Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:46:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081118.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_SRR3081118 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081118.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:46:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081118.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,689,121
Mapped reads	2,502,429 / 93.06%
Unmapped reads	186,692 / 6.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,895 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	109,222 / 4.06%
Duplication rate	3.51%
Clipped reads	914,807 / 34.02%

2.2. ACGT Content

Number/percentage of A's	49,012,915 / 28.54%
Number/percentage of C's	32,350,524 / 18.84%
Number/percentage of T's	53,805,431 / 31.33%
Number/percentage of G's	36,568,553 / 21.29%
Number/percentage of N's	1,972 / 0%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0555

Standard Deviation	0.4146

2.4. Mapping Quality

Mean Mapping Quality	47.06

2.5. Mismatches and indels

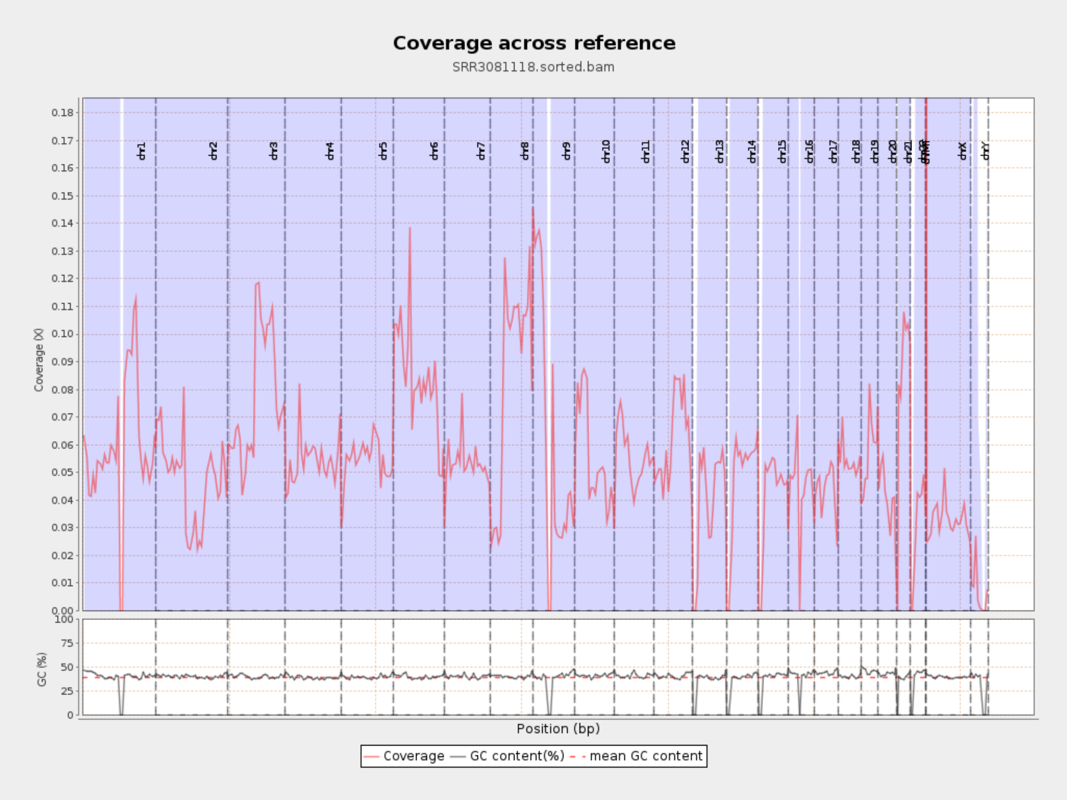
General error rate	0.86%
Mismatches	1,460,314
Insertions	12,982
Mapped reads with at least one insertion	0.51%
Deletions	37,151
Mapped reads with at least one deletion	1.47%
Homopolymer indels	48.3%

2.6. Chromosome stats

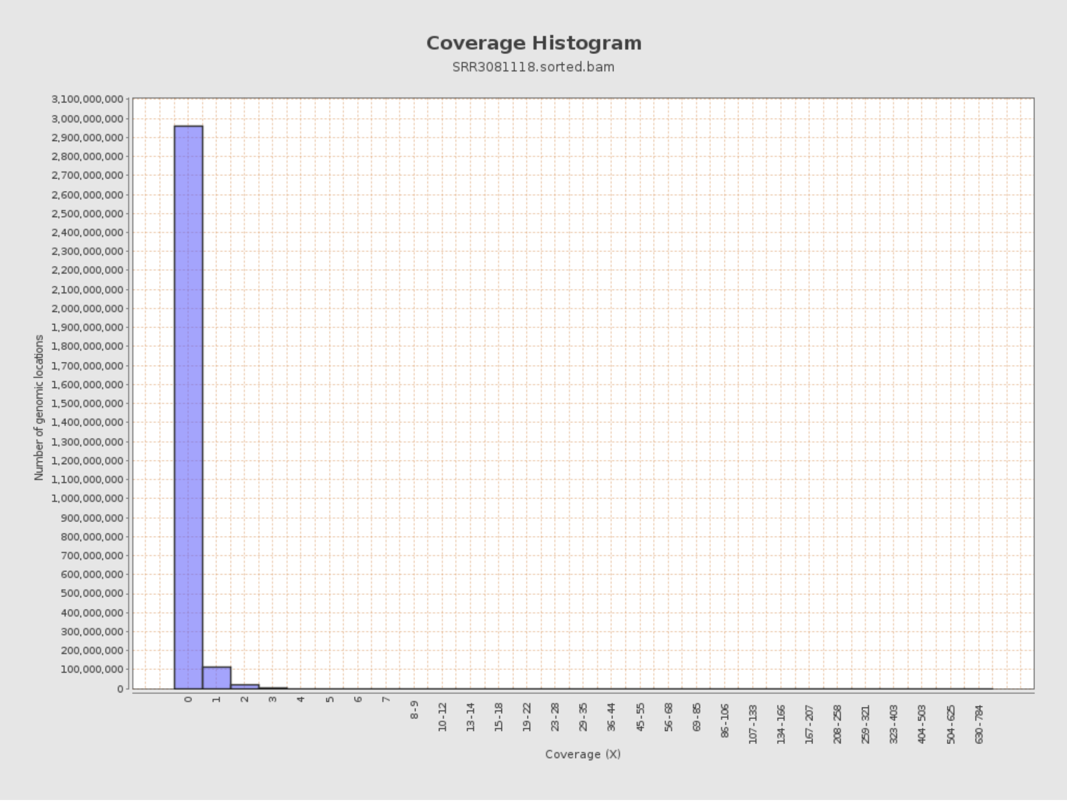
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14683265	0.0589	0.5796
chr2	243199373	11510876	0.0473	0.4253
chr3	198022430	15195165	0.0767	0.3323
chr4	191154276	10406245	0.0544	0.3098
chr5	180915260	9861559	0.0545	0.28
chr6	171115067	14461443	0.0845	0.5104
chr7	159138663	8474144	0.0533	0.4627

chr8	146364022	12374977	0.0845	0.4945
chr9	141213431	8632525	0.0611	0.503
chr10	135534747	7532143	0.0556	0.3981
chr11	135006516	7554943	0.056	0.3669
chr12	133851895	8261475	0.0617	0.3106
chr13	115169878	4536910	0.0394	0.2342
chr14	107349540	5081690	0.0473	0.3243
chr15	102531392	4163197	0.0406	0.2429
chr16	90354753	3926607	0.0435	0.3102
chr17	81195210	3615070	0.0445	0.2581
chr18	78077248	4259075	0.0545	0.9459
chr19	59128983	3416469	0.0578	0.4528
chr20	63025520	2629175	0.0417	0.2625
chr21	48129895	4130925	0.0858	0.4105
chr22	51304566	1537055	0.03	0.2023
chrMT	16571	24113	1.4551	1.5696
chrX	155270560	5116608	0.033	0.2516
chrY	59373566	420963	0.0071	0.1956

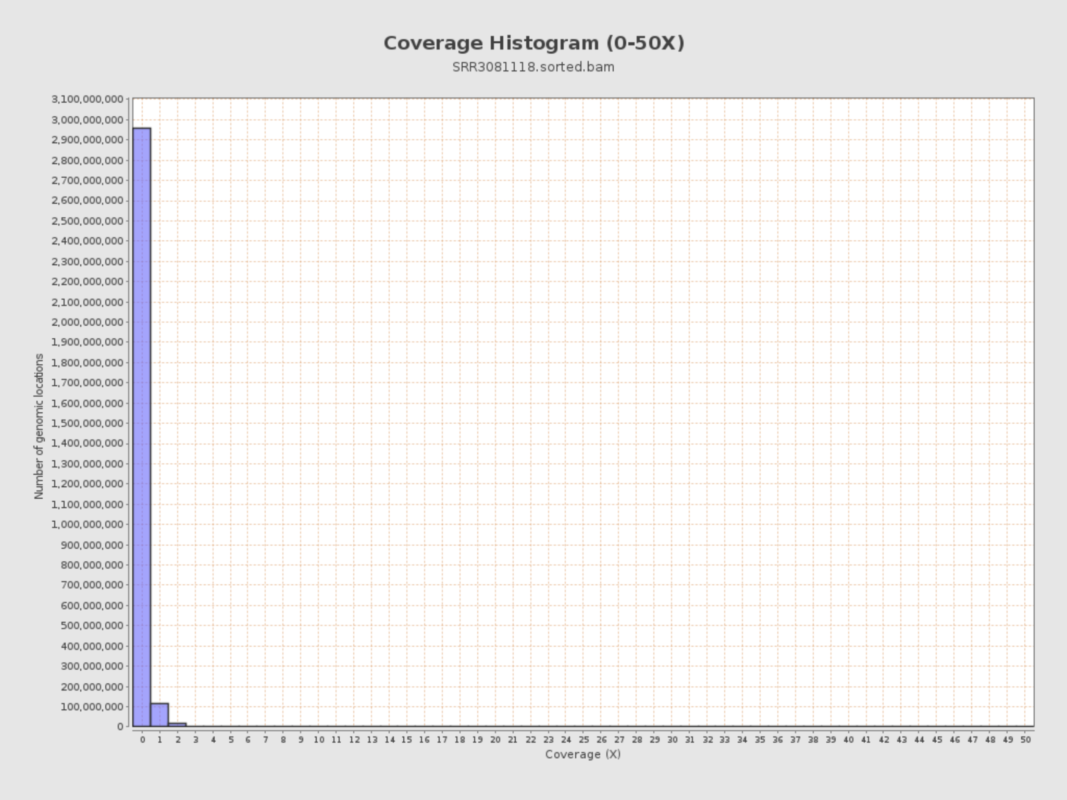
3. Results : Coverage across reference



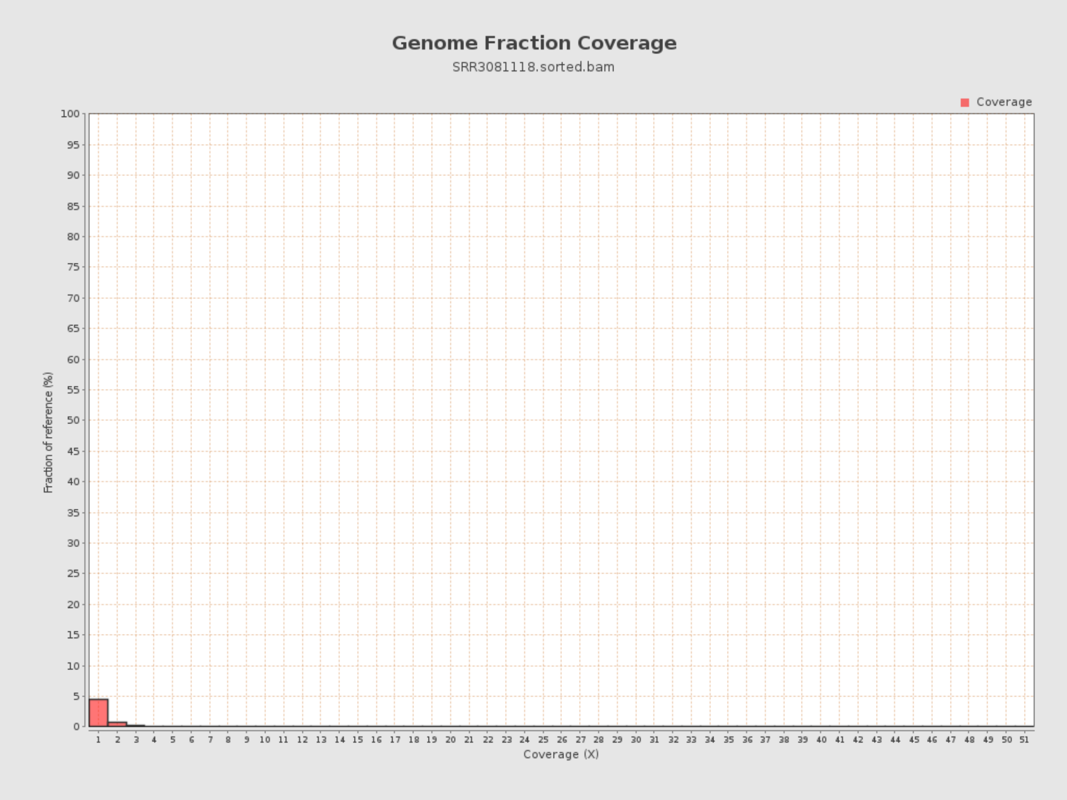
4. Results : Coverage Histogram



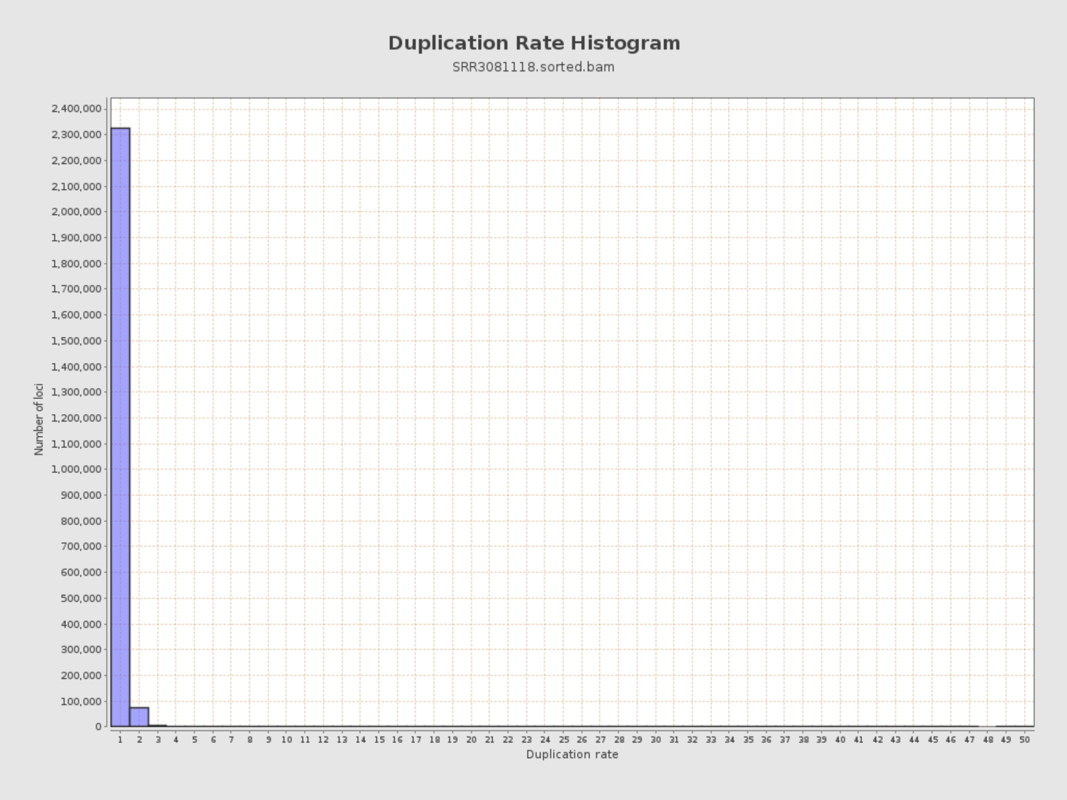
5. Results : Coverage Histogram (0-50X)



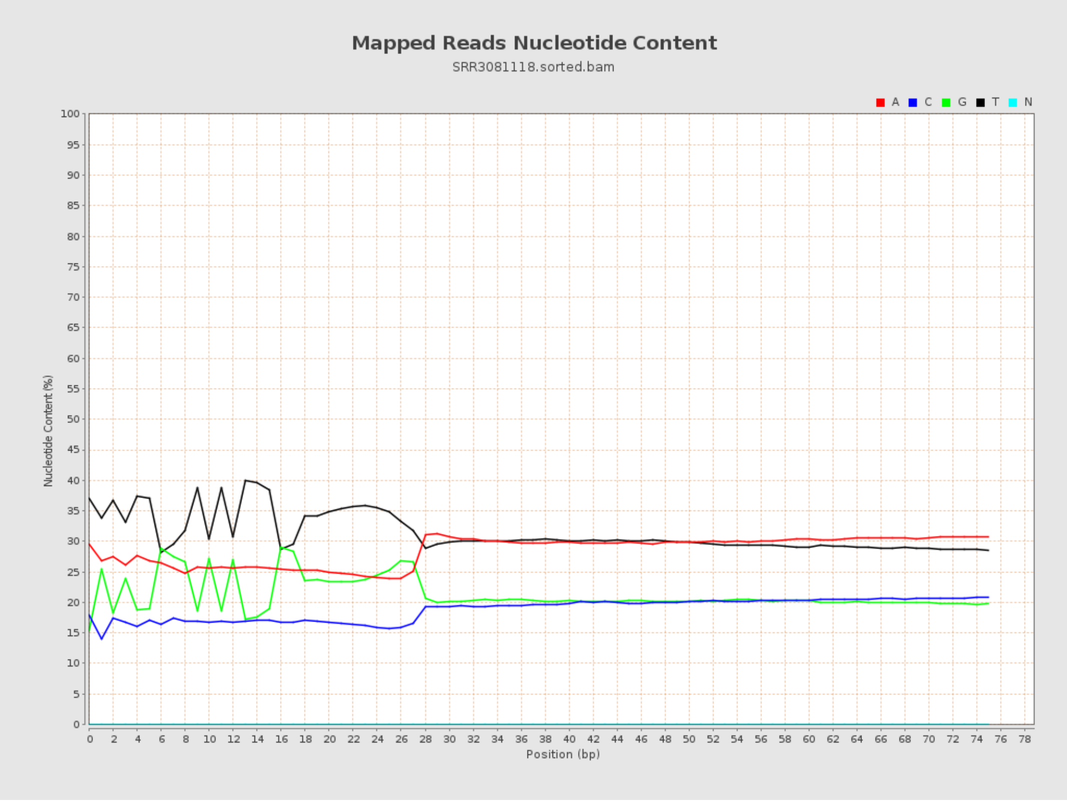
6. Results : Genome Fraction Coverage



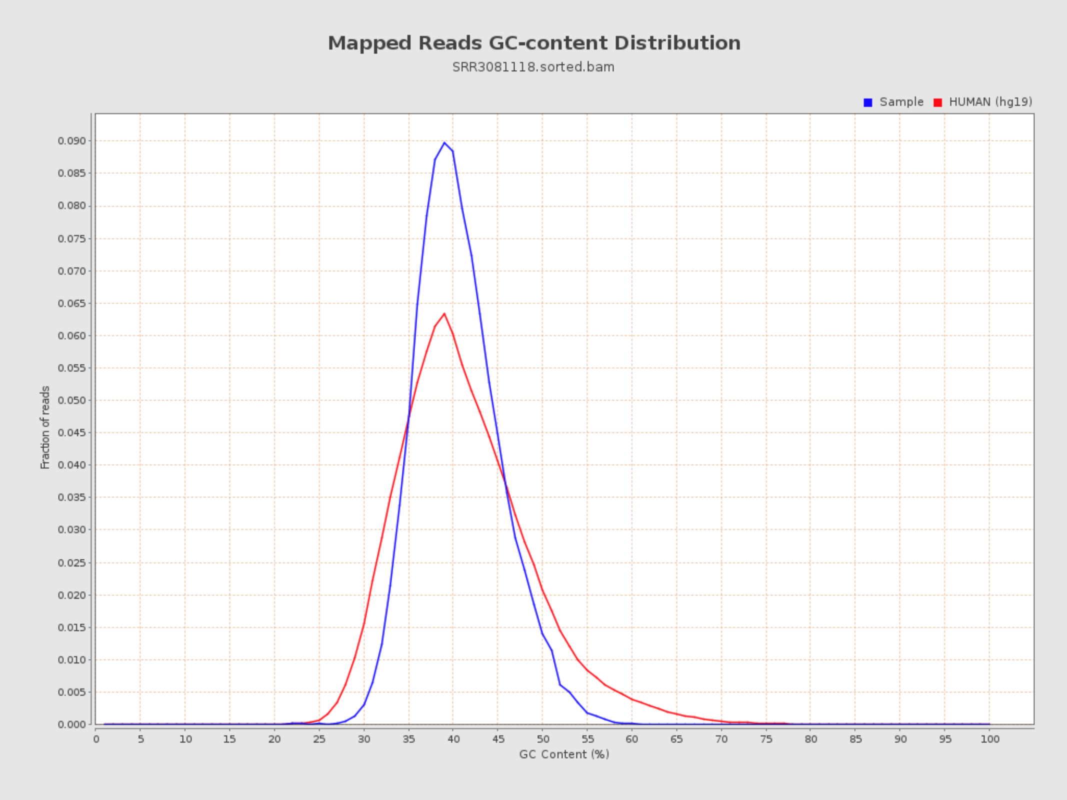
7. Results : Duplication Rate Histogram



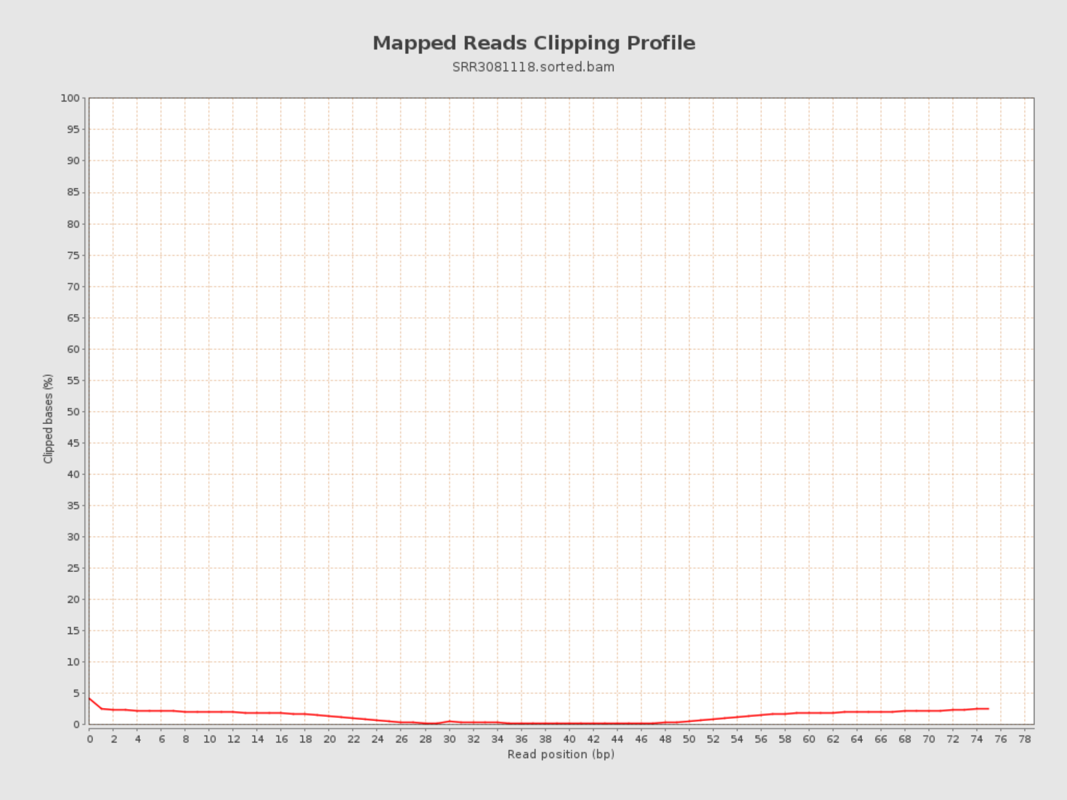
8. Results : Mapped Reads Nucleotide Content



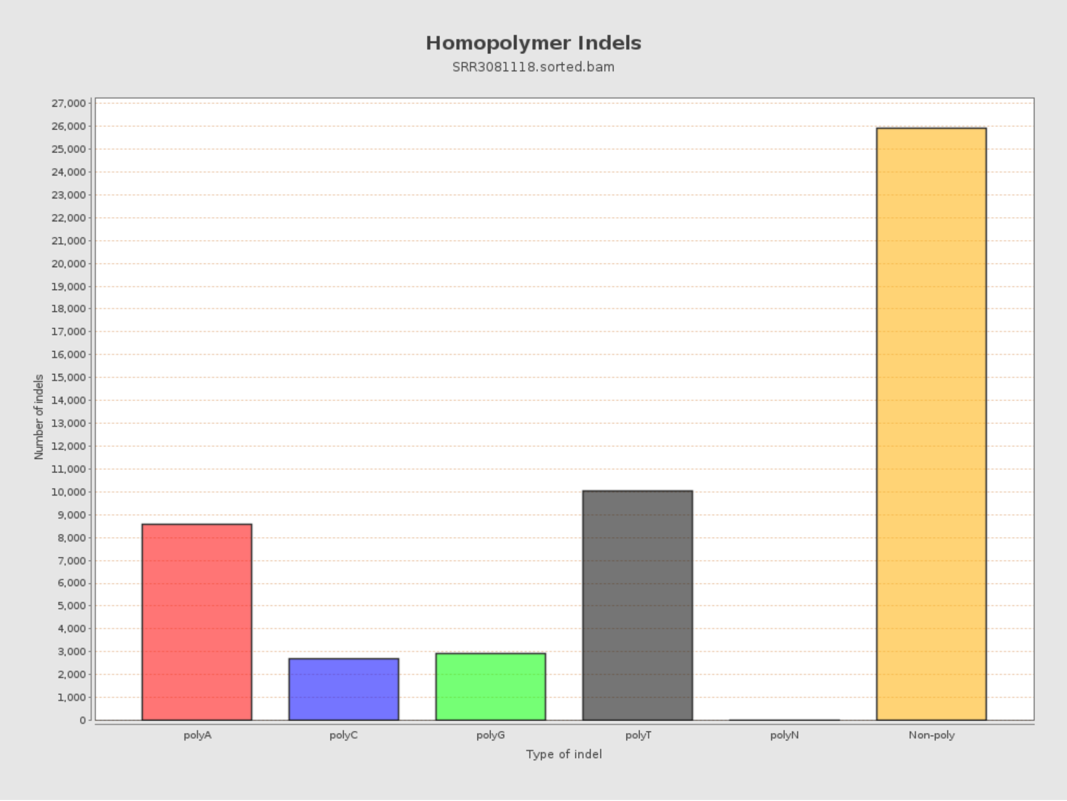
9. Results : Mapped Reads GC-content Distribution



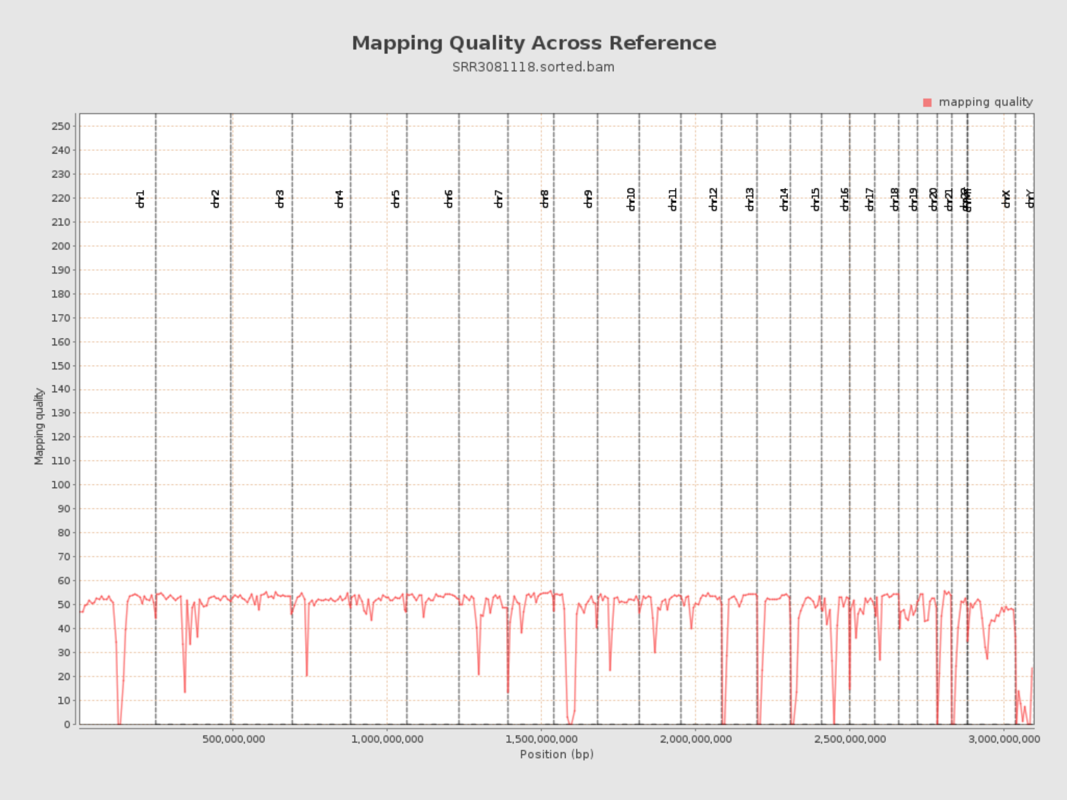
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram