

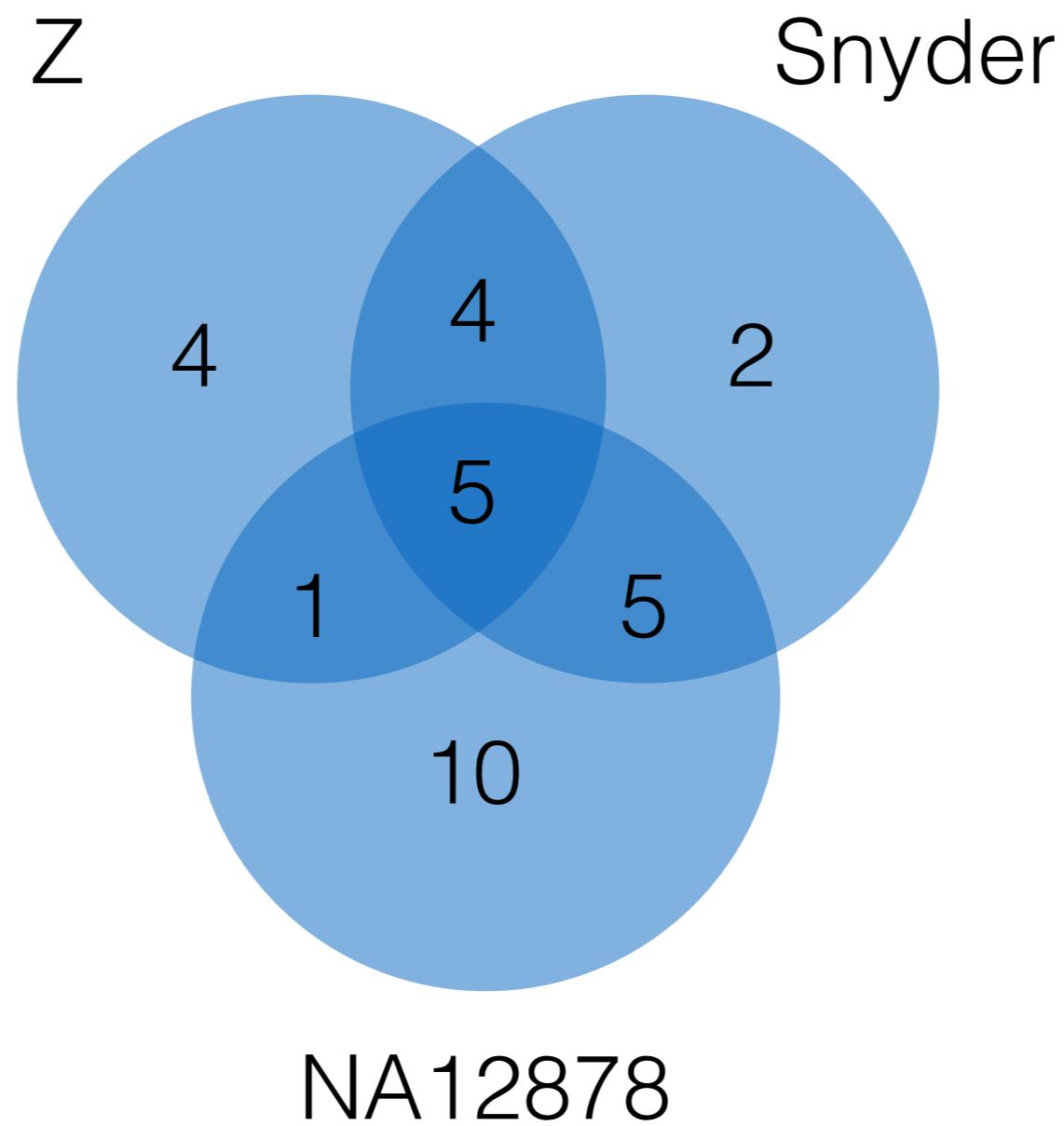
retroCNVs  
CZ; MS; NA12878  
FN - Tech

	Pseudogenes	Processed pseudogenes	Human specific processed pseudogenes
--	-------------	-----------------------	--------------------------------------

Human	~14,000	7,831	127
-------	---------	-------	-----

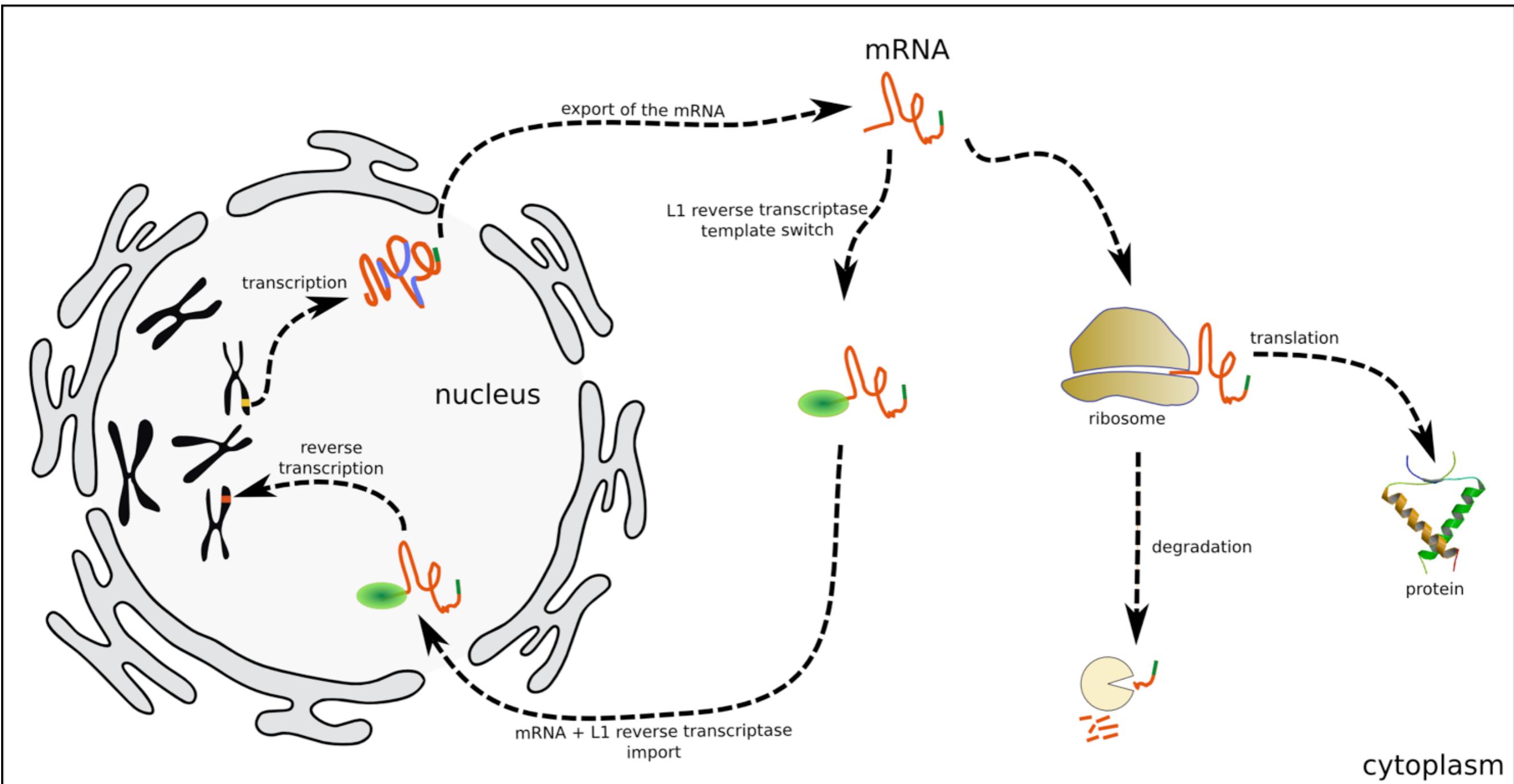
	# of ALUs in the genome	ALUY	Human specific ALUs
Human	1,238,995	146,308	?

# pseudogene absence



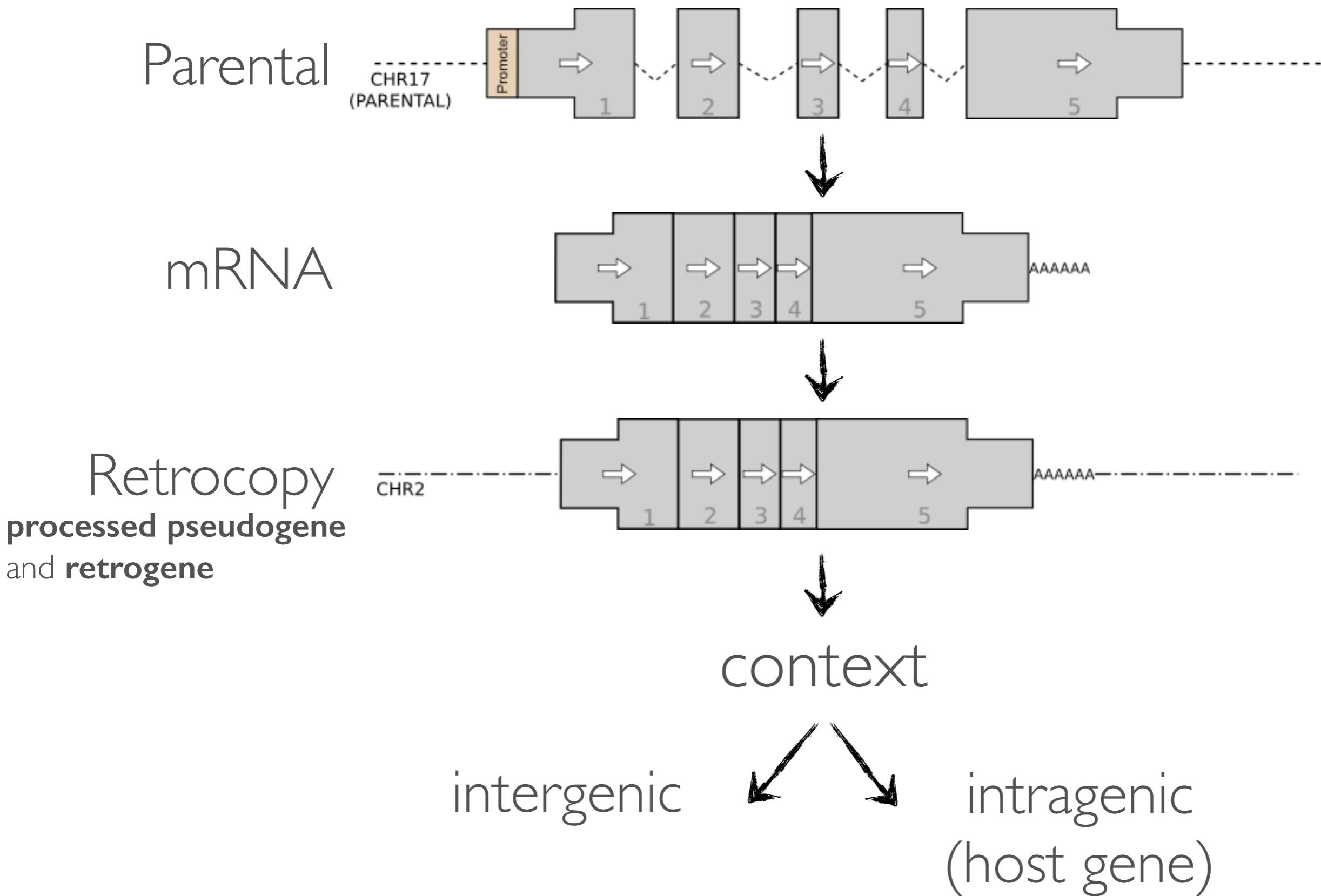
# Retrotransposition of mRNAs

origin of processed pseudogenes and retrogenes



