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NeuroX genotyping on DNA samples from PPMI

Dena G Hernandez
National Institute on Aging, Laboratory of Neurogenetics

Summary

SNP genotyping was performed using Illumina NeuroX array on 619 whole-blood extracted DNA samples collected according to the PPMI Research Biomarkers Laboratory Manual. The NeuroX array is an Illumina Infinium iSelect HD Custom Genotyping array containing 267,607 Illumina standard content exonic variants and an additional 24,706 custom variants designed for neurological disease studies. Of the custom variants, approximately 12,000 are designed to study Parkinson's disease and are applicable to both large population studies of risk factors and to investigations of familial disease and known mutations.

Method

Genotyping on Illumina NeuroX array was performed per manufacturers protocol (Illumina, Inc. San Diego). The Genotyping Analysis Module within Genome Studio version 1.9.4 was used to analyze data. The threshold call rate for sample inclusion was 95%. Quality control of sample handling was determined by comparing the subject's sex reported by Coriell Institute for Medical Research with the genotypic sex estimated from X chromosome heterogeneity. X chromosome heterogeneity calculations were based on common SNPs from the International HapMap Project that had genotypes with missingness <5% and hardy-Weinberg equilibrium (HWE) *p* values >1E-5. Samples containing discrepancies between reported sex and genotypic estimated sex were excluded.

References

Nalls MA, Pankratz N, Lill C, Do CB, Hernandez DG et al. Large Scale Meta Analysis of Genome-wide Association Data in Parkinson's Disease Reveals 28 Distinct Risk Loci. *Nature Genetics 2013. Under Review.*

Parkinson's Progression Marker Initiative Research Biomarkers Laboratory Manual (Biologic Manual) http://www.ppmi-info.org/wp-content/uploads/2011/05/PPMI-Biologics-Manual-April-2011-FINAL.pdf.

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About the Authors

This document was prepared by Dena G Hernandez, National Institute on Aging, Laboratory of Neurogenetics. For more information please contact Dena Hernandez by email at hernand@mail.nih.gov