Fill out the fields in the template file (PG_SNPsTemplate.docx, available at http://www.the-aps.org/mm/Publications/Journals/Physiol-Genomics/Article-Types/PG-SNPs.html) according to the required specifications detailed below:

Type the Title Here

**Authors and Institutions:**
(5 key authors, remainder listed under consortium name; online appendix)

**ABSTRACT**
(150 words, no subheadings within the abstract)

**Keywords**
(Provide up to 5 keywords, including SNP, phenotype, and gene)

**BACKGROUND/MOTIVATION FOR THE STUDY**
(250 words)

**PHENOTYPE**
(150 words for each subsection)
Include pre-specified name of the trait, how phenotype was measured, and details of measurement method/instrument used.

In the case of derived phenotypes, details of the calculation and formula should be described.

**Cohort details**
Include the following:
Type (retrospective, prospective, clinical trial, population cohort, disease case)
Inclusion/exclusion criteria
Ethnicity
Sample size
Brief demographic details

**Type of study**
1. Candidate SNP
2. Candidate gene
3. Bespoke genotyping array, for example Cardio-Metabochip, Exome Chip, etc.
4. GWAS - genome-wide association study
5. Sequencing analysis (exome or whole-genome sequencing)
Details of the SNP(s) studied
Specify SNP accession number (rs number) if candidate gene/or single SNP study. Add rs numbers to a maximum of 5 SNPs; if there are more, define as custom and give details in the supplement.

If an array or GWAS study, include the name and version of the array and the manufacturer. Indicate imputation, if done, and panel used.

Analysis model
Case control or quantitative; details of the statistical test used, for example regression model. Include covariates used in the model, including principal components and state the effective sample size if appropriate. Indicate thresholds used to report significance in this study. If replication/validation was performed, give details of the analysis if different from main study.

RESULTS
[150 words, provide a summary of the primary result(s)]
This is just a summary of the main result. Do not include interpretation of the result here. All figures will appear in the online supplement.

For single SNPs, include the rs number, allele frequency (effect allele) or both for case control studies, chromosome and base pair position of the variant (latest genome build), Hardy–Weinberg equilibrium (HWE).

For more than one SNP, include rs number of significant SNPs or top 5 (or 10) most significant in the study if no significant results.

Indicate P value, beta, and S.E., allele frequencies, chromosome and pair position, heterogeneity value.

For GWAS study, include Q-Q plot, report genomic control, forest plots, and if GWS include a locus plot.

INTERPRETATION
(50-100 words, provide a short statement)
Focus on the limitations and a statement on any other subsequent work that has been published in this area that may inform the results.

ACKNOWLEDGMENTS
Thank people indirectly involved with the research.

GRANTS
Indicate sources of funding, additional information to be included in Appendix 3

DISCLOSURES
Indicate any potential conflicts of interest

**AUTHOR CONTRIBUTIONS**
Describe author contributions

**REFERENCES**
(Provide 5 key references; additional references to be included in Appendix 3)

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**Supplemental Data:** (to be prepared and submitted online at http://pg.msubmit.net/cgi-bin/main.plex)

See samples of the Results template (PG_SNPs_results_template.xlsx) and Study genotyping/QC template (PG_SNPS_QC_table.xlsx) that must be completed by the author (http://www.the-aps.org/mm/Publications/Journals/Physiol-Genomics/Article-Types/PG-SNPs.html).

**Notes:**
For the reporting of single SNPs, there will be one line in the Results table.
For array and GWAS studies, please report a maximum of 20 SNPs

If an array or GWAS study is reported, please include a Q-Q plot and report the genomic control.

**Online Appendices:**
Appendix 1: Figures, may include a Q-Q plot or association plot
Appendix 2: The tables file
Appendix 3: Additional material, including extra references, list of consortium members, acknowledgments.