Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:47:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068110.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_SRR6068110 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068110.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:47:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068110.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,002,116
Mapped reads	4,738,526 / 94.73%
Unmapped reads	263,590 / 5.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,191 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	689,685 / 13.79%
Duplication rate	11.89%
Clipped reads	2,511,603 / 50.21%

2.2. ACGT Content

Number/percentage of A's	81,163,430 / 26.58%
Number/percentage of C's	54,342,361 / 17.8%
Number/percentage of T's	100,163,858 / 32.81%
Number/percentage of G's	69,599,266 / 22.8%
Number/percentage of N's	34,982 / 0.01%
GC Percentage	40.6%

2.3. Coverage

Mean	0.0987

Standard Deviation	0.9887

2.4. Mapping Quality

Mean Mapping Quality	46.13

2.5. Mismatches and indels

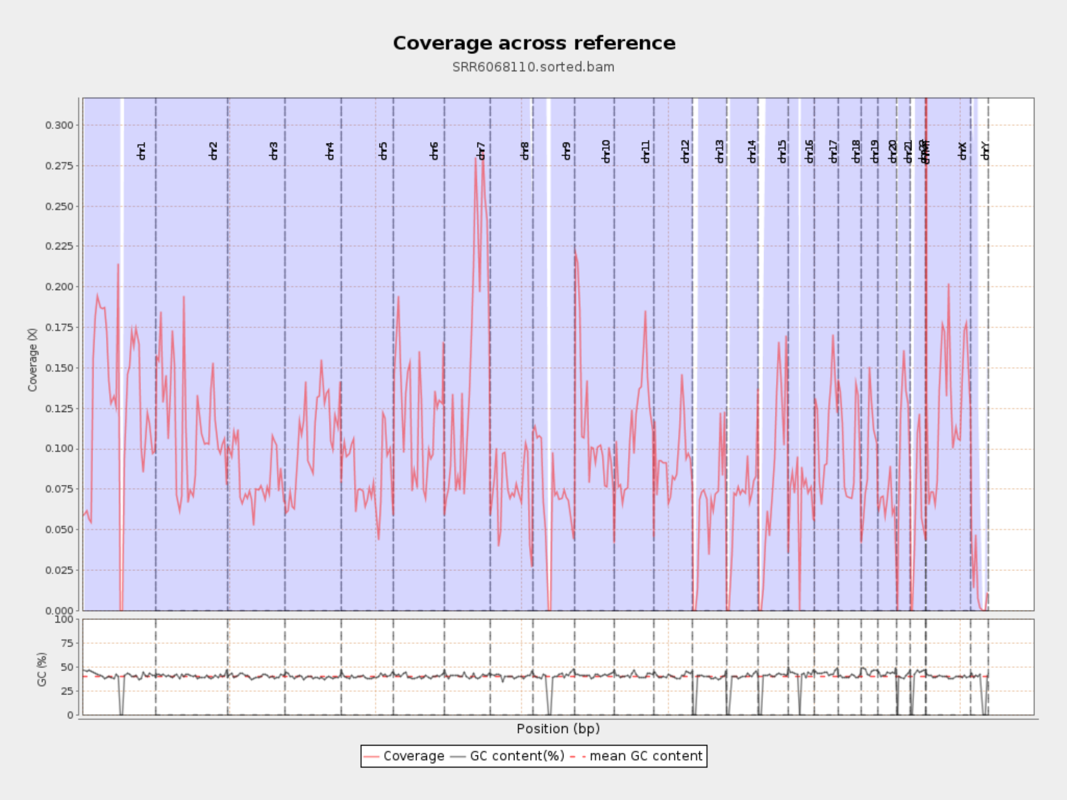
General error rate	0.55%
Mismatches	1,655,346
Insertions	19,859
Mapped reads with at least one insertion	0.42%
Deletions	66,237
Mapped reads with at least one deletion	1.38%
Homopolymer indels	45.06%

2.6. Chromosome stats

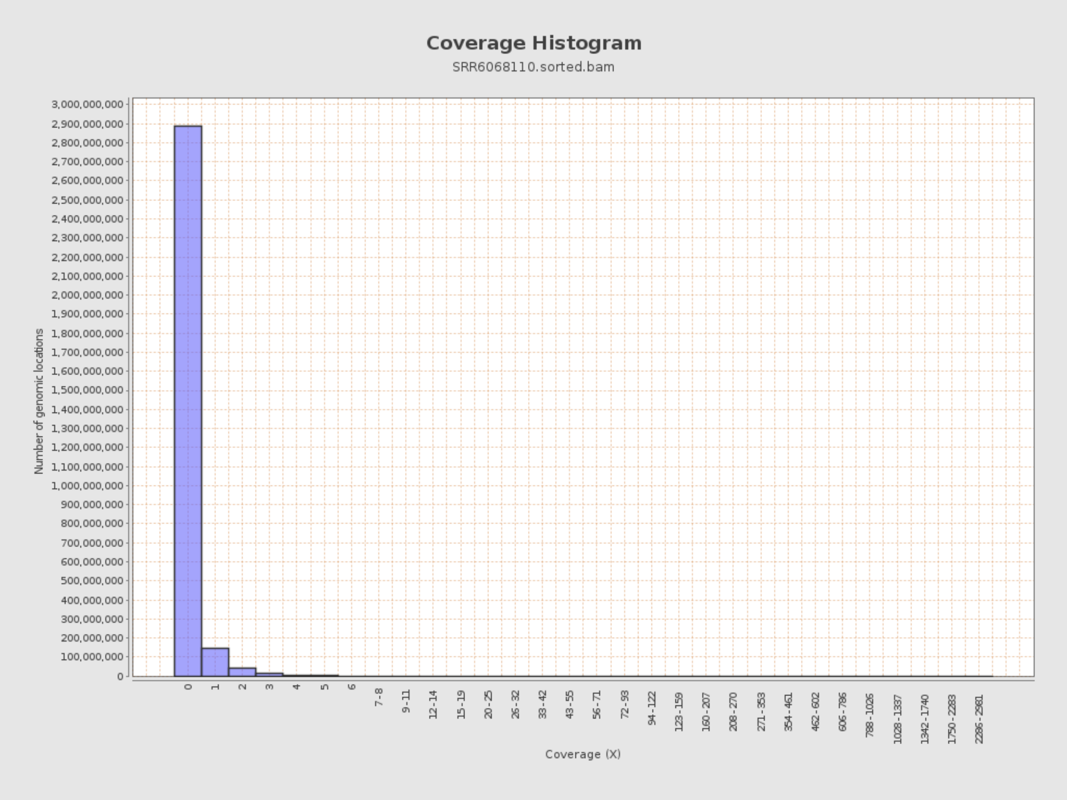
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31375801	0.1259	2.2091
chr2	243199373	28226464	0.1161	1.4974
chr3	198022430	16323251	0.0824	0.3967
chr4	191154276	20543418	0.1075	0.4998
chr5	180915260	15000411	0.0829	0.4058
chr6	171115067	20877168	0.122	0.657
chr7	159138663	24133918	0.1517	0.9735

chr8	146364022	10774602	0.0736	1.2847
chr9	141213431	9824216	0.0696	0.7208
chr10	135534747	15602492	0.1151	0.6769
chr11	135006516	15032841	0.1113	0.6539
chr12	133851895	12607091	0.0942	0.4707
chr13	115169878	7393778	0.0642	0.4038
chr14	107349540	6874820	0.064	0.4152
chr15	102531392	8560345	0.0835	0.4444
chr16	90354753	6238478	0.069	0.4152
chr17	81195210	9435368	0.1162	0.5217
chr18	78077248	7835197	0.1004	1.3614
chr19	59128983	5695540	0.0963	1.3504
chr20	63025520	4200202	0.0666	0.4004
chr21	48129895	5140769	0.1068	0.4787
chr22	51304566	2975227	0.058	0.322
chrMT	16571	500003	30.1734	18.7097
chrX	155270560	19391385	0.1249	0.6049
chrY	59373566	855627	0.0144	0.4603

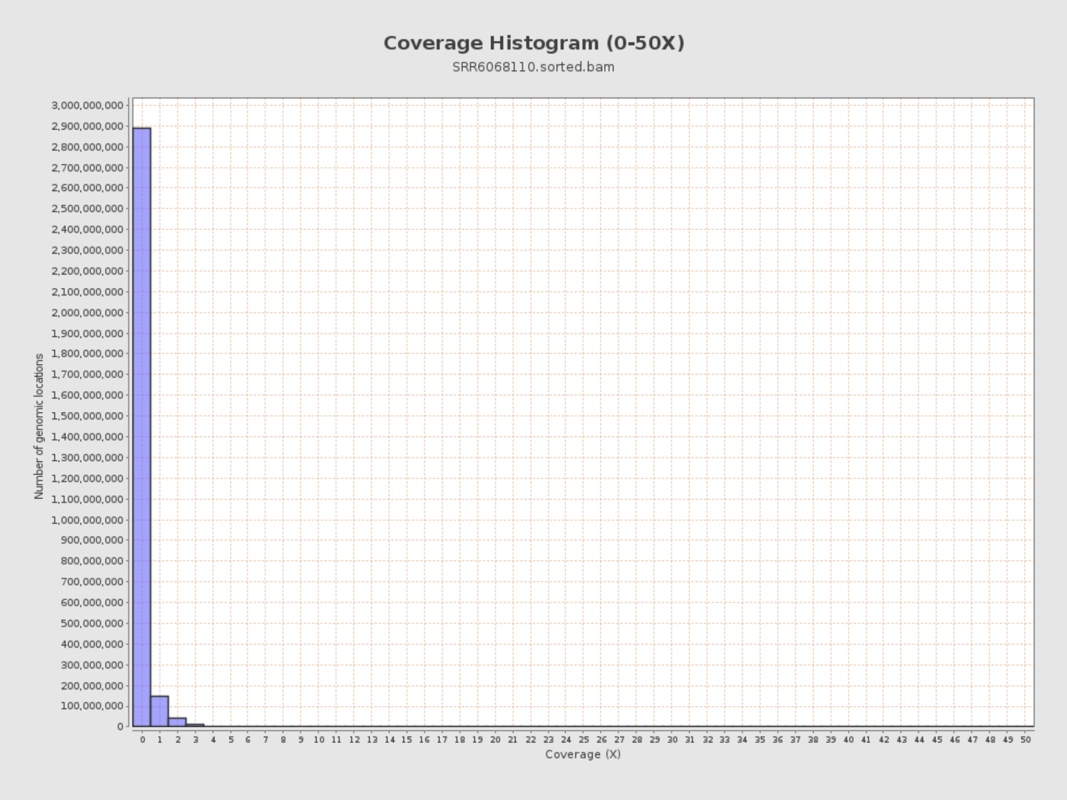
3. Results : Coverage across reference



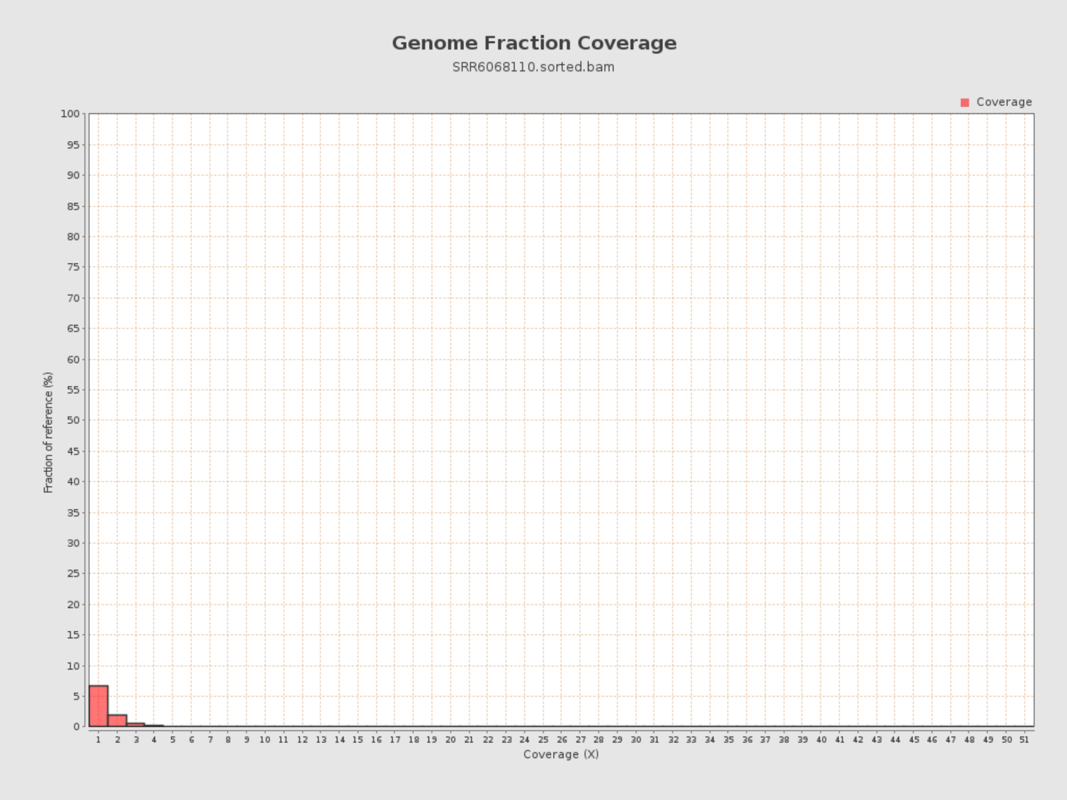
4. Results : Coverage Histogram



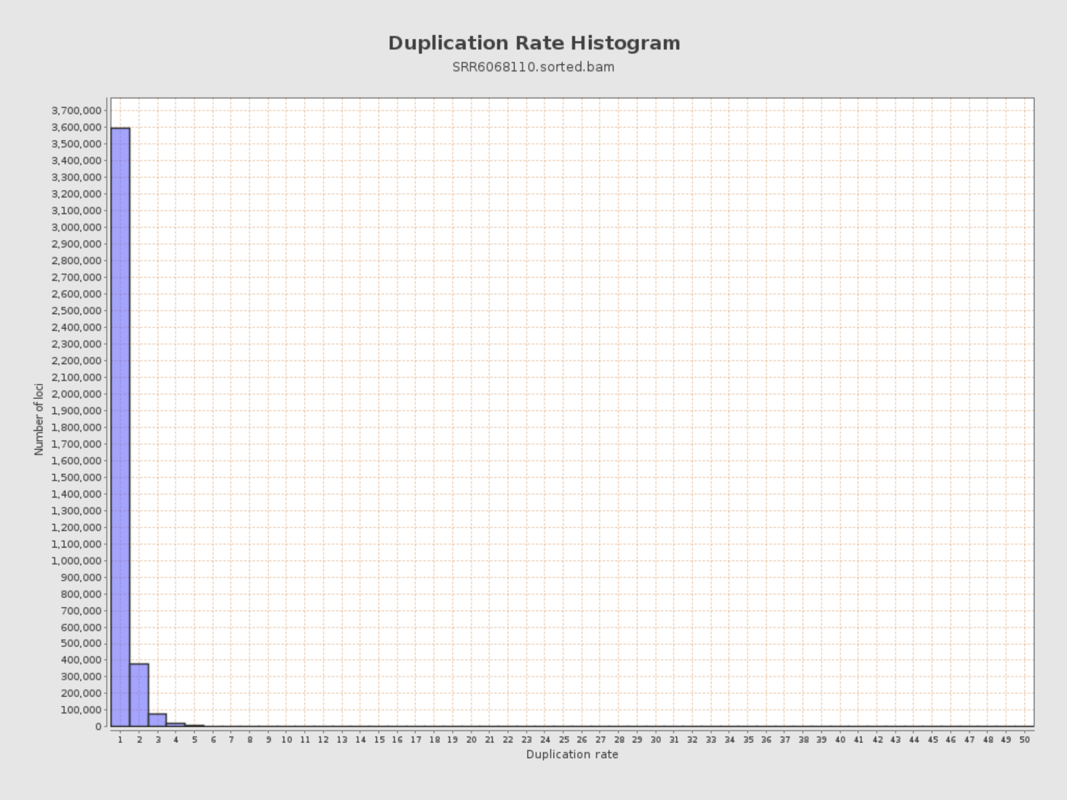
5. Results : Coverage Histogram (0-50X)



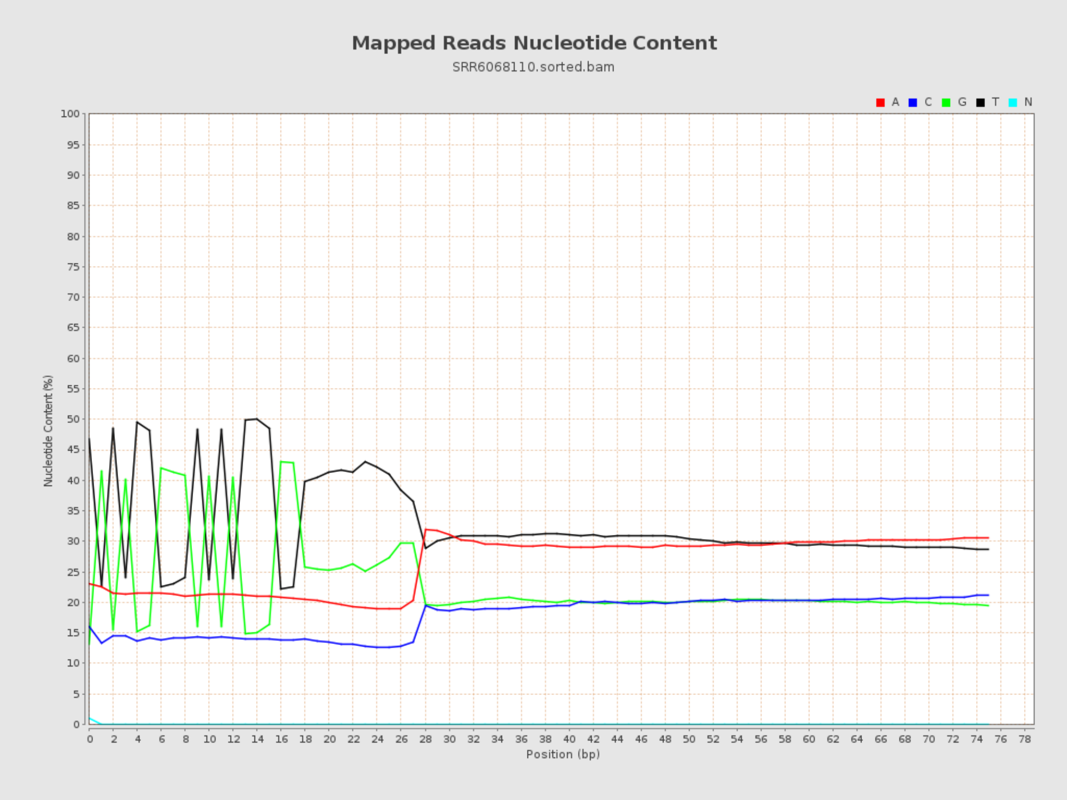
6. Results : Genome Fraction Coverage



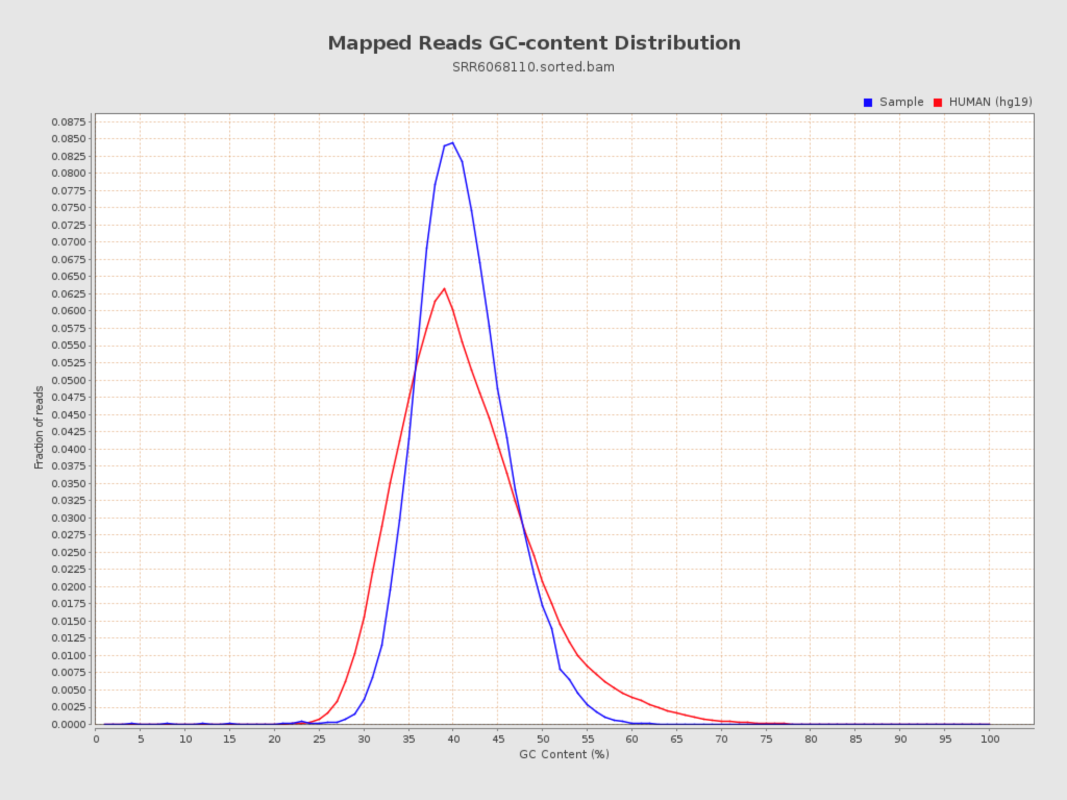
7. Results : Duplication Rate Histogram



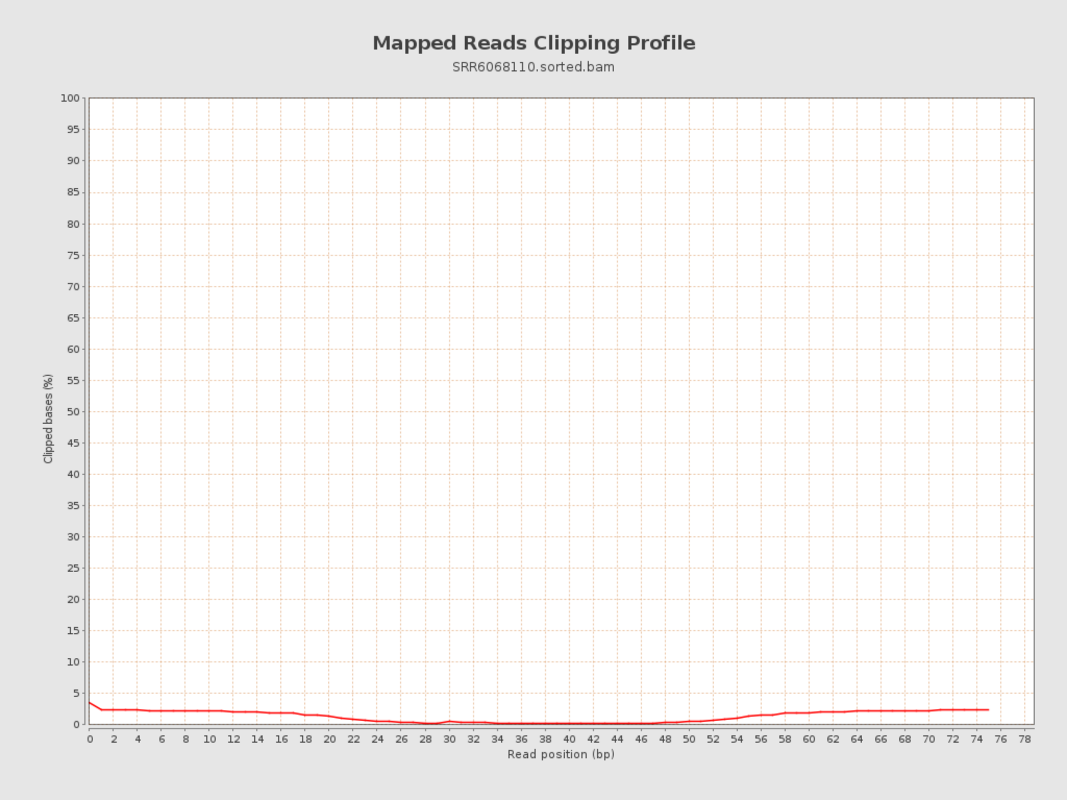
8. Results : Mapped Reads Nucleotide Content



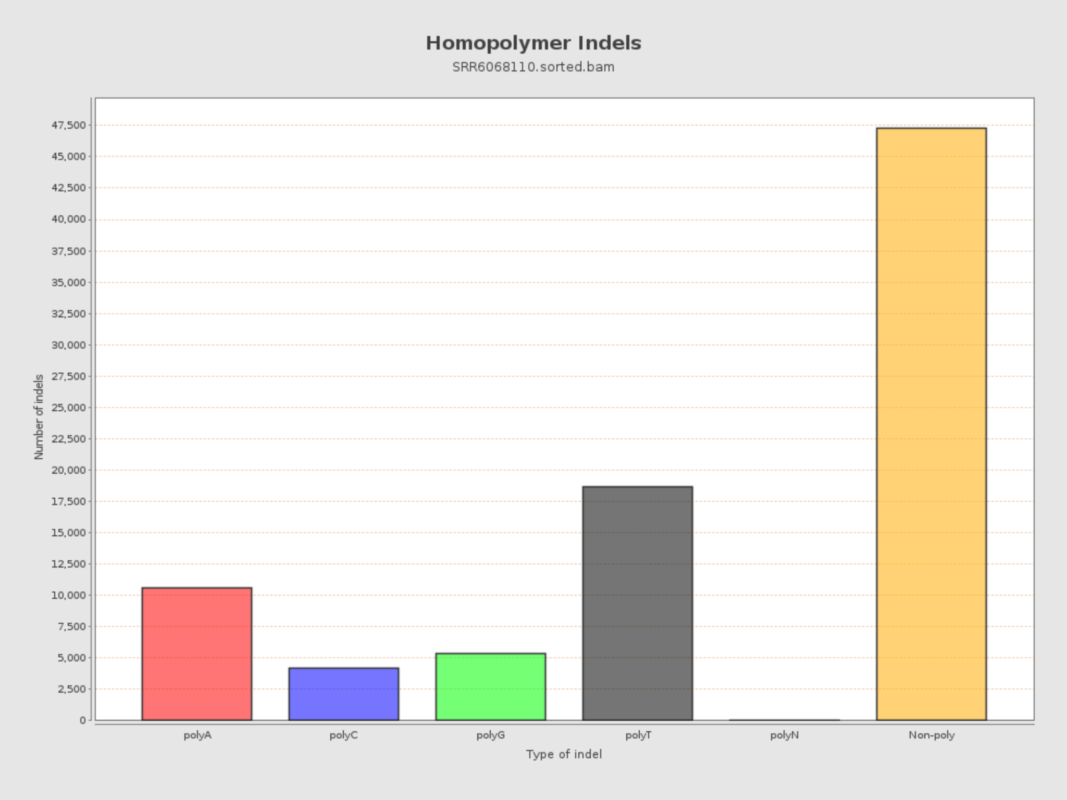
9. Results : Mapped Reads GC-content Distribution



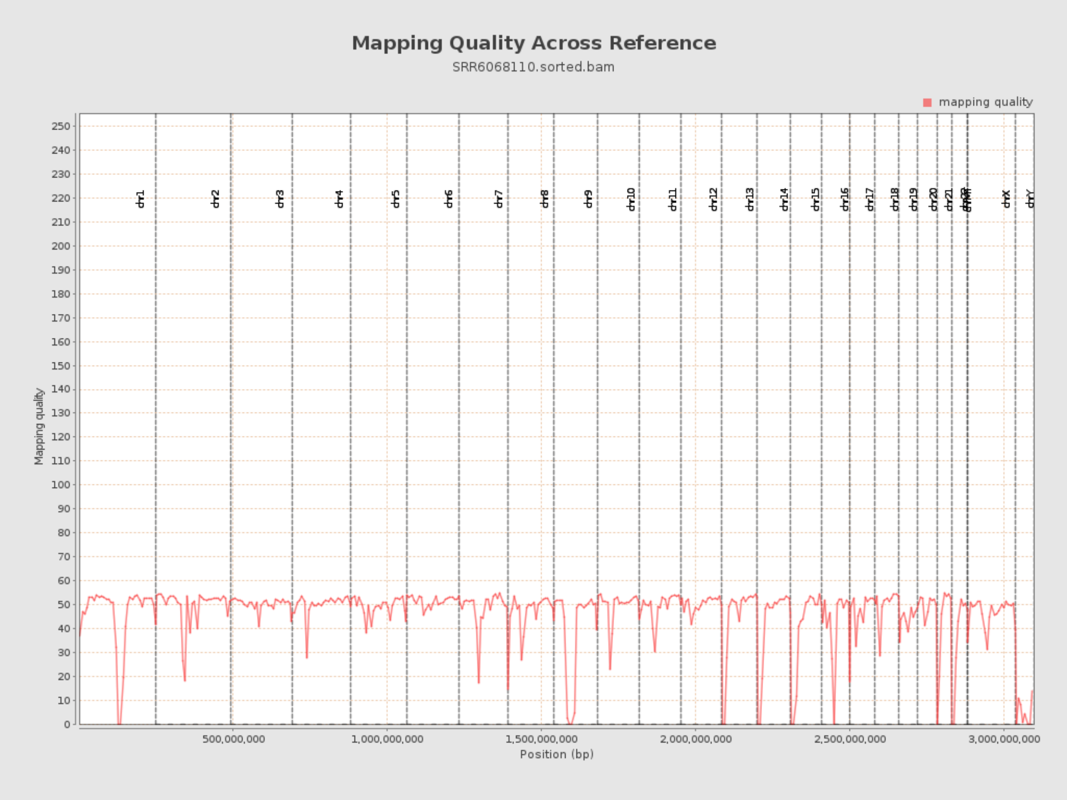
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram