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PARENT-OF-ORIGIN EFFECTS ON GENE EXPRESSION AND QUANTITATIVE
TRAITS IN A FOUNDER POPULATION

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For my family.

Especially my maternal grandmother and paternal grandfather,

Shamsi Joon (Shamsi Karimkhanzand) and Bababozorg (Hossein Mozaffari).

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ABSTRACT

Variants can affect traits differently depending on whether they are inherited from the mother or the father, but genome wide association studies (GWAS) treat maternal and paternal alleles as equivalent. In addition, the variants identified by GWAS do not account for a significant portion of the heritability for the corresponding trait and the “missing heritability” could be due to underlying biological mechanisms that are not yet well understood. My thesis addresses these limitations by disentangling the effects of maternal and paternal alleles on gene expression as well as on disease-associated phenotypes in the Hutterites, a founder population of European descent. With phased genotype data we can ask questions about parent of origin effects in this population. First, we tested for maternal and paternal genetic associations on cardiovascular disease and asthma associated traits and developed a novel method to detect variants that have opposite effects on the trait of interest depending on the parent of origin of the variant. We identified variants that have maternal-only or paternal-only effects, as well as variants that have opposite effects on traits, which would not be detected in a standard GWAS. This is the largest family based study of parent of origin effects on quantitative traits and the first to look for opposite parental effects. In the second chapter, we map RNA-seq reads from lymphoblastoid cell lines (LCLs) to parental haplotypes in 306 Hutterites and detect known imprinted genes and two novel imprinted genes (*PXDC1* and *PWAR6*). These imprinted gene patterns are validated using parent of origin expression from peripheral blood leukocytes (PBL) from 99 different Hutterites; imprinting control regions near the novel genes were validated using PBL methylation in the same 99 Hutterites. Finally, we explore searching for parent of origin effects on gene expression or parent of origin eQTLs, first for opposite effects and then for maternal and paternal specific effects.

CHAPTER 1

INTRODUCTION

1.1 Human Genetics and the Genetics of Complex Traits

A central goal of genetics is to understand the contribution of genetic variation to phenotypic variation. The mechanism by which genetic variants contribute to a phenotype is determined by the genetic architecture of the phenotype, however, the underlying rules that determine how genetic variants contribute to phenotype diversity are still not fully known.

Monogenic traits are determined by genetic variation in one gene whereas complex traits do not follow Mendelian rules of inheritance and have heterogenous phenotypes. Genetic variation in many genes, as well as interaction of genes with environmental factors typically contribute to complex trait phenotypes.

Genome wide association studies (GWAS) have been effective in detecting associations between common variants and common diseases since 2005, with the publication of the first large GWAS with good coverage of the genome in 2007 from the Wellcome Trust Case Control Consortium [115]. Although GWAS have resulted in the discovery of thousands of novel associations to hundreds of phenotypes, the loci identified by GWAS explain a small proportion of the estimated heritability of the trait, or the fraction of phenotypic variation in a population that is due to genetic variation. There are many explanations that could account for this “missing heritability,” or the proportion of heritability not accounted for by these significant GWAS loci, including gene-environment interactions, epistatic interactions, inflated heritability estimates, rare variants or structural variants not tagged by GWAS SNPs, common variants with small effect sizes, and parent-of-origin effects [116, 33, 39, 119]. Heritability of parent-of-origin effects on traits have been extensively studied in mice [9, 76, 10, 8] but is only beginning to be studied in humans [58]. The significant GWAS associations, or “low-hanging fruit” have been further investigated to determine causality

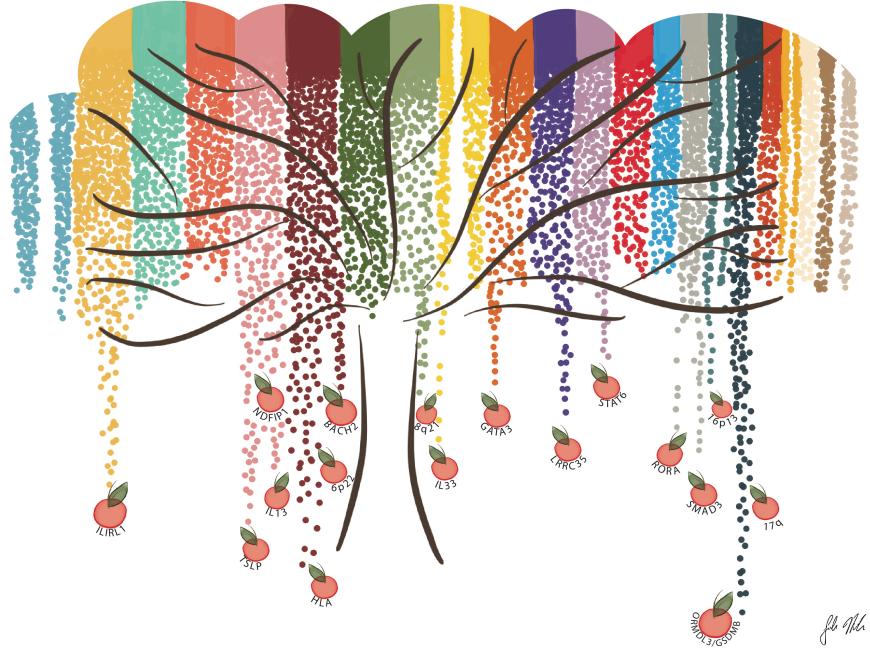


Figure 1.1: Asthma GWAS Manhattan Plot. Inverted manhattan plot for asthma GWAS highlighting “low hanging fruit” as apples hanging from the manhattan plot “tree.” Figure from Ober, 2016 [82] updated to reflect results from Demenais, 2018 [28].

but there still remains a lot of the genome, or “mid-hanging fruit,” that could contribute to a trait. Identifying which variants are causal among those with small p-values that are not genome wide-significant is challenging (Figure 1.1).

Additionally, in GWAS, the impact of parental origin of associated alleles has been largely ignored, and maternal and paternal alleles are treated as equivalent. Sequence variants could affect disease susceptibility or a quantitative trait differently depending on whether the variant was inherited from the father or the mother. Parent-of-origin effects include phenomena such as imprinting where epigenetic modifications determined by parental origin allows for differential gene expression of genes on homologous chromosomes [64, 59].

The classic examples of parent-of-origin effects are imprinted genes. More than 80% of imprinted genes in humans are found in genomic clusters, and at least thirteen clusters have been identified on eight chromosomes [59, 90, 91, 2]. These clusters contain both maternally

and paternally expressed genes as well as non-coding RNA genes [90, 2]. Parent-specific expression of the genes within a cluster is determined by cis-acting imprinting control regions (ICRs). ICRs show parental allele-specific DNA methylation and chromatin modifications. ICRs methylated in females during oogenesis typically contain the promoters of long non-coding RNA that are antisense to a protein- coding gene in the cluster and silence it. In contrast, ICRs that acquire methylation in the male germ line are located in intergenic regions [90].

The testing of maternal and paternal alleles separately can disentangle parent-of-origin effects. Parent-of-origin effects can alter gene expression levels that can ultimately affect other phenotypic traits including disease [59, 90]. Moreover, parent-of-origin eQTLs can provide insight into the molecular mechanisms that may underlie genetic associations with both rare and common diseases [59, 90, 56, 102, 35].

1.2 On The Origin of Genomic Imprinting

Genomic imprinting in its broadest sense suggests that a phenotype observed for a particular gene or genes depends on the sex of the parent from which the gamete containing that gene or genes originated [98]. A particular gene is imprinted if it results in a different phenotype when it is maternally inherited versus paternally inherited. The phenotype can be cytological, morphological, behavioral or biochemical [98].

The first use of the term “imprinting” was used in reference to the recognition and selective elimination of the paternal chromosomes in *Sciara* [25, 98]. “The ‘imprint’ a chromosome bears is unrelated to the genic constitution of the chromosome and is determined only by the sex of the germ line through with the chromosome has been inherited.” [25]

The preferential inactivation of the paternally-derived X chromosomes in mouse was the first demonstration of a functional imprint in mammalian genomes [106, 67, 20]. Imprinting on autosomes was first suggested by a deletion on mouse chromosome 17 that showed a

different phenotype based on which parent the deletion was inherited from [48, 94]. It was not until the development of the pronuclear transplantation technique that allowed for the creation of mice zygotes which contained only maternal or only paternal genetic contributions that there was any evidence that the maternal and paternal genomes are not equal. The differential imprinting on the parental chromosomes prevented complete embryonic development in these mice with complete uniparental disomy [98, 74]. Parental chromosomes have different regions silenced, or imprinted, such that one parental copy is expressed and having either both parental copies or neither expressed results in genetic and developmental abnormalities.

Further experiments suggested that imprinting occurs during gametogenesis and is necessary for full term development. An egg with a male pronucleus developed to term, but, an egg with two female pronuclei (gynogenetic embryos) or two male pronuclei (androgenetic) developed poorly[104, 74]. This provides evidence that input from both parents are required for normal development and the genome of the egg and sperm nuclei are not equal. Non-complementation in genetic crosses of translocated chromosomes provided a way to refine the imprinted regions of the genome[19].

Genetic characterization of Prader-Willi syndrome (PWS) was the first human genetic disease to be associated with maternal heterodisomy of chromosome 15q11-13[78]. It suggested that clinical phenotype of PWS arises from the absence of paternal contribution of 15q11-13 as opposed to a specific genetic mutation. Conversely the absence of maternal contribution to the same region should result in Angelman syndrome (AS) [78, 93]. This provided more evidence that, at “imprinted” regions, the functional differences depend on the sex of the transmitting parent and genetic input from both parents are required for normal human development [78]. Various other human imprinted syndromes due to loss or gain of expression of imprinted genes have been summarized in Table 1.1.

The evolution of genomic imprinting is not yet known and there are theories in place

to explain why it still exists. Genomic imprinting exposes recessive mutations since these regions are effectively haploid and thus results in a fitness cost. The evolution of genomic imprinting implies an advantage as the imprinting status of many genes have been conserved over millions of years [75, 91]. Genomic imprinting in animals exists in eutherian and marsupial mammals but not in non-mammalian vertebrates or monotremes (mammals that lay eggs) including the platypus and echidna [47, 91]. There are many theories to try and explain the evolution of imprinting, and two have gained the most popularity: the kinship (or parental conflict) theory and the maternal-offspring coadaptation theory. The kinship theory of genomic imprinting suggests that there exists a conflict between parental interests on maternal resources by the embryo: the paternally derived genes benefit from maximizing the resources at the expense of embryos from other fathers (in viviparous polyandrous, or multiple paternity species). In contrast, the maternally derived genes benefit from providing equal allocation of resources to all embryos since they are all equally related to the mother [91]. The kinship theory has been the most popular theory to explain the evolution of genomic imprinting since it is supported by dosage-dependent and opposing roles of reciprocally imprinted genes (i.e. *Igf2* and *Igf2r*) but it does fail to predict the direction of imprinting in some loci (*Meg1*). A second theory, maternal-offspring coadaptation theory, proposes that offspring are more likely to survive if they are more similar to the mother in species with extended maternal care [91]. This coadaptation theory could explain the predominance of maternally expressed genes in mice and plants.

Additional theories have been put forth including the Ovarian time bomb hypothesis (OTH), X-linked sex-specific selection hypothesis (XSSH), sexually antagonistic selection hypothesis (SASH), and imprinting as a barrier to parthenogenesis. OTH suggests that inactivation of early-acting growth enhancers and upregulation of growth inhibitors lowers the risk of unfertilized eggs in an ovary to develop into ovarian cancer [75, 47]. Both the kinship theory and OTH predict that growth affecting genes are likely targets of imprinting. XSSH

predicts patterns opposite of OTH and kinship theory, such that as a result of inactivation of maternal X-linked growth inhibitors and paternal X-linked growth enhancers, males will be larger, which is common in mammals. This imbalance is suggested to result from imprinting that augments any selection pressure that differs between sexes due to the X chromosome since maternal X will affect males more than females, and paternal X will only affect females [75]. SASH is an extension of XSSH to autosomal loci suggesting there is sex-specific imprinting [75]. The anti-parthenogenesis idea is that imprinting prevents an unfertilized egg from developing into a new individual and supports the idea that the genetic benefits of sexual reproduction for long-term evolutionary fitness outweigh the risk from imprinting a few genes [47, 57]. These theories do not provide a good mechanistic framework but focus on the evolutionary logic of imprinting. With characterization of more imprinted genes we will be able to understand how and why these have evolved.

1.3 The Search for Parent-of-Origin Effects

Parent-of-origin effects and imprinted genes have been most elegantly studied in mice, where two inbred strains are bred reciprocally to identify parent-of-origin effects on gene expression in progeny that have the same genotypes but different patterns of inheritance [8]. Such studies are obviously more challenging in humans. Previous studies have attempted to identify parent-of-origin alleles using different approaches, addressing parent-of-origin effects on gene expression and phenotypic traits.

In one study of gene expression, investigators examined whether genotypes fit Hardy Weinberg Equilibrium expectations and considered imprinted loci to be those with no or fewer than expected heterozygotes (C.T. Watson, ASHG 2014). Garg et al. used gene expression in lymphoblastoid cell lines (LCLs) from 29 CEU and 30 YRI HapMap trios to identify 30 imprinting eQTLs with parent-of-origin specific effects on expression by first comparing maternal alleles and paternal alleles associated with gene expression, and then

Human syndrome	Syn-	Location	Major features	Causes
Transient neonatal diabetes mellitus type 1[68]		6q24	Neonatal hyperglycaemia and intrauterine growth restriction	Overexpression of <i>PLAG1</i> and <i>HYMAI</i>
Silver-Russell syndrome[32, 109]		11p15.5 (65%), MatUPD7 (10%)	Dysmorphism, intrauterine growth restriction and postnatal growth retardation	Complex: 11p15.5: hypomethylation of <i>H19</i> DMR, silencing of <i>IGF2</i> and biallelic expression of <i>H19</i> ; <i>MEST</i> and <i>GRB10</i> are candidates for MatUPD7 cases
Beckwith-Wiedemann syndrome[22]		11p15.5	Prenatal and or postnatal overgrowth, enlarged tongue, abdominal wall defects, placental overgrowth and predisposition to embryonal tumours.	Complex: mostly epigenetic errors- silencing of <i>CDKN1C</i> or biallelic expression <i>IGF2</i> and silencing of <i>H19</i> ; inactivating mutations in <i>CDKN1C</i> ; PatUPD11
Temple Syndrome[46, 53] / MatUPD14 syndrome		14q32	Prenatal and postnatal growth retardation, premature puberty and obesity	Loss of paternal expression of <i>DLK1</i> and <i>RTL1</i>
Kagami-Ogata syndrome[52, 53, 84] / PatUPD14 syndrome		14q32	Dysmorphism, placentomegaly and excessive amniotic fluid	Increased expression of <i>RTL1</i>
Prader-Willi syndrome[17]		15q11-13	Developmental delay, obesity, hypogonadism, cognitive impairment	Loss of paternal expression up to 11 genes in 15q11-13 : paternal deletion of MatUPD15
Angelman syndrome[17]		15q11-13	Developmental delay, microcephaly, absent or limited speech, gait ataxia, characteristic EEG and behavioral profile with happy demeanour	loss of maternal expression of <i>UBE3A</i> , <i>UBE3A</i> mutation or patUPD15
Mulchandani-Bhoj-Conlin syndrome[77]		chr15	Prenatal growth restriction, severe short stature with proportional head circumference, and profound feeding difficulty	MatUPD20
Schaaf-Yang syndrome[36]		chr15	Delayed psychomotor development, intellectual disability, hypotonia, and behavioral abnormalities	inactivation of <i>MAGELO2</i> on paternal allele
Central precocious puberty 2[3]		chr15	Development of secondary sexual characteristics before age 8 in girls and age 9 in boys.	inactivation of <i>MKRN3</i> on paternal allele
Pseudo-hypoparathyroidism type 1a and type 1b[71, 34]		20q13.3	Dysmorphism, obesity, cognitive impairment, end-organ resistance to parathyroid hormone (which results in hypocalcemia and hyperphosphatemia) and resistance to other hormones	Inactivation/lack of maternal <i>GNAS</i>

Table 1.1: **Imprinted Gene Disorders.** Adapted from Peters (2014) and Mackay and Temple (2017) [90, 69], ordered by chromosome location of causal mutation. UPD = Uniparental Disomy

comparing reciprocal heterozygotes [38]. A study from the GTEx Consortium used RNA-seq data to determine allele specific expression (ASE) in 45 different tissues from various numbers of individuals to identify new imprinted genes [12]. By considering genes with monoallelic expression that were evenly distributed to both the reference and alternate alleles across individuals as evidence for imprinting, they identified 42 imprinted genes, both known and novel, and used family studies to confirm imprinting of 5 novel genes. Most recently, Santoni et al. identified nine novel imprinted genes using single-cell allele-specific gene expression and identified genes with mono-allelic expression in fibroblasts from 3 unrelated individuals and probands of 2 family trios, and then used the trios to confirm parent-of-origin of the alleles [97].

Not many studies have searched for parent-of-origin effects on binary and quantitative traits. In a study on 38,167 Icelanders with known status for 7 diseases, investigators identified variants that were associated with breast cancer only when paternally inherited and variants associated with type 2 diabetes only when maternally inherited [56]. Parent-of-origin associations with height in the same Icelandic population ($n=88,835$) identified four associations of which three were in known imprinted regions, one of which was also replicated in the Sardinia population [118].

1.3.1 Dissertation Overview

Large pedigrees are ideal for identifying parent-of-origin effects [12]. The advantages that large family studies have for these studies include: 1) formally proving parent-of-origin effects detected from ASE, and 2) detecting subtle imprinting that does not lead to strictly monoallelic expression [12]. The Hutterite population is ideally suited for these studies. The $>1,400$ Hutterite individuals studied by our group are related to each other in a 13-generation pedigree that includes 3,671 individuals, all of whom are descendants of only 64 founders. Ninety-eight Hutterites were initially selected for whole genome sequencing; alleles

were phased using Affymetrix framework markers in the 98 individuals and then imputed to the remaining 1,532 Hutterites who had been previously genotyped with the Affymetrix framework markers [63]. After quality control, parent-of-origin was assigned to more than 10 million variants. Of the 1,532 with genotype data, 431 also had RNA-seq expression data from LCLs, and between 600-1300 individuals have been phenotyped for cardiovascular disease (CVD) and asthma associated quantitative traits.

In this dissertation, I use a novel variation on GWAS to detect parent-of-origin effects on quantitative disease-related traits in the Hutterites that would be normally missed in standard GWAS. I am able to find maternal- and paternal-only effects, as well as opposite parent-of-origin effects. This method can be applied to any quantitative trait for which we know parent of origin of alleles, including gene expression. The method and results of testing this method with quantitative disease related traits is in Chapter 2. Using LCL gene expression and parent-of-origin allele information in the Hutterites, I develop a new method of mapping RNA-seq reads to parental haplotypes and detect known and novel imprinted genes in Chapter 3. The patterns of imprinted genes are validated in a different sample of Hutterite individuals for which we have peripheral blood leukocyte (PBL) RNA-seq and DNA methylation. In Chapter 4, I use methods, including one from Chapter 2, to try and find parent-of-origin variants that have opposite effects on gene expression. Additionally, we tested for maternal and paternal effects on maternal and paternal gene expression, respectively, and used a parent-of-origin ASE (PO-ASE) test to identify differences in maternal and paternal gene expression among reciprocal heterozygotes.

CHAPTER 2

PARENT-OF-ORIGIN EFFECTS ON QUANTITATIVE PHENOTYPES IN A FOUNDER POPULATION

2.1 Abstract¹

The impact of the parental origin of associated alleles in GWAS has been largely ignored. Yet sequence variants could affect traits differently depending on whether they are inherited from the mother or the father. To explore this possibility, we studied 21 quantitative phenotypes in a large Hutterite pedigree. We first identified variants with significant single parent (maternal-only or paternal-only) effects, and then used a novel statistical model to identify variants with opposite parental effects. Overall, we identified parent-of-origin effects (POEs) on 11 phenotypes, most of which are risk factors for cardiovascular disease. Many of the loci with POEs have features of imprinted regions and many of the variants with POE are associated with the expression of nearby genes. Overall, our results indicate that POEs, which can be opposite in direction, are relatively common in humans, have potentially important clinical effects, and will be missed in traditional GWAS.

2.2 Introduction

Genome-wide association studies (GWAS) typically treat alleles inherited from the mother and the father as equivalent, although variants can affect traits differently depending on whether they are maternal or paternal in origin. In particular, parent-of-origin effects (POEs) can result from imprinting, where epigenetic modifications allows for differential gene expression on homologous chromosomes that is determined by the parental origin of

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the chromosome. Mutations in imprinted genes or regions can result in diseases. For example, two very different diseases, Prader-Willi Syndrome (PWS) and Angelman Syndrome (AS), are due to loss of function alleles in genes within an imprinted region on chromosome 15q11-13. Inheriting a loss of function mutation for the *SNRPN* gene from the father results in PWS but inheriting a loss of function mutation for the *UBE3A* gene from the mother results in AS [90, 35]. Long noncoding RNA genes at this and other imprinted regions act to silence (i.e. imprint) genes in cis. Imprinted genes are often part of imprinted gene networks, suggesting regulatory links between these genes [88, 37, 108]. More than 150 imprinted loci have been described in humans [14] but there are likely many other, as yet undiscovered, imprinted loci. The kinship theory or conflict hypothesis suggests there is a conflict between the parent's interest on use of maternal resources by the fetus in utero. This theory promotes the idea that novel imprinted loci can affect more prominently phenotypes associated with fetal use of maternal resources, including early growth as well as downstream traits such as height, BMI, and metabolic disease [90].

Previous studies have utilized pedigrees to test maternal and paternal alleles separately for association with phenotypes or with gene expression to uncover new imprinted loci [56, 12, 38, 89, 14]. Kong *et al* [56] discovered one locus associated with breast cancer risk only when the allele is inherited from the father and another locus associated with type 2 diabetes risk only when the allele is inherited from the mother. Garg et al. reported parent-of-origin cis-eQTLs with known or putative novel imprinted genes affecting gene expression [38]. Two additional studies by Zoledziewska et al. and Benonisdottir et al. identified opposite POEs on adult height at known imprinted loci [118, 14]. Both studies reported associations with variants at the *KCNQ1* gene, and one showed additional opposite POEs with height at two known imprinted loci (*IGF2-H19* and *DLK1-MEG3*) [14]. These studies provide proof-of-principle that alleles at imprinted loci can show POEs, some with opposite effects, with common phenotypes.

Many existing studies and methods that identify POEs use case/parent trios or case/mother duos[23, 44, 4, 113, 112]. Similar to Kong *et al.* [56], our method does not require data on the parent and only uses the parent-of-origin informative alleles which were assigned and phased using PRIMAL [63]. In contrast to Kong *et al.* [56] which used binary traits, our method tests for POEs on quantitative traits, similar to Benonisdottir *et al.* [14] which tested for POEs on height.

No previous study has included a broad range of human quantitative phenotypes or has studied genome-wide variants with effects in different directions depending on the parent of origin. To address this possibility, we developed a statistical model that directly compares the effects of the maternal and paternal alleles to identify effects that are different, including those that are opposite. We applied this model in a study of 21 common quantitative traits that were measured in the Hutterites, a founder population of European descent for which we have phased genotype data [63]. We identified variants with maternally inherited or paternally inherited effects only and variants with opposite POEs. Some of the identified regions have characteristics similar to known imprinted genes. Overall, we show that this model can identify putative novel imprinted regions with POEs for a broad range of clinically relevant quantitative phenotypes.

2.3 Results

2.3.1 GWAS

We first performed standard genome-wide association studies (GWAS) of 21 traits in the Hutterites (Table 2.5). These studies identified one genome wide significant association ($p < 5 \times 10^{-8}$) with each of five of the 21 traits: low density lipoprotein level (LDL)-cholesterol, triglycerides, carotid artery intima media thickness (CIMT), left ventricular mass index (LVMI), and monocyte count. The results of all 21 GWAS are summarized in Table 2.7 and

Supplementary Figure 2.5a. Results for all variants for all GWAS are deposited in dbGaP (phs000185 - submission in progress).

2.3.2 Parent-of-Origin GWAS

We considered two possible mechanisms of POEs. In the first, the effect size of one parent's allele is close to zero and the effect size of the other parent's allele is significantly different from zero. For these cases, we performed a paternal only or maternal only GWAS. In other cases, the maternal and paternal alleles may both have effect sizes different from zero, but the effects are significantly different from each other or opposite in direction. To detect these types of POEs, we developed a model that tests for differences between parental effects (see Methods). This model is especially powerful to identify variants with parental effects in opposite directions.

2.3.3 Maternal and Paternal GWAS

Using the same phenotypes, genotypes, pedigree, and criteria for significance as in the standard GWAS, we tested for maternal and paternal effects on each trait by testing each parentally inherited allele with the trait of interest, similar to previous studies [56, 118, 38]. Variants were considered to have POEs if they had a p-value less than 5×10^{-8} in only one parent and were not significant in the standard GWAS (i.e., the LDL association on chromosome 19 and the triglycerides association chromosome 11 were not considered to have POEs; see Table 2.7). The most significant parent-of-origin associations are summarized in Table 2.1. All significant results of the parent-of-origin GWAS for all 21 phenotypes are included in Tables 2.10 and 2.12.

Overall, seven phenotypes had genome-wide significant parent-of-origin associations: four in the maternal only GWAS and three in the paternal only GWAS. Three cardiovascular disease (CVD)-associated phenotypes (age at menarche, CIMT, LVMI) and one lung function

Phenotype	rsid	chr:loc	Variant Location	Nearest Gene	MAF	N	Beta (SE)	Paternal GWAS p-value	Maternal GWAS p-value	Standard GWAS p-value
A. Maternal Associations										
Age at Menarche	rs7184983	16:56554709	Upstream (A/G)	<i>BBS2</i>	0.059	336	0.862 (0.154)	0.501	3.11E-08	6.75E-03
CIMT	rs4077567	2:216703202	Intronic (G/A)	<i>LINC00607*</i>	0.30	429	0.047 (0.008)	0.572	3.02E-08	4.21E-06
FEV ₁	rs9849387	3:77764243	Intergenic (A/G)	<i>ROBO2</i>	0.39	1029	-0.089 (0.015)	0.387	4.10E-09	4.38E-04
	rs6791779	3:74996505	Intergenic (C/G)	<i>MIR4444-1*</i>	0.24	879	-0.102 (0.021)	0.069	1.48E-08	0.0452
LVMI	rs574232282	1:41662388	Intronic (G/A)	<i>SCMH1</i>	0.018	537	0.239 (0.042)	0.552	1.39E-08	1.05E-03
B. Paternal Associations										
LDL	rs12024326	1:227146433	Intronic (A/G)	<i>ADCK3</i>	0.175	686	-0.295 (0.048)	8.06E-10	0.421	4.24E-05
	rs4843650	16:87683486	Intronic (A/G)	<i>JPH3</i>	0.448	621	0.211 (0.036)	6.57E-09	0.221	1.50E-04
SBP	rs1536182	13:46275415	Upstream (A/G)	<i>LINC01055*</i>	0.2	684	-0.028 (0.005)	1.53E-08	0.178	6.93E-04
Total cholesterol	rs113588203	1:228979156	Intergenic (G/T)	<i>RHOU</i>	0.099	703	-0.341 (0.060)	1.76E-08	0.074	8.08E-03

Table 2.1: **Phenotypes with significant single parent-of-origin associations.** *The most significant variant ($P < 5 \times 10^{-8}$) at each locus for the (A) maternal and (B) paternal associations associated with each phenotype is shown. *non-coding RNA genes

phenotype (forced expiratory volume in one second [FEV₁]) were associated with maternally-inherited alleles only.

When maternally inherited, the allele G at rs7184983 on chromosome 16 was associated with younger age of menarche ($P = 3.11 \times 10^{-8}$) (Figure 2.1). This SNP, rs7184983, is located upstream of the *BBS2* gene and is associated with increased expression of *OGFOD1* in transformed fibroblast cells and tibial nerve [40]. The maternally inherited G allele at rs4077567 on chromosome 2 was associated with decreased CIMT ($P = 3.02 \times 10^{-8}$) (Figure 2.6). This SNP is in the intron of a long intergenic noncoding gene, *LINC00607*, that is expressed in aorta, coronary, and tibial artery, all tissues potentially relevant to CIMT and atherosclerosis [40]. When maternally inherited, the allele G at rs574232282 in the intron of *SCMH1* on chromosome 1 was associated with increased LVMI ($P = 1.39 \times 10^{-8}$) (Supplementary Figure 2.7). *SCMH1* is expressed in aorta, coronary, and tibial artery [40]. *SCMH1* protein associates with the polycomb group multiprotein complexes required to maintain the transcriptionally repressive state of certain genes [40]. Lastly, maternally

inherited A allele at rs9849387 and maternally inherited C allele at rs6791779 on chromosome 3 were both associated with reduced FEV₁ ($P = 4.10 \times 10^{-9}$ and 1.48×10^{-8} , respectively) (Supplementary Figure 2.8). The nearest gene to rs9849387 is *ROBO2* (65kb, downstream), which is expressed in the lung as well as in brain, and ovary [40]. The nearest gene to rs6791779 is *MIR4444-1* (267kb) whose expression has not been characterized.

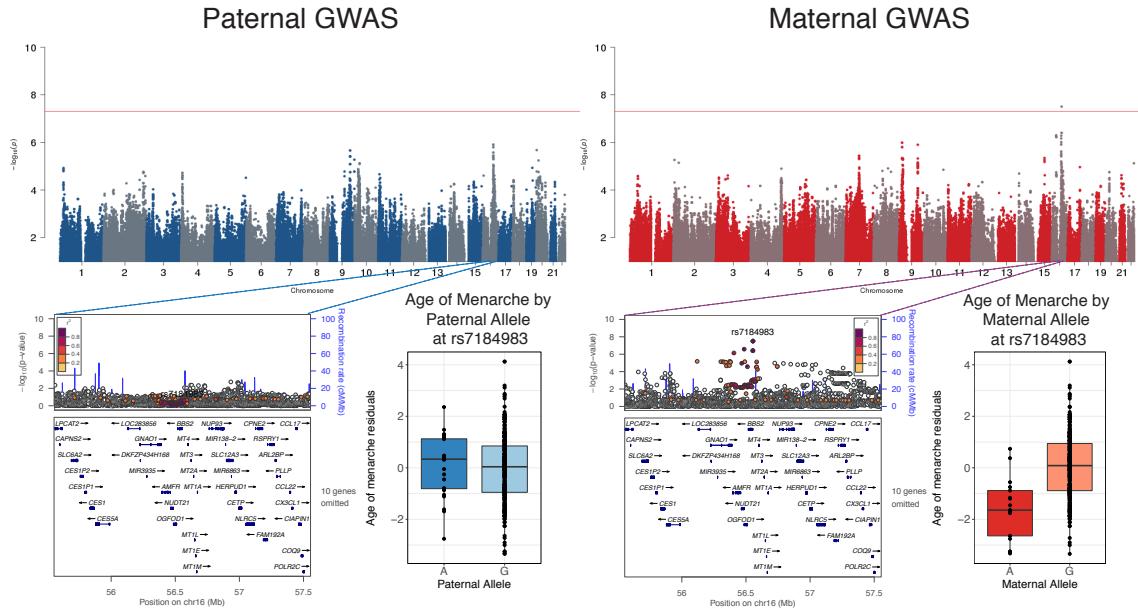


Figure 2.1: Maternal and Paternal GWAS results for Age of Menarche. The top panel shows the Manhattan plots from the paternal (left) and maternal (right) GWAS. LocusZoom plots for both GWAS are shown in the lower panel for the associated region in the GWAS. Boxplots show the distribution of age of menarche residuals (y-axes) by the corresponding maternal and paternal alleles at this SNP (x-axes). The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show $\pm 1.5 \times \text{IQR}$.

Three other CVD-related phenotypes (systolic blood pressure, LDL-C, and total cholesterol) had associations with paternally inherited alleles only. The paternally inherited A allele at rs12024326 on chromosome 1 was associated with lower LDL-cholesterol levels ($P = 8.06 \times 10^{-10}$) (Figure 2.2). rs12024326 is in the intron of gene *ADCK3*, and the same allele was associated with increased expression of *ADCK3* in whole blood, as well as decreased expression of a neighboring gene, *CDC42BPA* in brain (cerebellum), heart (left ventricle),

esophagus, and tibial artery [40]. When paternally inherited, the allele G at rs4843650 on chromosome 16 was associated with increased LDL-C and is located in the intron of *JPH3*, which is expressed predominantly in the brain [40]. A SNP on chromosome 13 (rs1536182) was associated with systolic blood pressure levels when it was inherited from the father (Figure 2.9). The paternally inherited A allele at this SNP was associated with decreased systolic blood pressure, as well as decreased expression of its closest gene, *LINC01055*, a long intergenic noncoding gene, in testis [40]. A paternally inherited allele at rs113588203 (G) on chromosome 1 was associated with lower total cholesterol ($P = 1.76 \times 10^{-8}$) (Figure 2.10). This SNP is intergenic between *RHOU* (96kb, downstream), which is expressed across multiple tissues, and *MIRR4454* (331kb), which is expressed in adipose, kidney and heart tissues [40].

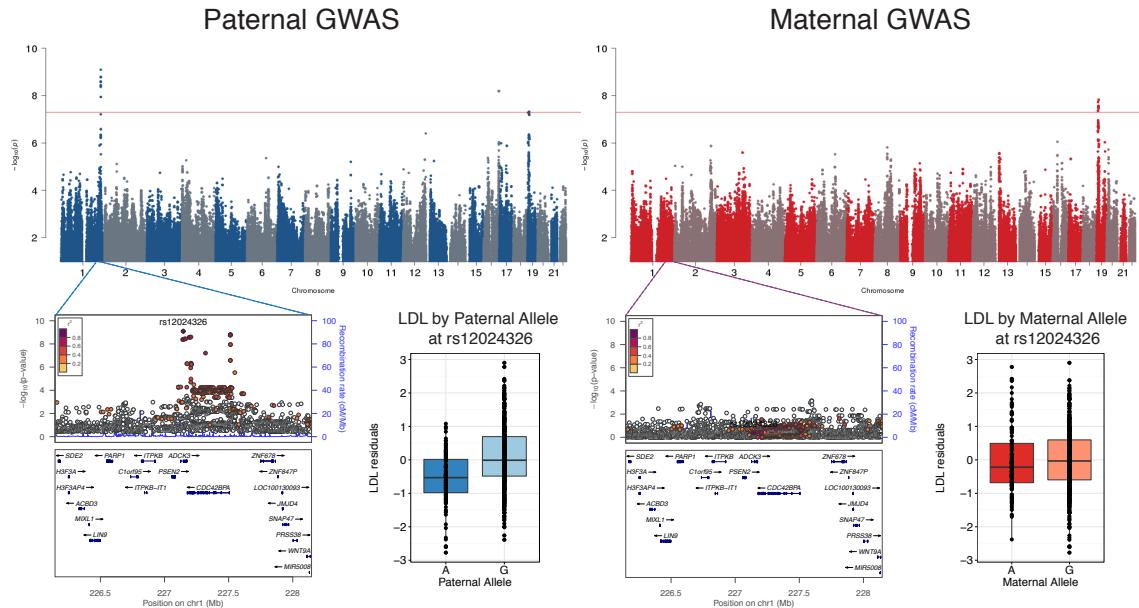


Figure 2.2: Maternal and Paternal GWAS results for LDL Cholesterol. The top panel shows the Manhattan plots from the paternal (left) and maternal (right) GWAS. LocusZoom plots for both GWAS are shown in the lower panel for the associated region in the GWAS. Boxplots show the distribution of LDL residuals (y-axes) by the corresponding maternal and paternal alleles at this SNP (x-axes). The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show $\pm 1.5 \times$ IQR.

Phenotype	rsid	chr:loc	Variant Location	Nearest Gene	MAF	$\beta_M - \beta_P$ (SE)	Opposite Effect GWAS	Paternal GWAS		Maternal GWAS		GWAS p-value
								P-value	Beta(SE)	P-value	Beta(SE)	
Age of menarche	rs12447191	16:62199299	Intergenic	<i>CDH8</i>	0.17	-0.654 (0.109)	5.27E-09	5.20E-06	0.391 (0.085)	1.85E-05 (0.085)	-0.368	0.868
BMI	rs77785972	5:97415767	Intergenic	<i>LINC01340</i> *	0.025	0.154 (0.025)	5.12E-10	5.84E-07	-0.094 (0.019)	1.58E-05 (0.019)	0.081	0.539
	rs17605739	6:22962798	Intronic	<i>RPI-209A6.1</i> *	0.17	0.053 (0.010)	3.01E-08	6.99E-05	-0.032 (0.008)	1.42E-06 (0.007)	0.034	0.156
Eosinophil count	rs2355879	1:18732860	Intergenic	<i>IGSF21</i>	0.14	0.091 (0.016)	1.69E-08	5.83E-08	-0.065 (0.012)	5.59E-04 (0.012)	0.043	0.253
FEV1	rs12714812	3:74813002	Intergenic	<i>CNTN3</i>	0.45	-0.119 (0.021)	4.52E-08	1.78E-03	0.052 (0.017)	6.35E-06 (0.016)	-0.073	0.958
LDL	rs1032596	16:86281537	Intronic	<i>LINC01081</i> *	0.30	-0.310 (0.056)	3.69E-08	1.05E-06	0.201 (0.041)	4.56E-04 (0.042)	-0.148	0.271
LVMI	rs16853098	2:168013281	Intronic	<i>XIRP2</i>	0.12	-0.091 (0.053)	4.18E-08	5.29E-06	0.064 (0.014)	2.04E-04 (0.013)	-0.048	0.926
Neutrophil count	rs14203084118:34371947	Intonic		<i>TPGS2</i>	0.042	-0.224 (0.041)	4.40E-08	2.25E-03	0.078 (0.025)	1.30E-07 (0.035)	-0.188	0.577
Triglycerides	rs7525463	1:218860879	Intronic	<i>MIR548F3</i> *	0.16	-0.401 (0.071)	2.51E-08	1.14E-03	0.195 (0.060)	5.52E-08 (0.049)	-0.267	0.028
Total cholesterol	rs7033776	9:36704465	Intergenic	<i>MELK</i>	0.41	0.230 (0.041)	4.12E-08	5.60E-08	-0.183 (0.034)	2.28E-03 (0.032)	0.099	0.067

Table 2.2: **Significant Opposite Parent-of-Origin Effect GWAS Associations.** The most significant variant at each locus for each phenotype is shown. $\beta_M - \beta_P$ represents difference in parental effect size. *non-coding RNA genes

2.3.4 GWAS for Differential Parent-of-Origin Effects

Because some imprinted regions include genes that have both maternal or paternal specific tissue expression, we next tested for such differential effects with these 21 phenotypes. In these analyses, we compared the effect and direction of the association between maternal and paternal alleles to identify variants that have different effects, including opposite effects, on the phenotype. Such loci would be completely hidden in standard GWAS in which paternally and maternally inherited alleles are combined. These opposite effect GWAS revealed 11 independent loci with opposite POEs for nine different traits, at least six of which are associated with CVD risk (Table 2.2, Figure 2.4).

A locus on chromosome 16, near the *CDH8* gene (128kb, upstream), was associated with opposite POEs with age of menarche (Figure 2.3). *CDH8* is highly expressed in the brain, as well as in the aorta artery and pituitary gland. Two loci on chromosomes 5 and 6 were associated with opposite POEs on body mass index (BMI) (Figure 2.4). The most significant variant on chromosome 5 (rs77785972) is near a long intergenic noncoding gene, *LINC01340* (409kb, downstream), whose expression has not been well characterized.

The SNP on chromosome 6 (rs17605739) is also in a long intergenic noncoding gene, *RP1-209A6.1*, which is expressed in low levels in the tibial artery, bladder, spleen, lung, pituitary gland, as well as testis.

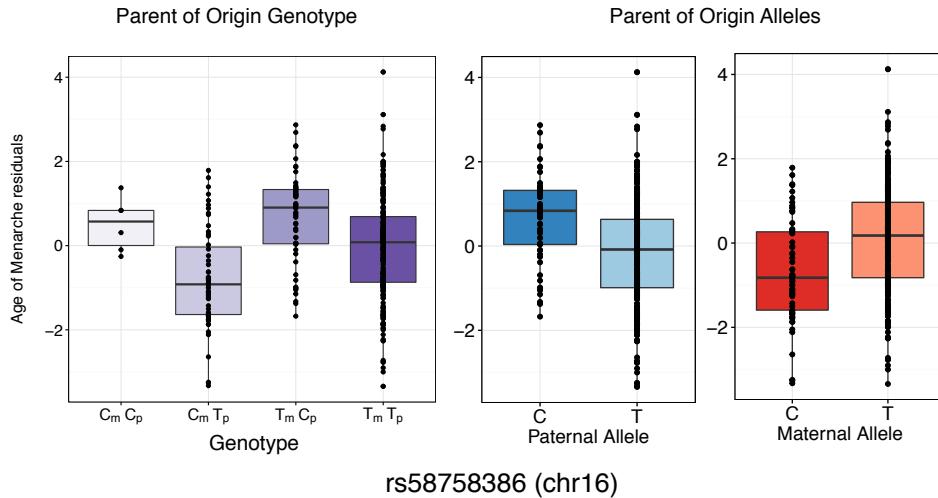


Figure 2.3: Opposite Effect Parent-of-Origin GWAS Result for Age of Menarche. Box plots of age of menarche residuals (y-axes) are shown for each of the four genotypes (left panel; x-axis), and for paternal (center panel; x-axis) and maternal (right panel; x-axis) alleles. The maternal C allele is associated with decreased and maternal T allele with increased age of menarche. The paternal C allele is associated with increased and the paternal T allele with decreased age of menarche. The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show +/-1.5 x IQR.

A SNP on chromosome 16 (rs1032596) was associated with opposite POEs on LDL-cholesterol (Figure 2.12). This SNP lies in the intron of another long noncoding RNA gene, *LINC01081*, which has been suggested to be imprinted because its downstream genes have also been shown to have parent- and tissue-specific activity [105]. A region on chromosome 2 has opposite effects associated with LVMI (Figure 2.13). The associated SNPs are in the intron of *XIRP2*, a cardiomyopathy associated protein that is expressed in skeletal muscle and heart left ventricle, suggesting that this gene could play a role in determining left ventricular mass [110, 81, 40]. In addition, the most significant SNP at this region, rs17616252 (and multiple SNPs in LD) is a strong eQTL ($P = 1.8 \times 10^{-13}$) for the gene *XIRP2* in skeletal

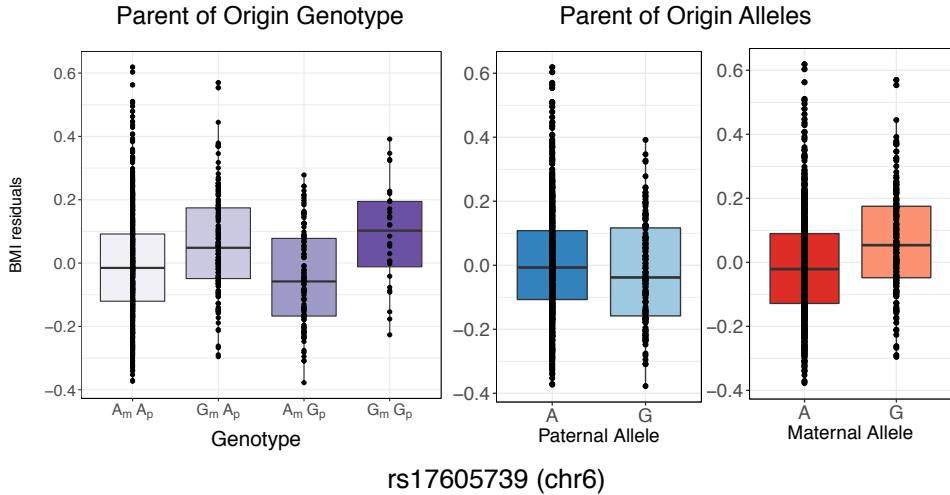


Figure 2.4: Opposite Effect Parent-of-Origin GWAS Result for BMI. Box plots of two significant loci plot BMI residuals (y-axes) for each of the four genotypes (left panel; x-axis), and for paternal (center panel; x-axis) and maternal (right panel; x-axis) alleles. For the (A) SNP on chromosome 5 the maternal A allele is associated with decreased and maternal G allele with increased BMI. The paternal A allele is associated with increased and the paternal G allele with decreased BMI. For the (B) SNP on chromosome 6 the maternal A allele is associated with decreased and maternal G allele with increased BMI. The paternal A allele is associated with increased and the paternal G allele with decreased BMI. The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show $\pm 1.5 \times \text{IQR}$.

muscle, *XIRP2-AS1* in testis, and *B3GALT1* in transformed fibroblast cells [40]. Four variants in a region on chromosome 1 in a microRNA gene, *MIR548F3*, were associated with opposite POEs on triglyceride levels (Figure 2.14). The expression of *MIR548F3* has not been characterized. SNP rs7033776 near *MELK* (27kb, downstream) on chromosome 9 was associated with opposite effects on total cholesterol (Figure 2.15). *MELK* is expressed in the colon and esophagus in addition to transformed lymphocytes and fibroblasts [40].

Nine linked variants on chromosome 1 were associated with opposite POEs of blood eosinophil count (Figure 2.16). These variants are near the gene *IGSF21* (27kb, downstream) which is a member of the immunoglobulin superfamily and likely acts as a receptor in immune response pathways [86]. A variant on chromosome 3, rs12714812, was associated with opposite POEs for FEV₁ (Figure 2.17). This variant has been shown to regulate the

expression of a gene *CNTN3* (45kb, upstream) in heart and brain [40]. Studies in mice have suggested that this gene is imprinted and maternally expressed in the murine placenta [16]. Variant rs142030841 in the intron of the gene *TPGS2* on chromosome 18 has opposite POEs with neutrophil levels (Figure 2.18). This SNP is an expression quantitative trait locus (eQTL) for the noncoding RNA gene *RP11-95O2.5* in skin, testis, breast, thyroid and adipose tissue, for *CELF4* in tibial nerve and lung, and for *TPGS2* in tibial artery and transformed fibroblast cells [40].

2.3.5 Parent-of-Origin Effects on Gene Expression

To determine if any of the associated variants also showed POEs on gene expression in the Hutterites, we used RNA-seq gene expression data from lymphoblastoid cell lines (LCLs) collected from 430 of the individuals in the GWAS sample. We first tested for association of maternal and paternal variants with genes detected as expressed in the LCLs and whose transcript start site was within 1Mb of each associated SNP. There were no significant associations after multiple testing correction, similar to a previous study [14]. However, because we considered this to be exploratory analyses, we show results for the five most significant parent-of-origin eQTLs (Table 2.3). We next used the opposite effect model for each SNP in Table 2.2 and expression of all genes that were detected as expressed in LCLs and whose transcript start site was within 1Mb of the associated SNP. This resulted in 57 tests (1 SNP for each of 8 phenotypes, and 57 genes). The five most significant opposite effect eQTLs, none of which passed the Bonferroni threshold of 8.77×10^{-4} , are shown in Table 2.4. The most significant opposite effect eQTL was for *POLR1E* expression with the SNP on chromosome 9 (rs7033776) that was associated with total cholesterol (opposite effect eQTL $P = 9.86 \times 10^{-4}$) (Figure 2.19). *POLR1E* is involved in the purine metabolism pathway as well as DNA-directed polymerase activity. The same SNP, rs7033776, had modest opposite effects with the expression of three other genes in the region (*PAX5*, *FBXO10*, and

Phenotype	Sample Size	rsid	chr:loc	Gene	Beta (SE)	Maternal eQTL p-value	Paternal eQTL p-value
A. Maternal Associations							
CIMT	334	rs4077567	1:216703202	<i>ABCA12</i>	0.039 (0.017)	0.0214	0.0153
Age at menarche	336	rs7184983	16:56554709	<i>POLR2C</i>	-0.085 (0.039)	0.0291	0.793
Age at menarche	336	rs7184983	16:56554709	<i>SLC12A3</i>	-0.064 (0.031)	0.0377	0.228
CIMT	334	rs4077567	1:216703202	<i>RPL37A</i>	0.030 (0.016)	0.0572	0.590
LVM	457	rs74232282	1:41662388	<i>SMAP2</i>	1.40 (0.159)	0.0582	0.112
B. Paternal Associations							
Total cholesterol	352	rs113588203	1:228979165	<i>HIST3H2A</i>	0.560 (0.308)	0.881	0.0685
Total cholesterol	352	rs113588203	1:228979165	<i>SPHAR</i>	0.073 (0.047)	0.601	0.120
LDL	352	rs1110603	16:87687317	<i>MAP1LC3B</i>	-0.024 (0.015)	0.435	0.125
LDL	352	rs1110603	16:87687317	<i>FBXO31</i>	-0.027 (0.018)	0.156	0.136
Total cholesterol	357	rs113588203	1:228979165	<i>RAB4A</i>	-0.039 (0.028)	0.616	0.159

Table 2.3: **Parent-of-Origin eQTLs in LCLs.** The most significant SNP for each phenotype (Table 2.1) was tested for association with gene expression for genes with TSS within 1Mb of the SNP. The effect sizes correspond to the maternal (A) or paternal (B) effect sizes.

FRMPD1), a signature consistent with an imprinted region. Another SNP with opposite POEs on LVMI, rs16853098, was an opposite effect eQTL for *STK39*, a gene that has been previously associated with hypertension [111].

2.4 Discussion

In this study, we introduced a novel statistical method that allows assessment of standard GWAS signals along with measures of differential POEs on common quantitative phenotypes. Similar to previous parent-of-origin studies of fewer phenotypes [56, 14, 38], we tested for associations of maternally- or paternally-derived alleles with each phenotype. We then extended this method to identify variants for which maternally- and paternally-derived alle-

Phenotype	Sample Size	rsid	chr:loc	Gene	$\beta_M - \beta_P$ (SE)	Opposite Effect p-value
Total cholesterol	381	rs7033776	9:36704465	<i>POLR1E</i>	0.0603 (0.399)	9.86E-04
Total cholesterol	381	rs7033776	9:36704465	<i>PAX5</i>	0.0608 (0.0253)	0.0162
Total cholesterol	381	rs7033776	9:36704465	<i>FBXO10</i>	0.0789 (0.0337)	0.019
LVMI	355	rs16853098	2:168013281	<i>STK39</i>	-0.238 (0.124)	0.055
Total cholesterol	381	rs7033776	9:36704465	<i>FRMPD1</i>	0.185 (0.0988)	0.060

Table 2.4: **Opposite Parent-of-Origin eQTLs in LCLs.** The most significant SNP for each phenotype (Table 2.2) was tested for opposite effect eQTLs with genes with TSS within 1Mb of the SNP. The effect size corresponds to the difference in maternal and paternal effect sizes.

les have different, including opposite, effects on phenotypic values. The focus on 21 common disease-associated phenotypes in a single large pedigree allowed us to broadly survey physiological effects of putative imprinted regions and the candidate genes at each associated locus. In contrast to previous studies, our new model can identify variants with opposite POEs that would be missed in traditional GWAS (Table 2.2).

Our studies of >1,000 Hutterites who are related to each other in a single pedigree allowed us to detect POEs, even when few genome-wide significant associations were detected in standard GWAS of the same phenotypes. Our method revealed parent-of-origin specific genome-wide significant associations for seven of the 21 phenotypes examined, with maternally-inherited alleles associated with four phenotypes, paternally-inherited alleles with three phenotypes (Table 2.1), and opposite parent-of-origin alleles with nine phenotypes, of which five also showed single POEs at different loci (Table 2.2). Overall, 11 of the 21 phenotypes examined showed genome-wide significant evidence of POEs with alleles at one or more loci. In contrast, standard GWAS of these same phenotypes and using the same markers in these same individuals revealed genome-wide significant association for only five traits.

It is notable that four of the nine significant opposite POEs (one each with LDL-C and triglycerides, and two with BMI) lie in or near long intergenic non-coding RNA genes (lincRNAs). LincRNAs are a feature of imprinted regions [90], where they can silence the expression of genes on the opposite chromosome [13, 88]. One of the variants, rs1032596, with an opposite parent-of-origin effect on LDL-C is located in the *LINC01081* gene. This noncoding RNA, along with *LINC01082*, regulates the *FOXF1* enhancer resulting in *FOXF1* parent- and tissue-specific activity[105] providing experimental support for tissue specific expression, a feature of imprinted regions.

Another variant with POEs in our study has been suggested to be imprinted in previously published work. The variant associated with opposite POEs for FEV₁ is an eQTL for the gene *CNTN3*. *CNTN3* was shown to have exclusive maternal allele-specific expression in murine placentas[16], although this finding may have been due to contaminating maternal cells [85, 92].

Other regions associated with POEs harbor genes involved in transcriptional repression (e.g., *SCMH1* with LVMI on chromosome 1) or the associated SNPs are reported as eQTLs in GTEx with expression in tissues relevant to the phenotype under investigation (e.g., the LVMI-associated SNPs are eQTLs for *XIRP2*, which is expressed in skeletal muscle and heart left ventricle) [40]. Overall, these patterns of expression provide additional support that the parent-of-origin associations in our study are flagging imprinted regions or regions involved in the regulation of gene expression. Finally, we used gene expression in LCLs from the Hutterites to directly test for parent-of-origin eQTLs among SNPs associated with phenotypes in the parent-of-origin GWAS. Although none of the parent-of-origin eQTLs met criteria for significance after correcting for multiple testing, the SNP on chromosome 9 with opposite POEs on total cholesterol levels was borderline significant as an opposite parent-of-origin eQTL for *POLR1E*, and possible for three other genes at the same locus (*PAX5*, *FBXO10*, and *FRMPD1*). The presence of multiple genes with potential parent-

of-origin expression patterns is further supportive of an imprinted locus. The availability of gene expression only in LCLs from the Hutterites limits the inferences we can draw about effects on expression because imprinted regions are often tissue-specific and sometimes developmentally regulated [90, 35]. Despite this limitation, the fact that many of the SNPs associated with POEs on phenotypes are themselves eQTLs in relevant tissues (GTEX) and some are suggestive of having POEs on expression in LCLs from the Hutterites is generally supportive of the suggestion that some of the regions identified in this study are imprinted or have network interactions with imprinted genes[21] in humans. Additionally, our data suggest that loci with POEs influence a broad spectrum of quantitative phenotypes that are themselves risk factors for common diseases.

In particular, the discovery of POEs for eight traits that are associated with cardiovascular disease risk is intriguing. These include metabolic phenotypes, such as BMI, total cholesterol, triglycerides, LDL, and age of menarche, that have indirect effects on cardiac health, as well as LVMI and CIMT, which more directly reflect cardiac health. Some of these phenotypes showed associations with paternally inherited alleles only (systolic blood pressure, LDL-C, total cholesterol), maternally inherited alleles only (LVMI, CIMT, and age at menarche), and/or with opposite effect variants (BMI, LDL-C, triglycerides, total cholesterol, LVMI, age at menarche). It has been suggested that genomic imprinting evolved in the mammalian lineage as a way to regulate maternally and paternally expressed genes in the placenta during pregnancy and modulate metabolic functions related to growth, where the parental interests may be in conflict — paternal alleles favoring growth of the fetus at the expense of the mother while maternal alleles favor restricting resources to the fetus to ensure preservation of her nutritional needs [41, 13, 88]. Our data show some effects that are consistent with this theory. For example, three independent paternally inherited alleles on chromosome 1 are associated with increased LDL-C (Fig. 2) and total cholesterol (Figure); a paternal allele on chromosome 13 is also associated with increased systolic blood pressure

(Figure). However, it is not always possible to interpret our results in light of this model, such as the association of maternal allele on chromosome 2 with decreased CIMT (Figure 2.7), or the maternal allele on chromosome 16 associated with decreased age of menarche (Figure 2.1), which confers increased cardiovascular risk [18]. However, because many of the traits associated with POEs in this study were measured in adults, and none were measured in neonates, we are likely observing the downstream effects of processes that occurred in utero. Nonetheless, this kinship theory, or parent-conflict hypothesis, could account for the enrichment of parent-of-origin associations, particularly those with opposite effects, among metabolic and CVD-associated traits [90].

Finally, we note that the parent-of-origin GWAS for 21 phenotypes in the Hutterites revealed overall twice as many genome-wide significant loci compared to standard GWAS of the same phenotypes in the same individuals, suggesting that variation at imprinted loci may represent some of the "missing heritability" of these phenotypes and potentially for the disease for which they confer risk. This idea is consistent with observations in both mice and humans [58]. POEs in mice contribute disproportionately to the heritability of 97 traits, including those related to total cholesterol, weight, HDL, and triglycerides [76]. Exactly how much loci with POEs in humans contribute to phenotypic variation and disease risk overall remains to be determined, but our study provides compelling evidence that it is likely to be significant for many important traits.

2.5 Methods

2.5.1 Sample Composition

The individuals in this study have participated in one or more of our studies on the genetics of complex traits in the Hutterites [26, 114, 1]. The more than 1,500 Hutterites in our study are related to each other in a 13-generation pedigree including 3,671 individuals.

2.5.2 Genotype Data

Variants detected in the whole genome sequences of 98 Hutterites were previously imputed to an additional 1,317 individuals using PRIMAL, a high-accuracy pedigree based imputation method [63]. PRIMAL was used to phase alleles and assign parent of origin for 83% of about 12 million autosomal SNPs. For these studies, we selected SNPs that had a MAF 1% and genotype call rate 85%. This yielded 5,891,982 autosomal SNPs. Parent-of-origin allele call rates differed among individuals and between phenotypes (Table 2.5).

2.5.3 Phenotype Data

We included 21 quantitative phenotypes that were previously measured in the Hutterites. Descriptions for each phenotype, as well as exclusion criteria, transformations, and covariates used with each phenotype in the GWAS, are available in the Supplementary Methods (Table 2.5).

Descriptions for 18 of the 21 phenotypes can be found in Cusanovich et al [26]. The remaining three are described here. Height was measured in cm on a stadiometer with shoes removed. BMI was calculated using weight (kg, measured on scale) divided by height (m) squared. Age at menarche was collected retrospectively by interview.

2.5.4 GWAS

We used a linear mixed model as implemented in GEMMA to test for genome wide association with 21 phenotypes using an additive model. We corrected for relatedness, as well as relevant covariates (Table 2.5).

2.5.5 Maternal and Paternal GWAS

To evaluated the evidence for POEs, we tested maternal and paternal alleles separately with each phenotype, comparing phenotypic differences between the maternally inherited alleles and between the paternally inherited alleles. We used a linear mixed model as implemented in GEMMA, which allows us to correct for relatedness as a random effect, as well as sex, age, and other covariates as fixed effects [117].The linear mixed model for the parent-of-origin GWAS for testing maternal alleles and paternal alleles is shown in Equation 2.1 and Equation 2.2, respectively.

$$Y = W\alpha + X_M\beta_M + g + \epsilon \quad (2.1)$$

$$Y = W\alpha + X_P\beta_P + g + \epsilon \quad (2.2)$$

n is the number of individuals, Y is an $n \times 1$ vector of quantitative traits, W is an $n \times c$ matrix of covariates (fixed effects) including intercept 1. α is a $c \times 1$ vector of covariate coefficients. X_M is an $n \times 1$ vector of maternal alleles, and X_P an $n \times 1$ vector of paternal alleles. β_M and β_P are the effect sizes of maternal and paternal alleles, respectively. g is a vector of genetic effects with $g \sim N(0, A(\sigma_g)^2)$ where A is the genetic relatedness matrix; ϵ is a vector of non-genetic effects with $\epsilon \sim N(0, I(\sigma_e)^2)$.

2.5.6 Differential Effect GWAS (PO-GWAS)

To test for a difference in the same allele inherited from each parent, including opposite effects, we re-parameterized the test model (Equation 2.3) from Garg et al [38]. The null model (Equation 2.4) is a standard GWAS model, ignoring parent of origin of alleles. The test model (Equation 2.3) is more significant when maternal and paternal alleles have differential effects on gene expression.

$$Y = W\alpha + X_M\beta_M + X_P\beta_P + g + \epsilon \quad (2.3)$$

$$Y = W\alpha + X_{MP}\beta_{MP} + g + \epsilon \quad (2.4)$$

This new model allows us to measure the difference in parental effect of the same allele when the genotype is a covariate in Equation 2.5.

$$Y = W\alpha + \frac{X_M - X_P}{2}(\beta_M - \beta_P) + X_{MP}\frac{(\beta_P + \beta_M)}{2} + g + \epsilon \quad (2.5)$$

X_{MP} is a $n \times 1$ vector of genotypes with possible values [0,1,2], equivalent to $X_P + X_M \cdot (\beta_M - \beta_P)$ is the difference in parental effect size. If the difference in parental effect size is large and significantly different from 0 it suggests a parent-of-origin effect exists at this variant. $((X_M - X_P))/2$ is a $n \times 1$ vector of genotypes with possible values [-1,0,1]. $((\beta_P + \beta_M))/2$ is the average parental effect size that is captured in normal GWAS using genotypes. The average genotypes are added in as a covariate, with the average parental effect size the corresponding covariate coefficient. This differential effect GWAS was implemented in GEMMA using BIMBAM format to use average genotype values [99].

2.5.7 Parent-of-Origin eQTL studies

RNA-seq data from LCLs were available from a previous study in the Hutterites [26]. For this study, sequencing reads were reprocessed as follows. Reads were trimmed for adaptors using Cutadapt (with reads <5 bp discarded) then remapped to hg19 using STAR indexed with gencode version 19 gene annotations [29, 72]. To remove mapping bias, reads were processed using the WASP mapping pipeline [107]. Gene counts were collected using HTSeq-count [6]. VerifyBamID was used to identify sample swaps to include individuals that were previously excluded [51]. Genes mapping to the X and Y chromosome were removed; genes with a

Counts Per Million (CPM) value of 1 (expressed with less than 20 counts in the sample with lowest sequencing depth) were also removed. The R/Bioconductor package edgeR was used to convert the RNA-seq counts to log2 TMM-normalized CPM values [96, 95]. Technical covariates that showed a significant association with any of the top principal components were regressed out (RNA Integrity Number and RNA concentration).

2.5.8 Maternal and Paternal Parent-of-Origin eQTL

LCL RNA-seq data was used to test the single parent model for the most significant SNP from the maternal or paternal only GWAS for each phenotype. We selected all genes detected as expressed in the LCLs and residing within 1Mb of each most significant associated SNP. A summary of the SNPs and genes tested are in Table 2.8.

2.5.9 Differential Parent-of-Origin eQTL

LCL RNA-seq data was used to test the opposite effect model for the most significant SNP in each region that was associated with a phenotype in the parent-of-origin opposite effects GWAS. We selected all genes detected as expressed in the LCLs and residing within 1Mb of each associated SNP. A summary of the SNPs and genes tested are in Table 2.9.

2.6 Supplementary Information

2.6.1 Supplementary Figures

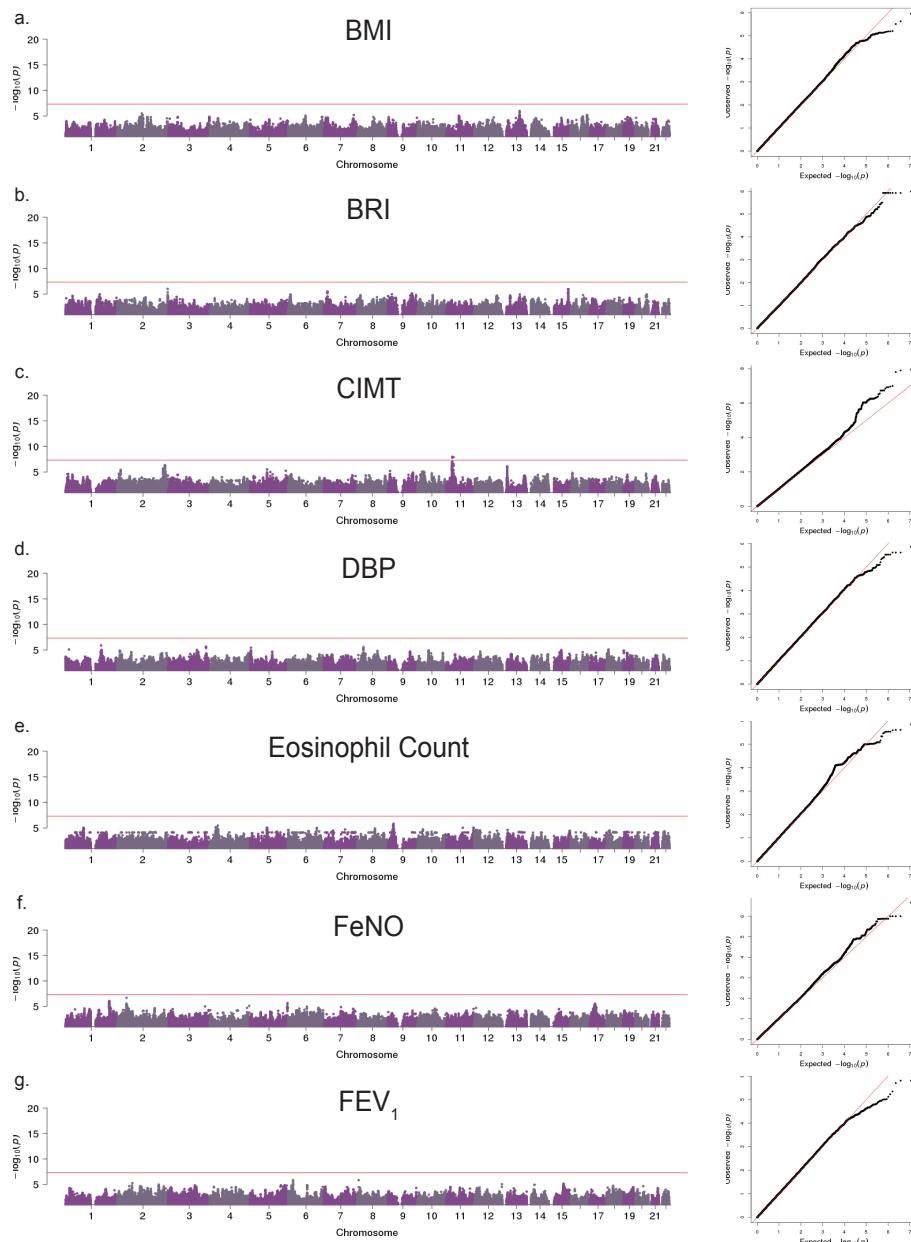


Figure 2.5a: Manhattan and QQ Plots from Standard GWAS of 21 Quantitative Phenotypes.

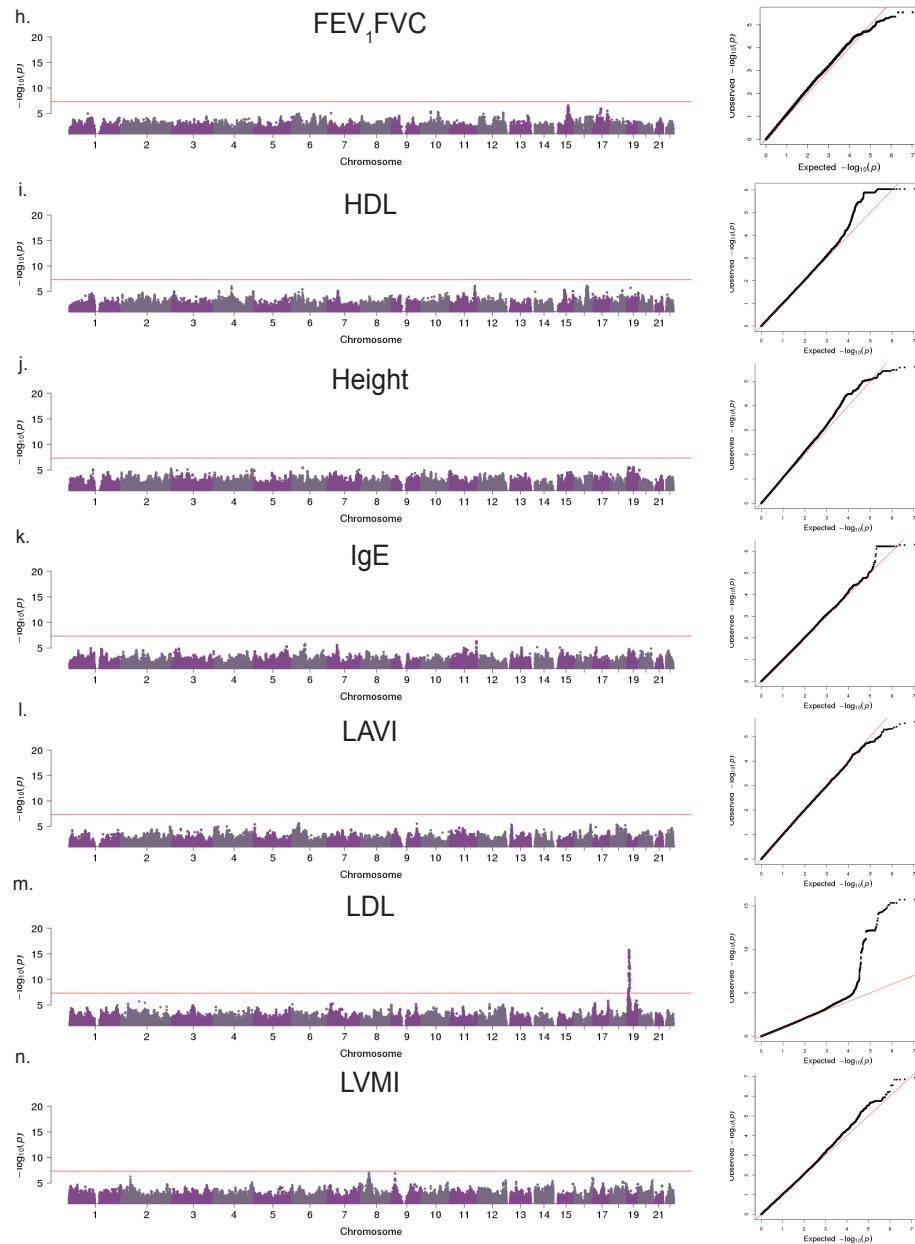


Figure 2.5b: Manhattan and QQ Plots from Standard GWAS of 21 Quantitative Phenotypes (Continued).

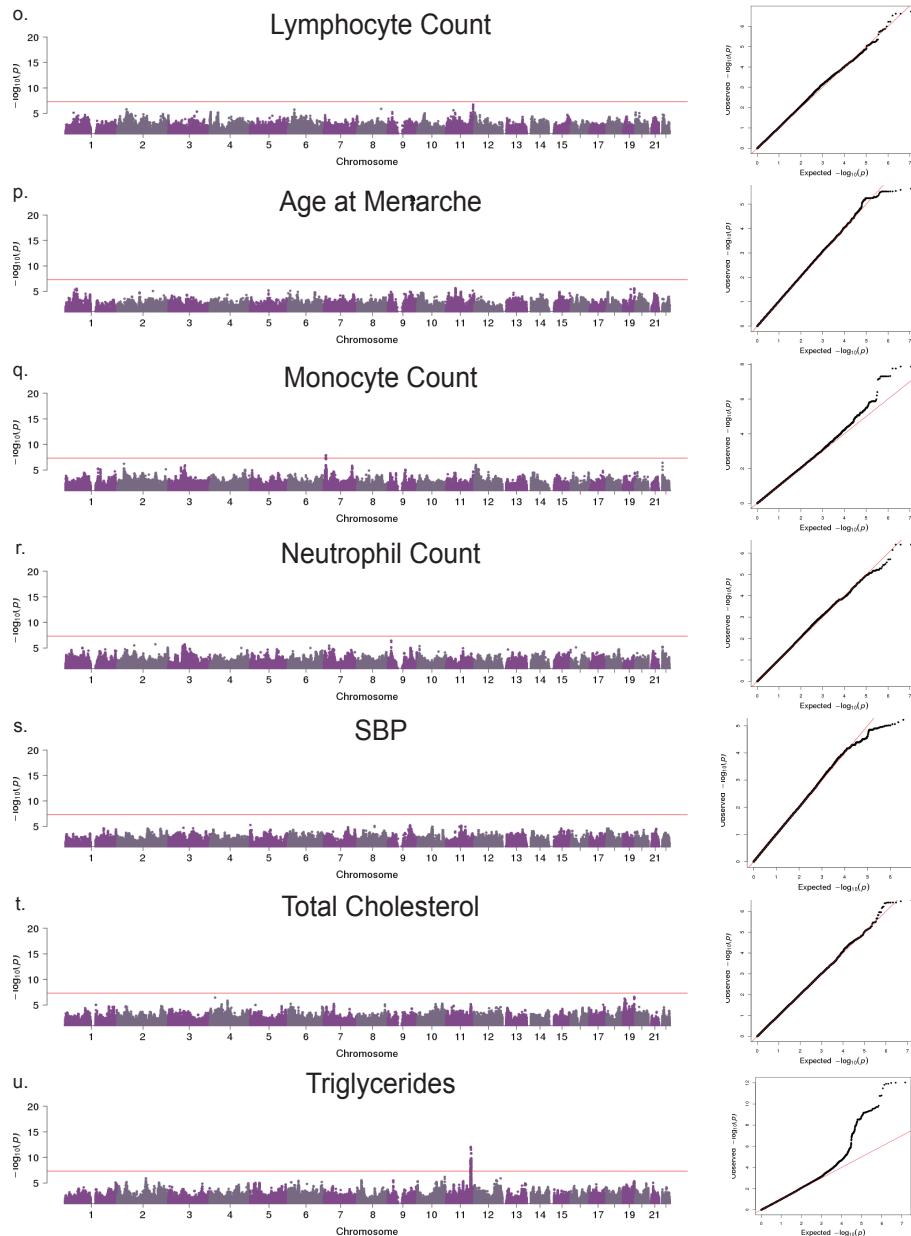


Figure 2.5c: Manhattan and QQ Plots from Standard GWAS of 21 Quantitative Phenotypes (Continued).

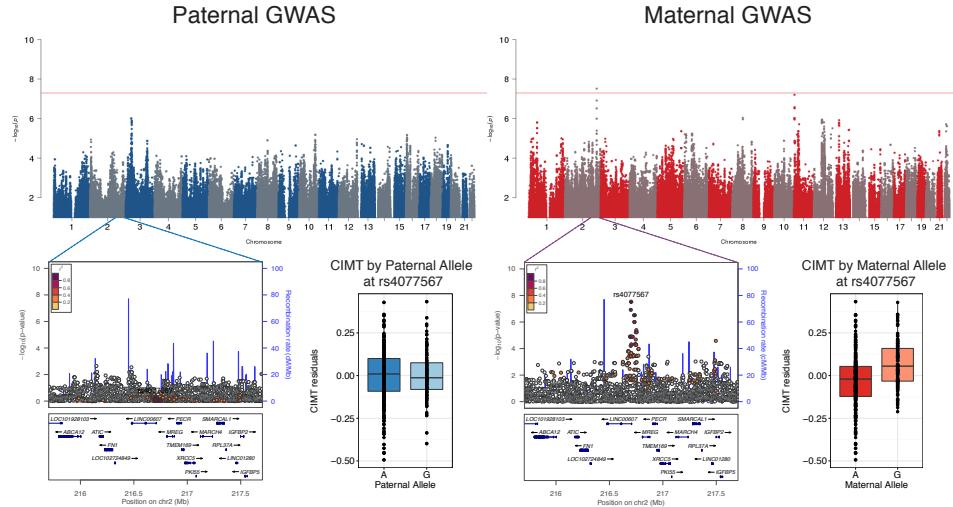


Figure 2.6: Maternal and Paternal GWAS results for CIMT. The top panel shows the Manhattan plots from the paternal (left) and maternal (right) GWAS. LocusZoom plots are shown in the lower panel for the associated region in the GWAS. Boxplots show the distribution of CIMT residuals (the residuals correspond to the inverse of raw CIMT values) (y-axes) by the corresponding maternal and paternal alleles at this SNP (x-axes). The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show $\pm 1.5 \times$ IQR.

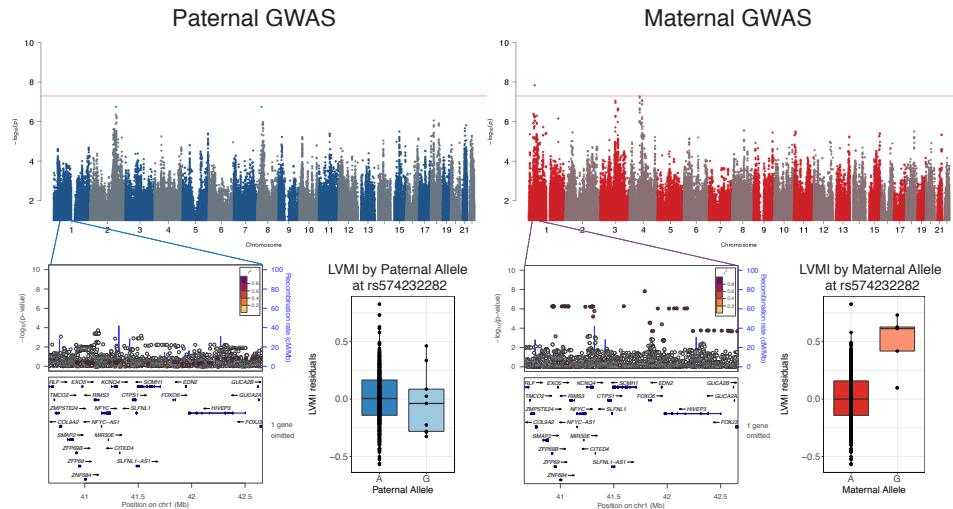


Figure 2.7: Maternal and Paternal GWAS results for LVMI. The top panel shows the Manhattan plots from the paternal (left) and maternal (right) GWAS. LocusZoom plots are shown in the lower panel for the associated region in the GWAS. Boxplots show the distribution of LVMI residuals (the residuals correspond to the inverse of raw CIMT values) (y-axes) by the corresponding maternal and paternal alleles at this SNP (x-axes). The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show $\pm 1.5 \times$ IQR.

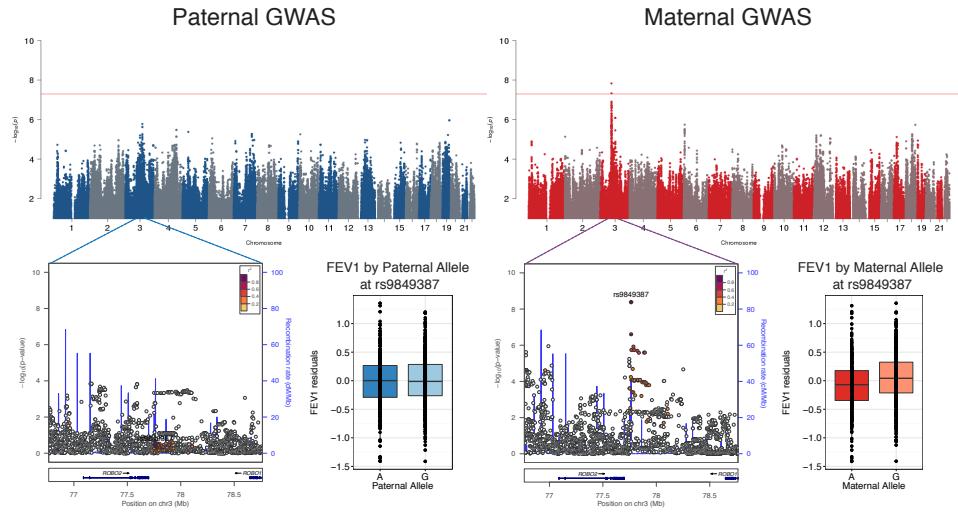


Figure 2.8: Maternal and Paternal GWAS results for FEV_1 . The top panel shows the Manhattan plots from the paternal (left) and maternal (right) GWAS. LocusZoom plots for both GWAS are shown in the lower panel for the associated region in the GWAS. Boxplots show the distribution of FEV_1 residuals (y-axes) by the corresponding maternal and paternal alleles at this SNP (x-axes). The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show $1.5 \times \text{IQR}$.

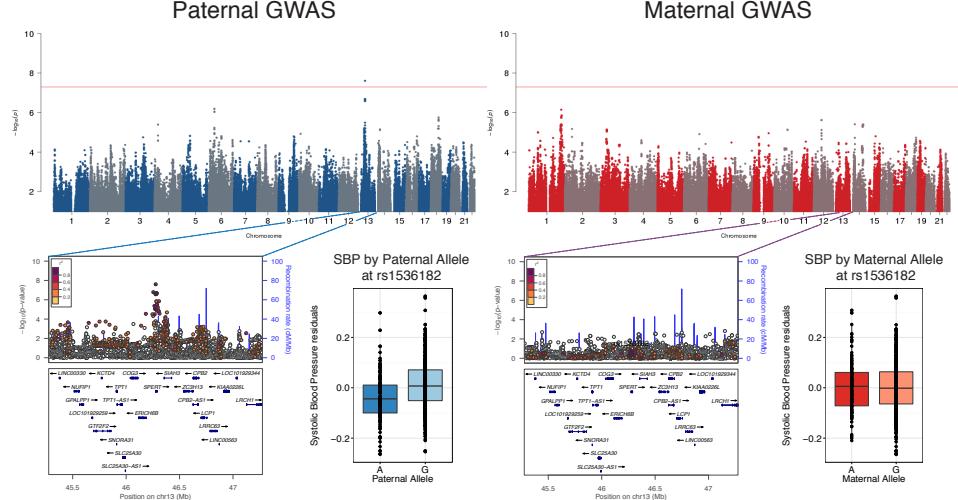


Figure 2.9: Maternal and Paternal GWAS results for Systolic Blood Pressure. The top panel shows the Manhattan plots from the paternal (left) and maternal (right) GWAS. LocusZoom plots for both GWAS are shown in the lower panel for the associated region in the GWAS. Boxplots show the distribution of systolic blood pressure residuals (y-axes) by the corresponding maternal and paternal alleles at this SNP (x-axes). The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show $1.5 \times \text{IQR}$.

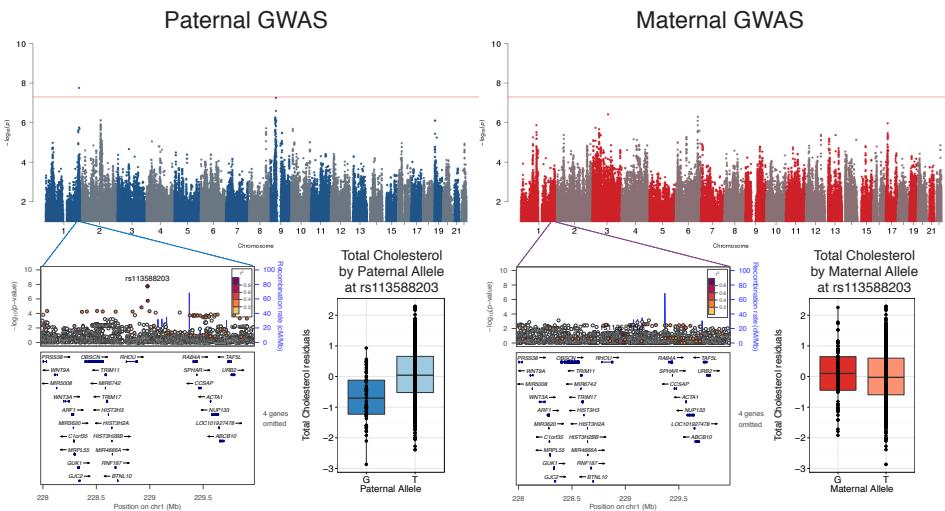


Figure 2.10: Maternal and Paternal GWAS results for Total Cholesterol. The top panel shows the Manhattan plots from the paternal (left) and maternal (right) GWAS. LocusZoom plots for both GWAS are shown in the lower panel for the associated region in the GWAS. Boxplots show the distribution of total cholesterol residuals (y-axes) by the corresponding maternal and paternal alleles at this SNP (x-axes). The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show 1.5 x IQR.

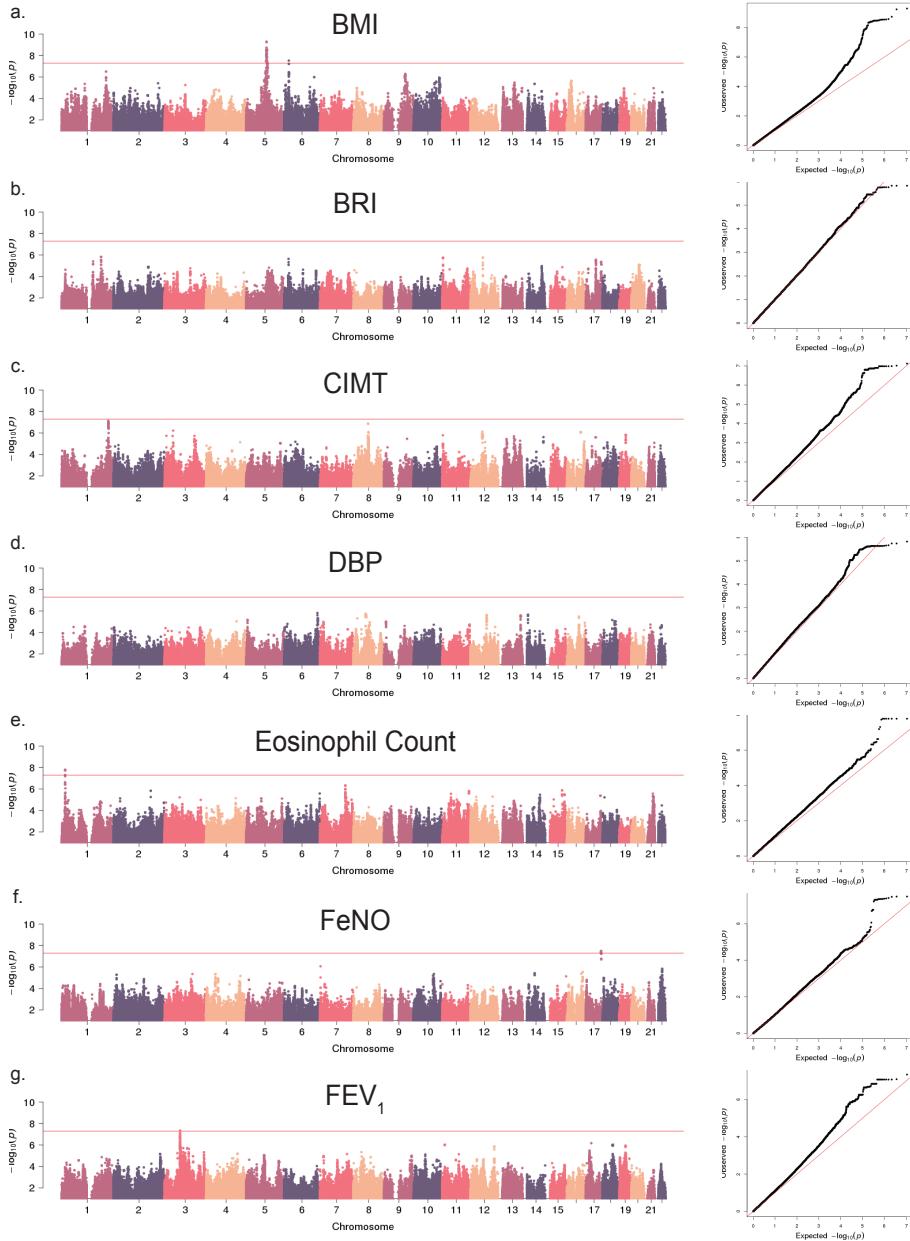


Figure 2.11: Manhattan and QQ Plots from Differential Effect GWAS of 21 Quantitative Phenotypes .

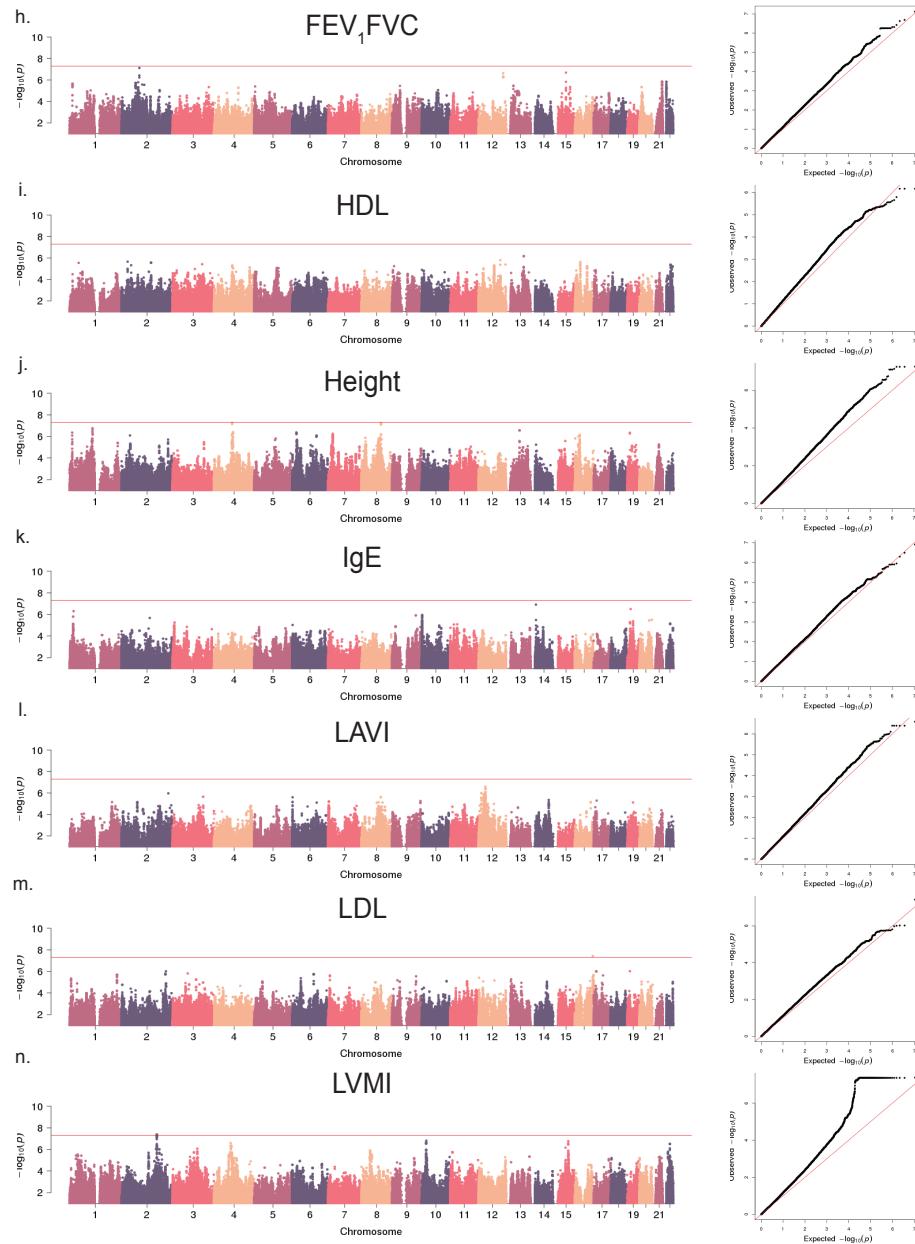


Figure 2.11a: Manhattan and QQ Plots from Differential Effect GWAS of 21 Quantitative Phenotypes (Continued).

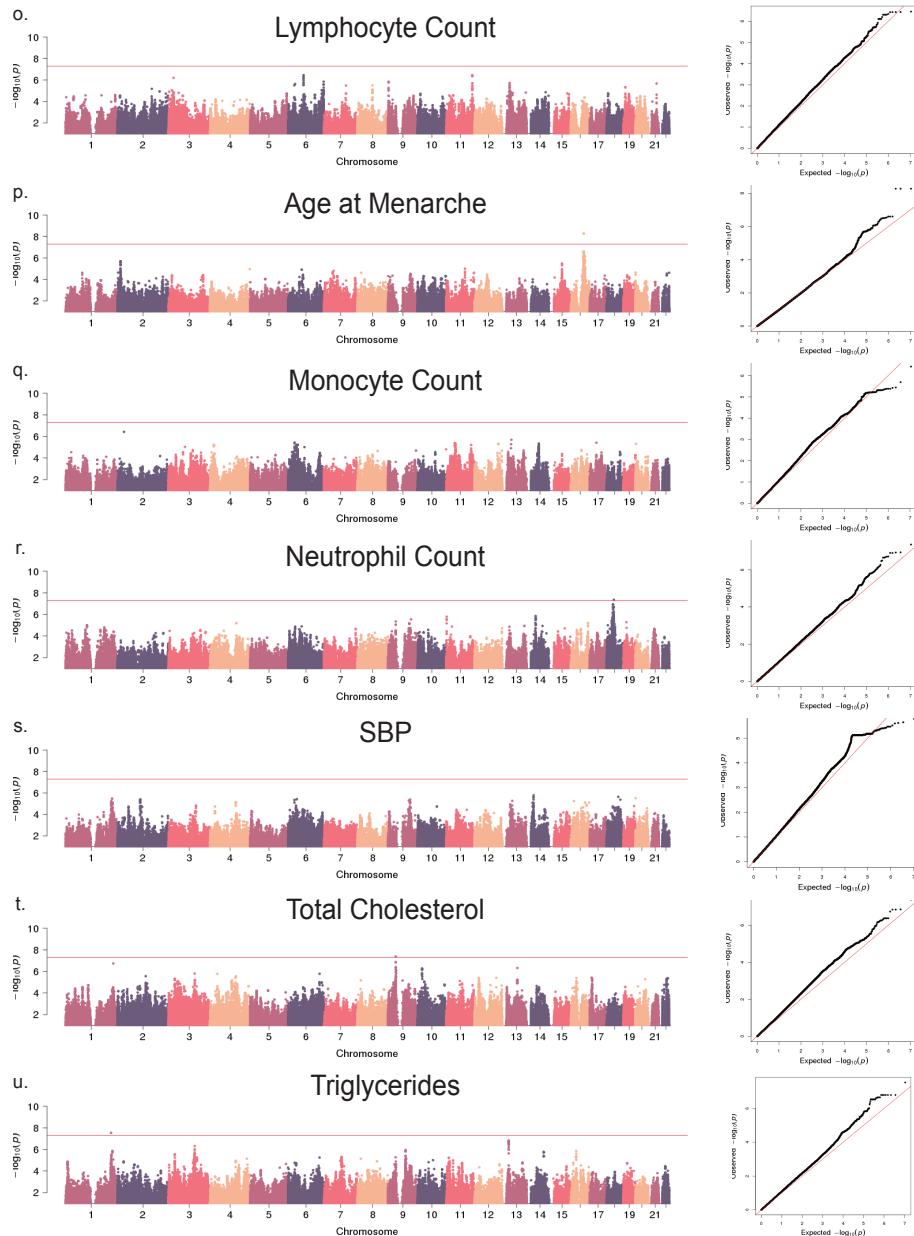


Figure 2.11b: Manhattan and QQ Plots from Differential Effect GWAS of 21 Quantitative Phenotypes (Continued).

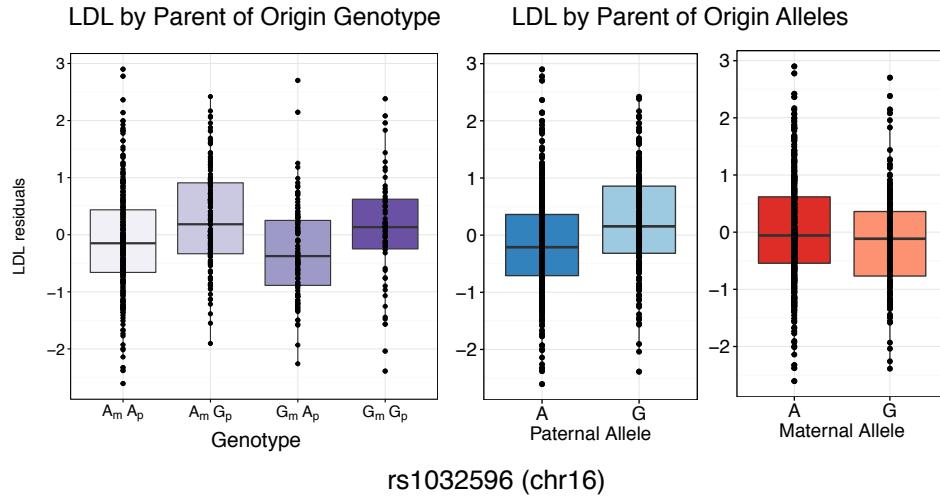


Figure 2.12: Opposite Effect Parent-of-Origin GWAS Result for LDL. Box plots of LDL residuals (y-axes) are shown for each of the four genotypes (left panel; x-axis), and for paternal (center panel; x-axis) and maternal (right panel; x-axis) alleles. The maternal G allele is associated with decreased and maternal A allele with increased LDL. The paternal G allele is associated with increased and the paternal A allele with decreased LDL. The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show +/-1.5 x IQR.

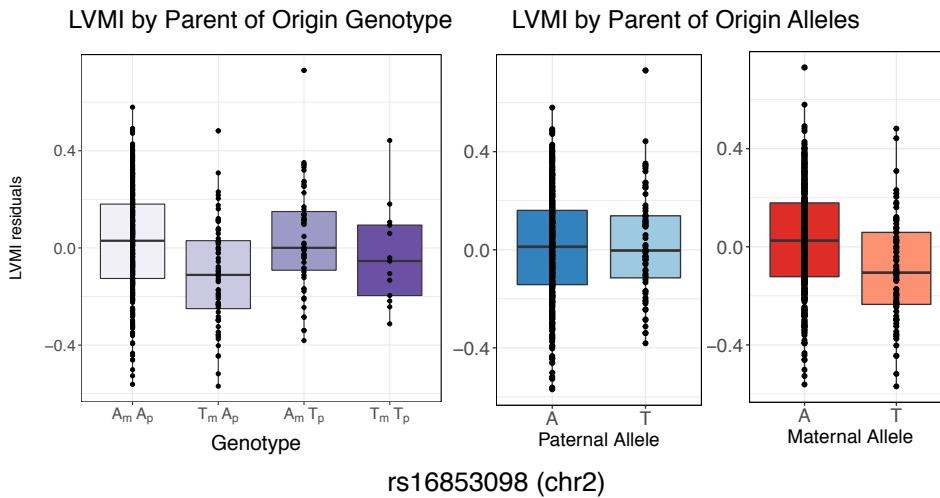


Figure 2.13: Opposite Effect Parent-of-Origin GWAS Result for LVMI. Box plots of LVMI residuals (y-axes) are shown for each of the four genotypes (left panel; x-axis), and for paternal (center panel; x-axis) and maternal (right panel; x-axis) alleles. The maternal T allele is associated with decreased and maternal A allele with increased LVMI. The paternal T allele is associated with increased and the paternal A allele with decreased LVMI. The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show +/-1.5 x IQR.

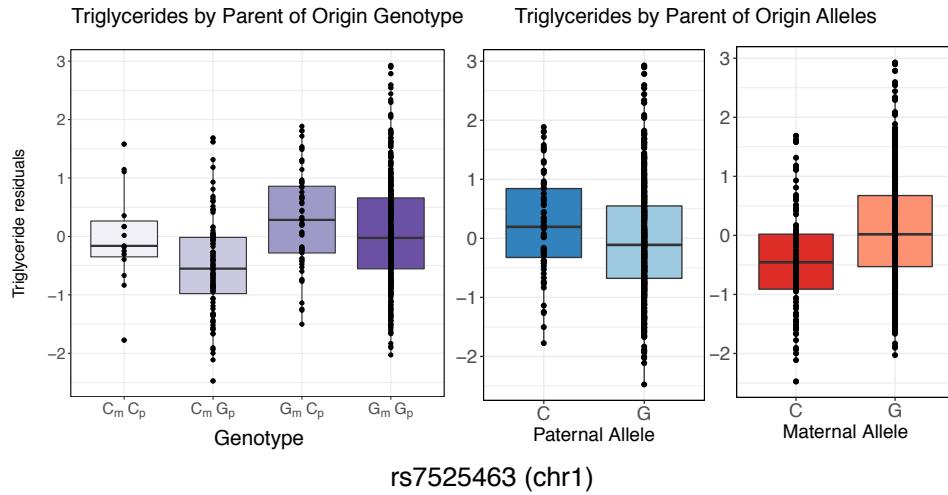


Figure 2.14: Opposite Effect Parent-of-Origin GWAS Result for Triglycerides. Box plots of triglyceride residuals (y-axes) are shown for each of the four genotypes (left panel; x-axis), and for paternal (center panel; x-axis) and maternal (right panel; x-axis) alleles. The maternal C allele is associated with decreased and maternal G allele with increased triglycerides. The paternal C allele is associated with increased and the paternal G allele with decreased triglycerides. The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show +/-1.5 x IQR.

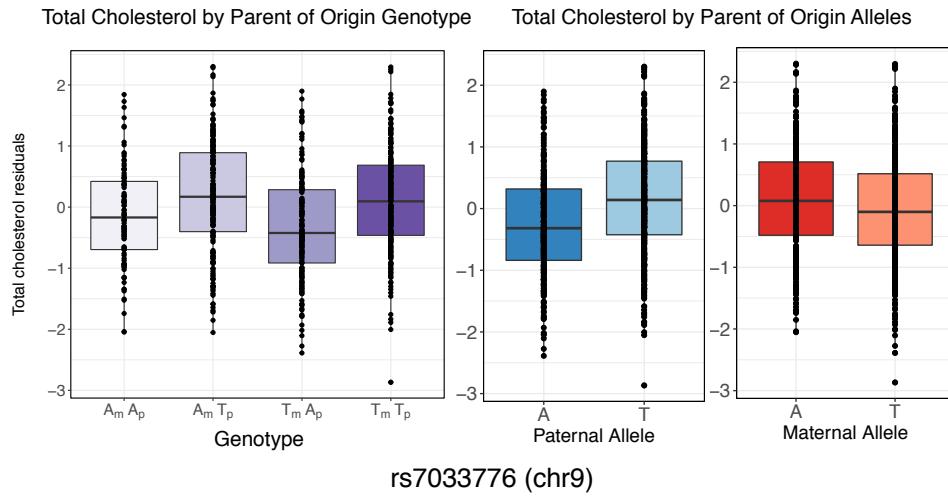


Figure 2.15: Opposite Effect Parent-of-Origin GWAS Result for Total Cholesterol. Box plots of total cholesterol residuals (y-axes) are shown for each of the four genotypes (left panel; x-axis), and for paternal (center panel; x-axis) and maternal (right panel; x-axis) alleles. The maternal T allele is associated with decreased and maternal A allele with increased total cholesterol. The paternal T allele is associated with increased and the paternal A allele with decreased total cholesterol. The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show +/-1.5 x IQR.

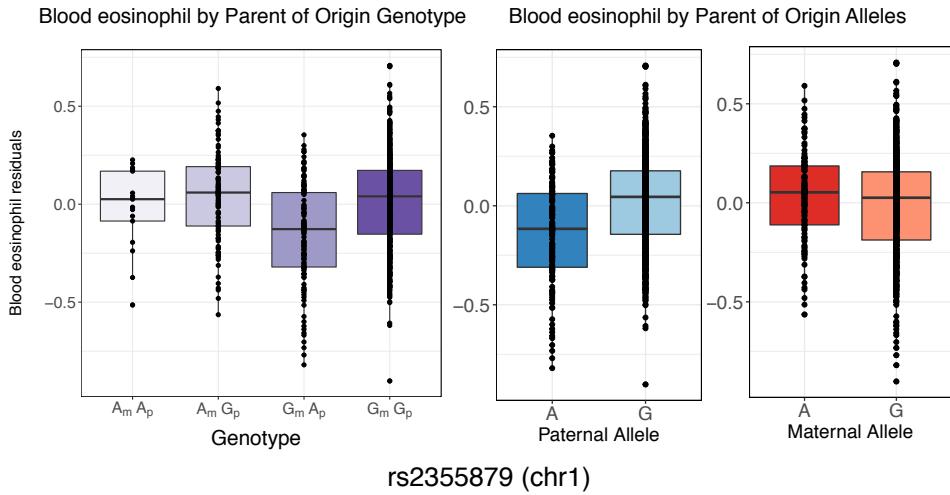


Figure 2.16: Opposite Effect Parent-of-Origin GWAS Result for Blood Eosinophil Count. Box plots of eosinophil residuals (y-axes) are shown for each of the four genotypes (left panel; x-axis), and for paternal (center panel; x-axis) and maternal (right panel; x-axis) alleles. The maternal G allele is associated with decreased and maternal A allele with increased eosinophil count. The paternal G allele is associated with increased and the paternal A allele with decreased eosinophil count. The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show +/-1.5 x IQR.

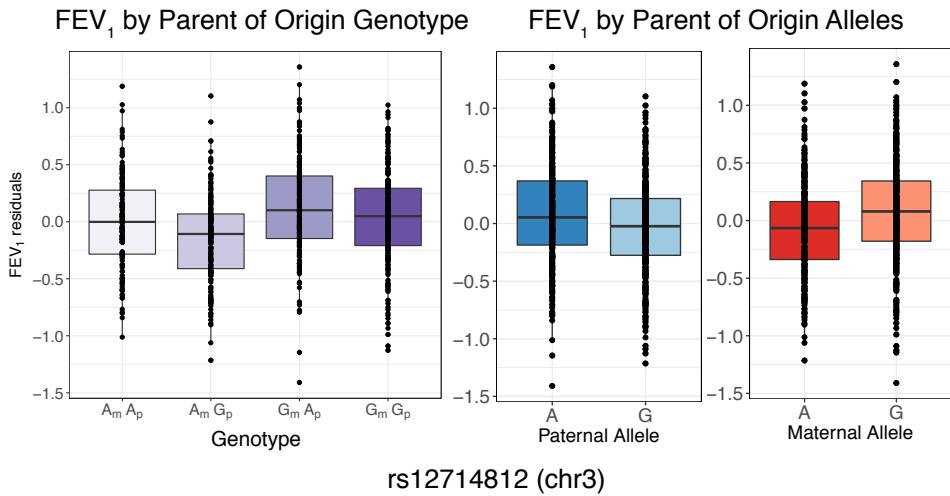


Figure 2.17: Opposite Effect Parent-of-Origin GWAS Result for FEV₁. Box plots of FEV₁ residuals (y-axes) are shown for each of the four genotypes (left panel; x-axis), and for paternal (center panel; x-axis) and maternal (right panel; x-axis) alleles. The maternal A allele is associated with decreased and maternal G allele with increased FEV₁. The paternal A allele is associated with increased and the paternal G allele with decreased FEV₁. The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show +/-1.5 x IQR.

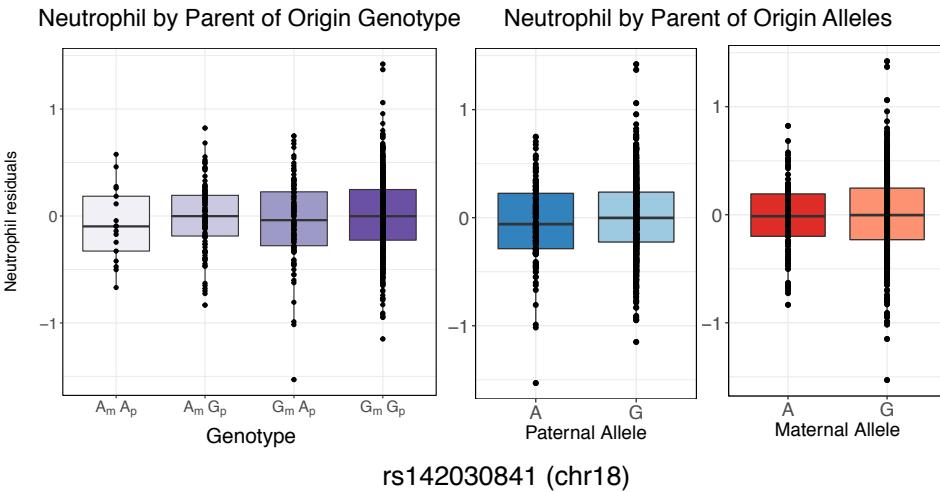


Figure 2.18: Opposite Effect Parent-of-Origin GWAS Result for Neutrophil Count. Box plots of neutrophil residuals (y-axes) are shown for each of the four genotypes (left panel; x-axis), and for paternal (center panel; x-axis) and maternal (right panel; x-axis) alleles. The maternal G allele is associated with decreased and maternal A allele with increased neutrophil count. The paternal G allele is associated with increased and the paternal A allele with decreased neutrophil count. The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show $\pm 1.5 \times \text{IQR}$.

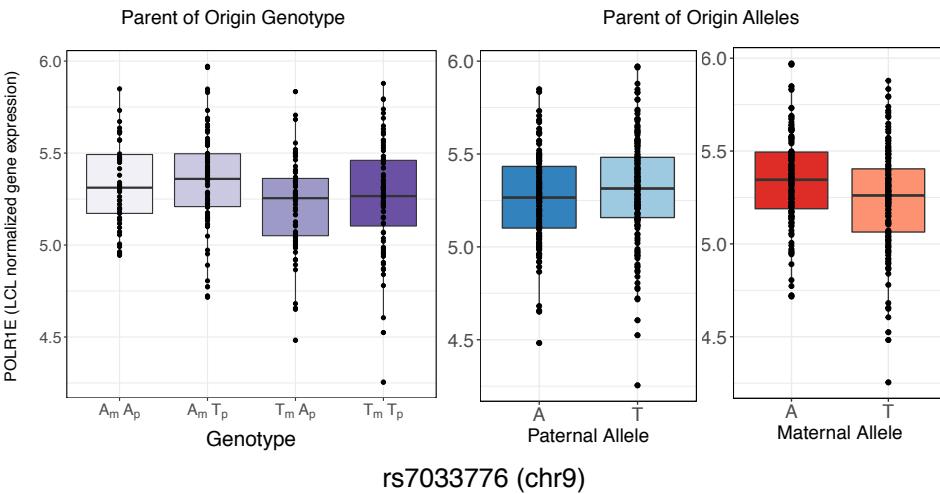


Figure 2.19: Opposite Effect eQTL for rs7033776. Box plots of two significant loci plot *POLR1E* gene expression residuals (y-axes) for each of the four genotypes (left panel; x-axis), and for paternal (center panel; x-axis) and maternal (right panel; x-axis) alleles. The maternal T allele is associated with decreased and maternal A allele with increased *POLR1E* expression. The paternal T allele is associated with increased and the paternal A allele with decreased *POLR1E* expression. The horizontal bar of the boxplot shows the median, the box delineates the first and third quartile, and the whiskers show $\pm 1.5 \times \text{IQR}$.

Quantitative Trait	Sample Size	M/F Ratio	Age range (years)	GWAS call rate	PO call rate	Transformation	Covariates	Exclusions
SBP	807	371/436	6-85	0.94	0.82	log	age, sex, age*sex, technician	Anti-hypertensive medication
DBP	807	371/436	6-85	0.94	0.82	log	age, sex, age*sex, technician	Anti-hypertensive medication
HDL	828	381/447	14-85	0.94	0.80	cube root	age, sex	Anti-hypercholesterolemia medication, hormone replacement therapy, birth control; diagnosis of sitosterolemia
LDL	807	367/440	14-85	-	0.80	cube root age, sex	age, sex	Anti-hypercholesterolemia medication, hormone replacement therapy, birth control; diagnosis of sitosterolemia
Triglycerides	828	382/446	0.94	0.80	log	age, sex	age, sex, breeding, technician	Anti-hypercholesterolemia medication, hormone replacement therapy, birth control; diagnosis of sitosterolemia
Total cholesterol/HDL	828	381/447	14-85	0.94	0.80	log	age, sex	Anti-hypercholesterolemia medication, hormone replacement therapy, birth control; diagnosis of sitosterolemia
Monocyte count	1069	503/566	5.47-85.10	0.94	0.81	log	age, sex, age*sex	Antibiotics, immunosuppressants, and/or steroids was an exclusion for all WBC count phenotypes. Antifungal medication was an exclusion for the Eosinophil count phenotype.
Lymphocyte count	1079	507/572	6-85	0.94	-	log	age	Pregnant, history of heart valve replacement, or poor quality echocardiography images
Eosinophil count	1068	502/566	5.47-85.10	0.94	0.81	square root(log())	sex	Aortic stenosis by history or echocardiogram Cholesterol and/or thyroid medication, or poor quality echocardiography images
Neutrophil count	1070	503/567	5.47-85.10	0.94	0.81	log	age, sex, age*sex, phase	Cholesterol and/or thyroid medication, history of liver disease, or poor quality imaging
LAVI	637	296/341	14-88	0.94	0.80	log	age, sex	Poor quality measurements
LVMI	621	286/335	14-88	0.94	0.79	log	age, sex	
CIMT	547	248/299	14-86	0.94	0.80	inverse	age, sex	
FeNO	825	381/444	6-85	0.95	0.82	log	age, sex, technician	

Table 2.5: **Summary of the Hutterite Phenotypes and Sample Composition.** *SBP: Systolic Blood Pressure, DBP: Diastolic Blood Pressure, HDL: High Density Lipoprotein, LDL: Low Density Lipoprotein, LAVI: Left Atrial Volume Index, LVMI: Left Ventricular Mass Index, CIMT: Carotid Intima Media Thickness, FeNO: Fraction of Exhaled Nitric Oxide, FEV₁: Forced Expiratory Volume at 1 s, FVC: Forced Vital Capacity, BRI: Bronchial Responsiveness Index

Quantitative Trait	Sample M/F Ratio Size	Age range (years)	GWAS PO call rate	Transformation	Covariates	Exclusions
BRI	950	445/505	6.11-78.22	0.94	0.82	none
FEV ₁	1102	509/593	5.47-8.47	0.94	0.82	none
FEV ₁ /FVC	1106	512/594	5.47-8.47	0.94	0.82	none
Total serum IgE	1219	562/657	6-91	0.94	0.81	log
BMI	1188	577/652	5.5-89.2	0.94	0.82	log
Height	1199	576/669	5-89	0.94	0.82	none
Age at menarche	477	0/719	9-17	0.92	0.71	none

Table 2.6: Summary of the Hutterite Phenotypes and Sample Composition (Continued). *SBP: Systolic Blood Pressure, DBP: Diastolic Blood Pressure, HDL: High Density Lipoprotein, LDL: Low Density Lipoprotein, LAVI: Left Atrial Volume Index, LVMI: Left Ventricular Mass Index, CIMT: Carotid Intima Media Thickness, FeNO: Fraction of Exhaled Nitric Oxide, FEV₁: Forced Expiratory Volume at 1 s, FVC: Forced Vital Capacity, BRI: Bronchial Responsiveness Index

Phenotype	Sample size	Most significant GWAS p-value	SNP Size	Sample rsid	(Ef-chr:loc)	Beta (SE)	Variant	(Nearest) Gene	MAF
BMI	1188	8.04E-07	1016	rs139659764 (A/G)	13:81:274241 (1.64E-02)	-8.16E-02 (6.47E-03)	intergenic <i>LINC00377</i>	0.07555	
BRI	950	3.05E-07	935	rs7498042 (T/G)	15:91:119014 (6.47E-03)	3.34E-02 (6.47E-03)	intron <i>CRTC3</i>	0.2921	
CIMT	547	1.51E-09	470	rs116908536 (A/G)	11:33:69981 (2.34E-02)	-0.144 (2.34E-02)	intron <i>LOC105376617</i>	0.05183	
DBP	807	9.66E-07	999	rs11619649 (T/C)	18:90:14768 (9.82E-03)	-4.84E-02 (9.82E-03)	intergenic <i>NDUFV2</i>	0.1312	
Eosinophil count	1068	1.44E-07	939	rs2544465 (A/G)	9:260:45558 (1.68E-02)	8.17E-02 (1.68E-02)	intergenic <i>LOC100506422</i>	0.147	
FeNO	825	2.15E-07	753	rs1121780 (T/C)	2:4296:1321 (2.28E-02)	0.157 (2.28E-02)	intron <i>MTA3</i>	0.4824	
FEV ₁	1102	1.22E-06	1102	rs13281444 (C/T)	8:652:20628 (2.28E-02)	1.11E-01 (2.28E-02)	intron <i>LOC100507530</i>	0.358	
FEV ₁ /FVC	1106	2.49E-07	1099	rs8028898 (A/G)	15:71:679543 (5.31E-02)	-2.75E-01 (5.31E-02)	intron <i>THSD4</i>	0.2049	
HDL	828	8.91E-07	828	rs18613312 (A/T)	16:58:850424 (9.73E-02)	-0.483 (9.73E-02)	intergenic <i>GOT2</i>	0.0687	
Height	1199	7.62E-07	1009	rs1318252 (G/A)	11:1653200 (0.278)	1.38 (0.278)	intergenic <i>KRTAP5-5</i>	0.4239	
IgE	1219	3.99E-07	1187	rs66498879 (C/T)	11:125495211 (5.31E-02)	-0.256 (5.31E-02)	5'UTR <i>CHEK1</i>	0.3243	
LDL	637	3.07E-06	573	rs17205373 (G/C)	6:32626210 (2.81E-02)	-0.1144 (2.81E-02)	intergenic <i>HLA-DQBI</i>	0.09724	
LVMI	807	2.83E-17	714	rs567778817 (T/C)	19:11305534 (1.3 (0.15))	1.3 (0.15)	intron <i>KANK2</i>	0.03382	
Lymphocyte count	1079	5.67E-08	894	rs113389683 (A/G)	8:360267788 (5.04E-02)	0.153 (5.04E-02)	intergenic <i>UNC5D</i> , <i>KCNU1</i>	0.08624	
Age at Menarche	477	3.17E-07	463	rs785474 (G/C)	11:129110347 (2.47E-02)	8.19E-02 (2.47E-02)	intergenic <i>ARHGAP32</i>	0.4395	
Monocyte count	1069	1.36E-08	902	rs31317434 (G/T)	7:9466593 (1.49E-02)	-0.27 (1.49E-02)	intergenic <i>NXPH1</i> , <i>PER4</i>	0.03361	
Neutrophil count	1070	2.11E-07	1070	rs1215134 (C/T)	9:15347518 (4.73E-02)	-8.97E-02 (4.73E-02)	intergenic <i>TTC39B</i>	0.4268	
SBP	807	5.23E-06	774	rs28742608 (G/T)	5:1440934 (1.05E-02)	-4.8E-02 (1.05E-02)	intron <i>LC6A3</i>	0.07549	
Total Cholesterol	828	1.20E-07	828	rs11084211 (A/G)	19:53460861 (5.39E-02)	0.287 (5.39E-02)	intron <i>ZNF816</i> , <i>ZNF816-2</i>	0.3071	
Triglycerides	828	7.12E-13	707	rs184333869 (T/C)	11:117947268 (0.175)	-1.28 (0.175)	intron <i>TMPRSS4</i>	0.02399	

Table 2.7: **GWAS Results.** Phenotype definitions, exclusions, transformations and covariates are summarized in Table 2.5

Phenotype	SNP	genes +/- 1Mb expressed in LCLs
A. Maternal Associations		
Age at Menarche	rs7184983	<i>AMFR, ARL2BP, BBS2, CCDC102A, CCL17, CCL22, CES5A, CETP, CIAPIN1, COQ9, CPNE2, CX2CL1, DOK4, FAM192A, GNAO1, HERPUD1, MR1E, MT1L, MT2A, NLRC5, NUDT21, NUP93, OGFOD1, PLLP, POLR2C, RSPRY1, SLC12A3</i>
CIMT	rs4077567	<i>ABCA12, ATIC, FN1, IGFBP2, MREG, PECR, RPL37A, SMARCAL1, TMEM169, XRCC5</i>
FEV1	rs9849387	<i>ROBO1</i>
FEV1	rs6791779	<i>ZNF717</i>
LVMI	rs574232282	<i>CITED4, COL9A2, FOXJ3, HIVEP3, KCNQ4, NFYC, RIMS3, RLF, SCMH1, SMAP2, ZMPSTE24, SNF684</i>
B. Paternal Associations		
LDL	rs12024326	<i>ADAMTS10, ANGPTL4, AHGEF18, CAMSAP3, CCL25, CD209, CD320, CERS4, CLEC4G, CTXN1, ELAVL1, EMR4P, EVI5L, FCER2, HNRNPM, INSR, KANK3, MAP2K7, MARCH2, MCOLN1, MYO1F, NDUFA, PCP2, PEX11G, PNPLA6, RAB11B, RAB11B-AS1, RPS28, SNAPC2, STXBP2, TIMM44, TRAPPC5, XAB2, ZNF358, ZNF414, ZNF557, ZNF558</i>
	rs4843650	<i>BANP, C16orf95, FBXO31, KLHDC4, MAP1LC3B, SLC7A5, ZC3H18, ZCCHC14, ZFPM1, ZNF469 SBP rs1536182 COG3, CTF2F2, KIAA0226L, LCP1, LRCH1, NUFIP1, SLC25A30, SLC25A30-AS1, TPT1, TPT1-AS1, ZC3H13</i>
Total Cholesterol	rs113588203	<i>ABCB10, ARF1, C1orf35, GUK1, HIST3H2A, IBA57, IBA57-AS1, MRPL55, NUP133, OBSCN, RAB4A, RHOU, RNF187, SNORA51, SPHAR, TAF5L, TRIM11, TRIM17, URB2, WNT3A</i>

Table 2.8: Candidate Genes for Parent-of-Origin eQTL.

Phenotype	SNP	Genes +/- 1Mb expressed in LCLs
Total Cholesterol	rs7033776	<i>CLTA, CREB3, FBXO10, FRMPD1, GBA2, GLIPE2, GNE, GRHPR, HINT2, MELK, MSMP, NRP2, PAX5, POLR1E, RECK, RGP1, SPAG8, TLN1, TMEM8B, TOMM5, ZBTB5, ZCCHC7</i>
BMI	rs77785972	<i>CHD1, RGMB, RGMB-AS1, RIOK2</i>
	rs17605739	-
LDL	rs1032596	<i>C16orf74, C16orf95, COX4I1, GINS2, IRF8, MTHFSD</i>
Triglycerides	rs7527236	<i>LYPLA1, RRP15, TGFB2</i>
LVMI	rs16853098	<i>STK39</i>
Age at menarche	rs58758366	-
Eosinophil count	rs2355879	<i>AKR7A2, ALDH4A1, ARHGEF10L, CAPZB, IFFO2, MRTO4, PQLC2, RCC2, UBR4</i>
Neutrophil count	rs142030841	<i>C18orf21, CELF4, ELP2, FHOD3, KIAA1328, MCOS, RPRD1A, SLC39A6, TPGS2</i>
FEV ₁	rs12714812	<i>FAM86DP</i>

Table 2.9: Candidate Genes for Parent-of-Origin Differential eQTL.

Phenotype	Chr	rsID	bp	Hutterite Variant	Gene	CGI id	NA (AF)	Beta	SE	Maternal pvalue	Paternal pvalue	sample size	GWASignal	
cint	2	rs4077567	216703202	0.3003	ncRNA intronic	<i>LINC00607</i>	1862234	0.312	0.04667999	0.00830	3.02E-08	0.5088493	429.00	
fev1	3	rs849387	7764243	0.3925	intergenic	<i>ROBO2</i>	2339106	0.418	-8.91E-02	1.51E-02	4.10E-09	3.87E-01	945.00	
fev1	3	rs6791779	74996505	0.2412	intergenic	<i>MIR4444-1</i>	2319821	0.243	-1.02E-01	1.80E-02	1.48E-08	6.88E-02	795.00	
fev1	3	rs4677464	75163736	0.1612	intergenic	<i>MIR4444-1</i>	2320625	0.158	-1.17E-01	2.13E-02	4.26E-08	4.02E-02	773.00	
fev1	3	rs4677461	75159504	0.1943	intergenic	<i>MIR4444-1</i>	2320603	0.157	-1.16E-01	2.13E-02	4.66E-08	3.60E-02	783.00	
LDL	19	rs14448349	13286582	0.03651	intergenic	<i>IER2</i>	11457751	0.046	5.31E-01	9.17E-02	1.49E-08	2.77E-04	658.00	Known GWAS signal
LDL	19	rs568448676	13324259	0.03651	intronic	<i>CACNA1A</i>	11458026	0.046	5.31E-01	9.17E-02	1.49E-08	2.77E-04	658.00	Known GWAS signal
LDL	19	rs190144917	9895661	0.0338	intergenic	<i>ZNF846</i>	11441358	0.044	5.27E-01	9.17E-02	1.87E-08	5.01E-07	689.00	Known GWAS signal
LDL	19	rs188874308	9905330	0.0338	intergenic	<i>FBXKL12</i>	11441397	0.044	5.27E-01	9.17E-02	1.87E-08	5.01E-07	689.00	Known GWAS signal
LDL	19	rs144213688	13163160	0.03571	intronic	<i>NFLX</i>	11457323	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs77679006	13163515	0.03571	intronic	<i>NFLX</i>	11457324	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs112429723	13163558	0.03571	intronic	<i>NFLX</i>	11457325	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs10410538	13163576	0.03571	intronic	<i>NFLX</i>	11457326	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs117712228	13165193	0.03571	intronic	<i>NFLX</i>	11457330	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs28412508	13165569	0.03571	intronic	<i>NFLX</i>	11457332	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs141821279	13168638	0.03571	intronic	<i>NFLX</i>	11457338	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs10423956	13170224	0.03571	intronic	<i>NFLX</i>	11457341	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs115864897	13170462	0.03571	intronic	<i>NFLX</i>	11457342	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs88686054	13171584	0.03571	intronic	<i>NFLX</i>	11457350	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs11295219	13172453	0.03571	intronic	<i>NFLX</i>	11457352	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs16978871	13176179	0.03571	intronic	<i>NFLX</i>	11457363	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs11733370	13176728	0.03571	intronic	<i>NFLX</i>	11457364	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs367872888	13178320	0.03532	intronic	<i>NFLX</i>	11457378	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs16978873	13179483	0.03571	intronic	<i>NFLX</i>	11457380	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs5113263	13179662	0.03571	intronic	<i>NFLX</i>	11457381	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs116307916	13183770	0.03571	intronic	<i>NFLX</i>	11457385	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs57339272	13187582	0.03571	intronic	<i>NFLX</i>	11457390	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs58848016	13191031	0.03571	intronic	<i>NFLX</i>	11457395	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs142927801	13191505	0.03571	intronic	<i>NFLX</i>	11457398	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs199732522	13194519	0.03571	intronic	<i>NFLX</i>	11457405	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs117332249	13194781	0.03571	intronic	<i>NFLX</i>	11457407	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs16978877	13195549	0.03571	intronic	<i>NFLX</i>	11457409	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs145316067	13199556	0.03571	intronic	<i>NFLX</i>	11457418	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs145333885	13200721	0.03571	intronic	<i>NFLX</i>	11457420	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs202138513	13200777	0.03571	intronic	<i>NFLX</i>	11457421	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs140567911	13204404	0.03571	intronic	<i>NFLX</i>	11457431	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs14412371	13204414	0.03571	intronic	<i>NFLX</i>	11457432	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs151187830	13204835	0.03571	intronic	<i>NFLX</i>	11457433	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs75550675	13208677	0.03571	UTR3	<i>NFLX</i>	11457446	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal

Table 2.10: **Maternal GWAS results with p-value < 5 × 10⁻⁸.** Significant results from the Maternal GWAS, not pruned for LD. GWAS variants are not excluded (LDL chromosome 19).

Phenotype	Chr	rsID	bp	Hutterite Variant	MAF	Gene	CGI id	NA (AF)	Beta	SE	Maternal pvalue	Paternal pvalue	sample size	GWASsignal
LDL	19	rs368995304	13211129	0.03571	intronic	<i>LYL1</i>	11457451	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs1003392	13212128	0.03571	intronic	<i>LYL1</i>	11457457	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs138326911	13213277	0.03571	intronic	<i>LYL1</i>	11457459	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs1122233	13213516	0.03571	UTR5	<i>LYL1</i>	11457460	0.045	5.21E-01	9.17E-02	2.77E-08	3.45E-04	672.00	Known GWAS signal
LDL	19	rs142462872	13065937	0.03551	intronic	<i>GADD45GPI1</i>	11456853	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs15114034	13073232	0.03551	intergenic	<i>GADD45GPI1</i>	11456882	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs112524225	13084849	0.03551	UTR3	<i>DAND5</i>	11456931	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs80073013	13087831	0.03551	intergenic	<i>DAND5</i>	11456944	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs6511847	13088366	0.03551	intergenic	<i>DAND5</i>	11456948	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs111683602	13090416	0.03551	intergenic	<i>DAND5</i>	11456956	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs113091342	130906388	0.03551	intergenic	<i>DAND5</i>	11456957	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs57061450	13091506	0.03551	intergenic	<i>DAND5</i>	11456960	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs111920263	13093227	0.03551	intergenic	<i>DAND5</i>	11456966	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs75853086	13094044	0.03551	intergenic	<i>DAND5</i>	11456972	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs78512588	13094218	0.035512	intergenic	<i>DAND5</i>	11456973	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs112367635	13095997	0.03551	intergenic	<i>DAND5</i>	11456982	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs74900983	13096147	0.03551	intergenic	<i>NFI</i>	11456983	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	.	13096726	0.03551	intergenic	<i>NFI</i>	11456986	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs61454251	13097043	0.03551	intergenic	<i>NFI</i>	11456987	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs58734454	13097959	0.03551	intergenic	<i>NFI</i>	11456988	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs117978586	13098059	0.03551	intergenic	<i>NFI</i>	11456989	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs11881865	13098993	0.03551	intergenic	<i>NFI</i>	11456991	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs115623314	13101359	0.03551	intergenic	<i>NFI</i>	11457104	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs111910178	13103344	0.03551	intergenic	<i>NFI</i>	11457114	0.045	5.20E-01	9.18E-02	2.97E-08	3.56E-04	671.00	Known GWAS signal
LDL	19	rs557778817	13105534	0.035382	intronic	<i>KANK2</i>	11448761	0.043	5.18E-01	9.18E-02	3.25E-08	6.53E-08	692.00	Known GWAS signal
LDL	19	rs201948164	13091706	0.03559	intergenic	<i>DAND5</i>	11456902	0.045	5.18E-01	9.19E-02	3.46E-08	3.72E-04	661.00	Known GWAS signal
LDL	19	rs569073306	9798489	0.03331	intergenic	<i>ZNF812</i>	11440834	0.041	5.25E-01	9.35E-02	4.23E-08	4.82E-07	679.00	Known GWAS signal
LDL	19	rs149995389	947570	0.03374	intronic	<i>ZNF559</i>	11439157	0.042	5.23E-01	9.37E-02	4.49E-08	6.16E-07	687.00	Known GWAS signal
						<i>ZNF177</i>								
LVM	1	rs57423282	41662388	0.01838	intronic	<i>SCMHI</i>	187718	0.01	2.39E-01	4.16E-02	1.39E-08	5.52E-01	537.00	
LVM	1	rs535685811	41790060	0.01877	intergenic	<i>FOXO6</i>	188284	0.01	2.38E-01	4.16E-02	1.45E-08	5.45E-01	524.00	
menarche	16	rs7184983	56554709	0.05921	upstream	<i>BBS2</i>	10497965	0.051	-8.62E-01	1.54E-01	3.11E-08	4.97E-01	336.00	

Table 2.11: **Maternal GWAS results with p-value <5 × 10⁻⁸ (Continued).** Significant results from the Maternal GWAS, not pruned for LD. GWAS variants are not excluded (LDL chromosome 19).

Phenotype	Chr	rsID	bp	Hutterite Variant MAF	Gene	CGI id	NA (AF)	Beta	SE	Paternal pvalue	Maternal pvalue	Sample Size	GWAS signal	
LDL	19	rs557493846	79708831	0.03045	intronic	<i>MAP2K7</i>	11430276	0.015	0.9765	0.1557	5.27E-10	1.62E-04	602.00	Known GWAS signal
LDL	19	rs186246405	8018607	0.03045	intronic	<i>ELAVL1</i>	11430573	0.015	0.9765	0.1557	5.27E-10	1.62E-04	602.00	Known GWAS signal
LDL	1	rs12024326	227146433	0.1745	intronic	<i>ADCK3</i>	850134	0.166	-0.2950	0.0476	8.06E-10	4.21E-01	686.00	
LDL	1	rs145511505	227512799	0.2347	intragenic	<i>CDC42BPA</i>	852812	0.192	-0.2697	0.0443	1.66E-09	2.35E-01	684.00	
LDL	1	rs10916122	227513033	0.2313	intragenic	<i>CDC42BPA</i>	852814	0.192	-0.2697	0.0443	1.66E-09	2.35E-01	684.00	
LDL	1	rs1037428	227513325	0.2315	intragenic	<i>CDC42BPA</i>	852816	0.192	-0.2697	0.0443	1.66E-09	2.35E-01	684.00	
LDL	1	rs682120	227513405	0.2315	intragenic	<i>CDC42BPA</i>	852817	0.192	-0.2697	0.0443	1.66E-09	2.35E-01	684.00	
LDL	1	rs6841784	227513482	0.2315	intragenic	<i>CDC42BPA</i>	852819	0.192	-0.2697	0.0443	1.66E-09	2.35E-01	684.00	
LDL	1	rs684803	227513724	0.2315	intragenic	<i>CDC42BPA</i>	852822	0.192	-0.2697	0.0443	1.66E-09	2.35E-01	684.00	
LDL	19	rs150113975	80960388	0.0342	intragenic	<i>CCL25</i>	11430921	0.018	0.8210	0.1563	2.34E-09	1.56E-04	621.00	Known GWAS signal
LDL	1	rs2005016	227206349	0.2221	intronic	<i>CDC42BPA</i>	850510	0.188	-0.2705	0.0449	2.51E-09	3.82E-01	681.00	
LDL	1	rs3818694	227192477	0.2225	intronic	<i>CDC42BPA</i>	850445	0.187	-0.2705	0.0450	2.63E-09	3.63E-01	684.00	
LDL	1	rs1079378	227195871	0.2225	intronic	<i>CDC42BPA</i>	850458	0.187	-0.2705	0.0450	2.63E-09	3.63E-01	684.00	
LDL	1	rs4653474	227201010	0.2261	intronic	<i>CDC42BPA</i>	850475	0.187	-0.2705	0.0450	2.63E-09	3.63E-01	684.00	
LDL	1	rs10916072	227155983	0.2223	intronic	<i>ADCK3</i>	850180	0.187	-0.2664	0.0447	3.64E-09	3.75E-01	686.00	
LDL	1	rs3806263	227165097	0.2227	intronic	<i>ADCK3</i>	850208	0.187	-0.2664	0.0447	3.64E-09	3.75E-01	686.00	
LDL	1	rs1888827	227141955	0.2196	intronic	<i>ADCK3</i>	850111	0.188	-0.2656	0.0448	4.25E-09	4.18E-01	686.00	
LDL	1	rs120611358	227146134	0.2196	intronic	<i>ADCK3</i>	850133	0.188	-0.2656	0.0448	4.25E-09	4.18E-01	686.00	
LDL	19	rs78618175	227149485	0.03175	intronic	<i>FCER2</i>	11429090	0.02	0.7808	0.1529	5.79E-09	1.65E-03	688.00	Known GWAS signal
LDL	16	rs4843650	87683486	0.4484	intronic	<i>JPH3</i>	10662505	0.483	0.2111	0.0361	6.46E-09	3.91E-02	621.00	
LDL	16	rs4843652	87684251	0.4455	intronic	<i>JPH3</i>	10662512	0.483	0.2111	0.0361	6.46E-09	3.91E-02	621.00	
LDL	16	rs4843653	87685216	0.4448	intronic	<i>JPH3</i>	10662514	0.483	0.2111	0.0361	6.46E-09	3.91E-02	621.00	
LDL	16	rs1077698	87686617	0.4435	intronic	<i>JPH3</i>	10662522	0.483	0.2111	0.0361	6.46E-09	3.91E-02	621.00	
LDL	16	rs1077699	87686675	0.4436	intronic	<i>JPH3</i>	10662524	0.483	0.2111	0.0361	6.46E-09	3.91E-02	621.00	
LDL	16	rs1077700	87686735	0.4433	intronic	<i>JPH3</i>	10662527	0.483	0.2111	0.0361	6.46E-09	3.91E-02	621.00	
LDL	16	rs1110604	87687216	0.438	intronic	<i>JPH3</i>	10662531	0.483	0.2111	0.0361	6.46E-09	3.91E-02	621.00	
LDL	16	rs1110603	87687317	0.4545	intronic	<i>JPH3</i>	10662534	0.485	0.2110	0.0361	6.57E-09	3.91E-02	621.00	
LDL	1	rs653823	227514024	0.3296	intragenic	<i>CDC42BPA</i>	852824	0.281	-0.2247	0.0389	1.14E-08	2.91E-01	684.00	
LDL	1	rs4653824	227514080	0.3296	intragenic	<i>CDC42BPA</i>	852826	0.281	-0.2247	0.0389	1.14E-08	2.91E-01	684.00	
LDL	19	rs686796	7598579	0.04296	intronic	<i>MCOLN1</i>	11427862	0.027	0.6194	0.1096	2.01E-08	3.68E-03	629.00	Known GWAS signal
LDL	19	rs145530718	105688833	0.03297	intronic	<i>PDE4A</i>	11445003	0.02	0.6326	0.1260	4.85E-08	1.40E-07	683.00	Known GWAS signal
LDL	19	.	10574007	0.03297	intronic	<i>PDE4A</i>	11445019	0.02	0.6326	0.1260	4.85E-08	1.40E-07	683.00	Known GWAS signal
LDL	19	rs138164292	10574510	0.03297	exonic	<i>PDE4A</i>	11445025	0.02	0.6326	0.1260	4.85E-08	1.40E-07	683.00	Known GWAS signal
LDL	19	rs35074907	10600418	0.03297	exonic	<i>KEAP1</i>	11445145	0.02	0.6326	0.1260	4.85E-08	1.40E-07	683.00	Known GWAS signal
systolic	13	rs1536182	46275415	0.1999	upstream	<i>LINC01055</i>	9200700	0.206	-0.0277	0.0049	1.53E-08	1.78E-01	684.00	
systolic	13	rs17068928	46276766	0.206	intronic	<i>SPPRT</i>	9200706	0.204	-0.0289	0.0052	2.46E-08	4.03E-01	602.00	
Total cholesterol	1	rs113588203	228079156	0.09874	intergenic	<i>RHOU</i>	858710	0.084	-0.3407	0.0800	1.76E-08	7.43E-02	703.00	

Table 2.12: **Paternal GWAS results with p-value < 5 × 10⁻⁸.** Significant results from the Paternal GWAS, not pruned for LD. GWAS variants are not excluded (LDL chromosome 19).

Phenotype	Chr	rsID	bp	Hutterite Variant	Gene	CGI id	Beta	SE	pvalue	Maternal Beta	Maternal SE	Maternal pvalue	Paternal Beta	Paternal SE	Paternal pvalue		
BMI	5	rs77785972	97415767	0.02493	intergenic	<i>LINC01340</i>	4132296	1.54E-01	2.45E-02	5.12E-10	8.06E-02	1.86E-02	1.58E-05	-9.39E-02	1.87E-02	5.84E-07	
BMI	5	rs144269495	97644763	0.02496	intergenic	<i>RGMB</i>	413347	1.54E-01	2.46E-02	5.80E-10	8.07E-02	1.86E-02	1.54E-05	-9.38E-02	1.87E-02	6.03E-07	
BMI	5	rs7729289	97086224	0.0257	intergenic	<i>LINC01340</i>	4130302	1.44E-01	2.38E-02	1.85E-09	8.05E-02	1.86E-02	1.61E-05	-8.05E-02	1.81E-02	9.38E-06	
BMI	5	rs183558720	90603341	0.02708	intergenic	<i>LOC100133050</i>	4141693	1.44E-01	2.40E-02	2.64E-09	8.54E-02	1.88E-02	6.25E-06	-7.90E-02	1.77E-02	8.33E-06	
BMI	5	rs6876509	98660952	0.0269	intergenic	<i>CTD-</i>	4137296	1.39E-01	2.32E-02	2.89E-09	7.81E-02	1.79E-02	1.38E-05	-7.92E-02	1.77E-02	7.99E-06	
BMI	5	rs10065471	97096444	0.02498	intergenic	<i>LINC01340</i>	4130391	1.44E-01	2.40E-02	2.82E-09	7.99E-02	1.86E-02	1.88E-05	-8.12E-02	1.81E-02	7.78E-06	
BMI	5	rs138319666	99804481	0.02671	intergenic	<i>FAM17A</i>	4142373	1.43E-01	2.39E-02	2.93E-09	8.59E-02	1.88E-02	5.53E-06	-7.85E-02	1.77E-02	9.56E-06	
BMI	5	rs36690309	97081264	0.02543	intergenic	<i>LINC01340</i>	4130288	1.44E-01	2.40E-02	2.86E-09	8.00E-02	1.86E-02	1.84E-05	-8.11E-02	1.81E-02	8.01E-06	
BMI	5	rs140335394	968935272	0.02562	ncRNA intronic	<i>LINC01340</i>	4129443	1.41E-01	2.36E-02	2.97E-09	7.62E-02	1.79E-02	2.24E-05	-8.11E-02	1.81E-02	8.03E-06	
BMI	5	rs17740326	98950533	0.02478	intergenic	<i>CTD-</i>	4138700	1.41E-01	2.37E-02	3.21E-09	8.18E-02	1.86E-02	1.18E-05	-7.93E-02	1.77E-02	7.77E-06	
BMI	5	rs12522765	98717177	0.02549	intergenic	<i>CTD-</i>	4137514	1.42E-01	2.37E-02	3.34E-09	8.18E-02	1.86E-02	1.17E-05	-7.93E-02	1.77E-02	7.82E-06	
BMI	5	rs148553558	96856793	0.02477	ncRNA intronic	<i>LINC01340</i>	4129293	1.44E-01	2.41E-02	3.41E-09	8.02E-02	1.86E-02	1.74E-05	-8.09E-02	1.81E-02	8.47E-06	
BMI	5	rs141542967	96861749	0.02477	ncRNA intronic	<i>LINC01340</i>	4129324	1.44E-01	2.41E-02	3.41E-09	8.02E-02	1.86E-02	1.74E-05	-8.09E-02	1.81E-02	8.47E-06	
BMI	5	rs18336124	96691061	0.02461	intergenic	<i>LINC01340</i>	4128633	1.44E-01	2.41E-02	3.35E-09	8.02E-02	1.86E-02	1.76E-05	-8.09E-02	1.81E-02	8.40E-06	
BMI	5	rs112966089	96148210	0.02596	intronic	<i>ERAP1</i>	4125752	1.41E-01	2.37E-02	3.49E-09	7.64E-02	1.79E-02	2.13E-05	-8.09E-02	1.81E-02	8.45E-06	
BMI	5	rs13187669	97269139	0.02553	intergenic	<i>LINC01340</i>	4131645	1.43E-01	2.41E-02	3.40E-09	8.01E-02	1.86E-02	1.78E-05	-8.10E-02	1.81E-02	8.34E-06	
BMI	5	rs4425526	97314428	0.02552	intergenic	<i>LINC01340</i>	4131794	1.43E-01	2.41E-02	3.40E-09	8.01E-02	1.86E-02	1.77E-05	-8.10E-02	1.81E-02	8.34E-06	
BMI	5	rs146317003	97322072	0.02552	intergenic	<i>LINC01340</i>	4131822	1.43E-01	2.41E-02	3.40E-09	8.01E-02	1.86E-02	1.77E-05	-8.10E-02	1.81E-02	8.34E-06	
BMI	5	rs14328145	98417440	0.02441	intergenic	<i>LOC100239230</i>	4136278	1.42E-01	2.40E-02	3.37E-09	8.20E-02	1.86E-02	1.12E-05	-7.89E-02	1.81E-02	1.41E-05	
BMI	5	.	914913526	97467475	0.02596	intergenic	<i>LINC01340</i>	4132735	1.40E-01	2.36E-02	3.87E-09	7.67E-02	1.79E-02	1.96E-05	-8.05E-02	1.81E-02	9.27E-06
BMI	5	.	9909892	0.02599	intergenic	<i>CTD-</i>	4139354	1.41E-01	2.38E-02	3.97E-09	8.23E-02	1.86E-02	1.05E-05	-7.88E-02	1.77E-02	8.87E-06	
BMI	5	rs150291236	97483641	0.02571	intergenic	<i>LINC01340</i>	4128290	1.43E-01	2.41E-02	4.00E-09	8.06E-02	1.86E-02	1.58E-05	-8.05E-02	1.81E-02	9.44E-06	
BMI	5	rs138752915	97483260	0.02569	intergenic	<i>LINC01340</i>	4132915	1.43E-01	2.41E-02	4.00E-09	8.06E-02	1.86E-02	1.58E-05	-8.05E-02	1.81E-02	9.44E-06	
BMI	5	rs148713283	96550111	0.02443	intergenic	<i>RIOK2</i>	4127599	1.43E-01	2.42E-02	4.03E-09	7.97E-02	1.86E-02	1.98E-05	-8.15E-02	1.81E-02	7.28E-06	
BMI	5	rs140013050	9897275	0.02562	intergenic	<i>CTD-</i>	4138786	1.41E-01	2.38E-02	4.29E-09	8.21E-02	1.86E-02	1.11E-05	-7.90E-02	1.77E-02	8.35E-06	
BMI	5	rs77489669	97902544	0.02682	intergenic	<i>RGMB</i>	4134327	1.43E-01	2.41E-02	4.46E-09	8.11E-02	1.86E-02	1.41E-05	-7.99E-02	1.81E-02	1.08E-05	
BMI	5	rs398084318	977470708	0.02547	intergenic	<i>RGMB</i>	4133681	1.40E-01	2.37E-02	4.51E-09	7.70E-02	1.86E-02	1.84E-05	-8.03E-02	1.81E-02	9.90E-06	
BMI	5	rs20066279	97746220	0.02522	intergenic	<i>RGMB</i>	4133686	1.40E-01	2.37E-02	4.51E-09	7.70E-02	1.86E-02	1.79E-05	-8.03E-02	1.81E-02	9.90E-06	
BMI	5	rs14330722	97764566	0.02522	intergenic	<i>RGMB</i>	4133737	1.40E-01	2.37E-02	4.51E-09	7.70E-02	1.86E-02	1.79E-05	-8.03E-02	1.81E-02	9.90E-06	
BMI	5	rs78112089	985851881	0.03345	intergenic	<i>CTD-</i>	413697	1.20E-01	2.06E-02	7.22E-09	6.69E-02	1.54E-02	1.46E-05	-6.45E-02	1.59E-02	5.14E-05	
BMI	5	rs140517163	97377767	0.02138	intergenic	<i>LINC01340</i>	4132134	1.55E-01	2.66E-02	6.89E-09	7.55E-02	2.03E-02	2.23E-04	-9.51E-02	1.97E-02	1.43E-06	
BMI	5	.	96121146	0.02587	intronic	<i>ERAP1</i>	4125556	1.45E-01	2.49E-02	7.50E-09	7.67E-02	1.79E-02	2.10E-05	-7.72E-02	1.92E-02	5.70E-05	
BMI	5	rs190558767	99561661	0.02701	intergenic	<i>LOC100133050</i>	41414571	1.40E-01	2.41E-02	8.24E-09	8.24E-02	1.86E-02	1.01E-05	-7.85E-02	1.81E-02	1.56E-05	
BMI	5	rs6557013	97207542	0.02584	intergenic	<i>LINC01340</i>	4131103	1.38E-01	2.38E-02	8.59E-09	7.11E-02	1.81E-02	9.30E-05	-8.10E-02	1.81E-02	8.14E-06	
BMI	5	rs115292822	93912840	0.02537	ncRNA intronic	<i>LOC101939710</i>	4124600	1.44E-01	2.50E-02	1.11E-08	7.59E-02	1.79E-02	2.54E-05	-7.80E-02	1.92E-02	4.73E-05	
BMI	5	rs181149134	95927651	0.02537	ncRNA intronic	<i>LOC101929710</i>	4124292	1.44E-01	2.50E-02	1.11E-08	7.60E-02	1.79E-02	2.48E-05	-7.79E-02	1.92E-02	4.84E-05	
BMI	5	rs114226267	95870876	0.02532	ncRNA intronic	<i>LOC101929710</i>	4121800	1.37E-01	2.38E-02	1.28E-08	7.21E-02	1.81E-02	7.51E-05	-8.01E-02	1.81E-02	1.05E-05	
BMI	5	rs1378438	97703974	0.02507	intergenic	<i>RGMB</i>	4133590	1.37E-01	2.38E-02	1.28E-08	7.21E-02	1.81E-02	7.51E-05	-8.01E-02	1.81E-02	1.05E-05	
BMI	5	rs6864552	97705646	0.02507	intergenic	<i>RGMB</i>	4133624	1.37E-01	2.38E-02	1.28E-08	7.21E-02	1.81E-02	7.51E-05	-8.01E-02	1.81E-02	1.05E-05	
BMI	5	rs2124263	97725019	0.02502	intergenic	<i>RGMB</i>	4133624	1.37E-01	2.38E-02	1.28E-08	7.21E-02	1.81E-02	7.51E-05	-8.01E-02	1.81E-02	1.05E-05	

Table 2.13: Differential Effect GWAS results with p-value $< 5 \times 10^{-8}$. Significant results from the Differential Effect GWAS, not pruned for LD.

Phenotype	Chr	rsID	bp	Hutterite Variant	Gene	CGI id	Beta	SE	pvalue	Maternal Beta	Maternal SE	Maternal pvalue	Paternal Beta	Paternal SE	Paternal pvalue	
BMI	5	rs4703065	97736141	0.0251	intergenic	<i>RGM</i>	4133654	1.37E-01	2.38E-02	1.28E-08	7.21E-02	1.81E-02	7.51E-05	-8.01E-02	1.81E-02	1.05E-05
BMI	5	rs77665200	90371047	0.0359	intergenic	<i>LOC100133050</i>	4140868	1.18E-01	2.07E-02	1.34E-08	6.77E-02	1.54E-02	1.15E-05	-6.37E-02	1.59E-02	6.37E-05
BMI	5	rs14461614	99271879	0.03498	intergenic	<i>CTD-</i>	4140453	1.18E-01	2.07E-02	1.40E-08	6.74E-02	1.54E-02	1.27E-05	-6.41E-02	1.59E-02	5.81E-05
BMI	5	rs184559335	99293072	0.03452	intergenic	<i>CTD-</i>	4140571	1.18E-01	2.07E-02	1.40E-08	6.74E-02	1.54E-02	1.27E-05	-6.41E-02	1.59E-02	5.81E-05
BMI	5	rs191715520	99490860	0.03466	intergenic	<i>LOC100133050</i>	4141410	1.19E-01	2.08E-02	1.46E-08	6.71E-02	1.54E-02	1.38E-05	-6.43E-02	1.59E-02	5.43E-05
BMI	5	rs187232727	99532646	0.03392	intergenic	<i>LOC100133050</i>	4141504	1.18E-01	2.07E-02	1.47E-08	6.73E-02	1.54E-02	1.35E-05	-6.39E-02	1.59E-02	6.10E-05
BMI	5	rs80201515	99390462	0.03455	intergenic	<i>CTD-</i>	4140651	1.18E-01	2.08E-02	1.47E-08	6.73E-02	1.54E-02	1.35E-05	-6.42E-02	1.59E-02	5.60E-05
BMI	5	.	98148676	0.01745	intergenic	<i>RGM</i>	4135144	1.61E-01	2.83E-02	1.78E-08	7.64E-02	2.03E-02	1.90E-04	-1.04E-01	2.30E-02	7.40E-06
BMI	5	rs77291665	98063683	0.01702	intergenic	<i>RGM</i>	4135135	1.61E-01	2.88E-02	1.92E-08	7.60E-02	2.03E-02	2.03E-04	-1.04E-01	2.30E-02	6.97E-06
BMI	5	.	978785952	0.02688	intergenic	<i>RGM</i>	4134200	1.43E-01	2.54E-02	2.48E-08	8.06E-02	1.86E-02	1.58E-05	-8.25E-02	2.05E-02	6.31E-05
BMI	5	rs116284915	97891262	0.02688	intergenic	<i>RGM</i>	4134282	1.43E-01	2.54E-02	2.48E-08	8.06E-02	1.86E-02	1.58E-05	-8.25E-02	2.05E-02	6.31E-05
BMI	6	rs17665739	23962798	0.1703	intergenic	<i>HDGF1L</i>	4604643	5.39E-02	9.65E-03	3.01E-08	3.40E-02	7.03E-03	1.42E-06	-3.17E-02	7.90E-03	6.99E-05
BMI	5	rs7861066	94593557	0.02994	intronic	<i>MCTP1</i>	4119855	1.38E-01	2.47E-02	3.44E-08	7.58E-02	1.75E-02	1.62E-05	-8.45E-02	4.68E-02	4.68E-05
BMI	5	rs14970464	100920184	0.01665	intergenic	<i>SLCO4C1</i>	4144691	1.57E-01	2.81E-02	3.41E-08	7.23E-02	1.83E-02	1.42E-04	-1.10E-01	2.44E-02	6.72E-06
BMI	5	rs562242498	99887689	0.02665	intronic	<i>FAM17A</i>	4142590	1.27E-01	2.31E-02	4.66E-08	7.60E-02	1.81E-02	2.92E-05	-7.82E-02	1.77E-02	9.91E-06
LDL	16	rs1032596	86287137	0.2967	ncRNA intronic	<i>LINC01081</i>	10653619	-3.10E-01	5.56E-02	3.69E-08	-1.48E-01	4.20E-02	2.47E-01	2.01E-01	4.09E-02	1.05E-06
LYM	2	rs16833098	168013281	0.1217	intronic	<i>XIRP2</i>	1665657	-9.14E-02	1.64E-02	4.18E-08	-4.82E-02	1.29E-02	2.04E-04	6.41E-02	1.37E-02	5.29E-06
LYM	2	rs10497311	168010712	0.1184	intronic	<i>XIRP2</i>	1665643	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs16833095	168012834	0.1168	intronic	<i>XIRP2</i>	1665654	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs16833097	168012870	0.1168	intronic	<i>XIRP2</i>	1665655	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs10497312	168013530	0.1171	intronic	<i>XIRP2</i>	1665659	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs16833101	168013617	0.1171	intronic	<i>XIRP2</i>	1665660	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs147685013	168013666	0.1168	intronic	<i>XIRP2</i>	1665661	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs16833103	168013703	0.1171	intronic	<i>XIRP2</i>	1665662	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs10497313	168013726	0.1171	intronic	<i>XIRP2</i>	1665663	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs73017988	168014000	0.1171	intronic	<i>XIRP2</i>	1665667	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs75316301	168014552	0.1171	intronic	<i>XIRP2</i>	1665669	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs73019948	168014552	0.1171	intronic	<i>XIRP2</i>	1665670	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs73019950	168014678	0.1171	intronic	<i>XIRP2</i>	1665671	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs73019953	168015225	0.1171	intronic	<i>XIRP2</i>	1665677	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs73019954	168015635	0.1171	intronic	<i>XIRP2</i>	1665674	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs79982267	168016782	0.1171	intronic	<i>XIRP2</i>	1665688	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs73019962	168017078	0.1171	intronic	<i>XIRP2</i>	1665689	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs75174695	168016944	0.1171	intronic	<i>XIRP2</i>	1665690	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs73019965	168017099	0.1171	intronic	<i>XIRP2</i>	1665691	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs111999067	168017394	0.1171	intronic	<i>XIRP2</i>	1665692	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs7558809	168017611	0.1171	intronic	<i>XIRP2</i>	1665693	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs7587904	168017798	0.1171	intronic	<i>XIRP2</i>	1665694	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs7561502	168017857	0.1171	intronic	<i>XIRP2</i>	1665695	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYM	2	rs7561801	168017879	0.1171	intronic	<i>XIRP2</i>	1665696	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06

Table 2.14: Differential Effect GWAS results with p-value < 5 × 10⁻⁸ (Continued).. Significant results from the Differential Effect GWAS, not pruned for LD.

Phenotype	Chr	rsID	bp	Hutterite Variant	Gene	CGI id	Beta	SE	pvalue	Maternal Beta	Maternal SE	Maternal pvalue	Paternal Beta	Paternal SE	Paternal pvalue	
LYMMI	2	rs7561812	168017915	0.1171	intronic	XIRP2	1665697	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7561839	168018085	0.1171	intronic	XIRP2	1665700	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73019970	168018143	0.1171	intronic	XIRP2	1665702	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73019972	168018350	0.1171	intronic	XIRP2	1665704	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73019975	168018516	0.1171	intronic	XIRP2	1665708	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs112608820	168018763	0.1171	intronic	XIRP2	1665709	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs113228222	168018895	0.1171	intronic	XIRP2	1665710	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73019980	168018968	0.1171	intronic	XIRP2	1665711	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73019981	168019271	0.1171	intronic	XIRP2	1665712	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs386652426	168019618	0.1171	intronic	XIRP2	1665713	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73019982	168019667	0.1171	intronic	XIRP2	1665714	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs13884735	168020067	0.1171	intronic	XIRP2	1665715	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73019985	168020091	0.1171	intronic	XIRP2	1665716	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73019986	168020375	0.1171	intronic	XIRP2	1665717	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73019987	168020472	0.1171	intronic	XIRP2	1665718	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73019991	168020523	0.1171	intronic	XIRP2	1665719	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs111768474	168020813	0.1171	intronic	XIRP2	1665727	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs118933377	168021121	0.1171	intronic	XIRP2	1665735	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs78400394	168021126	0.1171	intronic	XIRP2	1665736	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73020002	168021145	0.1171	intronic	XIRP2	1665737	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs11893509	168021232	0.1171	intronic	XIRP2	1665738	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs78619028	168021274	0.1171	intronic	XIRP2	1665739	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7606695	168021491	0.1171	intronic	XIRP2	1665741	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7607000	168021563	0.1171	intronic	XIRP2	1665742	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021964	168021631	0.1171	intronic	XIRP2	1665743	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs700549	168021639	0.1171	intronic	XIRP2	1665744	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7556854	168021731	0.1171	intronic	XIRP2	1665745	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7570780	168021925	0.1171	intronic	XIRP2	1665746	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7583301	168022013	0.1171	intronic	XIRP2	1665747	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021968	168022527	0.1171	intronic	XIRP2	1665750	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs672046	168022829	0.1171	intronic	XIRP2	1665751	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs700978	168022892	0.1171	intronic	XIRP2	1665752	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs6709079	168022908	0.1171	intronic	XIRP2	1665753	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs6709146	168023138	0.1171	intronic	XIRP2	1665755	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021970	168023277	0.1171	intronic	XIRP2	1665756	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs6709377	168023297	0.1171	intronic	XIRP2	1665758	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021971	168023617	0.1171	intronic	XIRP2	1665760	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021978	168023922	0.1171	intronic	XIRP2	1665763	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021981	168024415	0.1171	intronic	XIRP2	1665766	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs75737574	168024973	0.1171	intronic	XIRP2	1665770	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06

Table 2.15: **Differential Effect GWAS results with p-value $< 5 \times 10^{-8}$ (Continued)..** Significant results from the Differential Effect GWAS, not pruned for LD.

Phenotype	Chr	rsID	bp	Hutterite Variant	Gene	CGI id	Beta	SE	pvalue	Maternal Beta	Maternal SE	Maternal pvalue	Paternal Beta	Paternal SE	Paternal pvalue	
LYMMI	2	rs112330596	168025155	0.1216	intronic	XIRP2	16655771	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs112037476	168025177	0.1216	intronic	XIRP2	16655772	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs111963932	168025189	0.1216	intronic	XIRP2	16655773	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs113027543	168025196	0.1216	intronic	XIRP2	16655774	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021984	168025413	0.1171	intronic	XIRP2	16655776	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs75456957	168025545	0.1171	intronic	XIRP2	16655777	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021985	168025736	0.1171	intronic	XIRP2	16655779	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	.	.	.	intronic	XIRP2	16655780	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021986	168025866	0.1171	intronic	XIRP2	16655781	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021988	168025979	0.1171	intronic	XIRP2	16655782	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021990	168026100	0.1171	intronic	XIRP2	16655783	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021991	168026251	0.1171	intronic	XIRP2	16655784	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021992	168026271	0.1171	intronic	XIRP2	16655785	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73021994	168026337	0.1171	intronic	XIRP2	16655786	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73022001	168027043	0.1171	intronic	XIRP2	16655790	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73023904	168027022	0.1219	intronic	XIRP2	16655794	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73023906	168027025	0.1168	intronic	XIRP2	16655795	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs1319910	168027536	0.1171	intronic	XIRP2	16655801	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs2893038	168027579	0.1171	intronic	XIRP2	16655803	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs239615	168027783	0.1171	intronic	XIRP2	16655805	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs6744515	168028092	0.1171	intronic	XIRP2	16655806	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73023920	168028512	0.1171	intronic	XIRP2	16655813	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs112015900	168028572	0.1171	intronic	XIRP2	16655814	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs11858687	168028607	0.1171	intronic	XIRP2	16655815	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs147806340	168028633	0.1171	intronic	XIRP2	16655818	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs199677915	168028700	0.1171	intronic	XIRP2	16655819	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs20095327	168028703	0.1171	intronic	XIRP2	16655820	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs140239897	168028818	0.1171	intronic	XIRP2	16655821	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs4625871	168028820	0.1171	intronic	XIRP2	16655822	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs11295336	168029029	0.1171	intronic	XIRP2	16655824	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs112282731	168029226	0.1171	intronic	XIRP2	16655829	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73023984	168029231	0.1171	intronic	XIRP2	16655830	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73023988	16802936	0.1171	intronic	XIRP2	16655832	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs11663403	168030730	0.1171	intronic	XIRP2	16655834	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs112491758	168030745	0.1171	intronic	XIRP2	16655843	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73023997	168030903	0.1171	intronic	XIRP2	16655847	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs113467338	168030449	0.1171	intronic	XIRP2	16655840	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs1131318793	168030553	0.1171	intronic	XIRP2	16655841	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs114653070	168030730	0.1171	intronic	XIRP2	16655842	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs114653071	168030745	0.1171	intronic	XIRP2	16655843	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs114653072	168030750	0.1171	intronic	XIRP2	16655844	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs114653073	168030755	0.1171	intronic	XIRP2	16655845	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06

Table 2.16: Differential Effect GWAS results with p-value $< 5 \times 10^{-8}$ (Continued).. Significant results from the Differential Effect GWAS, not pruned for LD.

Phenotype	Chr	rsID	bp	Hutterite Variant	Gene	CGI id	Beta	SE	pvalue	Maternal Beta	Maternal SE	Maternal pvalue	Paternal Beta	Paternal SE	Paternal pvalue	
LYMMI	2	rs115339873	168031292	0.1171	intronic	XIRP2	1665850	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs4270315	168031613	0.1171	intronic	XIRP2	1665853	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs2082097	168031754	0.1168	intronic	XIRP2	1665855	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs2396547	168031776	0.1168	intronic	XIRP2	1665856	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs111584035	168032108	0.1171	intronic	XIRP2	1665857	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs113652088	168032120	0.1171	intronic	XIRP2	1665858	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs112680044	168032160	0.1171	intronic	XIRP2	1665859	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs112731427	168032163	0.1171	intronic	XIRP2	1665860	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs113761801	168032266	0.1171	intronic	XIRP2	1665862	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs112976808	168032353	0.1171	intronic	XIRP2	1665867	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs113124167	168032731	0.1171	intronic	XIRP2	1665868	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025706	168032761	0.1171	intronic	XIRP2	1665869	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025710	168032797	0.1171	intronic	XIRP2	1665870	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025711	168033357	0.1171	intronic	XIRP2	1665875	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025716	168033386	0.1171	intronic	XIRP2	1665876	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025722	168034128	0.1171	intronic	XIRP2	1665881	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025725	1680343492	0.1171	intronic	XIRP2	1665883	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025727	168034680	0.1172	intronic	XIRP2	1665886	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025729	168034780	0.1219	intronic	XIRP2	1665887	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025733	168035024	0.1171	intronic	XIRP2	1665891	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025737	168035337	0.1171	intronic	XIRP2	1665892	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025741	168035341	0.1171	intronic	XIRP2	1665893	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7600229	168035381	0.1219	intronic	XIRP2	1665894	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025736	1680353982	0.1171	intronic	XIRP2	1665899	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs113133603	168036020	0.1171	intronic	XIRP2	1665900	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs111677212	168036332	0.1171	intronic	XIRP2	1665903	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs113561873	168036322	0.1171	intronic	XIRP2	1665903	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs113566519	1680363174	0.1171	intronic	XIRP2	1665908	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73025796	168036326	0.1171	intronic	XIRP2	1665909	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs10497318	168036326	0.1171	intronic	XIRP2	1665911	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16853124	168036352	0.1171	intronic	XIRP2	1665913	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16853134	168036376	0.1171	intronic	XIRP2	1665914	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs5842143	168036387	0.1171	intronic	XIRP2	1665915	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16853136	168036387	0.1171	intronic	XIRP2	1665916	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16706115	168036393	0.1171	intronic	XIRP2	1665917	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs6748606	168036312	0.1171	intronic	XIRP2	1665918	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06

Table 2.17: Differential Effect GWAS results with p-value $< 5 \times 10^{-8}$ (Continued).. Significant results from the Differential Effect GWAS, not pruned for LD.

Phenotype	Chr	rsID	bp	Hutterite Variant	Gene	CGI id	Beta	SE	pvalue	Maternal Beta	Maternal SE	Maternal pvalue	Paternal Beta	Paternal SE	Paternal pvalue	
LYMMI	2	rs11510363	1680388473	0.1219	intronic	XIRP2	1665927	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73027809	1680388365	0.1171	intronic	XIRP2	1665929	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs77729004	1680388304	0.1171	intronic	XIRP2	1665930	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73027812	168038816	0.1171	intronic	XIRP2	1665931	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16833161	1680388941	0.1171	intronic	XIRP2	1665932	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16833163	168038935	0.1171	intronic	XIRP2	1665933	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16833164	168038935	0.1171	intronic	XIRP2	1665934	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs5700446	1680389406	0.1171	intronic	XIRP2	1665935	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73027816	168038968	0.1171	intronic	XIRP2	1665937	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7604418	16804046	0.1171	intronic	XIRP2	1665938	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73027817	168040101	0.1171	intronic	XIRP2	1665939	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7575058	168040115	0.1171	intronic	XIRP2	1665940	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7563857	168040273	0.1219	intronic	XIRP2	1665941	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs760024	168040558	0.1171	intronic	XIRP2	1665944	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs146010076	168040636	0.1171	intronic	XIRP2	1665945	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs10497320	168040700	0.1171	intronic	XIRP2	1665946	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16833169	168040152	0.1171	splicing	XIRP2	1665947	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs14750533	168041832	0.1171	intronic	XIRP2	1665948	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73027825	168042412	0.1171	intronic	XIRP2	1665953	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs79704019	168042760	0.1171	intronic	XIRP2	1665956	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs60361319	168042768	0.1171	intronic	XIRP2	1665957	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7577527	168042901	0.1171	intronic	XIRP2	1665958	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16833177	168043347	0.1171	intronic	XIRP2	1665962	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16833179	168043455	0.1171	intronic	XIRP2	1665963	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16833180	168043497	0.1171	UTR5	XIRP2	1665964	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73027831	168043487	0.1172	intronic	XIRP2	1665965	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs138492108	168043801	0.1172	intronic	XIRP2	1665966	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs75178620	168043469	0.1221	intronic	XIRP2	1665967	-9.14E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16833181	168044579	0.1188	intronic	XIRP2	1665968	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73027839	1680447394	0.1171	intronic	XIRP2	1665969	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs78733773	168044877	0.1171	intronic	XIRP2	1665970	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs34168219	168044900	0.1171	intronic	XIRP2	1665971	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73027841	1680449192	0.1171	intronic	XIRP2	1665982	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs73027843	168045059	0.1171	intronic	XIRP2	1665983	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16833189	168045067	0.1157	intronic	XIRP2	1665985	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs76138924	168051101	0.1158	intronic	XIRP2	1665987	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs7961379	168051461	0.1158	intronic	XIRP2	1665989	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs77816235	168051789	0.1158	intronic	XIRP2	1665991	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs16833201	168051808	0.1169	intronic	XIRP2	1665993	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs989007	168051816	0.1158	intronic	XIRP2	1666001	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06
LYMMI	2	rs2390548	168055739	0.1158	intronic	XIRP2	1666003	-9.15E-02	1.64E-02	4.34E-08	-4.78E-02	1.29E-02	2.28E-04	6.44E-02	1.37E-02	4.72E-06

Table 2.18: **Differential Effect GWAS results with p-value $< 5 \times 10^{-8}$ (Continued)..** Significant results from the Differential Effect GWAS, not pruned for LD.

Phenotype	Chromosome	rsID	bp	Hutterite Variant	MAF	Gene	CGI id	Beta	SE	pvalue	Maternal Beta	Maternal SE	Maternal pvalue	Paternal Beta	Paternal SE	Paternal pvalue
LYM1	2	rs78430257	1680536860	0.1155	intronic	<i>XIRP2</i>	1666005	-9.15E-02	1.64E-02	4.57E-08	-4.64E-02	1.29E-02	3.45E-04	6.56E-02	1.37E-02	3.04E-06
LYM1	2	rs16833221	168066491	0.1155	intronic	<i>XIRP2</i>	1666035	-9.15E-02	1.64E-02	4.57E-08	-4.64E-02	1.29E-02	3.45E-04	6.56E-02	1.37E-02	3.04E-06
LYM1	2	rs17616252	167976692	0.1183	intronic	<i>XIRP2</i>	1665492	-9.14E-02	1.64E-02	4.74E-08	-4.83E-02	1.29E-02	1.94E-04	6.38E-02	1.37E-02	5.66E-06
LYM1	2	rs75188073	167978397	0.1164	intronic	<i>XIRP2-4S1</i>	1665498	-9.14E-02	1.64E-02	4.74E-08	-4.83E-02	1.29E-02	1.94E-04	6.38E-02	1.37E-02	5.66E-06
LYM1	2	rs17616439	167992053	0.1158	ncRNA intronic	<i>XIRP2-4S1</i>	1665544	-9.14E-02	1.64E-02	4.74E-08	-4.83E-02	1.29E-02	1.94E-04	6.38E-02	1.37E-02	5.66E-06
LYM1	2	rs17515389	167997309	0.116	ncRNA intronic	<i>XIRP2-4S1</i>	1665561	-9.14E-02	1.64E-02	4.74E-08	-4.83E-02	1.29E-02	1.94E-04	6.38E-02	1.37E-02	5.66E-06
LYM1	2	rs1004769	167997817	0.1166	intronic	<i>XIRP2</i>	1665563	-9.14E-02	1.64E-02	4.74E-08	-4.83E-02	1.29E-02	1.94E-04	6.38E-02	1.37E-02	5.66E-06
trig	1	rs7525463	218860879	0.1561	ncRNA intronic	<i>MIR548F3</i>	815075	-4.01E-01	7.12E-02	2.51E-08	-2.67E-01	4.87E-02	5.55E-08	1.95E-01	5.96E-02	1.14E-03
trig	1	rs11465142	218833214	0.1862	ncRNA intronic	<i>MIR548F3</i>	814868	-3.89E-01	6.93E-02	2.91E-08	-2.48E-01	4.74E-02	5.66E-08	1.95E-01	5.66E-02	4.41E-04
trig	1	rs5781068	218838976	0.1728	ncRNA intronic	<i>MIR548F3</i>	814893	-3.89E-01	6.93E-02	2.91E-08	-2.48E-01	4.74E-02	5.66E-08	1.95E-01	5.66E-02	4.41E-04
trig	1	rs28420855	218840828	0.1728	ncRNA intronic	<i>MIR548F3</i>	814910	-3.89E-01	6.93E-02	2.91E-08	-2.48E-01	4.74E-02	5.66E-08	1.95E-01	5.66E-02	4.41E-04
trig	1	rs7527236	218846832	0.1534	ncRNA intronic	<i>MIR548F3</i>	814975	-4.10E-01	7.33E-02	3.16E-08	-2.55E-01	4.91E-02	1.99E-07	2.21E-01	6.12E-02	3.25E-04
totalcho	9	rs7033776	36704465	0.4104	intergenic	<i>MEIK</i>	6869852	2.30E-01	4.12E-02	4.12E-08	9.87E-02	3.22E-02	2.28E-03	-1.83E-01	3.35E-02	5.60E-08
eos	1	rs2553879	18732660	0.138	intergenic	<i>IGSF21</i>	91083	9.13E-02	1.61E-02	1.69E-08	4.28E-02	1.23E-02	5.53E-04	6.39E-02	1.21E-02	5.83E-08
eos	1	rs6661638	18734181	0.1386	intergenic	<i>IGSF21</i>	91092	9.13E-02	1.61E-02	1.69E-08	4.28E-02	1.23E-02	5.53E-04	6.39E-02	1.21E-02	5.83E-08
eos	1	rs6664427	18734604	0.1386	intergenic	<i>IGSF21</i>	91094	9.13E-02	1.61E-02	1.69E-08	4.28E-02	1.23E-02	5.53E-04	6.39E-02	1.21E-02	5.83E-08
eos	1	rs1009039	18734931	0.1386	intergenic	<i>IGSF21</i>	91096	9.13E-02	1.61E-02	1.69E-08	4.28E-02	1.23E-02	5.53E-04	6.39E-02	1.21E-02	5.83E-08
eos	1	rs1568342	18735266	0.1386	intergenic	<i>IGSF21</i>	91099	9.13E-02	1.61E-02	1.69E-08	4.28E-02	1.23E-02	5.53E-04	6.39E-02	1.21E-02	5.83E-08
eos	1	rs1547552	18736292	0.1386	intergenic	<i>IGSF21</i>	91101	9.13E-02	1.61E-02	1.69E-08	4.28E-02	1.23E-02	5.53E-04	6.39E-02	1.21E-02	5.83E-08
eos	1	rs2176655	18736474	0.1386	intergenic	<i>IGSF21</i>	91104	9.13E-02	1.61E-02	1.69E-08	4.28E-02	1.23E-02	5.53E-04	6.39E-02	1.21E-02	5.83E-08
eos	1	rs7513256	18732765	0.1381	intergenic	<i>IGSF21</i>	91082	9.11E-02	1.61E-02	1.69E-08	4.31E-02	1.23E-02	4.97E-04	-6.55E-02	1.21E-02	7.08E-08
eos	1	rs1878975	18733117	0.1457	intergenic	<i>IGSF21</i>	91085	8.98E-02	1.61E-02	4.97E-08	4.47E-02	1.26E-02	3.88E-04	-5.94E-02	1.23E-02	1.59E-06
fev1	3	rs12714812	74813002	0.4465	intergenic	<i>CNTN3</i>	2319085	-1.19E-01	2.15E-02	4.52E-08	-7.31E-02	1.62E-02	6.35E-06	5.15E-02	1.78E-03	
neuro	18	rs14230841	33371947	0.04242	intronic	<i>TPGS2</i>	1117155	-2.14E-01	4.06E-02	4.40E-08	-1.88E-01	3.54E-02	1.30E-07	7.81E-02	2.54E-03	
menarche	16	rs12447191	62199299	0.1712	intergenic	<i>CDH8</i>	10523440	-6.54E-01	1.00E-01	5.27E-09	-3.68E-01	8.53E-02	1.88E-05	3.91E-01	8.47E-02	5.04E-06
menarche	16	rs57477941	62200478	0.1712	intergenic	<i>CDH8</i>	10523452	-6.54E-01	1.00E-01	5.27E-09	-3.68E-01	8.53E-02	1.88E-05	3.91E-01	8.47E-02	5.04E-06
menarche	16	rs58758386	62201228	0.1715	intergenic	<i>CDH8</i>	10523456	-6.54E-01	1.00E-01	5.27E-09	-3.68E-01	8.53E-02	1.88E-05	3.91E-01	8.47E-02	5.04E-06

Table 2.19: **Differential Effect GWAS results with p-value < 5 × 10⁻⁸ (Continued)..** Significant results from the Differential Effect GWAS, not pruned for LD.

CHAPTER 3

PARENT-OF-ORIGIN GENE EXPRESSION IN A FOUNDER POPULATION IDENTIFIES TWO NOVEL IMPRINTED GENES AT KNOWN IMPRINTED REGIONS.

3.1 Abstract¹

Genomic imprinting is the phenomena that leads to silencing of one copy of a gene inherited from a specific parent. Mutations in imprinted regions have been involved in diseases showing parent-of-origin effects, such as Prader-Willi and Angelman syndrome, among others. Identifying genes with evidence of parent-of-origin expression patterns in family studies allows the detection of more subtle imprinting. Here we use allele-specific expression in lymphoblastoid cell lines from 306 Hutterites related in a single pedigree to provide formal evidence for parent-of-origin effects. Our approach identified known imprinted genes, two putative novel imprinted genes, and 14 genes with asymmetrical parent-of-origin gene expression. We used gene expression in peripheral blood leukocytes (PBL) to validate our findings, and then confirmed imprinting control regions (ICRs) using DNA methylation levels in the PBLs.

3.2 Introduction

Imprinted genes have one allele silenced in a parent-of-origin specific manner. In humans, approximately 105 imprinted loci have been identified, many of which play important roles in development and growth [35, 90]. Dysregulation of imprinted genes or regions can cause diseases that show parent-of-origin effects, such as Prader-Willi or Angelman syndrome, among others [90]. Imprinted regions have also been associated with complex traits, such as

1. Citation for chapter: Mozaffari SV, Stein MM, Magnaye KM, Nicolae DL, Ober C. Gene Expression and Methylation of Imprinted Genes in the Hutterites bioRxiv (2018).

height and age of menarche [14, 118], as well as common diseases such as obesity and some cancers [90]. More than 80% of imprinted genes in humans are clustered in genomic regions that contain both maternally and paternally expressed genes, as well as genes that encode non-coding RNAs. Parent-specific expression of the genes within a cluster are maintained by complex epigenetic mechanisms at cis-acting imprinting control regions (ICRs) [54], which show parent-of-origin specific DNA methylation patterns and chromatin modifications.

Using RNA-seq and allele-specific expression (ASE) we can map genes to parental haplotypes and identify those that are expressed when inherited from only the father or only from the mother, a hallmark feature of imprinted loci. Parent of origin effects and imprinted genes have been most elegantly studied in mice, where two inbred strains are bred reciprocally to identify parent-of-origin effects on gene expression in progeny that have the same genotypes but different patterns of inheritance [10]. Additionally, uniparental inheritance of imprinted regions in mice were associated with abnormal developmental phenotypes[19] before it was shown that imprinting defects are associated with human disease [78]. One approach to identifying imprinted loci in humans has been to test for parent-of-origin effects on gene expression and phenotypes in pedigrees [56, 14]. For example, Garg et al. used gene expression in LCLs from HapMap trios to identify 30 imprinting eQTLs with parent-of-origin specific effects on expression including two imprinted genes [38]. A study from the GTEx Consortium used RNA-seq data and ASE to identify allelic imbalance in 45 different tissues. By considering genes with monoallelic expression that was evenly distributed to both the reference and alternate alleles across individuals as evidence for imprinting, they identified 42 imprinted genes, both known and novel, and used family studies to confirm imprinting of 5 novel imprinted genes [12]. Santoni et al. identified nine novel imprinted genes using single-cell allele-specific gene expression and identifying genes with mono-allelic expression in fibroblasts from 3 unrelated individuals and probands of 2 family trios, and then using the trios to confirm parent of origin of the alleles [97].

Here, we perform a parent-of-origin ASE study in a large pedigree to characterize parent of origin specific gene expression in the Hutterites, a founder population of European descent, for which we have phased genotype data [63]. We use RNA-seq from lymphoblastoid cell lines (LCLs) to map transcripts to parental haplotypes and identify known and two not previously reported imprinted genes. We validated the two putative imprinted genes by showing the same patterns of parent of origin expression PBLs from different Hutterite individuals, and show DNA methylation signatures of imprinting in the PBLs at these regions.

3.3 Results

3.3.1 *Mapping Transcripts to Parental Haplotypes*

For each of 306 individuals, the total number of transcripts at each gene was assigned as maternally inherited, paternally inherited, or unknown parent of origin. The last group included transcripts without heterozygote SNPs or SNPs without parent of origin information. Transcripts were assigned to the parentally inherited categories using SNPs in the reads and matching alleles to either the known maternally or paternally inherited alleles. All the genes analyzed had some transcripts of neither maternal or paternal origin (average 97.8%, range 8.3-100%). For each gene we assigned parental origin to an average of 1.8% of transcripts (range: 0-34.7%), and for each individual we assigned parental origin to an average of 1.4% of transcripts (range: 0-1.7%). On average, about 40 SNPs per gene were used to assign the transcripts of a gene to parent (range 1-1839 SNPs).

After quality control (see Methods), transcripts in 15,889 genes were detected as expressed in 306 individuals. Some transcripts for 14,791 of those genes could be assigned to a parent. Of these, 75 genes were only expressed on the paternally-inherited allele in at least one individual and not on the maternally inherited allele in any individuals. Similarly, 64 genes were only expressed on the maternally-inherited allele in at least one individual and not on

	Mean	Standard Deviation	Range
Proportion of transcripts from each gene assigned to transcripts of unknown origin	0.978	0.031	(0.083, 1)
Proportion of transcripts from each gene assigned to parental origin	0.018	0.019	(0, 0.347)
Proportion of transcripts for each individual assigned to parental origin	0.014	0.0015	(0, 0.017)

Table 3.1: **Summary Statistics for Parental Origin of Transcripts.**

the paternally inherited allele in any individuals (S1 Table).

3.3.2 *Imprinted Genes in Lymphoblastoid Cell Lines (LCLs)*

Among the 139 genes with only paternally inherited expression or only maternally inherited expression, there are three known imprinted genes (*CDKN1C*, *NDN*, *SNRPN*) and one predicted to be imprinted (*IFITM1*) [65]. *CDKN1C* showed patterns opposite of what has been reported[42, 73], which could be due to the small sample (only three individuals showed expression from one parent) or to the different cell types used here (LCLs) and in previous studies (developing brain and embryonal tumors for *CDKN1C*).

We expect some imprinted genes to have “leaky” expression, such that there is some expression from the parental chromosome that is mostly silenced. To detect these genes, we used a binomial test to find patterns of gene expression asymmetry by parental transcript levels. This analysis identified 28 genes with an FDR <5% (Table 3.2). The 11 genes that showed the most asymmetry are known imprinted genes: *ZDBF2*, *PEG10*, *SNHG14*, *NHP2L1*, *L3MBTL1*, *ZNF331*, *LPAR6*, *FAM50B*, *KCNQ1*, *NAP1L5*, and *IGF1R*. Parent-of-origin expression for *ZDBF2* and *KCNQ1* are shown in Fig 3.1A and 3.1B, respectively. We identified two additional genes that showed asymmetry in parental expression from mostly one parent (*PXDC1*, *PWAR6*), which we consider potentially new imprinted genes. The remaining fourteen genes showed significant patterns of asymmetry but had expression from both maternal and paternal transcript levels. These genes are likely not imprinted but could

have asymmetry in expression due to an expression quantitative trait loci (eQTL).

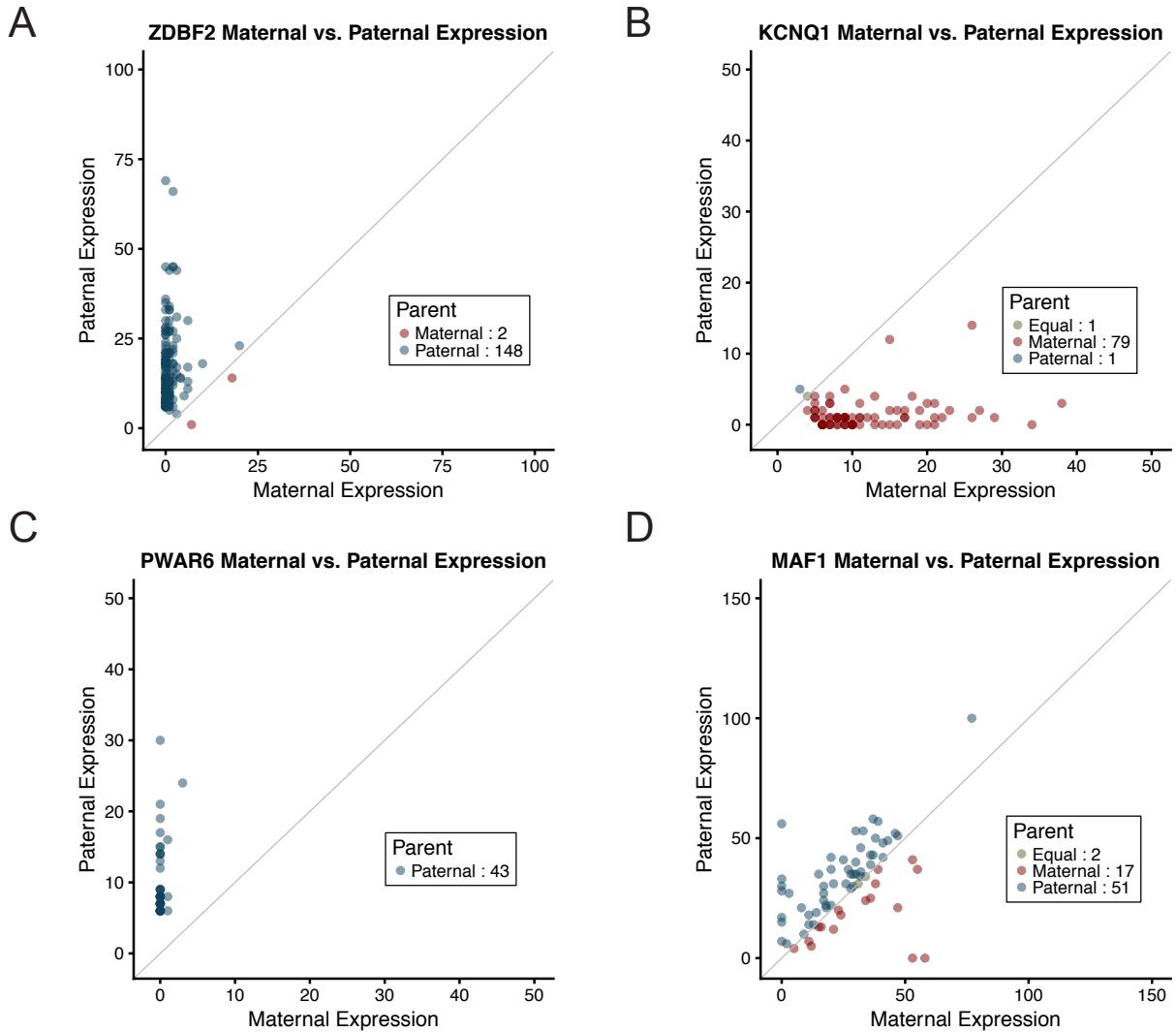


Figure 3.1: Plot of maternal (x-axis) and paternal (y-axis) gene expression for four genes. Plot of maternal (x-axis) and paternal (y-axis) gene expression for four genes. (A) maternally imprinted gene *ZDBF2* (paternally expressed), (B) paternally imprinted gene *KCNQ1* (maternally expressed), (C) novel maternally imprinted gene *PWAR6* (paternally expressed), (D) gene with asymmetry in parental expression *MAF1*. Each point represents one individual. Numbers in the legend represent the number of individuals with equal maternal and paternal expression, more maternal expression, or more paternal expression.

Two genes showed gene expression signatures consistent with imprinting but have not previously been specifically validated as imprinted genes. The first potentially new imprinted gene is *PXDC1*, which is in the same region and next to (<100kb) a known imprinted gene,

Gene	p-value	Number of individuals with more maternal expression than paternal expression	Number of individuals with more paternal expression than maternal expression	References
A. Known Imprinted				
<i>ZDBF2</i>	1.59E-41	2	148	geneimprint.com, Baran et al[12], and Babak et al.[10]
<i>PEG10</i>	5.51E-38	2	136	geneimprint.com, Baran et al[12], and Babak et al.[10]
<i>SNHG14</i>	1.64E-36	2	131	Baran et al[12]
<i>NHP2L1</i>	1.24E-33	23	189	Babak et al.[10] and Docherty et al. [30]
<i>L3MBTL1</i>	6.72E-31	2	107	geneimprint.com, and Li et al. [61]
<i>ZNF331</i>	4.05E-25	36	184	Daelemans et al.[27] and Baran et al[12]
<i>LPAR6</i>	2.65E-23	9	76	Baran et al[12]
<i>FAM50B</i>	5.29E-23	0	75	geneimprint.com, Baran et al[12]
<i>KCNQ1</i>	1.34E-22	79	1	geneimprint.com, Baran et al[12]
<i>NAP1L5</i>	3.76E-09	0	29	geneimprint.com
<i>IGF1R</i>	1.11E-05	14	49	geneimprint.com, Sun et al. [103], Kang et al. [55], Boucher et al. [15], and Al Adhami et al.[5]
B. Conflicting Evidence for Imprinting Status in the Literature				
<i>PRIM2</i>	5.53E-05	30	71	geneimprint.com, Santoni et al. [97]
C. New Imprinted Genes				
<i>PXDC1</i>	9.83E-14	12	81	-
<i>PWAR6</i>	2.27E-13	0	43	-
D. Genes with Asymmetrical Parent-of-Origin Expression				
<i>SNHG17</i>	6.2E-08	113	45	-
<i>ZNF813</i>	8.7E-07	63	132	-
<i>DAAM1</i>	1.78E-05	66	126	-
<i>RP11-379H18.1</i>	2.09E-05	52	106	-
<i>HMGN1P38</i>	2.09E-05	52	106	-
<i>MTX2</i>	3.05E-05	0	16	-
<i>ZNF714</i>	4.61E-05	35	79	-
<i>MAF1</i>	4.45E-05	17	51	-
<i>IL16</i>	5.71E-05	61	115	-
<i>CPNE1</i>	5.56E-05	111	58	-
<i>ATP6V0D1</i>	7.03E-05	32	7	-
<i>FAHD1</i>	9.34E-05	68	29	-
<i>CNN2</i>	1.18E-04	127	72	-
<i>HSP90AB3P</i>	1.16E-04	7	31	-

Table 3.2: **Results for Genes with Parent-of-Origin Expression Asymmetry.** Genes listed by category of imprinting status: (A) Known Imprinted, (B) Conflicting Evidence for Imprinted Status, (C) New Imprinted Genes, (D) Genes with Asymmetrical Parent-of-Origin Expression. Genes are ordered by significance within each category.

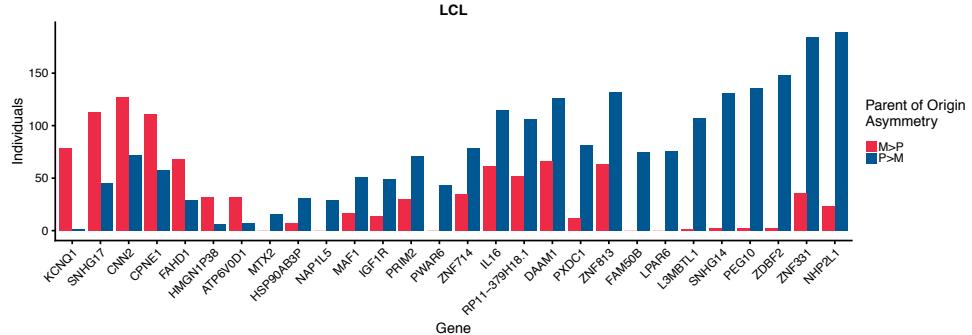
FAM50B. The second potentially novel imprinted gene is *PWAR6*, or Prader Willi Angelman Region RNA6, a gene encoding regulatory class of RNA. Although this gene is located within the intron of a known imprinted region, *SNHG14*, this noncoding RNA has not previously been recognized as having parent-of-origin specific expression (Fig 3.1C).

The remaining fourteen genes show significant asymmetry using the binomial test but do not have expression from mostly one parental chromosome. One of these genes, *SNHG17*, is a noncoding RNA. Another gene with parent-of-origin asymmetry, *ZNF813*, is next to a known imprinted gene, *ZNF331*. The remaining genes with asymmetrical parent origin expression have expression from both parental chromosomes, unlike imprinted genes. These genes include *DAAM1*, which is involved in cytoskeleton, specifically filopodia formation [43, 66], and has a suggested role for cytoskeleton organization during Mammalian testis morphogenesis and gamete progression [87]; *RP11-379H18.1*, a noncoding RNA gene; *HMGN1P38* [101]; *MTX2*, a nuclear gene that interacts with mitochondrial membrane protein metaxin 1 and is involved in mitochondrial protein import and metabolism of proteins in mice; *MAF1* a negative regulator of RNA polymerase 2; *ZNF714*, *CPNE1*, *IL16*, *ATP6V0D1*, *FAHD1*, *HSP90AB3P*, and *CNN2* are the remaining genes that show parent-of-origin asymmetry but not with a pattern consistent with imprinting (Figure 3.4).

3.3.3 Validation of Imprinted Genes in PBLs

Using the same methods described above, we assigned parent of origin to transcripts in PBLs from 99 Hutterite individuals not included in the LCL studies. Maternal and paternal expression in PBLs for all 28 genes identified in LCLs showed similar trends of asymmetry as in LCLs (Figure 3.2).

A



B

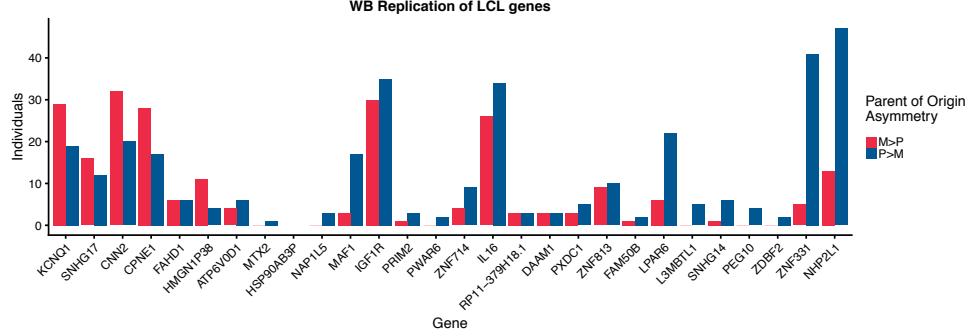


Figure 3.2: Validation in PBLs. Histogram showing the number of individuals with more maternal expression ($M > P$) or more paternal expression ($P > M$) for the 28 genes showing parent-of-origin asymmetry in LCLs (A) and PBLs (B). Genes are ordered by the magnitude of the difference in the number of individuals with more maternal expression than paternal expression in LCLs.

3.3.4 Methylation at Imprinting Control Regions

One of the mechanisms underlying parent-of-origin effects on expression at imprinted loci is differential methylation at cis-acting imprinting control regions (ICRs). DNA methylation from the Illumina HumanMethylation 450K array was available in PBLs from the same individuals included in the validation studies described above. To determine the expected patterns of methylation at known imprinted loci, we first looked at previously characterized methylated regions at known imprinted regions from Court et al. and Joshi et al. [24, 50].

The methylation patterns at the two potentially novel imprinted genes identified in this study, *PXDC1* and *PWAR6*, lie in or near known imprinted regions that contain previously

characterized ICRs. These previously characterized ICRs show about 50% methylation (beta value of between 0.25 and 0.75) in our DNA methylation data, which likely reflect methylation at only one parental chromosome in all the cells in the sample. Methylation patterns in PBLs at these two ICRs fall within this hemi-methylation range, further suggesting that these two genes are indeed imprinted (Fig 3.3).

3.4 Discussion

Dysregulation of imprinted genes can have a large impact on mammalian development and has been associated with significant diseases in humans. Studies aimed at identifying imprinted genes at genome-wide levels have used ASE and imbalance to infer parent of origin. Here we used a large pedigree with assigned parent-of-origin alleles to map transcripts to chromosomes with known parent of origin and identify imprinted genes.

Using this approach, we found transcripts with expression primarily from either the maternal or paternal haplotype. Because gene silencing at imprinted loci may be incomplete, we used a binomial test on parent-of-origin gene expression and identified 11 known imprinted genes and two potentially novel imprinted genes. Both of these novel genes, *PWAR6* and *PXDC1*, lie in known imprinted regions but have not themselves been characterized as imprinted. The remaining genes that have significant parent-of-origin asymmetry in gene expression do not show clear imprinting expression patterns. To validate these findings, we mapped gene expression in PBLs from Hutterite individuals not included in the LCL study. The same genes showed similar patterns of asymmetry in these different cell sources (transformed B cells and peripheral blood leukocytes) from different individuals.

In addition to validating gene expression, we characterized methylation patterns near genes showing asymmetry. Using results from studies that had previously characterized ICRs in patients with uniparental disomy at many imprinted regions [50, 24], we estimated regions for defining hemi-methylation near the genes identified in our study. Using this

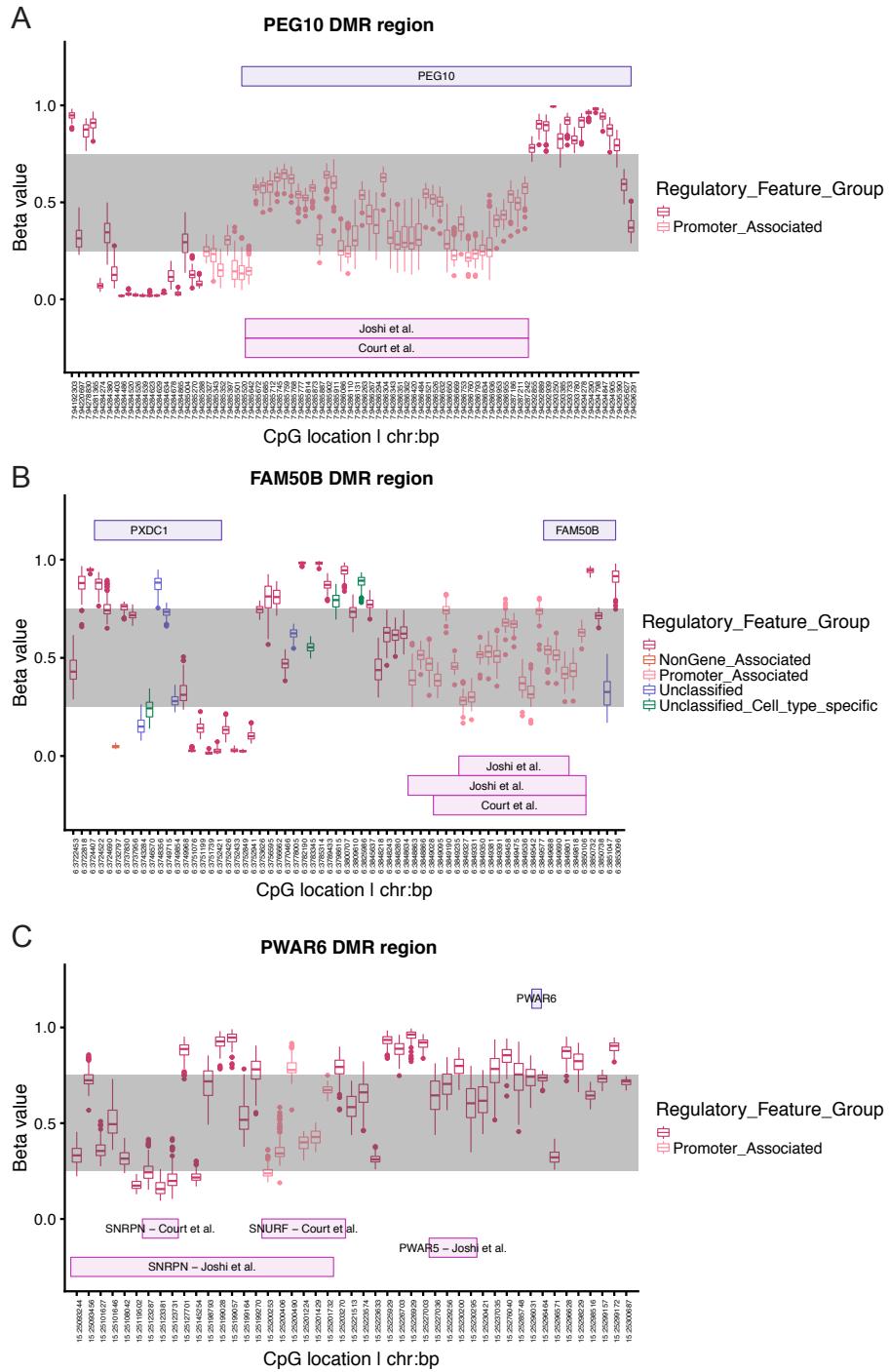


Figure 3.3: **Methylation at ICRs.** DNA methylation levels near known and novel imprinted genes previously defined by Joshi et al. and Court et al. (A) *PEG10*, (B) *PXDC1* and *FAM50B*, (C) *PWAR6*.

approach, we were able to provide additional supportive data for the two potentially novel imprinted genes to be true imprinted genes regulated by previously characterized ICRs.

Although our study is the largest pedigree-based study to date to search genome-wide for imprinted genes, it has limitations. First, we are able to determine the parent of origin for many transcripts in the Hutterites but we could not assign every RNA sequencing read to a parent due to lack of heterozygous sites or missing parent-of-origin information for alleles. Second, we conducted these studies in lymphoblastoid cell lines, and therefore could only study genes imprinted in this cell type and would miss the many imprinted genes that are tissue-specific and/or developmentally regulated. Third, while we can verify previously characterized ICRs, our study is not designed to identify novel ICRs because DNA methylation values from an array cannot be assigned to parental haplotype. Lastly, although we characterized the gene expression and methylation patterns for two potentially novel imprinted genes, replication of these genes in a different population and in different tissues, and functional characterization of these genes are required to confirm their status as imprinted genes. Similarly, most of the other genes with parent-of-origin asymmetry in the blood cells examined in this study may show more clear-cut evidence for imprinting in other tissues or at specific periods of development.

In summary, we have identified two new imprinted genes using gene expression from a founder population. The genes with asymmetrical parental expression had similar patterns of asymmetry in a different source of blood cells and in different individuals, and we were able to replicate the methylation patterns in known ICRs near the known and novel imprinted genes in this study. Our method and study population allowed us to map reads to parental haplotypes and uncovered *PWAR6* and *PXDC1* as new imprinted genes that could potentially impact disease risk and development.

3.5 Methods

3.5.1 *Genotypes*

Hutterite individuals ($n=1,653$) were genotyped using one of three Affymetrix genotype arrays, as previously described[63], of which 121 underwent whole genome sequencing by Complete Genomics, Inc (CGI) ($n=98$) or Illumina whole genome sequencing ($n=27$). A total of 10,235,233 variants present in the sequenced individuals were imputed and phased to the remaining 1532 genotyped individuals using PRIMAL [63]. Parent of origin was assigned to 89.85% of the alleles with call rate 81.6842% after QC. These include homozygous SNPs. For this study, we included individuals with genotyped parents in the primary analyses in LCLs. Written consents for these studies were obtained from the adult participants and parents of children under 18; written assents were obtained from all children. This study was approved by the University of Chicago Institutional Review Board.

3.5.2 *RNA-seq in Lymphoblastoid Cell Lines (LCLs).*

RNA-seq was performed in LCLs as previously described [26]. For this study, sequencing reads were reprocessed as follows. Reads were trimmed for adaptors using Cutadapt (reads less than 5 bp discarded) then remapped to hg19 using STAR indexed with gencode version 19 gene annotations [29, 72]. To remove mapping bias, reads were processed and duplicate reads removed using WASP [107]. We used a custom script modified from WASP to separate reads that overlap maternal alleles or paternal alleles. Instead of providing as input reference and alternate alleles in one file for all individuals, we input maternal and paternal alleles for each individual and separated out reads by matching alleles in the reads to the parentally inherited alleles. Reads without informative SNPs (homozygous, or no parent-of-origin information) were categorized as unknown where the unknown, maternal, and paternal make up the total gene expression. Gene counts were quantified using STAR for each category. VerifyBamID

was used to identify sample swaps [51]. Genes mapping to the X and Y chromosome were removed; genes with a CPM log transformed value less than 1 in less than 20 individuals were also removed.

3.5.3 RNA-seq in Peripheral Blood Leukocytes (PBLs)

RNA-seq was performed in whole blood as previously described [100]. For this study, sequencing reads were reprocessed as described above for the studies in LCLs. For all analyses, we excluded 32 individuals who were also in the LCL study.

3.5.4 Identifying Imprinted Genes

We used a binomial test to detect asymmetry in parent-of-origin gene expression. We generated a binomial Z-score for each individual for each gene (Z_i) and excluded those where $Z_i = 0$. For each gene, the number of subjects with $Z_i > 0$ can be modeled by a Binomial distribution with probability 1/2. For imprinted genes that show patterns of asymmetry, we expect a distribution of Z-scores that are skewed to one direction: right-skewed for genes asymmetrically maternally expressed and left-skewed for genes asymmetrically paternally expressed. Because we are only asking whether there are more individuals with more maternal expression or more paternal expression and not gene expression measures there is no need to model over-dispersion.

3.5.5 DNA methylation profiling and processing in PBLs

One milliliter of whole blood from 145 Hutterites was drawn into TruCulture (Myriad RBM; Austin, Texas) tubes containing proprietary TruCulture media. DNA was extracted using AllPrep DNA/RNA Mini Kits (Qiagen). DNA samples were bisulfite converted and hybridized to the Illumina HumanMethylation 450K array at the University of Chicago Functional Genomics Center. Samples were processed using default parameters using the

R package minfi [7], normalized using SWAN (subset within-array normalization [70]) and quantile normalized similar to previous methylation studies [79]. Probes were removed if: (1) mapped non-uniquely to a bisulfite-converted genome; (2) mapped to sex chromosomes; (3) had a probe detection p-value >0.01 in at least 25% of samples; and (4) contained common SNPs within the probe sequence, as previously described[11]. Principal components analysis (PCA) was used to identify significant technical covariates, and the ComBat function [49] within the R package sva [60] was used to correct for chip effect. Analyses of DNA methylation levels were conducted using beta values, which were converted from M-values using the lumi R package [31].

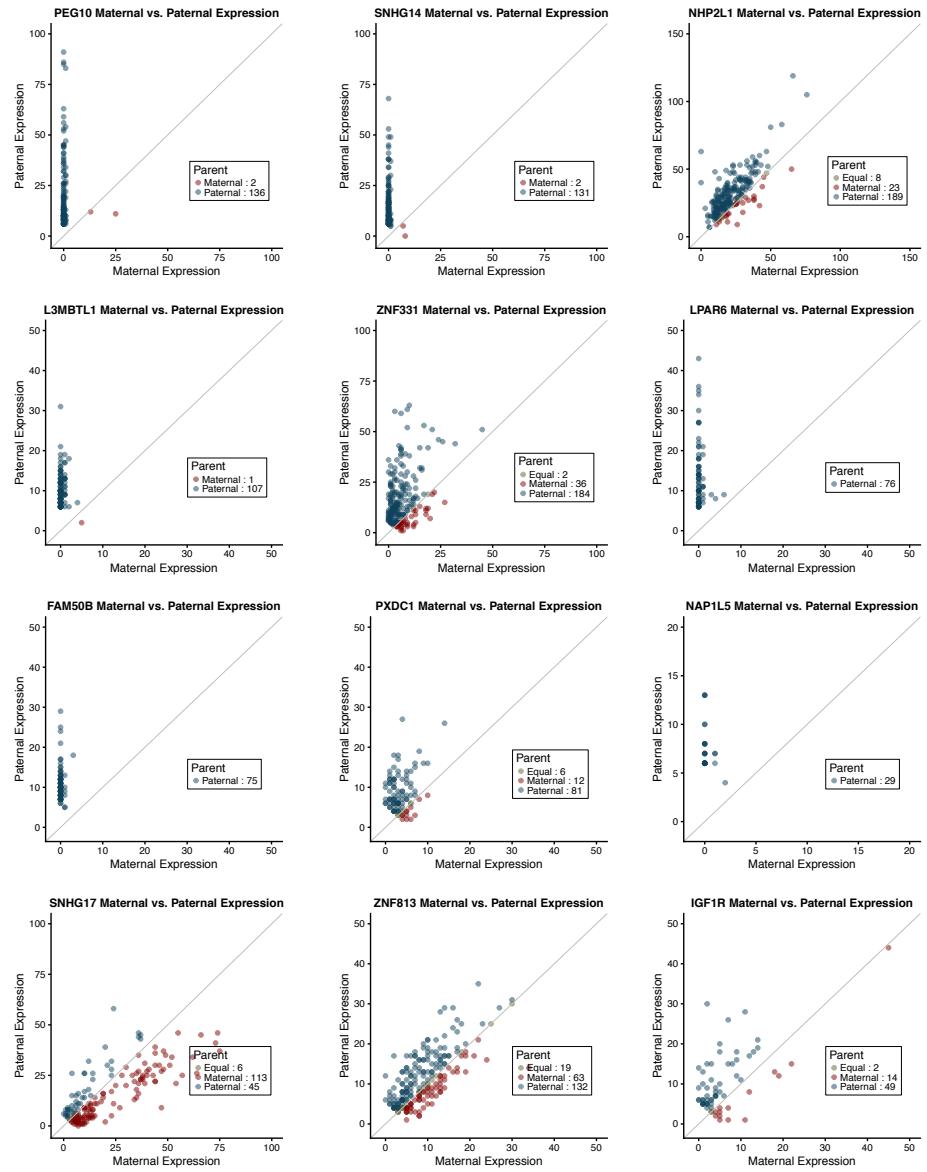


Figure 3.4: Plots of maternal and paternal expression for remaining genes with parent-of-origin asymmetry. Maternal gene expression along x-axis and paternal gene expression along y-axis.

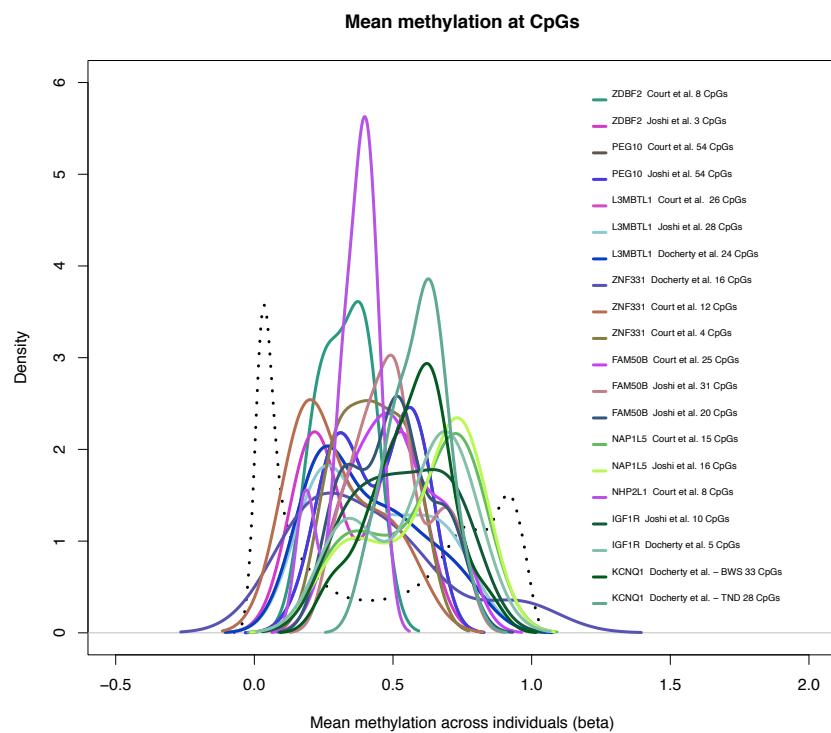


Figure 3.5: Density plot for DMRs for all imprinted genes. DNA methylation density plots for all imprinted genes with methylation levels in Joshi *et al*[50] and Court *et al.*[24]

Gene	Number of Individuals	Gene Name	Imprinted Status	Observed Expression Pattern in LCLs	Pattern consistent with known expression?
ENSG00000182636	22	<i>NDN</i>	Known	Paternal	Consistent
ENSG00000259261	11	<i>IGHV4OR15-8</i>		Maternal	
ENSG00000128739	9	<i>SNRPN</i>	Known	Paternal	Consistent
ENSG00000185044	9	<i>RP11-435B5.4</i>		Maternal	
ENSG00000089876	6	<i>DHX32</i>		Paternal	
ENSG00000262333	5	<i>HNRNPA1P16</i>		Paternal	
ENSG00000196378	5	<i>ZNF34</i>		Maternal	
ENSG00000198744	5	<i>RP5-857K21.11</i>		Maternal	
ENSG00000233757	5	<i>AC092835.2</i>		Maternal	
ENSG00000272933	5	<i>RP11-47A8.5</i>		Maternal	
ENSG00000154611	4	<i>PSMA8</i>		Paternal	
ENSG00000228109	4	<i>MFI2-AS1</i>		Paternal	
ENSG00000103269	4	<i>RHBDL1</i>		Maternal	
ENSG00000129654	4	<i>FOXJ1</i>		Maternal	
ENSG00000129757	3	<i>CDKN1C</i>	Known	Paternal	Inconsistent
ENSG00000137936	3	<i>BCAR3</i>		Paternal	
ENSG00000148926	3	<i>ADM</i>		Paternal	
ENSG00000204482	3	<i>LST1</i>		Paternal	
ENSG00000211669	3	<i>IGLV3-10</i>		Paternal	
ENSG00000223509	3	<i>RP11-632K20.7</i>		Paternal	
ENSG00000260442	3	<i>RP11-22P6.3</i>		Paternal	
ENSG00000270441	3	<i>RP11-694I15.7</i>		Paternal	
ENSG00000160828	3	<i>STAG3L2</i>		Maternal	
ENSG00000165886	3	<i>UBTD1</i>		Maternal	
ENSG00000181284	3	<i>TMEM102</i>		Maternal	
ENSG00000214269	3	<i>LGMNP1</i>		Maternal	
ENSG00000258561	3	<i>RP11-72M17.1</i>		Maternal	
ENSG00000075089	2	<i>ACTR6</i>		Paternal	
ENSG00000105518	2	<i>TMEM205</i>		Paternal	
ENSG00000115457	2	<i>IGFBP2</i>		Paternal	
ENSG00000137821	2	<i>LRRK49</i>		Paternal	
ENSG00000158517	2	<i>NCF1</i>		Paternal	
ENSG00000183604	2	<i>RP11-347C12.2</i>		Paternal	
ENSG00000211637	2	<i>IGLV4-69</i>		Paternal	
ENSG00000211940	2	<i>IGHV3-9</i>		Paternal	

Table 3.3: **Genes with only Maternal/ only Paternal gene expression.** Genes expressed only from one parent in number of individuals listed in column 2 (Number of Individuals). Imprinting status and pattern of gene expression in LCLs listed in columns 4 and 5.

Gene	Number of Individuals	Gene Name	Imprinted Status	Observed Expression Pattern in LCLs	Pattern consistent with known expression?
ENSG00000233426	2	<i>EIF3FP3</i>		Paternal	
ENSG00000240041	2	<i>IGHJ4</i>		Paternal	
ENSG00000240731	2	<i>RP5-890O3.9</i>		Paternal	
ENSG00000272145	2	<i>NFYC-AS1</i>		Paternal	
ENSG0000025156	2	<i>HSF2</i>		Maternal	
ENSG00000108298	2	<i>RPL19</i>		Maternal	
ENSG00000133216	2	<i>EPHB2</i>		Maternal	
ENSG00000133328	2	<i>HRASLS2</i>		Maternal	
ENSG00000134864	2	<i>GGACT</i>		Maternal	
ENSG00000158481	2	<i>CD1C</i>		Maternal	
ENSG00000169019	2	<i>COMMD8</i>		Maternal	
ENSG00000175701	2	<i>LINC00116</i>		Maternal	
ENSG00000196465	2	<i>MYL6B</i>		Maternal	
ENSG00000198155	2	<i>ZNF876P</i>		Maternal	
ENSG00000215030	2	<i>RPL13P12</i>		Maternal	
ENSG00000232640	2	<i>RP1-266L20.2</i>		Maternal	
ENSG00000233493	2	<i>TMEM238</i>		Maternal	
ENSG00000235400	2	<i>RP4-641G12.4</i>		Maternal	
ENSG00000240652	2	<i>RP11-832N8.1</i>		Maternal	
ENSG00000243364	2	<i>EFNA4</i>		Maternal	
ENSG00000255135	2	<i>RP11-111M22.3</i>		Maternal	
ENSG00000267152	2	<i>CTD-2528L19.6</i>		Maternal	
ENSG00000033122	1	<i>LRRC7</i>		Paternal	
ENSG00000096080	1	<i>MRPS18A</i>		Paternal	
ENSG00000100442	1	<i>FKBP3</i>		Paternal	
ENSG00000100632	1	<i>ERH</i>		Paternal	
ENSG00000109083	1	<i>IFT20</i>		Paternal	
ENSG00000111875	1	<i>ASF1A</i>		Paternal	
ENSG00000116819	1	<i>TFAP2E</i>		Paternal	
ENSG00000121089	1	<i>NACA3P</i>		Paternal	
ENSG00000122218	1	<i>COPA</i>		Paternal	
ENSG00000128011	1	<i>LRFN1</i>		Paternal	
ENSG00000129673	1	<i>AANAT</i>		Paternal	
ENSG00000140459	1	<i>CYP11A1</i>		Paternal	
ENSG00000148187	1	<i>MRRF</i>		Paternal	

Table 3.4: Genes with only Maternal/ only Paternal gene expression (Continued).
 Genes expressed only from one parent in number of individuals listed in column 2 (Number of Individuals). Imprinting status and pattern of gene expression in LCLs listed in columns 4 and 5.

Gene	Number of Individuals	Gene Name	Imprinted Status	Observed Expression Pattern in LCLs	Pattern consistent with known expression?
ENSG00000150456	1	<i>N6AMT2</i>		Paternal	
ENSG00000151366	1	<i>NDUFC2</i>		Paternal	
ENSG00000154640	1	<i>BTG3</i>		Paternal	
ENSG00000158716	1	<i>DUSP23</i>		Paternal	
ENSG00000158806	1	<i>NPM2</i>		Paternal	
ENSG00000163634	1	<i>THOC7</i>		Paternal	
ENSG00000165121	1	<i>RP11-213G2.3</i>		Paternal	
ENSG00000167286	1	<i>CD3D</i>		Paternal	
ENSG00000173715	1	<i>C11orf80</i>		Paternal	
ENSG00000173762	1	<i>CD7</i>		Paternal	
ENSG00000175550	1	<i>DRAP1</i>		Paternal	
ENSG00000179603	1	<i>GRM8</i>		Paternal	
ENSG00000181038	1	<i>METTL23</i>		Paternal	
ENSG00000181852	1	<i>RNF41</i>		Paternal	
ENSG00000183506	1	<i>PI4KAP2</i>		Paternal	
ENSG00000197568	1	<i>HHLA3</i>		Paternal	
ENSG00000198356	1	<i>ASNA1</i>		Paternal	
ENSG00000204472	1	<i>AIF1</i>		Paternal	
ENSG00000211594	1	<i>IGKJ4</i>		Paternal	
ENSG00000211595	1	<i>IGKJ3</i>		Paternal	
ENSG00000211965	1	<i>IGHV3-49</i>		Paternal	
ENSG00000215548	1	<i>RP11-764K9.4</i>		Paternal	
ENSG00000225329	1	<i>RP11-325F22.5</i>		Paternal	
ENSG00000226121	1	<i>AHCTF1P1</i>		Paternal	
ENSG00000233912	1	<i>AC026202.3</i>		Paternal	
ENSG00000239819	1	<i>IGKV1D-8</i>		Paternal	
ENSG00000239830	1	<i>RPS4XP22</i>		Paternal	
ENSG00000243312	1	<i>RP11-397E7.1</i>		Paternal	
ENSG00000244055	1	<i>AC007566.10</i>		Paternal	
ENSG00000253998	1	<i>IGKV2-29</i>		Paternal	
ENSG00000257261	1	<i>RP11-96H19.1</i>		Paternal	
ENSG00000259699	1	<i>HMGB1P8</i>		Paternal	
ENSG00000260219	1	<i>RP11-347C12.10</i>		Paternal	
ENSG00000260655	1	<i>CTA-250D10.23</i>		Paternal	
ENSG00000264473	1	<i>hsa-mir-4538</i>		Paternal	

Table 3.5: Genes with only Maternal/ only Paternal gene expression (Continued).
 Genes expressed only from one parent in number of individuals listed in column 2 (Number of Individuals). Imprinting status and pattern of gene expression in LCLs listed in columns 4 and 5.

Gene	Number of Individuals	Gene Name	Imprinted Status	Observed Expression Pattern in LCLs	Pattern consistent with known expression?
ENSG00000268568	1	<i>AC007228.9</i>		Paternal	
ENSG00000106211	1	<i>HSPB1</i>		Maternal	
ENSG00000118514	1	<i>ALDH8A1</i>		Maternal	
ENSG00000126709	1	<i>IFI6</i>		Maternal	
ENSG00000131773	1	<i>KHDRBS3</i>		Maternal	
ENSG00000135914	1	<i>HTR2B</i>		Maternal	
ENSG00000136104	1	<i>RNASEH2B</i>		Maternal	
ENSG00000136463	1	<i>TACO1</i>		Maternal	
ENSG00000148444	1	<i>COMMD3</i>		Maternal	
ENSG00000156873	1	<i>PHKG2</i>		Maternal	
ENSG00000163249	1	<i>CCNYL1</i>		Maternal	
ENSG00000164794	1	<i>KCNV1</i>		Maternal	
ENSG00000172586	1	<i>CHCHD1</i>		Maternal	
ENSG00000174871	1	<i>CNIH2</i>		Maternal	
ENSG00000178922	1	<i>HYI</i>		Maternal	
ENSG00000183426	1	<i>NPIPA1</i>		Maternal	
ENSG00000185885	1	<i>IFITM1</i>	Predicted	Maternal	Consistent
ENSG00000197279	1	<i>ZNF165</i>		Maternal	
ENSG00000199753	1	<i>SNORD104</i>		Maternal	
ENSG00000215302	1	<i>CTD-3092A11.1</i>		Maternal	
ENSG00000226085	1	<i>UQCRFS1P1</i>		Maternal	
ENSG00000227053	1	<i>RP11-395B7.4</i>		Maternal	
ENSG00000232573	1	<i>RPL3P4</i>		Maternal	
ENSG00000237973	1	<i>hsa-mir-6723</i>		Maternal	
ENSG00000240356	1	<i>RPL23AP7</i>		Maternal	
ENSG00000240449	1	<i>RP4-584D14.5</i>		Maternal	
ENSG00000253485	1	<i>PCDHGA5</i>		Maternal	
ENSG00000254681	1	<i>PKD1P5</i>		Maternal	
ENSG00000254887	1	<i>CTC-378H22.1</i>		Maternal	
ENSG00000261504	1	<i>RP11-317P15.4</i>		Maternal	
ENSG00000262691	1	<i>CTC-277H1.7</i>		Maternal	
ENSG00000266208	1	<i>CTD-2267D19.3</i>		Maternal	
ENSG00000268030	1	<i>AC005253.2</i>		Maternal	
ENSG00000272468	1	<i>RP1-86C11.7</i>		Maternal	

Table 3.6: **Genes with only Maternal/ only Paternal gene expression (Continued).** Genes expressed only from one parent in number of individuals listed in column 2 (Number of Individuals). Imprinting status and pattern of gene expression in LCLs listed in columns 4 and 5.

CHAPTER 4

PARENT-OF-ORIGIN EFFECTS ON GENE EXPRESSION

4.1 Abstract

In this chapter, I explore the impact of parental origin of genetic variation on gene expression. We are interested in identifying any variants that are eQTLs but differ in direction by the parent the variant was inherited from. We performed opposite effect eQTL (oeQTL) and *cis* maternal and paternal eQTL (mat-eQTL, pat-eQTL) using lymphoblastoid cell line (LCL) gene expression in 306 Hutterites. We did not find any variants that have opposite effects by parental origin on gene expression with either of these two approaches. We also used a χ^2 test to search for parent specific effects on reciprocal heterozygotes using parent specific gene expression and identified SNPs that have modest parent-of-origin eQTL effects that need to be investigated further.

4.2 Introduction

Imprinted genes have one allele silenced in a parent-of-origin specific manner. In humans, approximately 150 imprinted loci have been identified, many of which play important roles in development and growth [35, 90, 14]. Dysregulation of imprinted genes or regions can cause diseases that show parent-of-origin effects, such as Prader-Willi or Angelman syndrome, among others [90]. Dysregulation of imprinted genes can be caused by large deletions but also by single variant mutations. Imprinted regions have also been associated with complex traits, such as height and age of menarche [14, 118], as well as common diseases such as obesity and some cancers [90]. We know that SNPs associated with traits are more likely to be eQTLs [80], and here we explore if different parentally inherited alleles can have different impacts on gene expression and can be identified as parent-of-origin eQTLs with potential impacts on traits. We are not the first to look for parent-of-origin effects on gene expression:

Garg et al. used gene expression in LCLs from HapMap trios to identify thirty imprinting eQTLs with parent-of-origin specific effects on expression of which two were known imprinted genes [38]. Garg et al. looked for impact of parent-of-origin specific effects on gene expression [38], but no one has yet looked for eQTLs on parent specific expression coming from the same haplotype as the parentally inherited allele.

Using RNA-seq and allele specific expression (ASE) we can map genes to parental haplotypes that will inform us of gene expression from parental chromosomes. With parentally mapped gene expression data, we can ask if genetic variation on the parental haplotype can influence gene expression from the same haplotype. We are the first to look for 1) parental genetic variation that can have opposite effects on gene expression, as well as 2) maternal or paternally inherited genetic variation that could affect parental gene expression on the same chromosome.

We use methods to detect opposite parent-of-origin effects on total expression, as well as parent-specific expression in the Hutterites, a founder population of European descent, for which we have phased genotype data [63]. We use RNA-seq from LCLs to map transcripts to parental haplotypes and use the parental gene expression to look for variation in *cis* that would effect gene expression. Our study is likely underpowered to identify any opposite effect parent-of-origin eQTLs but we do identify a few parent-of-origin eQTLs where parentally inherited variation affects parent specific gene expression from the same haplotype. There is no known biological mechanism as to why parent-of-origin eQTLs could exist outside of imprinted loci.

4.3 Results

For each of 306 individuals, the total number of transcripts at each gene was assigned as maternally inherited, paternally inherited, or unknown parent of origin. The last group included transcripts without heterozygote SNPs or SNPs without parent-of-origin information.

Transcripts were assigned to the parentally inherited categories using SNPs in the reads and matching alleles to either the known maternally or paternally inherited alleles. All the genes analyzed had some transcripts of unknown origin (average 97.8%, range 8.3-100%). For each gene we assigned parental origin to an average of 1.8% of transcripts (range: 0-34.7%), and for each individual we assigned parental origin to an average of 1.4% of transcripts (range: 0-1.7%). On average, about 40 SNPs per gene were used to assign the transcripts of a gene to a parent (range 1-1839 SNPs).

4.3.1 Opposite Parent-of-Origin eQTL (oeQTL)

Our original oeQTL identified three significant opposite effect associations but these associations were driven by one individual's genotype. The significant associations are shown in Figures 4.1. Once we subset SNPs on having at least three individuals in each of three genotype groups, we did not find any significant results (Bonferroni corrected p-value).

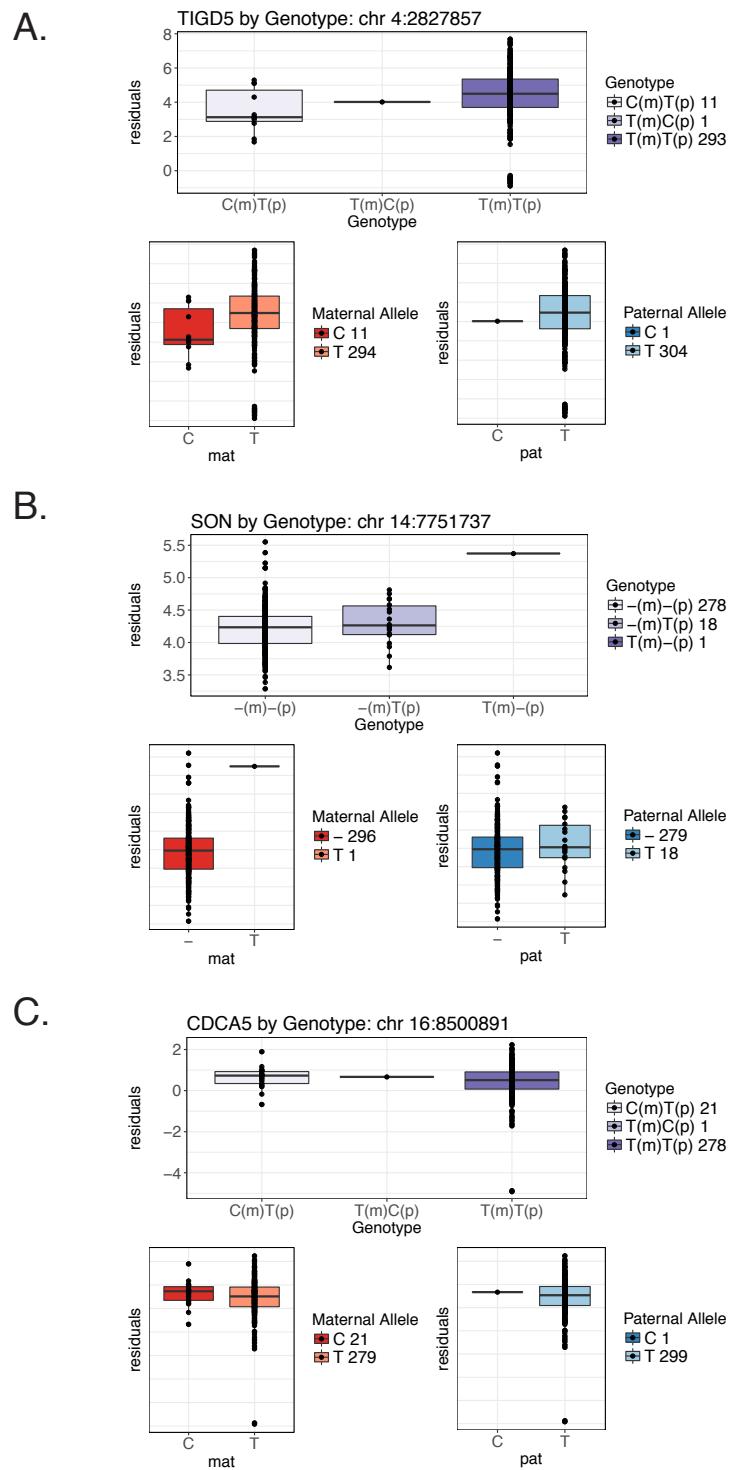


Figure 4.1: **Opposite effect eQTLs driven by one individual's genotype.** The three most significant opposite effect eQTLs for genes A) *TIGD5* (p-value 3.1×10^{-9}), B) *SON* (4.3×10^{-9}) and C) *CDCA5* (p-value 3.5×10^{-9}). The parent-of-origin eQTL is driven by one heterozygous individual for each gene.

4.3.2 Single Parent eQTL (mat-eQTL, pat-eQTL)

We performed the mat-eQTL and pat-eQTL analysis, using parent-of-origin normalized expression. We normalized the parental gene expression data using library sizes from the total gene expression(see Methods). However, the data was sparse and zeros drove most of the analysis. The significant maternal and paternal associations were driven by zeros in the data shown in Figures 4.2 and 4.3.

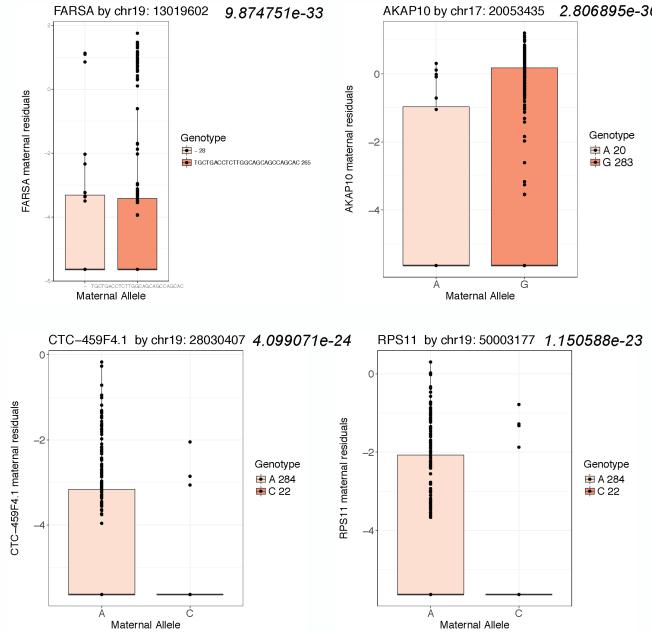


Figure 4.2: Maternal eQTL Associations Driven by Null Values. The four most significant maternal eQTL associations. Most of the individuals have no value of expression for these genes, we see most of the genes have a median that corresponds to a value of zero after normalization.

To address this problem, we redid the same analysis using only informative reads, removing zeros that were due to absence of heterozygous SNPs in the gene (see Methods for more detail). There were 7,398,096 SNP-gene pairs we could compare across both single parent eQTLs. For eQTLs significant in both, (60,549 SNP gene pairs), the effect sizes were all

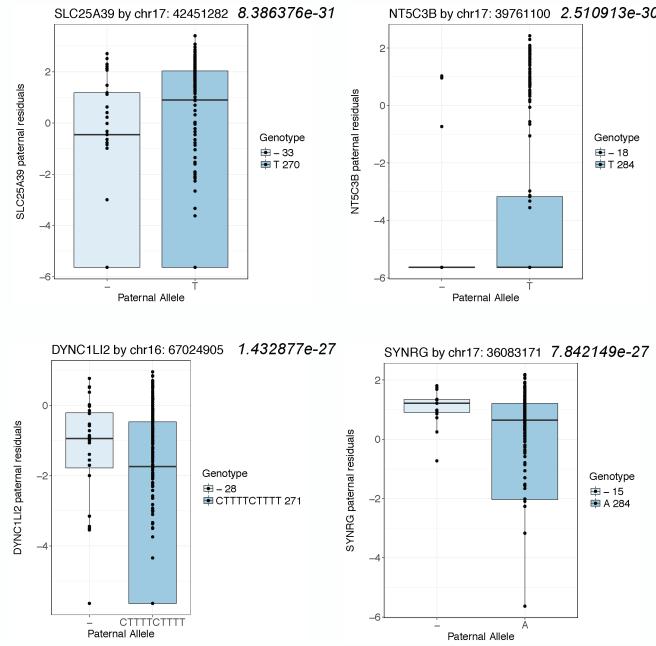


Figure 4.3: Paternal eQTL Associations Driven by Null Values. The four most significant paternal eQTL associations. Most of the individuals have no value of expression for these genes, we see most of the genes have a median that corresponds to a value of zero after normalization.

in the same direction: no SNPs had opposite effects on their corresponding parental gene expression (Figure 4.4). The imbalance of positive and negative effect sizes in Figure 4.4 is likely due in large part to the sparsity of the data, where most individuals have an expression value of zero and any individuals with some measure of expression drive the effect size to be positive.

We compared SNP gene pairs that were significant (Bonferroni) in one parent, and not significant ($p > 0.05$) in the other parent. 7,712 SNP-gene pairs were maternally significant and not paternally significant and 10,815 paternal significant associations were not maternally significant. An example of each is shown in Figure 4.5 where the maternally inherited A allele at 20:20036897 in Figure 4.5A is associated with increased maternal expression, but at least half of the individuals with the paternally inherited A allele at the same SNP have

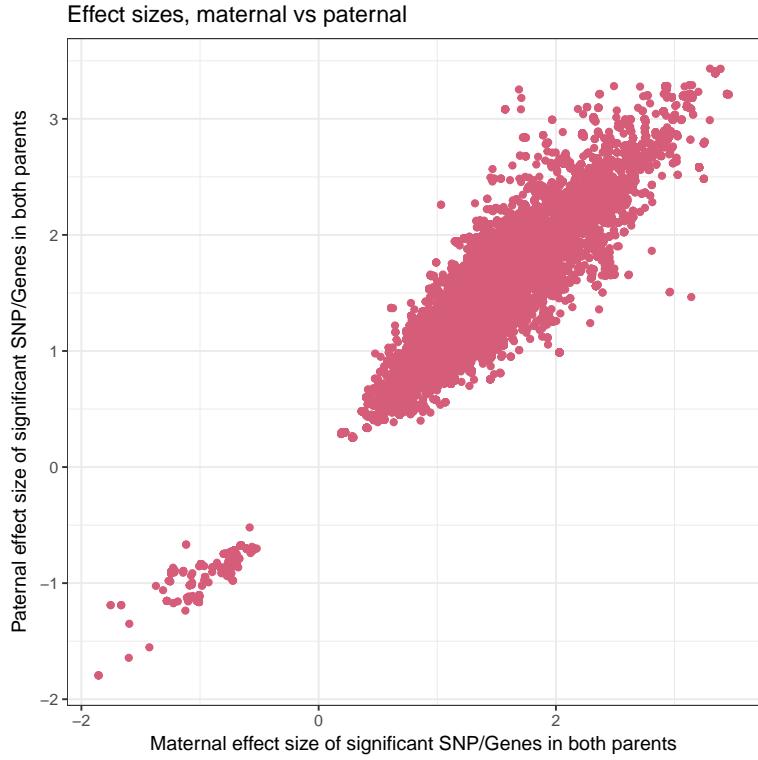


Figure 4.4: **Similar effect sizes across mat-eQTL and pat-eQTL.**

no expression from the paternal haplotype. In Figure 4.5 B, the A allele at 9:134850002 is associated with increased paternal expression when inherited from the father but not when inherited from the mother.

4.3.3 Parent-of-Origin (PO) - ASE Test

To detect parent-of-origin effects on expression using a different approach, we did a PO ASE test (see Methods) using parental gene expression count data. We identified 56,800 significant results using a Bonferroni corrected p-value . The top ten significant genes with their most significant SNPs are included in Table 4.1. The top four genes with their most significant SNPs shown in Figures 4.6, 4.7, 4.8, and 4.9. Of the 10 most significant genes, 5 are imprinted (*SNHG14*, *ZDBF2*, *PEG10*, *L3MBTL1*, *FAM50B*.)

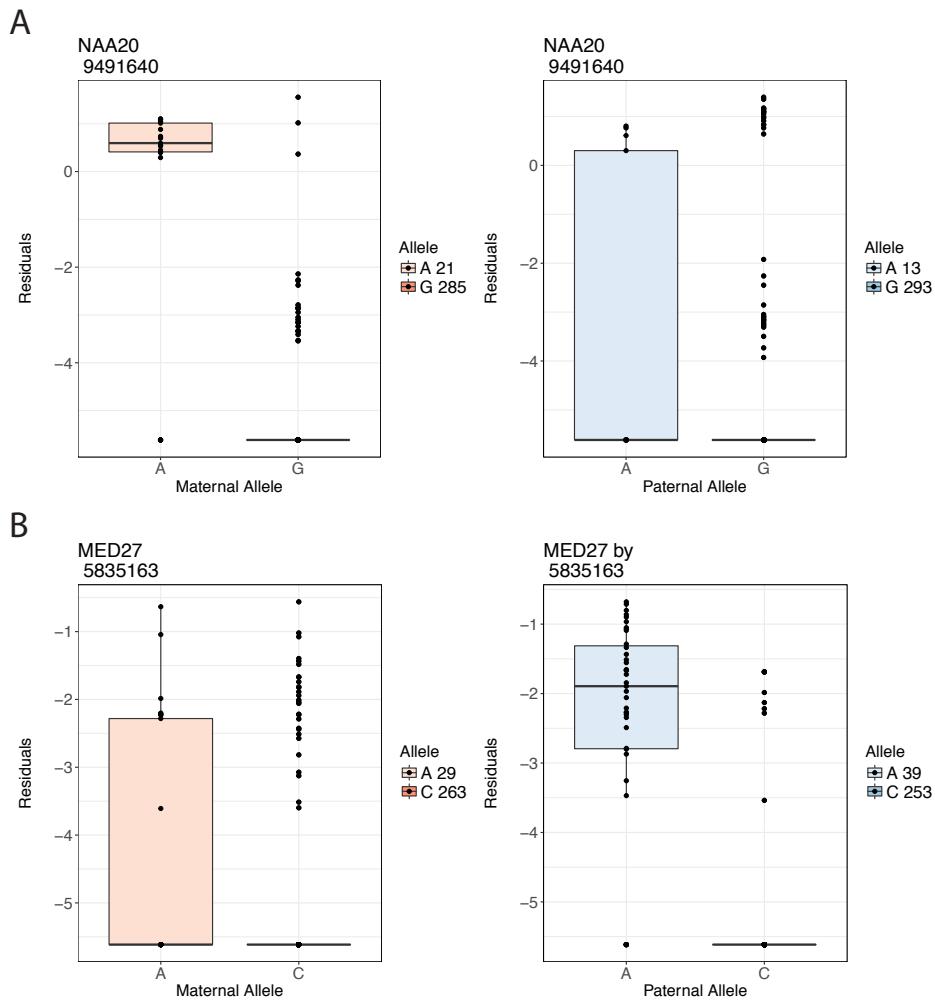


Figure 4.5: Parent specific eQTLs significant in one parent and not the other. (A) Variant on chromosome 20:20036897 has a significant mat-eQTL association (left) with gene *NAA20* ($p\text{-value} = 2.32 \times 10^{-27}$) where the pat-eQTL (right) from the same variant is not significant ($p\text{-value} = 2.18 \times 10^{-2}$). In contrast, (B) Variant on chromosome 9:134850002 has a significant pat-eQTL association (right) with gene *MED27* ($p\text{-value} = 4.7 \times 10^{-32}$) and mat-eQTL is not significant ($p\text{-value} = 2.75 \times 10^{-3}$) (left).

Chr	bp	Gene	Maternal Reads (Ref/Alt)	Paternal Reads (Ref/Alt)	p-value
15	8034579	<i>SNHG14</i> *	15/11	587/983	0
2	1459666	<i>ZDBF2</i> *	34/49	638/1190	0
5	3342675	<i>ERAP2</i>	3948/2445	4790/7067	0
7	4671649	<i>PEG10</i> *	42/4	635/1073	0
8	5271050	<i>PABPC1</i>	600/2564	21/494	0
20	9548868	<i>L3MBTL1</i> *	13/18	527/699	9.88E-248
14	8007882	<i>IGHG1</i>	794/156	1711/918	5.15E-191
6	3666034	<i>FAM50B</i> *	0/6	481/362	1.58E-180
22	9799426	<i>IGLV2-5</i>	240/499	23/1	6.56E-145
6	3758995	<i>BTN3A2</i>	3609/1049	3328/3330	8.40E-144

Table 4.1: **Top Ten Significant Genes from PO-ASE Test.** Five of the top ten significant genes from the PO-ASE test are imprinted genes (* represents imprinted genes). P-value of 0 corresponds to a really small p-value ($<10 \times 10^{-248}$)

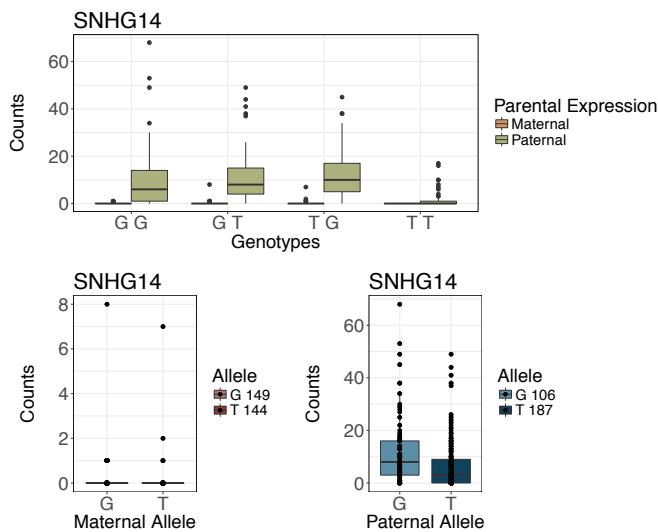


Figure 4.6: **Significant PO-ASE association with gene *SNHG14*.** For imprinted gene *SNHG14* we see variation in expression based on the allele and the parent it was inherited from. The paternally inherited T and G allele have different expression levels. Due to the imprinted status of the gene, we also see consistently more paternal expression from both alleles than maternal expression.

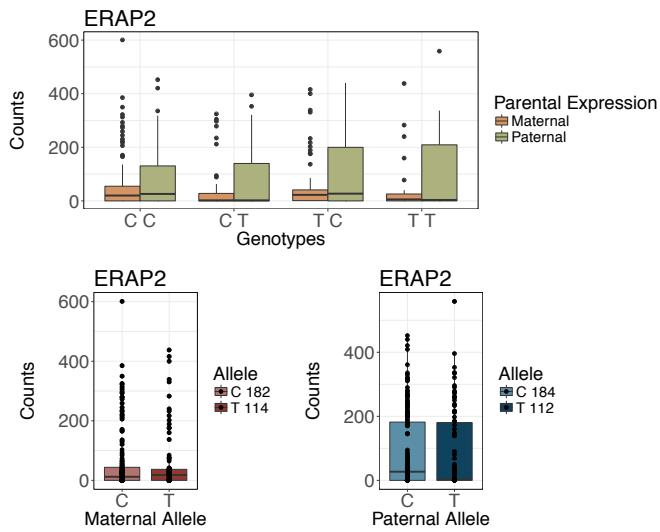


Figure 4.7: **Significant PO-ASE association with gene *ERAP2*.** For gene *ERAP2* Alleles C and T have different expression levels based on which parent the allele was inherited from. We see more expression form the paternal G allele than the paternal A allele in the reciprocal heterozygotes. Similar to imprinted genes, we see more paternal expression and less maternal expression across both alleles.

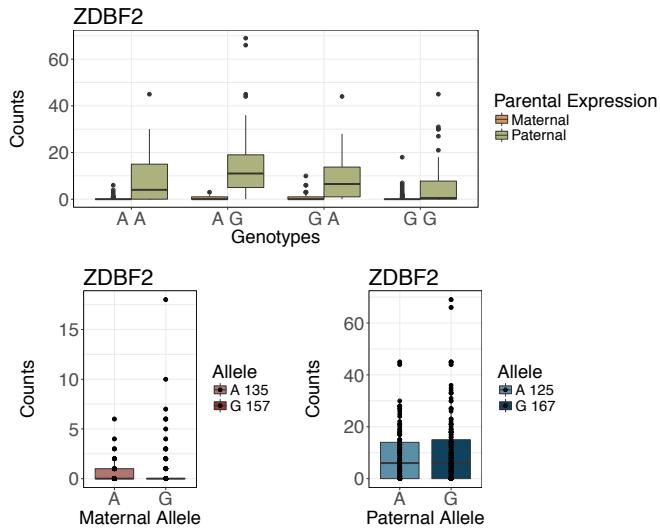


Figure 4.8: **Significant PO-ASE association with gene *ZDBF2*.** In *ZDBF2*, a maternally imprinted gene, there is consistently less maternal expression but still different in expression among parentally inherited expression, as well as by parentally inherited allele where there is more expression from the parental haplotype with the paternal G allele than the paternal A allele in the two reciprocal heterozygotes.

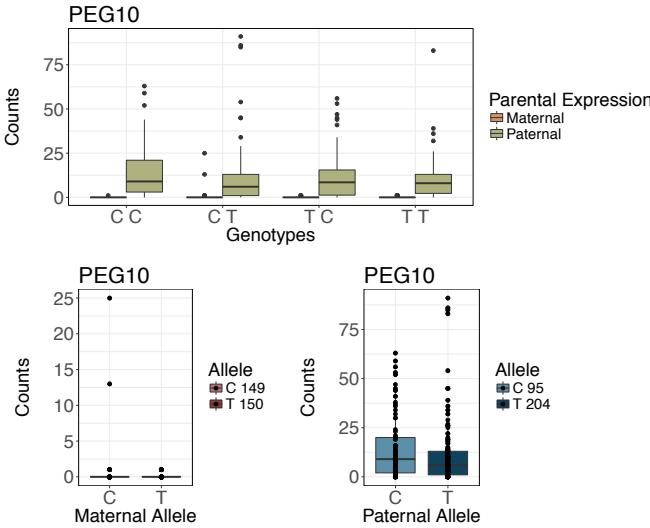


Figure 4.9: Significant PO-ASE association with gene **PEG10.** For maternally imprinted gene *PEG10* we see significant differences between maternal and paternal expression as well as paternally expression in the reciprocal heterozygotes. There is consistently less maternal expression due to the imprinting status of the gene and then more expression from the haplotype with the paternal expression with the C allele compared to the T allele in the reciprocal heterozygotes.

4.3.4 Modified ASE Test on Symmetrically Expressed Genes

We were not surprised to find that the most significant genes from the PO-ASE test were imprinted genes since one haplotype of imprinted genes is silenced, and the other haplotype will be expressed contributing to the significant difference in parental gene expression. We are searching for genes that have different parental expression based on a parentally inherited allele in *cis*. Imprinted genes, as those we identified in Figures 4.6, 4.8, and 4.9, are consistently not expressed from the imprinted haplotype, irrespective of which allele was inherited. We wanted to identify a parent-of-origin allele effect on expression.

To exclude imprinted genes in the analysis we only tested genes that did not have significant asymmetrical expression (see Methods). We were searching for genes that were more symmetrically expressed from each parental haplotype to identify if a parentally inherited allele can affect expression from the same haplotype in *cis*. We identified 15,340 significant

SNPs (not pruned for LD) with 518 genes (using Bonferroni p-value 5.99×10^{-9}). The two most significant genes from the PO-ASE test and with symmetric expression are plotted with their most significant SNPs in Figures 4.10 and 4.11. The top ten genes and their most significant SNPs are listed in Table 4.2.

Chr	bp	Gene	Maternal reads (Ref/Alt)	Paternal reads (Ref/Alt)	p-value
1	404610	SEC22B	148/101	513/478	1.11E-98
3	2222154	ZMAT3	1320/1650	257/2085	3.53E-83
8	5425272	PARP10	128/334	324/1018	1.06E-71
12	7253839	OAS3	4465/939	2069/4327	1.06E-65
11	6368707	IRF7	620/2463	2079/167	2.94E-62
14	8008568	IGHV2-5	291/295	22/135	1.80E-62
17	8884867	CCDC137	1449/865	173/1819	1.45E-57
14	7958818	ITPK1	387/686	862/1056	2.48E-57
17	8865144	SEPT9	560/2595	2594/1305	7.50E-50
17	8730038	SLFN5	2528/3084	1678/2539	1.27E-48

Table 4.2: Top Ten Significant Genes from PO-ASE Test after Filtering Asymmetrically Expressed Genes. Filtering on symmetrical expression removed imprinted genes from being the most significant genes from PO-ASE test.

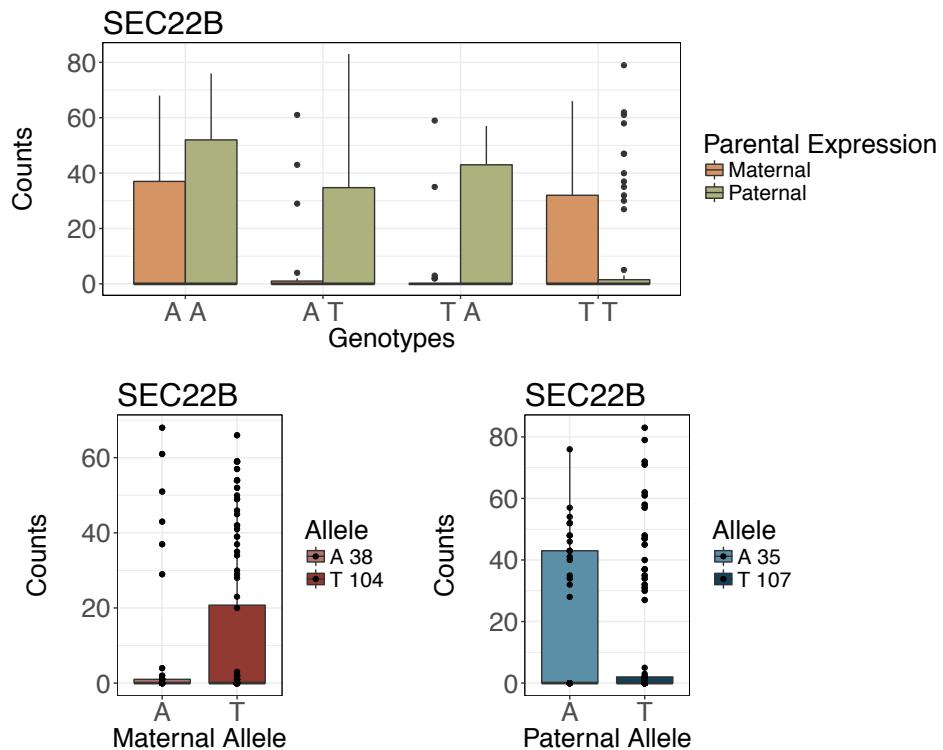


Figure 4.10: **Significant Association from PO-ASE test with *SEC22B*.** The most significant SNP (1:404610) with the most significant gene *SEC22B*. In the top plot with all four genotypes we see expression from the paternal allele in all four genotypes except TT. Maternal expression is only seen in the homozygotes. In the plots by parental allele below, it is clear that the maternal T allele is associated with increased maternal expression compared to the maternal A allele at this SNP. We see the opposite effect with paternal allele where the paternal A allele is associated with increased paternal expression and the paternal T allele with decreased expression. Based on the parental origin of the allele, the expression from the haplotype is different.

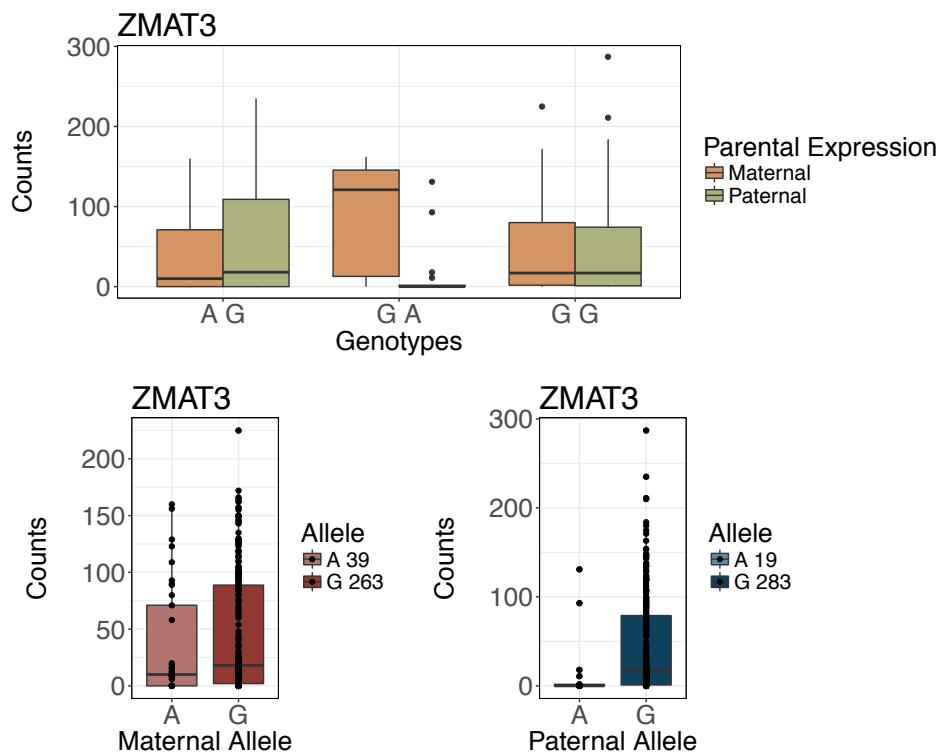


Figure 4.11: **Significant Association from PO-ASE test with *ZMAT3*.** The most significant SNP (3:2222154) with the second most significant gene *ZMAT3*. In the top plot with all three genotypes we see expression from the paternal allele in all four genotypes except GA. Maternal expression in all genotypes. In the plots by parental allele below, it is clear that the maternal alleles are associated with maternal expression, but the paternal A allele, in contrast to the paternal G allele, is not associated with paternal expression.

4.4 Discussion

Previous studies using parental alleles and gene expression have identified imprinted genes and genetic variation that affects quantitative traits [118, 12, 14, 38], but none to our knowledge have looked at how genetic variation can impact parent-of-origin expression from the same haplotype as the genetic variation.

Here we used parental specific gene expression in 306 Hutterites to characterize genetic effects on parental expression. We first performed a parent-of-origin opposite effect eQTL (oeQTL) test using total gene expression. We then did a maternal and a paternal eQTL study of maternal and paternal gene expression (mat-eQTL, pat-eQTL), respectively. Finally, we tested for parent-of-origin effects among reciprocal heterozygotes.

Our opposite effect model has been successful in identifying opposite effects of parentally inherited variants on quantitative traits in the Hutterites but we were not able to find any with gene expression in LCLs. These could be due to a number of reasons, including sample size and the tissue studied. LCLs are transformed cell types and the transformation could alter imprinting mechanisms. We also performed a *cis* mat-eQTL and pat-eQTL study. This test identified known significant eQTLs that showed up in both the mat-eQTL and pat-eQTL results since the effect does not depend on the parent of origin. None of the variants compared across the mat-eQTL and pat-eQTL showed opposite effects by parent of origin. We were not able to find any maternal or paternally only effects on gene expression without modifying our test.

We found that most of the negative results were driven by sparsity in the data. Null expression values for gene expression could be due to two factors: 1) no heterozygous/parent-of-origin SNPs in the gene such that homozygous reads could not be assigned to a parent, or 2) there are heterozygous SNPs in the genes but there are no reads. Genes without any heterozygous SNPs for an individual were considered missing and not included in the analysis. We maintained the values for those genes for the individuals with at least one

heterozygous site in a gene. Although this resulted in different numbers of individuals and genes to be tested, and provided a more conservative and informative data set, we still did not find any significant opposite effects on gene expression.

Finally, we performed a PO- ASE test among reciprocal heterozygotes to identify effects of parental variation on gene expression. The missing gene expression (i.e. uninformative) for some individuals decreased the numbers of reciprocal heterozygotes we could test for each gene.

These few results from the PO-ASE test and the opposite effect eQTL could be due to many limitations of our study. Although we were able to determine the parent of origin for many transcripts in the Hutterites, we could not assign every RNA sequencing read to a parent due to lack of heterozygous sites or missing parent-of-origin information for alleles. Missing parental gene expression resulted in very sparse data. Second, we conducted these studies in LCLs, and therefore would miss effects in other tissues or developmental time points. Additionally, our models to test for parent-of-origin eQTL effects are effective but could be much improved, such as to model over-dispersion in gene expression.

In summary, we did not identify any genetic variation with opposite parental effects on either parentally mapped gene expression or total gene expression. We did identify SNPs with parent-of-origin eQTLs even though our data are noisy and underpowered. Deeper sequencing and better modeling could potentially identify more genetic variation that impacts parental gene expression if such a biological mechanism exists. We expect these possible parent-of-origin eQTLs from the PO-ASE test to represent variation that can impact imprinting or other gene silencing mechanisms by parent of origin. For example, for the *ZMAT3* gene in Figure 4.11 we see expression from all haplotypes except from the paternal A allele. It could suggest that the paternal G allele is disrupting the mechanism that turns off paternal expression at this gene or that the paternal A allele activates a mechanism to silence the gene expression from the paternal haplotype. If more evidence for such effects are identified,

it could lead to new approaches to understanding genetic variation and its impact on gene expression and, ultimately, disease and human health.

4.5 Methods

4.5.1 Genotypes and Sample Information

LCL RNA-seq transcripts for 306 individuals were mapped to parental haplotypes as in Chapter 3. We used the measures of total as well as maternal and paternal expression in this study. We used multiple approaches to characterize parent-of-origin effects on gene expression. To be conservative, we used 306 Hutterite individuals for which we have parental genotypes and tested SNPs for which we have at least three individuals in at least three of four parent-of-origin genotype classes (such that we have at least three individuals in at least one heterozygote category and one heterozygote individual will not drive our analysis). We used QCed SNPs with MAF >5%.

4.5.2 RNA-seq QC

Multiple approaches required different QC methods. For the total gene expression, we used normalized gene expression. First, we removed lowly expressed genes with a log count per million (cpm) greater than 1 in at least 20 individuals. The R/Bioconductor package edgeR was used to convert the RNA-seq counts to log2 TMM-normalized CPM values[96, 95]. Technical covariates correlated with gene expression Principal Components were regressed out (RIN, DNA concentration, RNA concentration, Flowcell/Lane).

4.5.3 Parent-of-Origin Expression QC

Maternal gene expression was used as both counts and as normalized gene expression. Maternal gene expression counts were used directly from STAR gene count output[29] subsetted

on genes included in the total gene expression analysis. Normalized maternal expression was calculated similar to total gene expression using edgeR and converting RNA-seq counts to log₂ TMM normalized CPM values using normalization factors (library sizes) from the total gene expression (maternal gene expression too sparse on its own). The same method was used to get paternal gene expression counts and normalized paternal gene expression.

4.5.4 Informative Genes

To separate informative parental gene expression from uninformative parental gene expression I compiled all of the heterozygous SNPs for each individual for each gene that was expressed in LCLs. If a gene for an individual did not have any heterozygous parent-of-origin SNPs (i.e. informative SNPs), the gene was considered missing (converted to NA for downstream analysis). If there was at least one heterozygous parent-of-origin SNP in the corresponding gene, the gene expression value was not altered, since zero expression for that gene for that parent could be informative. This resulted in different numbers of genes for different individuals (Figure 4.12).

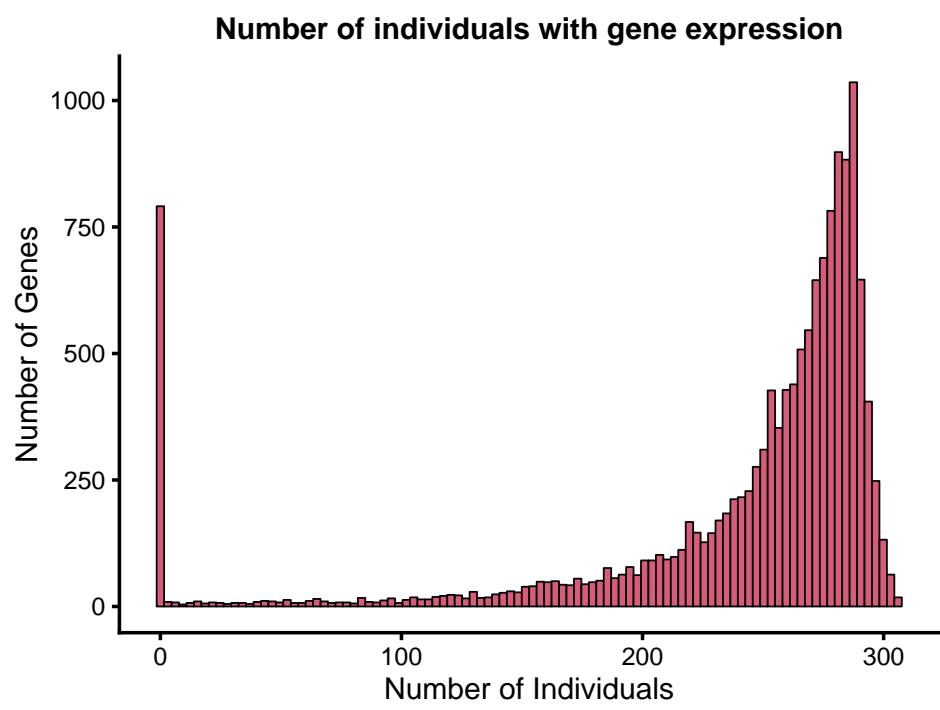


Figure 4.12: Number of Individuals with Gene Expression.

4.5.5 Opposite Parent-of-Origin eQTL

We used the same method outlined in Chapter 2 to detect if SNPs had opposite effects on total gene expression by parental origin. We tested SNPs in *cis*, defined as +/-250kb from the TSS of the gene. The model was implemented in GEMMA[117] where we used sex and age as covariates and corrected for relatedness (see Methods from Chapter 2).

4.5.6 Single Parent eQTL

To use the parent-of-origin expression, we performed a *cis* eQTL testing for specific parental effects on the same parental gene expression as follows, where n is the number of individuals, Y_P and Y_M are an $n \times 1$ vector of quantitative traits corresponding to paternal and maternal expression. W is an $n \times c$ matrix of covariates (fixed effects) including intercept 1. α is a $c \times 1$ vector of covariate coefficients. X_M is an $n \times 1$ vector of maternal alleles, and X_P an $n \times 1$ vector of paternal alleles. β_M and β_P are the effect sizes of maternal and paternal alleles, respectively. g is a vector of genetic effects with $g \sim N(0, A(\sigma_g)^2)$ where A is the genetic relatedness matrix; ϵ is a vector of non-genetic effects with $\epsilon \sim N(0, I(\sigma_e)^2)$.

$$Y_M = W\alpha + X_M\beta_M + g + \epsilon \quad (4.1)$$

$$Y_P = W\alpha + X_P\beta_P + g + \epsilon \quad (4.2)$$

We defined *cis* as +/- 250kb from the TSS of the gene. The model was implemented in GEMMA[117] where we used sex and age as covariates and corrected for relatedness.

4.5.7 PO ASE Test

We used a simple χ^2 test on the reciprocal heterozygotes on their corresponding allelic expression using maternal and paternal count data corresponding to haplotype specific expression.

Layout of the matrix for the test is in Table 4.3.

Genotype	C allele (ref) expression	G allele (alt) expression
$C_M G_P$	148 (maternal expression)	478 (paternal expression)
$G_M C_P$	513 (paternal expression)	101 (maternal expression)

Table 4.3: **Setup for PO-ASE test.** For reciprocal genotypes we use the maternal and paternal gene expression counts corresponding to opposite alleles. The chi-squared test here will determine if there is an allele and parental effect. The C and G allele in genotype refer to the reference and alternate alleles, respectively. The M and P subscript refer to maternal or paternal inherited allele.

4.5.8 Not Asymmetrically Expressed Genes

We used a binomial test to determine which genes had more maternal expression than paternal expression. We summed paternal and maternal gene expression across all individuals for a gene and used the sum of maternal and paternal gene expression in a binomial test to determine if the ratio of maternal to the sum of maternal and paternal expression is only 1/2. We kept genes not significant (Bonferroni, $p > 3.5 \times 10^{-6}$) for the Modified ASE Test.

CHAPTER 5

CONCLUSION

As we look past the "low hanging fruit" of GWAS, we turn to other biological mechanisms where genetics can influence our traits, including studies of rare variation [45, 62], gene by environment interactions, and parent-of-origin effects, among others. The Hutterites are an ideal population to look for parent-of-origin effects on quantitative disease related traits and gene expression because of their common environmental exposures and similar genetic background [114, 1, 83]. With the availability of RNA-seq data, novel methods for imputing and phasing data at a population scale [63], and extensive phenotyping of the Hutterites, we are able to start investigating such questions related to parent-of-origin effects.

5.1 A novel method to detect opposite effects of parentally inherited variants on cardiovascular disease and asthma associated traits

In Chapter 2, I describe our study to detect genetic variation than can impact cardiovascular disease and asthma associated traits when inherited from one parent and not the other. In order to maximize our data, we developed a novel method that can be used to detect parentally inherited alleles with opposite effects on quantitative traits, depending on which parent they were inherited from. These associations would be missed in traditional GWAS. Previous studies have explored parent-of-origin effects but mostly using trios [38, 4, 44] and on binary disease status [56, 4]. Only a few studies have searched for parent-of-origin effects on quantitative traits, starting with height [14, 118].

Using our method, we identify parent-of-origin effects (POEs) on 11 phenotypes in the Hutterites, most of which are risk factors for cardiovascular disease. Most of the loci we identified have features of imprinted regions and many of the variants are associated with

expression of nearby genes. Most of the phenotypes are also associated with metabolic traits consistent with the parent conflict hypothesis of imprinted genes first put forward by Haig [41, 13, 88]. The idea suggests that parental interests may be in conflict such that paternal alleles favor growth of the fetus at the expense of the mother while maternal alleles favor restricting resources to the fetus to ensure preservation of her own nutritional needs. We show that POEs, which can be opposite in direction, are relatively common in humans, are possible imprinted regions, and have potentially important clinical effects.

It is necessary to replicate the parent-of-origin effects we identified in a different population to verify these effects exist. The associations did not replicate in the Sardinia population, although there were few suggestively significant. Additionally a power analysis will need to be done to confirm our method would pick up genetic variants of the effect size and minor allele frequency that we identified.

It is important to further investigate these regions. One of the regions with a POE identified in our study with *LINC01081* has been studied in detail by another group showing that a parent-of-origin effect exists at this region [105]. Others have shown POEs at known imprinted regions that affect height [14, 118] that we were not able to replicate in the Hutterites likely due to our smaller sample size. It would be the next step to show whether or not the regions we identify with POEs lie in or near previously unidentified imprinted regions.

5.2 Identifying two novel imprinted genes in known imprinted regions using parent-of-origin gene expression

In Chapter 3, I identified two new imprinted genes using parent-of-origin and allele specific expression. Using a novel method as a variation on WASP [107], I mapped RNA-seq reads to parental haplotypes using SNPs in the reads and parent-of-origin information of SNPs. We identified known imprinted genes and two novel imprinted genes, *PXDC1* and *PWAR6*,

among our genes with asymmetrical parent-of-origin gene expression. We validated the patterns of gene expression using RNA-seq from peripheral blood leukocytes (PBLs). To validate the imprinted genes further, we used DNA methylation levels in the PBLs to confirm imprinting control regions (ICRs) previously defined [50, 24]. Our two new imprinted genes lie in known imprinted regions with known ICRs providing more evidence for their imprinting status.

This is the largest pedigree based genome-wide scan for imprinted regions to date with 306 Hutterite individuals. We also provide a new way of mapping reads to parent-of-origin haplotypes and identify two new possible imprinted genes.

We would still need to further validate *PXDC1* and *PWAR6* as imprinted genes in a different population and possibly in additional cell types. Further characterization of these loci are still required. We identified these genes as imprinted but had overall very few parentally mapped reads. This would need to be replicated with many more parentally mapped reads. It was somewhat surprising they were not previously discovered as imprinted genes since they are in known and somewhat well characterized imprinted regions. It is possible they are tissue and/or developmentally specific as has been shown for other imprinted genes [12]. It is also possible that, although imprinted, variation at these imprinted genes does not affect disease, contrary to other imprinted genes and how they have been previously identified.

5.3 Can genetic variation by parent of origin influence gene expression on the same haplotype?

In Chapter 4, I explored if parentally inherited genetic variation can affect gene expression as well as haplotype specific gene expression (maternal and paternal specific expression). Using the method described in Chapter 2 to detect opposite effect associations, we did not identify any SNPs that had opposite effects on total gene expression depending on which parent the allele as inherited from. To get at the same opposite effects in a different way, we

performed a maternal eQTL (mat-eQTL) with maternal alleles on maternal expression as well as a paternal eQTL (pat-eQTL) with paternal alleles on paternal expression. Across all the SNP-gene pairs analyzed we did not identify any effects that were opposite in direction.

To determine if any alleles had a specific effect on gene expression when inherited from one parent or the other, we used a parent-of-origin allele specific expression (PO-ASE) test and identified alleles that when inherited from one parent, and not the other, had a different effect on gene expression from the same haplotype as the allele.

While our model detected genes that look like they could have a PO allele specific effect, there is still room for improvement. We use gene expression counts but our model is not accounting for overdispersion, which needs to be accounted for when looking at gene expression. We also looked for PO-ASE effects with very few parentally mapped reads. For standard eQTL studies we require at least 10 million reads, whereas, here, we have on average 1.8% of 10 million reads mapped to a parental haplotype resulting in, on average, about half of 1.8 million reads to use for an eQTL study. Our study is likely, therefore, underpowered to identify SNPs that have opposite effects on gene expression depending on which parent it was inherited from. More reads are required to perform this study and find parent specific effects.

Even with these parent-of-origin eQTLs identified in Chapter 4, it is not clear what biological mechanism could lead to such an effect. It is possible that the parentally inherited allele that contributes to gene expression differently from the rest could disrupt normal expression by inducing silencing of the gene in a chromosome specific manner. It is also possible that the opposite allele - from the same parent - results in aberrant over expression of the allele. Both of these would result in a parent-of-origin effect on gene expression but why or how these would occur is unknown.

5.4 Future Directions

With this large pedigree data we are able to answer some questions about parent-of-origin effects on gene expression and quantitative traits. However, it barely scratches the surface of biological mechanisms that we don't yet have a pipeline for or the ideal dataset to detect such effects, in contrast to genome wide association studies. From Chapter 2, our method to detect opposite parent-of-origin effects represents progress in this direction. The method needs to be tested on multiple datasets to confirm the results are accurate. There would also need to be a power analysis done to confirm that most of the associations are not false positives. Although these opposite effect variants don't show an effect on gene expression in our study or others [14], we still need to understand the mechanism by which these variants are acting. Better characterization of the expression of genes nearby these variants needs to be done, across different tissues, to get at whether these effects are a result of imprinting. Methylation and chromatin in these regions could be studied once the gene or genes contributing to the parent-of-origin phenotype are identified to characterize epigenetic marks that define an imprinted region. Characterization of allele specific interactions using chromatin conformation capture at heterozygous SNPs could also help unravel the different interactions among parental alleles if one is not imprinted and both genes are actively expressed. Ultimately, functional characterization of these SNPs remains necessary to understand the mechanism behind these opposite parental effects and the traits they impact.

In Chapter 3 we identify known imprinted genes in lymphoblastoid cell lines as well as two novel imprinted genes. Using a larger dataset, with accurate parent-of-origin calls, more parent-of-origin calls, more sequencing reads, and across different tissues is necessary to confirm these novel imprinted genes as well as confirm more known imprinted genes. Imprinted genes have been shown to be tissue specific [12] and thus performing a similar study in more tissues and samples could increase the resolution on imprinted genes and their mechanisms of gene expression.

Although we were not able to do it in Chapter 4, it remains necessary to identify variation that can impact imprinted genes or impact gene expression by parent of origin. Similar to diseases that result from mutations in imprinted genes, it is possible genetic variation that affects gene expression in a parent-of-origin manner can affect diseases or disease associated traits.

In this dissertation, I characterize parent-of-origin effects of some variants, and their small effects on quantitative disease associated traits, but there still remains a lot to be discovered and better understood for us to have a better understanding of the genome and its impact on human health and disease. These parent-of-origin effects, although small, likely do contribute to heritability of traits as more researchers, including us, have identified genetic variation that can impact traits by parent of origin [14, 118, 38, 56].

5.5 Concluding remarks

In this thesis, I contribute to the growing knowledge of additional biological mechanisms, specifically, parent-of-origin effects, that can contribute to phenotypes and disease risk missed in standard GWAS. In all the chapters of this dissertation we are able to leverage the parent-of-origin information for alleles in the Hutterites and use them to uncover novel effects of genetic variation on gene expression and quantitative traits. In Chapter 2 I developed a new method to test for opposite effects of parentally inherited genetic variation on quantitative traits and we find 11 parent-of-origin effects, including maternal, paternal, and opposite parental effects. In Chapter 3, I mapped RNA-seq to parental haplotypes using parent of origin of alleles and uncover known and new imprinted genes (*PXDC1* and *PWAR6*), which show similar patterns of expression in PBLs and have well characterized ICRs in the region. In Chapter 4, I explored how parent-of-origin genetic variation could influence gene expression. We did not find any opposite effects on gene expression but identified alleles that when inherited from one parent showed altered gene expression patterns.

Throughout this research, I investigated the basis for parent-of-origin effects for which we have not had the methodology and or the appropriate dataset I have today to explore such a phenomenon. The novelty of these data and the questions I asked has allowed for the expansion of this research from one original aim to a full dissertation covering 3 separate projects and future directions such as measuring parent-of-origin heritability on traits and gene expression. The research in this dissertation provides methods and a basis for studying parent-of-origin effects and other less well characterized effects that could contribute to heritability of traits and disease risk.

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