Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:19:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082718.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_SRR3082718 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082718.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:19:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082718.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,341,860
Mapped reads	3,055,666 / 91.44%
Unmapped reads	286,194 / 8.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,949 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	137,510 / 4.11%
Duplication rate	3.02%
Clipped reads	1,540,442 / 46.1%

2.2. ACGT Content

Number/percentage of A's	54,169,357 / 27%
Number/percentage of C's	34,536,054 / 17.21%
Number/percentage of T's	66,765,843 / 33.27%
Number/percentage of G's	45,134,833 / 22.49%
Number/percentage of N's	51,031 / 0.03%
GC Percentage	39.7%

2.3. Coverage

Mean	0.0648

Standard Deviation	0.6121

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

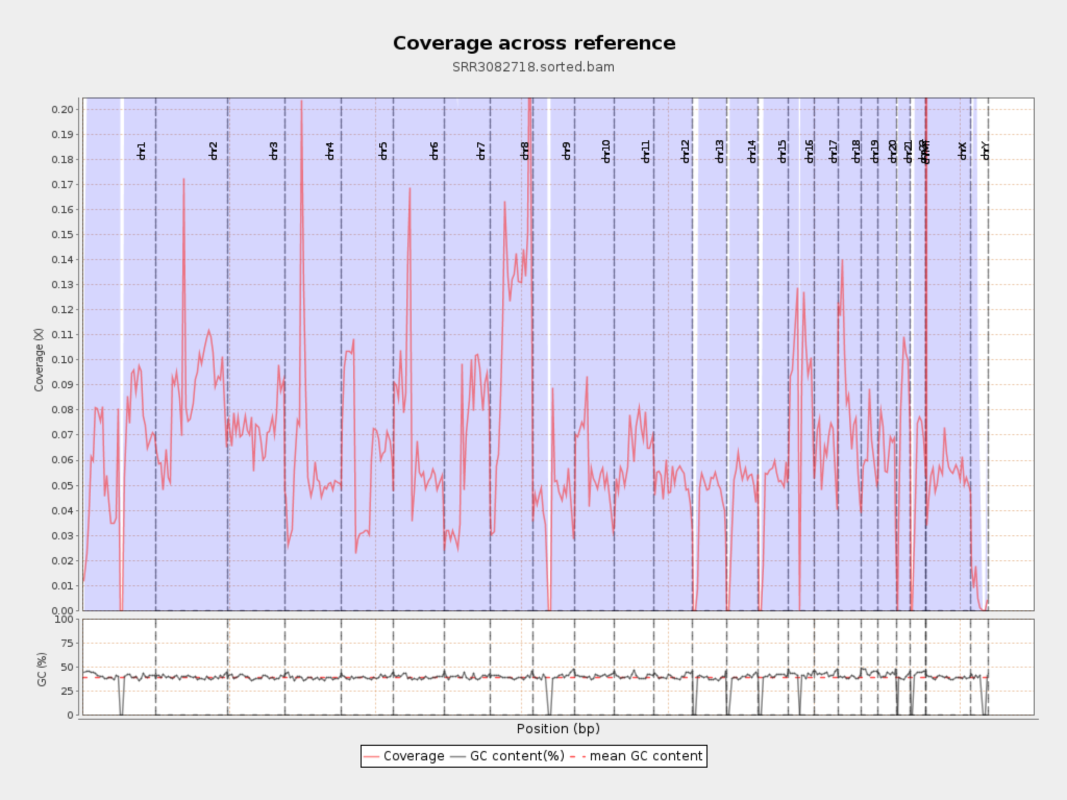
General error rate	0.94%
Mismatches	1,853,147
Insertions	18,796
Mapped reads with at least one insertion	0.61%
Deletions	49,696
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.81%

2.6. Chromosome stats

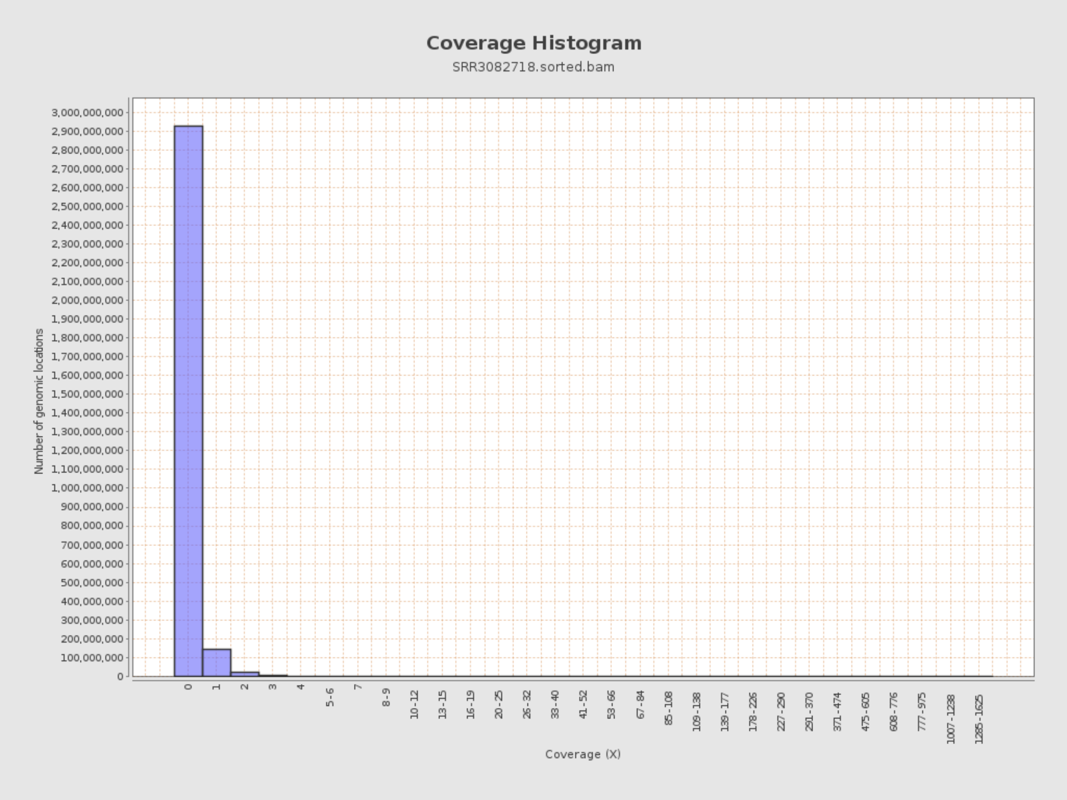
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15226333	0.0611	0.7634
chr2	243199373	21160922	0.087	1.0198
chr3	198022430	14567617	0.0736	0.3151
chr4	191154276	11640996	0.0609	0.303
chr5	180915260	11412007	0.0631	0.2946
chr6	171115067	12130563	0.0709	0.5704
chr7	159138663	10466175	0.0658	0.8379

chr8	146364022	17442275	0.1192	0.7184
chr9	141213431	6011253	0.0426	0.7862
chr10	135534747	7888834	0.0582	0.4641
chr11	135006516	8657118	0.0641	0.5745
chr12	133851895	6888624	0.0515	0.2856
chr13	115169878	4735448	0.0411	0.2299
chr14	107349540	4883893	0.0455	0.3572
chr15	102531392	4528669	0.0442	0.2412
chr16	90354753	8115400	0.0898	0.4015
chr17	81195210	5227780	0.0644	0.4204
chr18	78077248	6836708	0.0876	1.4469
chr19	59128983	3672518	0.0621	0.7096
chr20	63025520	4125033	0.0655	0.3291
chr21	48129895	3659559	0.076	0.3398
chr22	51304566	2609181	0.0509	0.2586
chrMT	16571	36001	2.1725	2.8418
chrX	155270560	8439753	0.0544	0.4226
chrY	59373566	374116	0.0063	0.1368

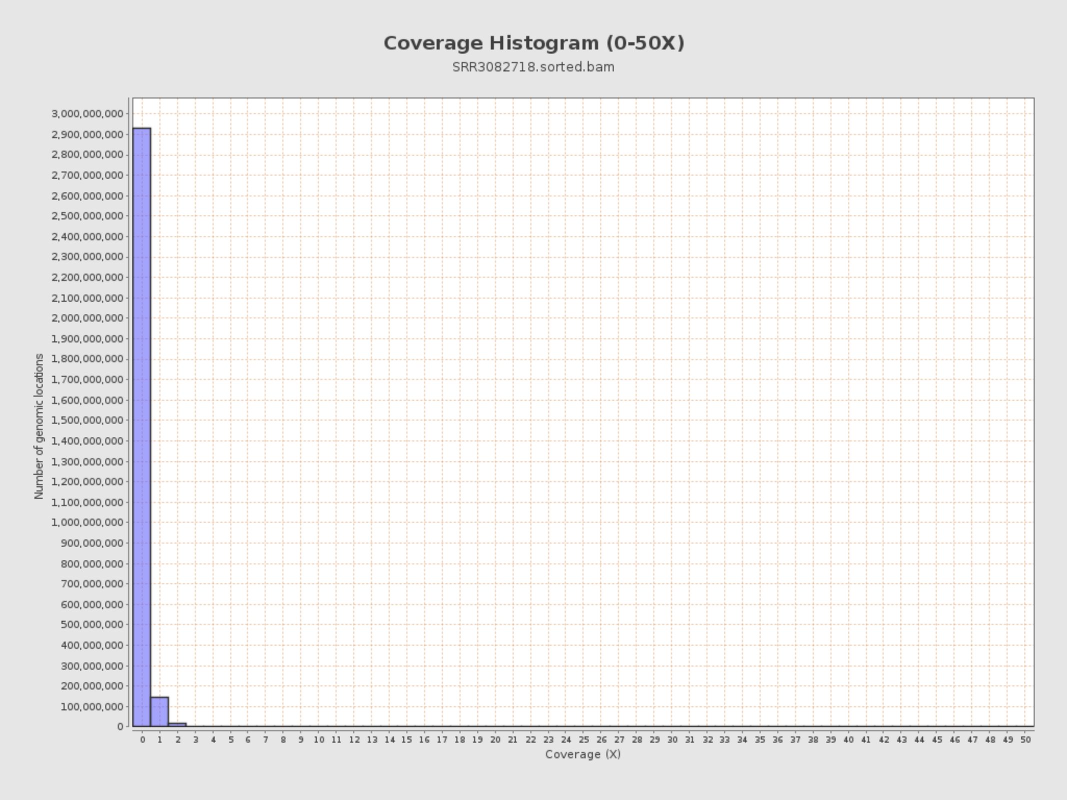
3. Results : Coverage across reference



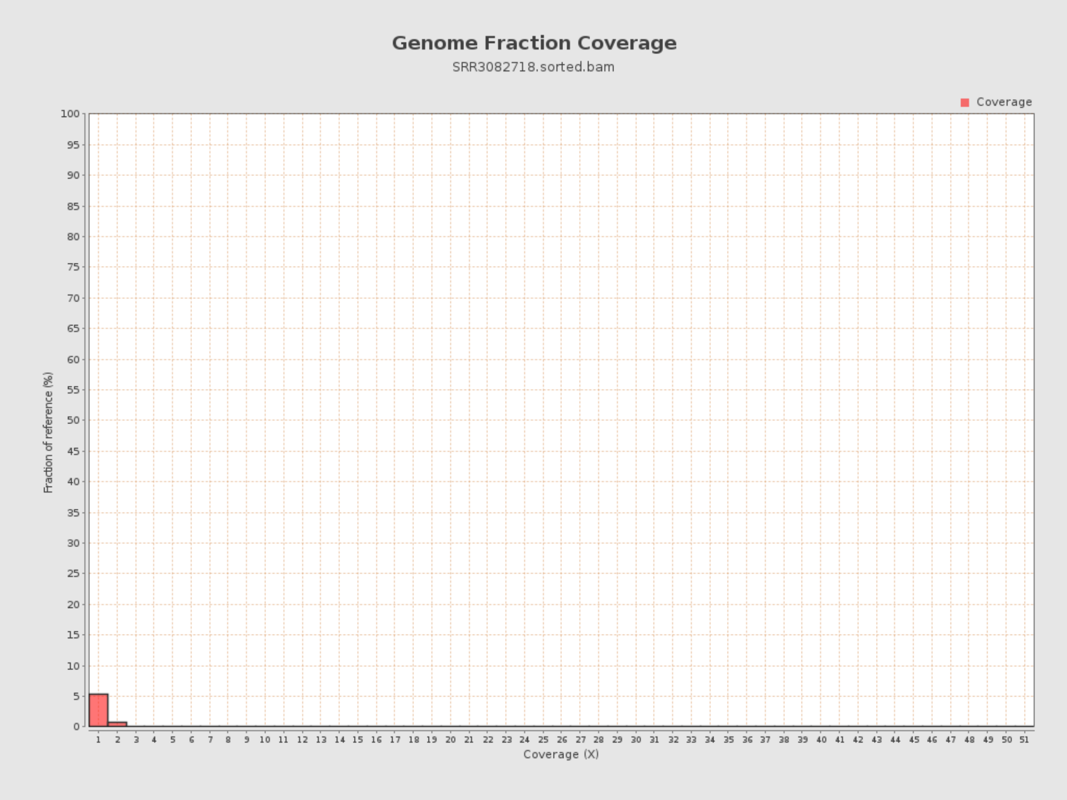
4. Results : Coverage Histogram



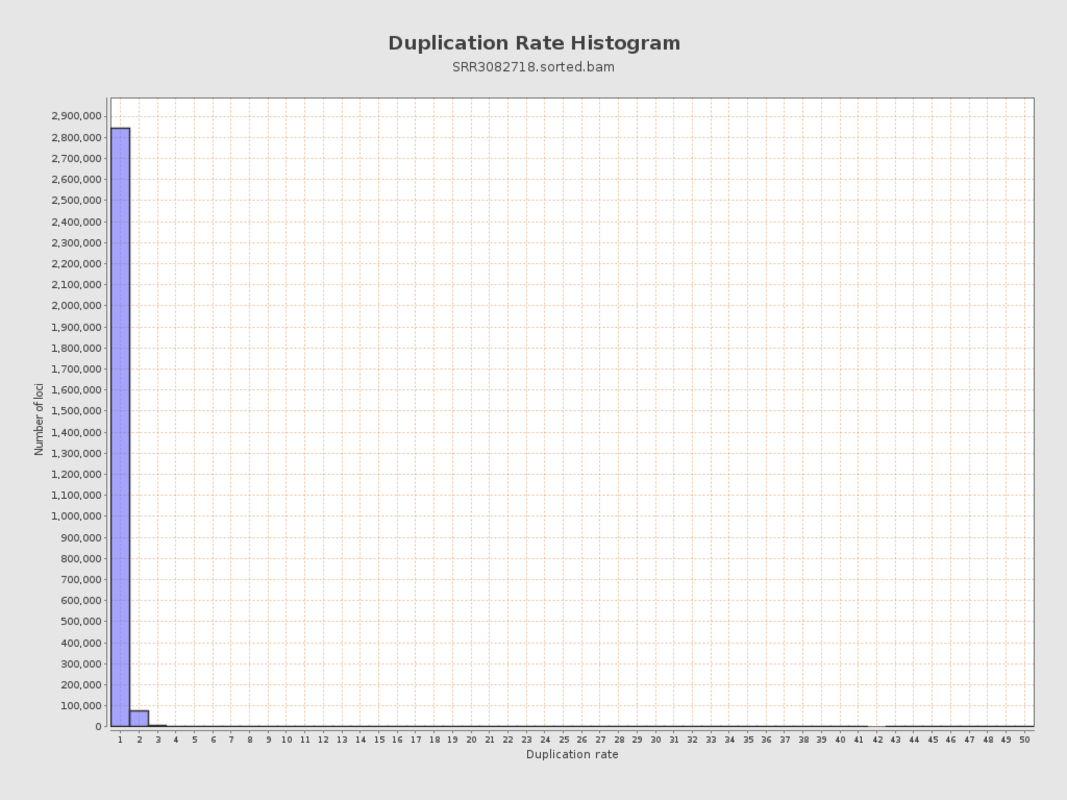
5. Results : Coverage Histogram (0-50X)



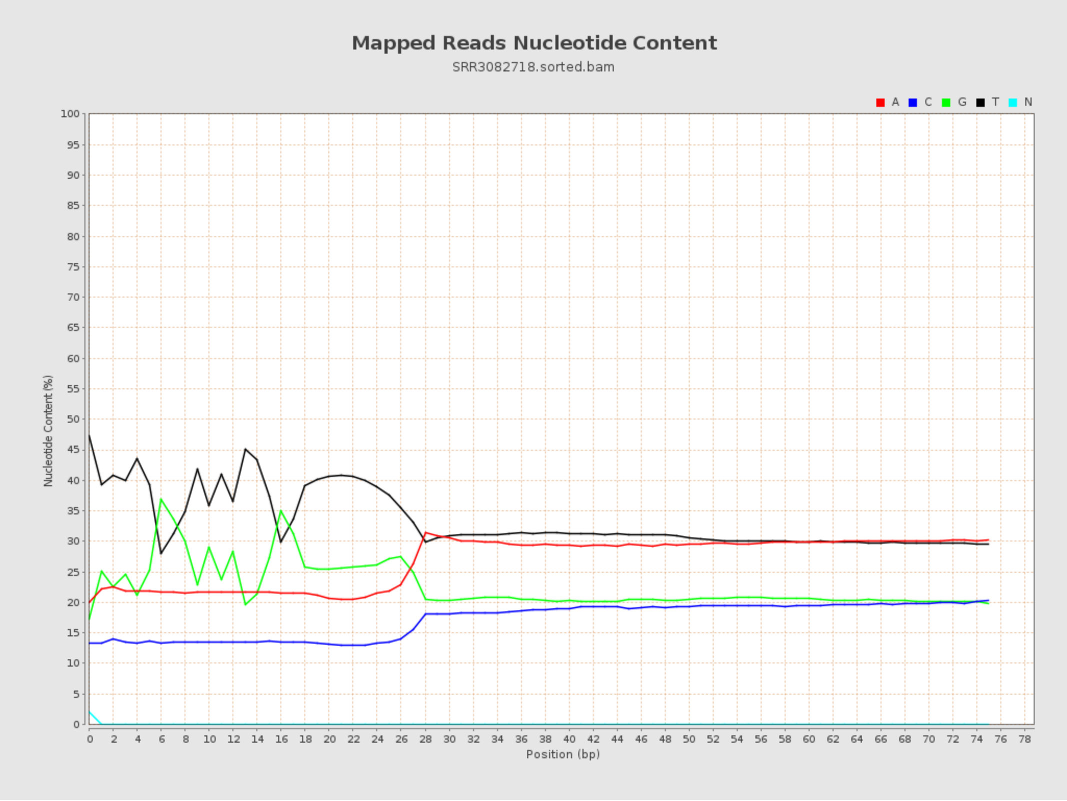
6. Results : Genome Fraction Coverage



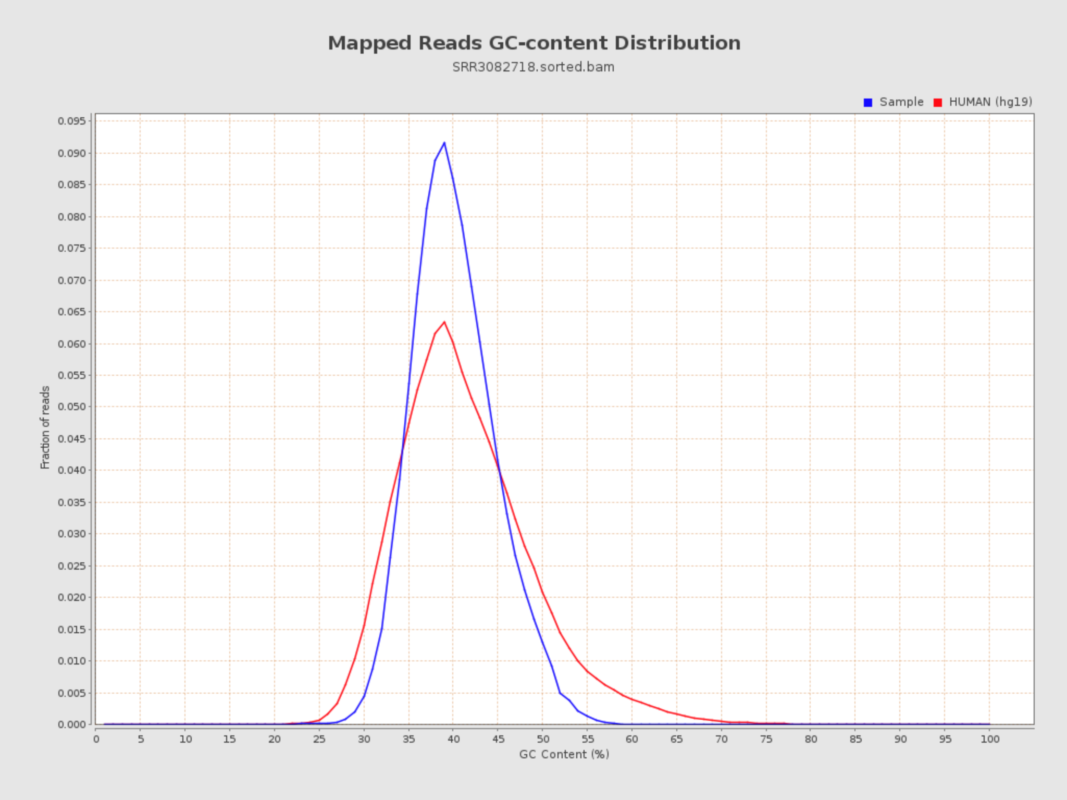
7. Results : Duplication Rate Histogram



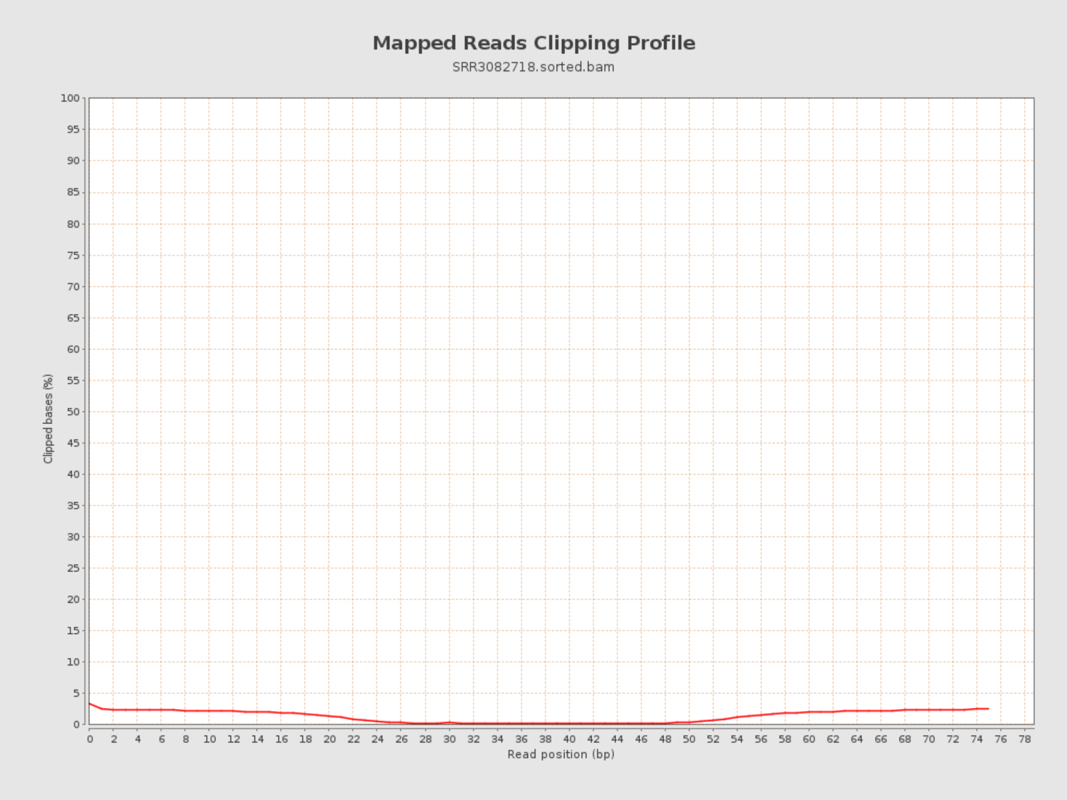
8. Results : Mapped Reads Nucleotide Content



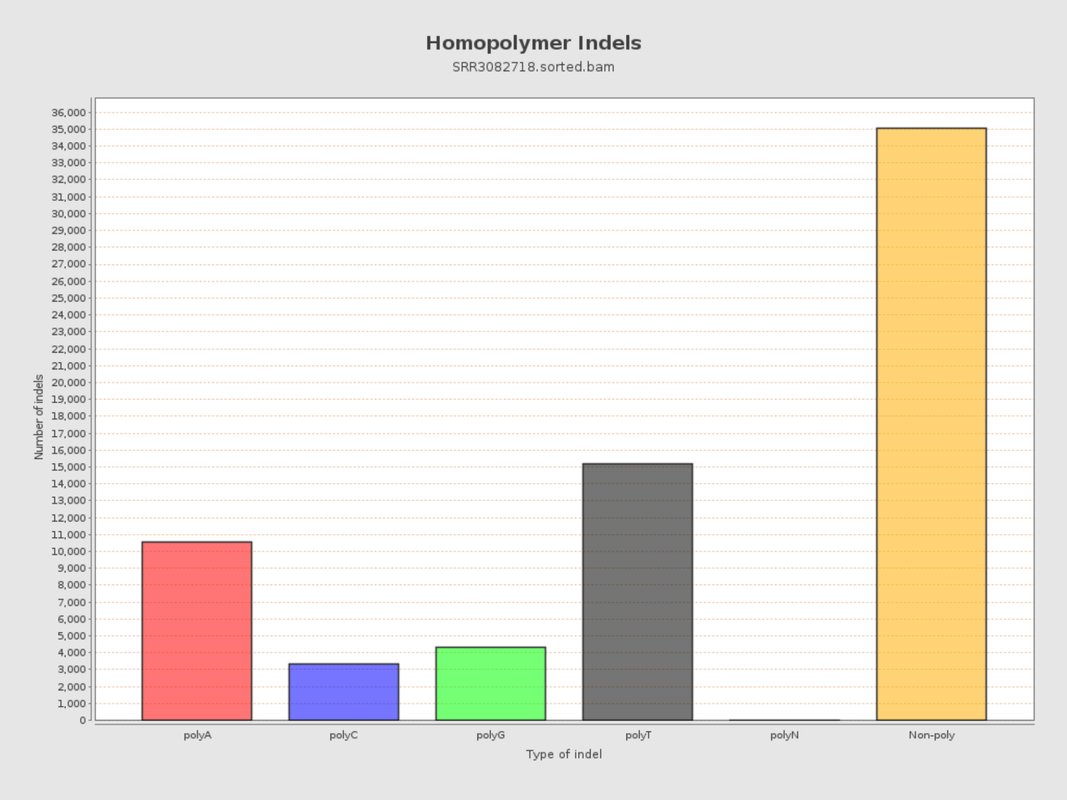
9. Results : Mapped Reads GC-content Distribution



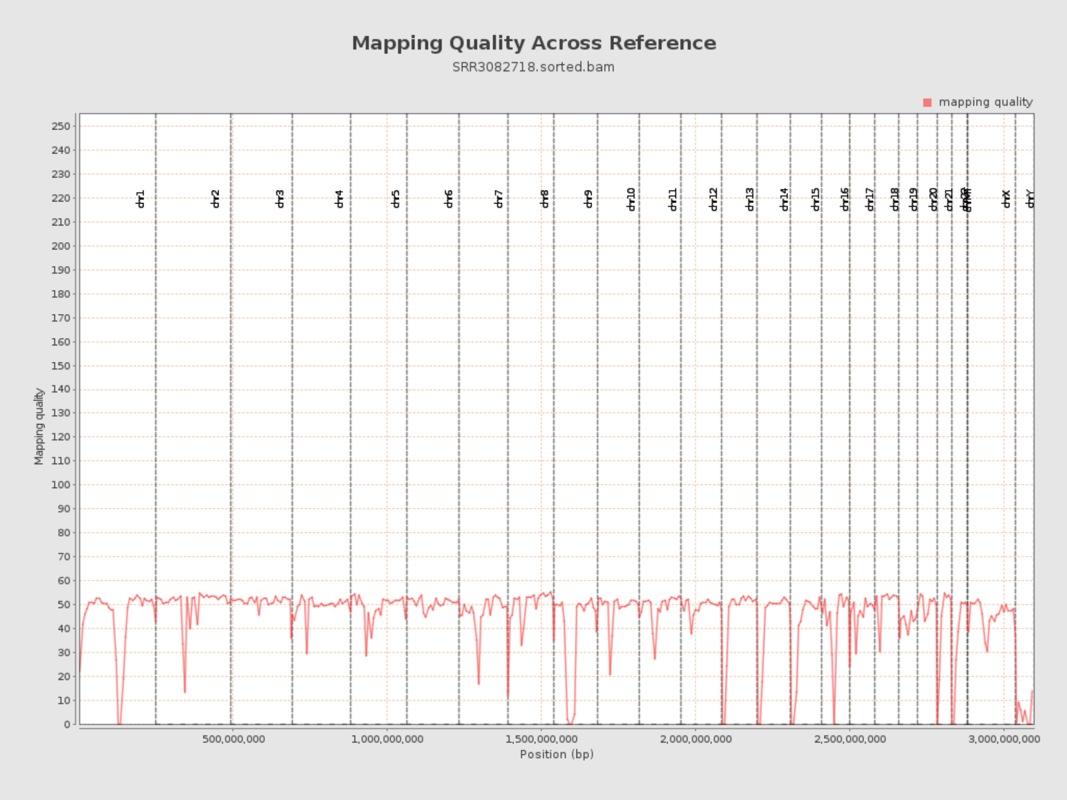
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram