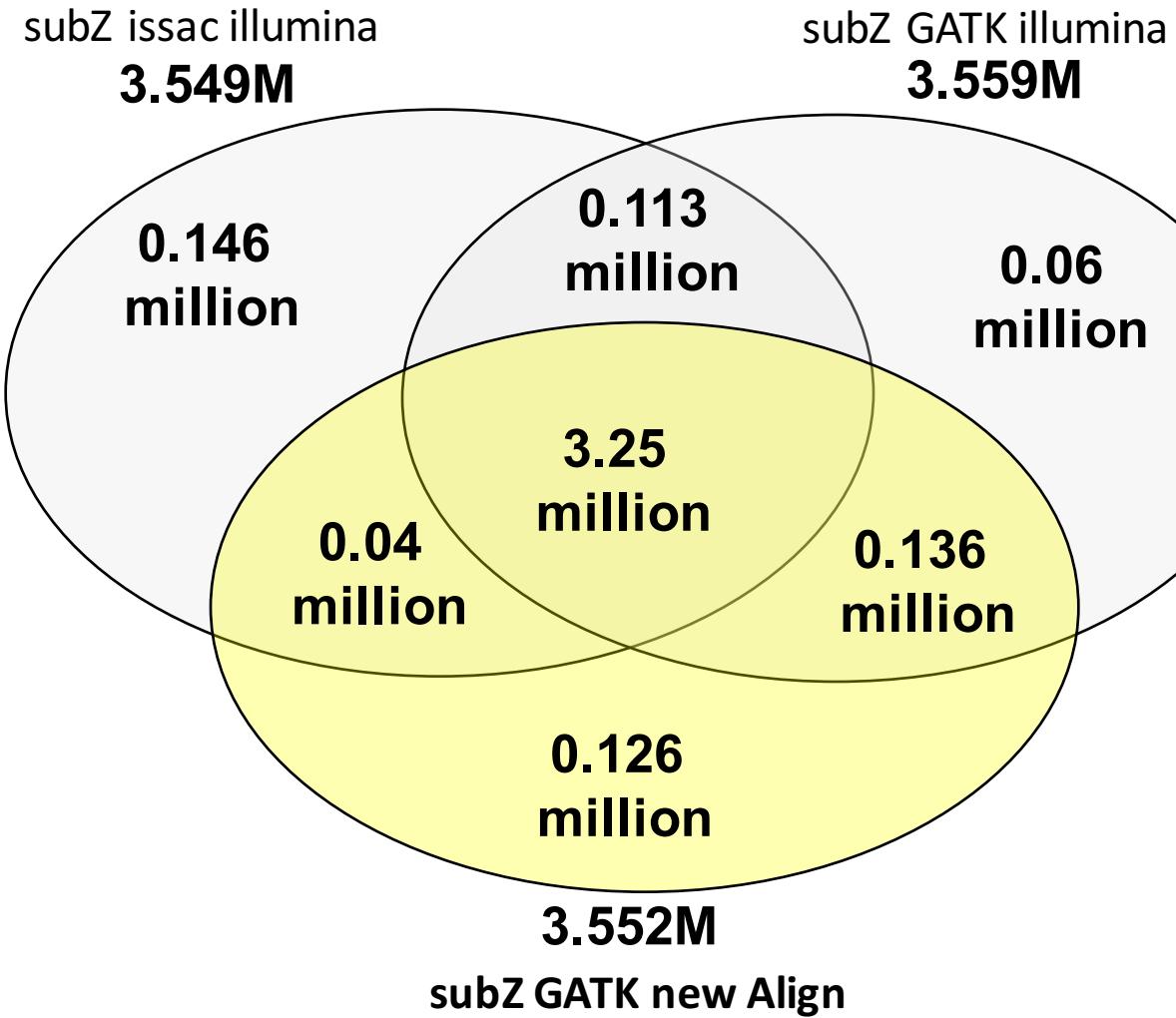


Personal Genome Analysis

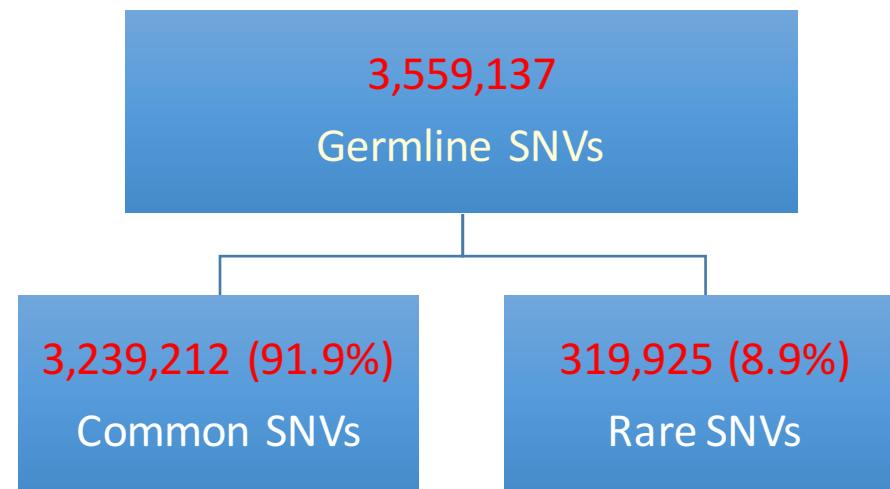
Variant calling and Examples

Comparison of variant calls for subject Z

SNPs

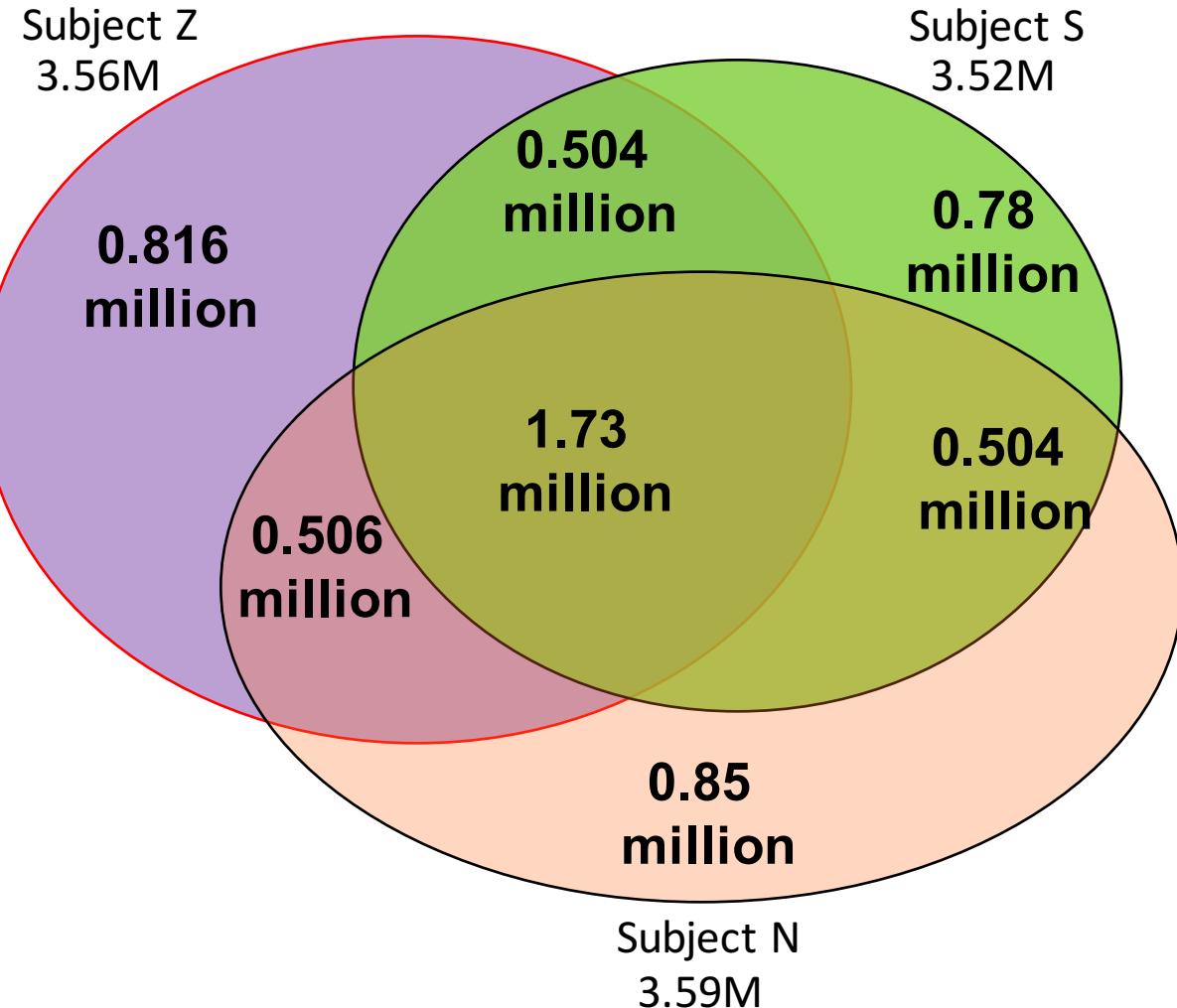


- Original approach (146K specific events):
 - Aligner: CASAVA; Variant Caller: Isaac
- Hybrid approach (60K specific events):
 - Aligner: CASAVA; Variant Caller: GATK
- Gold standard approach (126K specific events):
 - Aligner: BWA; Variant Caller: GATK

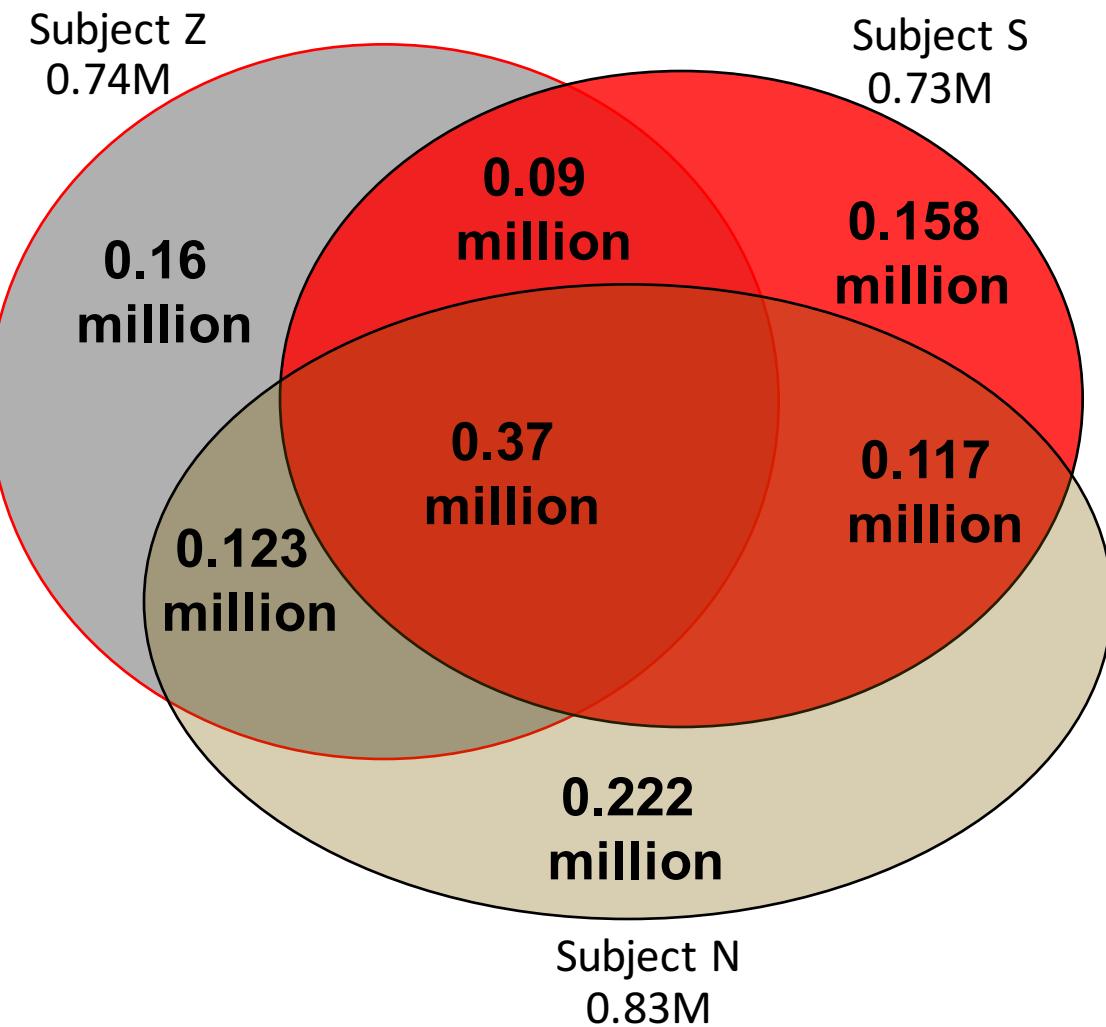


Comparison of SNVs & INDELs across three genomes

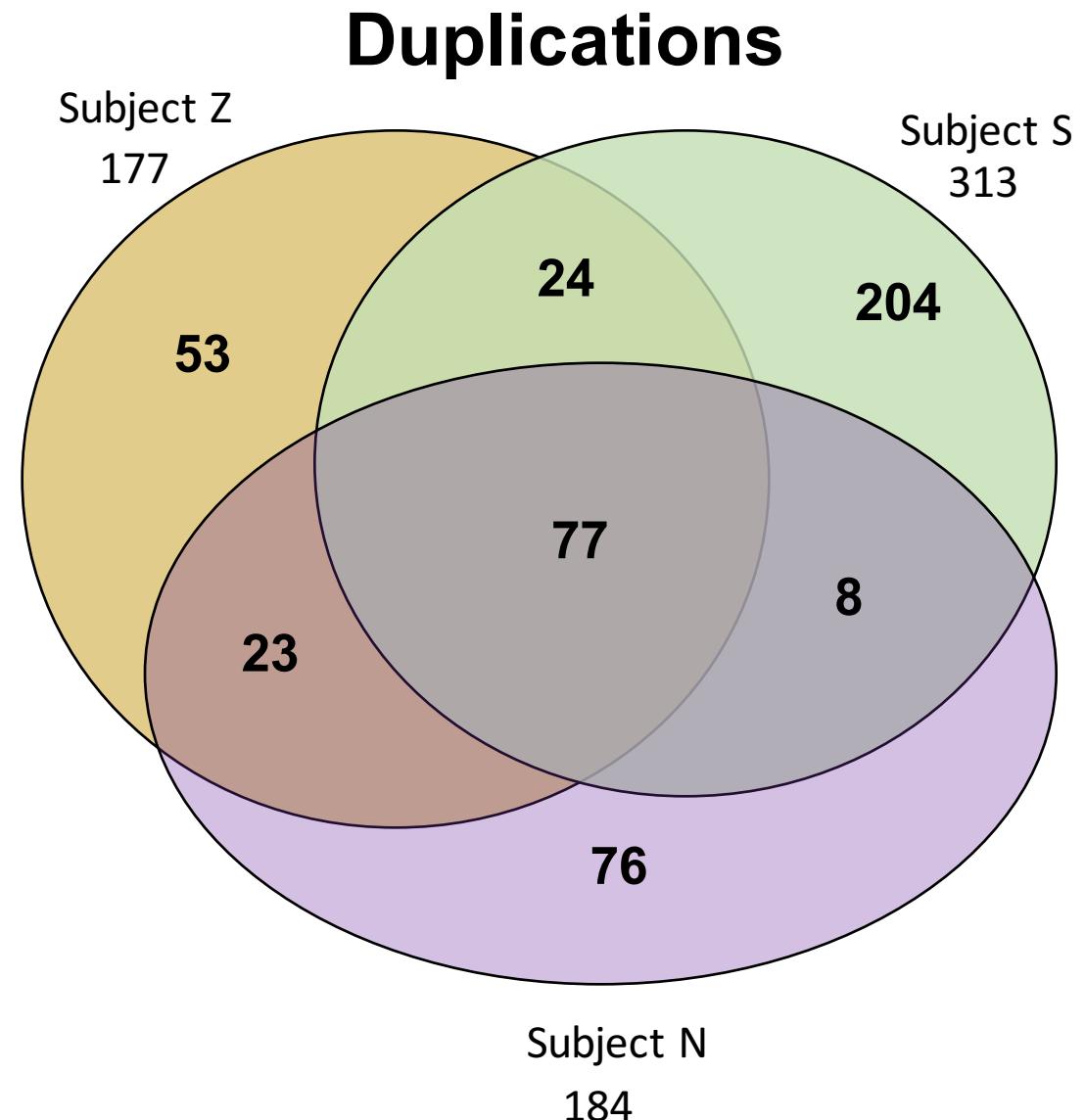
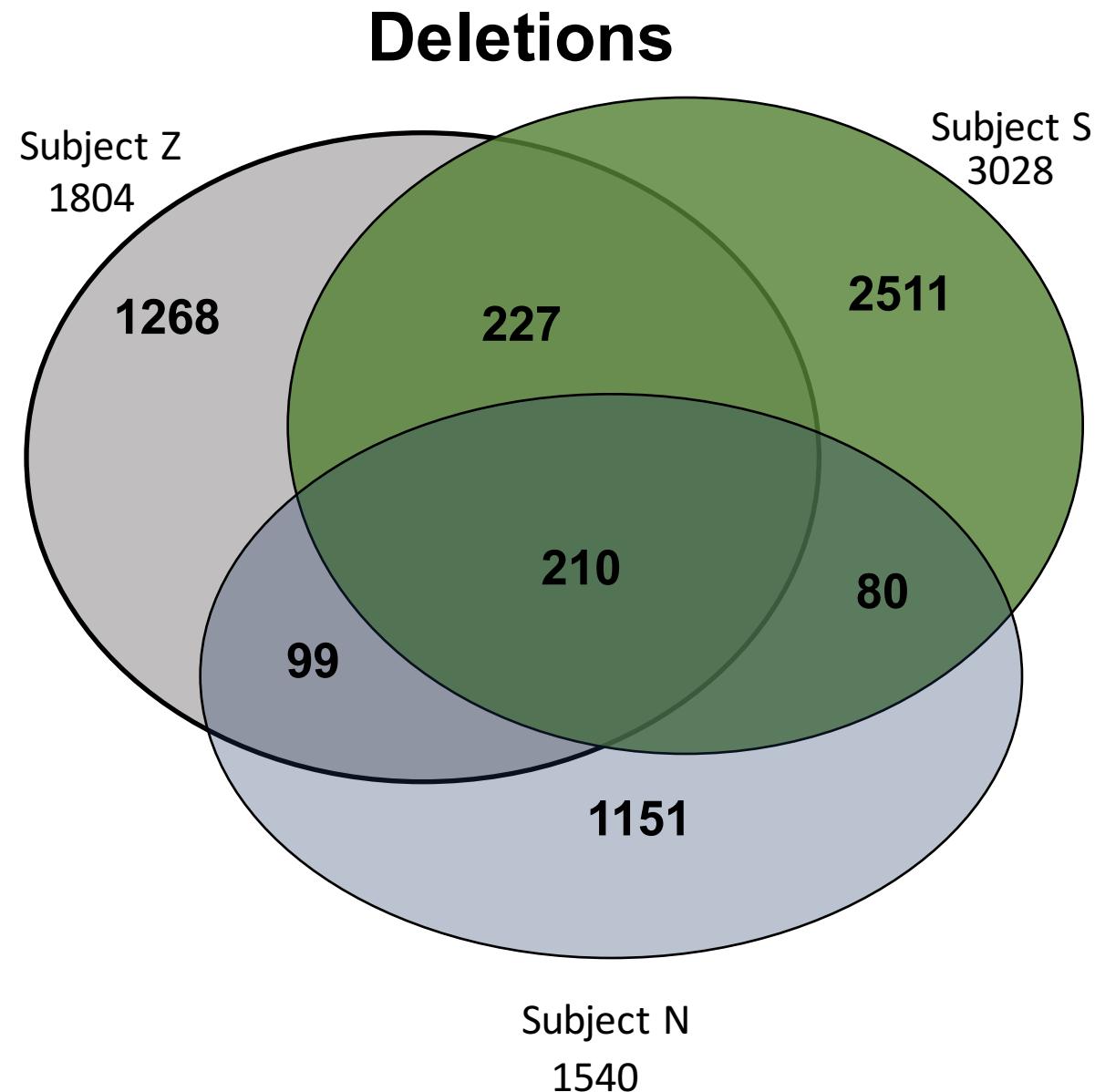
SNPs



