

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:40:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234150.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_SRR6234150 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234150.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:40:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234150.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	757,250
Mapped reads	466,739 / 61.64%
Unmapped reads	290,511 / 38.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,043 / 0.53%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	21,001 / 2.77%
Duplication rate	3.81%
Clipped reads	249,006 / 32.88%

2.2. ACGT Content

Number/percentage of A's	8,452,408 / 28.35%
Number/percentage of C's	5,010,515 / 16.8%
Number/percentage of T's	10,000,921 / 33.54%
Number/percentage of G's	6,349,995 / 21.3%
Number/percentage of N's	4,148 / 0.01%
GC Percentage	38.1%

2.3. Coverage

Mean	0.0096

Standard Deviation	0.1483
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2.4. Mapping Quality

Mean Mapping Quality	46.27
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2.5. Mismatches and indels

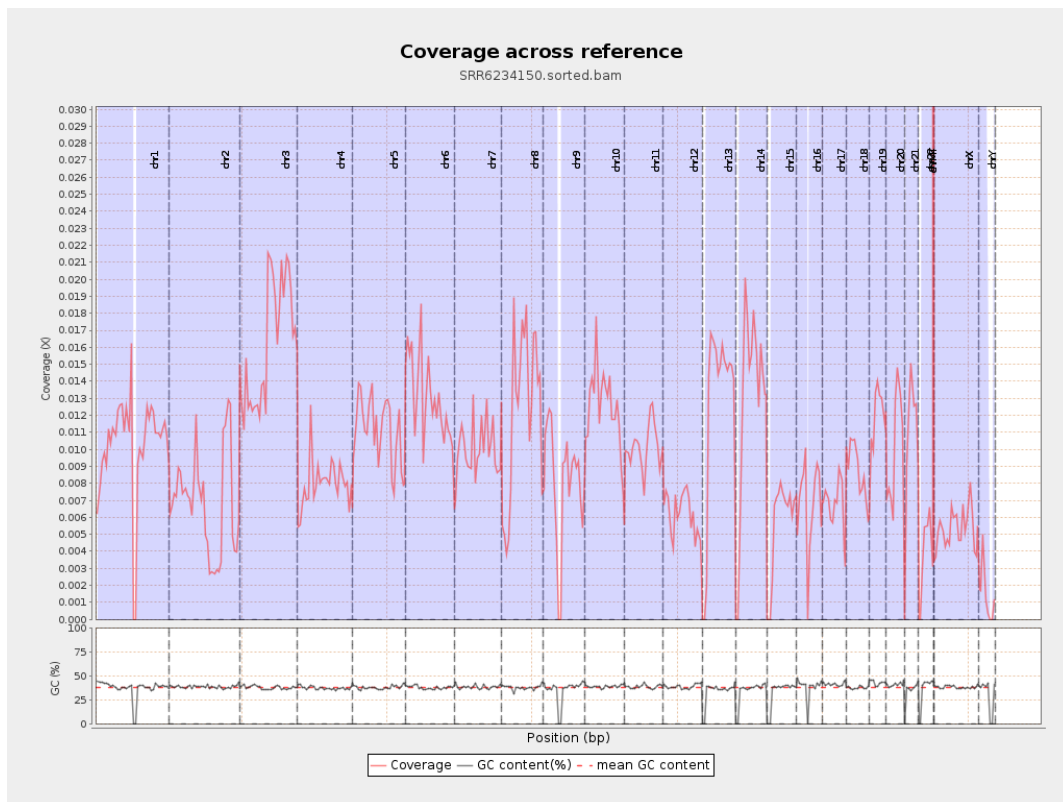
General error rate	0.98%
Mismatches	287,466
Insertions	2,612
Mapped reads with at least one insertion	0.55%
Deletions	15,662
Mapped reads with at least one deletion	3.28%
Homopolymer indels	42.32%

2.6. Chromosome stats

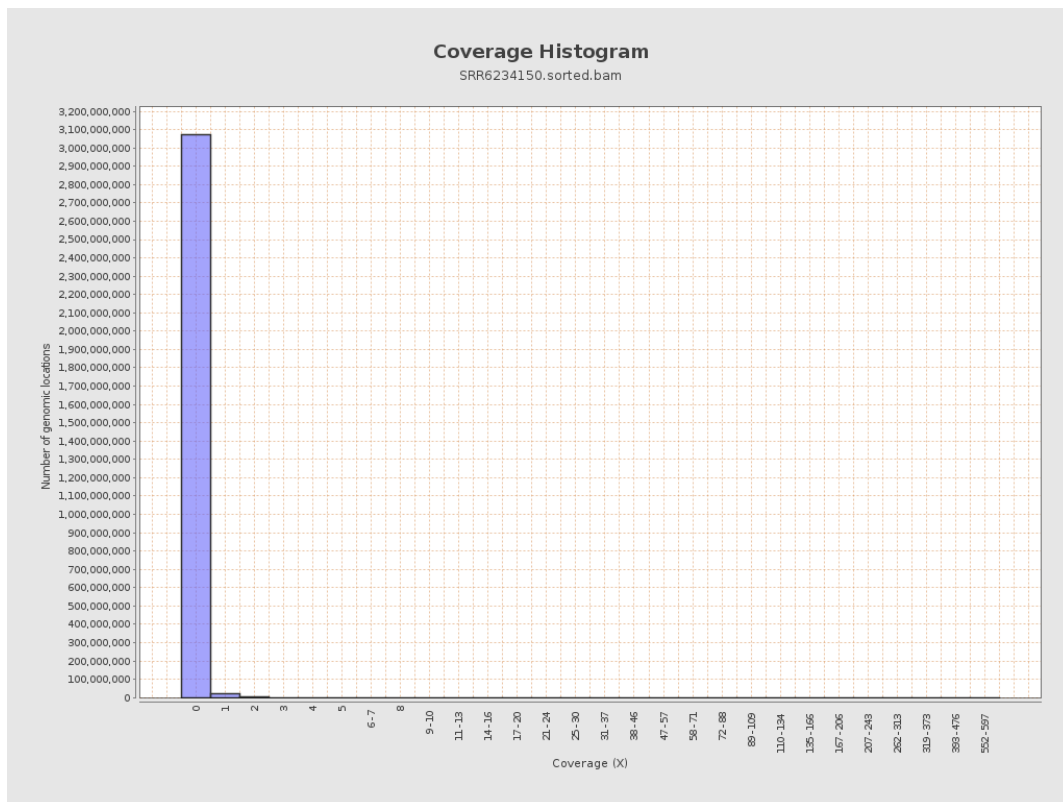
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2563665	0.0103	0.2007
chr2	243199373	1660413	0.0068	0.1083
chr3	198022430	3212777	0.0162	0.1456
chr4	191154276	1524548	0.008	0.1048
chr5	180915260	2001807	0.0111	0.1206
chr6	171115067	2216976	0.013	0.1406
chr7	159138663	1603224	0.0101	0.1272

chr8	146364022	1786787	0.0122	0.366
chr9	141213431	1147479	0.0081	0.1101
chr10	135534747	1710267	0.0126	0.1403
chr11	135006516	1360700	0.0101	0.1221
chr12	133851895	826508	0.0062	0.0937
chr13	115169878	1446779	0.0126	0.1301
chr14	107349540	1393606	0.013	0.1313
chr15	102531392	586320	0.0057	0.0959
chr16	90354753	617889	0.0068	0.0951
chr17	81195210	539290	0.0066	0.0931
chr18	78077248	685987	0.0088	0.1833
chr19	59128983	705210	0.0119	0.1445
chr20	63025520	626035	0.0099	0.1141
chr21	48129895	521260	0.0108	0.1196
chr22	51304566	198730	0.0039	0.0684
chrMT	16571	10563	0.6374	0.939
chrX	155270560	816951	0.0053	0.0845
chrY	59373566	81846	0.0014	0.0474

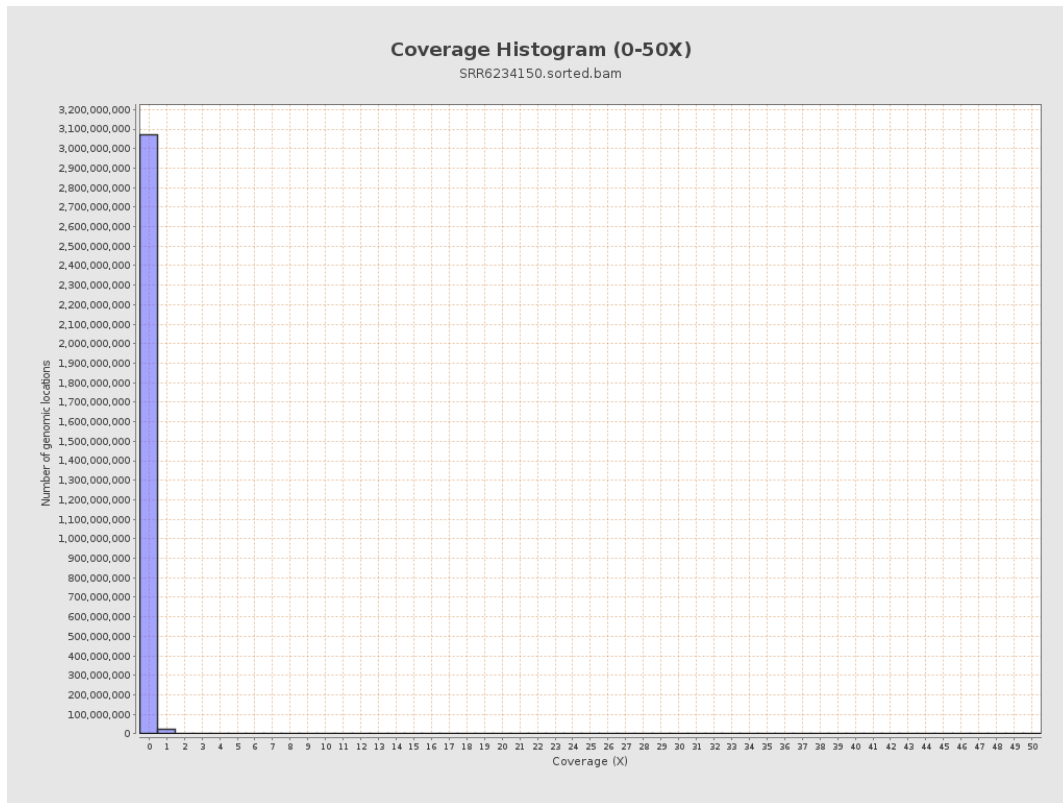
3. Results : Coverage across reference



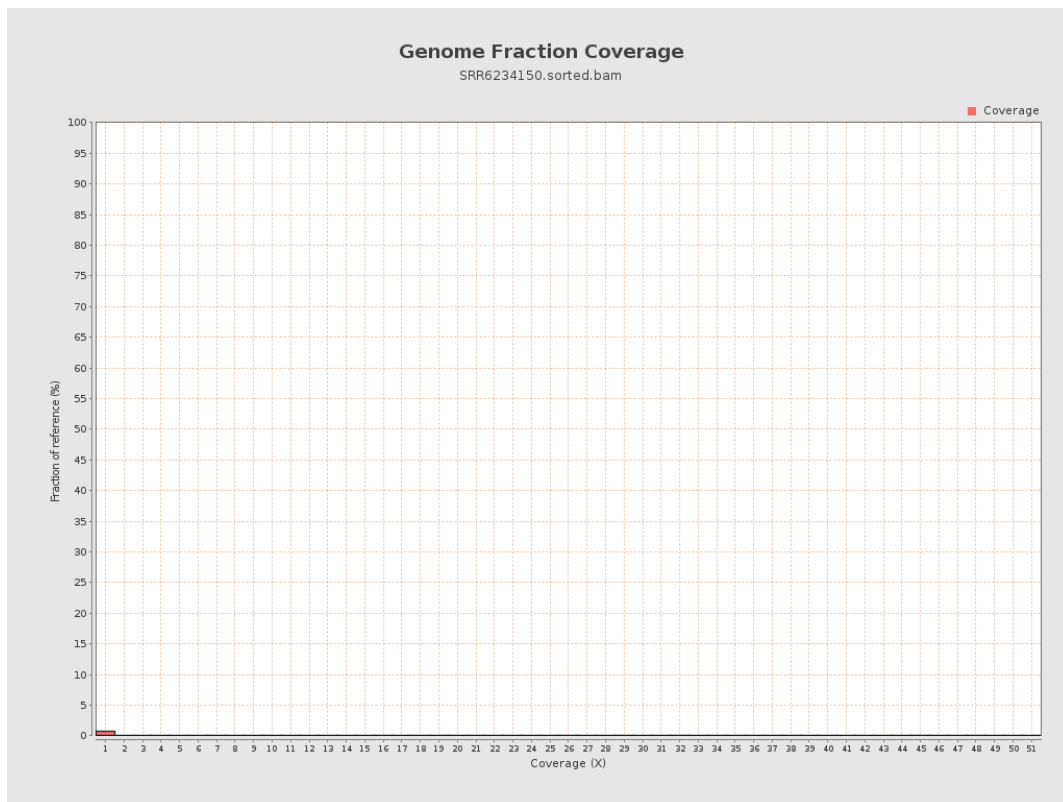
4. Results : Coverage Histogram



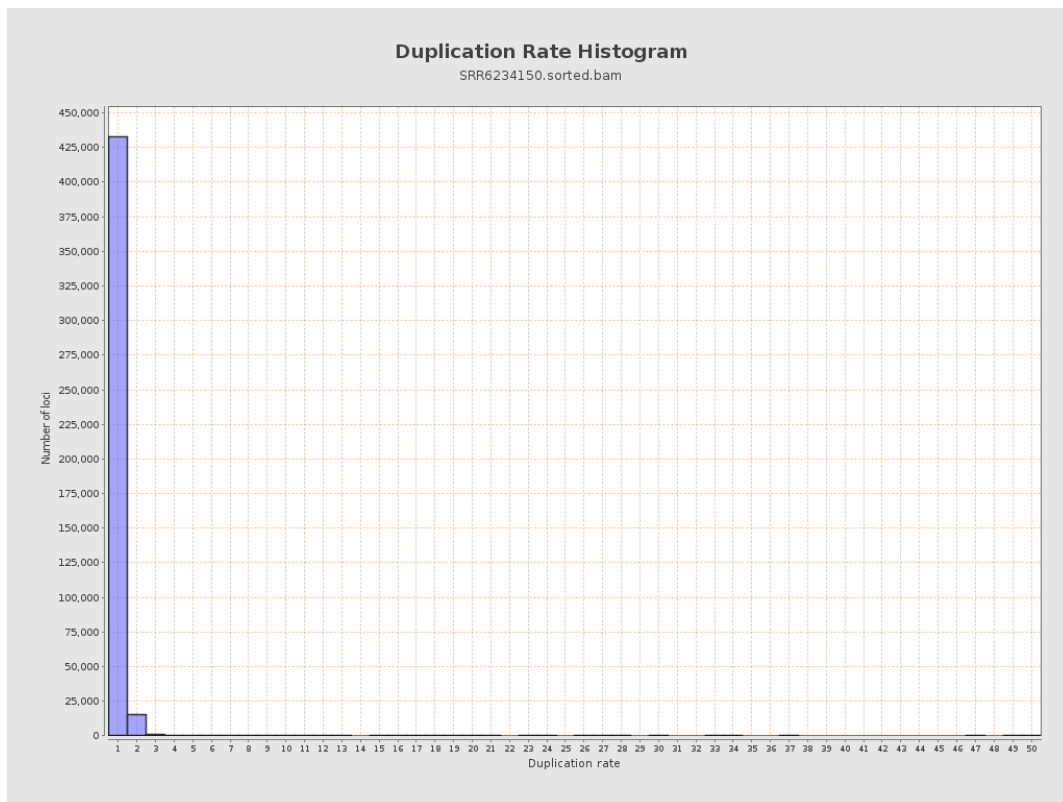
5. Results : Coverage Histogram (0-50X)



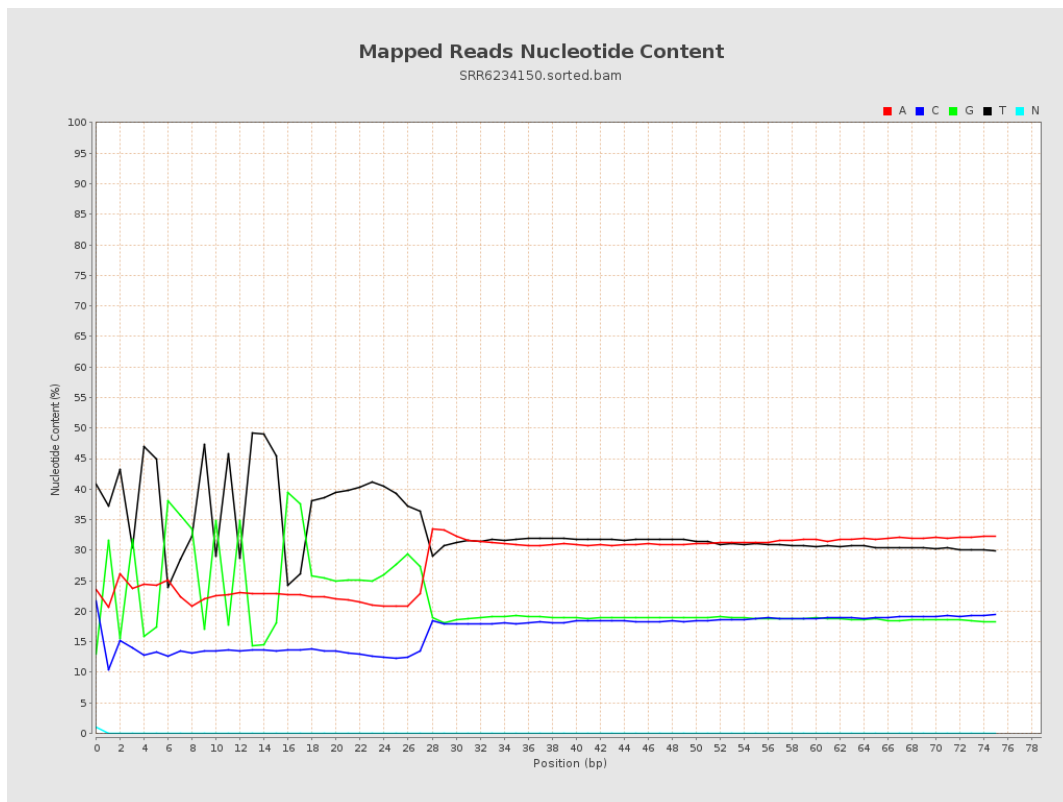
6. Results : Genome Fraction Coverage



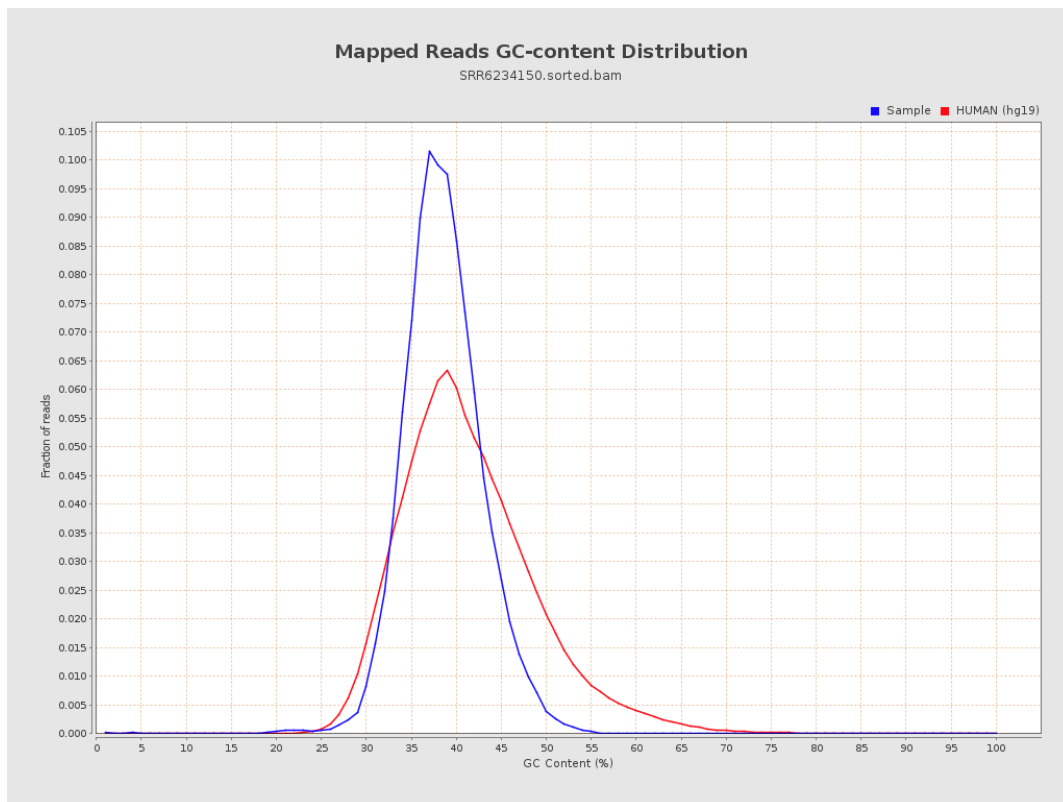
7. Results : Duplication Rate Histogram



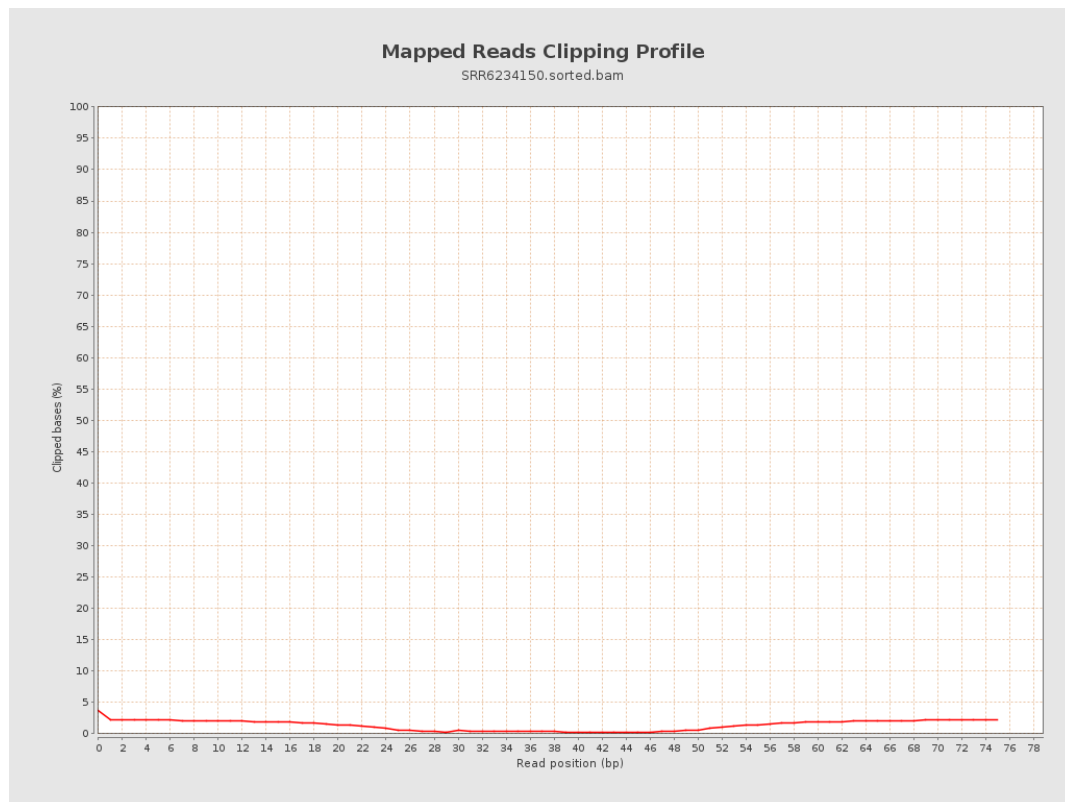
8. Results : Mapped Reads Nucleotide Content



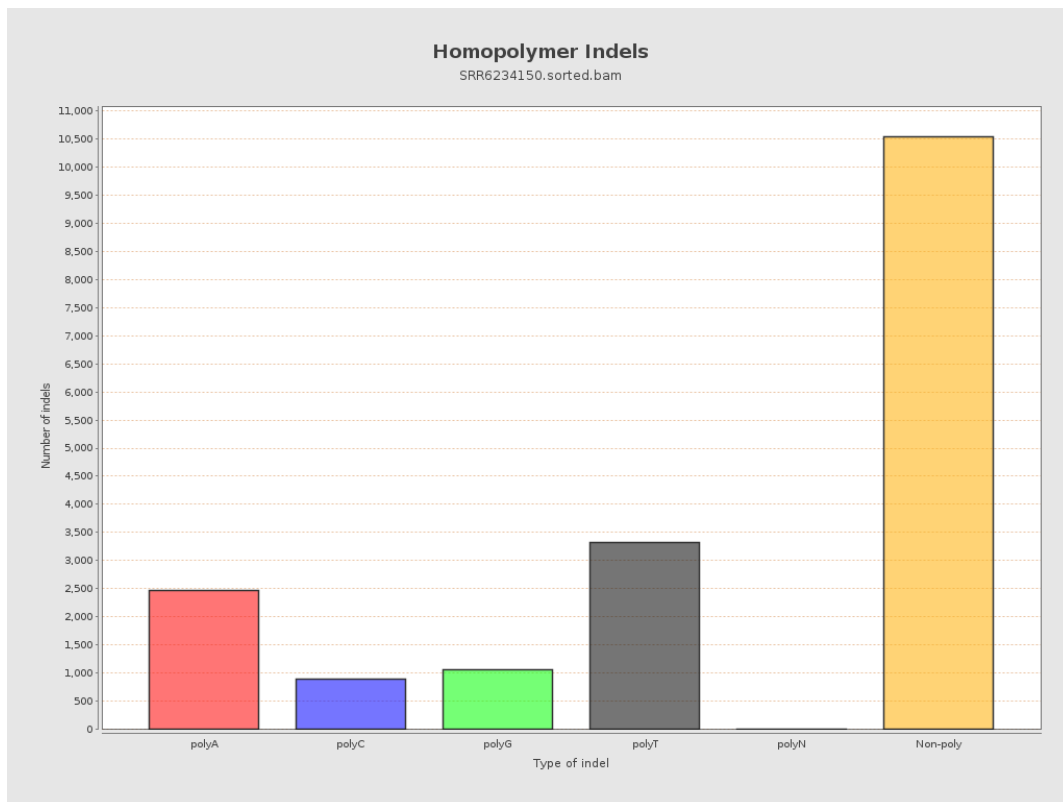
9. Results : Mapped Reads GC-content Distribution



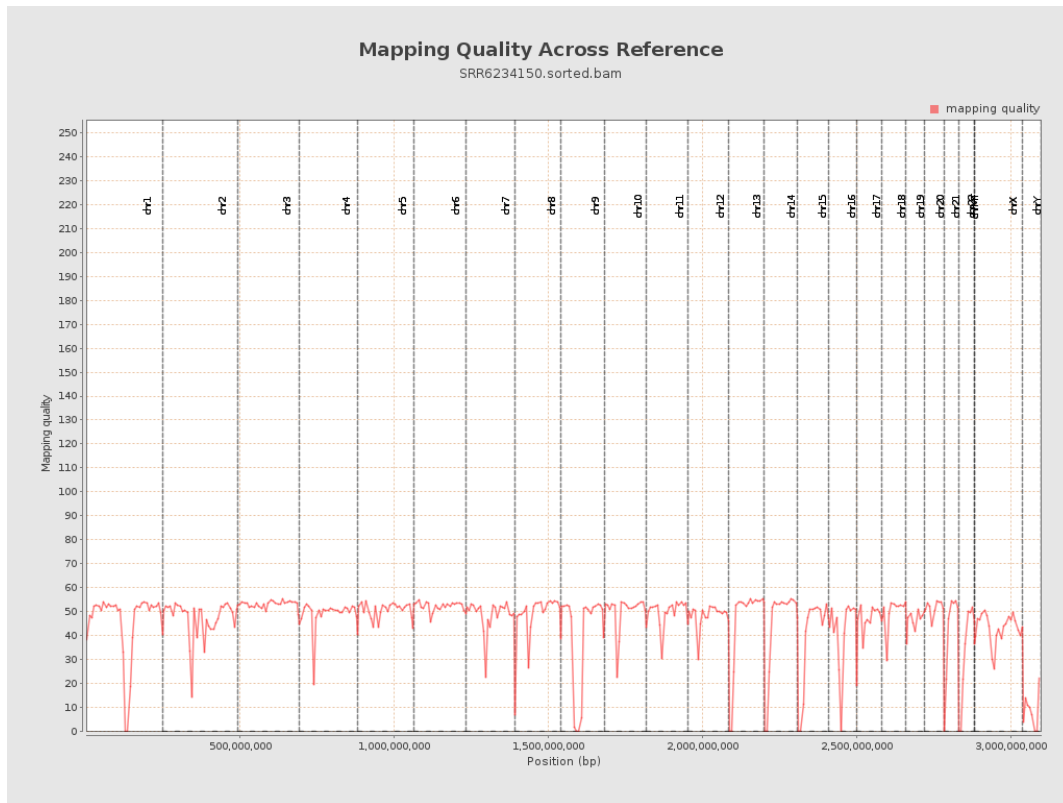
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

