Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:23:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819038.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_SRR1819038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819038.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:23:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,825,377
Mapped reads	3,452,608 / 90.26%
Unmapped reads	372,769 / 9.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,952 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	154,335 / 4.03%
Duplication rate	3.38%
Clipped reads	3,466,968 / 90.63%

2.2. ACGT Content

Number/percentage of A's	48,244,926 / 24.46%
Number/percentage of C's	39,916,666 / 20.24%
Number/percentage of T's	59,855,327 / 30.35%
Number/percentage of G's	49,195,443 / 24.94%
Number/percentage of N's	4,201 / 0%
GC Percentage	45.18%

2.3. Coverage

Mean	0.0637

Standard Deviation	0.4159

2.4. Mapping Quality

Mean Mapping Quality	43.75

2.5. Mismatches and indels

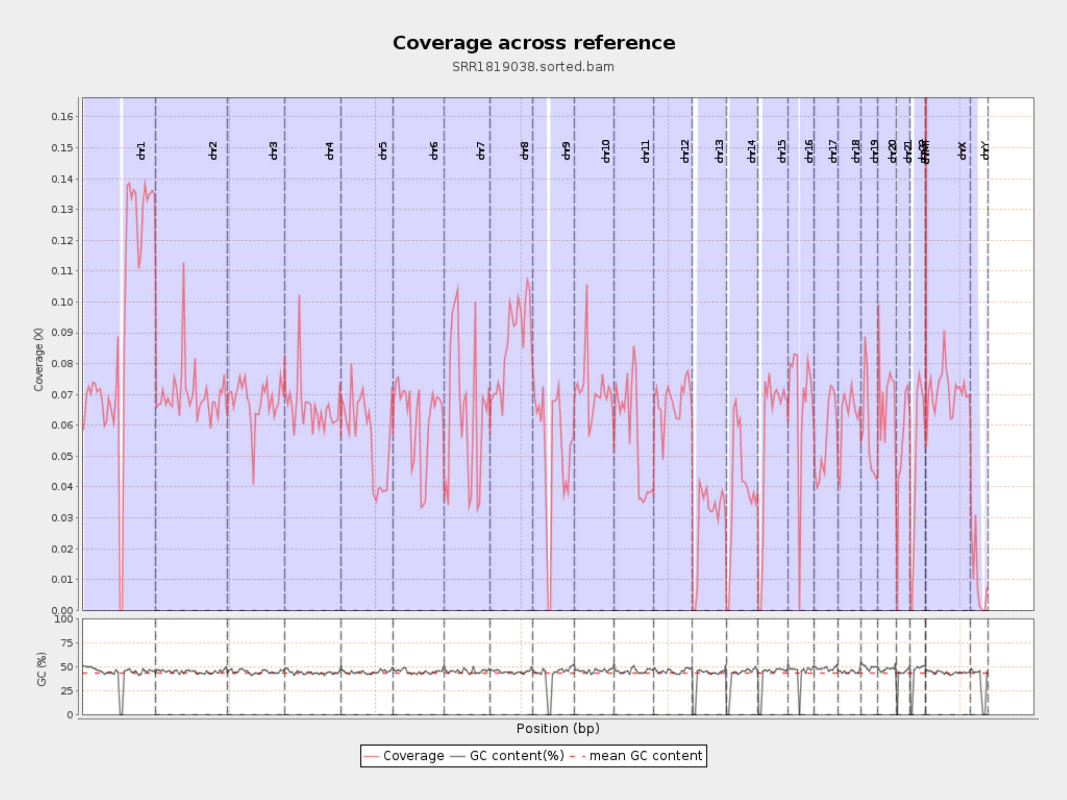
General error rate	0.49%
Mismatches	950,483
Insertions	10,128
Mapped reads with at least one insertion	0.29%
Deletions	29,920
Mapped reads with at least one deletion	0.86%
Homopolymer indels	42.48%

2.6. Chromosome stats

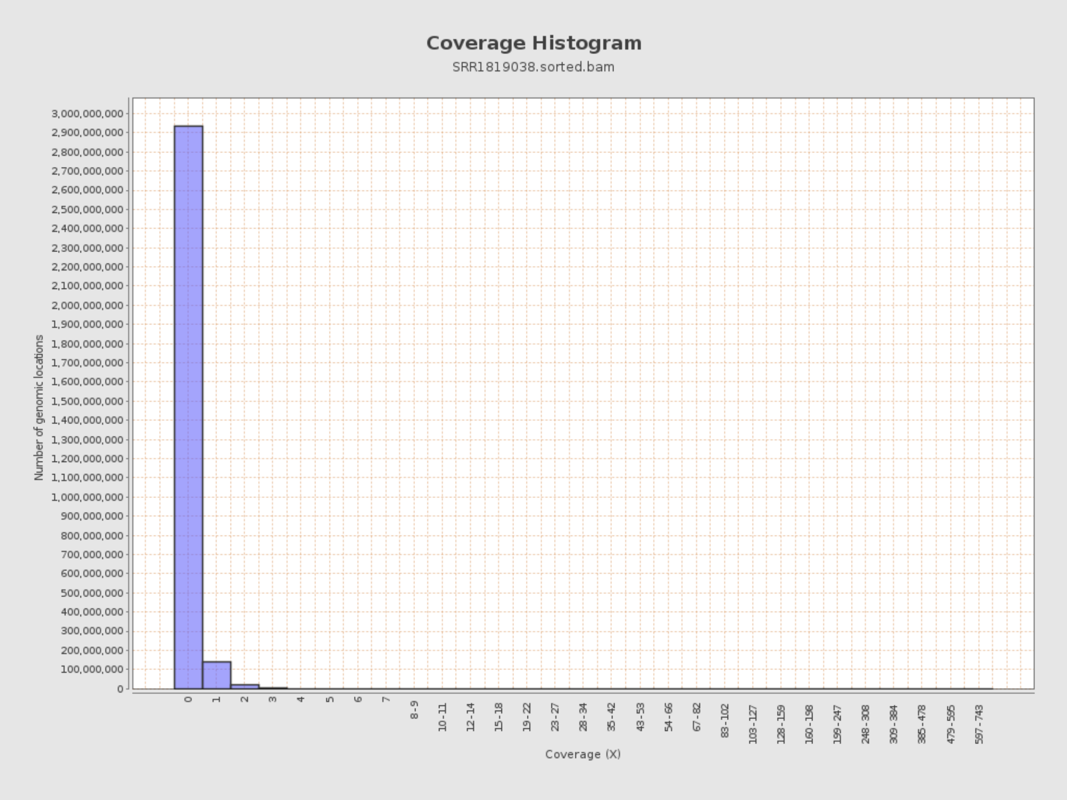
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22692541	0.091	0.6424
chr2	243199373	17059924	0.0701	0.5167
chr3	198022430	13461109	0.068	0.3108
chr4	191154276	12656228	0.0662	0.351
chr5	180915260	10315014	0.057	0.2891
chr6	171115067	10612377	0.062	0.3288
chr7	159138663	10215754	0.0642	0.4001

chr8	146364022	12676875	0.0866	0.423
chr9	141213431	7402408	0.0524	0.4476
chr10	135534747	9650904	0.0712	0.4645
chr11	135006516	7659424	0.0567	0.4179
chr12	133851895	9126467	0.0682	0.3134
chr13	115169878	3433993	0.0298	0.2025
chr14	107349540	4303239	0.0401	0.2795
chr15	102531392	5824099	0.0568	0.2832
chr16	90354753	6070705	0.0672	0.3537
chr17	81195210	4560943	0.0562	0.2966
chr18	78077248	4931891	0.0632	0.8139
chr19	59128983	3425435	0.0579	0.469
chr20	63025520	4432604	0.0703	0.3306
chr21	48129895	2576122	0.0535	0.3231
chr22	51304566	2517287	0.0491	0.2607
chrMT	16571	36113	2.1793	1.9634
chrX	155270560	11049269	0.0712	0.3794
chrY	59373566	577087	0.0097	0.2022

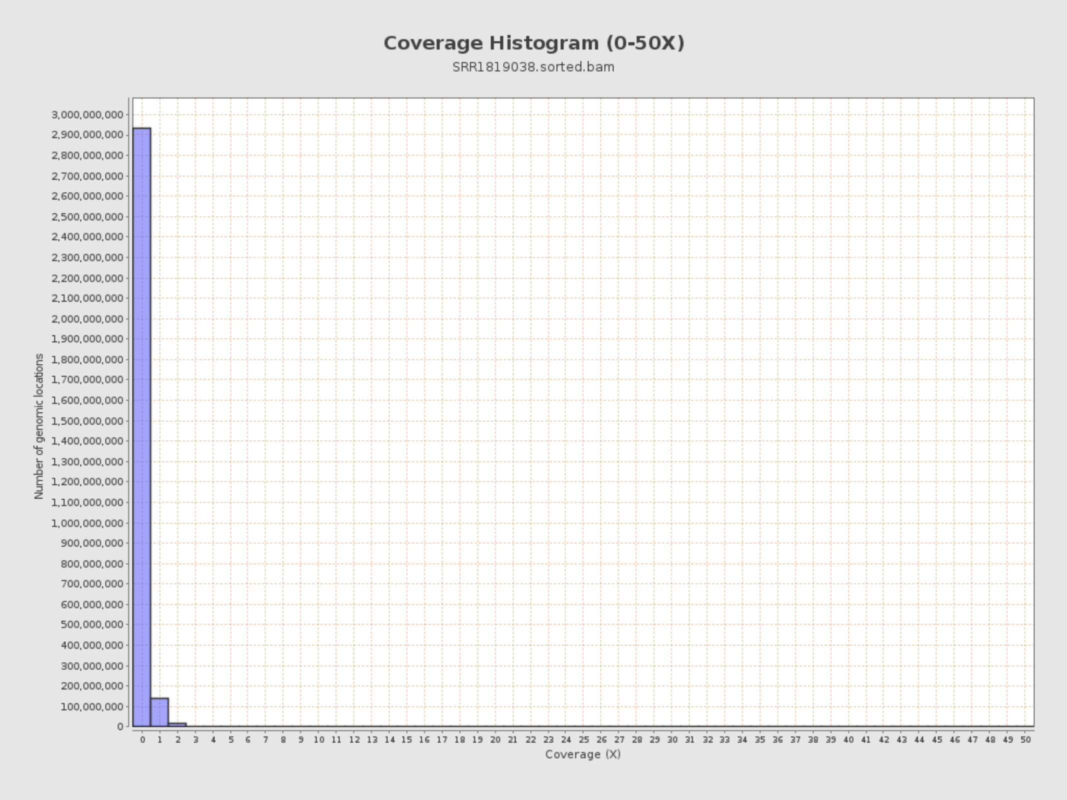
3. Results : Coverage across reference



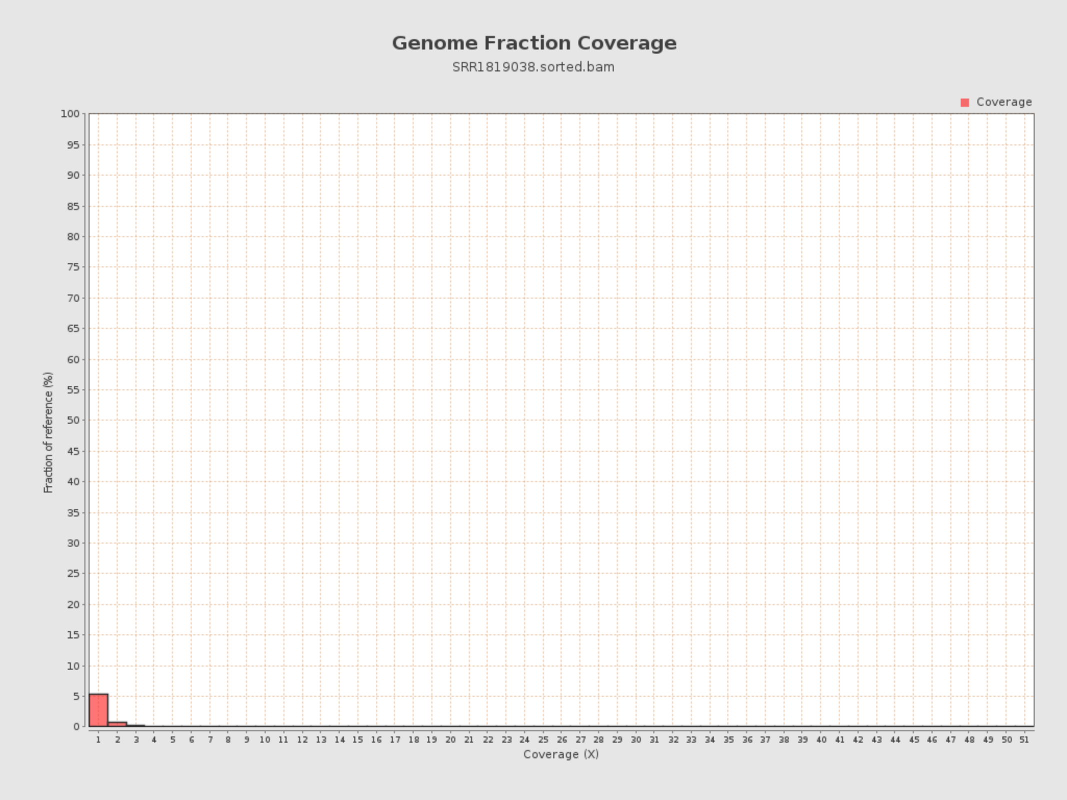
4. Results : Coverage Histogram



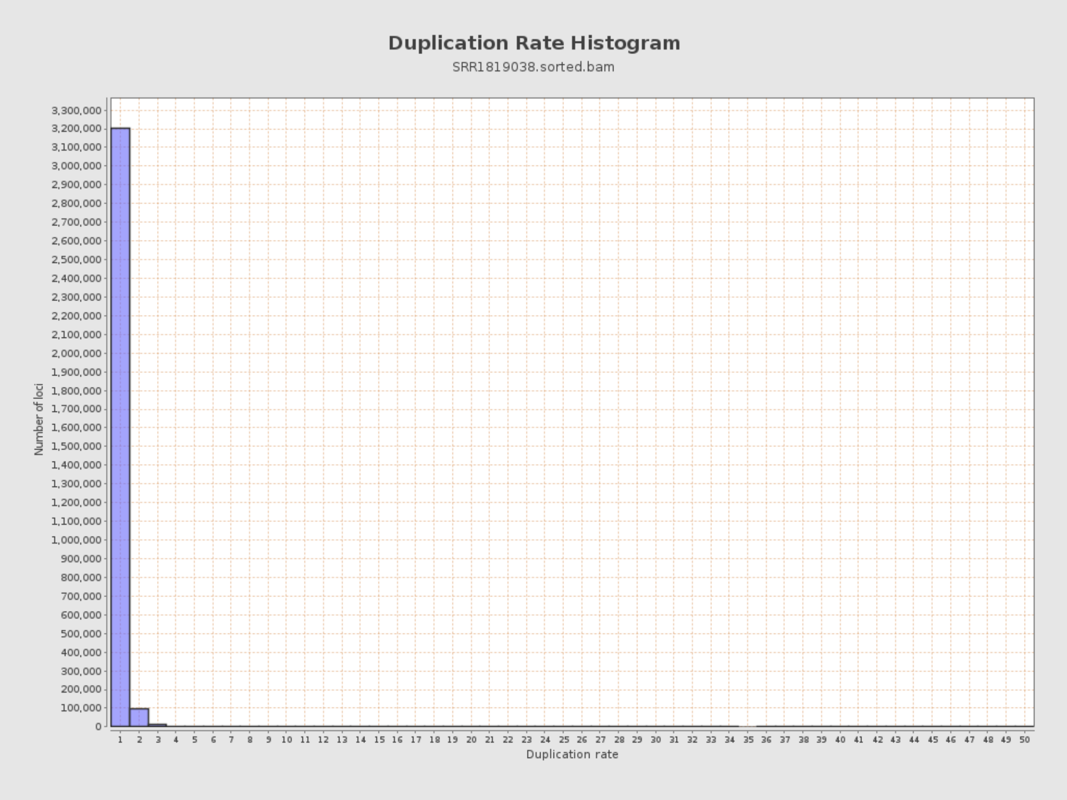
5. Results : Coverage Histogram (0-50X)



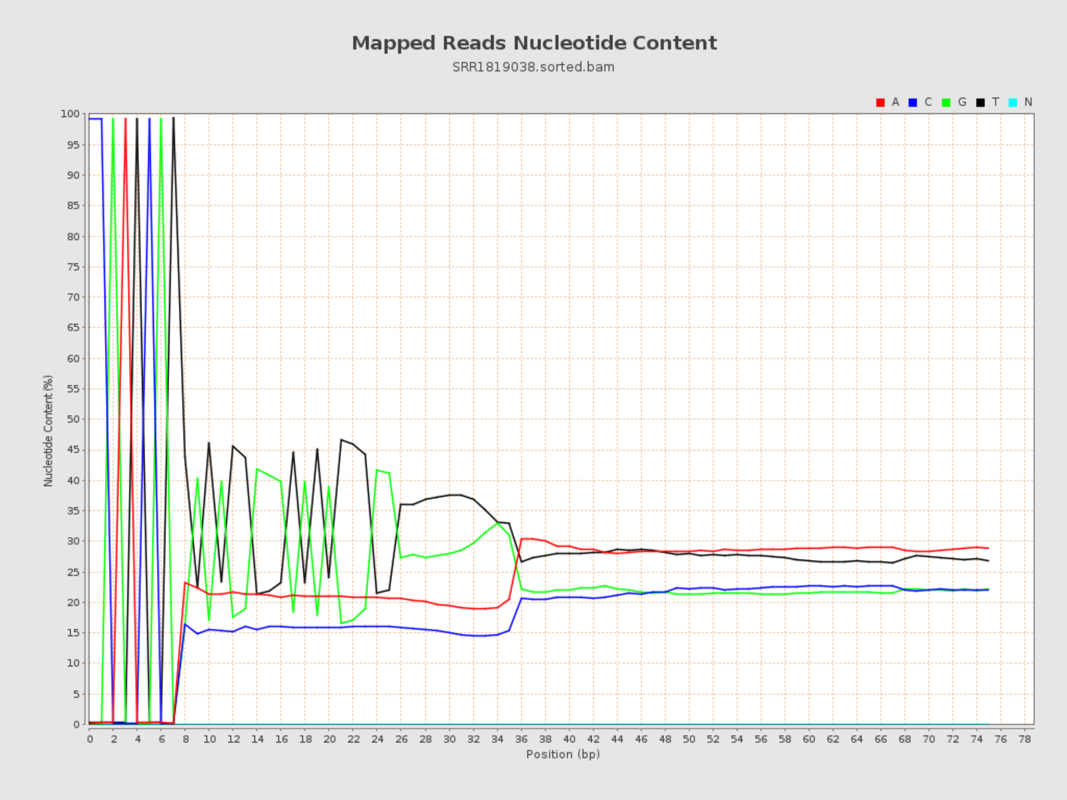
6. Results : Genome Fraction Coverage



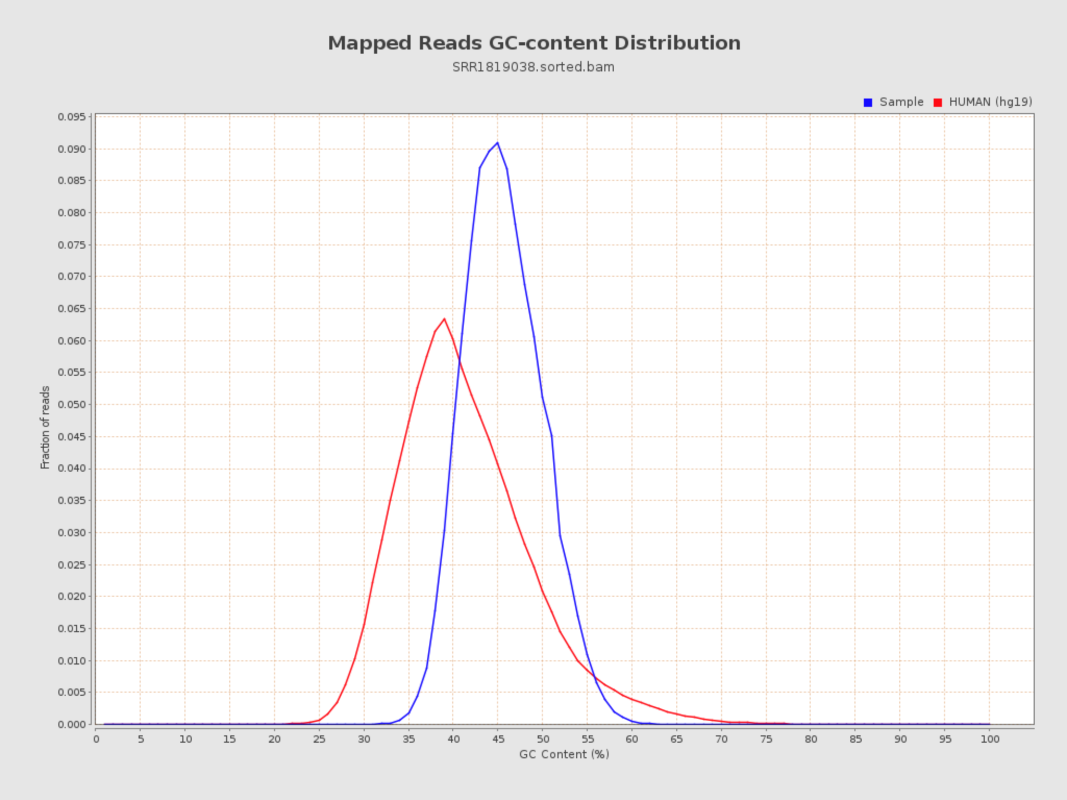
7. Results : Duplication Rate Histogram



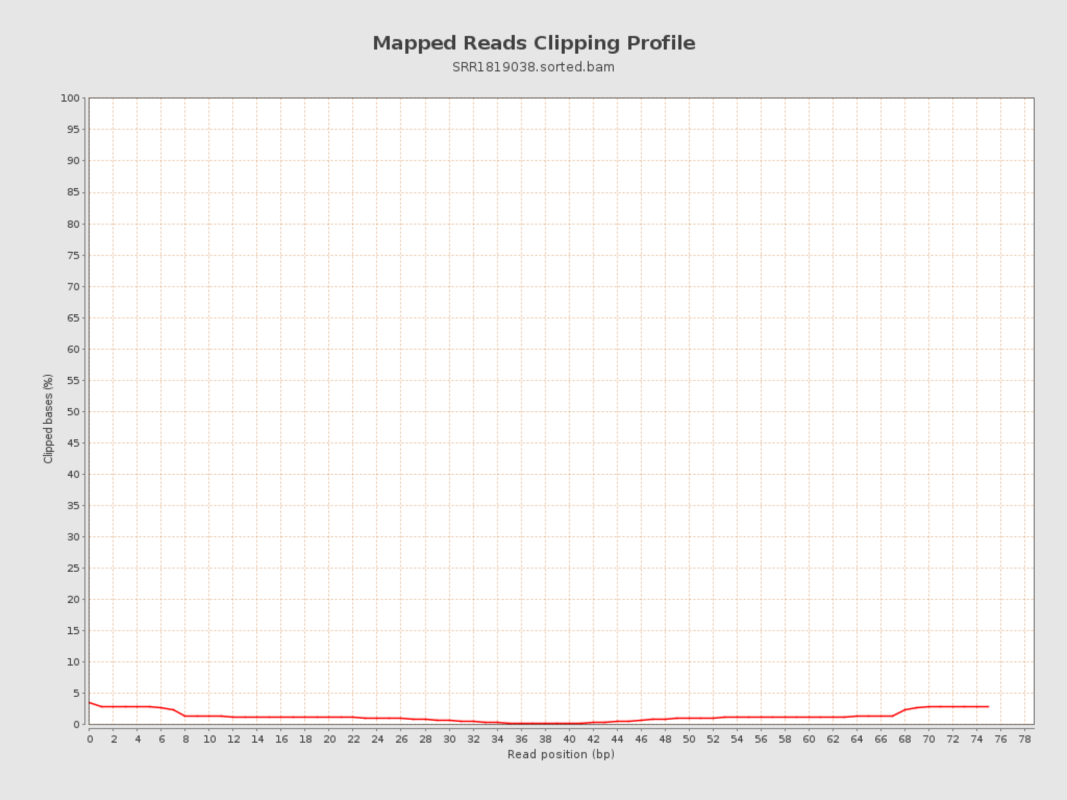
8. Results : Mapped Reads Nucleotide Content



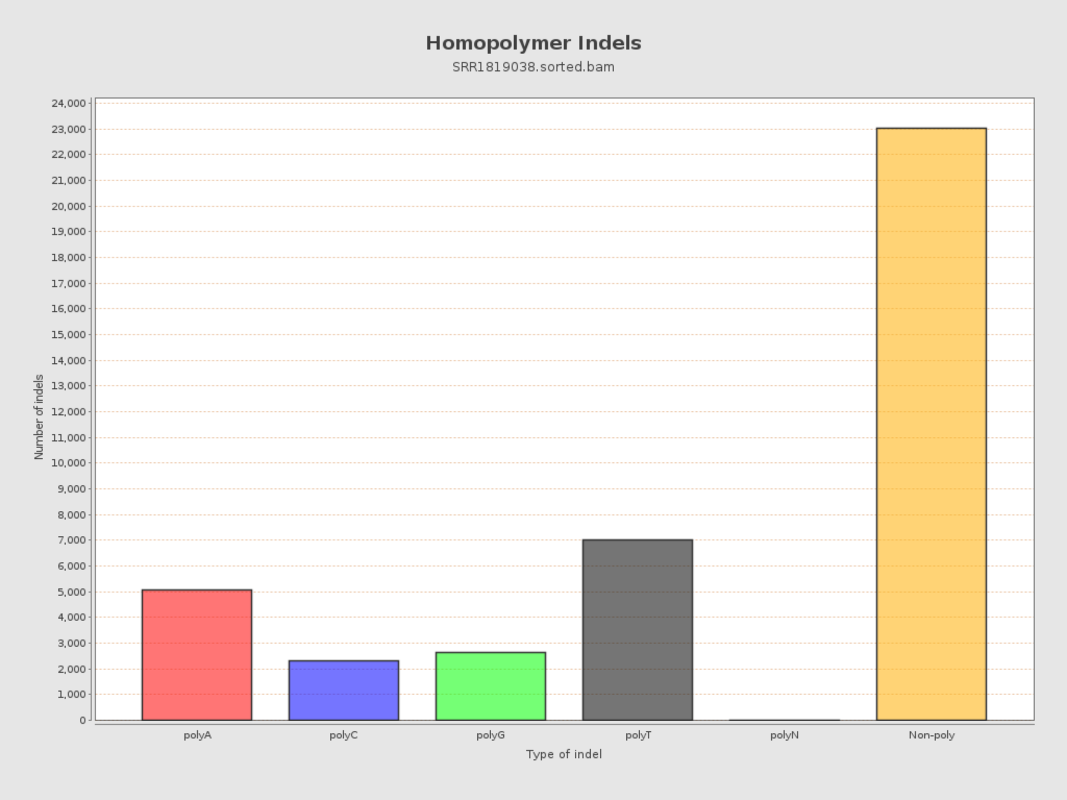
9. Results : Mapped Reads GC-content Distribution



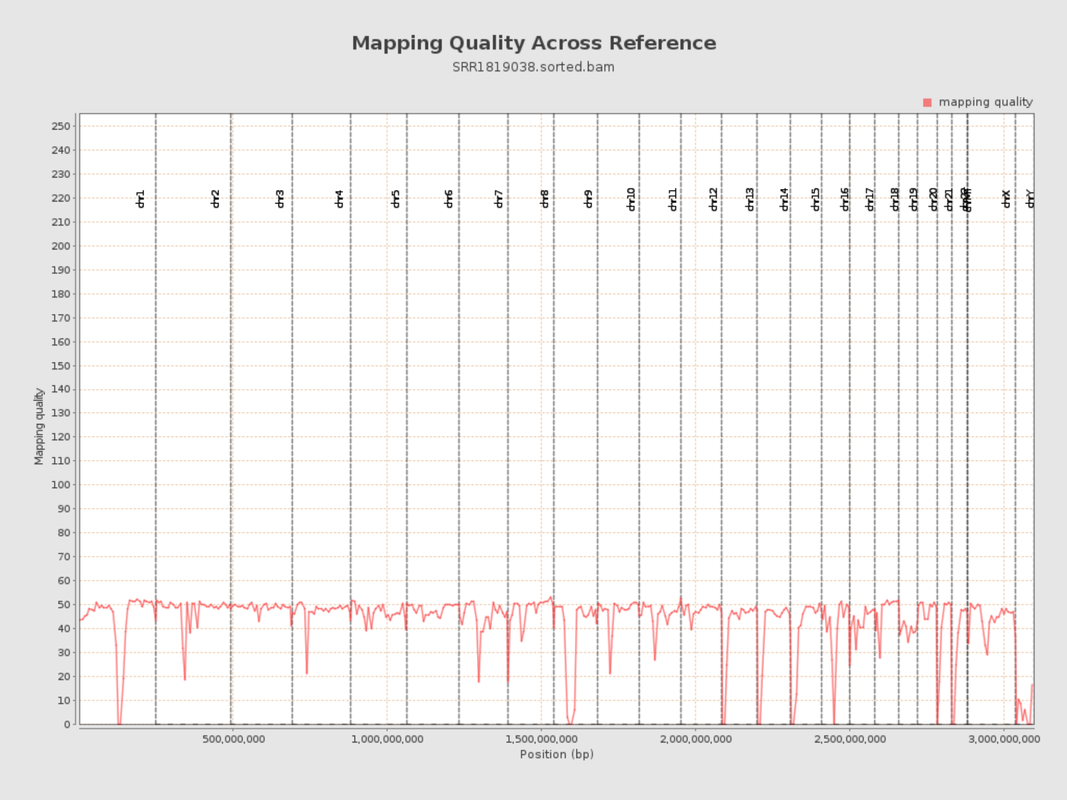
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram