Structural Variant Detection Notes

# Reproducing Andrew’s Code: Haploid data

MethodCompare.m is the script Andrew used to run his code (uses 2 SPIRAL scripts, 1 for each noise type)

compare\_methods\_haploid.m is the script I am working with (uses 1 SPIRAL script with 2 noisetype cases)

Data:

* 1 parent, 1 child (haploid)
* novel,

|  |  |
| --- | --- |
| MethodCompare.m |  |
| Andrew’s data:  Chart, line chart  Description automatically generated  iter\_p = 10, iter\_nb = 10 | Reproduced data:  Chart  Description automatically generated  iter\_p = 10, iter\_nb = 10 |
| compare\_methods\_haploid.m |  |
|  |  |
| Andrew’s data:  Chart, line chart  Description automatically generated  iter\_p = 62, iter\_nb = 164 | Reproduced data:  Chart, line chart  Description automatically generated  iter\_p = 5, iter\_nb = 108 |