Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:04:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081738.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_SRR3081738 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081738.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:04:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081738.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,247,736
Mapped reads	1,991,031 / 88.58%
Unmapped reads	256,705 / 11.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,610 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	74,830 / 3.33%
Duplication rate	2.68%
Clipped reads	991,694 / 44.12%

2.2. ACGT Content

Number/percentage of A's	36,225,510 / 27.76%
Number/percentage of C's	25,262,256 / 19.36%
Number/percentage of T's	39,423,796 / 30.21%
Number/percentage of G's	29,590,403 / 22.67%
Number/percentage of N's	1,497 / 0%
GC Percentage	42.03%

2.3. Coverage

Mean	0.0422

Standard Deviation	0.3937

2.4. Mapping Quality

Mean Mapping Quality	43.3

2.5. Mismatches and indels

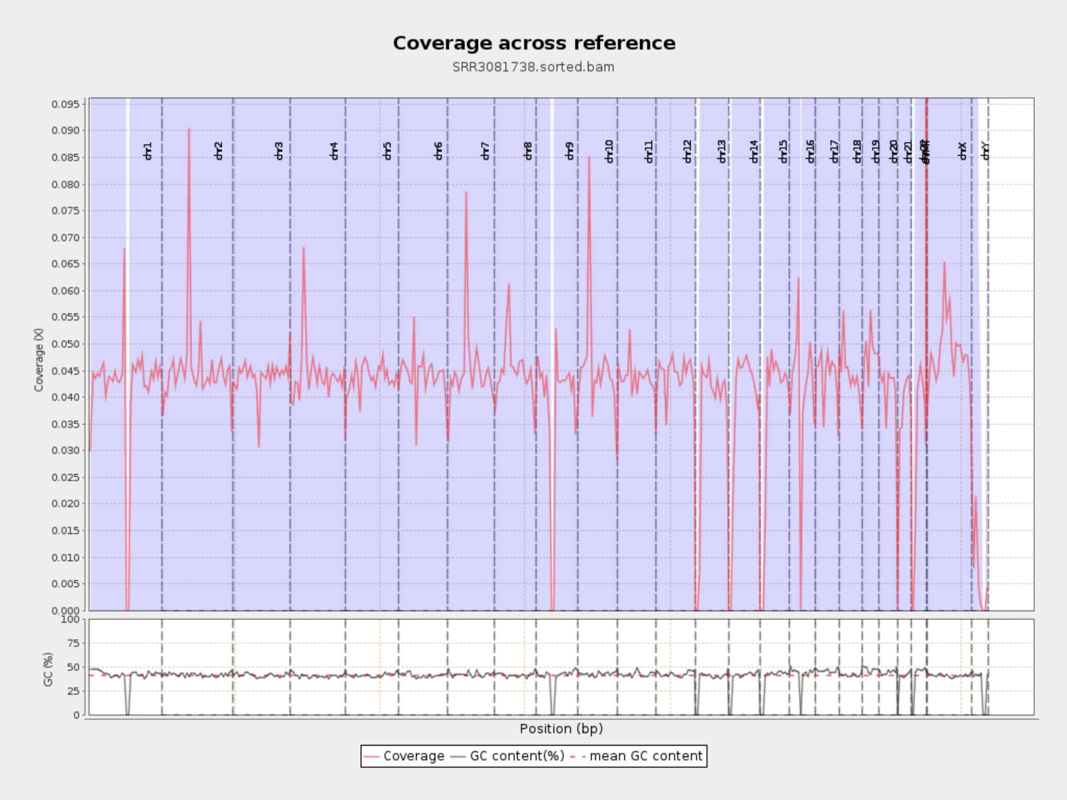
General error rate	0.87%
Mismatches	1,110,189
Insertions	10,544
Mapped reads with at least one insertion	0.52%
Deletions	29,781
Mapped reads with at least one deletion	1.48%
Homopolymer indels	45.74%

2.6. Chromosome stats

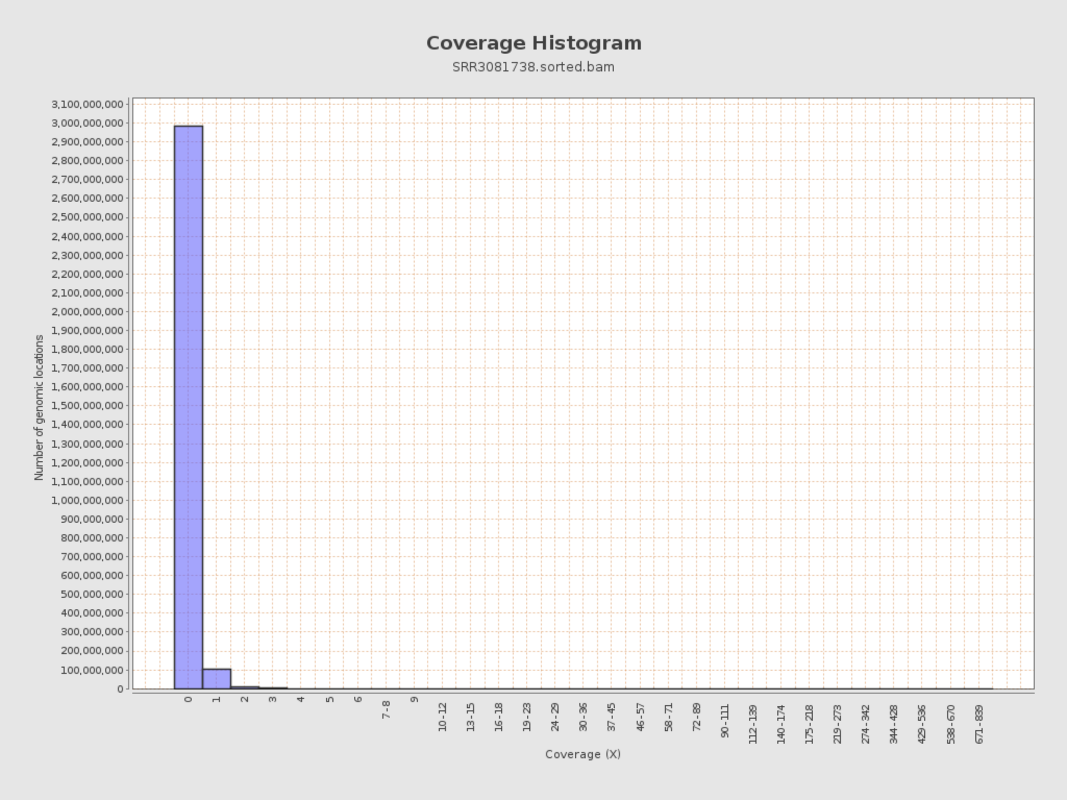
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10376557	0.0416	0.6775
chr2	243199373	11096017	0.0456	0.5117
chr3	198022430	8689370	0.0439	0.2342
chr4	191154276	8493892	0.0444	0.2731
chr5	180915260	7931091	0.0438	0.2333
chr6	171115067	7557100	0.0442	0.276
chr7	159138663	7243261	0.0455	0.5462

chr8	146364022	6583438	0.045	0.5046
chr9	141213431	5390298	0.0382	0.3622
chr10	135534747	6226795	0.0459	0.43
chr11	135006516	5867858	0.0435	0.3359
chr12	133851895	5927374	0.0443	0.2368
chr13	115169878	4066408	0.0353	0.2078
chr14	107349540	3980173	0.0371	0.2374
chr15	102531392	3725119	0.0363	0.2192
chr16	90354753	3747530	0.0415	0.2718
chr17	81195210	3572705	0.044	0.2506
chr18	78077248	3492113	0.0447	0.6748
chr19	59128983	2848410	0.0482	0.5323
chr20	63025520	2617583	0.0415	0.2372
chr21	48129895	1705956	0.0354	0.2388
chr22	51304566	1487394	0.029	0.1881
chrMT	16571	9052	0.5463	0.791
chrX	155270560	7528401	0.0485	0.2835
chrY	59373566	392181	0.0066	0.1768

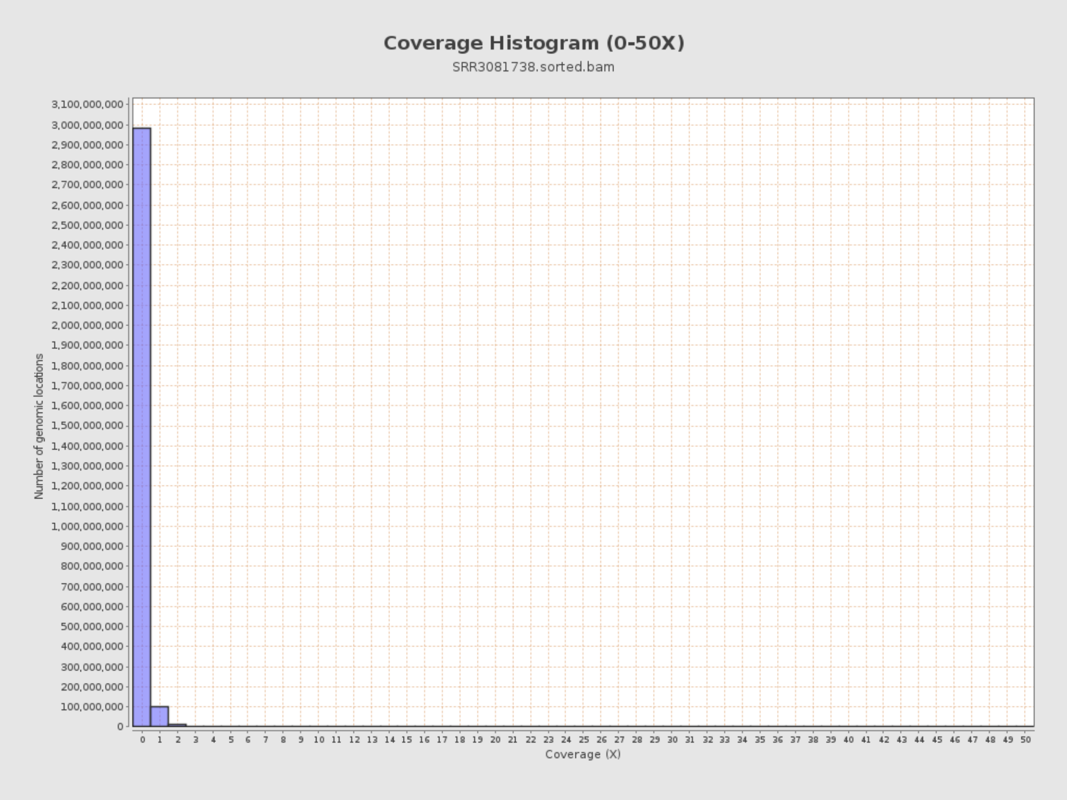
3. Results : Coverage across reference



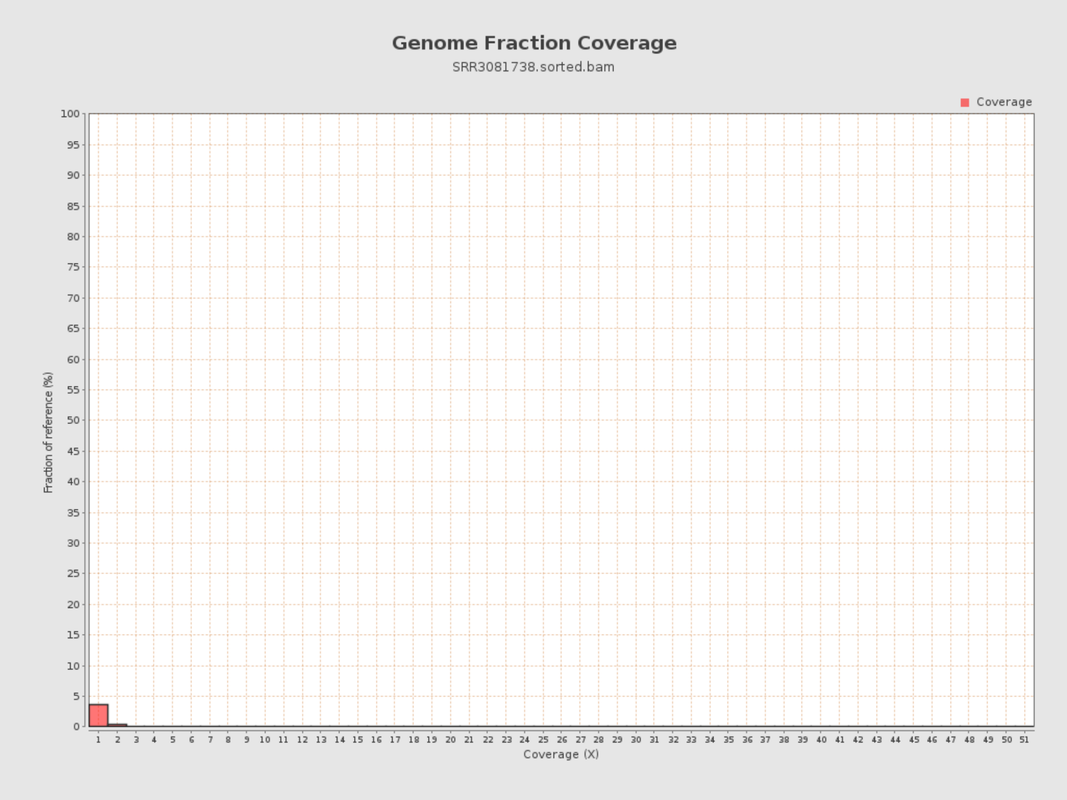
4. Results : Coverage Histogram



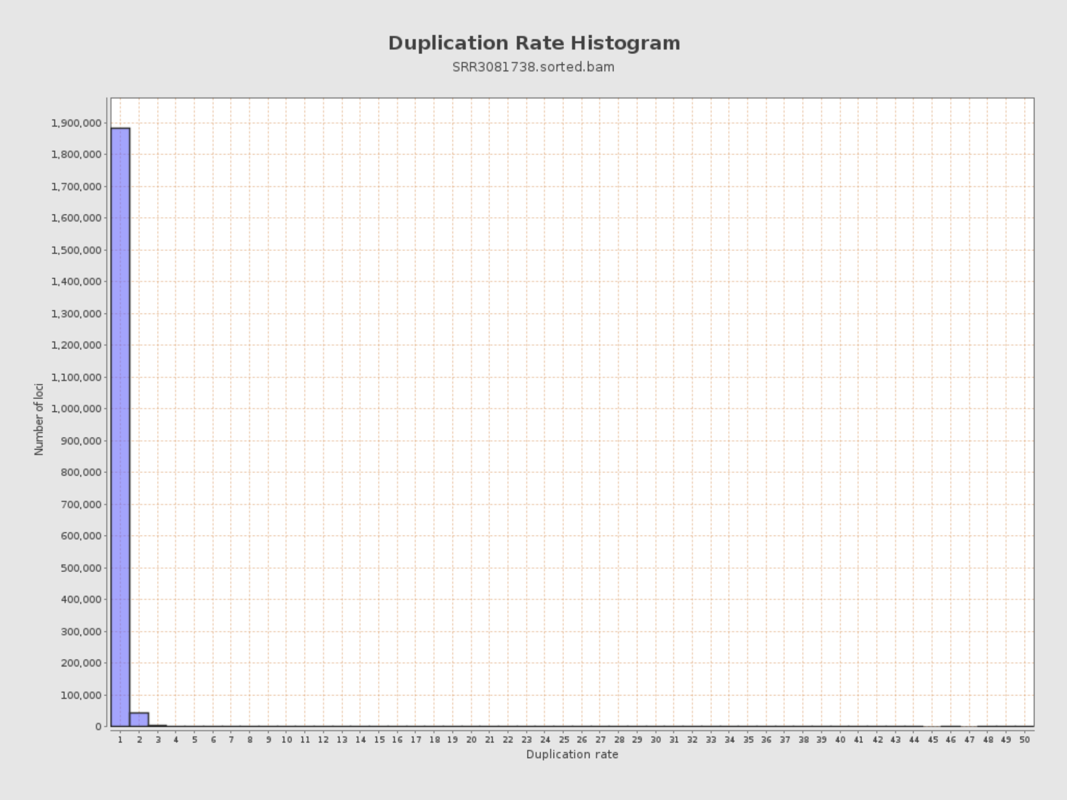
5. Results : Coverage Histogram (0-50X)



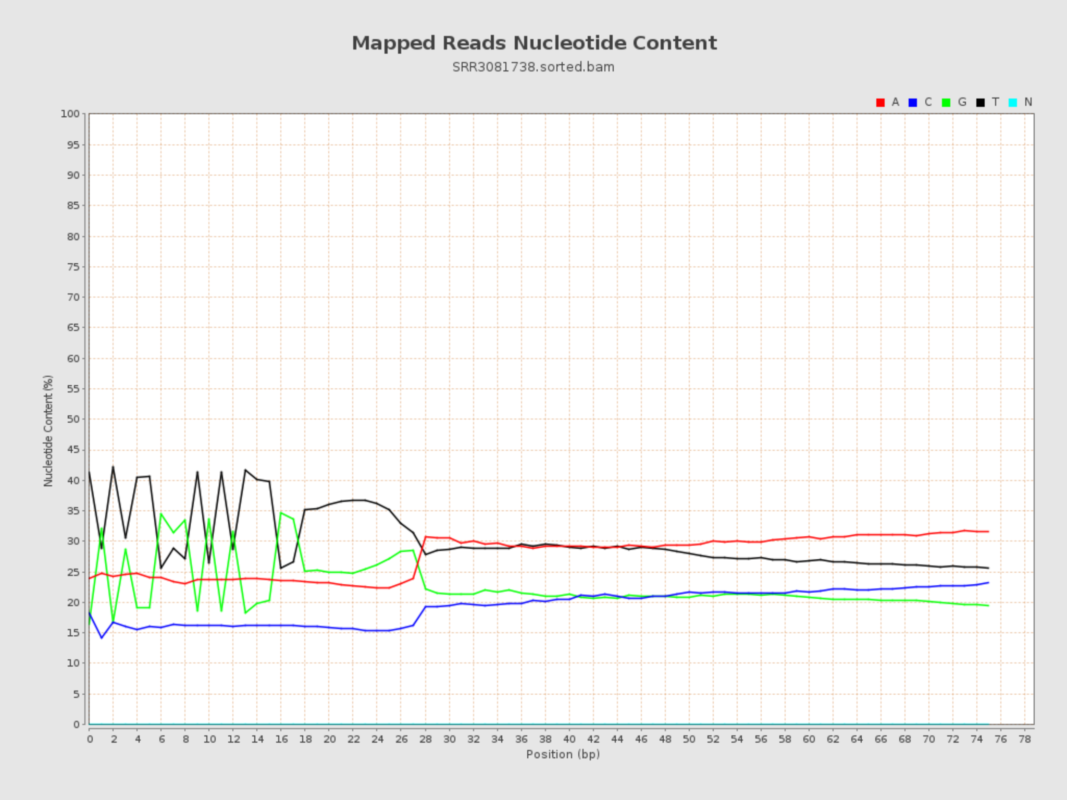
6. Results : Genome Fraction Coverage



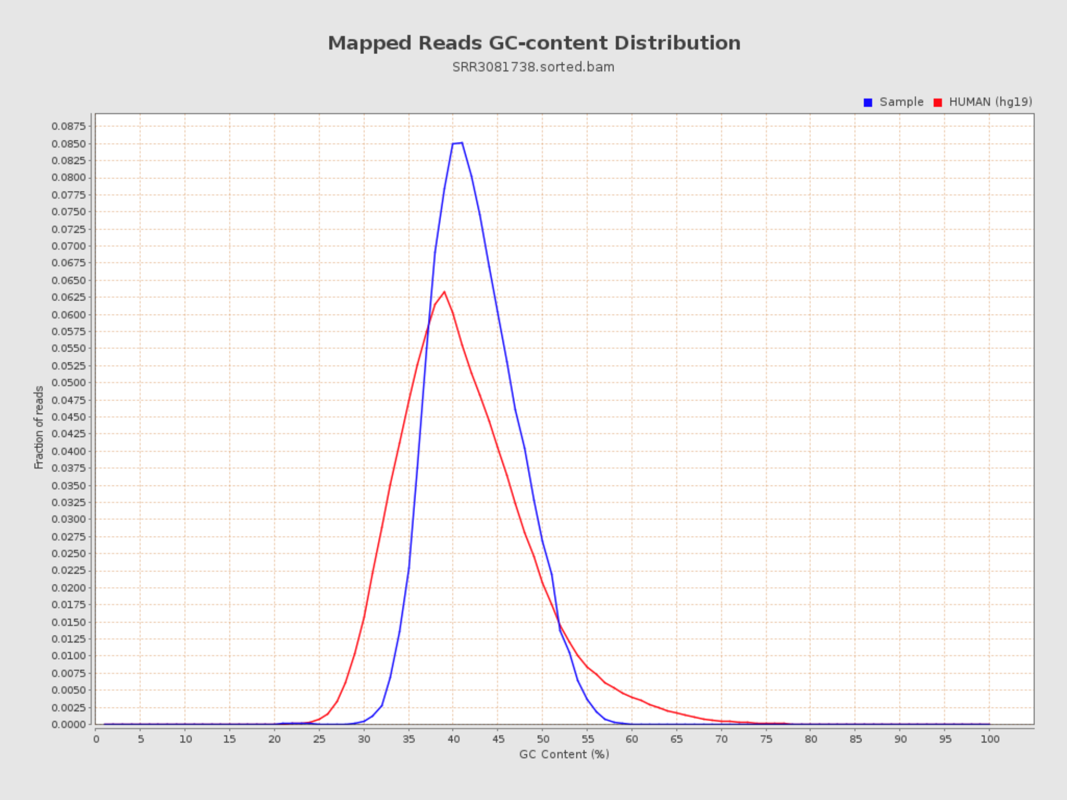
7. Results : Duplication Rate Histogram



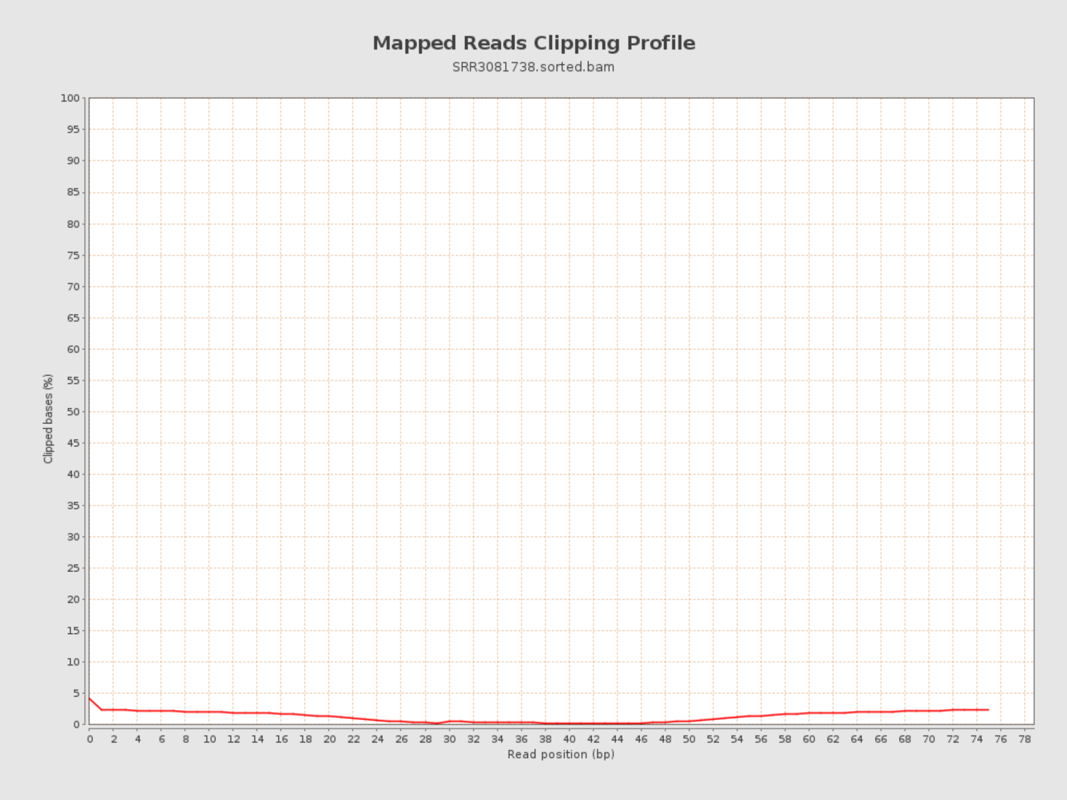
8. Results : Mapped Reads Nucleotide Content



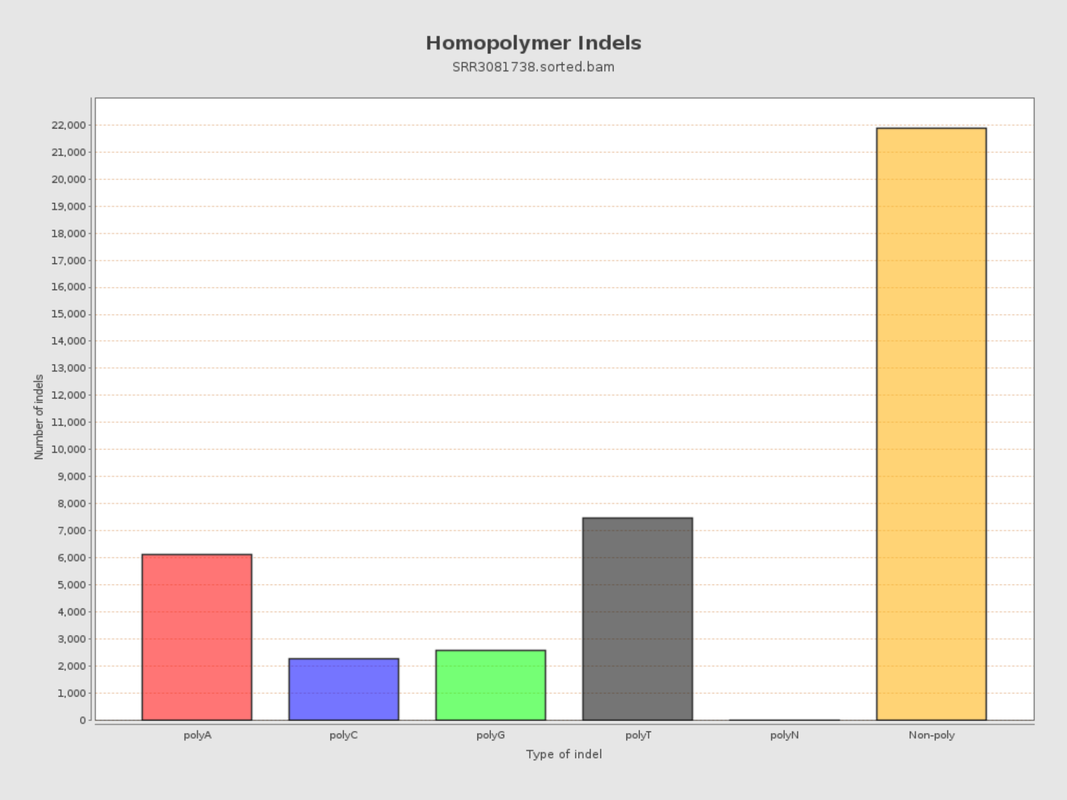
9. Results : Mapped Reads GC-content Distribution



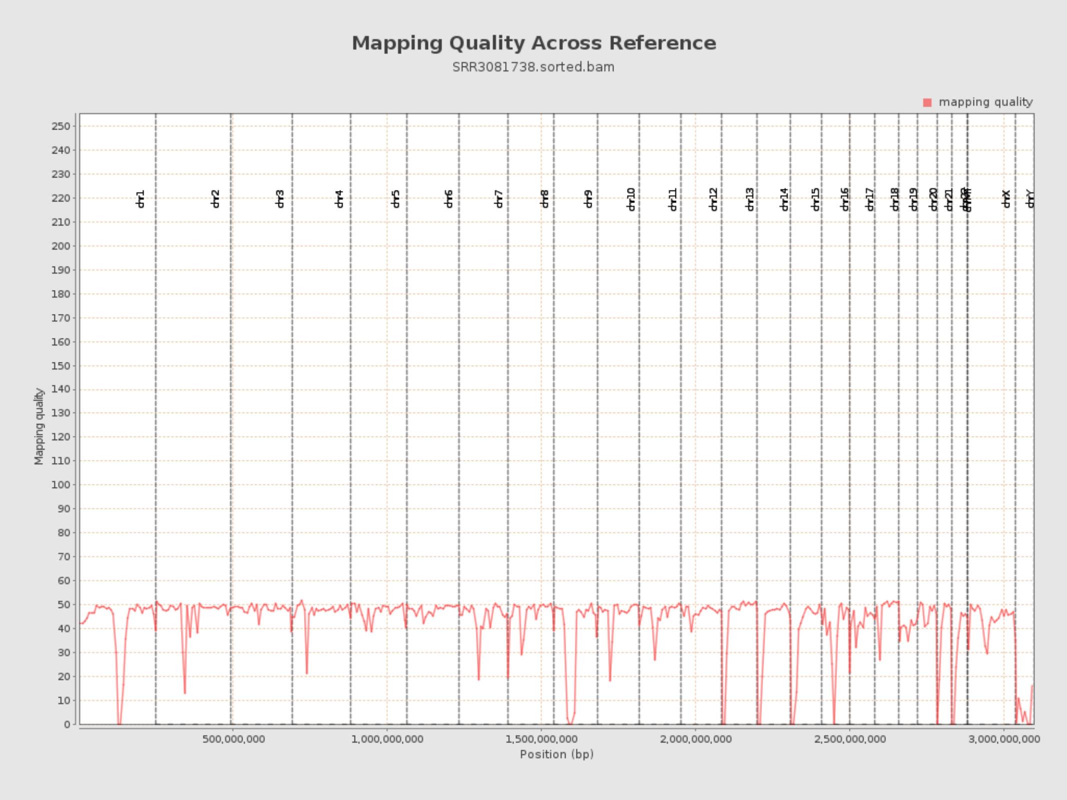
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram