Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:33:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068091.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_SRR6068091 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068091.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:33:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068091.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,471,626
Mapped reads	3,759,810 / 84.08%
Unmapped reads	711,816 / 15.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,082 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	1,420,930 / 31.78%
Duplication rate	20.93%
Clipped reads	2,198,277 / 49.16%

2.2. ACGT Content

Number/percentage of A's	58,912,292 / 24.96%
Number/percentage of C's	42,889,235 / 18.17%
Number/percentage of T's	76,669,041 / 32.49%
Number/percentage of G's	57,516,879 / 24.37%
Number/percentage of N's	25,316 / 0.01%
GC Percentage	42.54%

2.3. Coverage

Mean	0.0763

Standard Deviation	0.9925

2.4. Mapping Quality

Mean Mapping Quality	44.97

2.5. Mismatches and indels

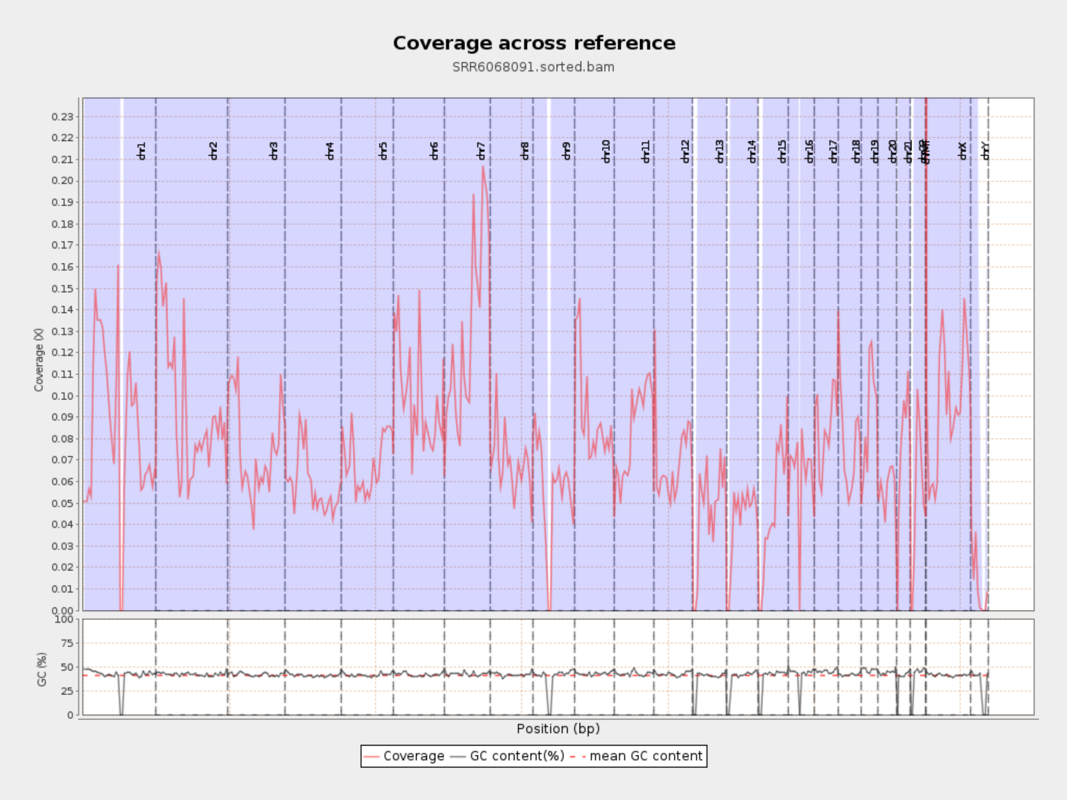
General error rate	0.66%
Mismatches	1,518,309
Insertions	14,646
Mapped reads with at least one insertion	0.39%
Deletions	78,256
Mapped reads with at least one deletion	2.05%
Homopolymer indels	45.06%

2.6. Chromosome stats

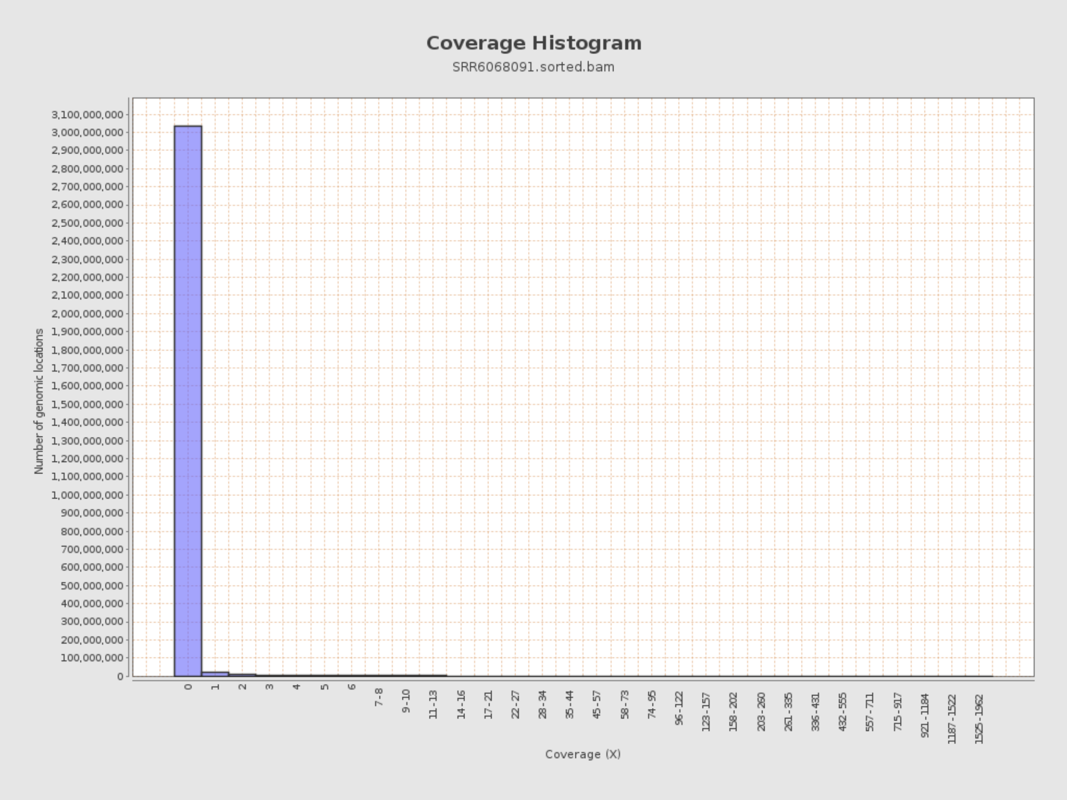
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21177082	0.085	1.6445
chr2	243199373	23222124	0.0955	1.3028
chr3	198022430	15006330	0.0758	0.7807
chr4	191154276	11227046	0.0587	0.6821
chr5	180915260	12515141	0.0692	0.7333
chr6	171115067	17033013	0.0995	0.972
chr7	159138663	20903872	0.1314	1.3742

chr8	146364022	9942992	0.0679	1.0221
chr9	141213431	7859843	0.0557	0.7343
chr10	135534747	12247243	0.0904	0.9413
chr11	135006516	11362055	0.0842	0.8846
chr12	133851895	9330703	0.0697	0.7595
chr13	115169878	5320631	0.0462	0.5974
chr14	107349540	4563749	0.0425	0.5794
chr15	102531392	4719969	0.046	0.6206
chr16	90354753	5613167	0.0621	0.7212
chr17	81195210	6973116	0.0859	0.8636
chr18	78077248	6071233	0.0778	1.1987
chr19	59128983	5354281	0.0906	1.291
chr20	63025520	3600991	0.0571	0.687
chr21	48129895	3620227	0.0752	0.7929
chr22	51304566	2689073	0.0524	0.6398
chrMT	16571	344818	20.8085	18.2032
chrX	155270560	14730613	0.0949	0.8897
chrY	59373566	723927	0.0122	0.3753

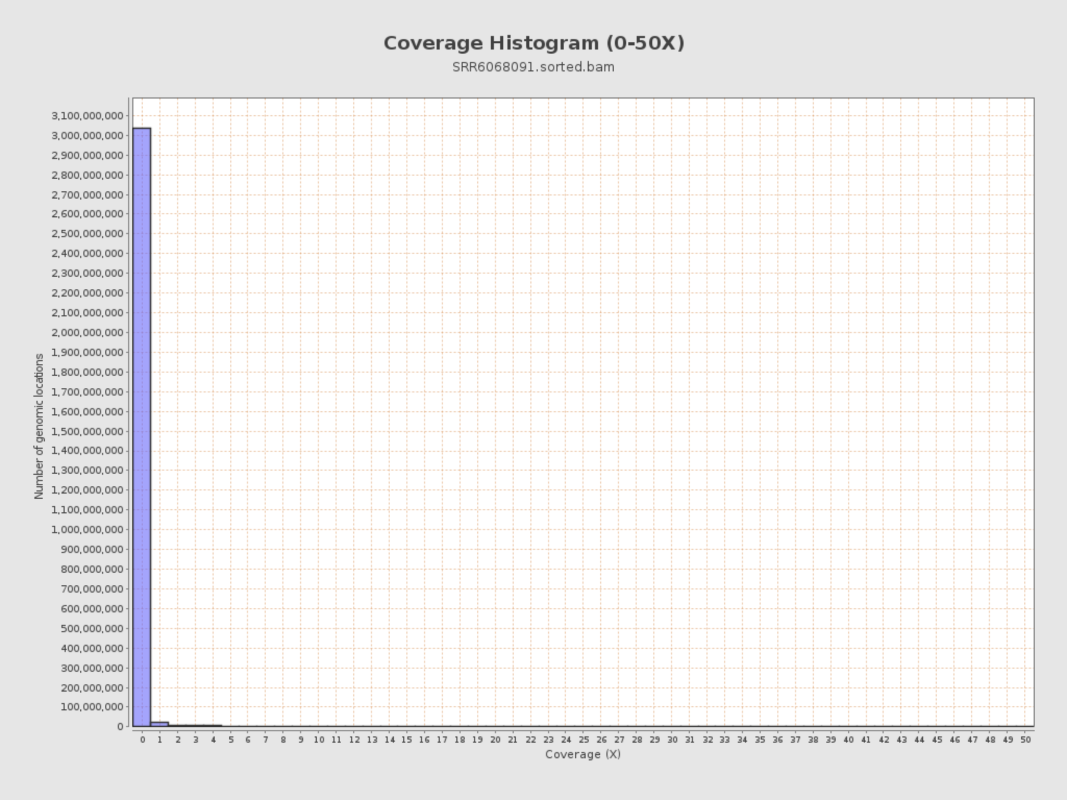
3. Results : Coverage across reference



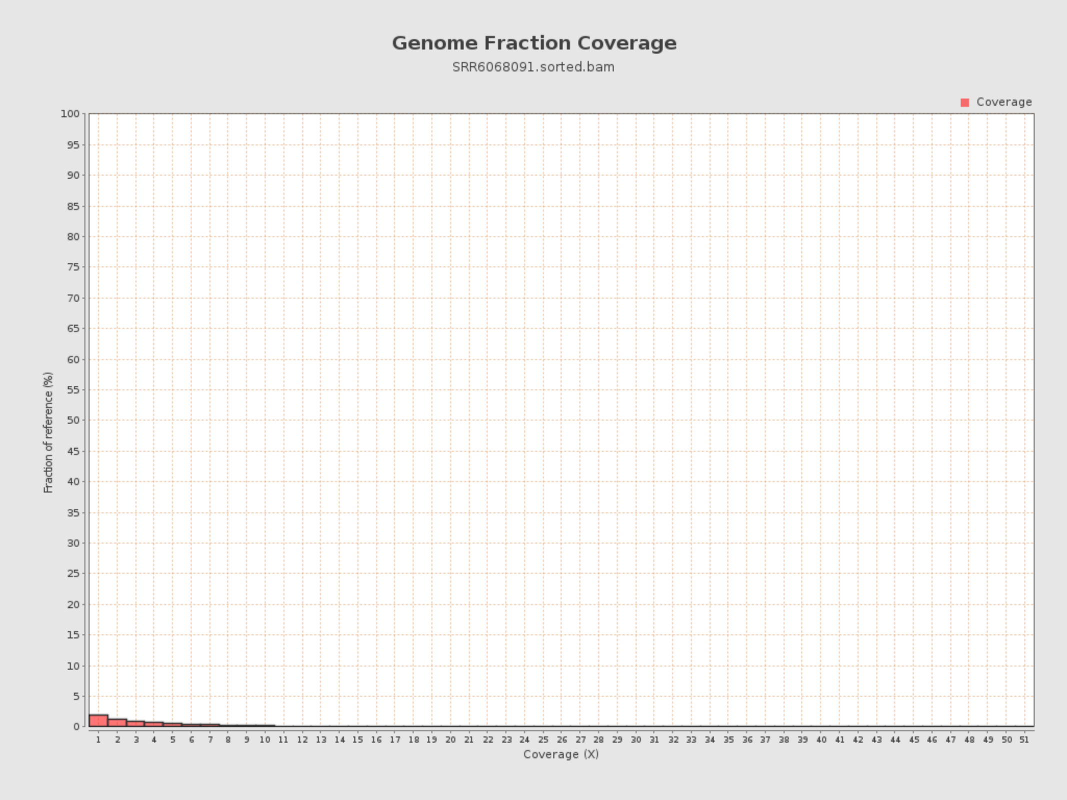
4. Results : Coverage Histogram



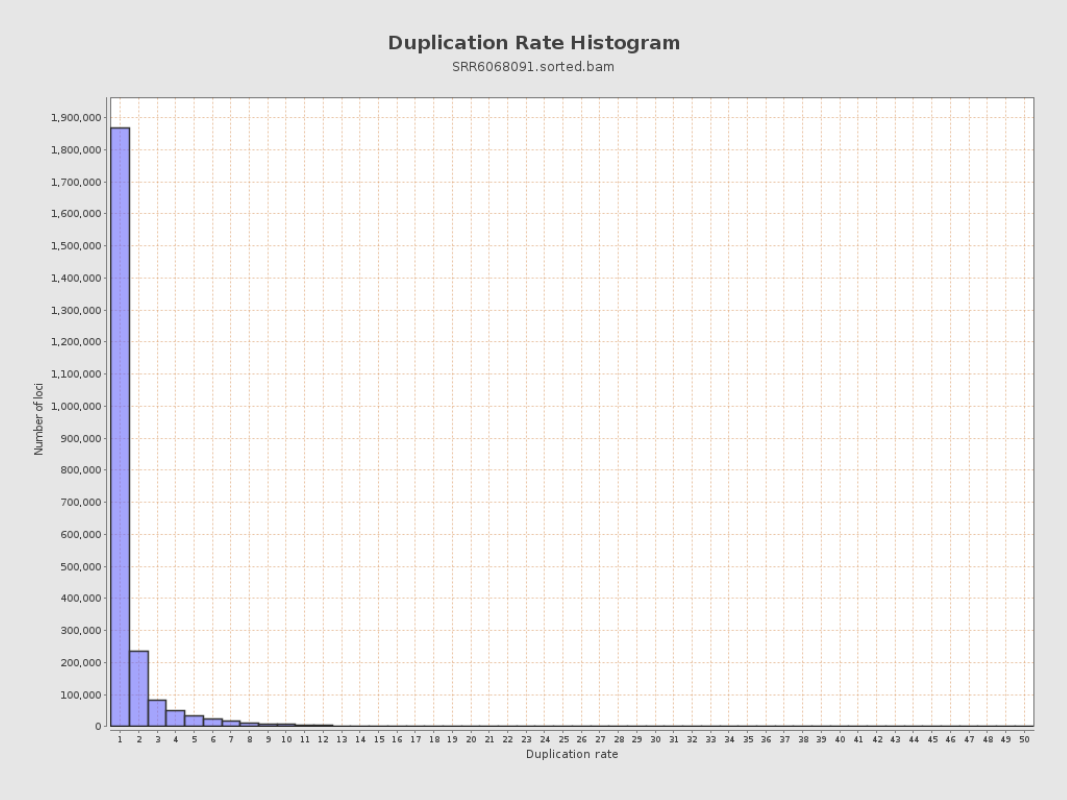
5. Results : Coverage Histogram (0-50X)



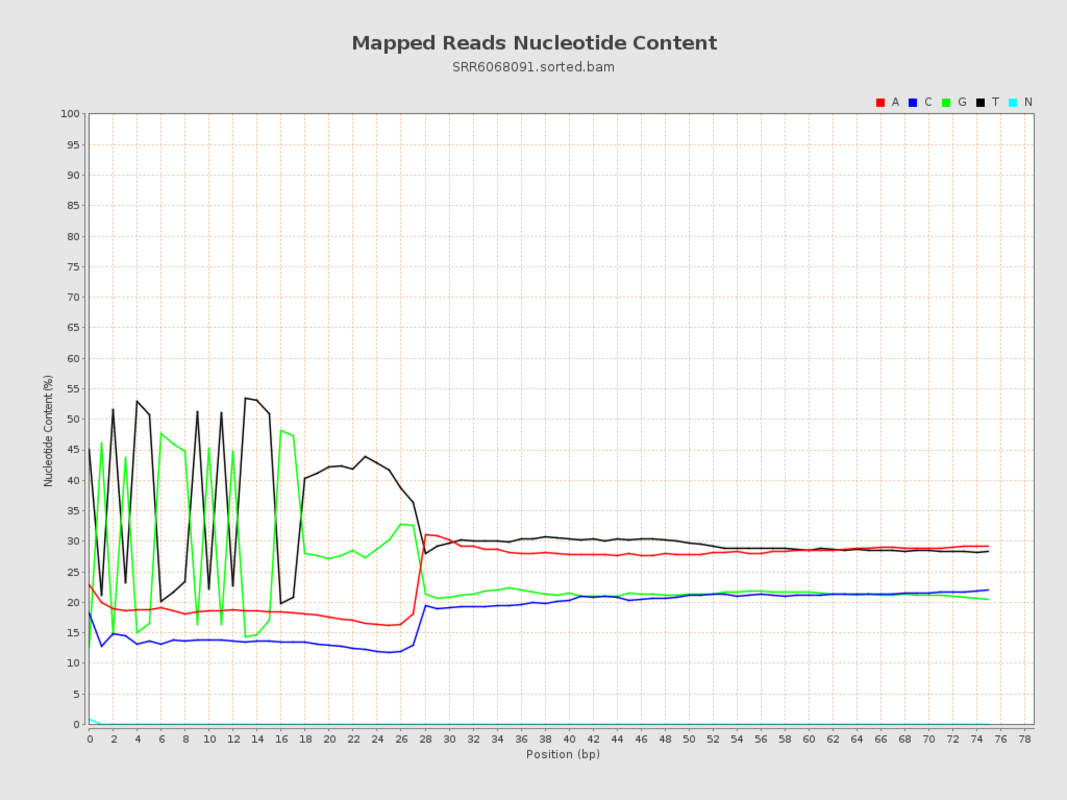
6. Results : Genome Fraction Coverage



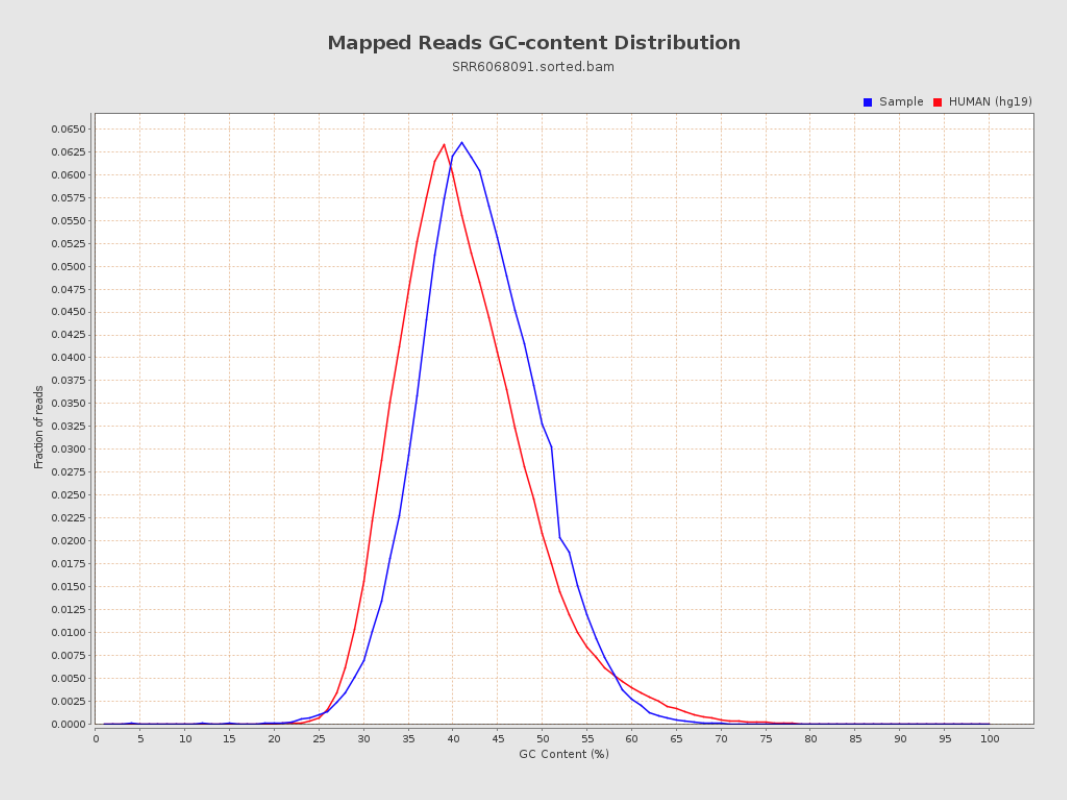
7. Results : Duplication Rate Histogram



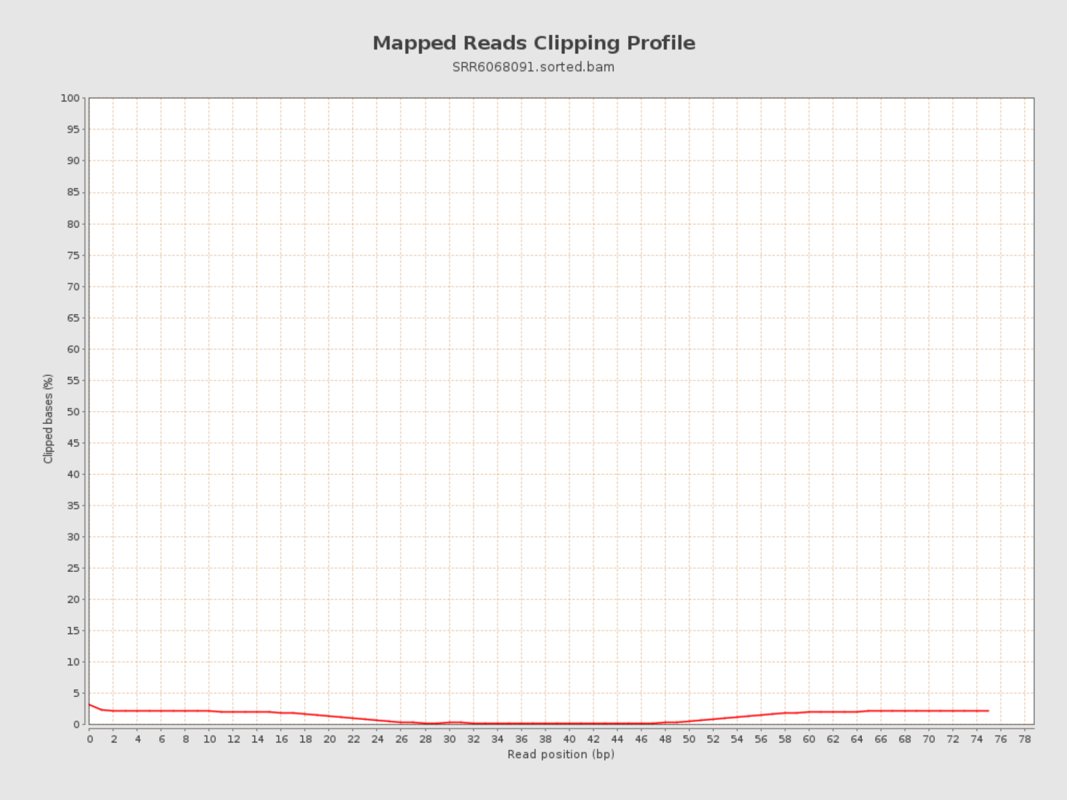
8. Results : Mapped Reads Nucleotide Content



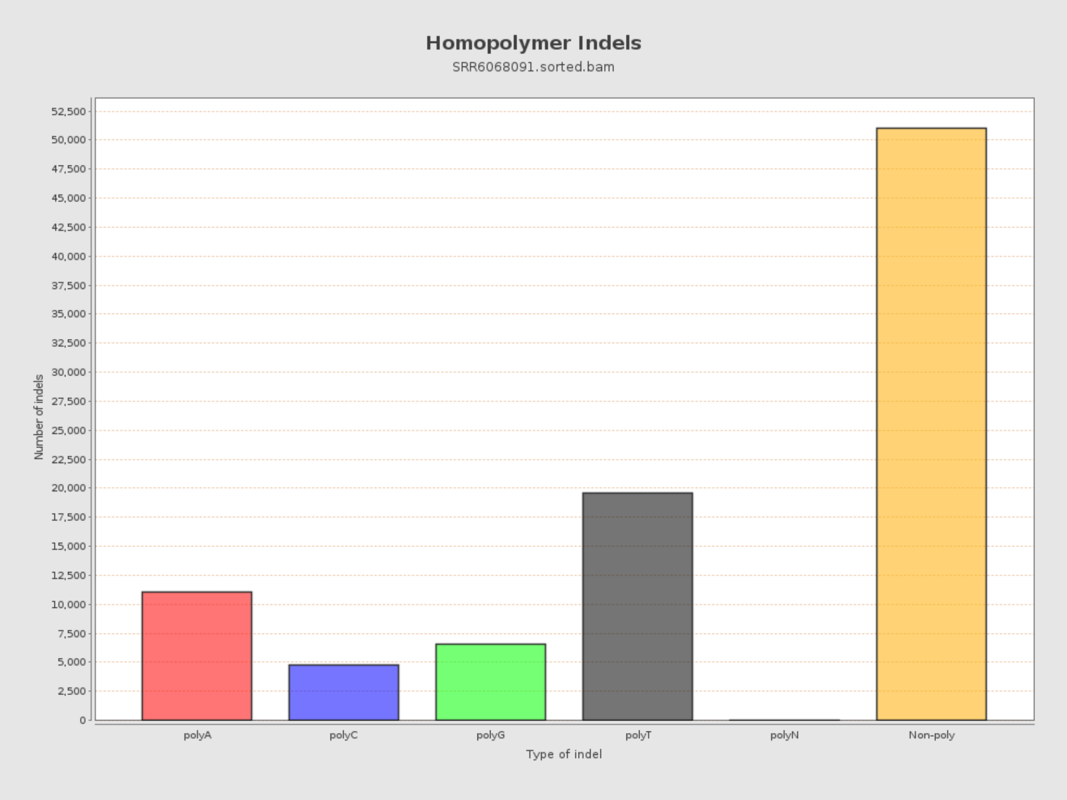
9. Results : Mapped Reads GC-content Distribution



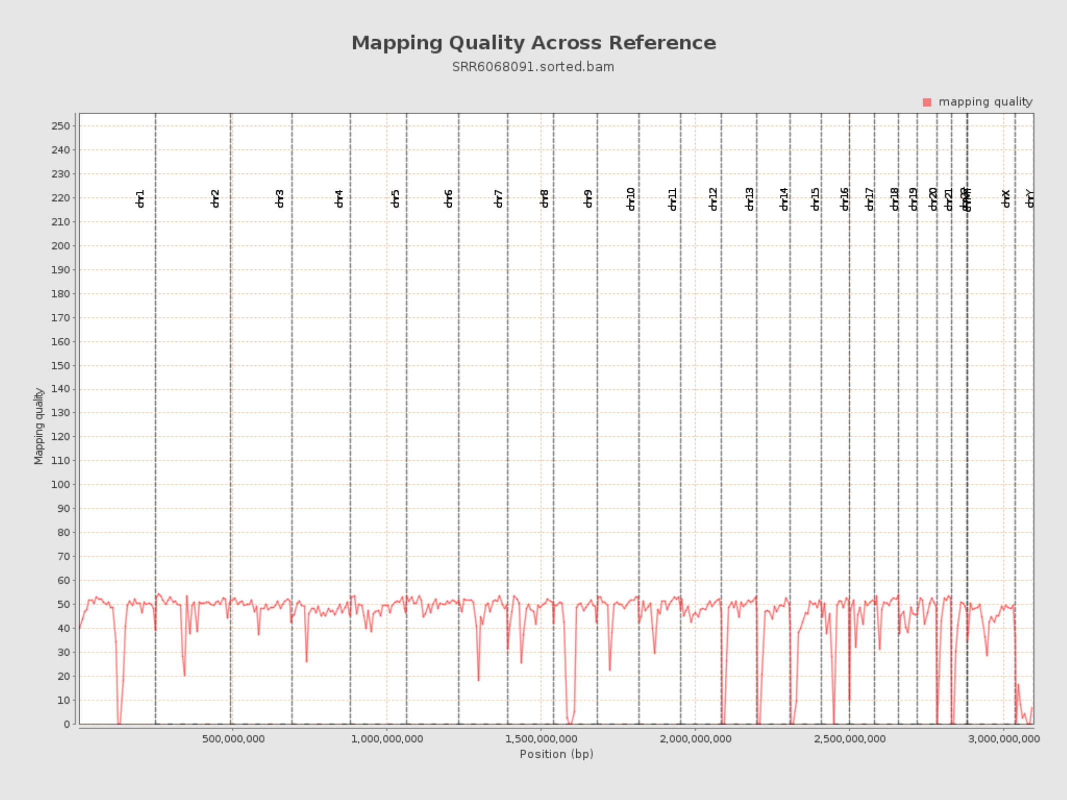
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram