

Contents

Support for comprehensive amplicon analysis: SNV, RNA-fusion, CNV and SV

```
dragen -r ${1} --fastq-file1=${2} --fastq-file2=${3} \  
--output-directory=${4} --output-file-prefix=${5} \  
--RGSM ${5} --RGID Illumina_RGID \  
--enable-dna-amplicon true \  
--enable-map-align=true --enable-sort=true --enable-map-align-output=true \  
--enable-variant-caller=true --enable-cnv=true --enable-sv=true \  
--vc-use-somatic-hotspots false \  
--amplicon-target-bed=${6}
```

maximum amplicon primer length is set to 50

```
--amplicon-primer-length 50
```

The CNV segmentation bed can be modified using **cnv-segmentation-bed**