**2018 Exome Array Summary Statistics**

**WHR Exome Array Summary Statistics**

**File name structure:** PublicRelease.WHRadjBMI.\*.\*.\*.txt.gz

**Abbreviations in filenames:**

C-Combined Sexes

M-Men

W-Women

All- All Ancestries

Eur- European descent only

Add- Additive genetic model

Rec- Recessive genetic model

**File headers:**

1. snpname - dbSNP rsID

2. chr - chromosome

3. pos - position

4. markername - chr:pos

5. ref - reference allele (hg19 + strand)

6. alt - alternate allele (hg19 + strand)

7. beta - beta

8. se - standard error

9. pvalue - P value

10. n - sample size

11. gmaf/eur\_maf - alternate allele frequency in 1000 Genome Combined/European Ancestries

12. exac\_maf/exac\_nfe\_maf -alternate allele frequency in ExAC Combined/Non-Finnish European Ancestries