Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:10:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068150.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_SRR6068150 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068150.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:10:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068150.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,588,119
Mapped reads	3,376,922 / 94.11%
Unmapped reads	211,197 / 5.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,839 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,145,830 / 31.93%
Duplication rate	20.82%
Clipped reads	1,981,624 / 55.23%

2.2. ACGT Content

Number/percentage of A's	54,610,781 / 25.66%
Number/percentage of C's	36,972,684 / 17.37%
Number/percentage of T's	70,994,312 / 33.35%
Number/percentage of G's	50,245,249 / 23.61%
Number/percentage of N's	22,488 / 0.01%
GC Percentage	40.98%

2.3. Coverage

Mean	0.0688

Standard Deviation	1.3876

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

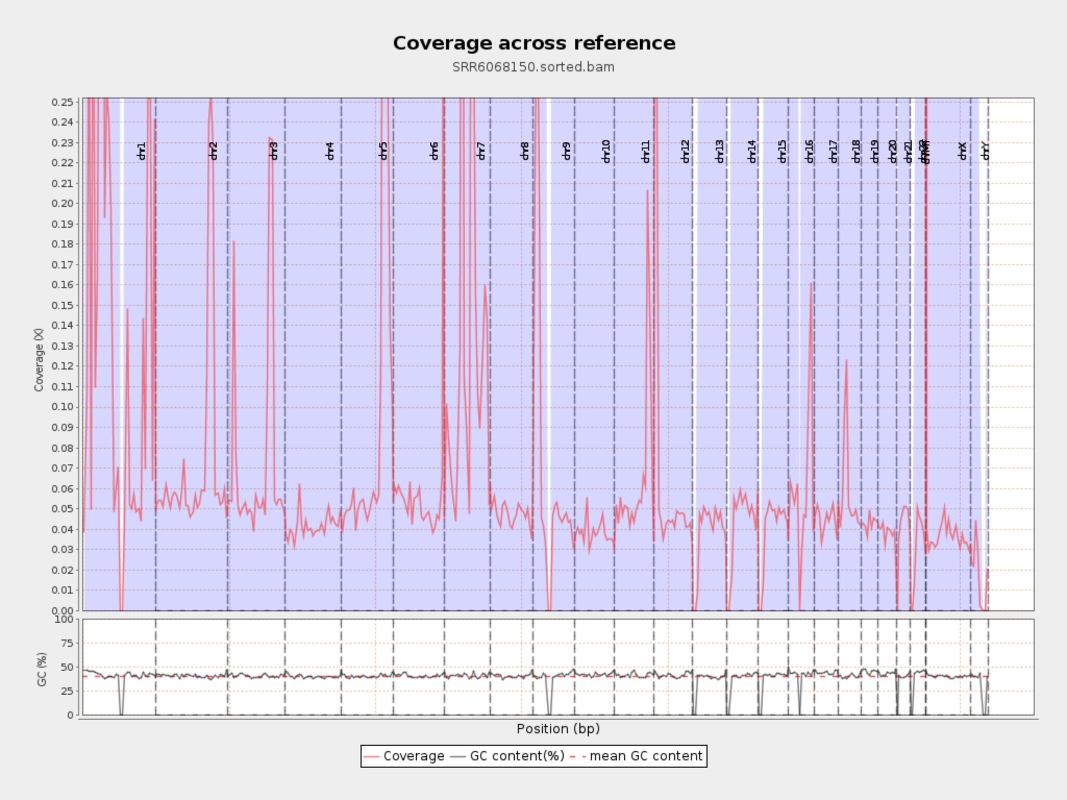
General error rate	0.57%
Mismatches	1,190,353
Insertions	13,069
Mapped reads with at least one insertion	0.38%
Deletions	54,228
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.17%

2.6. Chromosome stats

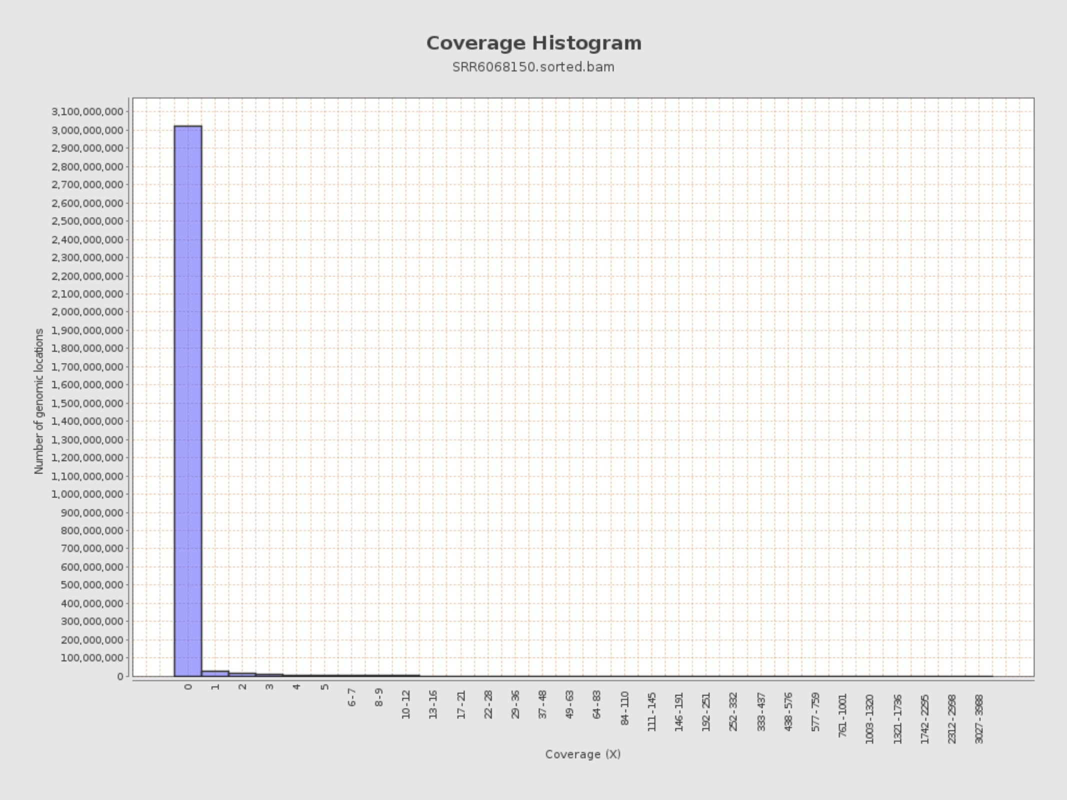
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37592537	0.1508	0.9586
chr2	243199373	18133339	0.0746	1.1145
chr3	198022430	14513560	0.0733	0.6219
chr4	191154276	7984213	0.0418	0.4773
chr5	180915260	17828886	0.0985	0.7176
chr6	171115067	9714470	0.0568	0.6144
chr7	159138663	24310010	0.1528	5.3816

chr8	146364022	6870094	0.0469	0.6909
chr9	141213431	10336834	0.0732	0.6459
chr10	135534747	5227418	0.0386	0.4896
chr11	135006516	8855469	0.0656	0.6235
chr12	133851895	9781029	0.0731	0.6335
chr13	115169878	4341029	0.0377	0.4669
chr14	107349540	4572324	0.0426	0.4839
chr15	102531392	3961701	0.0386	0.4745
chr16	90354753	5225517	0.0578	0.5417
chr17	81195210	3682594	0.0454	0.5024
chr18	78077248	4669745	0.0598	0.9025
chr19	59128983	2538305	0.0429	0.5525
chr20	63025520	2422522	0.0384	0.4484
chr21	48129895	1966829	0.0409	0.464
chr22	51304566	1531244	0.0298	0.3863
chrMT	16571	189324	11.425	9.7107
chrX	155270560	5659364	0.0364	0.4358
chrY	59373566	1033386	0.0174	0.2838

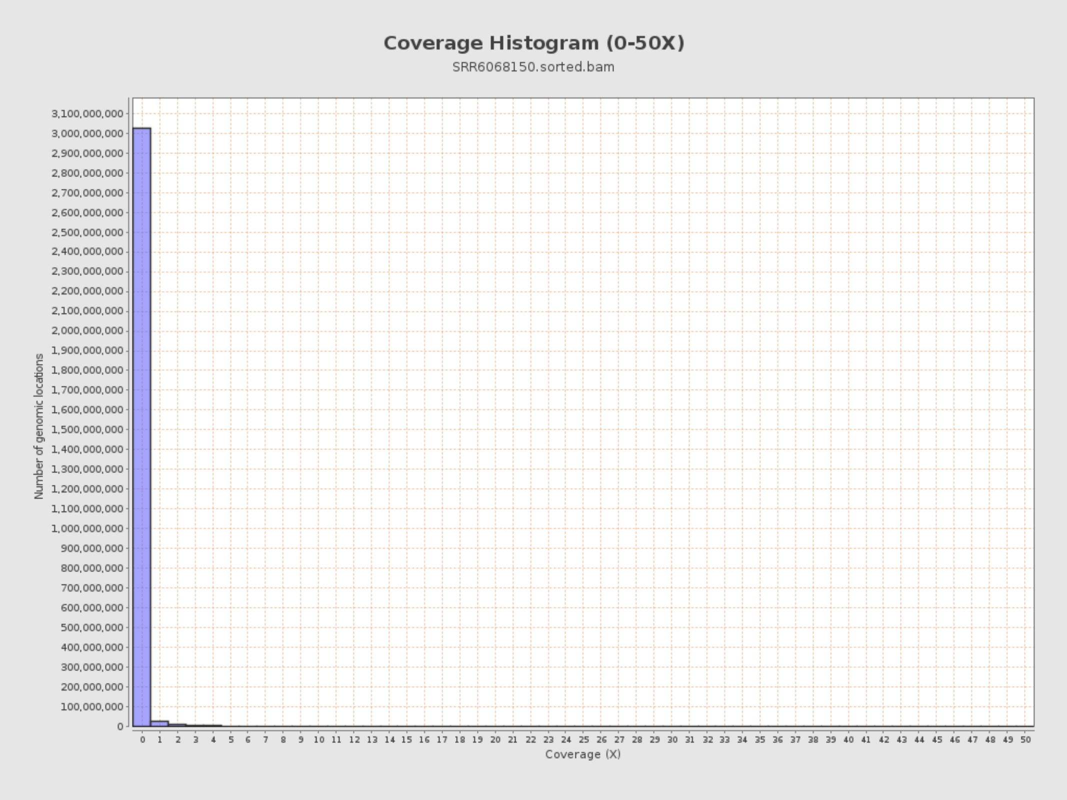
3. Results : Coverage across reference



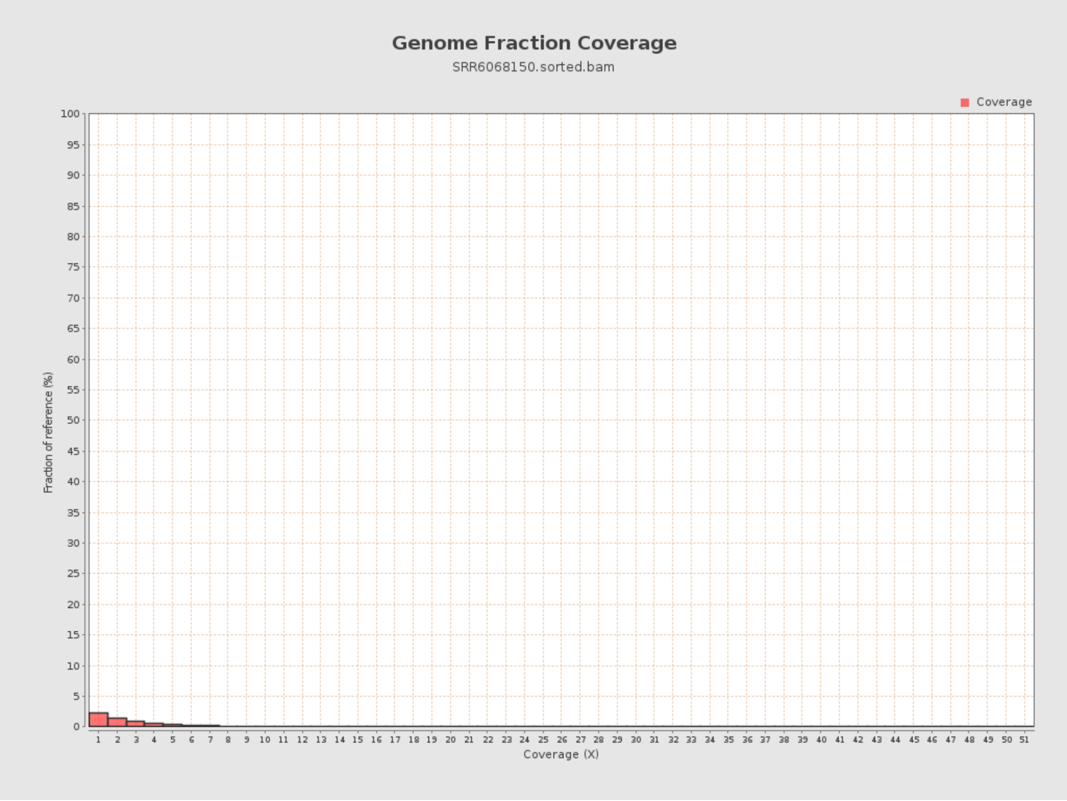
4. Results : Coverage Histogram



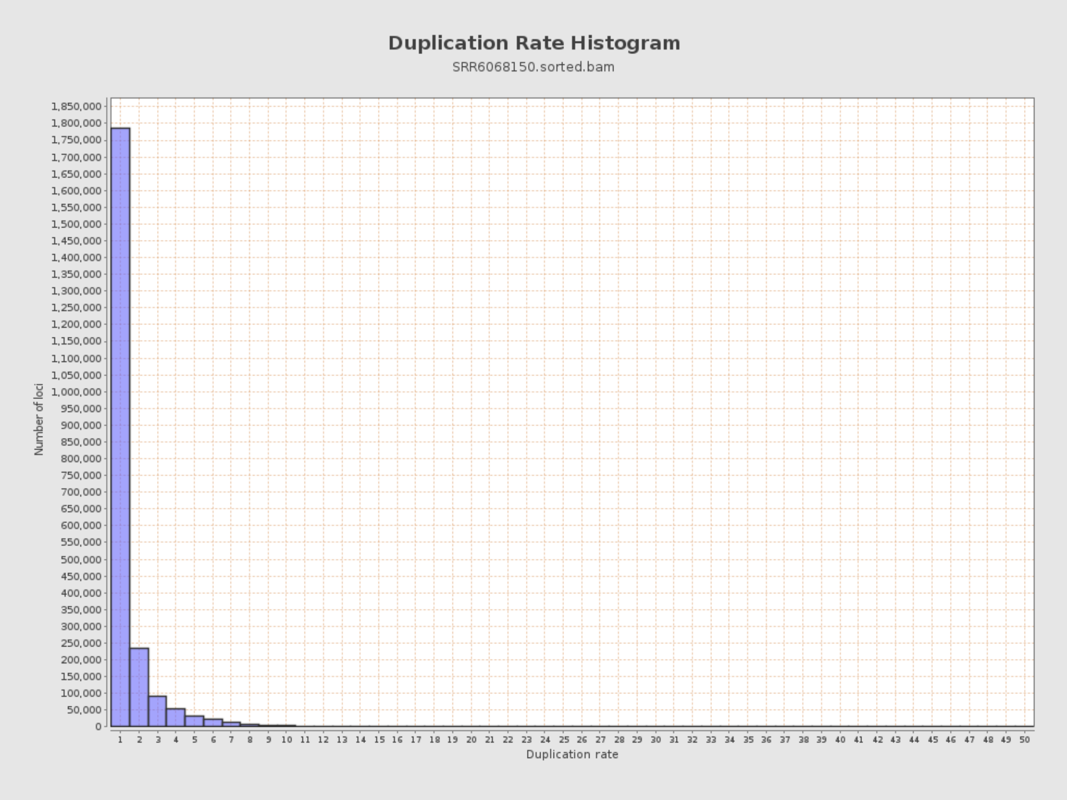
5. Results : Coverage Histogram (0-50X)



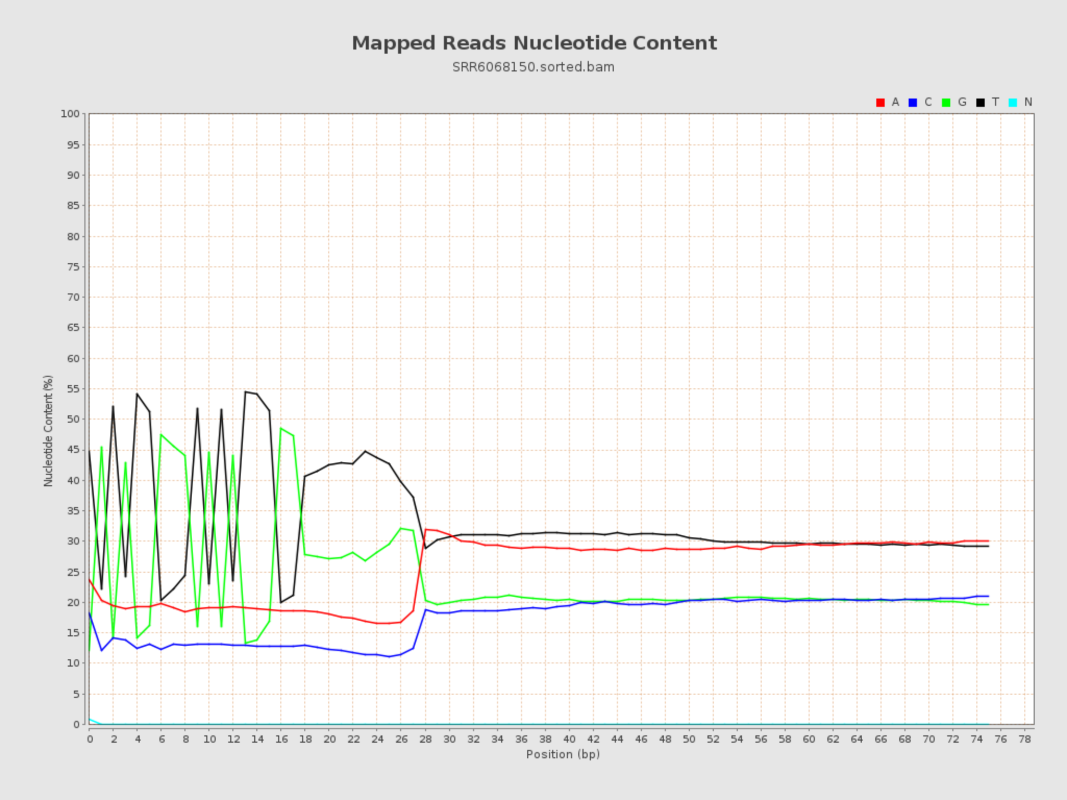
6. Results : Genome Fraction Coverage



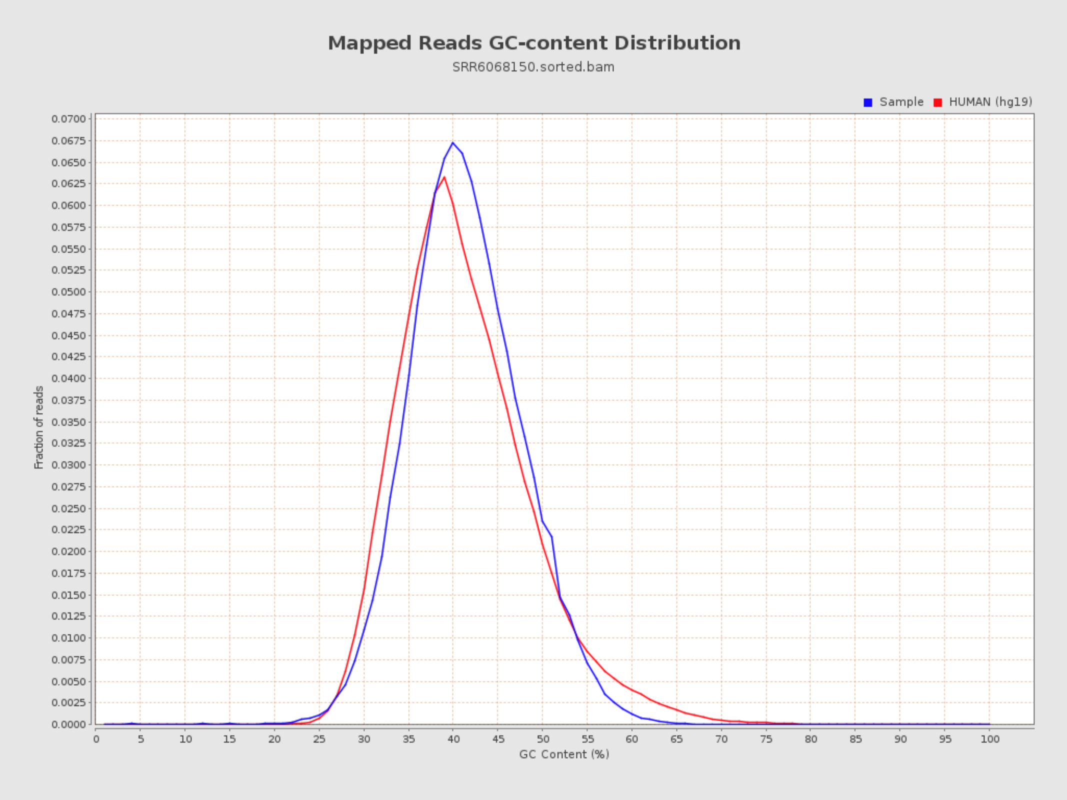
7. Results : Duplication Rate Histogram



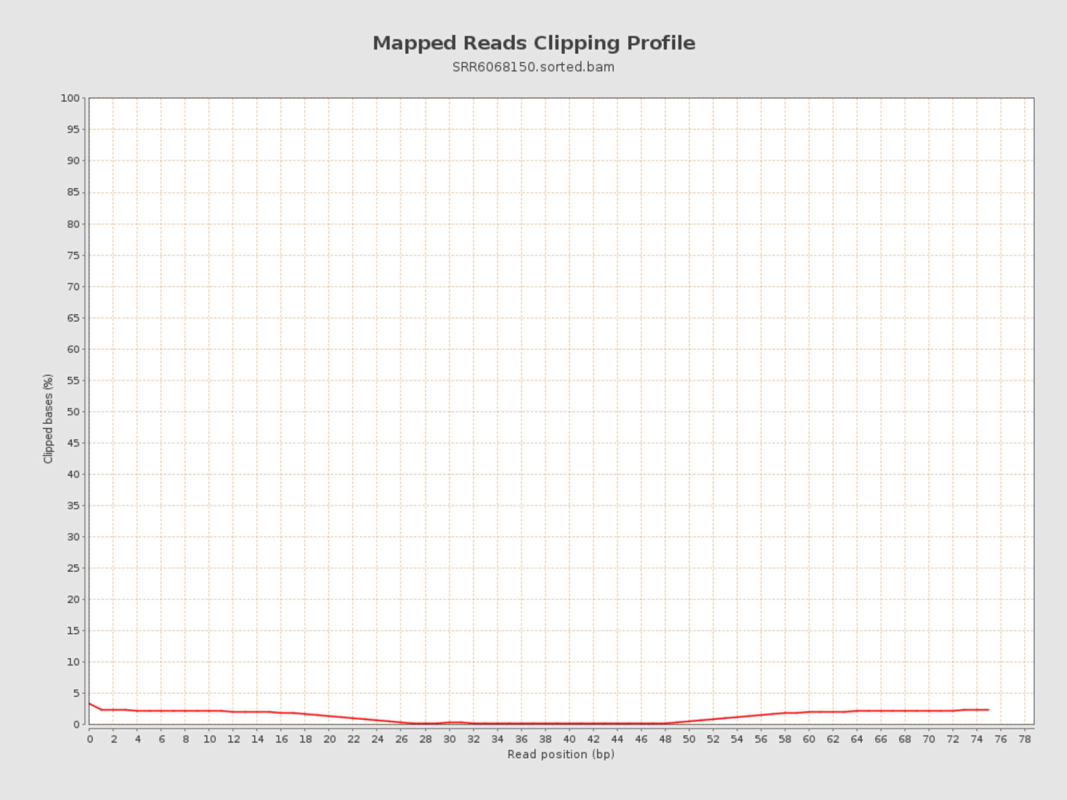
8. Results : Mapped Reads Nucleotide Content



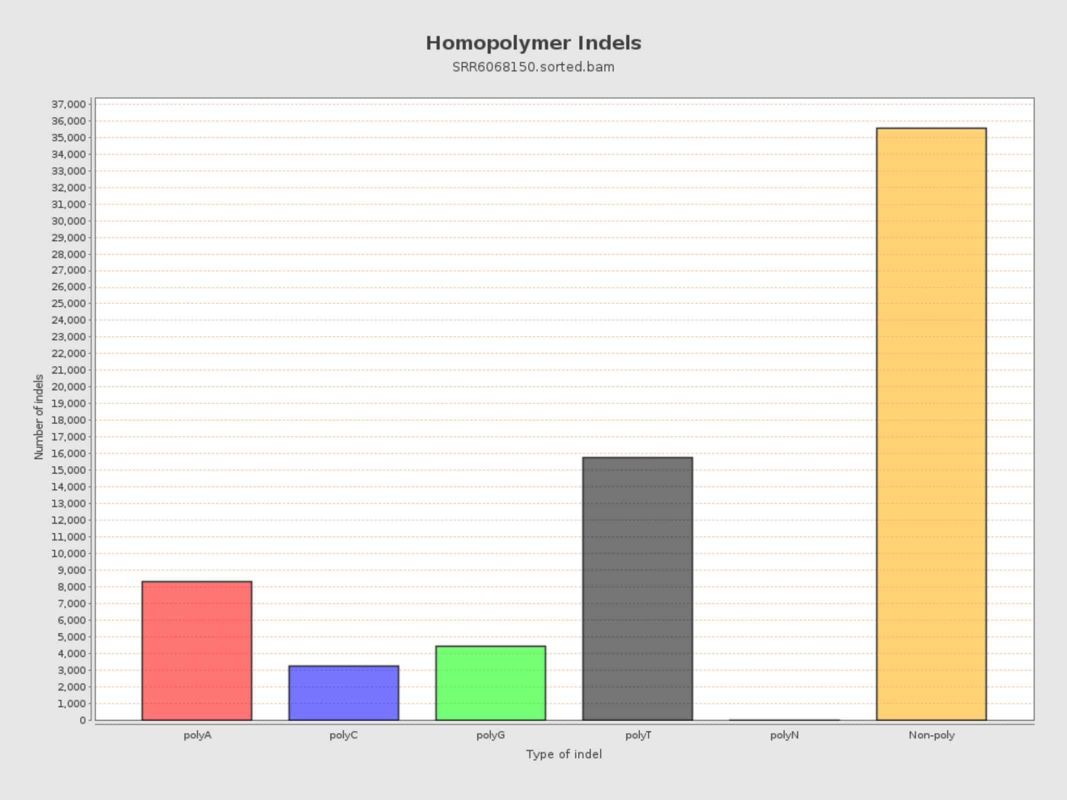
9. Results : Mapped Reads GC-content Distribution



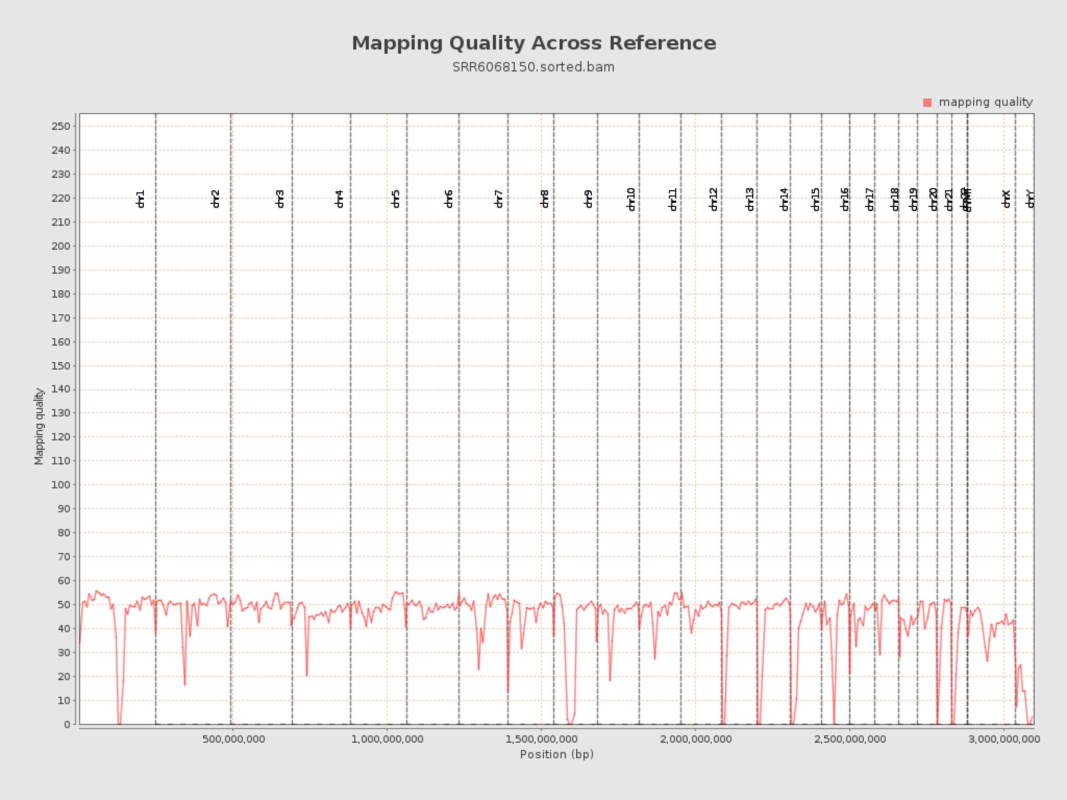
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram