

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:33:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013303.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_SRR6013303 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013303.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:33:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013303.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,535,079
Mapped reads	1,023,293 / 66.66%
Unmapped reads	511,786 / 33.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,424 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	80,660 / 5.25%
Duplication rate	6.67%
Clipped reads	841,666 / 54.83%

2.2. ACGT Content

Number/percentage of A's	16,804,226 / 29.49%
Number/percentage of C's	11,013,738 / 19.33%
Number/percentage of T's	16,928,812 / 29.71%
Number/percentage of G's	12,234,528 / 21.47%
Number/percentage of N's	686 / 0%
GC Percentage	40.8%

2.3. Coverage

Mean	0.0184

Standard Deviation	0.2061
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2.4. Mapping Quality

Mean Mapping Quality	43.23
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2.5. Mismatches and indels

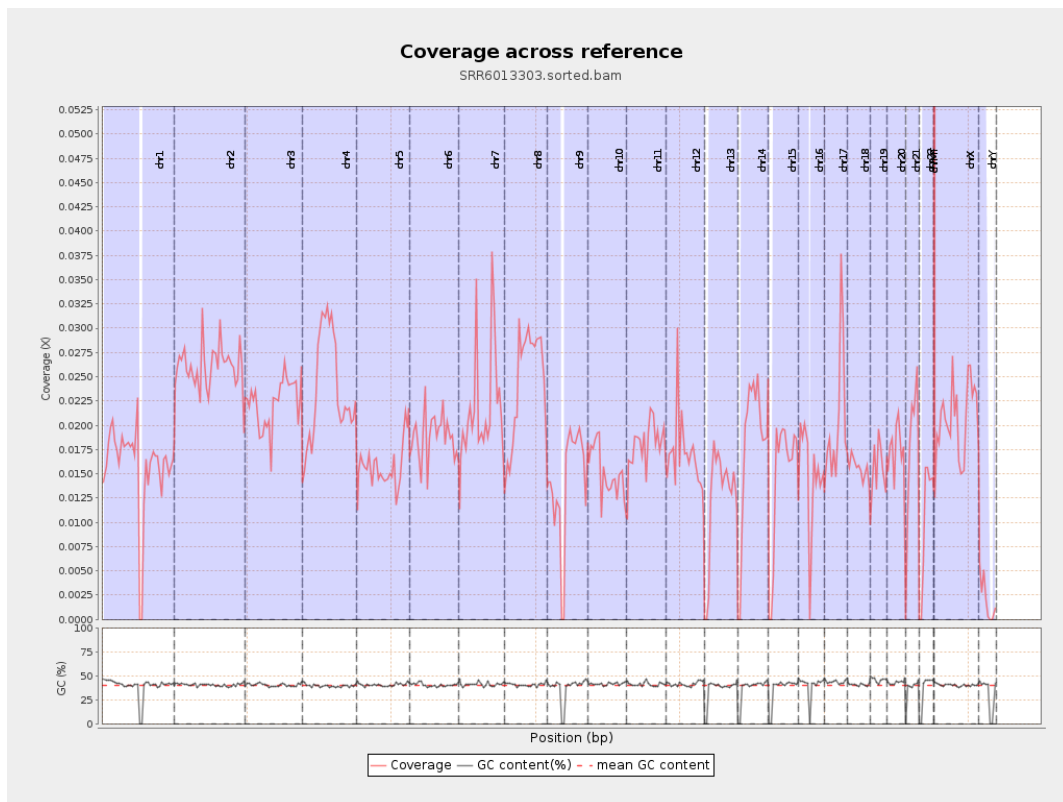
General error rate	0.81%
Mismatches	457,451
Insertions	3,658
Mapped reads with at least one insertion	0.36%
Deletions	13,761
Mapped reads with at least one deletion	1.33%
Homopolymer indels	46.72%

2.6. Chromosome stats

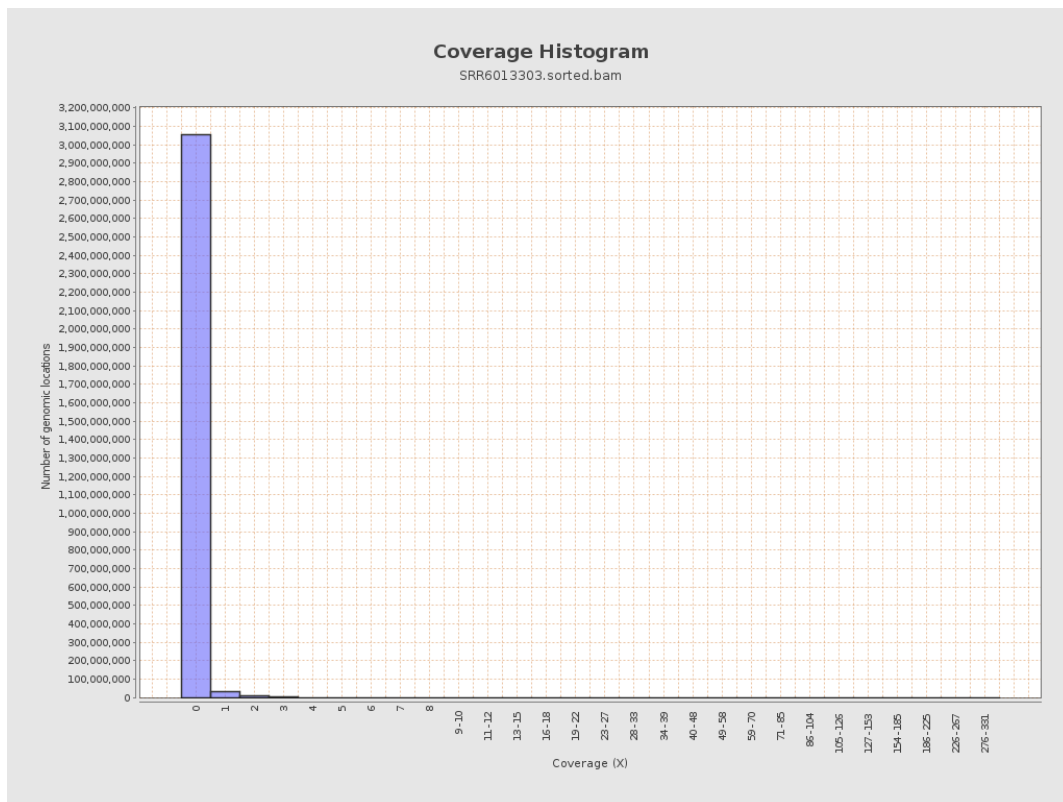
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3948464	0.0158	0.2421
chr2	243199373	6341311	0.0261	0.2565
chr3	198022430	4425442	0.0223	0.1941
chr4	191154276	4524701	0.0237	0.2051
chr5	180915260	2861776	0.0158	0.1603
chr6	171115067	3210601	0.0188	0.1872
chr7	159138663	3457871	0.0217	0.3215

chr8	146364022	3586383	0.0245	0.2759
chr9	141213431	1980821	0.014	0.1726
chr10	135534747	2041281	0.0151	0.1721
chr11	135006516	2442114	0.0181	0.186
chr12	133851895	2276842	0.017	0.1659
chr13	115169878	1433895	0.0125	0.144
chr14	107349540	1933294	0.018	0.1754
chr15	102531392	1501024	0.0146	0.1599
chr16	90354753	1317834	0.0146	0.154
chr17	81195210	1660422	0.0204	0.1864
chr18	78077248	1214196	0.0156	0.2261
chr19	59128983	925366	0.0156	0.1998
chr20	63025520	1091714	0.0173	0.1702
chr21	48129895	853956	0.0177	0.1711
chr22	51304566	539346	0.0105	0.1291
chrMT	16571	90942	5.488	5.1297
chrX	155270560	3224555	0.0208	0.1918
chrY	59373566	120207	0.002	0.0555

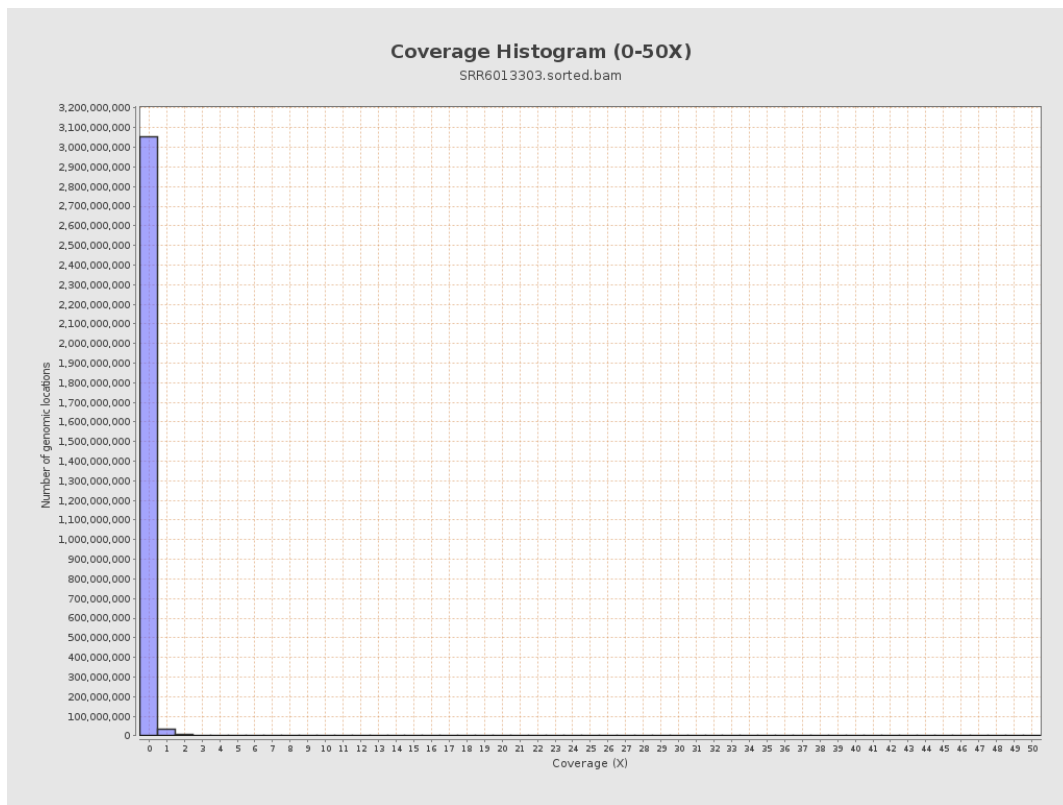
3. Results : Coverage across reference



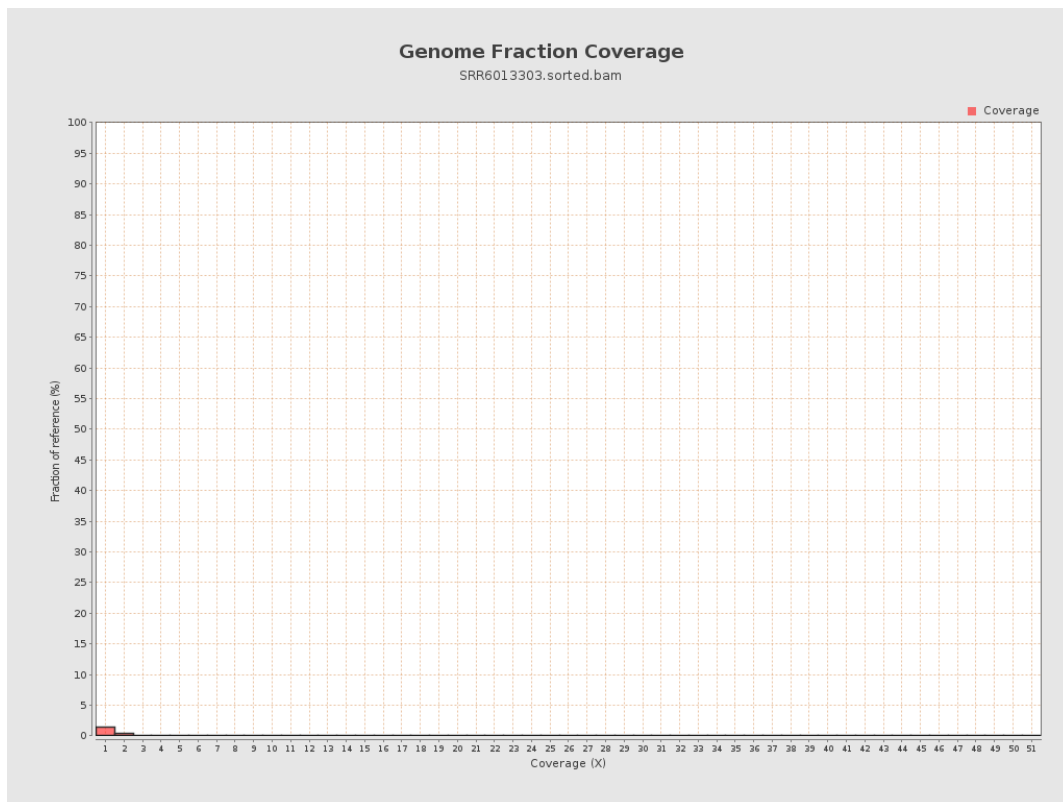
4. Results : Coverage Histogram



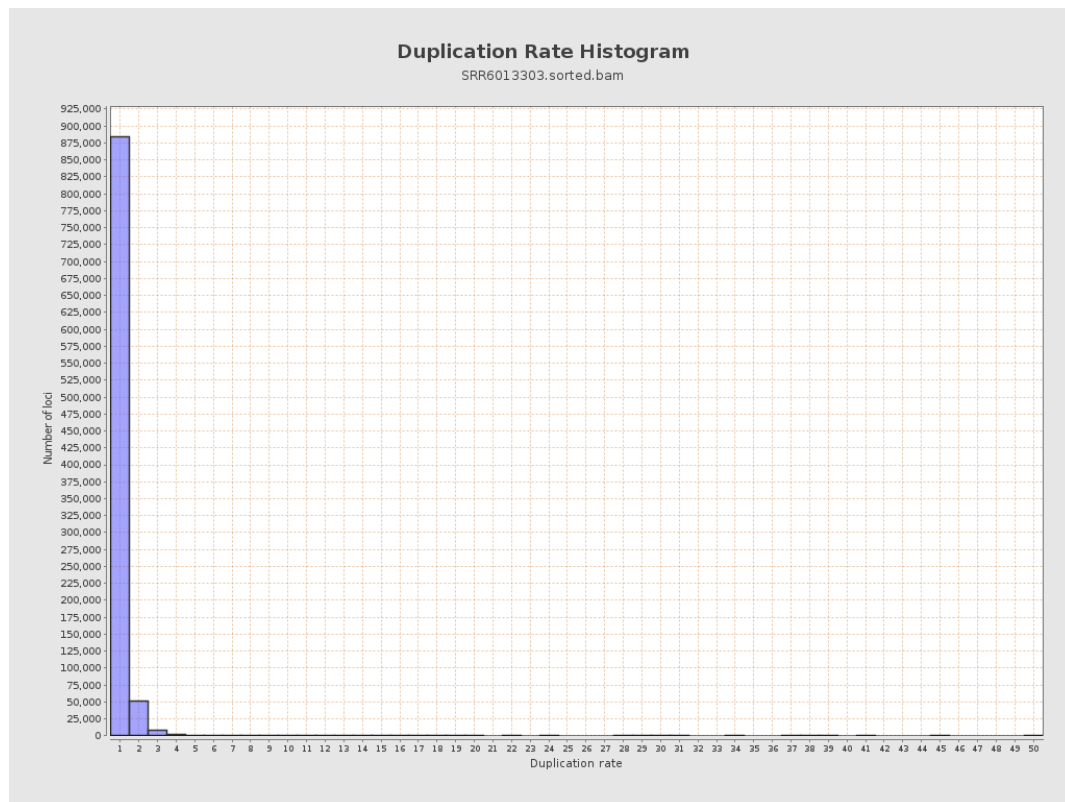
5. Results : Coverage Histogram (0-50X)



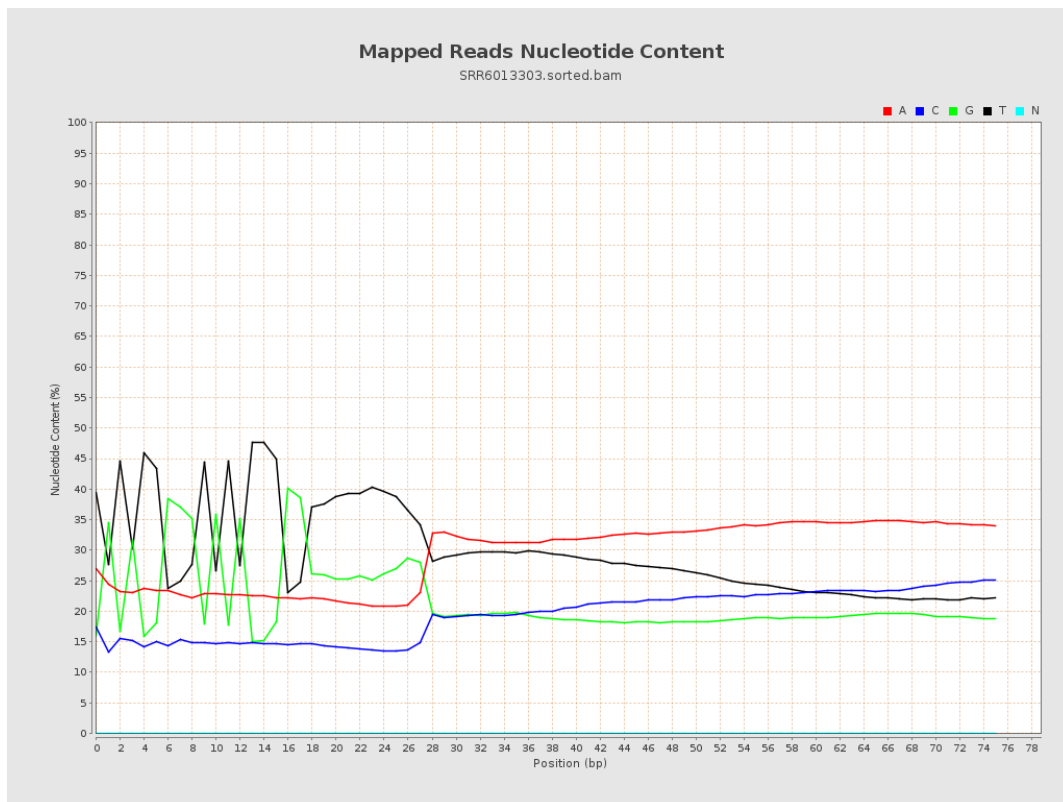
6. Results : Genome Fraction Coverage



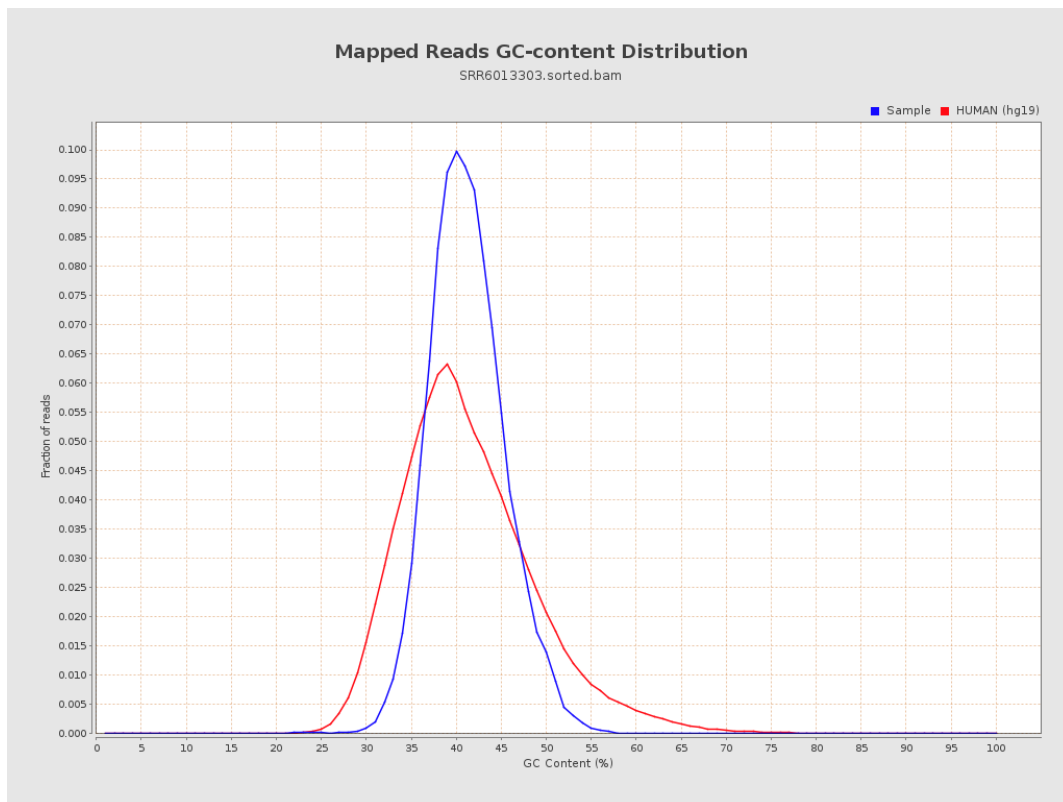
7. Results : Duplication Rate Histogram



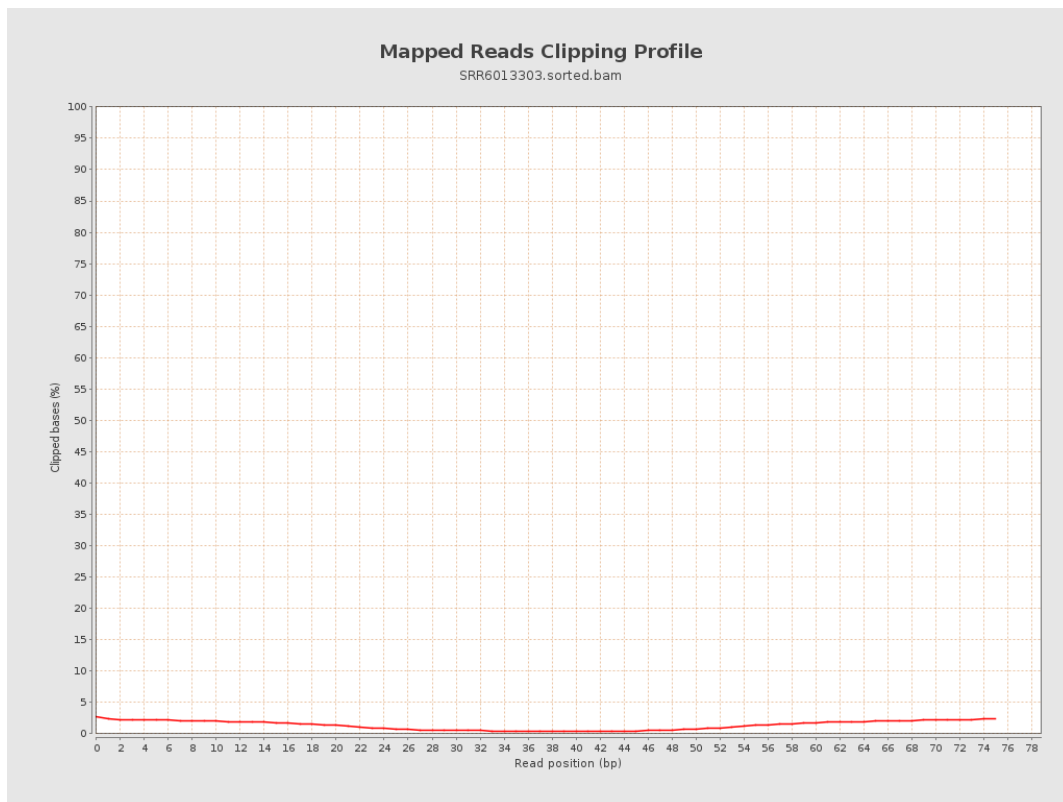
8. Results : Mapped Reads Nucleotide Content



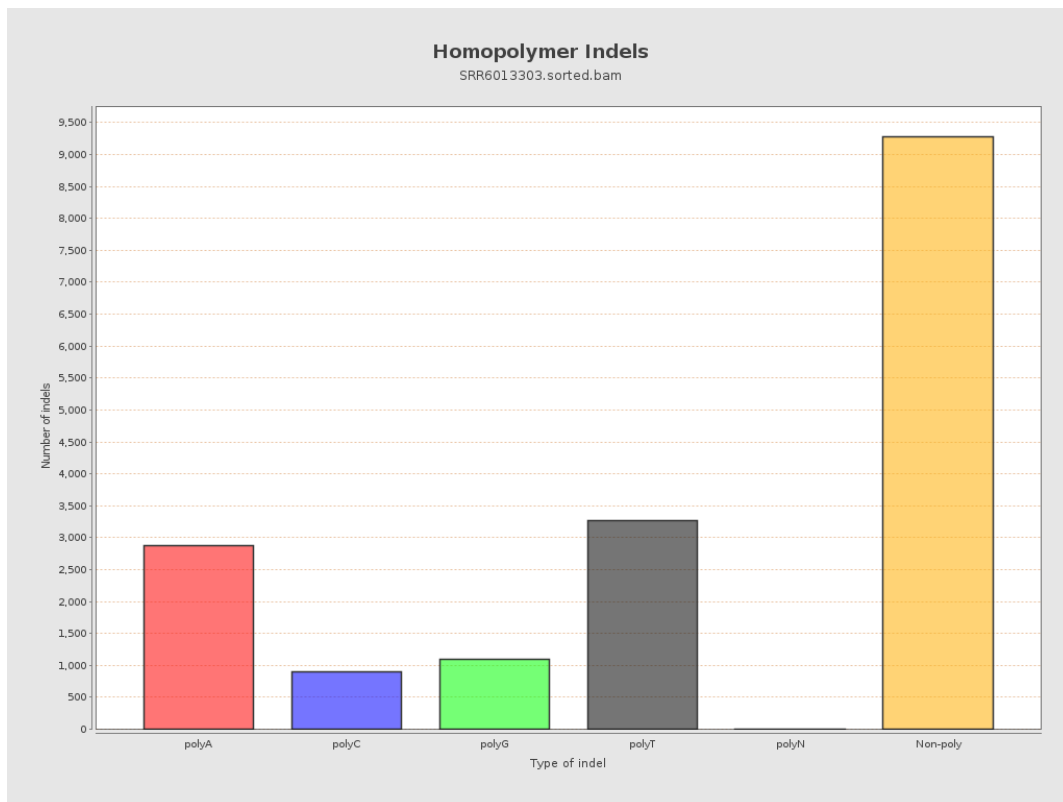
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

