Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:32:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081034.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_SRR3081034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081034.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:32:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,817,652
Mapped reads	2,180,088 / 57.11%
Unmapped reads	1,637,564 / 42.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,411 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	83,592 / 2.19%
Duplication rate	3.22%
Clipped reads	1,329,249 / 34.82%

2.2. ACGT Content

Number/percentage of A's	38,103,062 / 28.24%
Number/percentage of C's	27,395,962 / 20.31%
Number/percentage of T's	39,311,582 / 29.14%
Number/percentage of G's	30,093,218 / 22.31%
Number/percentage of N's	1,709 / 0%
GC Percentage	42.61%

2.3. Coverage

Mean	0.0436

Standard Deviation	0.3072

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

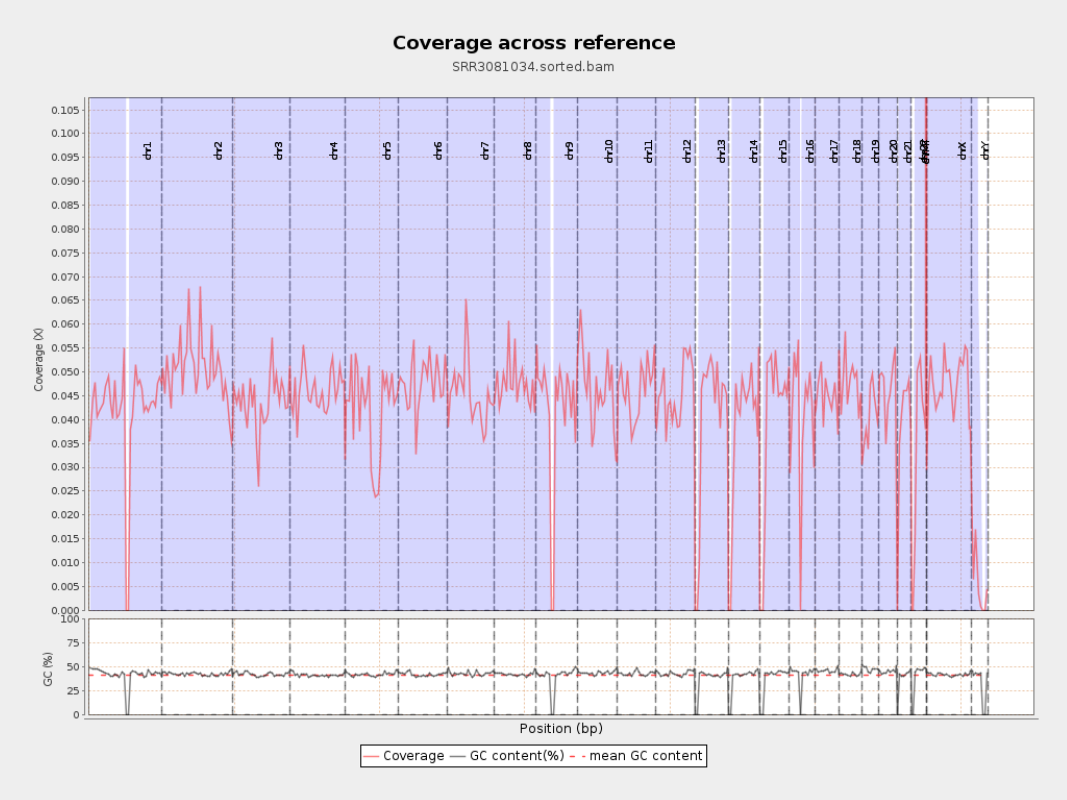
General error rate	0.76%
Mismatches	1,012,836
Insertions	8,585
Mapped reads with at least one insertion	0.39%
Deletions	25,079
Mapped reads with at least one deletion	1.14%
Homopolymer indels	46.09%

2.6. Chromosome stats

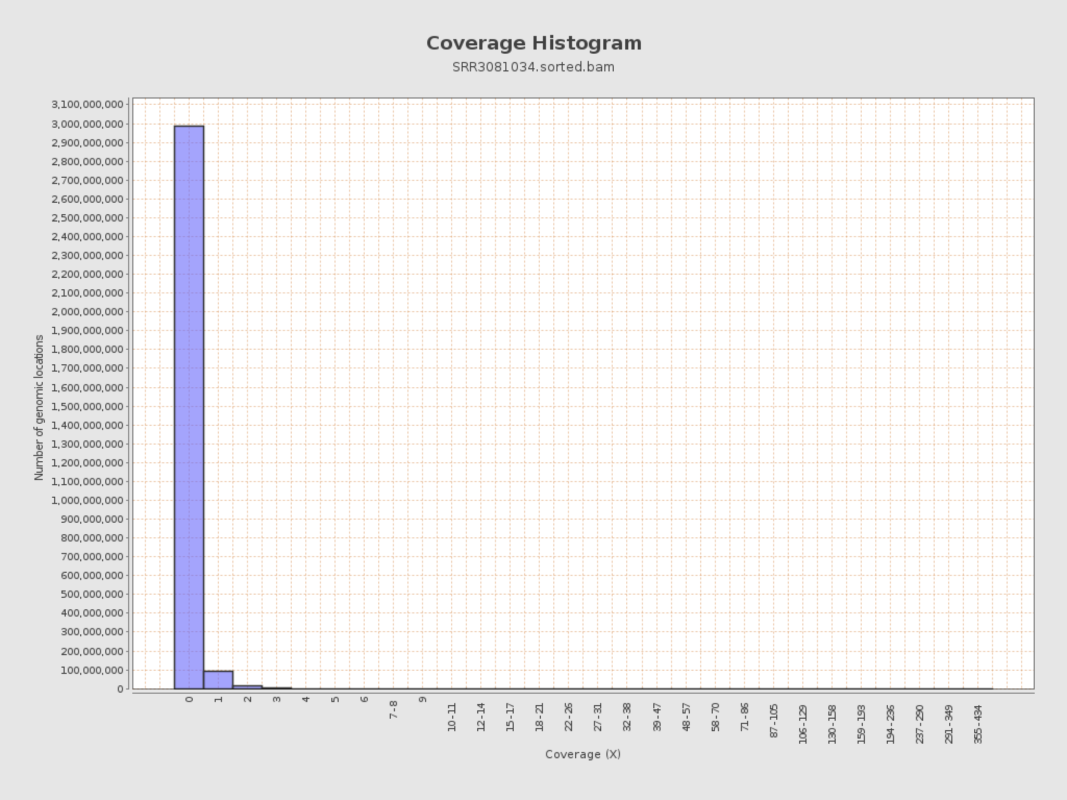
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10373415	0.0416	0.4153
chr2	243199373	12341331	0.0507	0.3588
chr3	198022430	8658229	0.0437	0.2446
chr4	191154276	8802223	0.046	0.2623
chr5	180915260	7645222	0.0423	0.2425
chr6	171115067	8206136	0.048	0.2873
chr7	159138663	7221980	0.0454	0.4332

chr8	146364022	6945672	0.0475	0.3205
chr9	141213431	5777346	0.0409	0.2975
chr10	135534747	6363846	0.047	0.3032
chr11	135006516	6227431	0.0461	0.2905
chr12	133851895	6082089	0.0454	0.2535
chr13	115169878	4600713	0.0399	0.2362
chr14	107349540	4028801	0.0375	0.2389
chr15	102531392	4062996	0.0396	0.244
chr16	90354753	3657746	0.0405	0.2503
chr17	81195210	3628374	0.0447	0.271
chr18	78077248	3752001	0.0481	0.4805
chr19	59128983	2401113	0.0406	0.3437
chr20	63025520	2913508	0.0462	0.2601
chr21	48129895	1858932	0.0386	0.2454
chr22	51304566	1648805	0.0321	0.2094
chrMT	16571	92118	5.559	4.6804
chrX	155270560	7326531	0.0472	0.2758
chrY	59373566	332365	0.0056	0.1179

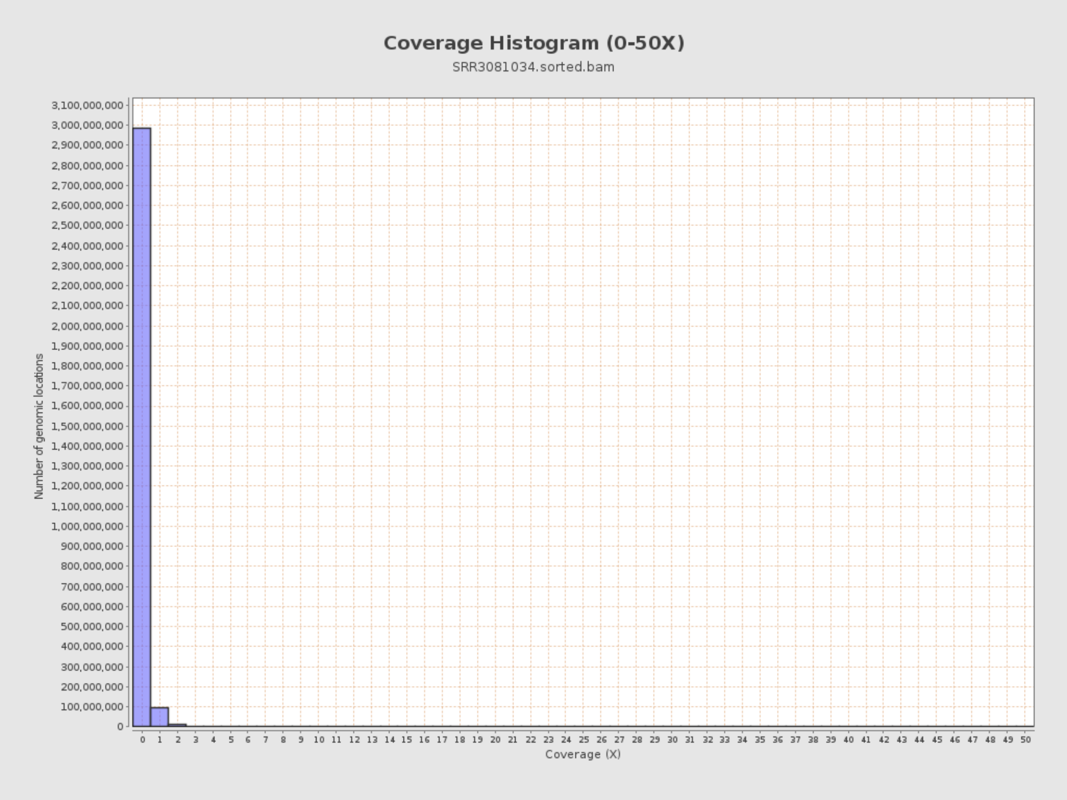
3. Results : Coverage across reference



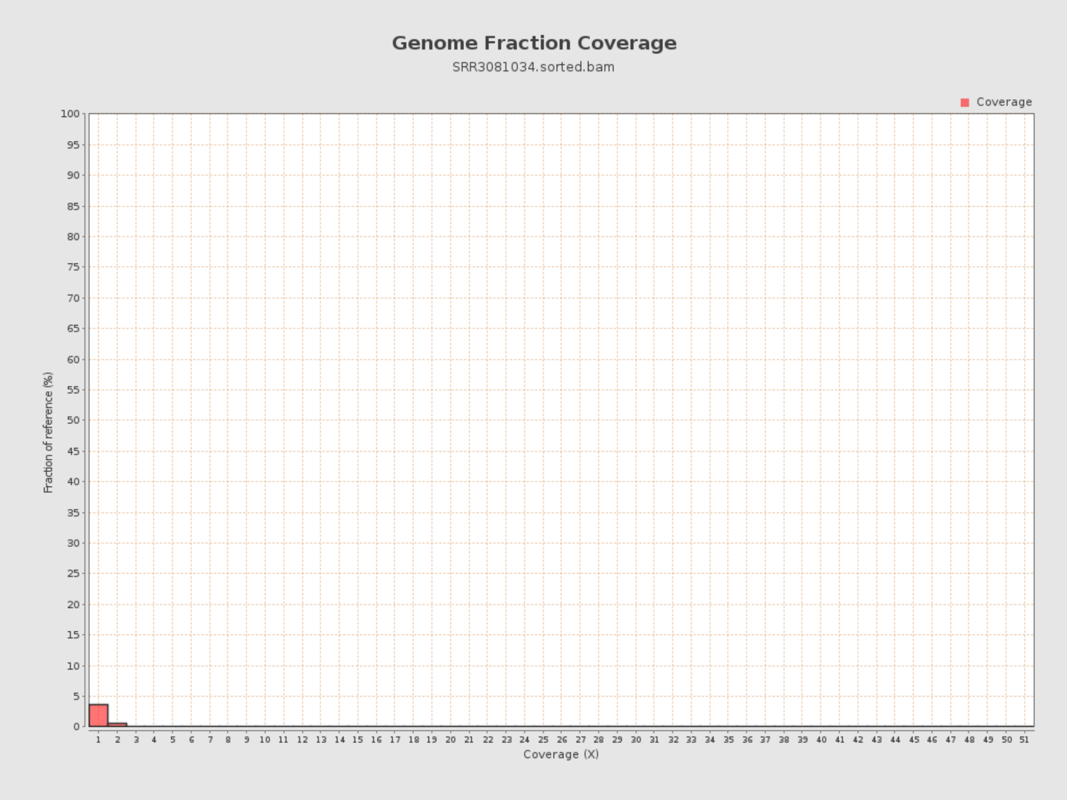
4. Results : Coverage Histogram



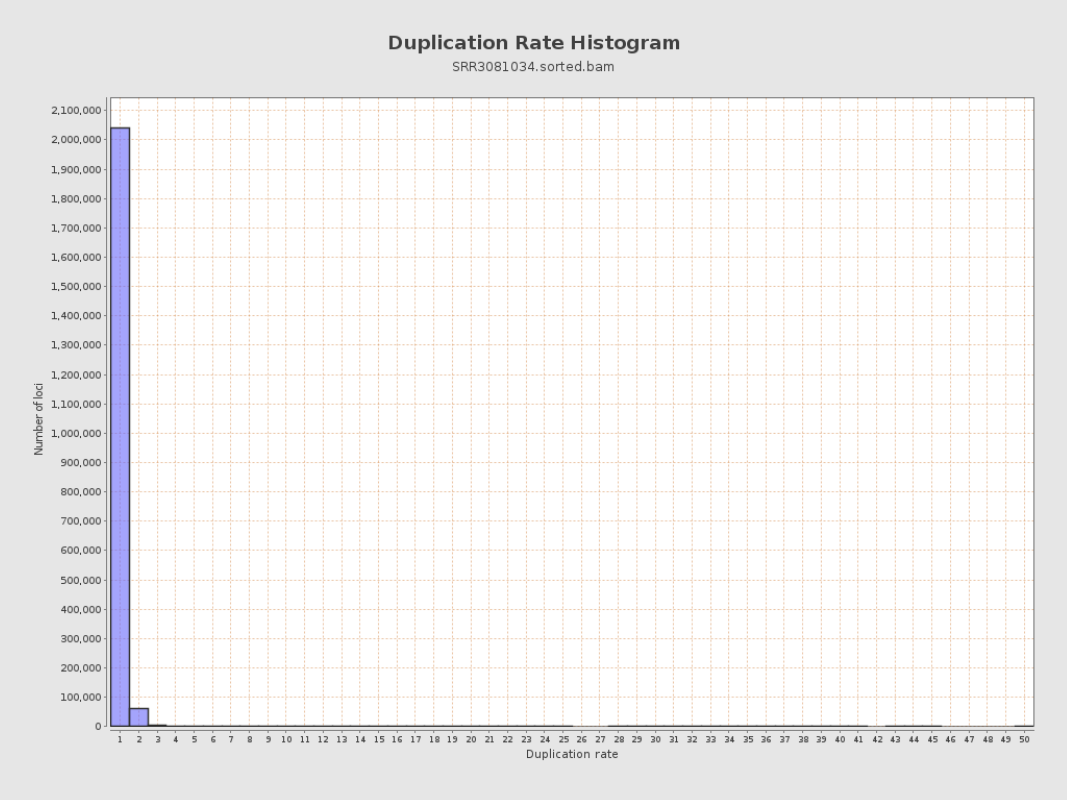
5. Results : Coverage Histogram (0-50X)



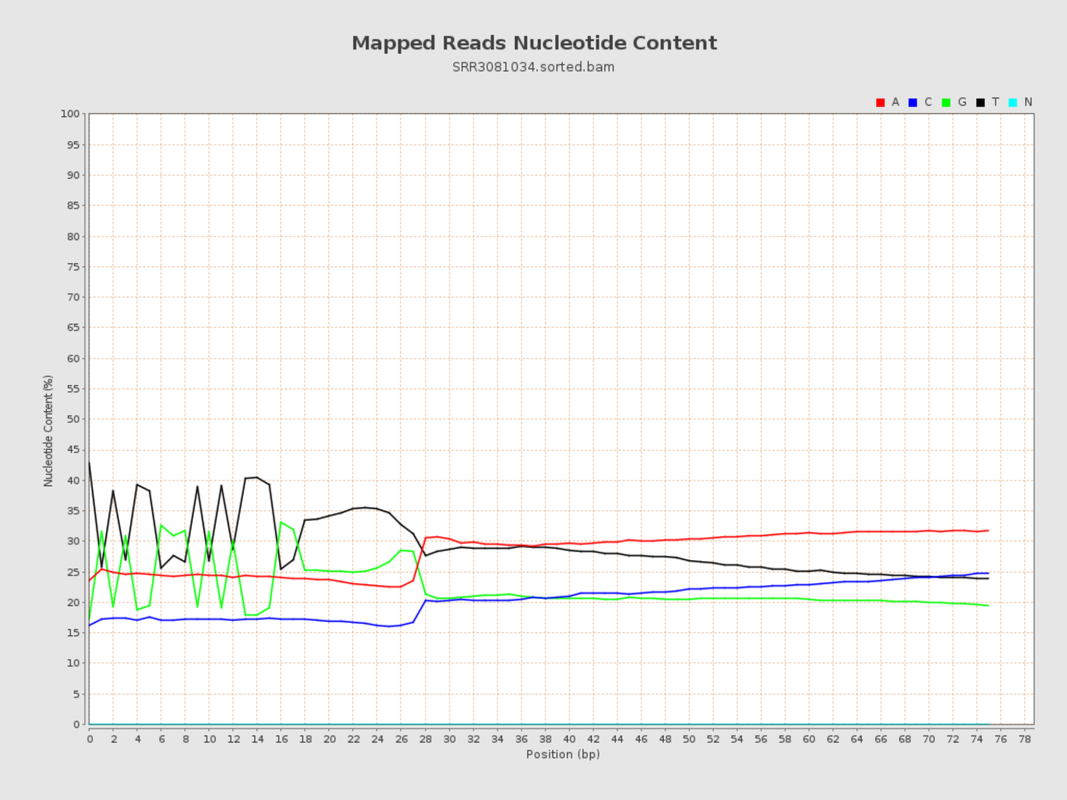
6. Results : Genome Fraction Coverage



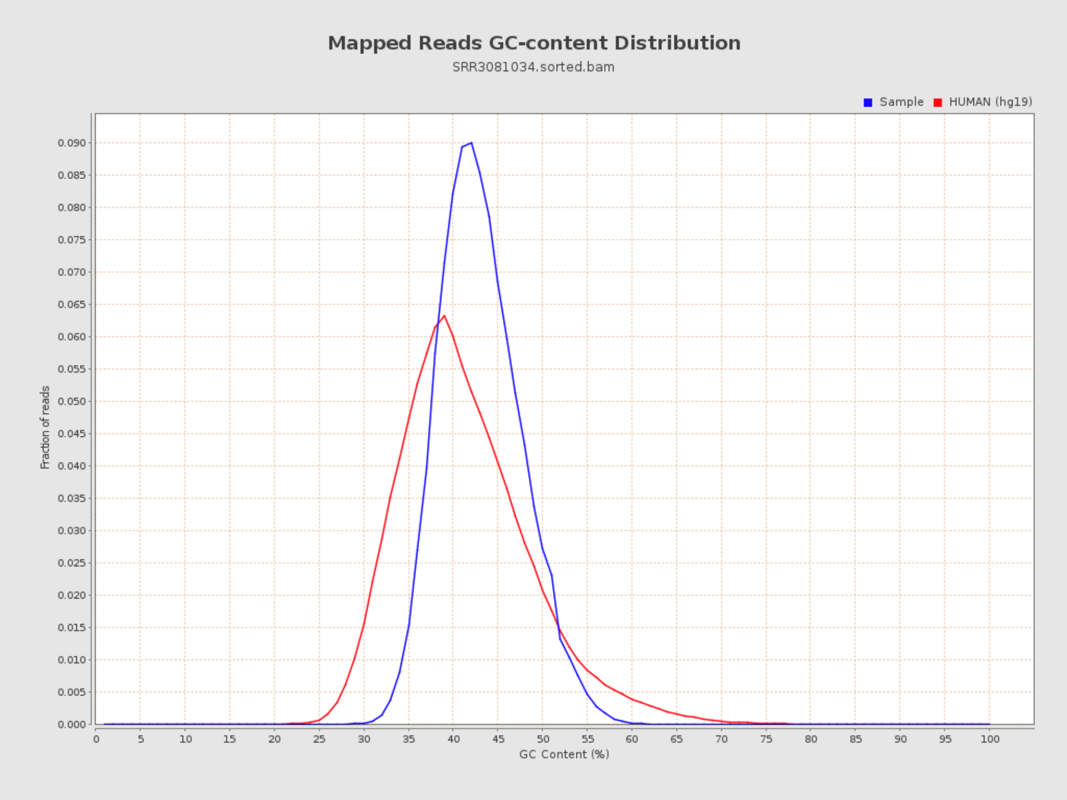
7. Results : Duplication Rate Histogram



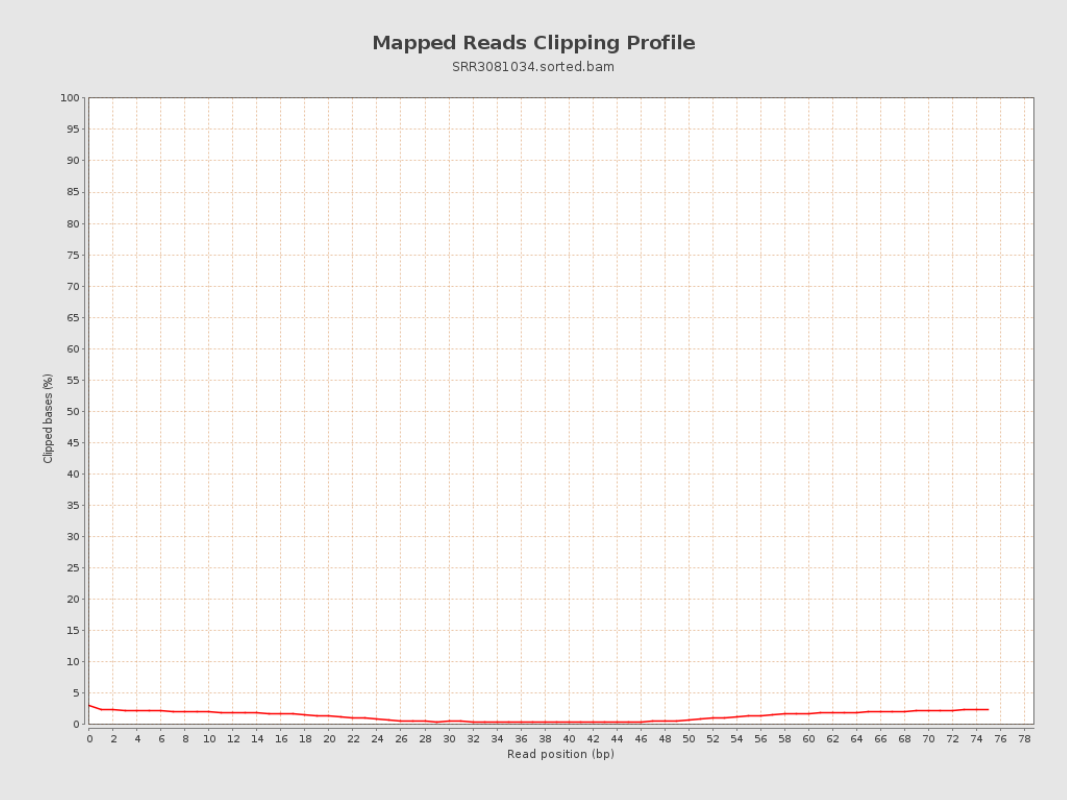
8. Results : Mapped Reads Nucleotide Content



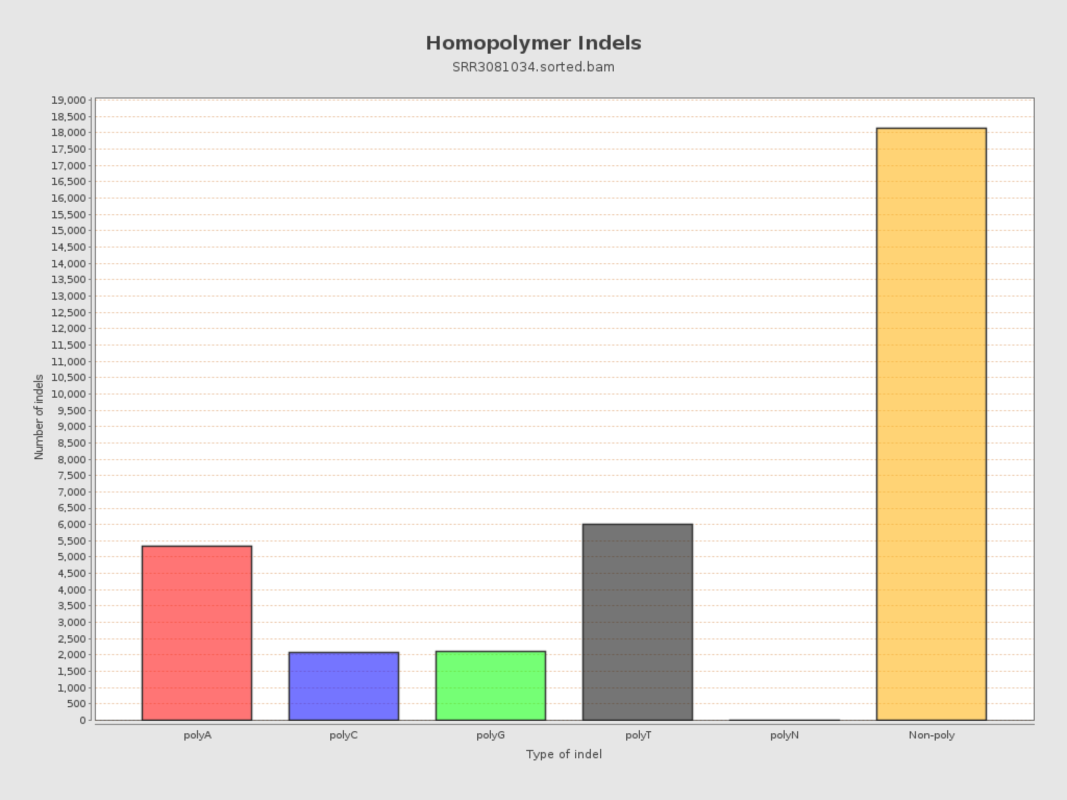
9. Results : Mapped Reads GC-content Distribution



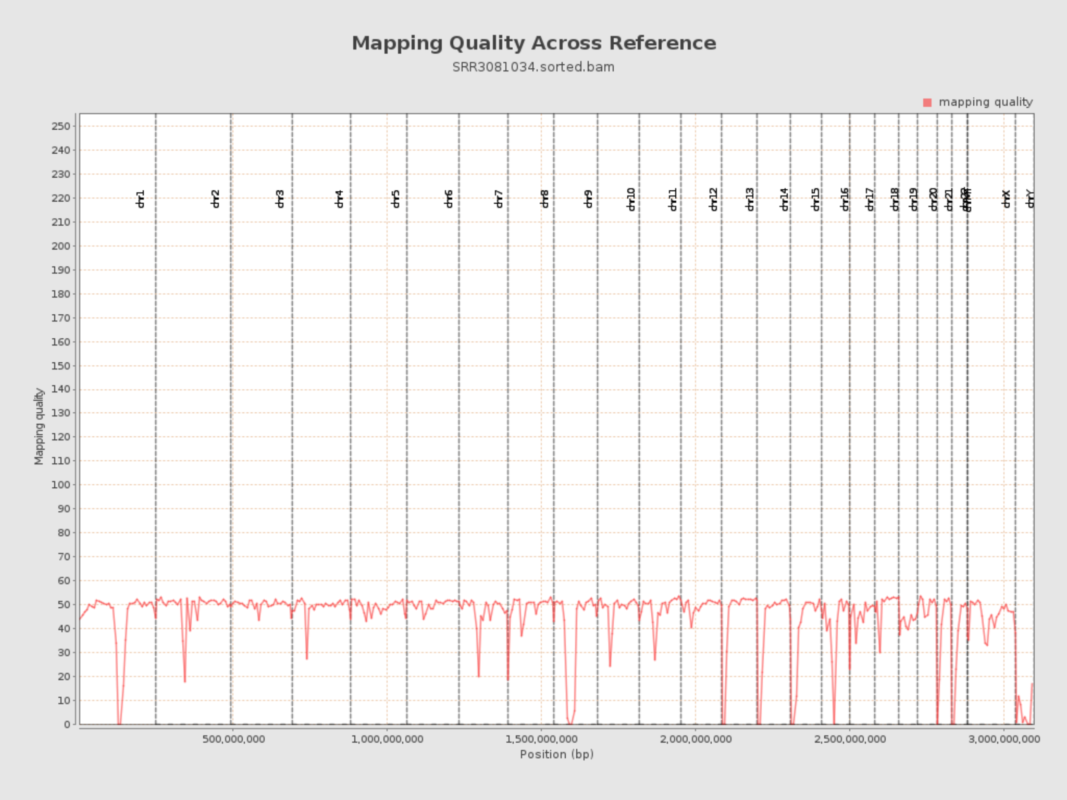
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram