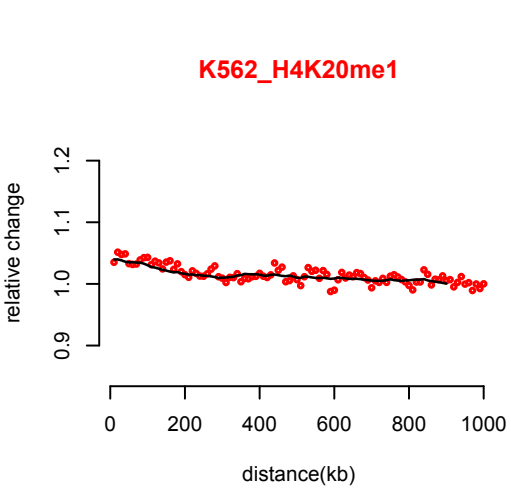
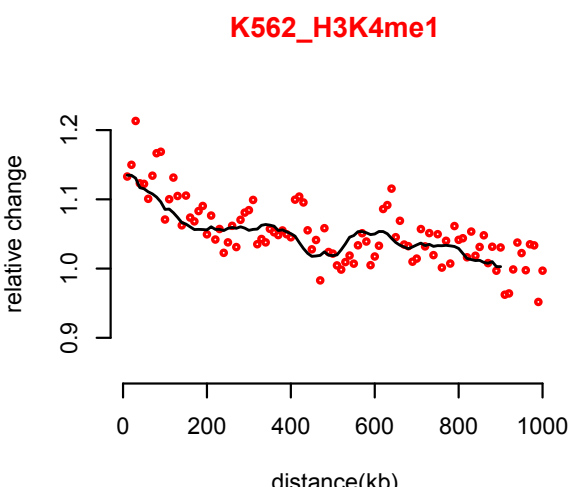
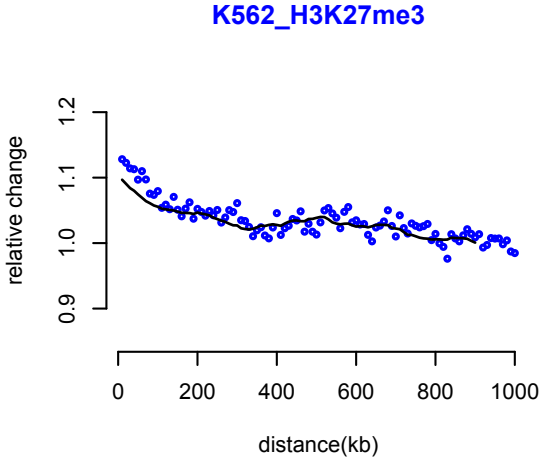

K562_H4K20me1
relative change
0.9
1.0
1.1
1.2
0
200
400
600
800
1000
distance(kb)


K562_H3K4me1
relative change
0.9
1.0
1.1
1.2
0
200
400
600
800
1000
distance(kb)


K562_H3K27me3
relative change
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1.1
1.2
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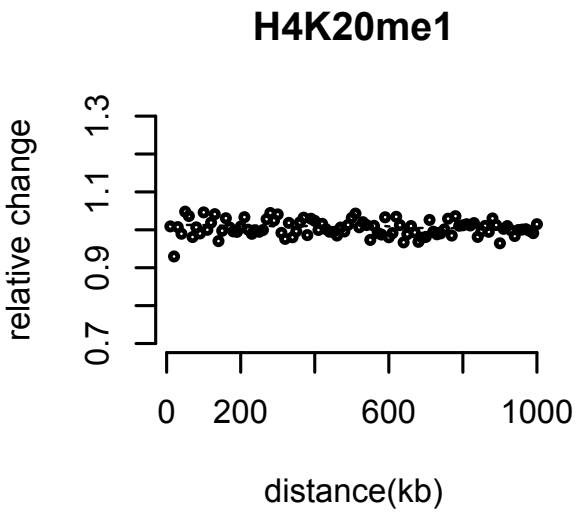
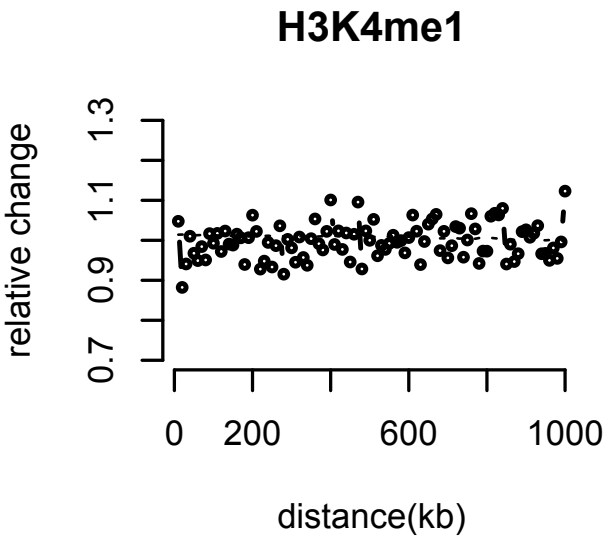
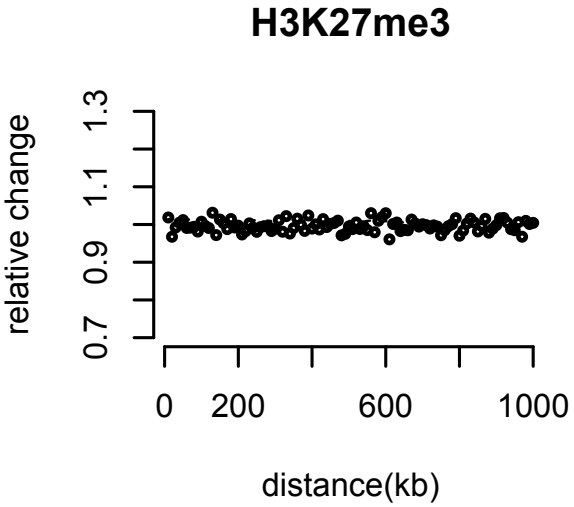
200
400
600
800
1000
distance(kb)


H4K20me1
relative change
0.7
0.9
1.1
1.3
0
200
600
1000
distance(kb)

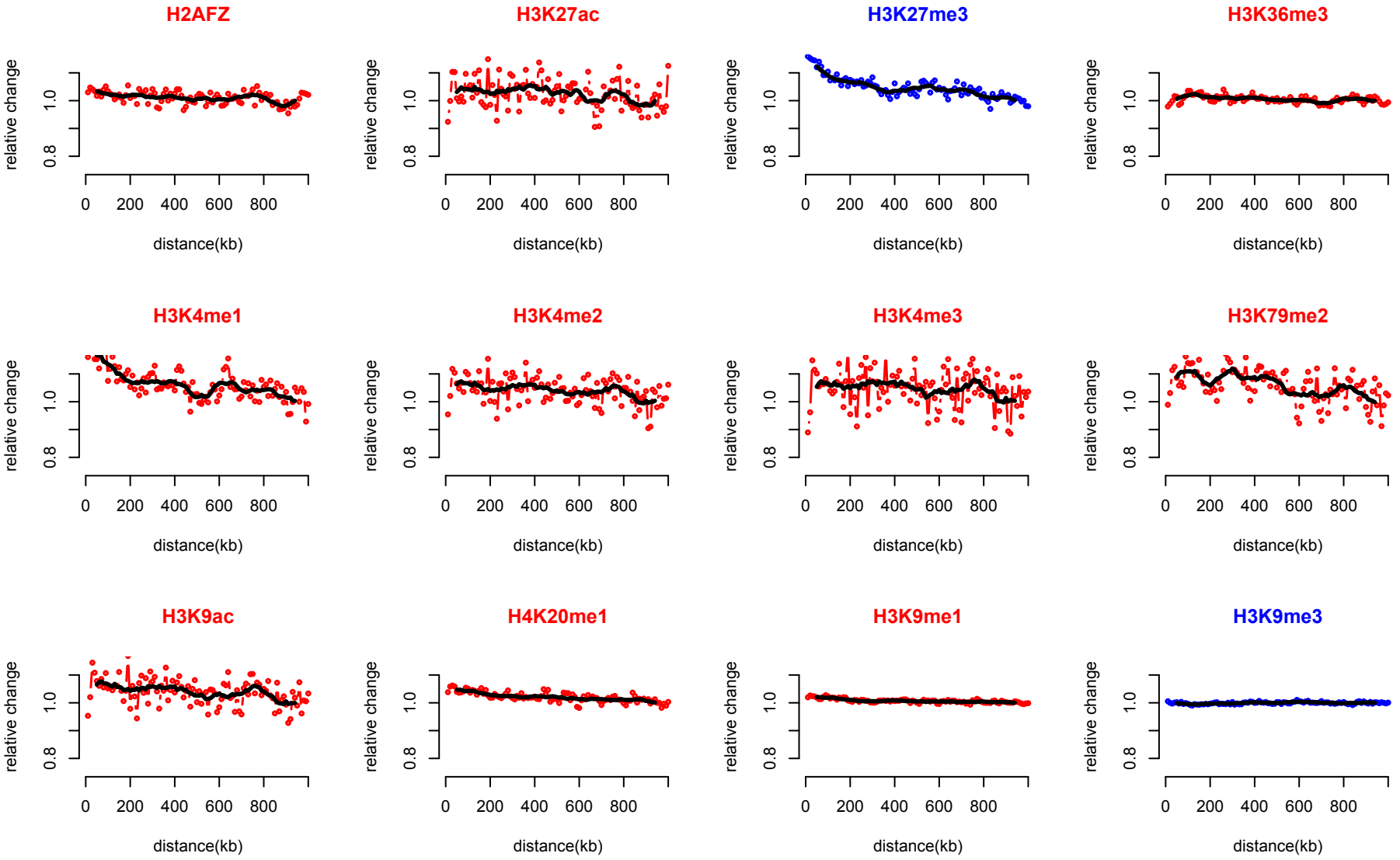

H3K4me1
relative change
0.7
0.9
1.1
1.3
0
200
600
1000
distance(kb)


H3K27me3
relative change
0.7
0.9
1.1
1.3
0
200
600
1000
distance(kb)

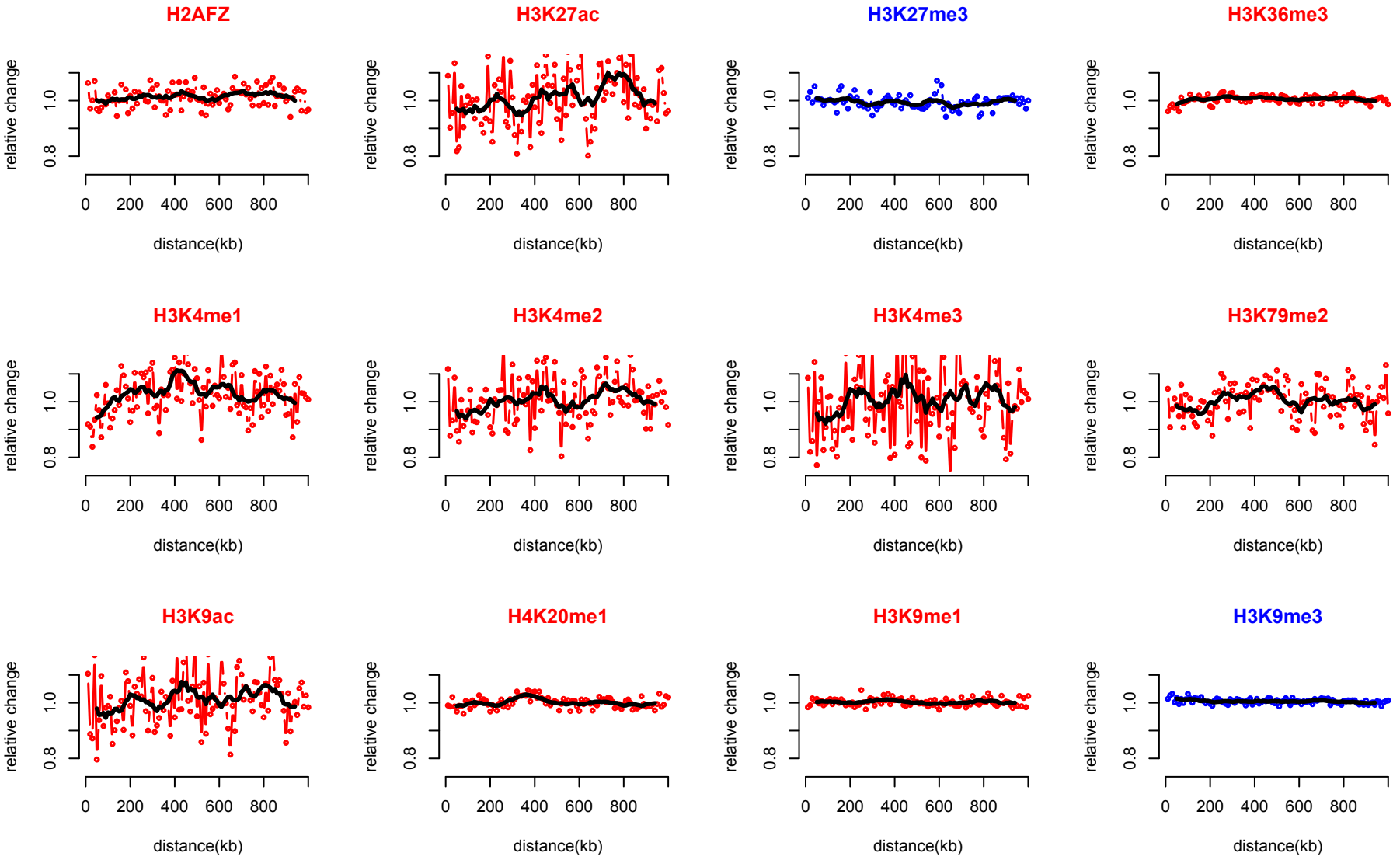
Aggregation thoughts

- Just an association or causality?
  - SVs are impactful events and likely disrupt local epigenetics (impact)
  - Certain HM makes local genome prone to SVs (predisposition)
  - They might go two different directions
- Bkpts paper: predisposition
  - We applied pulled cohort SVs on one cell line from an indiv.
- K562 private SVs: more likely SVs leads to HM change (impact)
  - Certainly confounded by predisposition by we assume the effect of impact is larger and thus dominant
  - We certainly also compare with germline SVs…but no signal
    - Low power due to low SV counts?
    - Somatic SVs have different impact profile?
    - Confounded by strong selection
- K562 private SVs have contradicted results on pulled CML cohort data
  - Because patients do not have these SVs…
  - They are not somatic, or germline

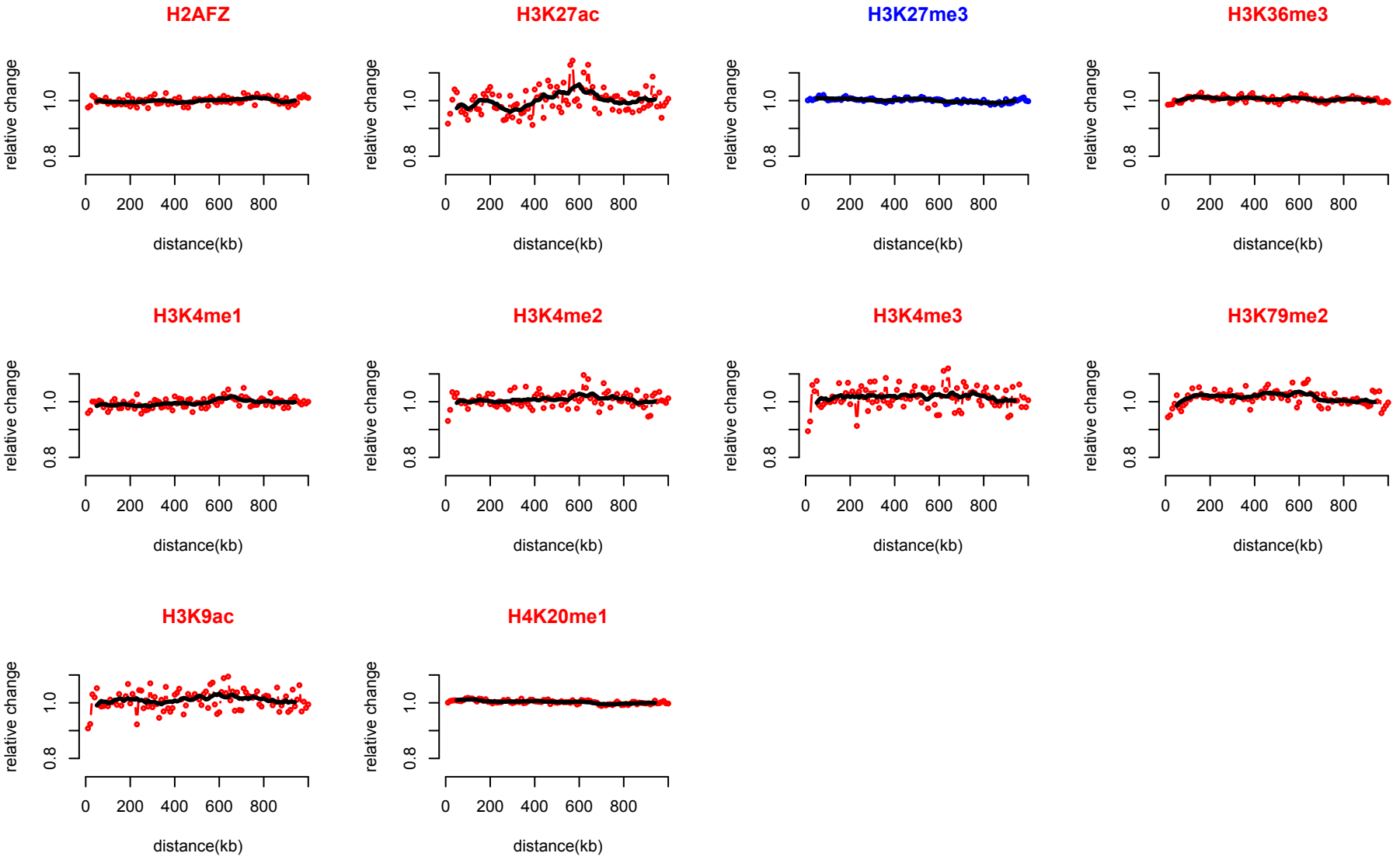
Private K562 SV ~ HM in K562



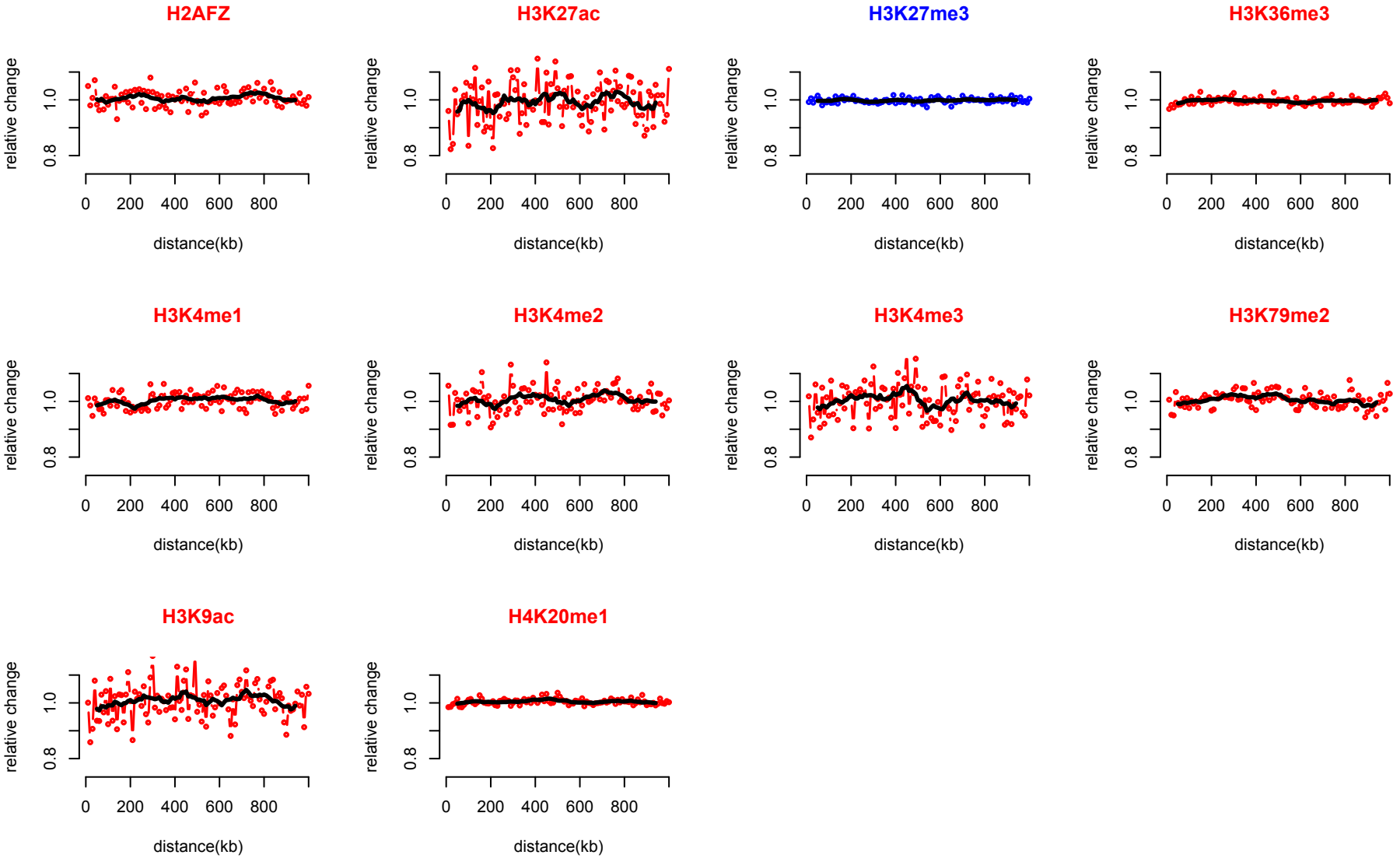
Common 1KG SV ~ HM in K562

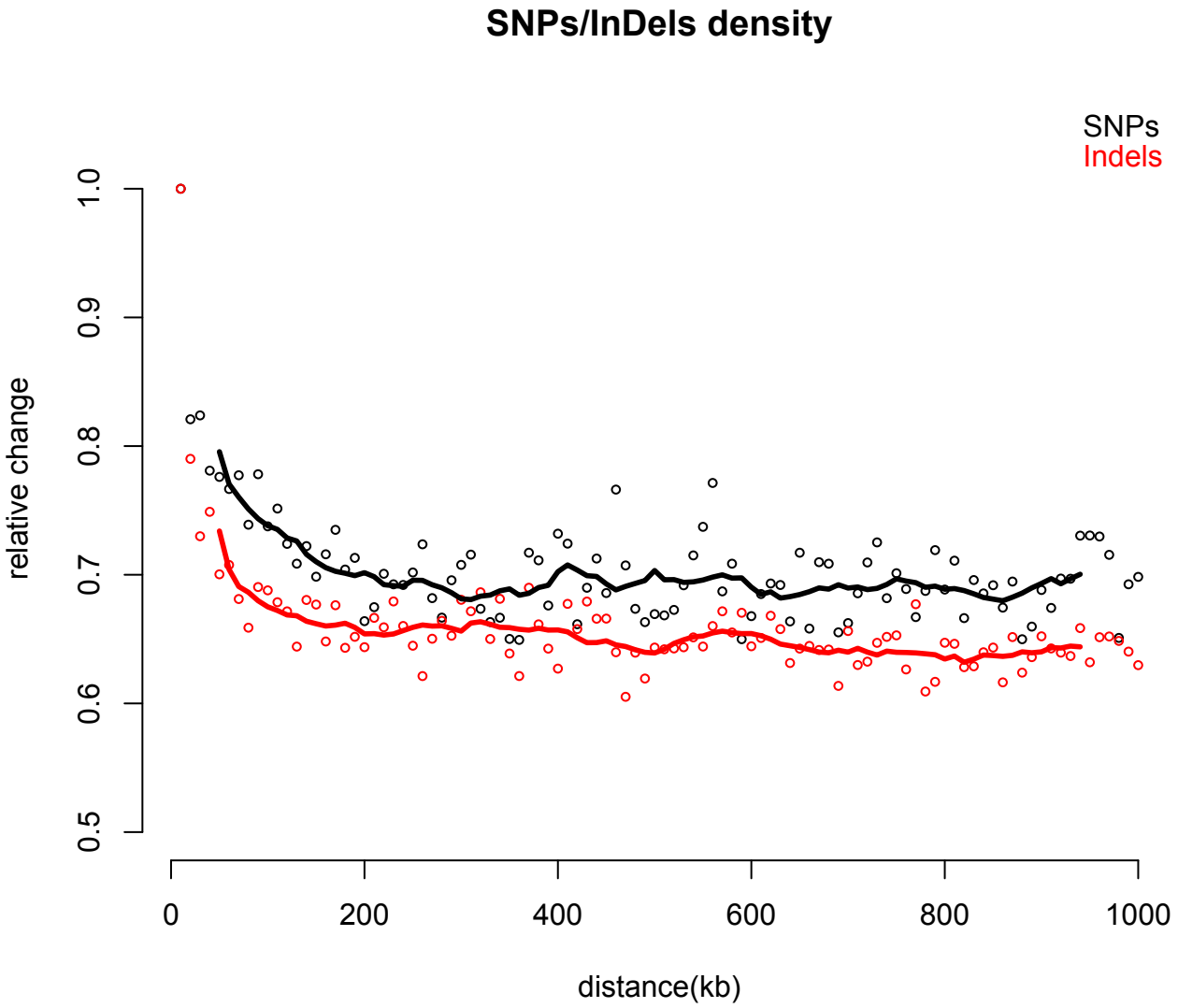


Private K562 SV ~ HM in Gm12878



Common 1KG SV ~ HM in Gm12878



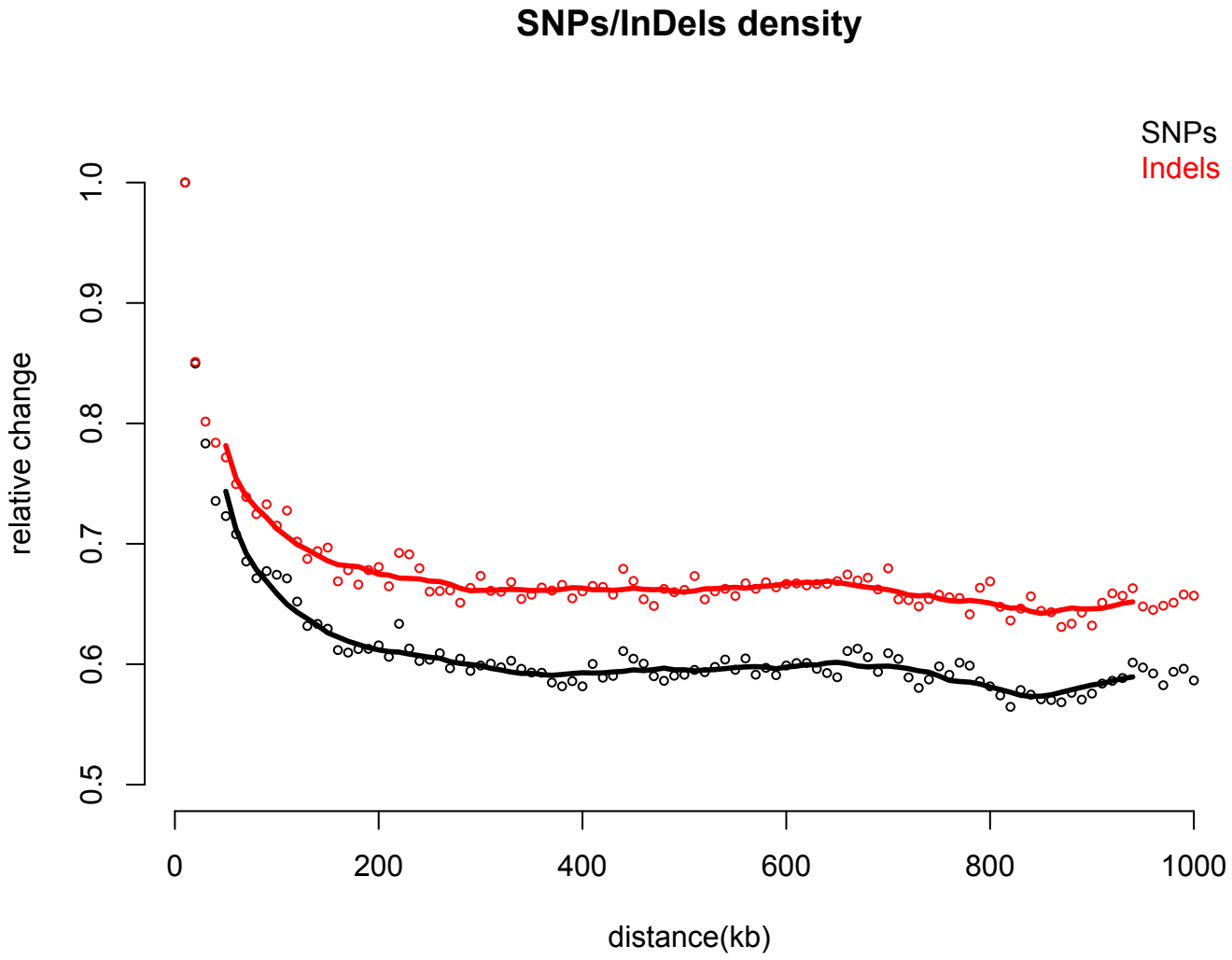


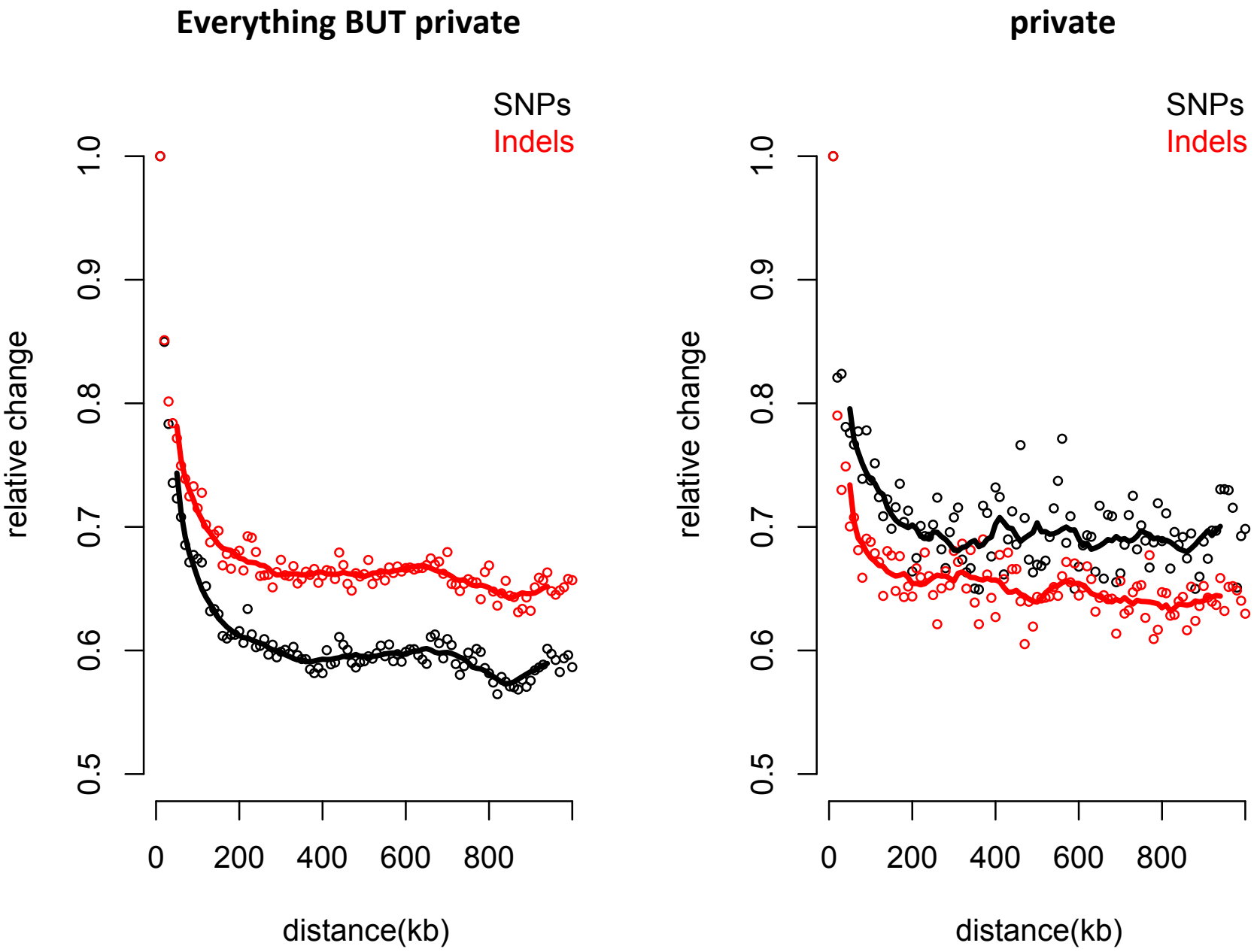
Cannot run common SV bkpts on private SNVs in K562…no overlap within 1MB!

- Now we try the Urban K562 call that overlaps with dbSNP…
- Definitely dominated by germline. Although better to use 1KG for stringent filtering…

- Now something really spooky…
  - K562 private SNV density is ~24/MB when 1MB far away from bkpts…The average mutation rate is about 20/MB (60k+ mutations)
  - Also high density with germline SNVs (~1K/MB)
  - Germline SNV density is only ~0.2/MB (average mutation rate should be 1K/MB?)
  - Almost no K562 private mutation

Using germline SNVs




Everything BUT private
SNPs
Indels
relative change
1.0
0.9
0.8
0.7
0.6
0.5
0
200
400
600
800
distance(kb)
private
SNPs
Indels
relative change
1.0
0.9
0.8
0.7
0.6
0.5
0
200
400
600
800
distance(kb)