INDELs

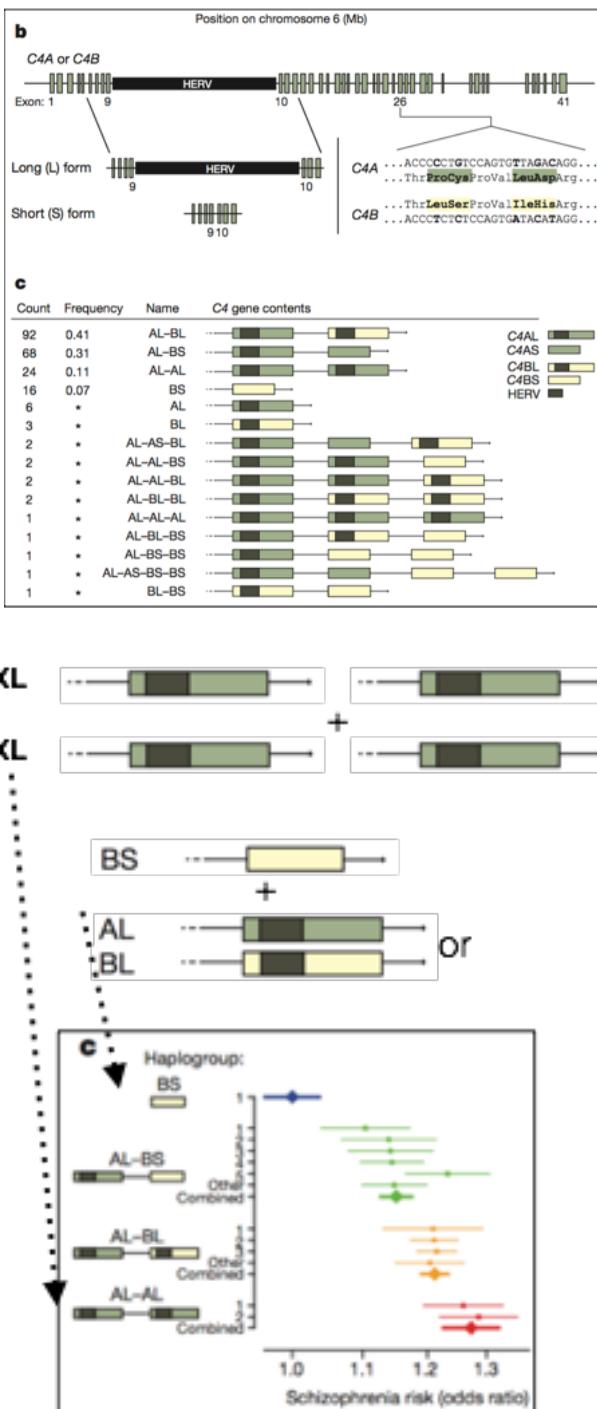
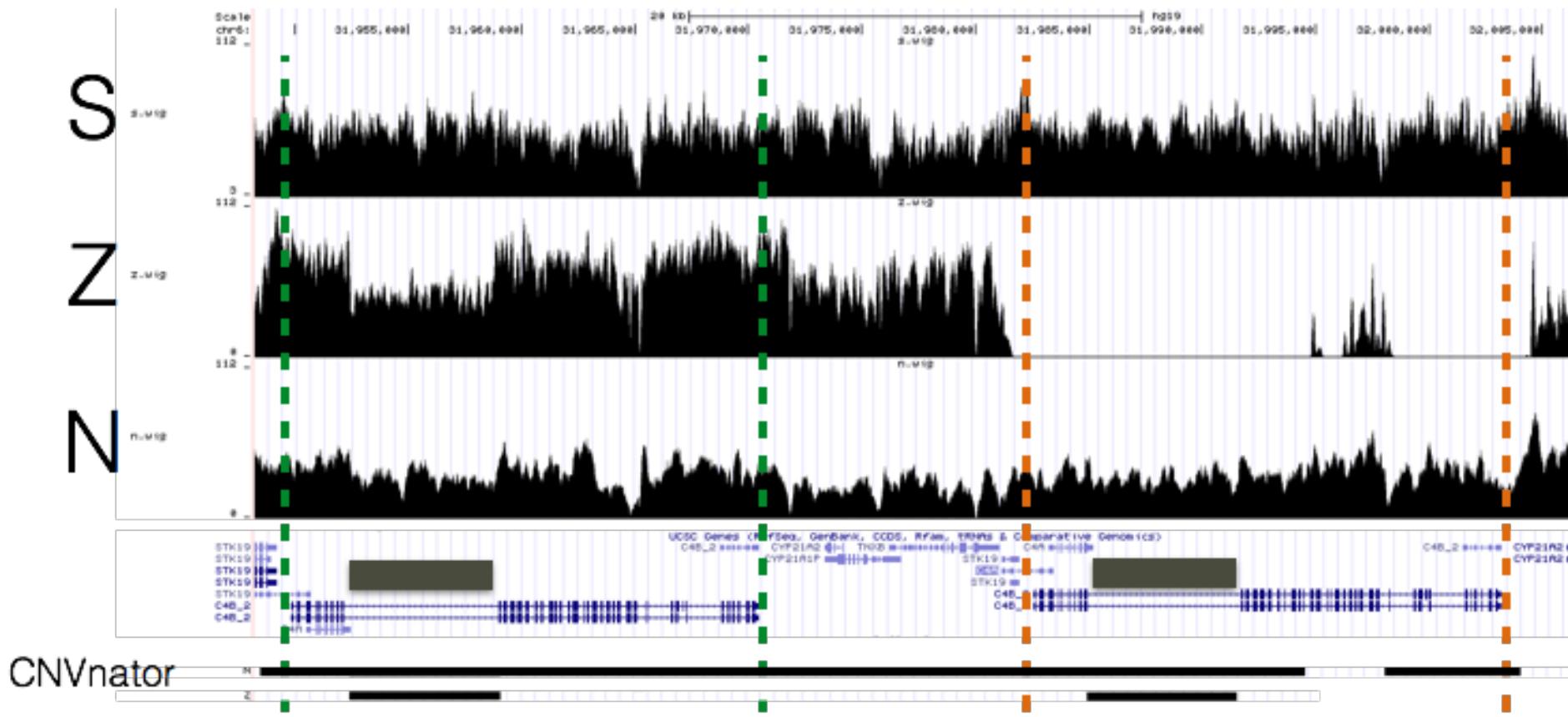


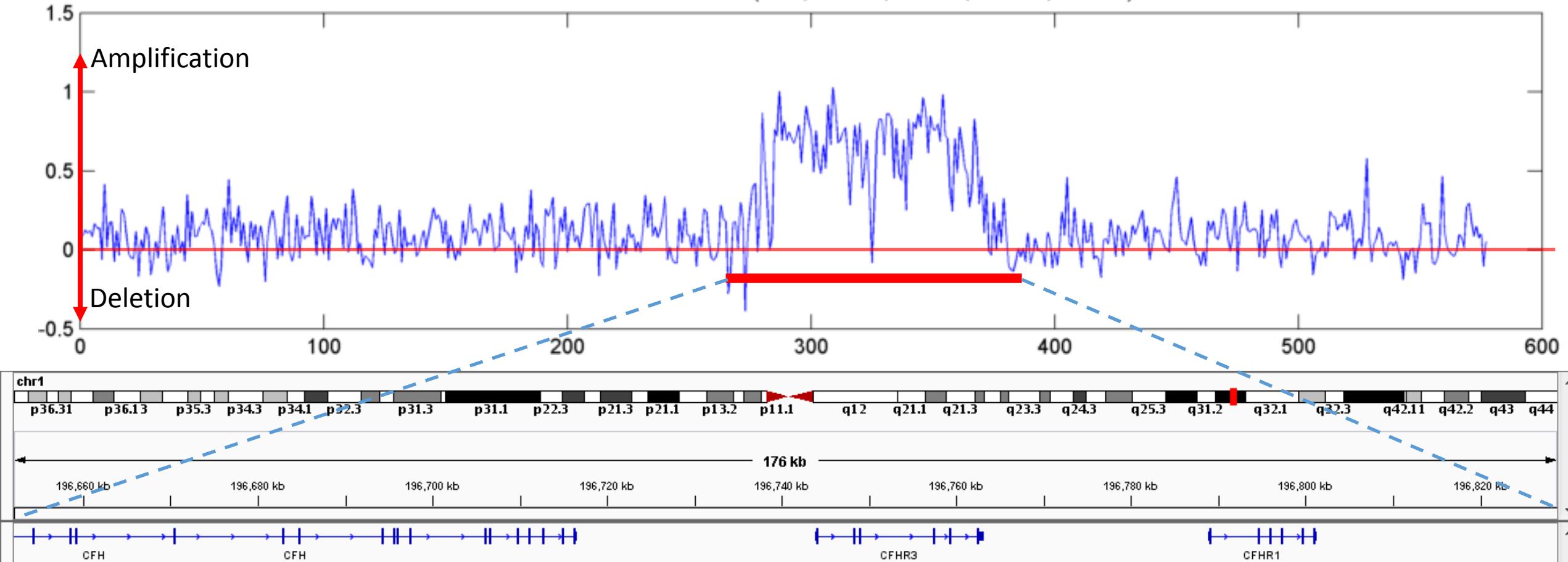
Consensus structural variations across three genomes



Schizophrenia risk from complex variation of complement component 4

Aswin Sekar^{1,2,3}, Allison R. Bialas^{4,5}, Heather de Rivera^{1,2}, Avery Davis^{1,2}, Timothy R. Hammond⁴, Nolan Kamitaki^{1,2}, Katherine Tooley^{1,2}, Jessy Presumey⁵, Matthew Baum^{1,2,3,4}, Vanessa Van Doren¹, Giulio Genovese^{1,2}, Samuel A. Rose², Robert E. Handsaker^{1,2}, Schizophrenia Working Group of the Psychiatric Genomics Consortium*, Mark J. Daly^{2,6}, Michael C. Carroll⁵, Beth Stevens^{2,4} & Steven A. McCarroll^{1,2}

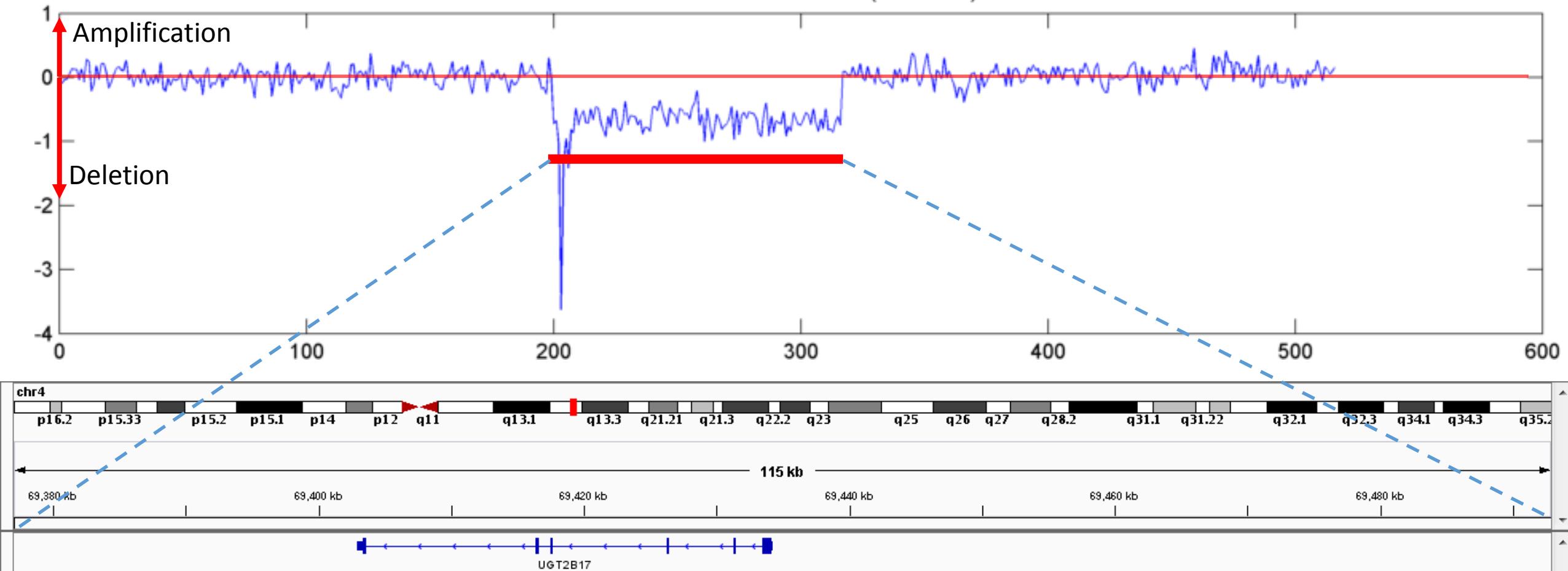




A common *CFH* haplotype, with deletion of *CFHR1* and *CFHR3*, is associated with lower risk of age-related macular degeneration

Anne E Hughes¹, Nick Orr¹, Hossein Esfandiary¹, Martha Diaz-Torres², Timothy Goodship² & Usha Chakravarthy³

chr4:69377002-69493001 (UGT2B17)



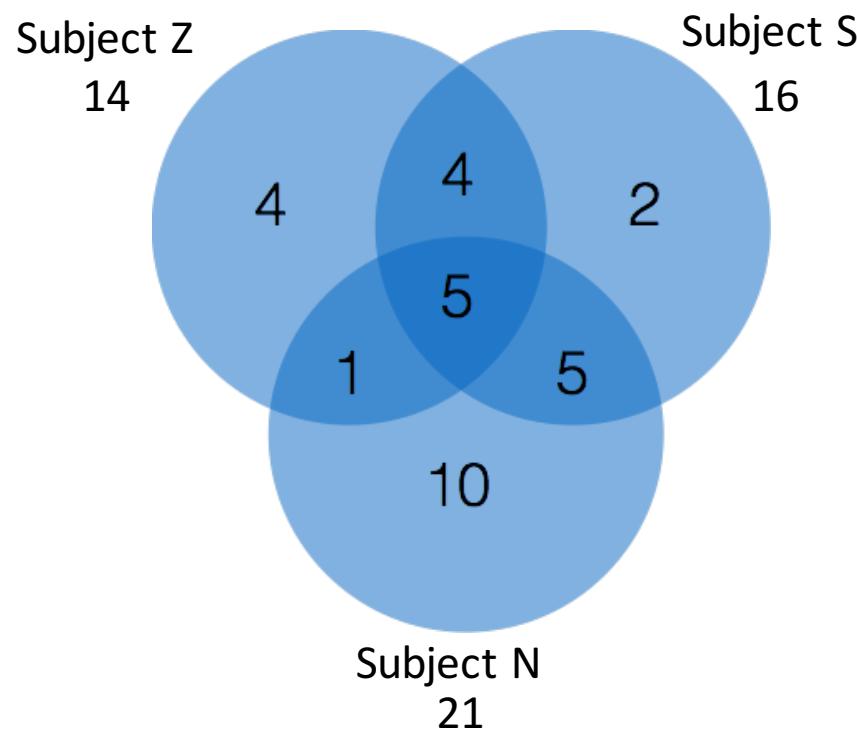
Deletion Polymorphism of UDP-Glucuronosyltransferase 2B17 and Risk of Prostate Cancer in African American and Caucasian Men

can American controls, respectively. When all subjects were considered, a significant association was found between the *UGT2B17* deletion polymorphism and prostate cancer risk

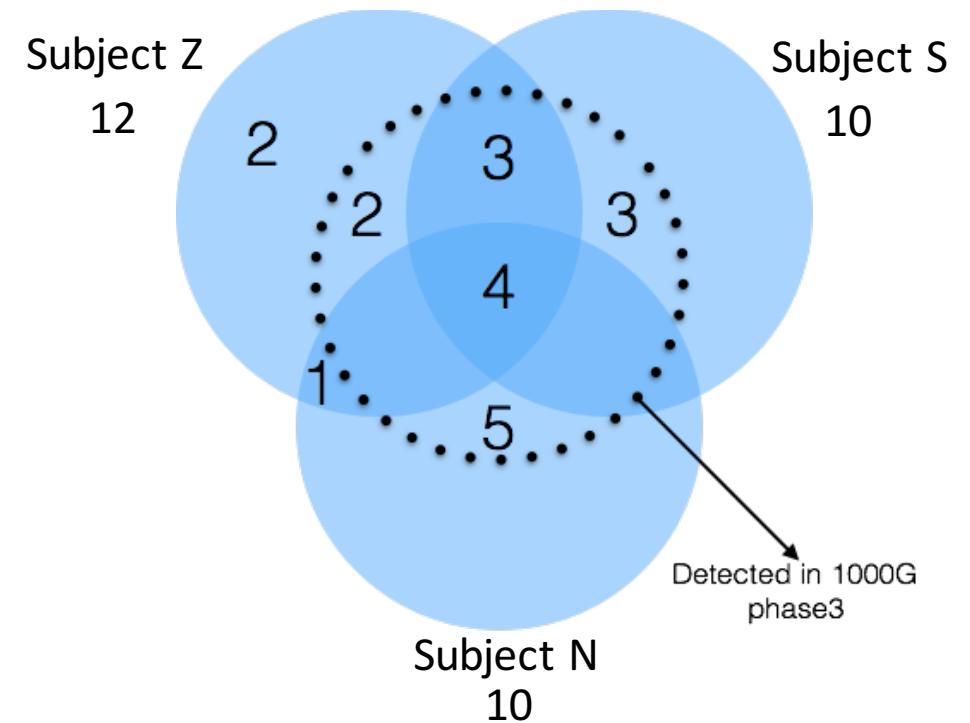
Processed Pseudogene CNV

	Pseudogenes	Processed pseudogenes	Human specific processed pseudogenes
Human	~14,000	7,831	127

Pseudogene absence

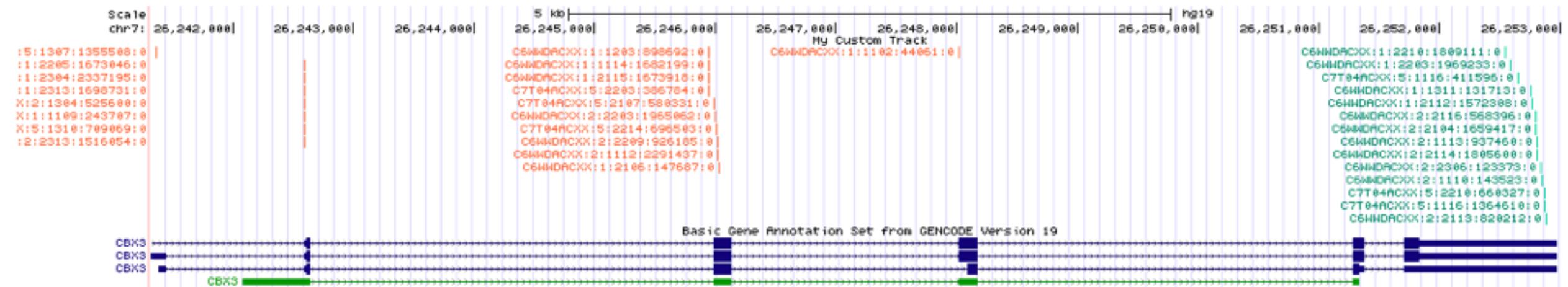


Pseudogene insertion

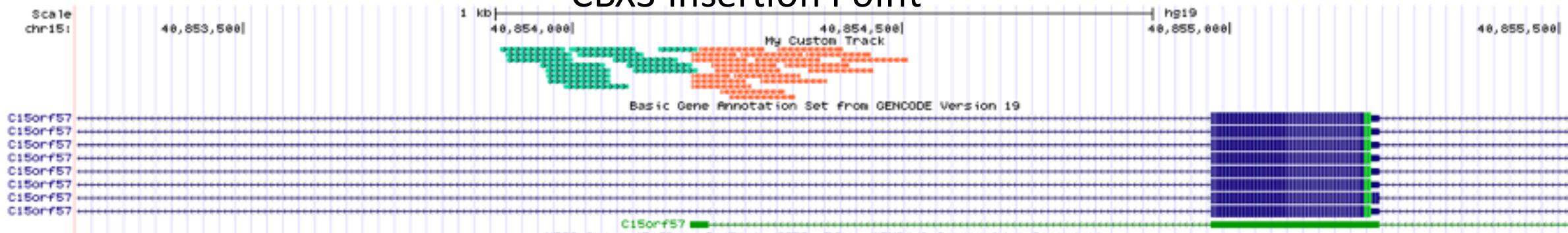


Pseudogene CNV – Example I

CBX3 Parental gene



CBX3 Insertion Point



ALU variation

	# of Alu in the genome	AluY
Human	1,238,995	146,308

