iPSYCH-PGC ASD GWAS results — November 2017 release

This is the GWAS results file from the meta-analysis of ASD by the Lundbeck Foundation Initiative for Integrative Psychiatric Research (iPSYCH) and the Psychiatric Genomics Consortium (PGC). The summary data was released in November 2017, the paper published March 2019.

Citation for studies using these data

J. Grove, S. Ripke, T. D. Als, M. Mattheisen, R. K. Walters, H. Won, J. Pallesen, E. Agerbo, O. A. Andreassen, R. Anney, S. Awashti, R. Belliveau, F. Bettella, J. D. Buxbaum, J. Bybjerg-Grauholm, M. Bækvad-Hansen, F. Cerrato, K. Chambert, J. H. Christensen, C. Churchhouse, K. Dellenvall, D. Demontis, S. De Rubeis, B. Devlin, S. Djurovic, A. L. Dumont, J. I. Goldstein, C. S. Hansen, M. E. Hauberg, M. V. Hollegaard, S. Hope, D. P. Howrigan, H. Huang, C. M. Hultman, L. Klei, J. Maller, J. Martin, A. R. Martin, J. L. Moran, M. Nyegaard, T. Nærland, D. S. Palmer, A. Palotie, C. B. Pedersen, M. G. Pedersen, T. dPoterba, J. B. Poulsen, B. S. Pourcain, P. Qvist, K. Rehnström, A. Reichenberg, J. Reichert, E. B. Robinson, K. Roeder, P.Roussos, E. Saemundsen, S. Sandin, F. K. Satterstrom, G. Davey Smith, H. Stefansson, S. Steinberg, C. R. Stevens, P. F. Sullivan, P. Turley, G. B. Walters, X. Xu, Autism Spectrum Disorder Working Group of the Psychiatric Genomics Consortium, BUPGEN, Major Depressive DisorderWorking Group of the Psychiatric Genomics Consortium, 23andMe Research Team, K. Stefansson, D. H. Geschwind, M. Nordentoft, D. M. Hougaard, T.Werge, O. Mors, P. B. Mortensen, B. M. Neale, M. J. Daly, and A. D. Børglum (Mar. 2019). "Identification of common genetic risk variants for autism spectrum disorder." *Nature genetics* 51 (3), pp. 431–444. doi: 10.1038/s41588-019-0344-8. PMID: 30804558

Disclaimer

These data are provided "as is", and without warranty, for scientific and educational use only. If you download these data, you acknowledge that these data will be used only for non-commercial research purposes; that the investigator is in compliance with all applicable state, local, and federal laws or regulations and institutional policies regarding human subjects and genetics research; that secondary distribution of the data without registration by secondary parties is prohibited; and that the investigator will cite the appropriate PGC publication in any communications or publications arising directly or indirectly from these data.

Data Use Agreement

1. Investigators acknowledge that these data are provided on an "as-is" basis, without warranty of any type, expressed or implied, including but not limited to any warranty as to their performance, merchantability, or fitness for any particular purpose;
2. Investigators will use these results for scientific research and educational use only.
3. The downloaded results can be shared among collaborators but the reposting or public distribution of the result file is prohibited;
4. Investigators certify that they are in compliance with all applicable local, state, and federal laws or regulations and institutional policies regarding human subjects and genetics research;
5. Investigators will cite the appropriate publication in any communications or publications arising directly or indirectly from these data;
6. Investigators will never attempt to identify any participant who contributed to these data;

7. Investigators may not use these data to develop any type of risk or predictive test for an unborn individual;
8. For any risk or predictive test for a child or adult, investigators must acknowledge that this is an experimental use of these data and that essentially all psychiatric disorders have important non-genetic etiological components;
9. When these data are made available prior to publication, investigators agree to respect and not compete with the scientific priorities of the iPSYCH team according to the Fort Lauderdale principles.

Experience has taught us that the appropriate use of these data requires considerable attention to detail, prior experience, and technical skill. Errors are easy to make. If investigators use these data, any and all consequences are entirely their responsibility.

Non-Compete Request for Pre-Publication Summary Statistics
Consistent with the responsibilities of resource users under 2003 Fort Lauderdale principles and PGC data sharing policies, we request that investigators do not compete with the following analyses before publication of the submitted paper:

(i) analyses in the submitted paper named at the beginning of this document, and
(ii) ongoing cross-disorder/trait studies between ASD and the significantly correlated traits identified in the paper: Intelligence, educational attainment (incl. college yes/no), selfreported tiredness, neuroticism, subjective well-being, schizophrenia, major depression, depressive symptoms, ADHD, and chronotype.

File Description
iPSYCH-PGC_ASD_Nov2017.gz: Full ASD GWAS meta-analysis of samples of European ancestry
(18,382 cases, 27,969 controls, see manuscript for methods)

CHR Chromosome (hg19)
SNP Marker name
BP Base pair location (hg19)
A1 Allele 1 (may or may not be minor allele)
A2 Allele 2
INFO Imputation information score
OR Odds ratio for the effect of the A1 allele
SE Standard error of the log(OR)
P P-value for association test in the meta-analysis

Additional Notes
- For long insertion/deletion variants, the A1/A2 alleles are truncated to the first 13 bases with a specification of the remaining length (e.g. AACACACACACAC+16)
- For multiallelic variants, “m” is appended to the marker name for different alternative alleles in order to insure that the marker name is unique.
- The reported imputation INFO score is a weighted average across the cohorts contributing to meta-analysis for that variant
- Allele frequencies and case/control counts per variant are currently omitted from public release for data privacy. For inquiries about accessing this data, please contact the ASD Data Access Committee (DAC) representative (pgc.dac.aut@gmail.com).