

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:11:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008827.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_SRR6008827 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008827.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:11:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008827.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,750,441
Mapped reads	939,733 / 34.17%
Unmapped reads	1,810,708 / 65.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,331 / 0.19%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	56,640 / 2.06%
Duplication rate	3.79%
Clipped reads	452,402 / 16.45%

2.2. ACGT Content

Number/percentage of A's	16,440,493 / 26.83%
Number/percentage of C's	11,894,028 / 19.41%
Number/percentage of T's	18,746,308 / 30.59%
Number/percentage of G's	14,116,261 / 23.03%
Number/percentage of N's	85,915 / 0.14%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0198

Standard Deviation	0.4064
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2.4. Mapping Quality

Mean Mapping Quality	44.74
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2.5. Mismatches and indels

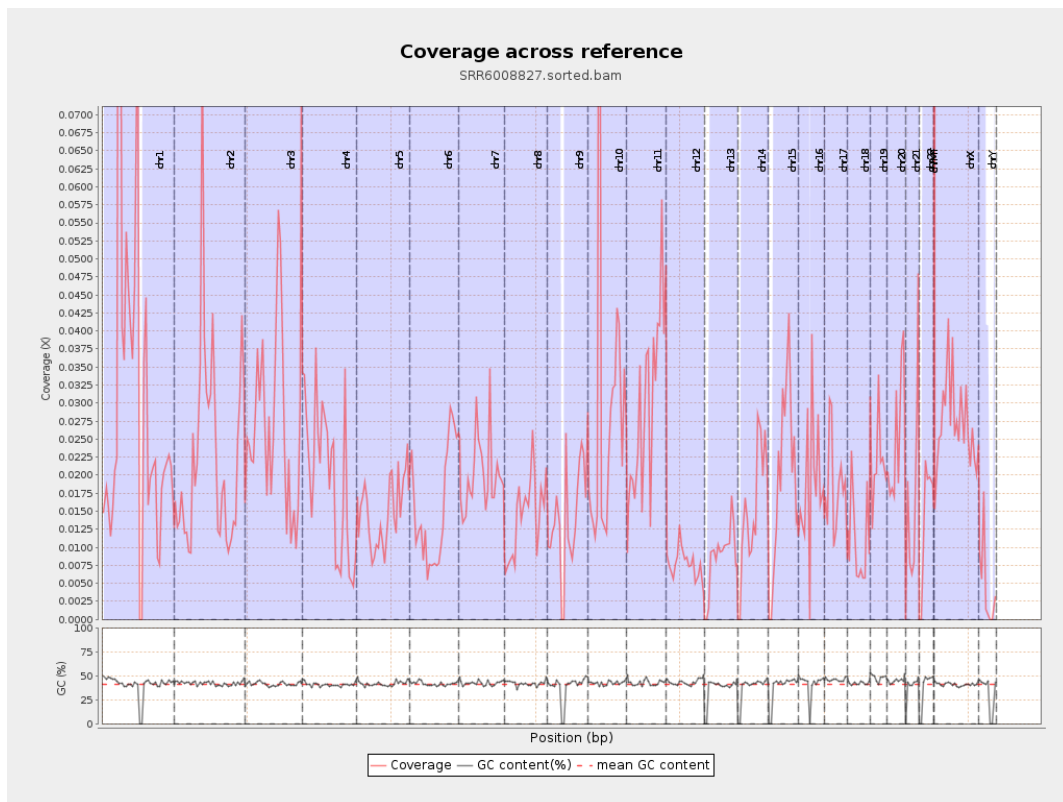
General error rate	0.95%
Mismatches	569,850
Insertions	4,950
Mapped reads with at least one insertion	0.52%
Deletions	17,406
Mapped reads with at least one deletion	1.83%
Homopolymer indels	43.38%

2.6. Chromosome stats

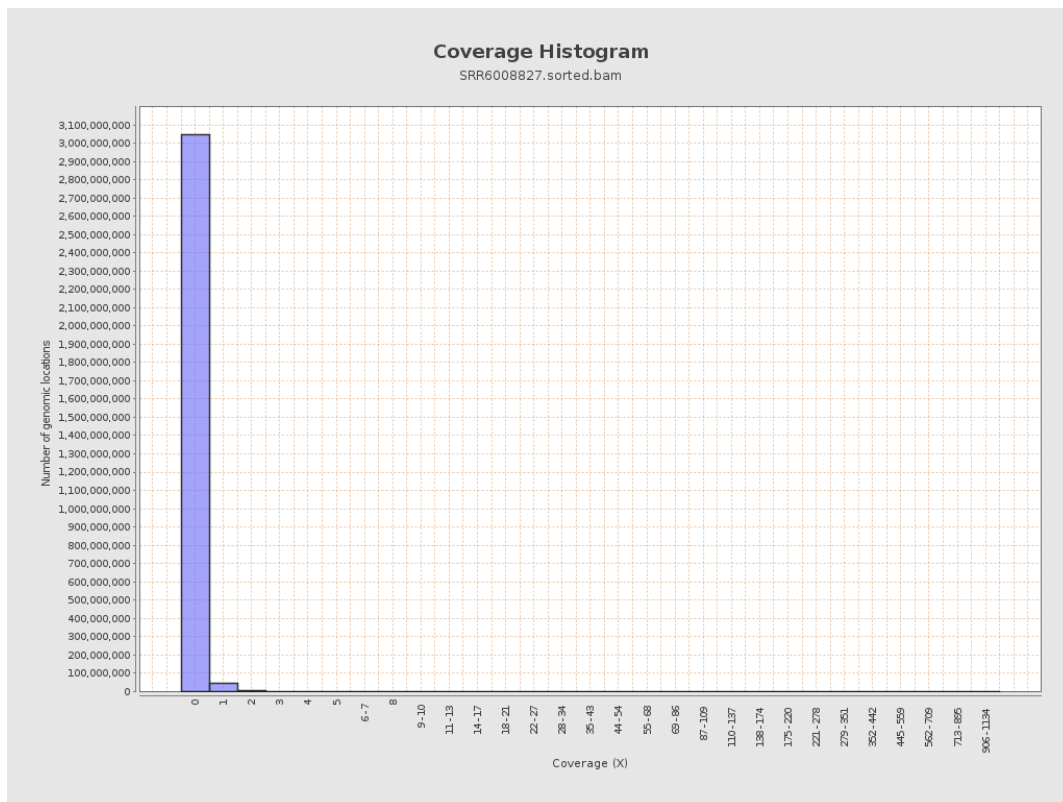
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7430655	0.0298	0.9023
chr2	243199373	5547195	0.0228	0.3452
chr3	198022430	5329363	0.0269	0.281
chr4	191154276	3756225	0.0197	0.1978
chr5	180915260	2693246	0.0149	0.1442
chr6	171115067	2659427	0.0155	0.1524
chr7	159138663	3210691	0.0202	0.2205

chr8	146364022	2131121	0.0146	0.2973
chr9	141213431	1963087	0.0139	0.2107
chr10	135534747	4009972	0.0296	1.0577
chr11	135006516	4001703	0.0296	0.2273
chr12	133851895	1032407	0.0077	0.1295
chr13	115169878	1000948	0.0087	0.1089
chr14	107349540	1610329	0.015	0.1797
chr15	102531392	2029875	0.0198	0.1688
chr16	90354753	1678802	0.0186	0.3146
chr17	81195210	1499690	0.0185	0.21
chr18	78077248	813470	0.0104	0.3494
chr19	59128983	1297519	0.0219	0.4965
chr20	63025520	1608913	0.0255	0.1933
chr21	48129895	797219	0.0166	0.2614
chr22	51304566	728443	0.0142	0.1384
chrMT	16571	19301	1.1647	1.3933
chrX	155270560	4196394	0.027	0.2203
chrY	59373566	268666	0.0045	0.18

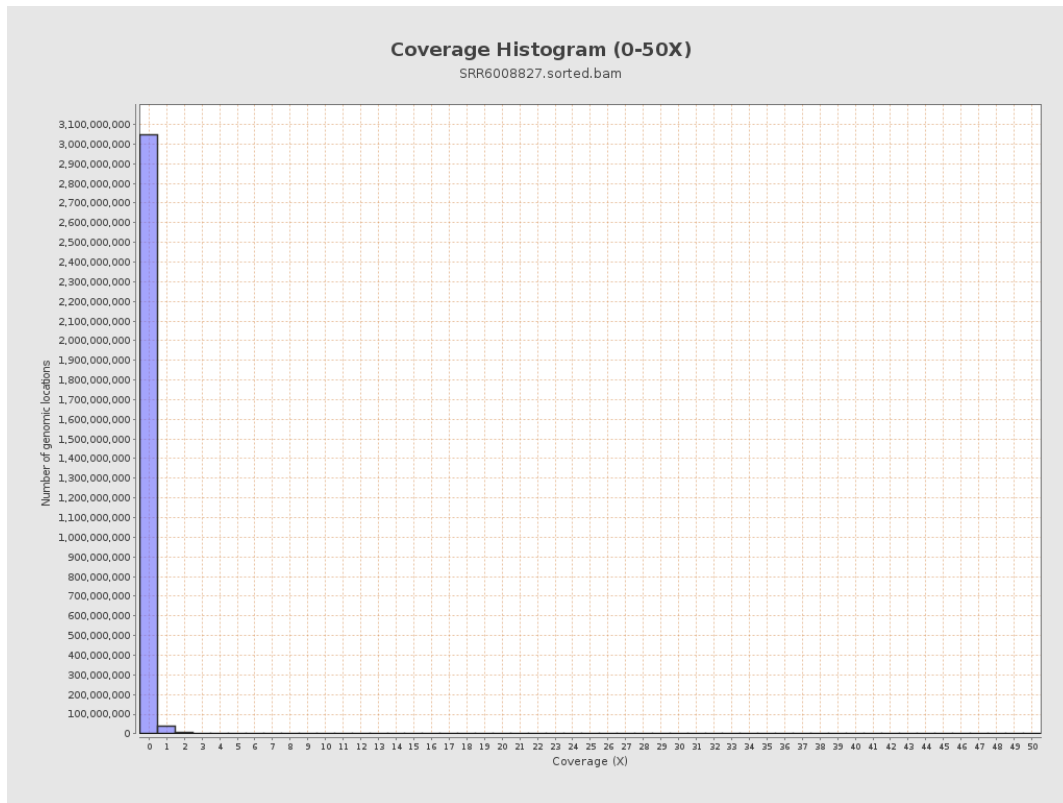
3. Results : Coverage across reference



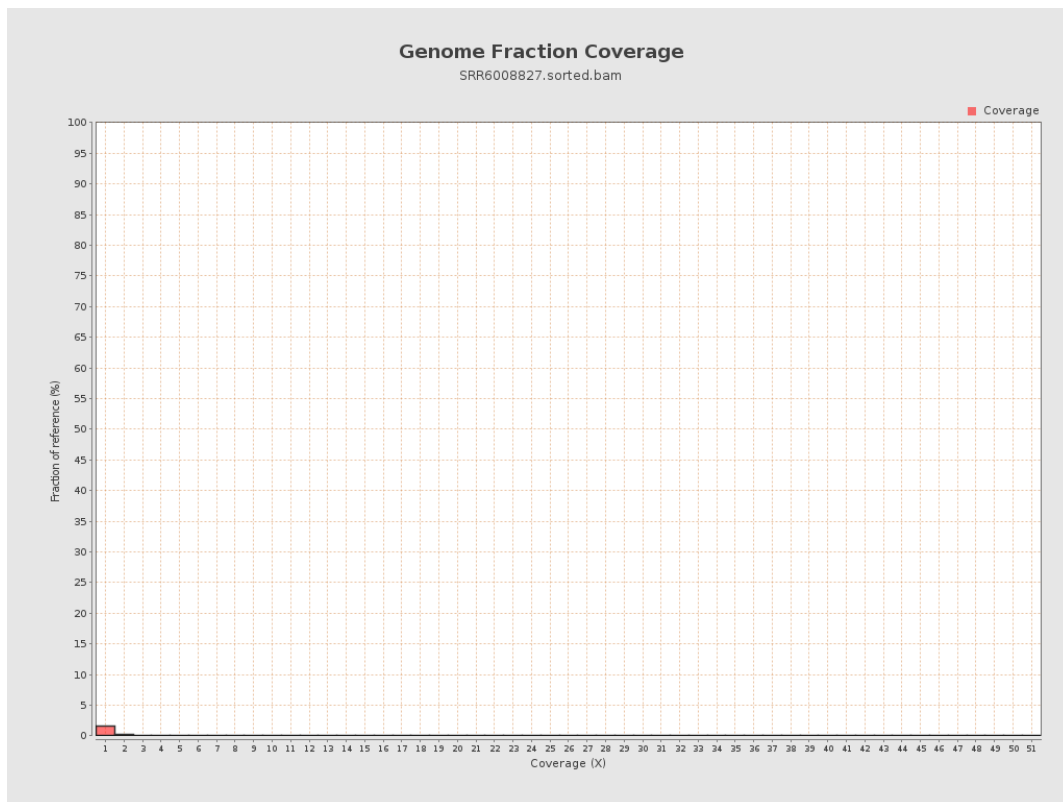
4. Results : Coverage Histogram



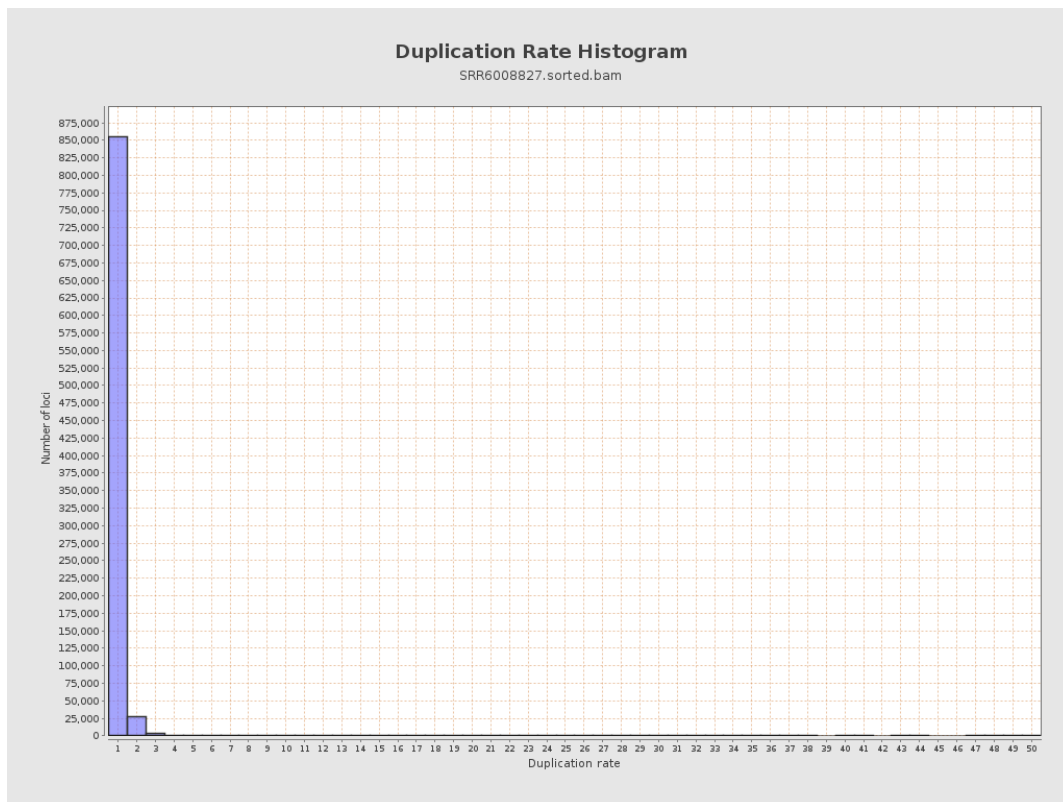
5. Results : Coverage Histogram (0-50X)



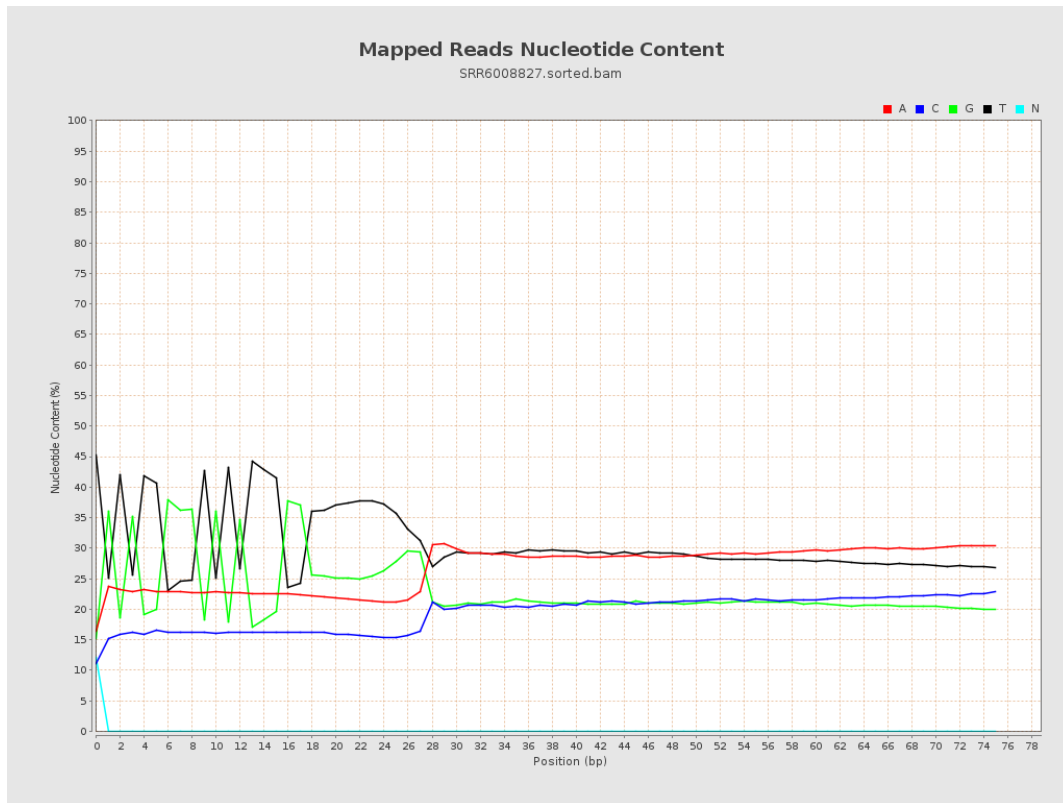
6. Results : Genome Fraction Coverage



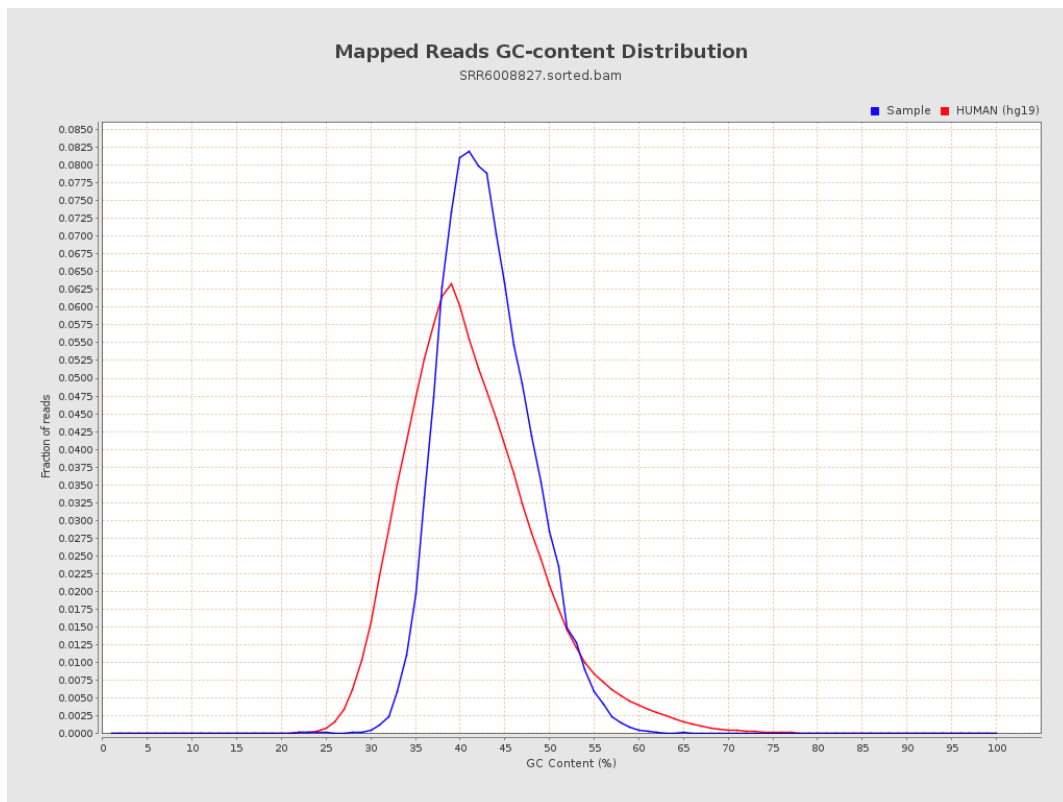
7. Results : Duplication Rate Histogram



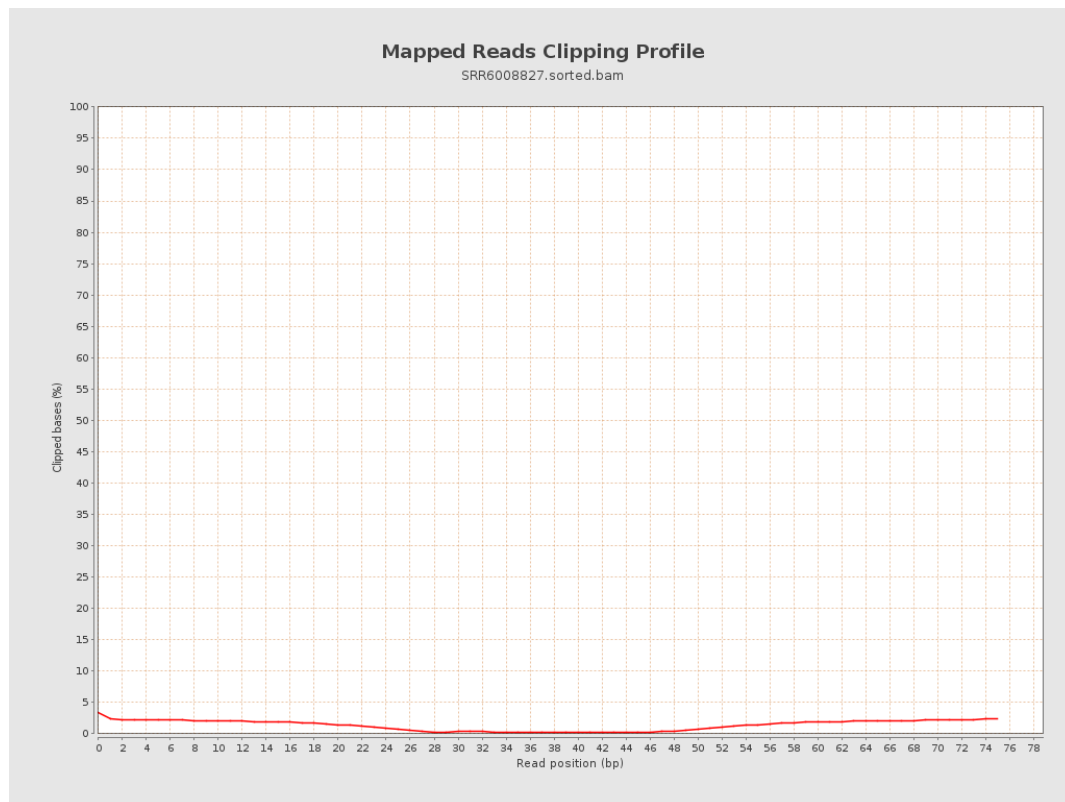
8. Results : Mapped Reads Nucleotide Content



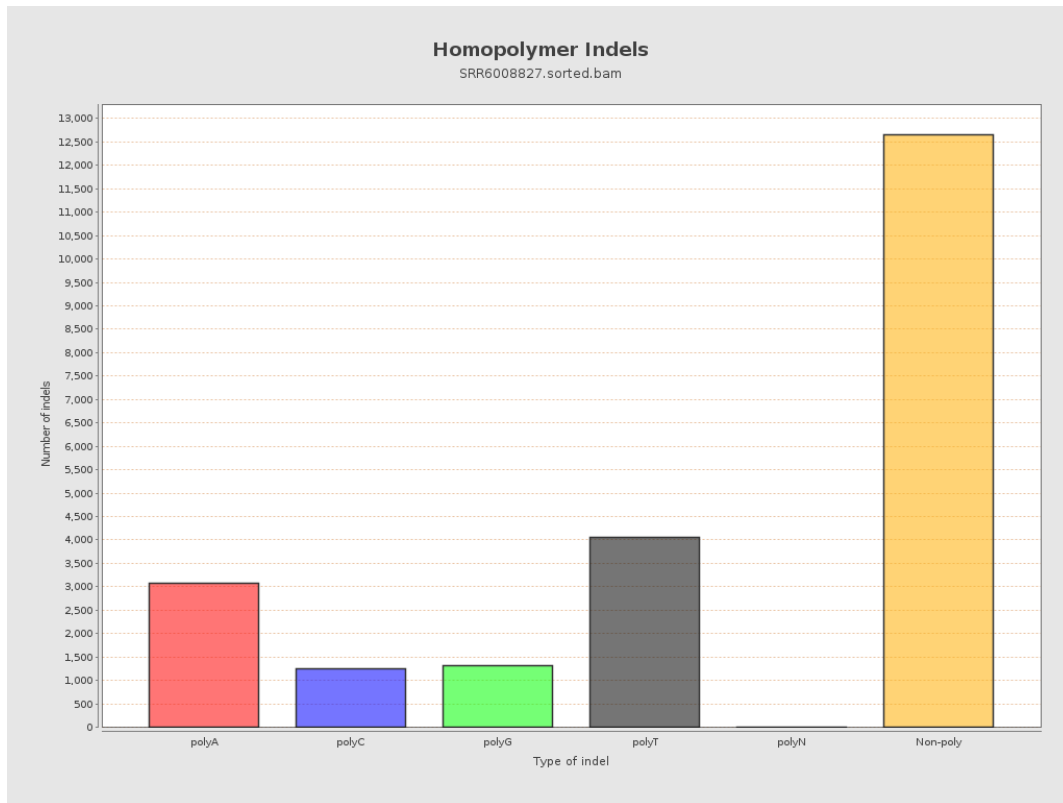
9. Results : Mapped Reads GC-content Distribution



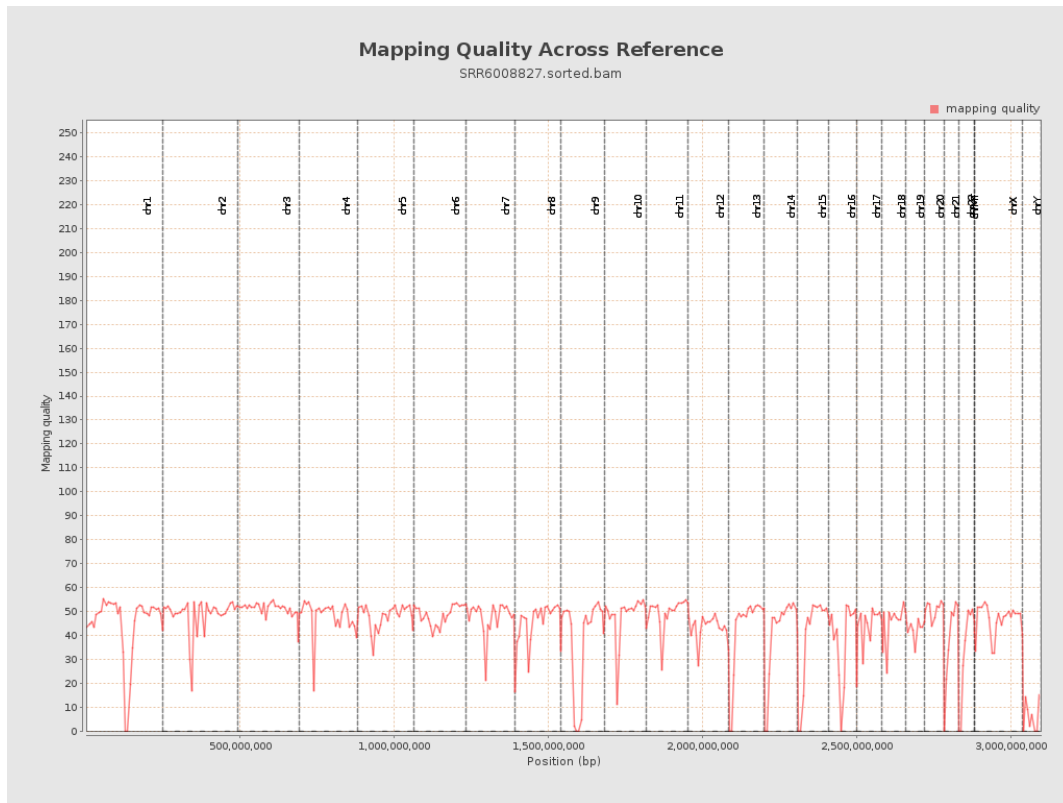
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

