Supplemental Information for:

Genomic Variants Associated with Resistance to High Fat Diet Induced Obesity

in a Primate Model

R. Alan Harris PhD^{1,2}, Callison E. Alcott³, Elinor L. Sullivan PhD^{4,5}, Diana Takahashi⁴, Carrie E. McCurdy PhD⁶, Sarah Comstock PhD⁷, Karalee Baquero⁴, Peter Blundell⁴, Antonio E. Frias, MD^{4,8}, Maike Kahr MD¹, Melissa Suter PhD¹, Stephanie Wesolowski PhD⁹, Jacob E. Friedman PhD⁹, Kevin L. Grove PhD⁴, and Kjersti M. Aagaard MD PhD^{§1,2,3,4,10}

Affiliations:

¹Department of Obstetrics & Gynecology, Division of Maternal-Fetal Medicine at Baylor College of Medicine and Texas Children's Hospital, Houston, TX.

²Department of Molecular and Human Genetics at Baylor College of Medicine, Houston, TX.

³ Developmental Biology Interdisciplinary Program at Baylor College of Medicine, Houston, TX.

⁴Oregon National Primate Research Center, Oregon Health & Science University (OHSU), Beaverton, OR.

⁵ Department of Biology, University of Portland

⁶Department of Human Physiology, University of Oregon, Eugene, OR.

⁷Department of Biology, Corban University, Salem, OR.

⁸Department of Obstetrics & Gynecology, Division of Maternal-Fetal Medicine, OHSU, Portland, OR.

⁹Departments of Pediatrics, University of Colorado Anschutz Medical Campus, Aurora, CO.

¹⁰Department of Molecular and Cell Biology at Baylor College of Medicine, Houston, TX.

[§]Correspondence to: Kjersti Aagaard, M.D. Ph.D. Baylor College of Medicine Department of Obstetrics & Gynecology Houston, TX 77030 aagaardt@bcm.edu



Supplemental Figure 1. Exon capture array design.



Supplemental Figure 2. SNP Calling





Supplemental Figure 3. Significant (p < 0.05) genotype-phenotype NOIA three loci models based on genotypes for the extended panel of high fat diet exposed Japanese macaques. The Genotype axis shows the genotypes (1 = homozygous most frequent allele, 2 = heterozygous, 3 = homozygous least frequent allele) for each of the loci (ordered as *PLA2G4A*, *APOB.1 APOB.2*) and the Genotypic Effects axis shows the NOIA predicted effect of the genotype on a phenotype.