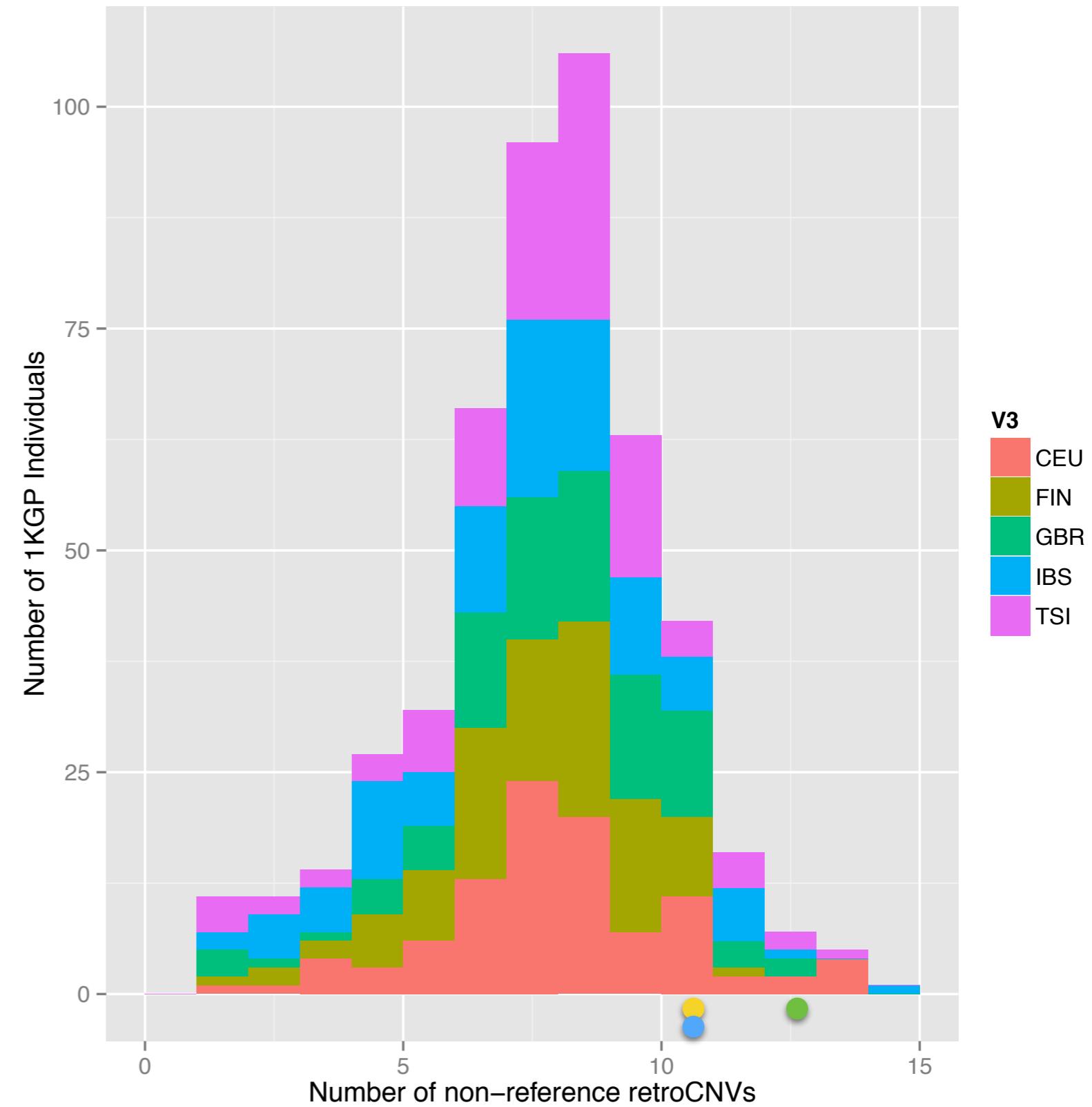
adapted from Non-LTR retrotransposons encode noncanonical RRM domains in their first open reading frame. E. Khazina, et al. PNAS, 2009.

# Involved sequences



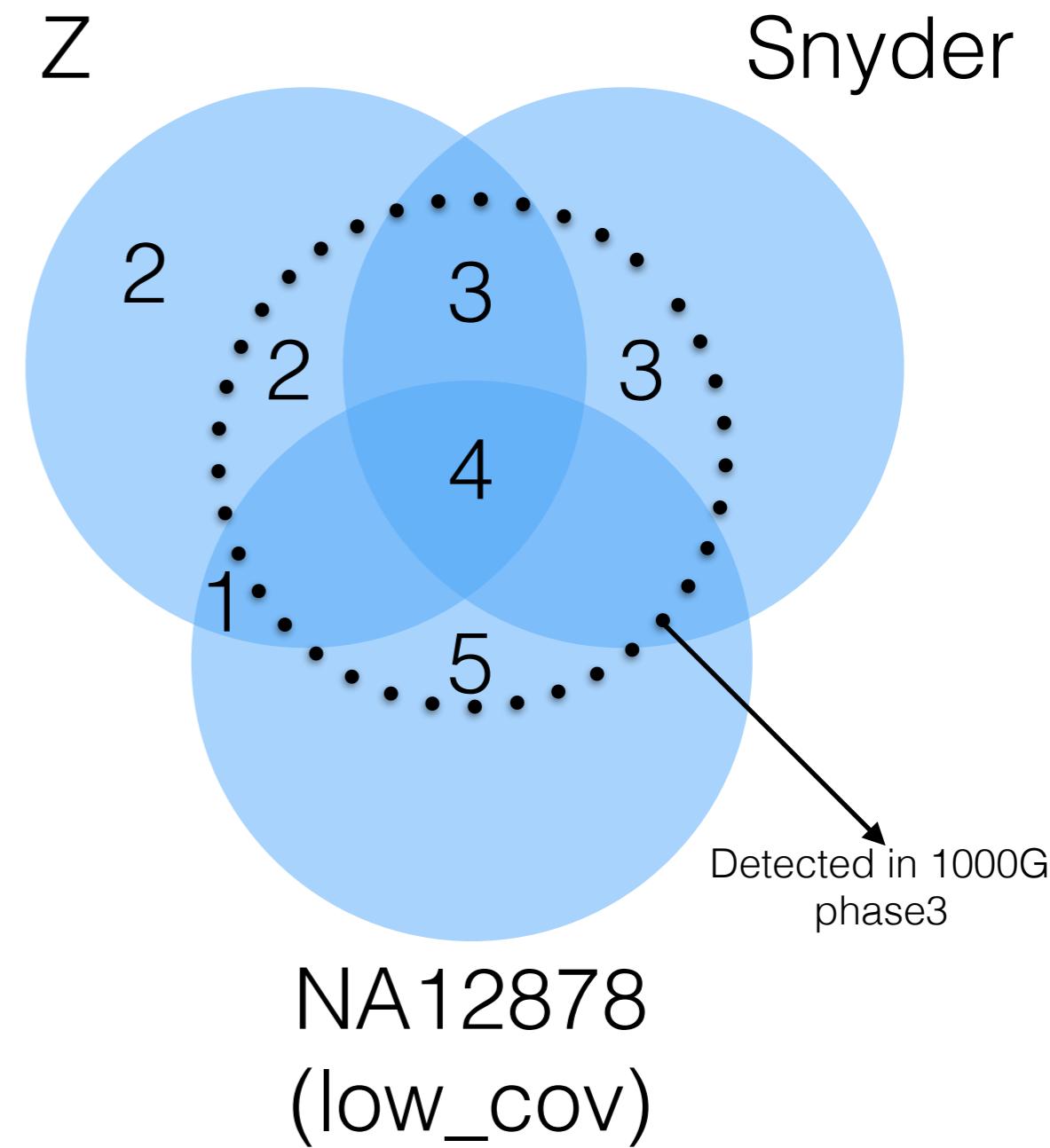
# 1000 Genomes retroCNVs

- Z: 12 retroCNVs
- M. Snyder: 10 retroCNVs
- NA12878: 10 retroCNVs



# Shared and Specific retroCNVs

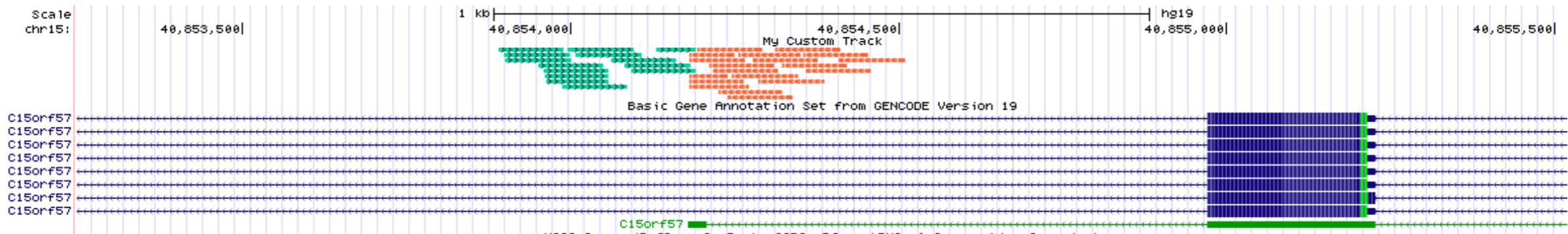
- Z specific insertions:
  - MFF\_chr15: freq. in AFR
  - FAM136A\_chrA: rare variant
- Snyder specific insertions:
  - ANPEP\_chr13: freq. in ASN
  - PPIA\_chr4: freq. south EUR
  - PRKRA\_chr3: freq. in ASN



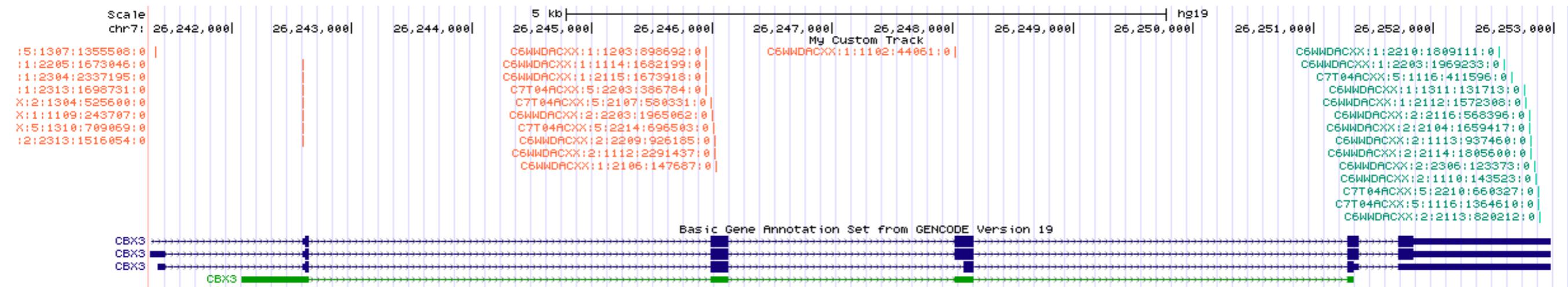
# New retroCNVs

- TENM4 (Z and NA12878)  
Small segment 3'UTR  
Intergenic insertion close to ORs (3kb)  
"neural development, regulating the establishment of proper connectivity within the nervous system"
- FAM230  
Could be a huge deletion (only evidence from one extremity)  
Intergenic - gene desert  
unknown function
- ANKDR36  
3'UTR (only evidence from one extremity)  
Intragenic (NBPF25P)

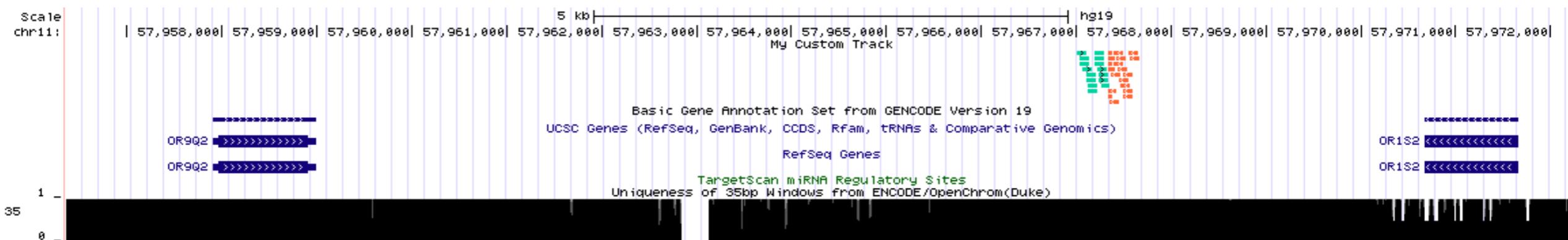
# CBX3: Insertion Point



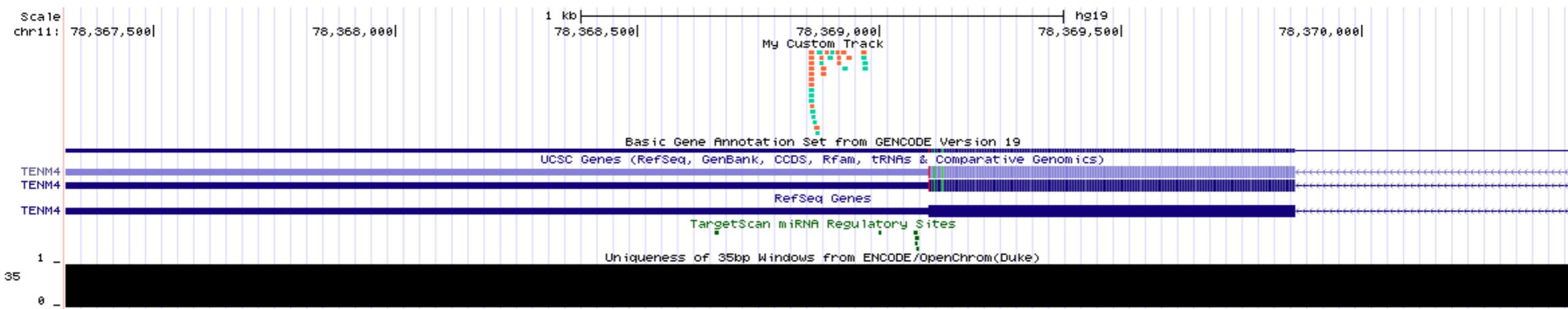
# CBX3: Parental



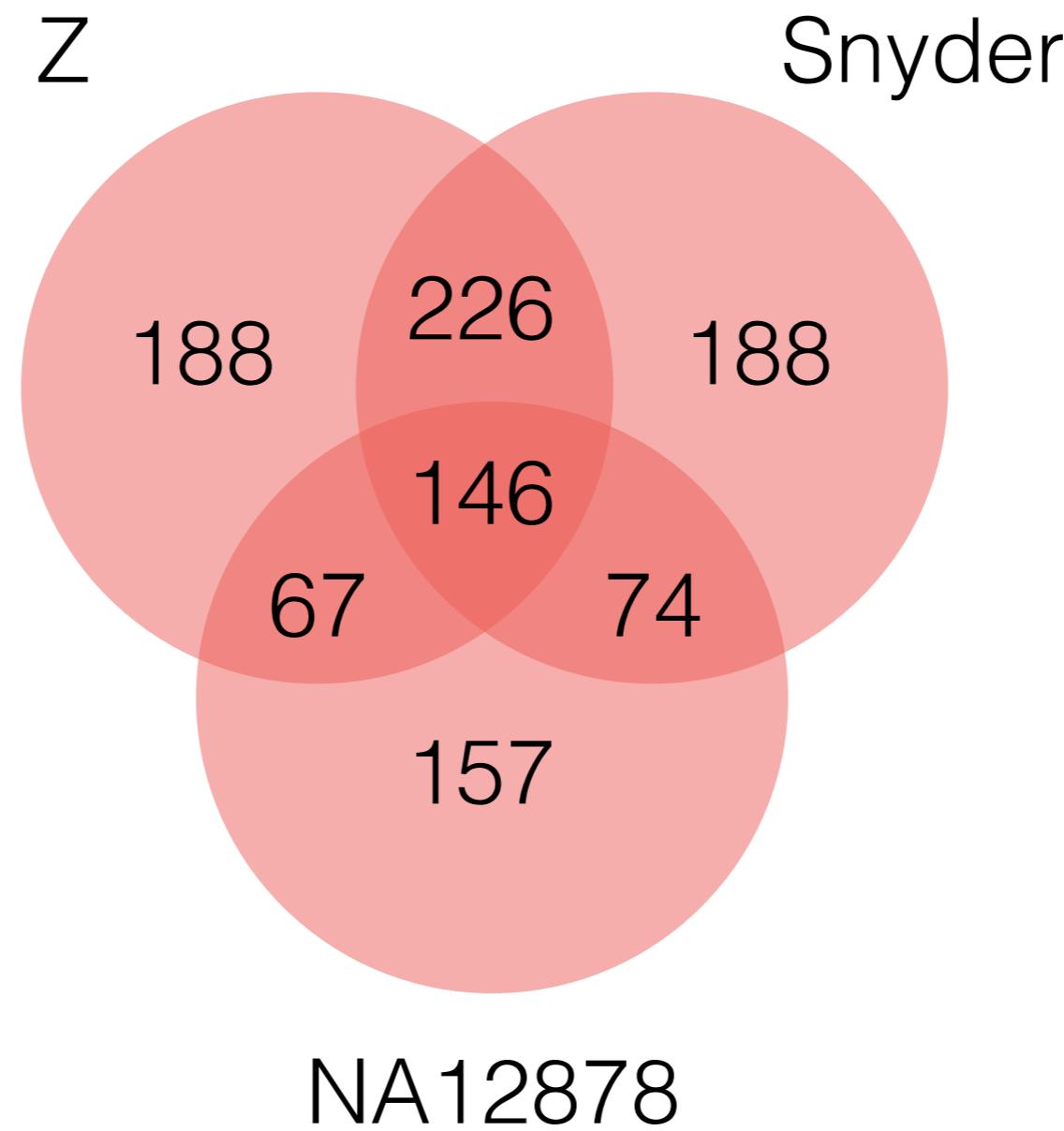
# TENM4: Insertion Point



# TENM4: Parental

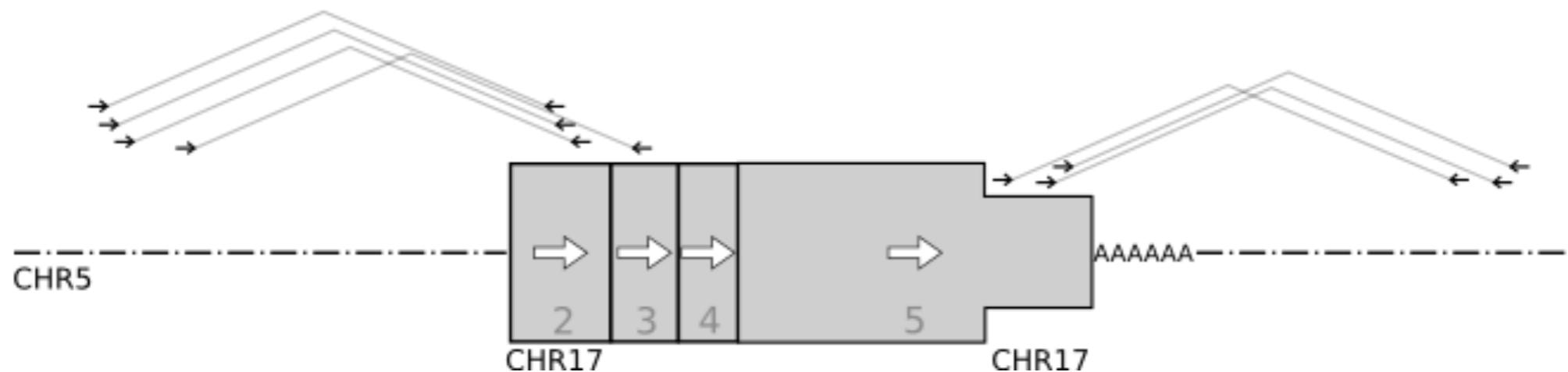


# Shared and Specific ALUs



# Detection of new retrocopies

population/individual specific retrocopies



Alignment in the reference genome:

