

A Single Complex *Agpat2* Allele In A Patient With Partial Lipodystrophy

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Running title: *AGPAT2* Affected In Partial Lipodystrophy

Supplementary Data

R script to determine the association of common genetic variants with partial lipodystrophic phenotype.

Supplementary Figure 1. Whole genome sequencing data showing the *AGPAT2* variants in a patient with partial lipodystrophy. WGS reads of our patient aligned to the human reference genome GRCh37 (bottom). WGS results show that patient is heterozygous for rs2236514 and c.199G>A/c.500T>C, respectively. Please note that the reads are shown in reverse.

Supplementary Table 1. Overview of *AGPAT2* mutations in lipodystrophy.

Overview of previously described mutations in *AGPAT2*. Genbank accession no. NM_006412.3 and NP_006403.2.# Originally described as c.636c>A. § Originally described as c.713A>T * Originally described as c.645 A>T

Supplementary Table 2. SNP genotype of patient with partial lipodystrophy. In the patient WGS data was used to genotype 53 genomic regions that were previously identified to be associated with a reduced ability to store adipose tissue in peripheral compartments (Lotta et al., 2017). We identified 60 risk alleles.

R script to determine the association of common genetic variants with partial lipodystrophic phenotype.

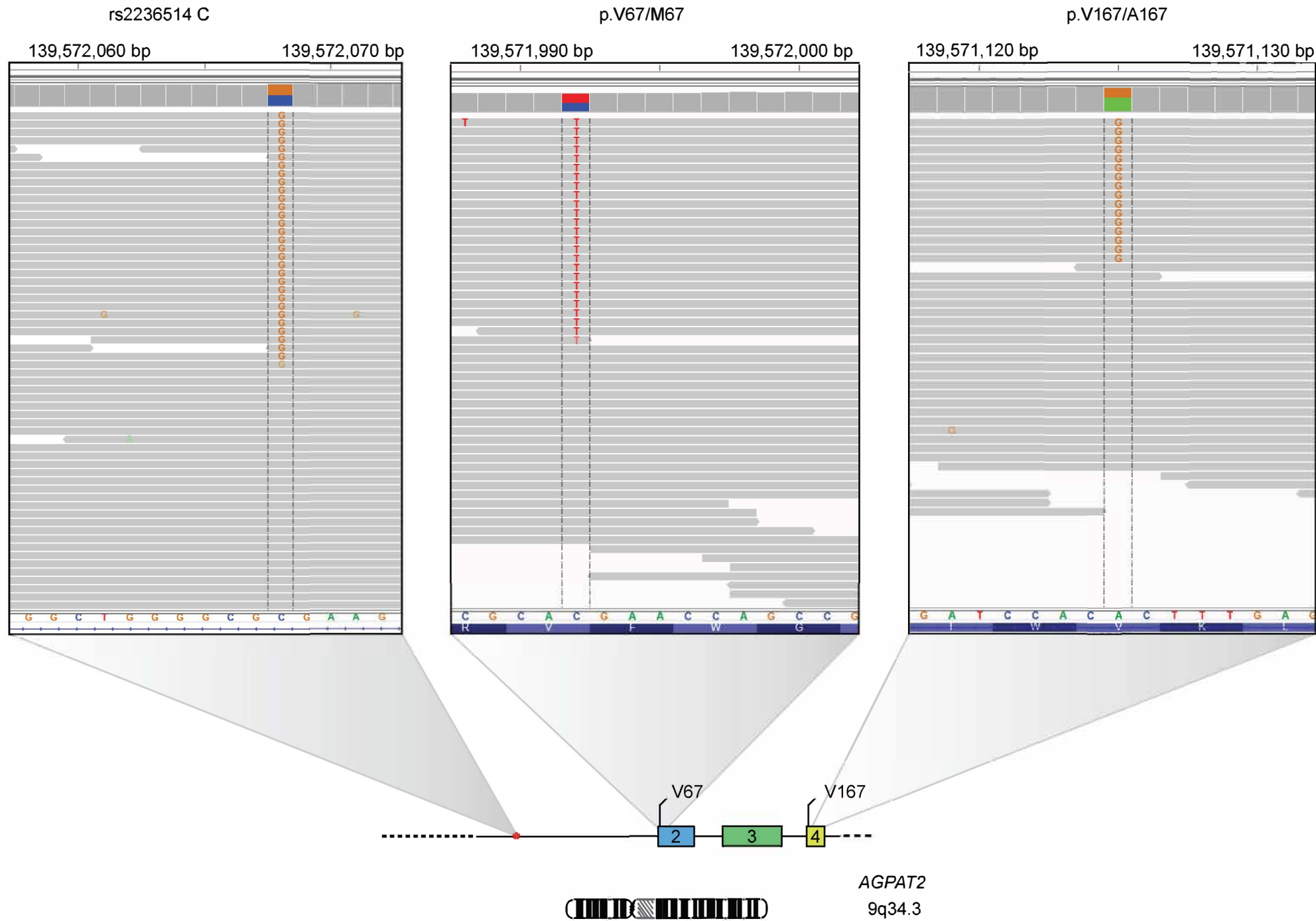
```
library("ggplot2")
setwd("53SNPs")
# Read relevant data
dosage <- read.table("UKHLS.dosage.txt.assoc.dosage",sep=",",header=F, stringsAsFactors=F,
col.names=c("CHR","SNP","BP","A1","A2","FRQ","INFO","OR","SE","P"), skip=1 )
head(dosage)
gts <- read.table("plink.ped",sep=' ',header=F, stringsAsFactors=F)
head(gts[,1:10])
snpinfo <- read.table("SNPdata.txt",sep='\t',header=T, stringsAsFactors=F)
colnames(gts) <-
c("sample","family","pat","mat","gender","phenotype",as.character(snpinfo$SNP))
# Selecting females only
gts <- subset(gts, gender=="2")
# Determine where reference allele != non-risk allele
snpinfo$flip <- snpinfo$Effect.Allele!=dosage$A1
# Convert genotypes to risk scores
scores <- gts[,7:ncol(gts)]
scores[scores==0]<-NA
scores[scores==11]<-0
scores[scores==12]<-1
scores[scores==21]<-1
scores[scores==22]<-2
# Adjust risk scores for 'flipped' positions
scores[,snpinfo$SNP[snpinfo$flip]] <- scores[,snpinfo$SNP[snpinfo$flip]]-2
scores <- abs(scores)
# Determine missing genotypes to prevent over scoring
liponas <- apply(scores, 1, function(x) sum(is.na(x)))
liporisk <- rowSums(scores, na.rm=T)
liporiskfrac <- liporisk/((53-liponas)*2)
rownames(scores) <- gts$sample
```

```

scores$liporiskfrac <- liporiskfrac
scores$riskalleles <- scores$liporiskfrac*106
# Plot results of patient relative to population
pdf(file="LipoRiskDistribution_Paper.pdf",width=6,height=10,useDingbats=F, fontsize=10 )
aplot <- ggplot(scores, aes(x=riskalleles)) + geom_histogram(binwidth=1, fill="#4396F0",
color="#4396F0", alpha=.5)
bplot <- aplot + ylab("UKHLS controls, n") + xlab("Number of risk alleles") + theme_bw() +
theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor
= element_blank(), axis.line = element_line(colour = "black")) +
scale_x_continuous(breaks=round(seq(40,80,by=5),1)) +
scale_y_continuous(breaks=round(seq(0,900,by=100),1))
cplot <- bplot + theme(axis.text = element_text(size=15)) + theme(axis.title =
element_text(size=20))
print(cplot + geom_vline(xintercept=53, color="red"))
dev.off()
# Calculate z-score
pop_sd <- sd(scores$riskalleles)*sqrt((length(scores$riskalleles)-
1)/(length(scores$riskalleles)))
pop_mean <- mean(scores$riskalleles)
zscore <- (53 - pop_mean)/pop_sd
print(zscore)

```

Supplementary Figure 1: Whole genome sequencing data showing the AGPAT2 variants in a patient with partial lipodystrophy.



Supplementary Table 1. Overview of *AGPAT2* mutations in lipodystrophy.

	Protein	Genomic change	Location	Modes of inheritance	Reference
Missense	C48R	c.142T>C	Exon 1	Homozygous	(Ramanathan et al., 2013)
	V67M	c.199G>A	Exon 2	Homozygous/ single complex allele	(Poovazhagi et al., 2013; Current study)
	S100N	c.299G>A	Exon 2	Homozygous	(Agarwal et al., 2003; Cortés et al., 2014; Miranda et al., 2009)
	P112L	c.335C>T	Exon 2	Homozygous/ Compound heterozygous	(Pelosini et al., 2011; Taleban et al., 2008)
	G136R	c.406G>A	Exon 3	Compound heterozygous	(Agarwal et al., 2002)
	V167A	c.500T>C	Exon 4	Single complex allele	(Current study)
	E172K	c.514G>A	Exon 4	Homozygous	(Haghighi et al., 2012; Magré et al., 2003)
	L228P	c.683T>C	Exon 6	Compound heterozygous	(Agarwal et al., 2002)
	A238G	c.712C>G	Exon 6	Compound heterozygous	(Magré et al., 2003)
	A239V	c.716C>T	Exon 6	Compound heterozygous	(Agarwal et al., 2003)
Nonsense	S45X	c.134C>A	Exon 1	Homozygous	(Haghighi et al., 2016)
	C48X	c.144C>A	Exon 1	Homozygous	(Akinci et al., 2016)
	W65X	c.194G>A	Exon 2	Homozygous	(Magré et al., 2003)
	R68X	c.202C>T	Exon 2	Homozygous/ Compound heterozygous	(Agarwal et al., 2002; Akinci et al., 2016; Haghighi et al., 2016; Magré et al., 2003; Taleban et al., 2008)
	Y72X	c.216C>G	Exon 2	Homozygous	(Haghighi et al., 2016)
	F189X	c.567C>A [#]	Exon 4	Compound heterozygous	(Fu et al., 2004)
	Y190X	c.570C>A	Exon 4	Compound heterozygous	(Agarwal et al., 2003)
	K215X	c.645A>T [§]	Exon 5	Homozygous	(Fu et al., 2004)
	K216X	c.647A>T [*]	Exon 5	Homozygous	(Akinci et al., 2016; Magré et al., 2003)
	Q226X	c.676C>T	Exon 6	Homozygous	(Magré et al., 2003)
E229X	c.685G>T	Exon 6	Homozygous	(Akinci et al., 2016; Haghighi et al., 2012)	
Insertion	L126fsX	c.377insT	Exon 3	Compound heterozygous	(Agarwal et al., 2002)
	Q87GfsX	c.258_259insGGCTG	Exon 2	Homozygous	(Shetty et al., 2016)
Deletion	R90VfsX	c.268delC	Exon 2	Homozygous	(Akinci et al., 2016)
	140delIF	c.418delITTC	Exon 3	Compound heterozygous	(Agarwal et al., 2002)
	V167fsX	c.504delGA	Exon 4	Compound heterozygous	(Agarwal et al., 2002)
	D180fsX	c.538delG	Exon 4	Compound heterozygous	(Agarwal et al., 2002; Haque et al., 2005)

	V223LfsX	c.667-705delinsCTGCG	Exon 6	Homozygous	(Akinci et al., 2016)
	252deIMRT	c.755delTGAGGACCA	Exon 6	Homozygous	(Agarwal et al., 2002)
	G106fsX188	c.317-588del	Exon 2-4	Homozygous	(Agarwal et al., 2002; Fu et al., 2004; Gomes et al., 2004; Magré et al., 2003)
Splice		IVS1+1G>A	Intron 1	Compound heterozygous	(Agarwal et al., 2003)
	F60fsX102	IVS1-2A>G	Intron 1	Compound heterozygous	(Magré et al., 2003)
		IVS2+1G>T	Intron 2	Homozygous	(Akinci et al., 2016)
		IVS3+1G>A	Intron 3	Compound heterozygous	(Agarwal et al., 2003)
	N164fsX	IVS3-1G>C	Intron 3	Homozygous/Compound heterozygous	(Agarwal et al., 2003; Cortés et al., 2014; Fu et al., 2004; Haque et al., 2005; Magré et al., 2003; Miranda et al., 2009)
	Q196fsX	IVS4-2A>G	Intron 4	Homozygous/Compound heterozygous	(Agarwal et al., 2002, 2003; Fu et al., 2004; Haghghi et al., 2016; Magré et al., 2003)
		IVS5+2T>G	Intron 5	Homozygous	(Magré et al., 2003)
	221delIGT	IVS5-2A>C	Intron 5	Homozygous	(Agarwal et al., 2002; Akinci et al., 2016)
3'UTR	c.916C>G		3'UTR	Compound heterozygous	(Agarwal et al., 2002)

Genbank accession no. NM_006412.3 and NP_006403.2.

Originally described as c.636c>A.

§ Originally described as c.713A>T

* Originally described as c.645 A>T

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Supplementary Table 2: SNP genotype of patient with atypical partial lipodystrophy.

SNP	Chromosome	Position	Effect Allele	Other Allele	Genotype	Risk Allele
rs683135	1	39895460	A	G	GG	0
rs17386142	1	50815783	C	T	CC	2
rs11577194	1	110500175	T	C	TT	2
rs9425291	1	172312769	A	G	GG	0
rs4846565	1	219722104	G	A	GG	2
rs2249105	2	65287896	A	G	AG	1
rs10195252	2	165513091	T	C	TT	2
rs492400	2	219349752	T	C	CT	1
rs2943645	2	227099180	T	C	CT	1
rs308971	3	12116620	G	A	AA	0
rs3864041	3	15185634	T	C	TT	2
rs295449	3	47375955	A	G	AA	2
rs11130329	3	52896855	A	C	AA	2
rs9881942	3	123082416	A	G	AG	1
rs645040	3	135926622	T	G	TT	2
rs2699429	4	3480136	C	T	TC	1
rs3822072	4	89741269	A	G	AA	2
rs6822892	4	157734675	A	G	GG	0
rs4865796	5	53272664	A	G	AA	2
rs459193	5	55806751	G	A	AA	0
rs4976033	5	67714246	G	A	AA	0
rs6887914	5	112711486	C	T	CT	1
rs1045241	5	118729286	C	T	CT	1
rs2434612	5	158022041	G	A	AA	0
rs966544	5	173350405	G	A	AA	0
rs12525532	6	35004819	T	C	CC	0
rs6937438	6	43815364	A	G	AA	2
rs2745353	6	127452935	T	C	CT	1
rs9492443	6	130398731	C	T	CC	2
rs3861397	6	139828916	G	A	AA	0
rs17169104	7	15883727	G	C	CG	1
rs972283	7	130466854	G	A	AA	0
rs2126259	8	9185146	T	C	CC	0
rs1011685	8	19830769	C	T	CC	2
rs4738141	8	72469742	G	A	AA	0
rs7005992	8	126528955	C	G	CC	2
rs498313	9	78034169	A	G	AA	2
rs10995441	10	64869239	G	T	GT	1
rs11231693	11	63862612	A	G	GG	0
rs17402950	12	14571671	G	A	AA	0
rs718314	12	26453283	G	A	AG	1
rs7973683	12	124449223	C	A	CC	2
rs7323406	13	111628195	A	G	GG	0
rs7176058	15	39464167	A	G	AA	2
rs8032586	15	73081067	C	T	CC	2
rs754814	17	4657034	T	C	TT	2
rs7227237	18	47174679	C	T	CC	2
rs8101064	19	7293119	T	C	TC	1
rs4804833	19	7970635	A	G	AG	1
rs4804311	19	8615589	A	G	AA	2
rs731839	19	33899065	G	A	GG	2
rs6066149	20	45602638	G	A	GG	2
rs132985	22	38563471	C	T	CT	1