Activities in SVs, focusing on breakpoint characterization

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Our Activities Related to SVs

- SV calling (eg Retroduplications)
- Functional enrichment
- Breakpoints/Mechanism study

Breakpoint characterization in 1000G

TEI

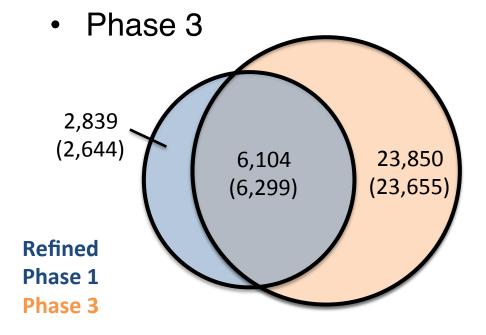
NH

VNTR

 Breakseq #1 w/ ~2000 breakpoints [Lam et al. Nat. Biotech. ('10)]

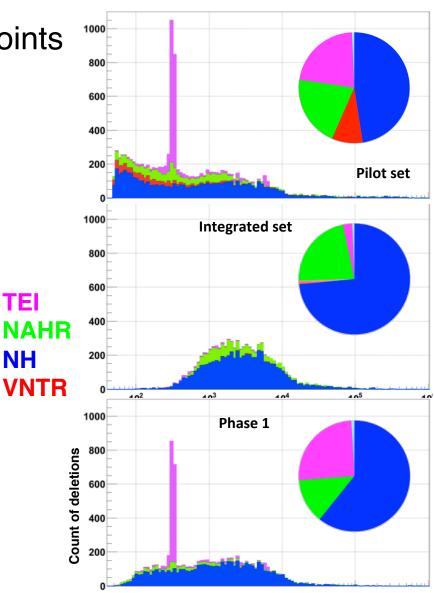
Pilot

Phase 1 "Integrated" & Phase 1 refined



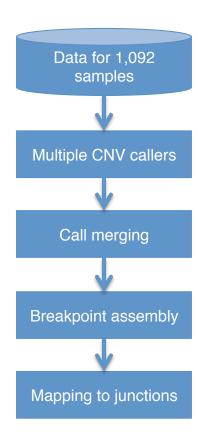
Exact match

Number in parentheses: >50% reciprocal match

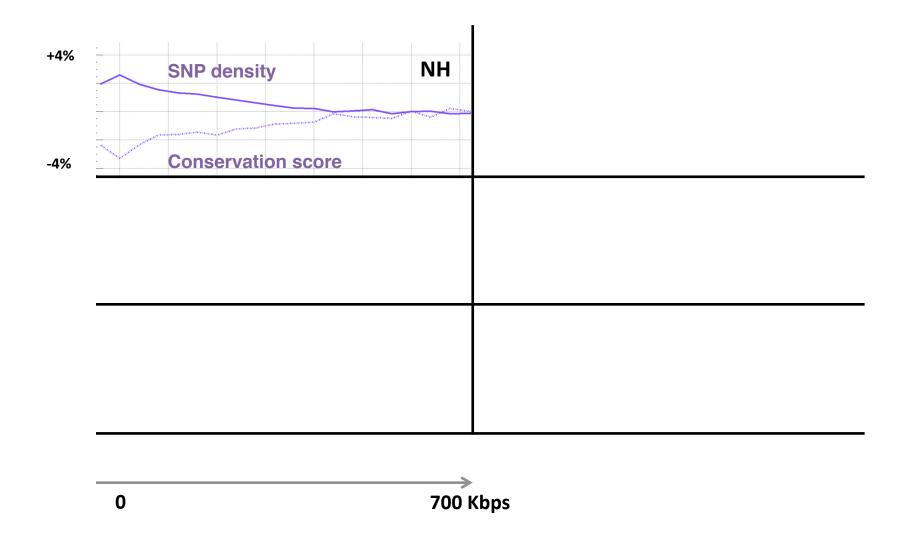


8,943 Deletion Breakpoints (Phase I Refined)

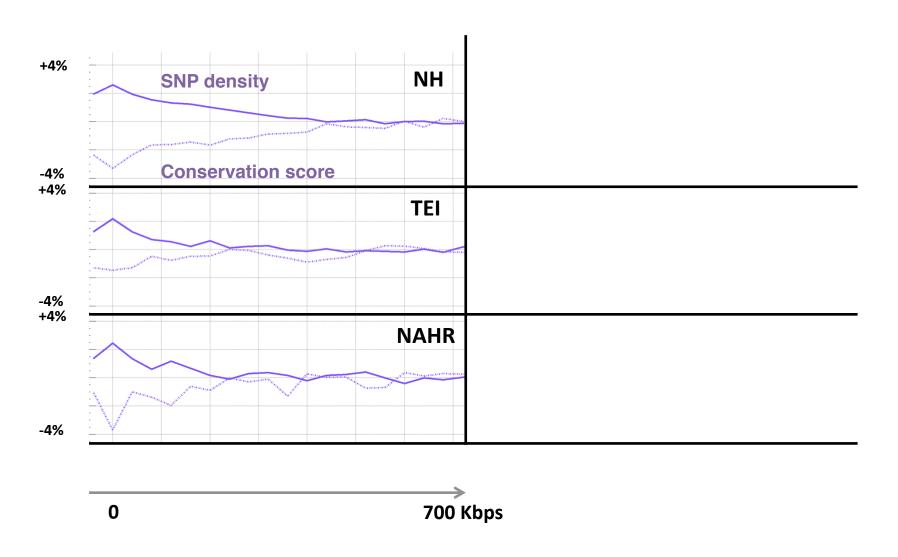
- FDR from IRS, PCR, and high-coverage trios
 - − ~7% for site existence
 - 13% for site existence + sequence precision



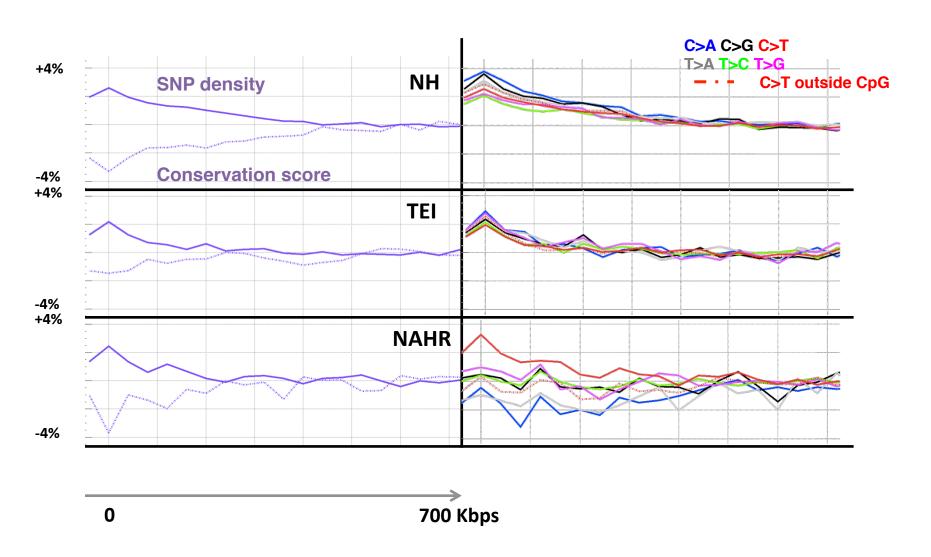
Higher SNP Density and Relaxed Selection at NH Breakpoints



Higher SNP Density and Relaxed Selection at all Breakpoints



SNP Density at NAHR is Driven by High C>T



NAHR breakpoint are associated with open chromatin environment

1.3

1.2

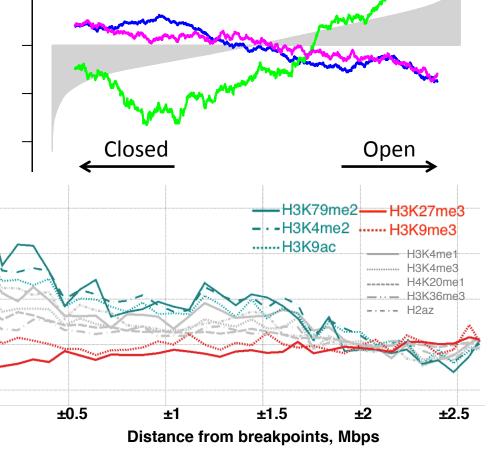
1.1

0.9

 Supported by Hi-C and Histone modification

 Hypothesis: Some NAHR deletions occur w/o cell Replication

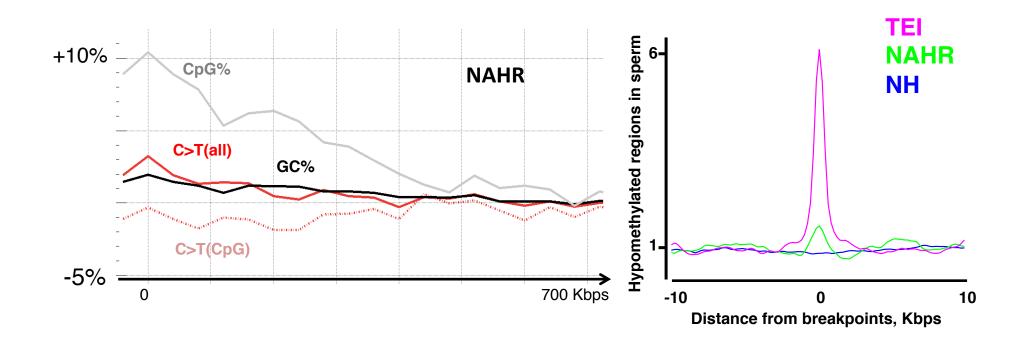
* H1 & GM12878 cells



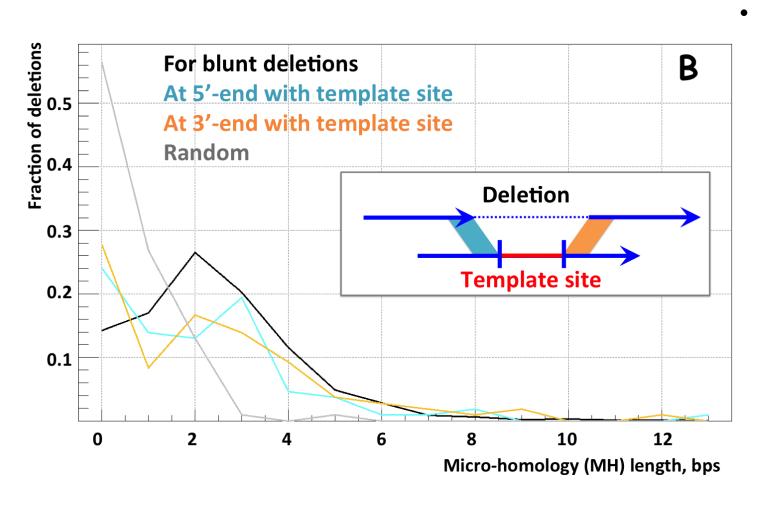
NAHR NH

Methylation pattern associated with breakpoints mechanisms

- Lower C>T in CpG around NAHR breakpoints
 - indicates lower methylation level in germline & embryonic cells
- Confirmed in male gamete



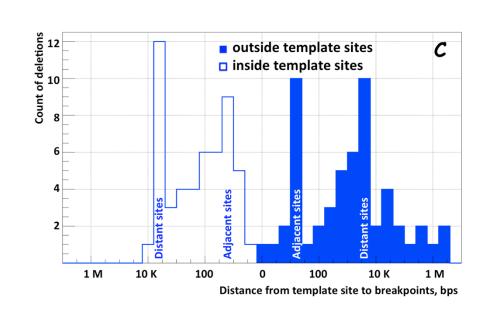
Micro-homologies Identified around Breakpoints

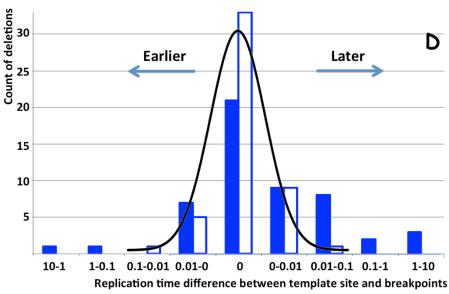


Breakpoints
have
Microhomologous
sequences
with the
template sites.

NH deletions are often coupled with micro-insertions

- Templates located at 2 characteristic distances from breakpoints, which tend to replicate late
- Suggests spatial & temporal configuration of DNA during template switching





More about breakpoints/ mechanisms

See shadow

More Functional Characterization of SVs

See shadow

More SV calling & retrodups

See shadow

Acknowledgements

Refined Phase 1
 Breakpoints Analysis

 Alexej Abyzov,
 Shantao Li,

Daniel Rhee Kim, Marghoob Mohiyuddin, Adrian Stuetz, Nicholas F. Parrish, Xinmeng Jasmine Mu, Wyatt Clark, Ken Chen, Matthew Hurles, Jan Korbel, Hugo Y.K. Lam, Charles Lee

- Other SV participants
 - Y Zhang, J Zhang,F Navarro, S Kumar



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