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| **SNP** | **Locus** | **Phenotype** | **Effect Allele** | **Effect Allele Frequency in the discovery sample** | **Discovery p-value** | **Discovery Odds Ratio [CI95]** | **Caucasian Replication p-value** | **Caucasian Replication Odds Ratio [CI95]** | **RACE replication p-value** | **RACE Replication Odds Ratio [CI95]** | **Overall meta-analysis p-value** | **Overall meta-analysis Odds Ratio [CI95]** |
| rs342920 | PLSCR5 | IS | T | 0.3760 | 3.2E-7 | 1.11 [1.07-1.15] | 0.5154 | 1.01 [0.97- 1.04] | 0.4597 | 1.03 [0.95- 1.11] | 8.2E-5 | 1.05 [1.02- 1.07] |
| rs9683944 | PCDH18 | IS | A | 0.7974 | 1.5E-6 | 0.88 [0.84-0.93] | 0.1688 | 0.97 [0.92-1.01] | 0.6564 | 1.02 [0.92- 1.12] | 0.00012 | 0.94 [0.91- 0.97] |
| rs9330355 | PCDH18 | IS | A | 0.7975 | 3.0E-6 | 0.89 [0.84-0.93] | 0.2000 | 0.97 [0.93- 1.01] | 0.6645 | 1.02 [0.92- 1.12] | 0.00023 | 0.94 [0.91- 0.97] |
| rs60436833 | intergenic | IS | A | 0.0681 | 1.0E-5 | 1.19 [1.12-1.26] | 0.3382 | 1.03 [0.96- 1.11] | 0.5223 | 1.04 [0.92- 1.17] | 0.00027 | 1.09 [1.04- 1.14] |
| rs3777209 | GLRX | IS | T | 0.9418 | 6.6E-7 | 0.81 [0.75-0.88] | 0.8482 | 0.99 [0.91-1.078] | 0.8959 | 0.99 [0.79- 1.23] | 0.00036 | 0.90 [0.85- 0.95] |
| rs13148045 | PCDH18 | IS | T | 0.8347 | 9.3E-6 | 0.88 [0.83-0.93] | 0.3007 | 0.98 [0.93- 1.02] | 0.9076 | 1.00 [0.87-1.16] | 0.00047 | 0.94 [0.90- 0.97] |
| rs318373 | intergenic | IS | T | 0.5135 | 9.7E-8 | 0.90 [0.86-0.93] | 0.4152 | 1.01 [0.97- 1.05] | 0.3359 | 0.95 [0.86- 1.04] | 0.0013 | 0.95 [0.93- 0.98] |
| rs10489625 | IL12RB2 | IS | T | 0.9525 | 1.9E-6 | 1.26 [1.14-1.38] | 0.8165 | 0.99 [0.91-1.07] | 0.2389 | 1.20 [0.88- 1.65] | 0.0021 | 1.09 [1.03- 1.16] |
| rs6664757 | IL12RB2 | IS | T | 0.0626 | 2.0E-6 | 0.81 [0.74-0.88] | 0.9618 | 1.00 [0.93--1.07] | 0.8897 | 0.99 [0.86-1.13] | 0.0054 | 0.93 [0.88- 0.97] |
| rs342919 | PLSCR5 | IS | C | 0.3726 | 0.0055 | 1.06 [1.02-1.10] | 0.3989 | 1.01 [0.97- 1.05] | 0.4571 | 1.03 [0.95- 1.11] | 0.0095 | 1.03 [1.00- 1.06] |
| rs16944241 | SHISA6 | IS | A | 0.9788 | 2.1E-6 | 0.71 [0.62-0.82] | 0.06618 | 1.13 [0.99- 1.30] | 0.1457 | 1.10 [0.97-1.24] | 0.19\* | 0.97 [0.90- 1.05] |
| rs78160483 | SHISA6 | IS | T | 0.9800 | 9.4E-5 | 0.74 [0.64-0.86] | 0.08015 | 1.13 [0.99- 1.29] | 0.1496 | 1.10 [0.97- 1.24] | 0.88 | 0.99 [0.91- 1.07] |

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| rs79472290 | GUCY1A3 | LVD | T | 0.0149 | 1.4E-6 | 2.24 [1.61-3.11] | 0.3205 | 1.15 [0.87-1.53] | 0.01219 | 2.44 [1.21- 4.91] | 8.3E-6 | 1.59 [1.29- 1.95] |
| rs74443985 | NACC2 | LVD | A | 0.0282 | 2.9E-7 | 2.32 [1.68-3.21] | 0.05472 | 1.20 [1.00-1.46] | NA | NA | 2.0E-5 | 1.43 [1.21- 1.68] |
| rs184207444 | intergenic | LVD | A | 0.9865 | 1.4E-7 | 0.42 [0.31-0.58] | 0.6072 | 0.91 [0.65- 1.28] | NA | NA | 3.0E-5 | 0.61 [0.48- 0.76] |
| rs9472313 | SUPT3H | LVD | A | 0.3179 | 4.5E-7 | 1.23 [1.13-1.33] | 0.3677 | 1.03 [0.96- 1.10] | 0.6924 | 0.96 [0.80- 1.15] | 0.00019 | 1.10 [1.04- 1.15] |
| rs112713881 | UBR5 | LVD | A | 0.0450 | 6.3E-7 | 1.64 [1.35-1.99] | 0.5248 | 1.06 [0.89-1.26] | 0.5192 | 0.69 [0.22- 2.10] | 0.00022 | 1.27 [1.12- 1.44] |
| rs556621 | SUPT3H | LVD | T | 0.3220 | 5.8E-5 | 1.18 [1.09-1.27] | 0.4046 | 1.02 [0.96- 1.10] | 0.6880 | 0.96 [0.81- 1.14] | 0.0023 | 1.08 [1.02- 1.13] |
| rs112447110 | UBR5 | LVD | C | 0.0434 | 3.1E-6 | 1.62 [1.32-1.90] | 0.9793 | 0.99 [0.83- 1.20] | 0.5599 | 0.71 [0.22- 2.22] | 0.0025 | 1.23 [1.07- 1.40] |
| rs77935123 | intergenic | LVD | A | 0.9789 | 3.5E-6 | 0.50 [0.37-0.67] | 0.9350 | 1.01 [0.75-1.37] | 0.9344 | 0.99 [0.70- 1.37] | 0.0050 | 0.77 [0.64- 0.92] |
| rs12258032 | CTNNA3 | LVD | T | 0.7053 | 2.1E-6 | 0.82 [0.76-0.89] | 0.9273 | 1.00 [0.93-1.07] | 0.7737 | 1.03 [0.86- 1.21] | 0.0050 | 0.92 [0.88- 0.97] |
| rs151212397 | PCDH15 | LVD | A | 0.0140 | 7.7E-7 | 2.32 [1.66-3.23] | 0.3170 | 0.88 [0.69- 1.12] | NA | NA | 0.039 | 1.22 [1.01- 1.48] |
| rs2660040 | CTNNA3 | LVD | A | 0.2967 | 1.8E-6 | 1.22 [1.13-1.33] | 0.5666 | 0.98 [0.91-1.05] | 0.4523 | 0.92 [0.73- 1.15] | 0.015 | 1.07 [1.01- 1.12] |
| rs73143582 | intergenic | LVD | C | 0.0249 | 1.4E-6 | 2.05 [1.53-2.74] | 0.1178 | 0.83 [0.66- 1.04] | 0.9670 | 0.99 [0.72- 1.35] | 0.13 | 1.12 [0.96- 1.31] |

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| rs9533106 | TNFSF11 | CE | T | 0.7595 | 7.6E-9 | 0.78 [0.72-0.85] | 0.05497 | 0.94 [0.87- 1.00] | 0.1458 | 0.88 [0.74- 1.04] | 1.03E-7 | 0.87 [0.83- 0.91] |
| rs9525624 | TNFSF11 | CE | T | 0.2410 | 6.0E-9 | 1.28 [1.18-1.39] | 0.07639 | 1.06 [0.99- 1.13] | 0.1668 | 1.12 [0.95- 1.32] | 1.7E-7 | 1.14 [1.08- 1.19] |
| rs4941428 | TNFSF11 | CE | A | 0.2511 | 3.3E-9 | 1.28 [1.18-1.39] | 0.3482 | 1.03 [0.96- 1.10] | 0.1228 | 1.17 [0.96- 1.34] | 2.5E-6 | 1.12 [1.07- 1.18] |
| rs78636564 | MYO3B | CE | T | 0.9283 | 4.5E-7 | 0.68 [0.59-0.79] | 0.05627 | 0.89 [0.80- 1.00] | 0.5652 | 1.14 [0.72- 1.82] | 1.4E-5 | 0.82 [0.75- 0.90] |
| rs531905 | CBFA2T3 | CE | T | 0.9594 | 3.8E-6 | 0.61 [0.49-0.75] | 0.2298 | 0.91 [0.78- 1.05] | 0.02644 | 0.32 [0.12- 0.87] | 9.7E-5 | 0.78 [0.69- 0.88] |
| rs4039572 | CBFA2T3 | CE | A | 0.9609 | 3.0E-6 | 1.65 [1.34-2.04] | 0.2736 | 0.92 [0.79- 1.06] | 0.009492 | 0.24 [0.08- 0.71] | 0.00016\* | 0.79 [0.70- 0.89] |
| rs7252106 | EMR3 | CE | A | 0.0149 | 7.3E-7 | 2.57 [1.77-3.72] | 0.2265 | 1.15 [0.91- 1.44] | 0.3245 | 1.11 [0.86- 1.52] | 0.00041 | 1.33 [1.13- 1.56] |
| rs2975831 | KCNB2 | CE | A | 0.6550 | 1.7E-6 | 1.21 [1.12-1.31] | 0.9748 | 0.99 [0.94-1.06] | 0.4189 | 0.93 [0.77- 1.11] | 0.0089 | 1.06 [1.01- 1.11] |
| rs2929558 | KCNB2 | CE | A | 0.6631 | 7.4E-7 | 1.22 [1.13-1.32] | 0.6170 | 0.98 [0.90- 1.04] | 0.3515 | 0.91 [0.76- 1.09] | 0.022 | 1.05 [1.00- 1.10] |

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| rs117481954 | GCH1 | SVD | A | 0.9846 | 1.2E-6 | 0.46 [0.34-0.63] | 0.0741 | 0.79 [0.62- 1.02] | 0.7151 | 0.92 [0.60- 1.40] | 3.3E-5 | 0.69 [0.57- 0.82] |
| rs13220913 | AKAP12 | SVD | T | 0.4007 | 6.0E-7 | 1.24 [1.14-1.35] | 0.5981 | 1.02 [0.94- 1.10] | 0.2193 | 1.13 [0.92- 1.39] | 5.2E-5 | 1.12 [1.06- 1.18] |
| rs74712762 | TMEM108 | SVD | T | 0.0204 | 3.6E-7 | 2.27 [1.66-3.11] | 0.3611 | 1.13 [0.86- 1.48] | NA | NA | 6.5E-5 | 1.51 [1.23- 1.86] |
| rs79380341 | TMEM108 | SVD | T | 0.9808 | 2.6E-7 | 0.42 [0.30-0.59] | 0.4275 | 0.89 [0.67- 1.17] | NA | NA | 8.6E-5 | 0.65 [0.53- 0.80] |
| rs10457874 | AKAP12 | SVD | T | 0.3991 | 7.0E-7 | 1.24 [1.14-1.34] | 0.5141 | 1.02 [0.95- 1.10] | 0.2263 | 1.13 [0.92- 1.38] | 8.9E-5 | 1.11 [1.05- 1.17] |
| rs75725351 | intergenic | SVD | A | 0.0687 | 1.2E-7 | 1.67 [1.38-2.02] | 0.5393 | 0.94 [0.79- 1.12] | 0.4991 | 1.36 [0.55- 3.40] | 0.0016 | 1.22 [1.07- 1.38] |
| rs77420780 | KIAA1217 | SVD | A | 0.0170 | 1.2E-7 | 2.49 [1.78-3.49] | 0.8704 | 0.97 [0.72- 1.30] | 0.09854 | 0.61 [0.34- 1.09] | 0.0044\* | 1.30 [1.06- 1.60] |
| rs12259419 | KIAA1217 | SVD | A | 0.0170 | 1.9E-7 | 2.52 [1.78-3.57] | 0.8506 | 0.97 [0.72- 1.30] | 0.09187 | 0.60 [0.34- 1.08] | 0.0065\* | 1.28 [1.04- 1.58] |
| rs59078057 | LRRTM4 | SVD | A | 0.7003 | 4.6E-7 | 0.80 [0.73-0.87] | 0.1243 | 1.07 [0.98- 1.16] | NA | NA | 0.015 | 0.92 [0.87- 0.98] |

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| rs118000664 | KIAA1217 | SVD | T | 0.0138 | 3.4E-8 | 3.09 [2.07-4.61] | 0.6563 | 0.93 [0.69- 1.25] | 0.1056 | 0.61 [0.33- 1.10] | 0.016\* | 1.27 [1.01- 1.58] |

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| rs57569024 | LRRTM4 | SVD | A | 0.7002 | 5.1E-7 | 0.80 [0.73-0.87] | 0.2154 | 1.05 [0.97- 1.13] | NA | NA | 0.016 | 0.93 [0.87- 0.98] |
| rs17014247 | LRRTM4 | SVD | T | 0.7006 | 4.6E-7 | 0.80 [0.73-0.87] | 0.1245 | 1.06 [0.98- 1.14] | NA | NA | 0.028 | 0.93 [0.88- 0.99] |
| rs7256023 | MOB3A | SVD | T | 0.0810 | 1.8E-6 | 1.44 [1.24-1.67] | 0.07074 | 0.89 [0.78- 1.01] | 0.4591 | 1.15 [0.78- 1.68] | 0.064 | 1.09 [0.99- 1.1986] |

**Table e-3**: Meta-analysis results for all IS and subtypes: Listed are all SNPs undergoing replication analysis in the current study that did not reach genome-wide significance in the final trans-ethnic meta-analysis. Results are shown for the discovery sample, the Caucasian and South Asian replication samples and the final trans-ethnic meta-analysis. Results are sorted by stroke phenotype and meta-analysis p-value. NA signifies that no information on that SNP was available for QC reasons. An asterisk indicates that the resulting trans-ethnic meta-analysis p-value is derived from the Han-Eskin random effects model