**Supplemental Digital Content 3**

Overview of top pooling findings

The pooling results were compared with the expected p values. For example with ~620000 Single Nucleotide Polymorphisms (SNPs) (original number of SNPs interrogated on the Illumina microarray), ~6200 SNPs would be expected to yield p-values <0.01 under the null hypothesis of no associations. The proportion of SNPs at the different thresholds is shown in the table below. It is noticeable that the proportion of SNPs exceeding the threshold is close to that expected under the null hypothesis for p-value threshold of 0.01. Conversely, for smaller thresholds, there are more positive results than expected by chance. This result is consistent with there being more positive associations for this sample. For example, at the 0.0001 we would expect to see ~62 SNPs under the null hypothesis of no associations but we in fact observe 646 SNPs.

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| p-value threshold | Proportion of SNPs exceeding threshold |
| 0.01 | 0.019 |
| 0.001 | 0.0045 |
| 0.0001 | 0.0011 |
| 0.00001 | 0.00028 |
| 0.000001 | 0.000081 |
| 0.0000001 | 0.0000145 |