

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:09:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013191.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6013191 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013191.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:09:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013191.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,558,899
Mapped reads	1,215,205 / 77.95%
Unmapped reads	343,694 / 22.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,534 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	81,524 / 5.23%
Duplication rate	5.8%
Clipped reads	727,147 / 46.64%

2.2. ACGT Content

Number/percentage of A's	20,285,781 / 26.62%
Number/percentage of C's	13,267,461 / 17.41%
Number/percentage of T's	25,142,710 / 32.99%
Number/percentage of G's	17,512,462 / 22.98%
Number/percentage of N's	927 / 0%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.2335
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2.4. Mapping Quality

Mean Mapping Quality	45.68
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2.5. Mismatches and indels

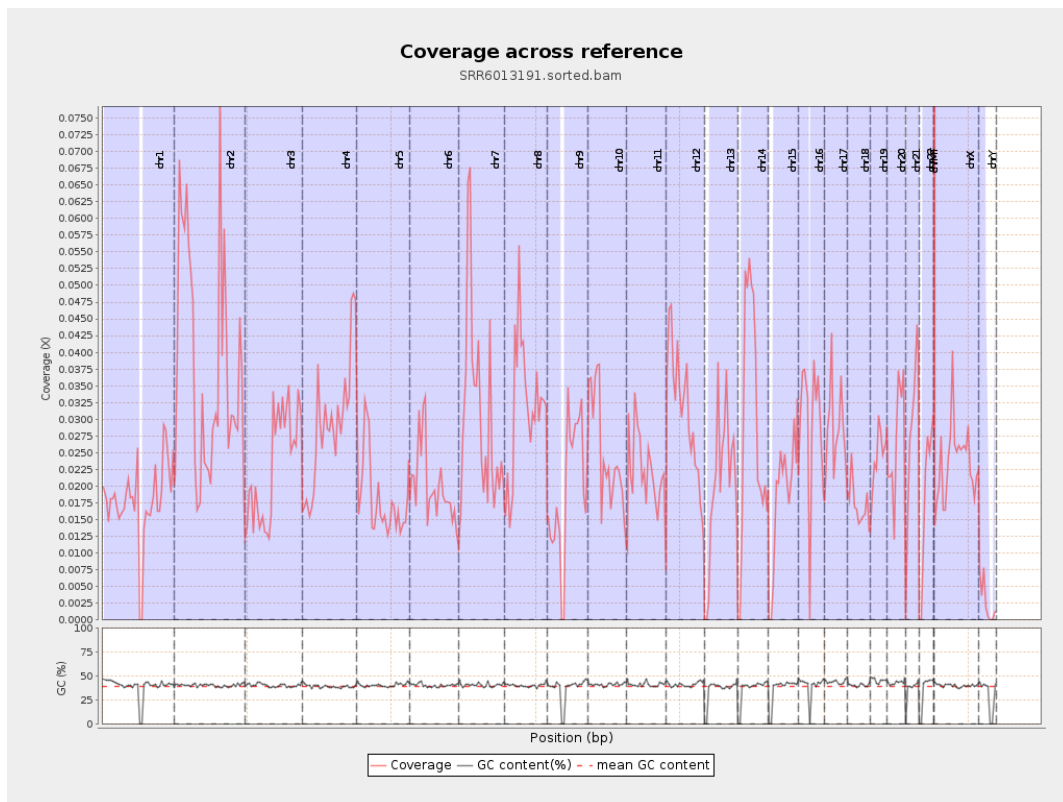
General error rate	0.83%
Mismatches	623,148
Insertions	5,264
Mapped reads with at least one insertion	0.43%
Deletions	22,389
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.03%

2.6. Chromosome stats

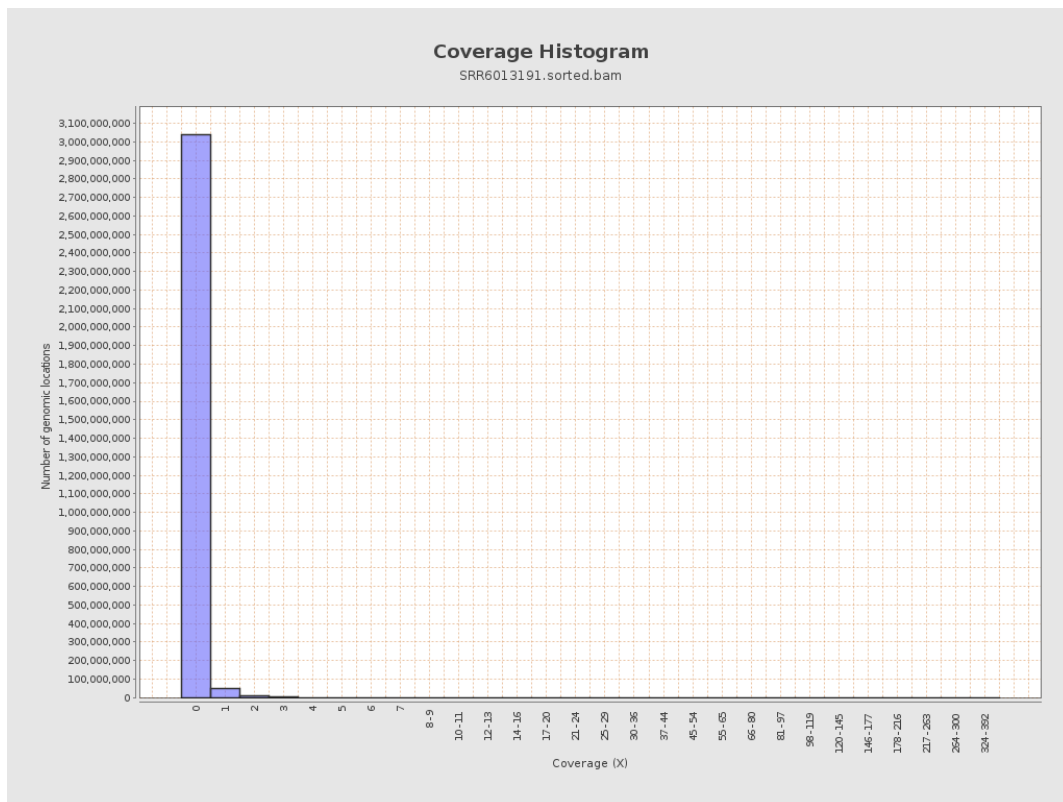
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4438912	0.0178	0.3029
chr2	243199373	9253680	0.038	0.3099
chr3	198022430	4584388	0.0232	0.1893
chr4	191154276	5581327	0.0292	0.2153
chr5	180915260	3255590	0.018	0.1671
chr6	171115067	3413264	0.0199	0.1975
chr7	159138663	4843951	0.0304	0.2838

chr8	146364022	4679984	0.032	0.2847
chr9	141213431	2728640	0.0193	0.2053
chr10	135534747	3378953	0.0249	0.238
chr11	135006516	3024553	0.0224	0.2057
chr12	133851895	4176673	0.0312	0.2208
chr13	115169878	2347199	0.0204	0.1789
chr14	107349540	3138625	0.0292	0.2154
chr15	102531392	1899803	0.0185	0.1709
chr16	90354753	2615236	0.0289	0.2139
chr17	81195210	2304286	0.0284	0.2216
chr18	78077248	1333929	0.0171	0.3096
chr19	59128983	1450288	0.0245	0.2568
chr20	63025520	1655866	0.0263	0.2056
chr21	48129895	1356475	0.0282	0.2136
chr22	51304566	952282	0.0186	0.1666
chrMT	16571	25644	1.5475	2.0963
chrX	155270560	3655118	0.0235	0.2023
chrY	59373566	153266	0.0026	0.0736

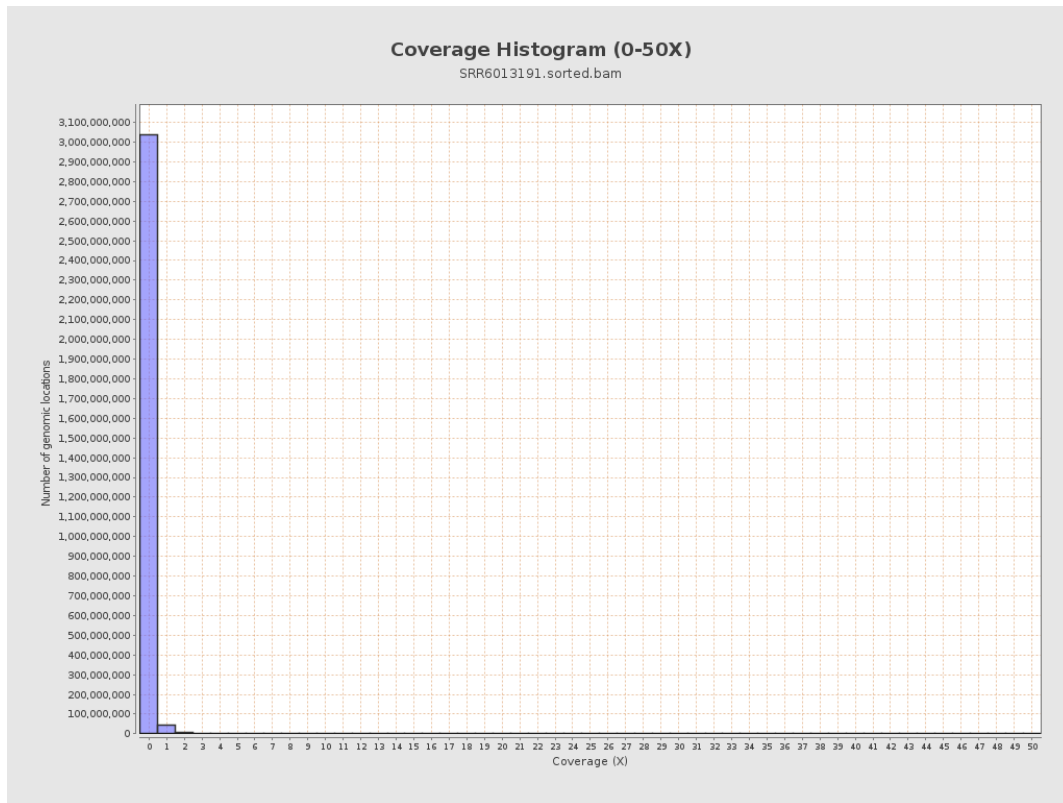
3. Results : Coverage across reference



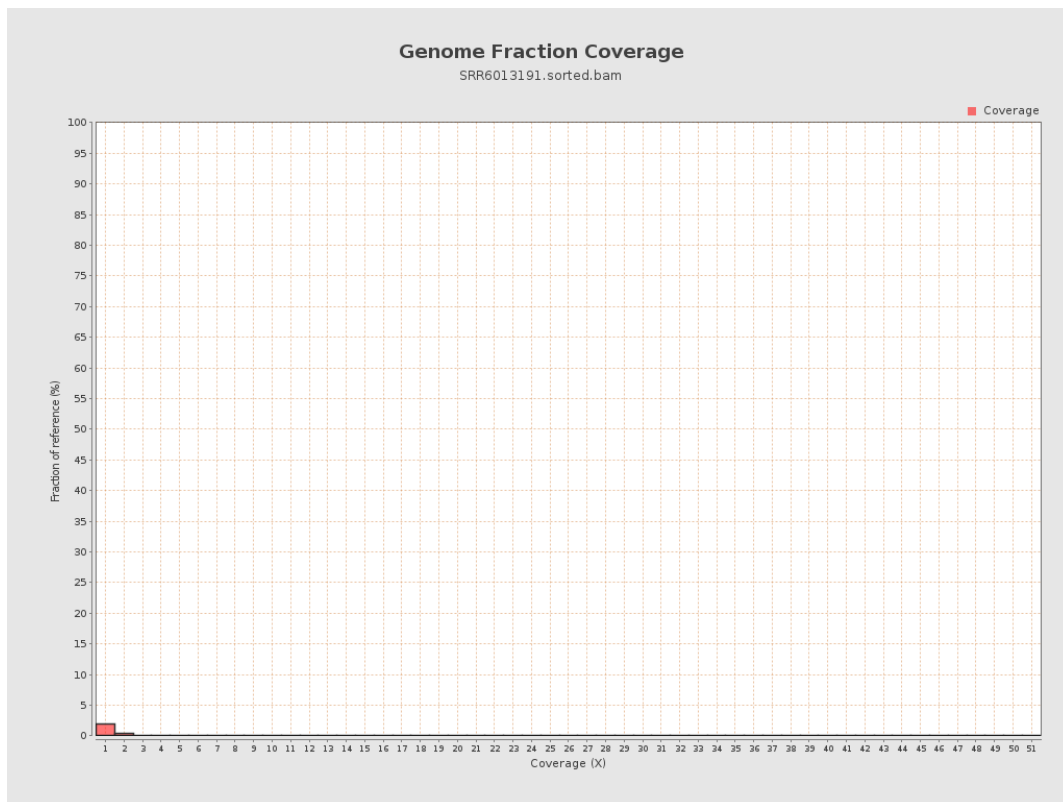
4. Results : Coverage Histogram



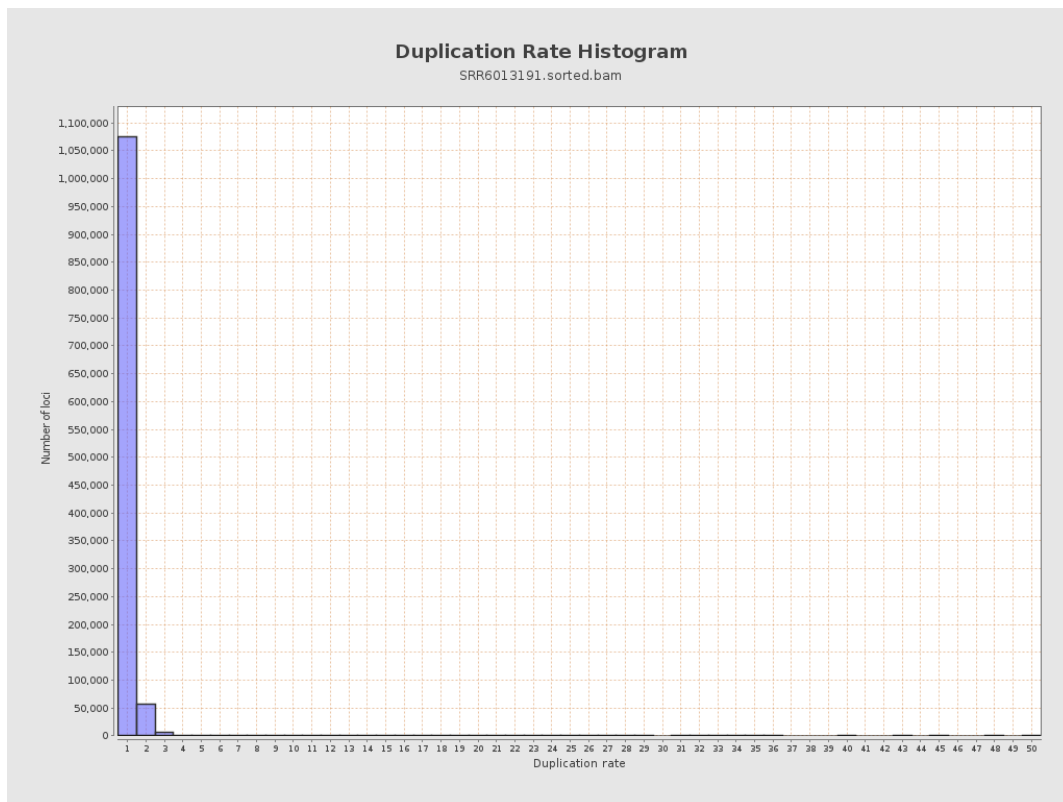
5. Results : Coverage Histogram (0-50X)



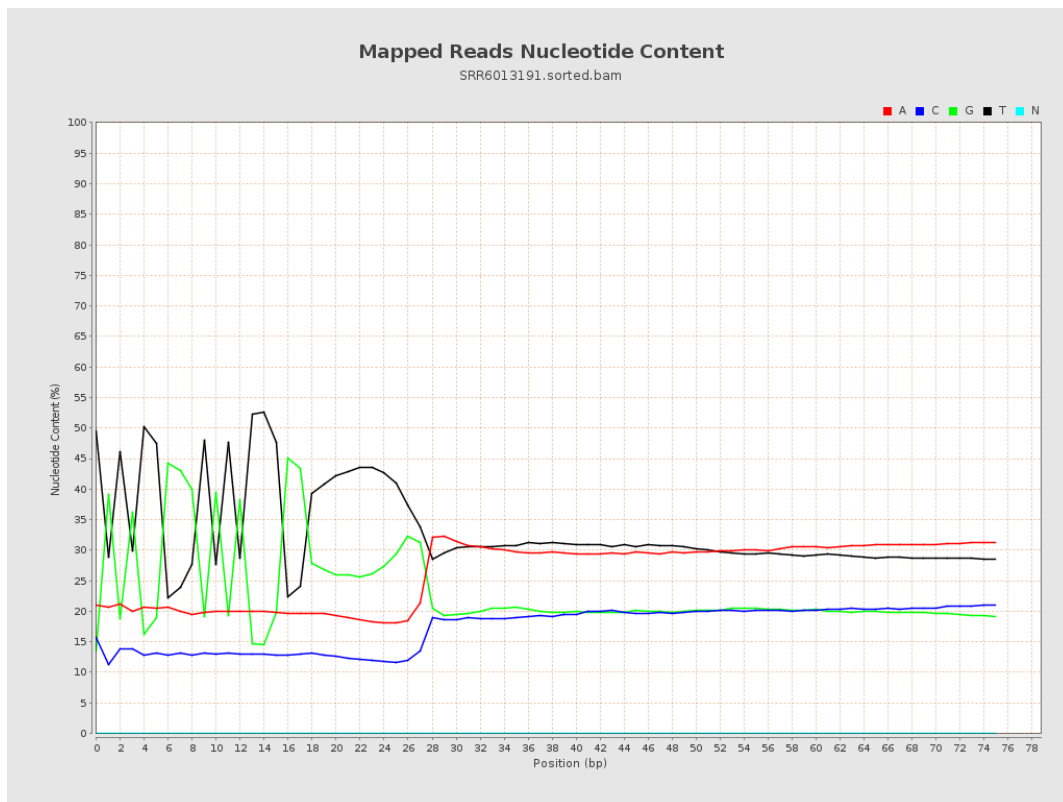
6. Results : Genome Fraction Coverage



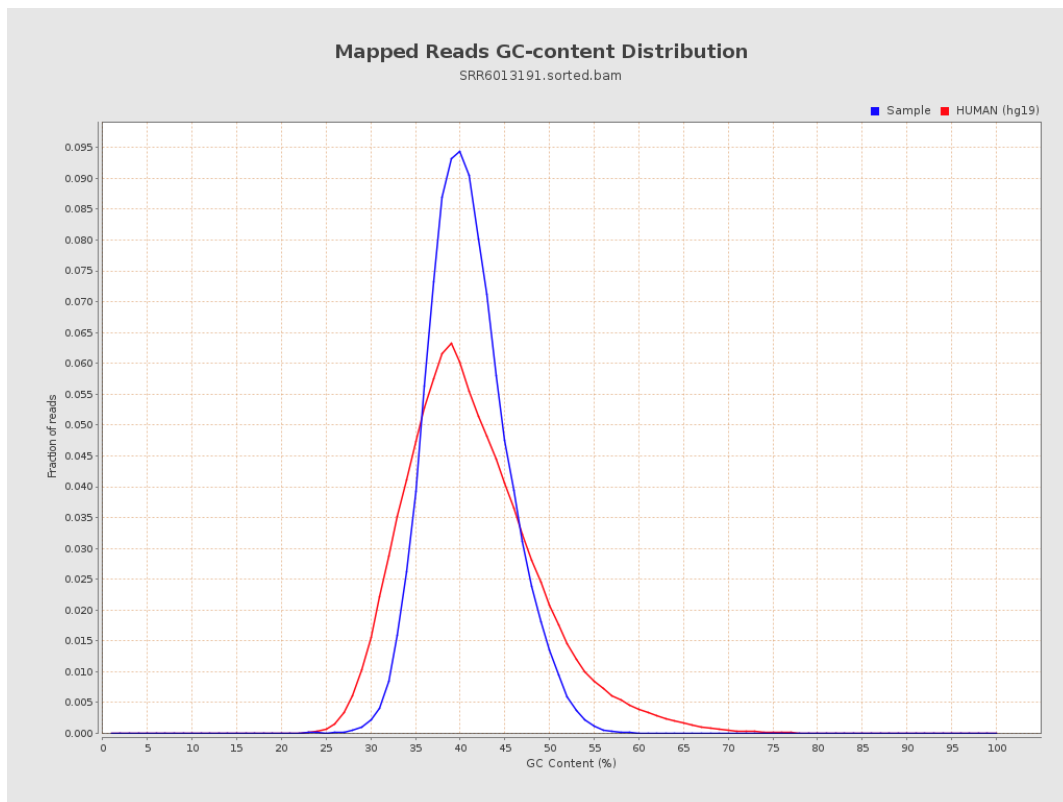
7. Results : Duplication Rate Histogram



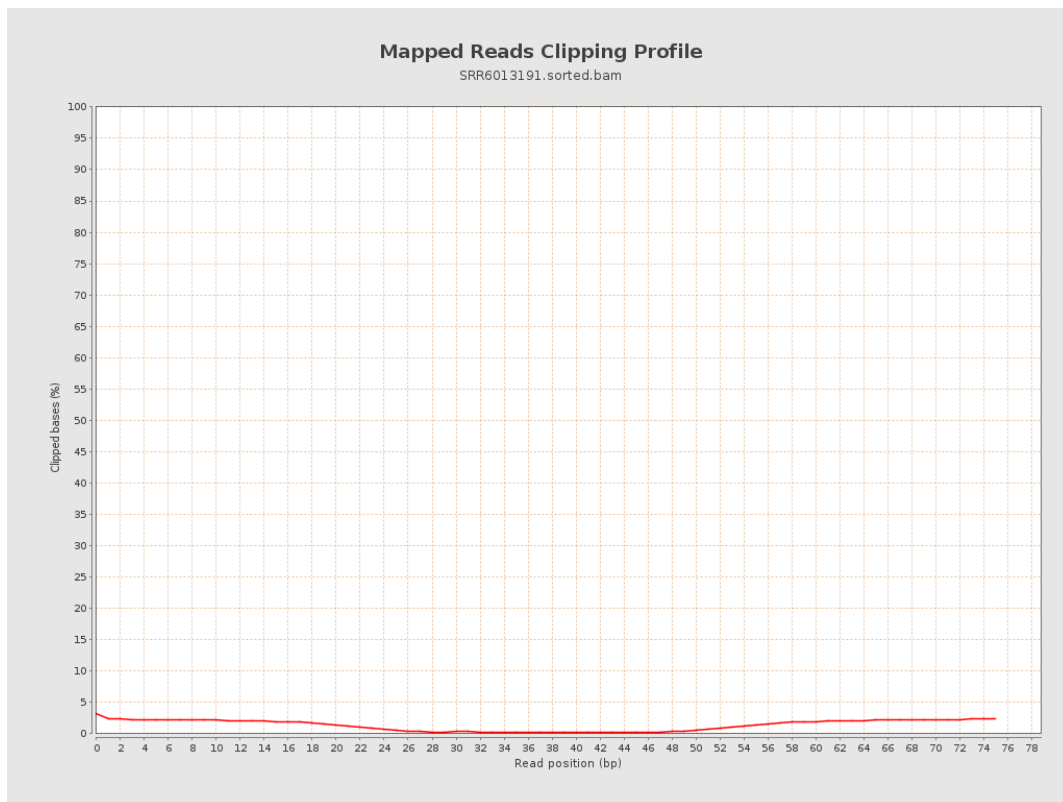
8. Results : Mapped Reads Nucleotide Content



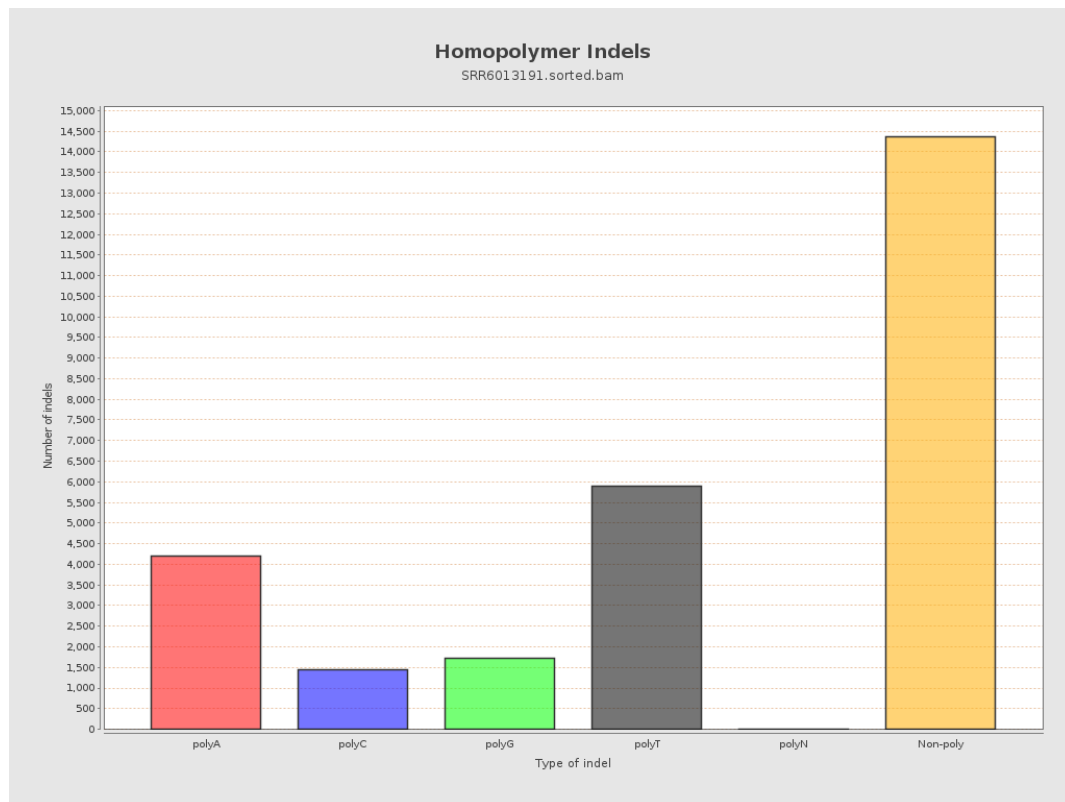
9. Results : Mapped Reads GC-content Distribution



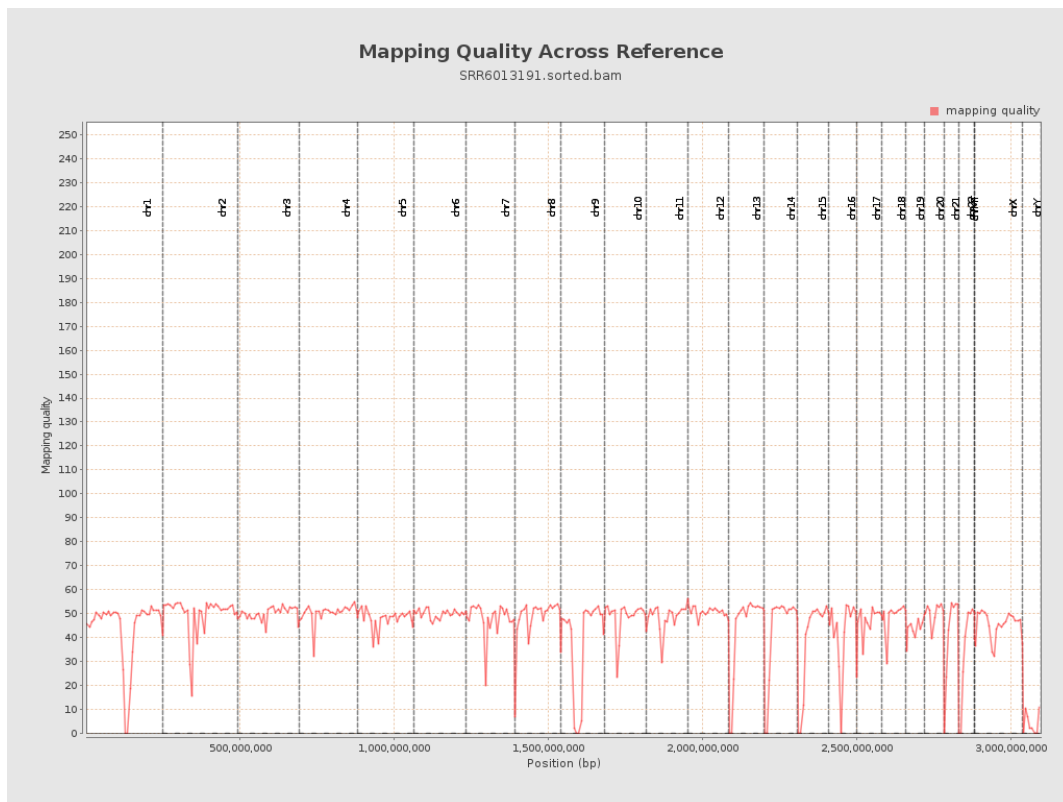
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

