



# **DNA Methylation Signatures in MZ Twins Discordant for Smoking**

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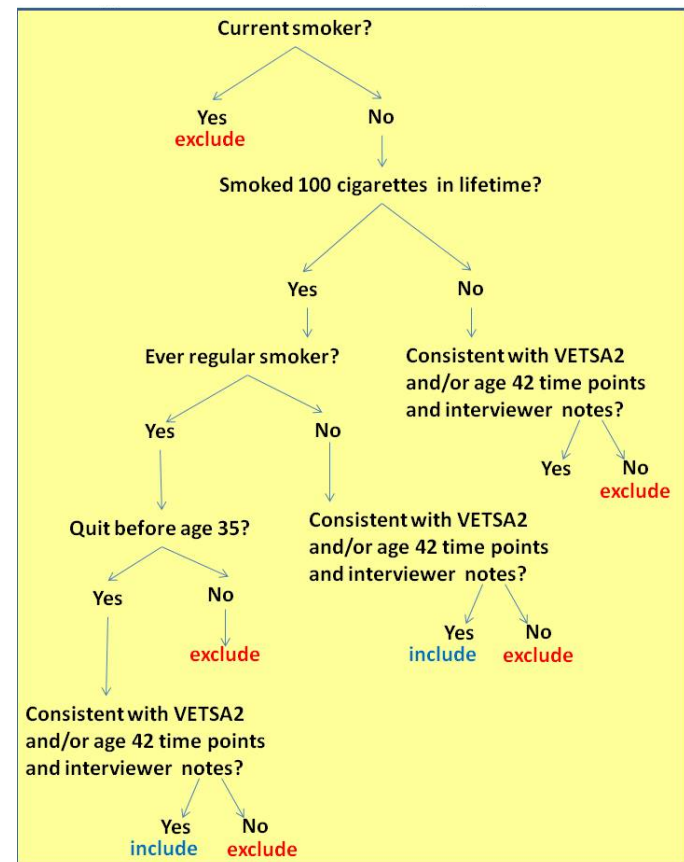
# Study Participants



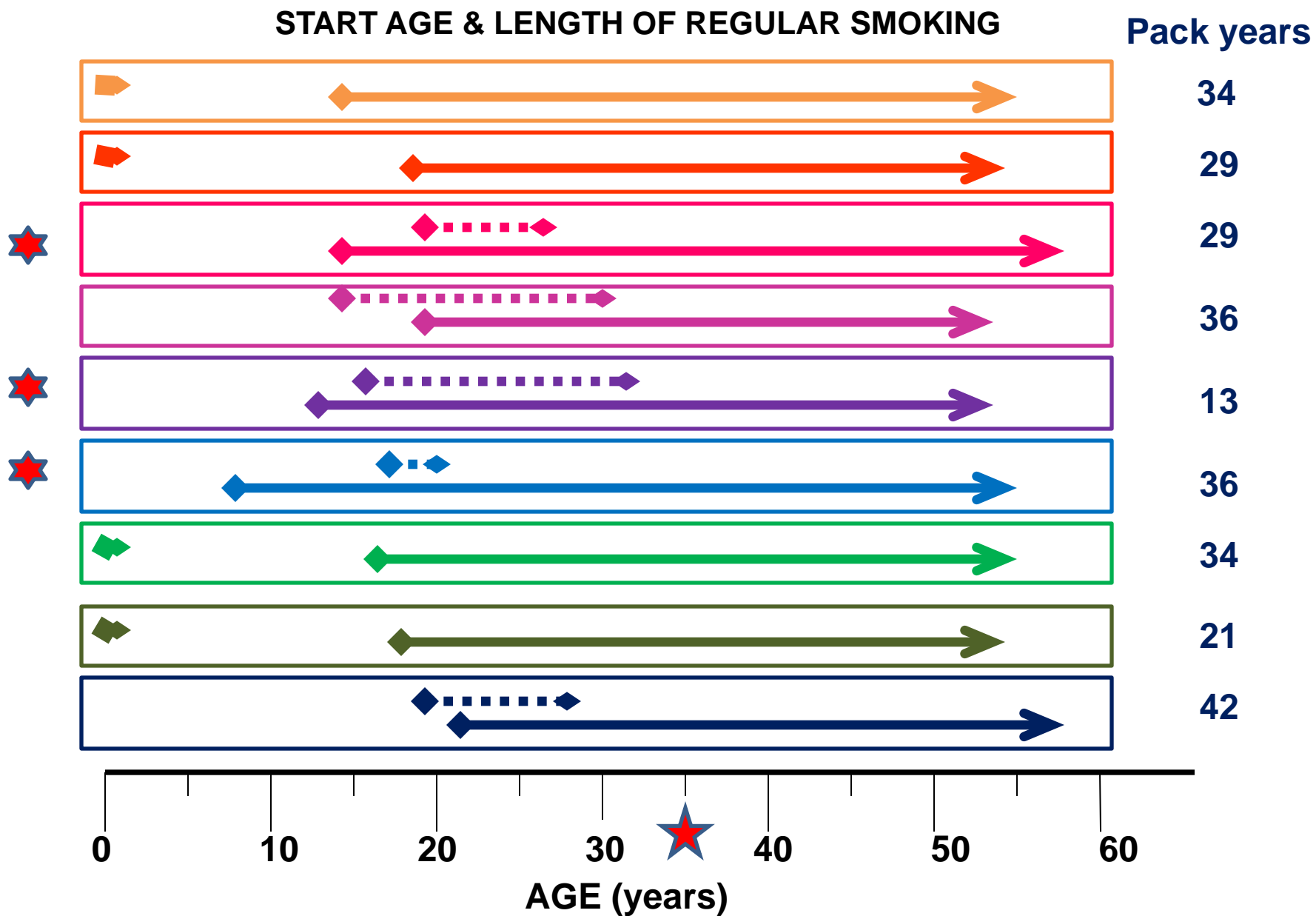
Wave 1: 349 Male MZ Twin Pairs  
51-59 years old

Pilot Study:  
9 MZ Twin Pairs Discordant for Smoking

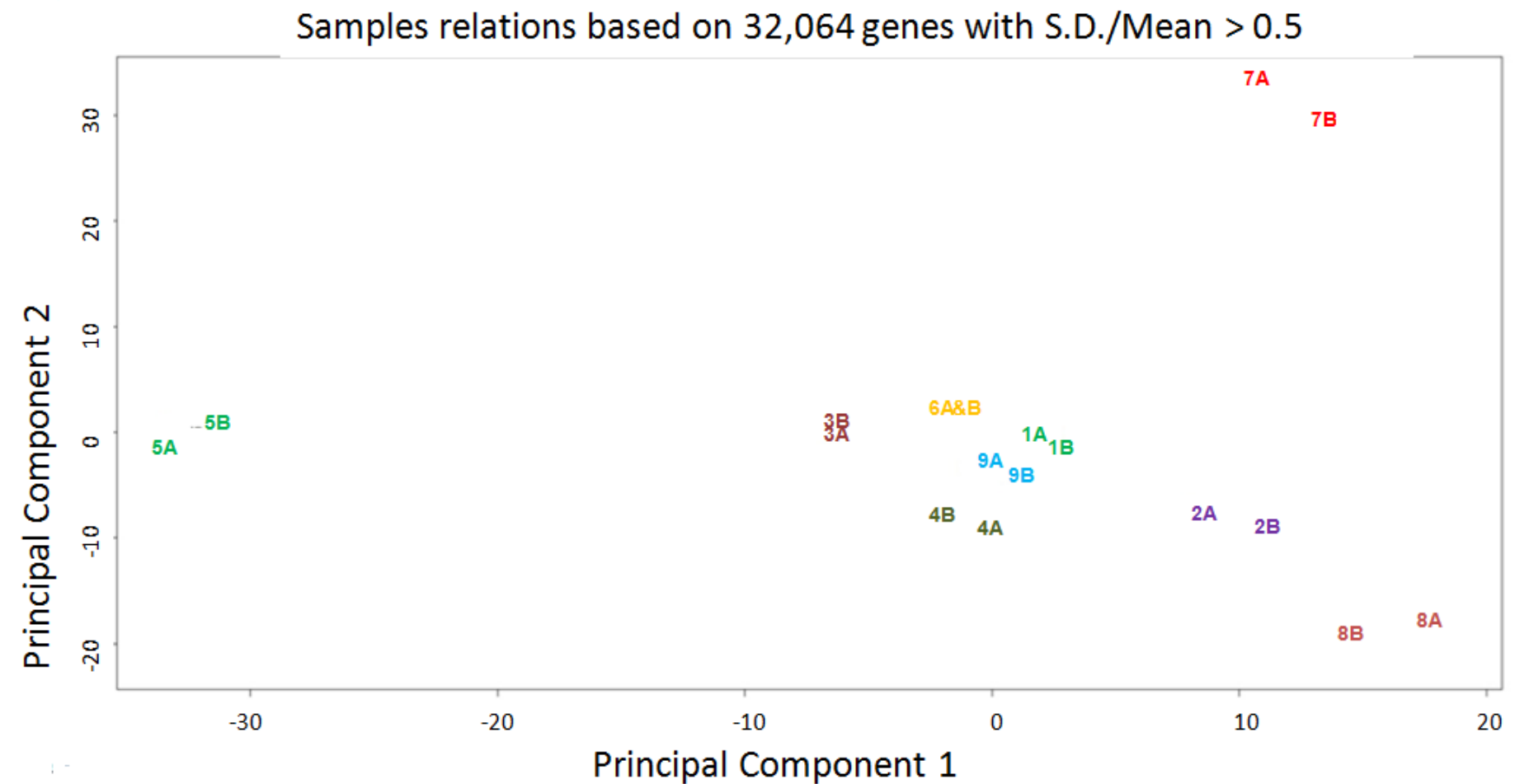
Tobacco use and history assessed  
through a 40-item questionnaire  
administered during a face-to-face  
interview



# TWIN PAIRS DISCORDANT FOR CURRENT SMOKING



# Principal Component Analysis Demonstrates Methylation Patterns of Twin Pairs Cluster Together & Separate from Other Twin Pairs



# Identification of Three Sites Differentially Methylated between Smokers and Non-Smokers at Genome-Wide Significance Levels

CpG Locus	Gene	Protein	Mean $\beta$ -value Difference	unadjusted p value	FDR adjusted p value
cg05575921	<i>AHRR</i>	Aryl hydrocarbon receptor repressor	-0.268	$1.5 \times 10^{-9}$	0.00056
cg09935388	<i>GFI1</i>	Zinc Finger Protein Gfi-1	-0.158	$2.9 \times 10^{-8}$	0.00493
cg03636183	<i>F2RL3</i>	Protease-activated receptor 4	-0.159	$1.1 \times 10^{-6}$	0.10083

$\beta$ -value Difference =  $\beta$ -value Smokers -  $\beta$ -value Non-smokers

$\beta$ -value in Non-smokers higher for all three loci  $\rightarrow$  hypomethylated in smokers

# Results of Co-Twin Control Design versus Case Control Studies

			Our Pilot Data 9 Discordant MZ twin pairs Current smoker vs. non-smoker European Illumina 450K BeadChip			Zeilinger et. al (2012) N=262 Current Smokers N=749 Never smokers European Illumina 450K BeadChip		Elliott et al. (2014) N= 36 Current Smokers N=129 Never smokers South Asian & European Illumina 27K BeadChip		Elliott et al. (2014) N= 190 (smoker non-smoker breakdown not available)	
CpG Locus	Gene	Protein	Mean $\beta$ -value Difference <sup>a</sup>	unadjusted p value	FDR adjusted p value	Median $\beta$ -value Difference	unadjusted p value (rank <sup>b</sup> )	Median $\beta$ -value Difference	unadjusted p value (rank <sup>b</sup> )	Median $\beta$ -value Difference	unadjusted p value (rank <sup>b</sup> )
cg05575921	AHRR	Aryl hydrocarbon receptor repressor	-0.268	$1.5 \times 10^{-9}$	0.00056	-0.244	$2.5 \times 10^{-18}$ (1)	-.22	$6.1 \times 10^{-59}$ (1)	-.14	$1.7 \times 10^{-9}$ (1)
cg09935388	GFI1	Zinc Finger Protein Gfi-1	-0.158	$2.9 \times 10^{-8}$	0.00493	n.s.	n.s.	-.30	$1.0 \times 10^{-10}$ (6)	n.s.	n.s.
cg03636183	F2RL3	Protease-activated receptor 4	-0.159	$1.1 \times 10^{-6}$	0.10083	-0.1474	$2.4 \times 10^{-80}$ (4)	-.12	$10 \times 10^{-17}$ (3)	-.07	$3.8 \times 10^{-7}$ (4)

<sup>a</sup> Median  $\beta$ -value Difference =  $\beta$ -value Smokers -  $\beta$ -value Non-smokers

<sup>b</sup> Rank of locus by p value in each study

n.s. = not significant at epigenome wide level in study

# Conclusion

With only 18 samples (9 twin pairs discordant for smoking), we were able to identify three loci, with genome wide significance, that were hypomethylated in smokers versus their non-smoking co-twin.

1. **Aryl Hydrocarbon Receptor Repressor (AHRR)**: part of the aryl hydrocarbon pathway that metabolizes cigarette smoke components (dioxins).
2. **F2RL3**: A GPCR involved in platelet activation. F2RL3 hypomethylation associated with increased mortality among individuals with coronary heart disease [Eur Heart J 33(22):2841–2848 (2012)]
3. **GFI1**: Transcription repressor essential for hematopoiesis. Mutations that alter the expression of this gene cause neutropenia.

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