**2017 Gene x Environment Summary Statistics**

**Summary Statistics for Smoking Stratified Models**

**Column headers:**

1. Chromosome

2. rs\_id: dbSNP ID

3. markername: chr:pos

4. position\_hg18: base pair position on build hg18

5. Effect\_allele

6. Other\_allele

7. EAF\_HapMapCEU: The allele frequency of Allele1 in the HapMap CEU population

8. N\_SMK: sample size for smokers

9. Effect\_SMK: beta in smokers

10. StdErr\_SMK: standard error in smokers

11. P\_value\_SMK: p- value for smokers after correction for inflation of test statistics using genomic control both at the individual study level and again after meta-analysis

12. N\_NONSMK: sample size for nonsmokers

13. Effect\_NonSMK: beta in nonsmokers

14. StdErr\_NonSMK: standard error in nonsmokers

15. P\_value\_NonSMK: p- value for nonsmokers after correction for inflation of test statistics using genomic control both at the individual study level and again after meta-analysis