Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:24:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234123.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_SRR6234123 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234123.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:24:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234123.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,425,594
Mapped reads	3,155,698 / 92.12%
Unmapped reads	269,896 / 7.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,046 / 1.02%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	527,172 / 15.39%
Duplication rate	6.83%
Clipped reads	1,175,497 / 34.32%

2.2. ACGT Content

Number/percentage of A's	54,942,080 / 25.41%
Number/percentage of C's	37,888,603 / 17.52%
Number/percentage of T's	59,411,166 / 27.47%
Number/percentage of G's	63,953,727 / 29.58%
Number/percentage of N's	46,313 / 0.02%
GC Percentage	47.1%

2.3. Coverage

Mean	0.0699

Standard Deviation	42.4913

2.4. Mapping Quality

Mean Mapping Quality	46.22

2.5. Mismatches and indels

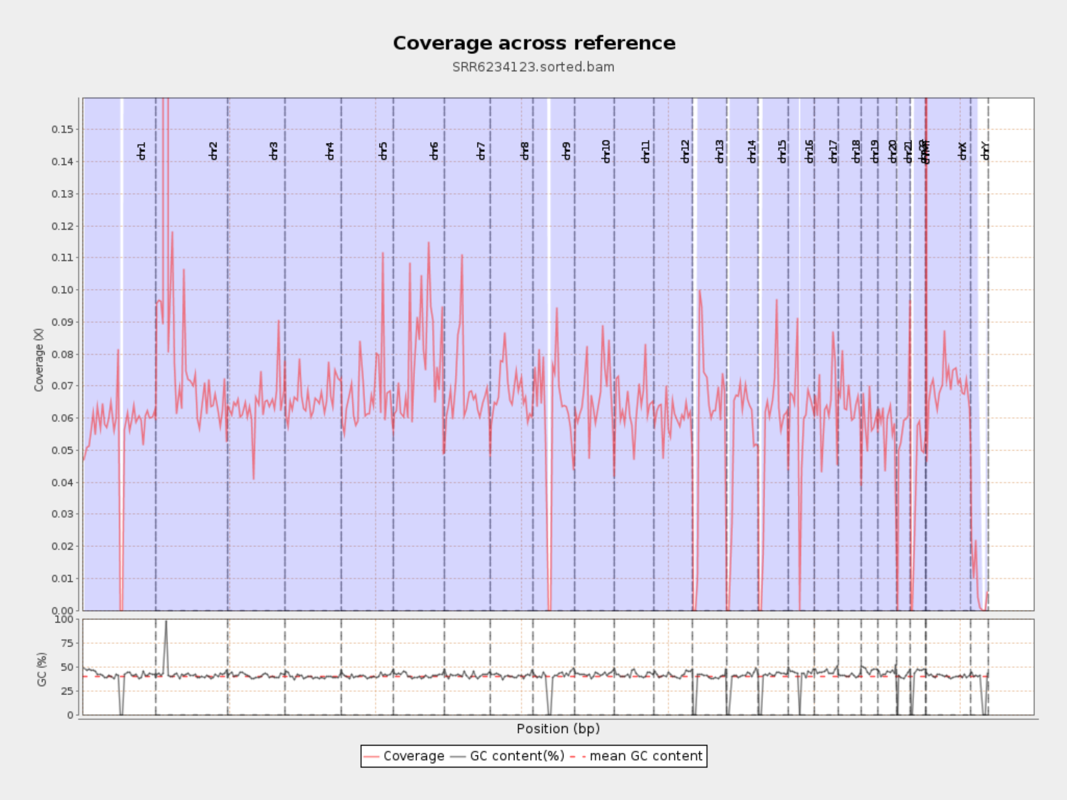
General error rate	0.62%
Mismatches	1,316,112
Insertions	14,447
Mapped reads with at least one insertion	0.45%
Deletions	41,853
Mapped reads with at least one deletion	1.31%
Homopolymer indels	47.08%

