R,D | 0.9793 | 0.9097 | 0.279 | 0.7922 | 0.8065 |
| rs55908560 | 6 | 12882732 | C,T | 0.9761 | 0.8353 | 0.237 | 0.8183 | 0.7828 |
| rs9463511 | 6 | 13178259 | G,A | 0.7174 | 0.6374 | 0.111 | 0.821 | 0.5261 |
| rs10948524 | 6 | 13188493 | A,G | 0.7674 | 0.8039 | 0.102 | 0.8267 | 0.5209 |
| rs9367369 | 6 | 13189941 | A,G | 0.7668 | 0.7946 | 0.102 | 0.8272 | 0.5207 |
| rs3823445 | 6 | 13182995 | G,A | 0.7697 | 0.8447 | 0.099 | 0.8276 | 0.5217 |
| rs9381812 | 6 | 13183998 | A,G | 0.7691 | 0.8415 | 0.098 | 0.83 | 0.5233 |
| rs9381810 | 6 | 13183121 | T,C | 0.7692 | 0.8459 | 0.097 | 0.8313 | 0.5246 |
| rs9367368 | 6 | 13189275 | T,C | 0.7644 | 0.7857 | 0.098 | 0.834 | 0.5236 |
| rs17617584 | 6 | 12882064 | A,G | 0.9747 | 0.79 | 0.195 | 0.8506 | 0.7383 |
| 6:12775414:AT_A | 6 | 12775414 | R,D | 0.6385 | 0.6408 | -0.065 | 0.859 | 0.417 |
| rs6941624 | 6 | 12775930 | T,C | 0.6382 | 0.6436 | -0.064 | 0.859 | 0.4175 |
| rs59802022 | 6 | 12882105 | C,A | 0.9742 | 0.7765 | 0.182 | 0.8604 | 0.7367 |
| rs2876298 | 6 | 12800727 | C,A | 0.8933 | 0.6857 | 0.095 | 0.8658 | 0.7929 |
| rs9367253 | 6 | 12888047 | A,T | 0.8948 | 0.605 | 0.084 | 0.8775 | 0.5099 |
| rs10948235 | 6 | 12770823 | T,C | 0.6381 | 0.6218 | -0.054 | 0.8824 | 0.4283 |
| rs950720 | 6 | 12773990 | C,T | 0.6385 | 0.6312 | -0.054 | 0.8824 | 0.4283 |
| rs9395520 | 6 | 13183523 | C,T | 0.7395 | 0.9769 | 0.059 | 0.8857 | 0.5716 |

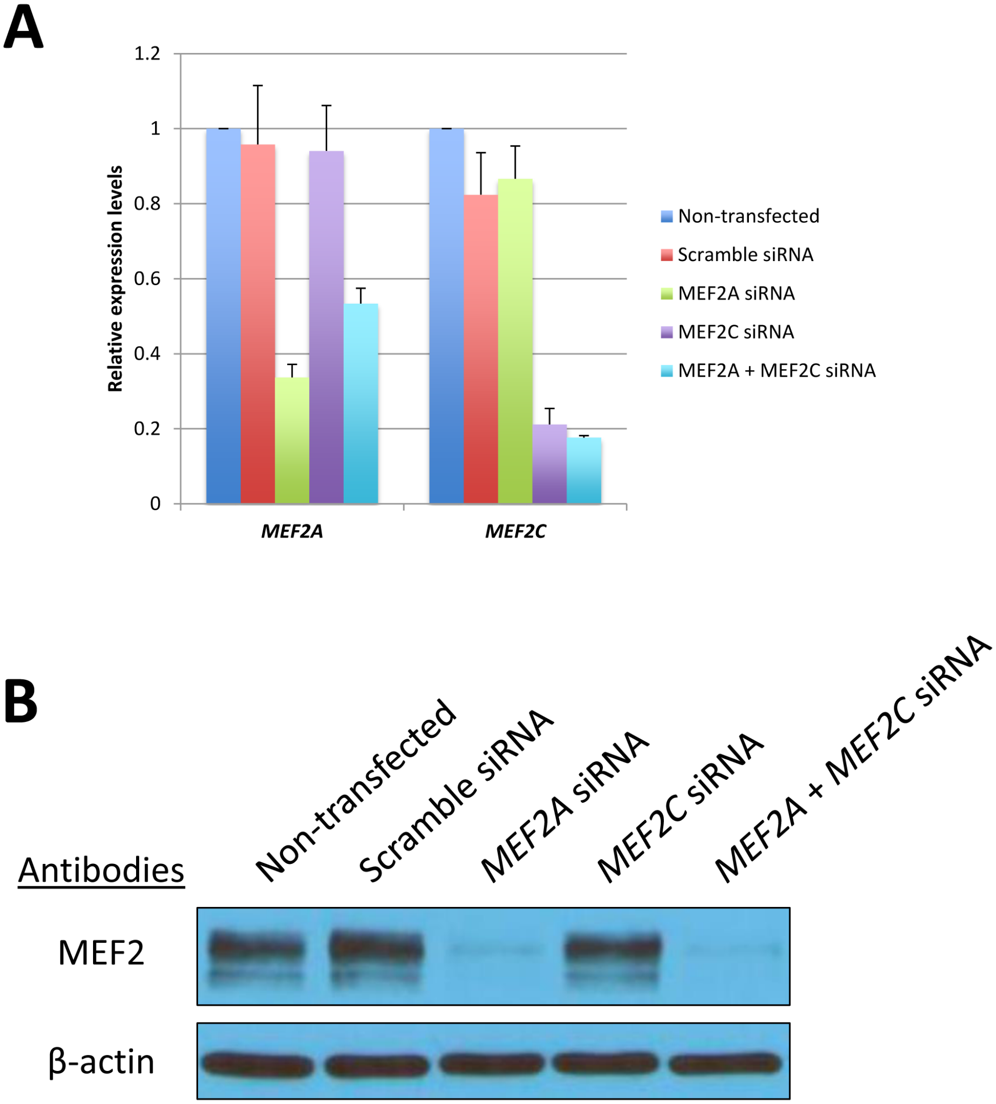
| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| rs9296494 | 6 | 12859886 | A,G | 0.6196 | 1 | -0.042 | 0.8899 | 0.4236 |
| rs9395190 | 6 | 12860080 | T,C | 0.6196 | 1 | -0.042 | 0.8899 | 0.4236 |
| rs6921974 | 6 | 12865376 | T,C | 0.6197 | 1 | -0.042 | 0.8902 | 0.4238 |
| rs9381456 | 6 | 12865148 | A,G | 0.6197 | 1 | -0.042 | 0.8902 | 0.4238 |
| rs11757278 | 6 | 13180454 | T,C | 0.7398 | 1 | 0.052 | 0.8958 | 0.5781 |
| rs6914513 | 6 | 12805843 | C,T | 0.5802 | 0.7623 | 0.039 | 0.9014 | 0.5452 |
| rs6901070 | 6 | 12865243 | G,A | 0.6233 | 0.9985 | -0.035 | 0.9095 | 0.4635 |
| rs16873383 | 6 | 12800443 | A,T | 0.6341 | 0.7955 | -0.03 | 0.9254 | 0.447 |
| rs7758513 | 6 | 12777571 | C,T | 0.6451 | 0.6492 | -0.032 | 0.9288 | 0.4505 |
| rs9463138 | 6 | 12803792 | A,G | 0.6386 | 0.8107 | -0.028 | 0.9292 | 0.4245 |
| rs11758650 | 6 | 12778109 | C,A | 0.6415 | 0.6652 | -0.031 | 0.9298 | 0.4467 |
| rs11753864 | 6 | 12778218 | G,A | 0.6419 | 0.6657 | -0.031 | 0.9302 | 0.447 |
| rs7776079 | 6 | 12819572 | A,G | 0.5346 | 0.9747 | 0.023 | 0.9338 | 0.5415 |
| rs9472590 | 6 | 12801104 | C,G | 0.6352 | 0.803 | -0.027 | 0.9341 | 0.4493 |
| rs4714930 | 6 | 12852478 | T,G | 0.5529 | 0.965 | 0.024 | 0.9343 | 0.6214 |
| rs9472583 | 6 | 12799417 | C,A | 0.6354 | 0.7979 | -0.026 | 0.9346 | 0.4495 |
| rs12523719 | 6 | 12800824 | T,G | 0.6353 | 0.8015 | -0.026 | 0.9348 | 0.4496 |
| rs12530186 | 6 | 12800690 | T,C | 0.6353 | 0.8007 | -0.026 | 0.9348 | 0.4495 |
| rs1412749 | 6 | 12774363 | C,G | 0.5627 | 0.6558 | 0.028 | 0.935 | 0.5115 |
| rs9472587 | 6 | 12800874 | A,T | 0.6353 | 0.8023 | -0.026 | 0.9352 | 0.4499 |
| rs13203883 | 6 | 12802560 | T,C | 0.6365 | 0.804 | -0.025 | 0.9372 | 0.4528 |
| rs7760286 | 6 | 12810937 | A,G | 0.634 | 0.8576 | -0.024 | 0.9373 | 0.4557 |
| 6:12785347:AC_A | 6 | 12785347 | R,D | 0.6387 | 0.7144 | -0.026 | 0.9381 | 0.4532 |
| rs7760140 | 6 | 12782968 | G,T | 0.639 | 0.7074 | -0.026 | 0.9387 | 0.4533 |
| rs1412738 | 6 | 12805995 | A,G | 0.6346 | 0.8275 | -0.024 | 0.9388 | 0.4552 |
| rs12524974 | 6 | 12784785 | A,G | 0.6387 | 0.7119 | -0.026 | 0.9389 | 0.4537 |
| rs9296464 | 6 | 12784293 | T,C | 0.6389 | 0.7091 | -0.026 | 0.9389 | 0.4537 |
| rs7747656 | 6 | 12790872 | A,G | 0.6378 | 0.7421 | -0.025 | 0.9398 | 0.4495 |
| rs6913075 | 6 | 12805821 | G,C | 0.6339 | 0.8292 | -0.024 | 0.9402 | 0.4543 |
| rs1953089 | 6 | 12804619 | C,T | 0.6339 | 0.8238 | -0.024 | 0.9407 | 0.4544 |
| rs6916334 | 6 | 12801594 | G,T | 0.6347 | 0.8069 | -0.024 | 0.9407 | 0.4542 |
| rs4714870 | 6 | 12797055 | T,G | 0.6363 | 0.7584 | -0.024 | 0.9409 | 0.4519 |
| rs6930873 | 6 | 12805039 | A,T | 0.6338 | 0.8266 | -0.023 | 0.941 | 0.4544 |
| rs9472594 | 6 | 12803223 | C,A | 0.6343 | 0.8157 | -0.024 | 0.941 | 0.4544 |
| rs9472595 | 6 | 12803718 | C,T | 0.6341 | 0.8193 | -0.023 | 0.941 | 0.4542 |
| rs13214313 | 6 | 12802428 | G,A | 0.6345 | 0.8109 | -0.024 | 0.9411 | 0.4543 |
| rs2327619 | 6 | 12790353 | G,A | 0.6374 | 0.7405 | -0.025 | 0.9411 | 0.4516 |
| rs9463137 | 6 | 12803582 | G,T | 0.6342 | 0.8181 | -0.023 | 0.9411 | 0.4544 |
| rs1412752 | 6 | 12788776 | A,T | 0.6373 | 0.7344 | -0.025 | 0.9412 | 0.452 |
| rs6909834 | 6 | 12805582 | C,T | 0.6337 | 0.8283 | -0.023 | 0.9412 | 0.4545 |
| rs9472558 | 6 | 12789655 | C,T | 0.6372 | 0.7381 | -0.025 | 0.9413 | 0.4518 |
| rs10948247 | 6 | 12786511 | C,A | 0.6379 | 0.7251 | -0.025 | 0.9415 | 0.452 |
| rs28451666 | 6 | 12802374 | G,A | 0.6346 | 0.8089 | -0.023 | 0.9415 | 0.4549 |
| rs6458473 | 6 | 12804934 | G,C | 0.6338 | 0.8262 | -0.023 | 0.9415 | 0.4547 |
| rs1412753 | 6 | 12791207 | G,C | 0.6373 | 0.7438 | -0.024 | 0.9417 | 0.4521 |
| rs9463136 | 6 | 12803416 | T,C | 0.6343 | 0.8173 | -0.023 | 0.9417 | 0.4548 |
| rs7757835 | 6 | 12798443 | A,G | 0.6364 | 0.7627 | -0.024 | 0.9421 | 0.4523 |
| rs883947 | 6 | 12787714 | C,T | 0.6378 | 0.7287 | -0.024 | 0.9423 | 0.4527 |
| rs9463134 | 6 | 12802815 | G,C | 0.635 | 0.8112 | -0.023 | 0.9423 | 0.4544 |
| rs6935309 | 6 | 12804882 | T,C | 0.6366 | 0.8148 | -0.022 | 0.9437 | 0.4598 |
| rs13203774 | 6 | 12802502 | T,C | 0.6352 | 0.8095 | -0.022 | 0.9445 | 0.4561 |
| rs2095123 | 6 | 12790079 | A,G | 0.6355 | 0.7357 | -0.023 | 0.9457 | 0.4506 |
| rs7762417 | 6 | 12807829 | C,T | 0.6324 | 0.8341 | -0.021 | 0.9458 | 0.454 |
| rs9296465 | 6 | 12784464 | A,G | 0.5628 | 0.7232 | 0.021 | 0.9475 | 0.5079 |
| rs6458461 | 6 | 12789191 | C,T | 0.5601 | 0.751 | 0.021 | 0.9478 | 0.5062 |
| rs944766 | 6 | 12787449 | C,T | 0.5607 | 0.7424 | 0.021 | 0.9479 | 0.5061 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| rs4714868 | 6 | 12791878 | T,C | 0.5595 | 0.7612 | 0.021 | 0.9482 | 0.506 |
| rs6924150 | 6 | 12795621 | C,T | 0.559 | 0.7689 | 0.02 | 0.9482 | 0.506 |
| rs6458460 | 6 | 12789038 | C,A | 0.5581 | 0.75 | 0.021 | 0.9483 | 0.5055 |
| rs9472551 | 6 | 12786272 | C,A | 0.5608 | 0.7394 | 0.021 | 0.9483 | 0.5058 |
| 6:12788487:TA_T | 6 | 12788487 | R,D | 0.5584 | 0.7483 | 0.021 | 0.9484 | 0.5055 |
| rs4714866 | 6 | 12791802 | G,A | 0.5595 | 0.7608 | 0.02 | 0.9484 | 0.5058 |
| rs7757858 | 6 | 12798477 | A,C | 0.5583 | 0.7789 | 0.02 | 0.9485 | 0.5058 |
| rs2015764 | 6 | 12788283 | G,A | 0.5606 | 0.7468 | 0.021 | 0.9487 | 0.5052 |
| rs1412751 | 6 | 12787247 | G,A | 0.5608 | 0.7405 | 0.021 | 0.9489 | 0.5053 |
| rs1572000 | 6 | 12769487 | G,A | 0.5732 | 0.6321 | 0.022 | 0.9493 | 0.4976 |
| rs9463110 | 6 | 12782602 | T,G | 0.5622 | 0.7202 | 0.02 | 0.9512 | 0.5071 |
| rs6919327 | 6 | 12803410 | A,G | 0.5538 | 0.8326 | 0.018 | 0.9521 | 0.5067 |
| rs7762547 | 6 | 12807877 | C,A | 0.5538 | 0.8565 | 0.018 | 0.9521 | 0.5068 |
| 6:12796108:AT_A | 6 | 12796108 | R,D | 0.5579 | 0.7665 | 0.018 | 0.9534 | 0.5051 |
| rs7757205 | 6 | 12777449 | G,A | 0.5688 | 0.6636 | 0.019 | 0.9557 | 0.5054 |
| 6:12801131:G_GA | 6 | 12801131 | R,I | 0.6522 | 0.6861 | -0.019 | 0.9565 | 0.4201 |
| rs17617207 | 6 | 12800332 | G,A | 0.5549 | 0.8151 | 0.016 | 0.9576 | 0.502 |
| rs6922969 | 6 | 12780032 | T,C | 0.5633 | 0.7106 | 0.017 | 0.958 | 0.5016 |
| rs9463106 | 6 | 12778864 | G,A | 0.5652 | 0.681 | 0.017 | 0.9591 | 0.5009 |
| rs6938417 | 6 | 12780185 | G,A | 0.5632 | 0.712 | 0.017 | 0.9593 | 0.5008 |
| rs1572002 | 6 | 12780990 | G,A | 0.5631 | 0.7143 | 0.017 | 0.9595 | 0.501 |
| rs6941422 | 6 | 12775753 | T,C | 0.5675 | 0.6637 | 0.017 | 0.9606 | 0.5008 |
| rs9296487 | 6 | 12849031 | T,C | 0.5279 | 0.9772 | -0.014 | 0.9606 | 0.4209 |
| rs7764490 | 6 | 12817237 | A,G | 0.5445 | 0.9558 | 0.014 | 0.9614 | 0.522 |
| rs10948244 | 6 | 12786085 | T,C | 0.6628 | 0.6998 | 0.013 | 0.9696 | 0.4873 |
| rs6917493 | 6 | 12801488 | C,G | 0.6533 | 0.7413 | -0.011 | 0.9732 | 0.4595 |
| rs2327617 | 6 | 12785023 | C,T | 0.6488 | 0.6621 | -0.012 | 0.9738 | 0.4807 |
| rs6917492 | 6 | 12801487 | C,T | 0.6523 | 0.7449 | -0.01 | 0.9756 | 0.4602 |
| rs1332840 | 6 | 12818865 | G,C | 0.5421 | 0.9674 | 0.008 | 0.9765 | 0.5251 |
| rs1412740 | 6 | 12817590 | A,G | 0.5444 | 0.9603 | 0.008 | 0.9767 | 0.5268 |
| rs9472752 | 6 | 12864134 | T,C | 0.5402 | 0.9759 | 0.008 | 0.9796 | 0.5187 |
| rs2026457 | 6 | 12825805 | G,A | 0.54 | 1 | 0.007 | 0.9801 | 0.5233 |
| rs9349344 | 6 | 12826479 | T,C | 0.5395 | 1 | 0.006 | 0.983 | 0.5222 |
| rs9296495 | 6 | 12865649 | G,A | 0.5391 | 0.9937 | 0.005 | 0.9873 | 0.5147 |
| rs9395172 | 6 | 12850534 | G,A | 0.5398 | 0.99 | 0.004 | 0.9884 | 0.5155 |
| rs6917097 | 6 | 12851768 | T,C | 0.5398 | 0.9893 | 0.004 | 0.9887 | 0.5152 |
| rs9349346 | 6 | 12827334 | A,T | 0.5238 | 0.9776 | -0.004 | 0.9903 | 0.4364 |
| rs9381391 | 6 | 12781416 | C,T | 0.5332 | 0.7294 | 0.004 | 0.9904 | 0.3887 |
| rs6915402 | 6 | 12821491 | A,T | 0.5341 | 0.9645 | 0.003 | 0.9911 | 0.4991 |
| rs7454135 | 6 | 12855542 | T,G | 0.5405 | 0.9913 | 0.002 | 0.9934 | 0.5121 |
| rs13196135 | 6 | 12804875 | G,A | 0.6561 | 0.788 | 0.002 | 0.9945 | 0.4749 |

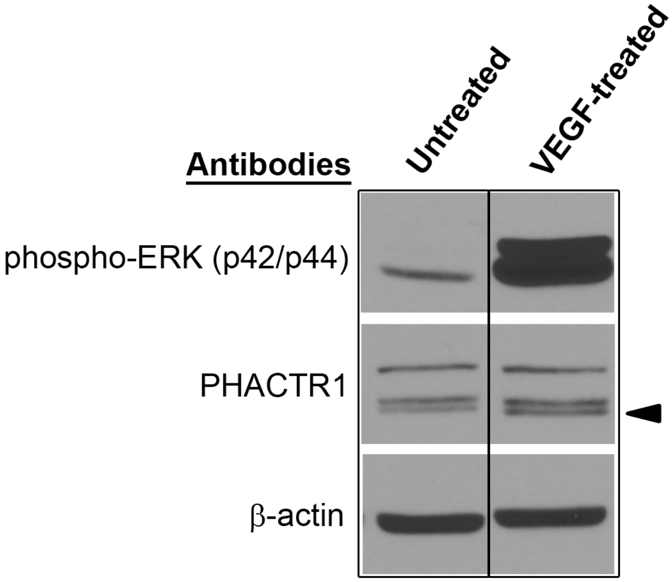
**Supplemental Figure I.** Expression of genes located 1-megabase on either side of *PHACTR1*-rs9349379 in right coronary arteries from 25 human donors. We did not measure the expression of a pseudogene or predicted non-coding RNA within the locus. We used linear regression to test the association between genotypes at rs9349379 and gene expression levels. We did not detect significant cis-eQTL effect for these eight genes. (**A**) EDN1. (**B**) GFOD1. (**C**) HIVEP1. (**D**) MCUR1. (**E**) NOL7. (**F**) RanBP9. (**G**) SIRT5. (**H**) TBC1D7.


A
EDN1 relative expression
r2= 0.0125
pval= 0.5947
0.5
1.0
1.5
2.0
2.5
A/A
A/G
G/G
rs9349379
B
GFOD1 relative expression
r2= 0.04204
pval= 0.3255
0.4
0.6
0.8
1.0
1.2
A/A
A/G
G/G
rs9349379
C
Hivep1 relative expression
r2= 0.002528
pval= 0.8113
0.5
1.0
1.5
2.0
2.5
3.0
A/A
A/G
G/G
rs9349379
D
MCUR1 relative expression
r2= 0.07226
pval= 0.1938
1.0
1.5
2.0
2.5
3.0
3.5
4.0
A/A
A/G
G/G
rs9349379
E
NOL7 relative expression
r2= 0.0008472
pval= 0.8902
0.5
1.0
1.5
2.0
2.5
A/A
A/G
G/G
rs9349379
F
RanBP9 relative expression
r2= 0.0008182
pval= 0.8969
1.0
1.5
2.0
2.5
A/A
A/G
G/G
rs9349379
G
SIRT5 relative expression
r2=0.001546
pval=0.852
0.5
1.0
1.5
A/A
A/G
G/G
rs9349379
H
TBC1D7 relative expression
r2=0.000928
pval=0.8851
0.6
0.8
1.0
1.2
A/A
A/G
G/G
rs9349379

**Supplemental Figure II.** The anti-MEF2 antibody (Santa Cruz-313) preferentially recognizes MEF2A in HUVEC. (**A**) We used siRNA to knockdown the expression of *MEF2A* and *MEF2C* in HUVEC, and measured transcript levels by real-time PCR. We reduced the expression of *MEF2A* by 65% and the expression of *MEF2C* by 80%. There is no non-specific knockdown of the other *MEF2* transcript (*e.g.* when we knockdown *MEF2A*, the levels of *MEF2C* do not change). (**B**) At the protein levels, the knockdown of *MEF2A*, but not *MEF2C*, reduces the Western blot signal of the protein detected by the anti-MEF2 antibody.



**Supplemental Figure III.** VEGF treatment activates ERK/MAPK. Experiment to demonstrate that HUVEC used in our experiments respond to VEGF treatment, as demonstrated by the phosphorylation of ERK (p42/p44). HUVEC cells were serum-starved overnight and treated with VEGF at 20ng/mL for five minutes before preparing the protein extracts. Different times (5-60 min) or VEGF concentration (2-100ng/mL) had no impact on *PHACTR1* expression levels. β-actin is the loading control. PHACTR1 is the lower band in the doublet, as indicated by the arrowhead. These results come from the same experiment and gel, but samples were loaded on non-consecutive lanes.



## Supplemental References

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