**Supplementary Fig. S3. Regional plot for top variant in African American meta-analysis.** One variant (rs139558732, OR=2.19, p=3.33e-8) nominally exceeds genome-wide significance, but statistical significance decreased in the trans-ethnic meta-analysis (OR=2.05, p=1.31e-07) and upon meta-analysis of the present AA results with the AA results from the Army STARRS Consortium (rs11085374, p=1.74e-05).