2.6. Chromosome stats

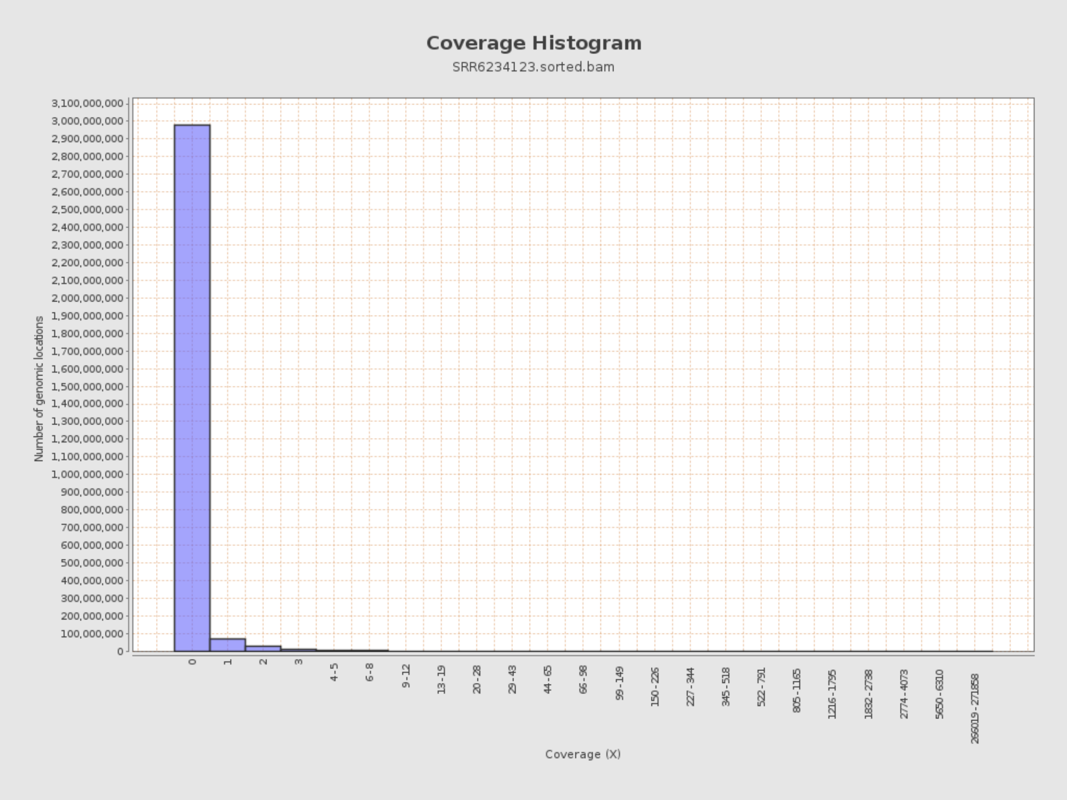
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13865370	0.0556	0.6783
chr2	243199373	39475687	0.1623	151.5876
chr3	198022430	12772270	0.0645	0.3923
chr4	191154276	12693161	0.0664	0.4115
chr5	180915260	12179733	0.0673	0.4033
chr6	171115067	13385584	0.0782	0.5242
chr7	159138663	10970173	0.0689	0.8869

chr8	146364022	9971698	0.0681	0.9482
chr9	141213431	8534927	0.0604	0.5433
chr10	135534747	9118557	0.0673	0.4944
chr11	135006516	8644566	0.064	0.5621
chr12	133851895	8072102	0.0603	0.3911
chr13	115169878	6830764	0.0593	0.3781
chr14	107349540	5676615	0.0529	0.4681
chr15	102531392	5473244	0.0534	0.3603
chr16	90354753	5293813	0.0586	0.4027
chr17	81195210	5295012	0.0652	0.4827
chr18	78077248	5142256	0.0659	0.9492
chr19	59128983	3476314	0.0588	0.5516
chr20	63025520	3584087	0.0569	0.3822
chr21	48129895	2659245	0.0553	0.3917
chr22	51304566	1939905	0.0378	0.2983
chrMT	16571	18166	1.0963	1.4515
chrX	155270560	10792257	0.0695	0.4378
chrY	59373566	444275	0.0075	0.1753

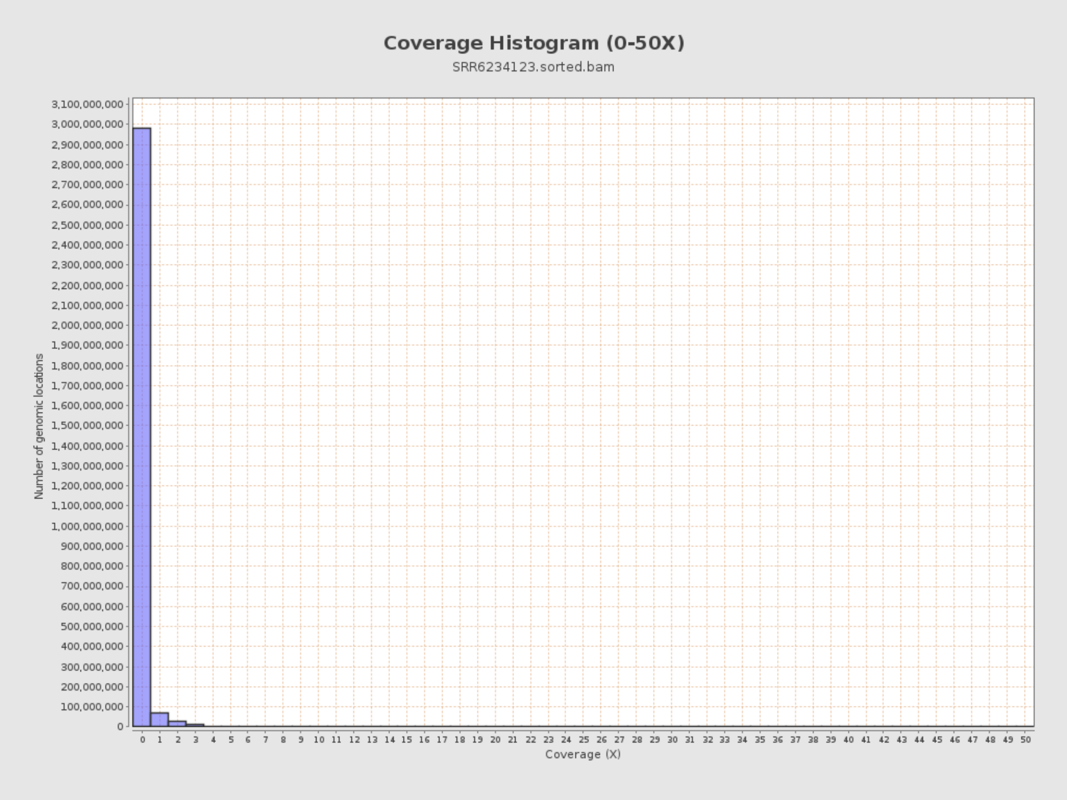
3. Results : Coverage across reference



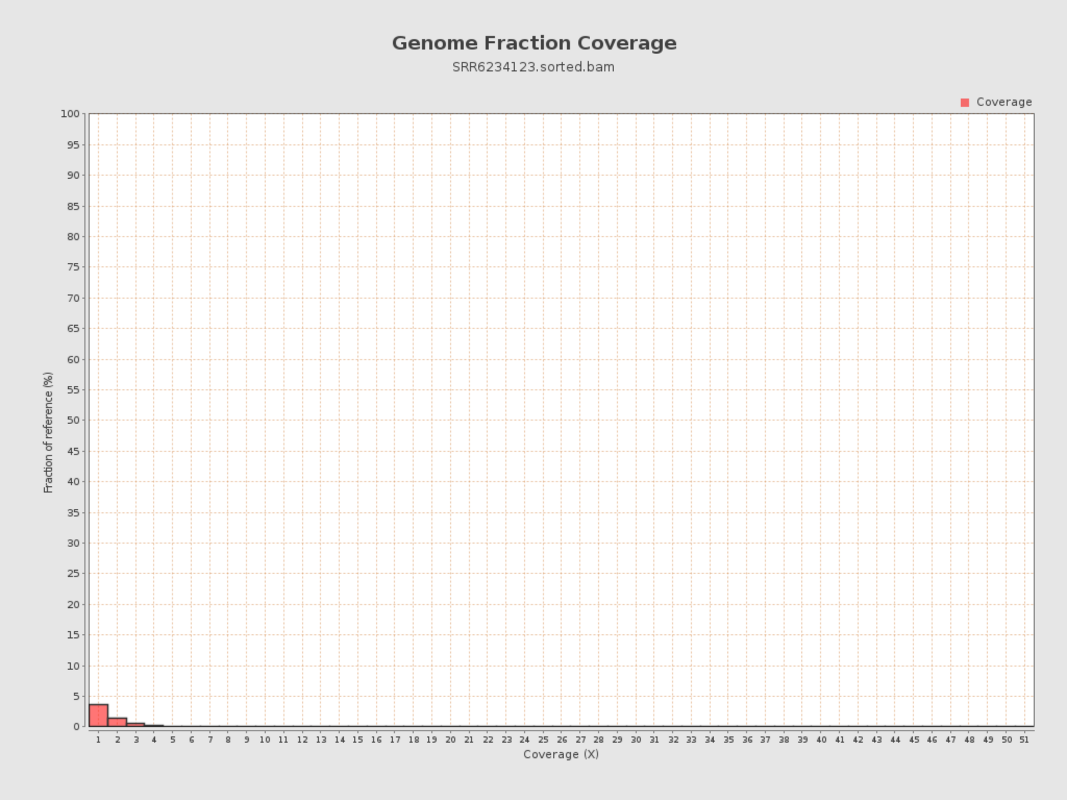
4. Results : Coverage Histogram



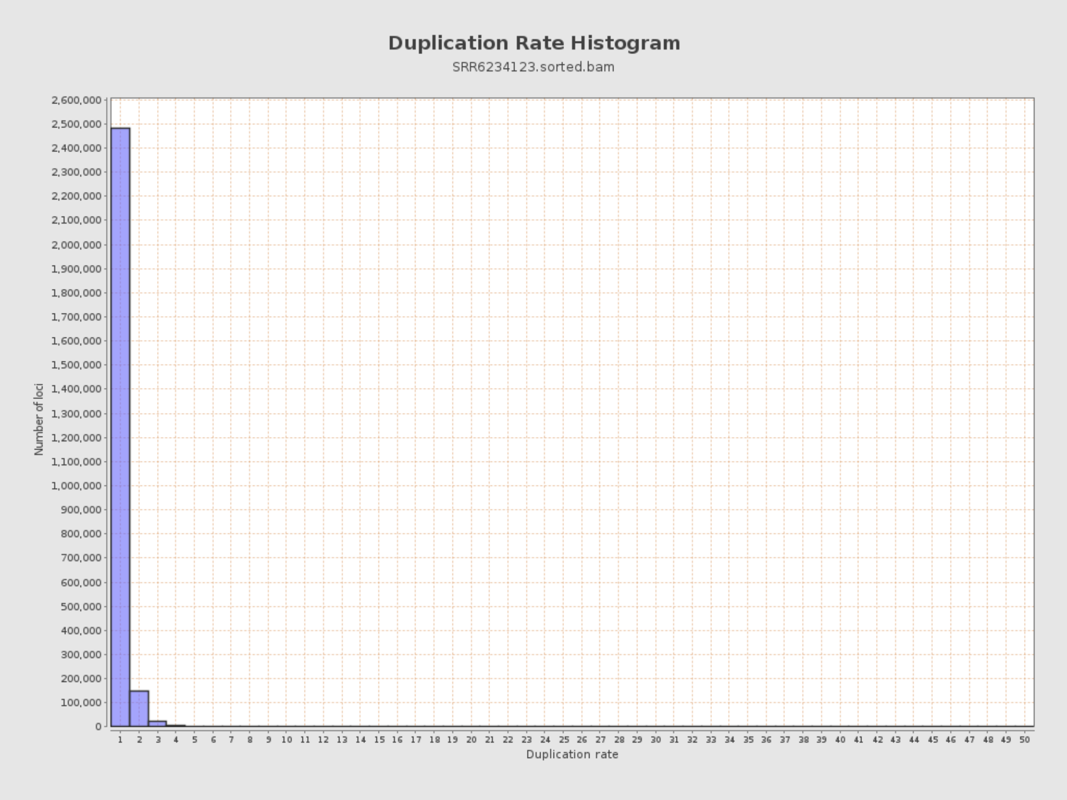
5. Results : Coverage Histogram (0-50X)



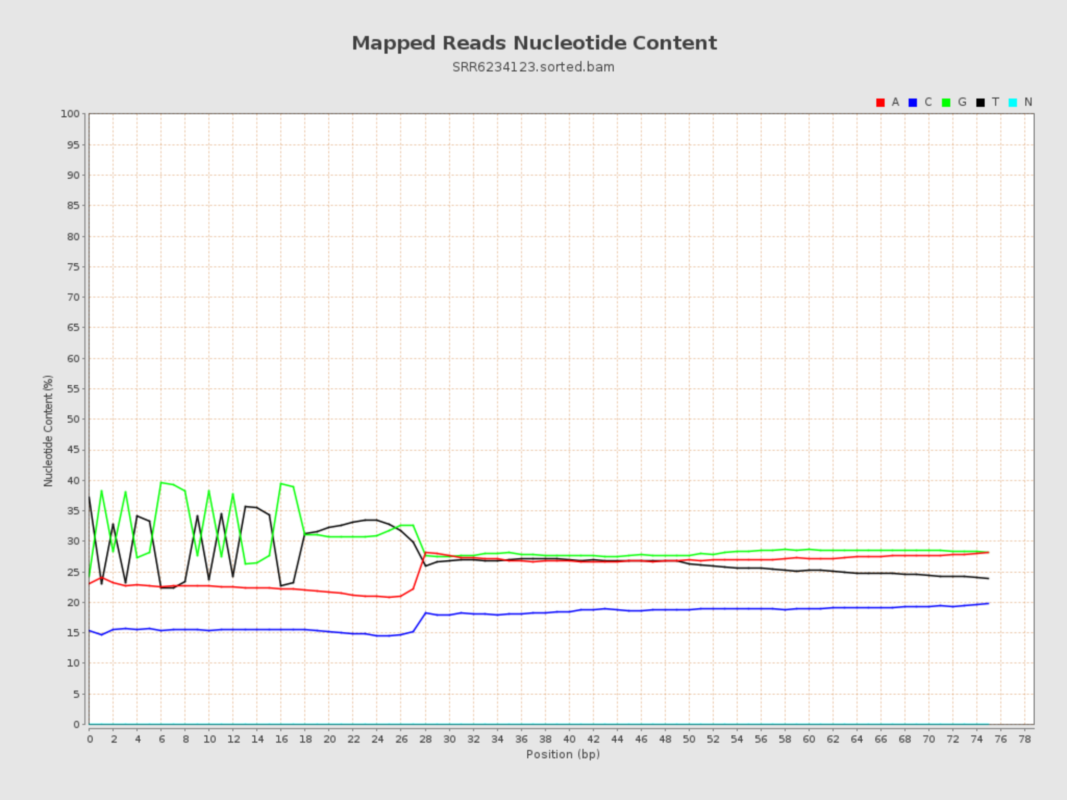
6. Results : Genome Fraction Coverage



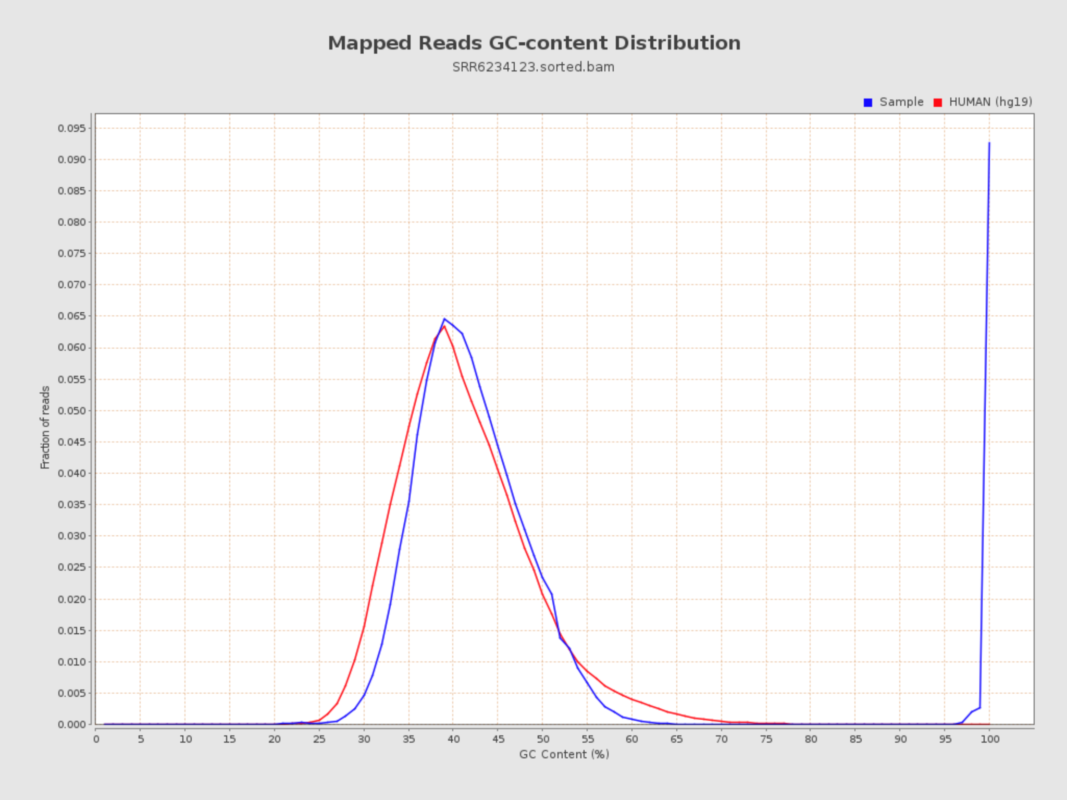
7. Results : Duplication Rate Histogram



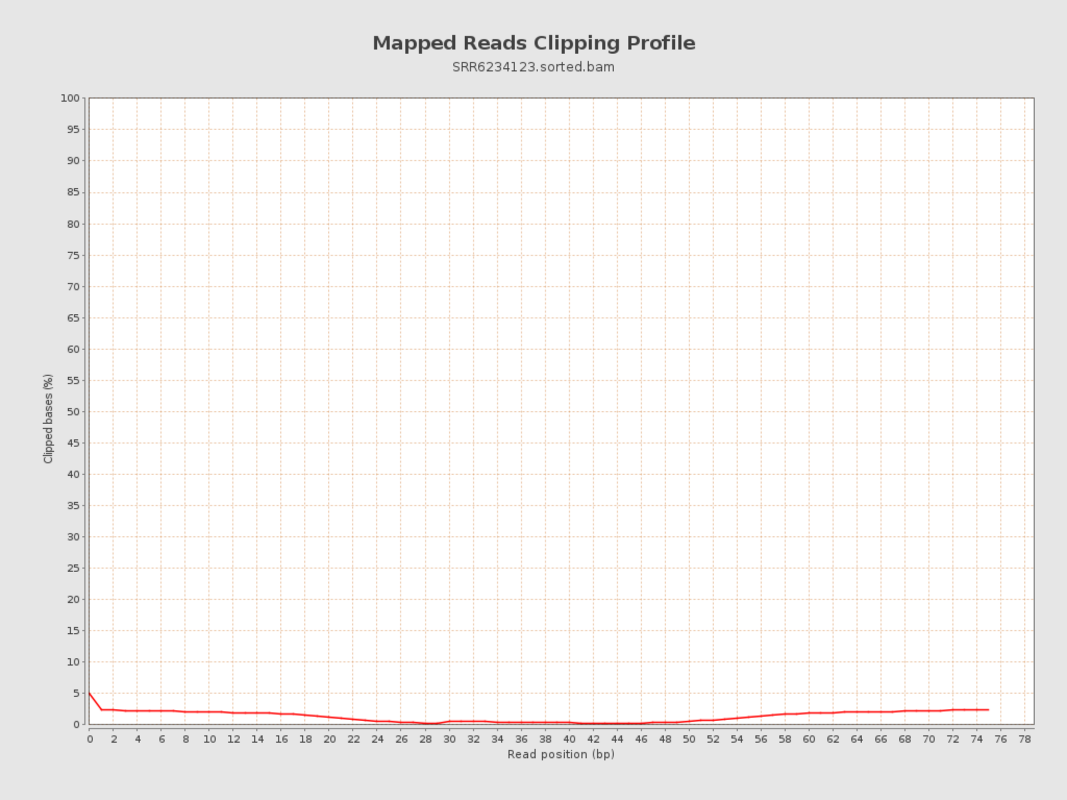
8. Results : Mapped Reads Nucleotide Content



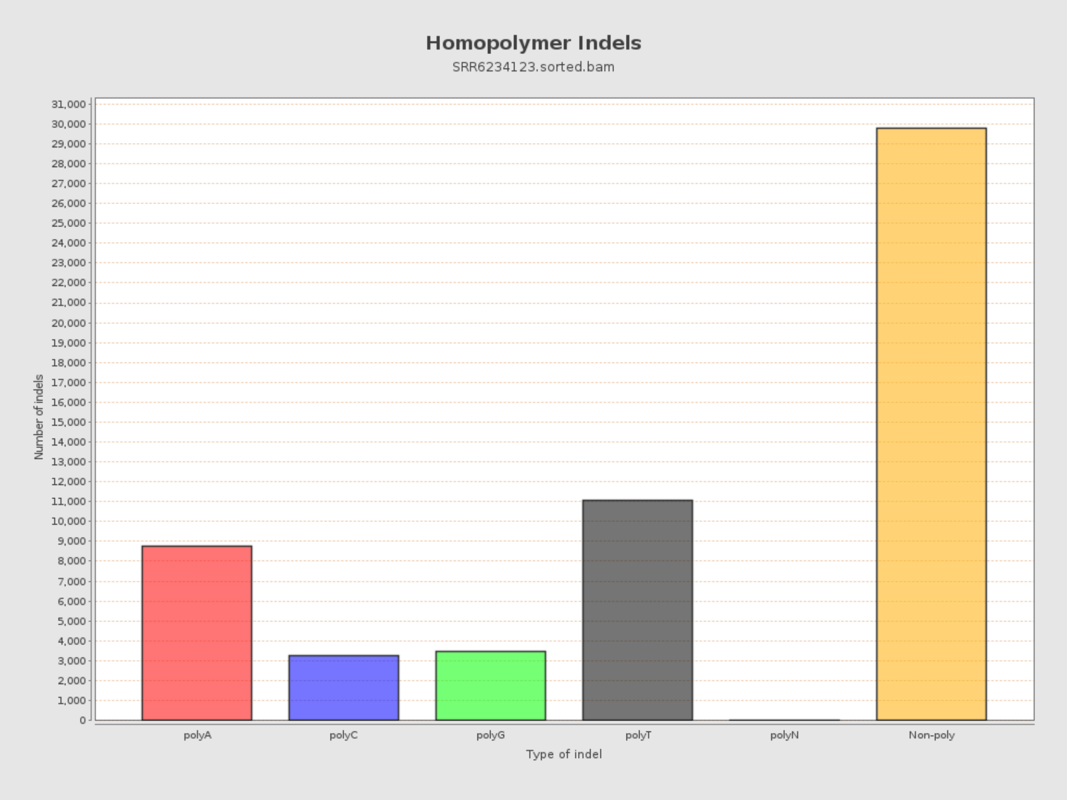
9. Results : Mapped Reads GC-content Distribution



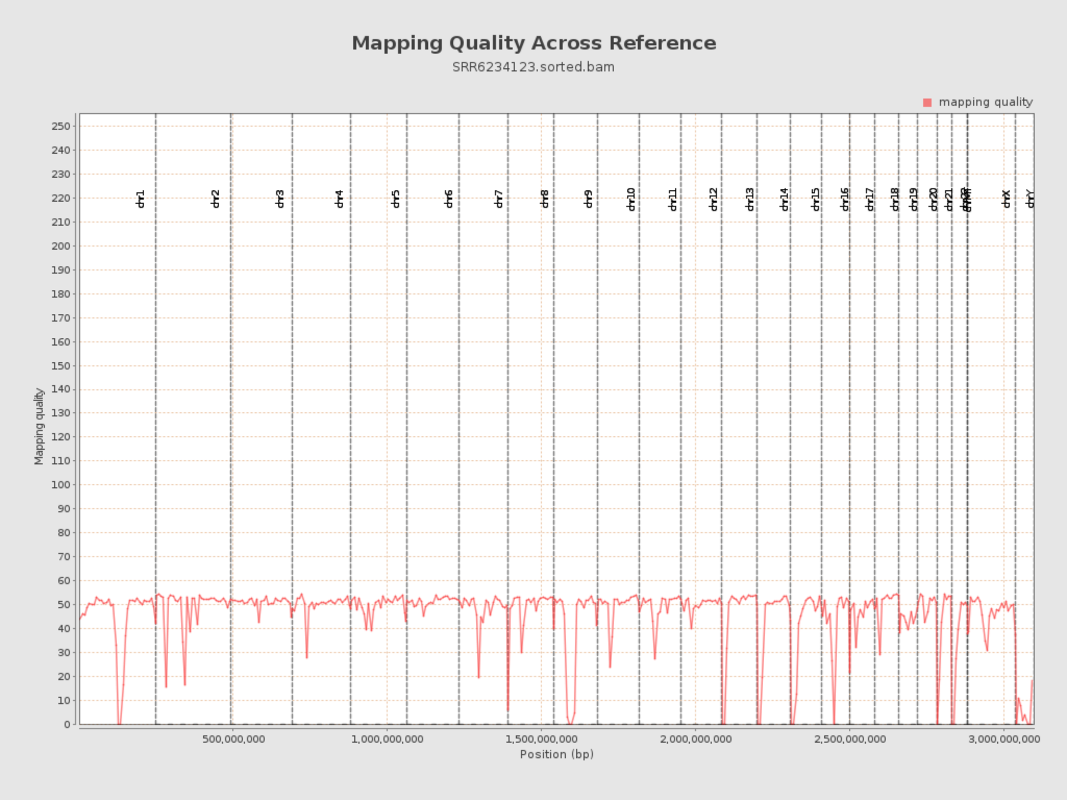
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram