Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:49:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081954.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_SRR3081954 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081954.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:49:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,791,217
Mapped reads	2,597,853 / 93.07%
Unmapped reads	193,364 / 6.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,724 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	122,822 / 4.4%
Duplication rate	3.84%
Clipped reads	944,292 / 33.83%

2.2. ACGT Content

Number/percentage of A's	50,596,401 / 28.46%
Number/percentage of C's	32,842,673 / 18.47%
Number/percentage of T's	56,413,264 / 31.73%
Number/percentage of G's	37,930,155 / 21.33%
Number/percentage of N's	23,274 / 0.01%
GC Percentage	39.8%

2.3. Coverage

Mean	0.0575

Standard Deviation	0.432

2.4. Mapping Quality

Mean Mapping Quality	47

2.5. Mismatches and indels

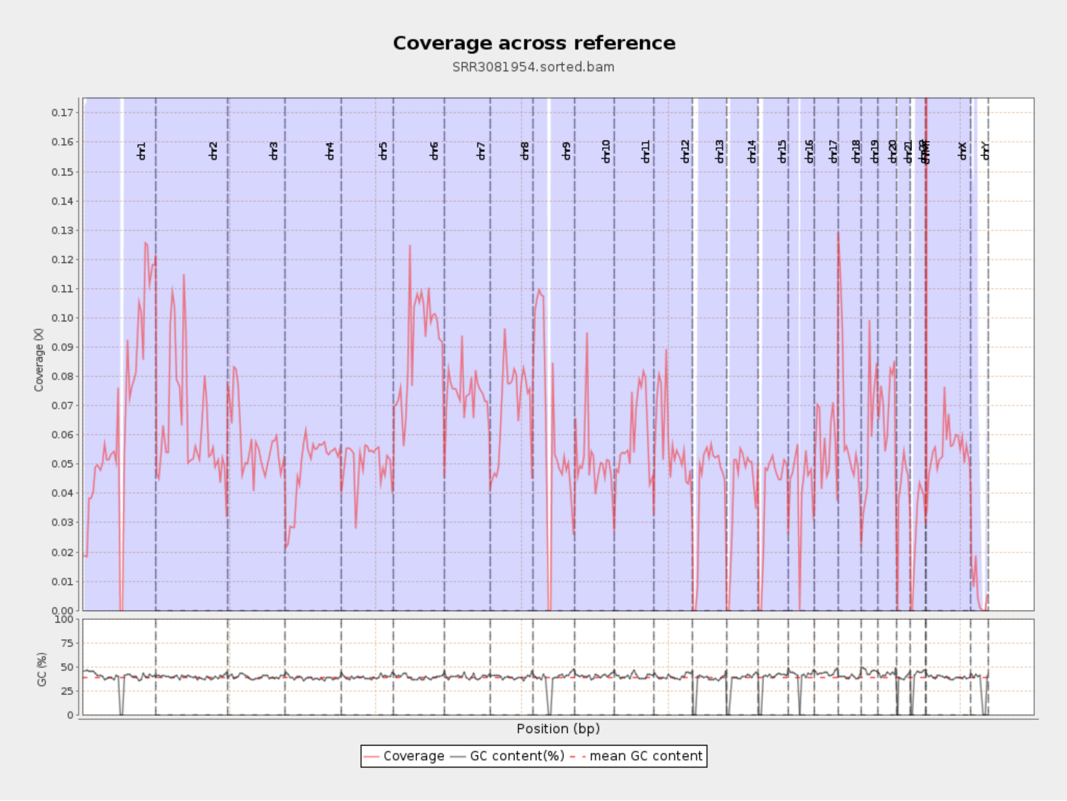
General error rate	0.74%
Mismatches	1,288,930
Insertions	12,013
Mapped reads with at least one insertion	0.46%
Deletions	35,412
Mapped reads with at least one deletion	1.35%
Homopolymer indels	49.01%

2.6. Chromosome stats

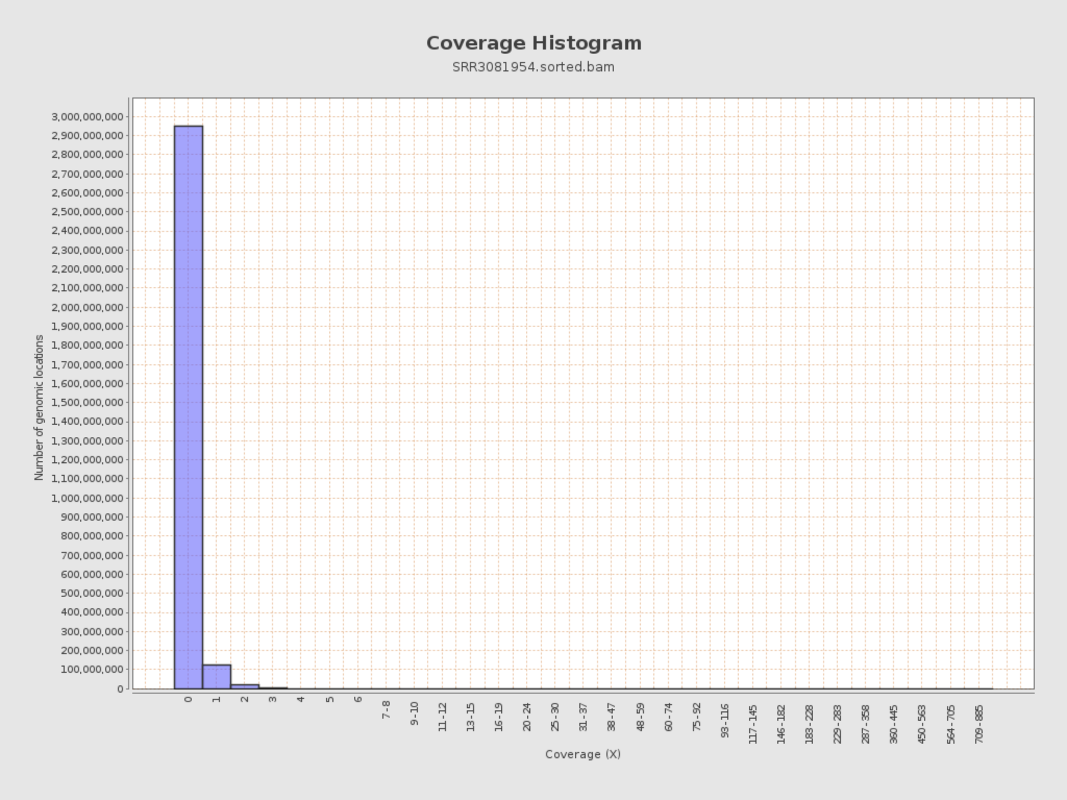
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16396538	0.0658	0.7155
chr2	243199373	15508135	0.0638	0.5576
chr3	198022430	11389105	0.0575	0.276
chr4	191154276	9324667	0.0488	0.2661
chr5	180915260	9048877	0.05	0.2583
chr6	171115067	15651803	0.0915	0.4457
chr7	159138663	11748980	0.0738	0.5284

chr8	146364022	10201615	0.0697	0.6474
chr9	141213431	8709810	0.0617	0.4534
chr10	135534747	6994033	0.0516	0.415
chr11	135006516	8044737	0.0596	0.3454
chr12	133851895	7671416	0.0573	0.2829
chr13	115169878	4871184	0.0423	0.2363
chr14	107349540	4418930	0.0412	0.2527
chr15	102531392	4050642	0.0395	0.2288
chr16	90354753	3759612	0.0416	0.2671
chr17	81195210	4660725	0.0574	0.3027
chr18	78077248	5067171	0.0649	0.695
chr19	59128983	3530192	0.0597	0.5357
chr20	63025520	4462935	0.0708	0.3107
chr21	48129895	1949495	0.0405	0.2559
chr22	51304566	1434559	0.028	0.1901
chrMT	16571	50423	3.0428	2.3128
chrX	155270560	8553308	0.0551	0.3062
chrY	59373566	369664	0.0062	0.1401

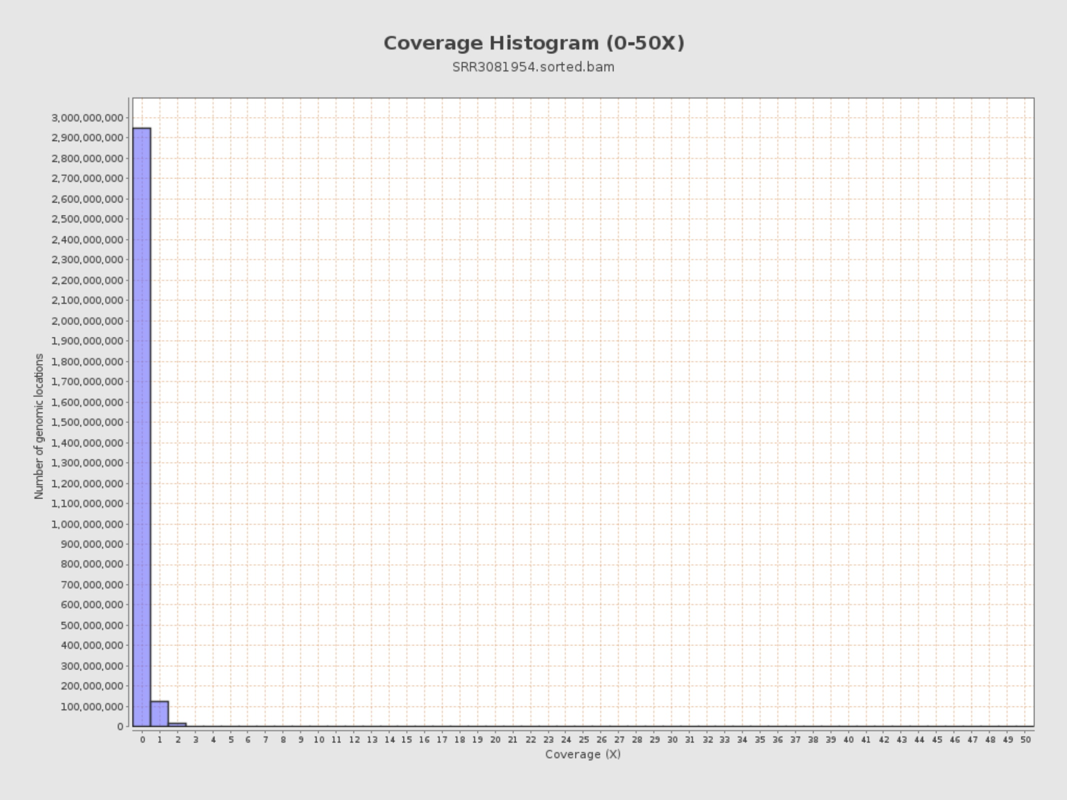
3. Results : Coverage across reference



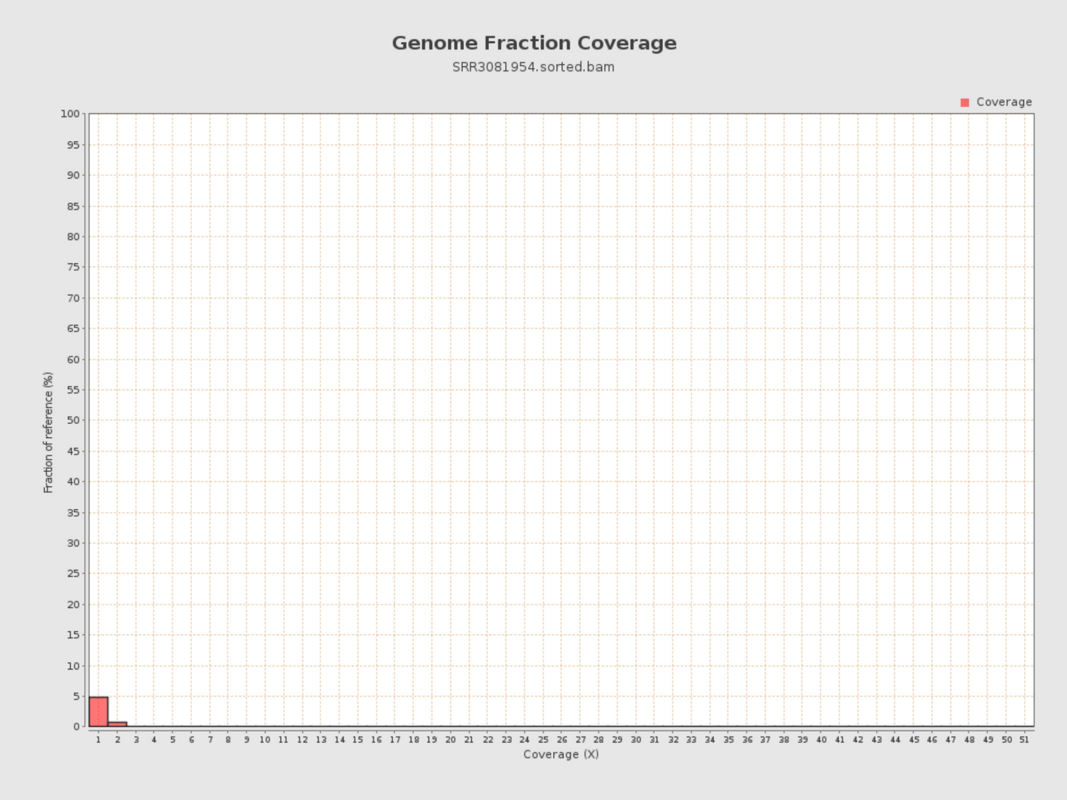
4. Results : Coverage Histogram



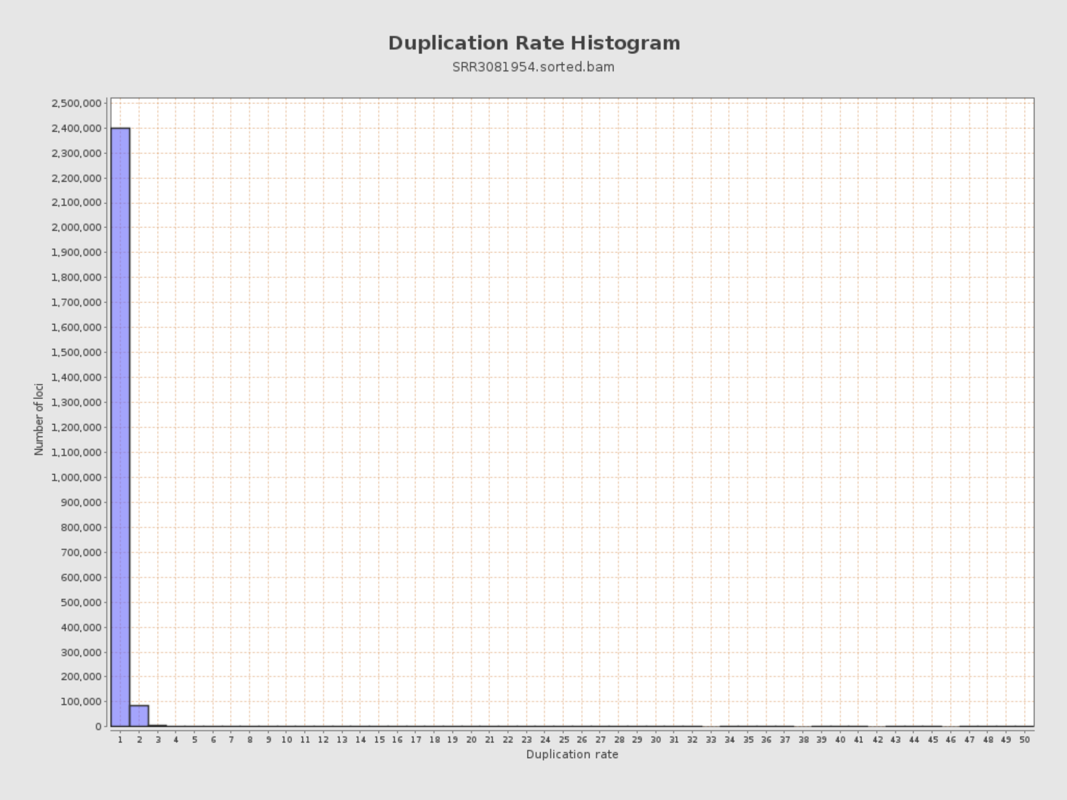
5. Results : Coverage Histogram (0-50X)



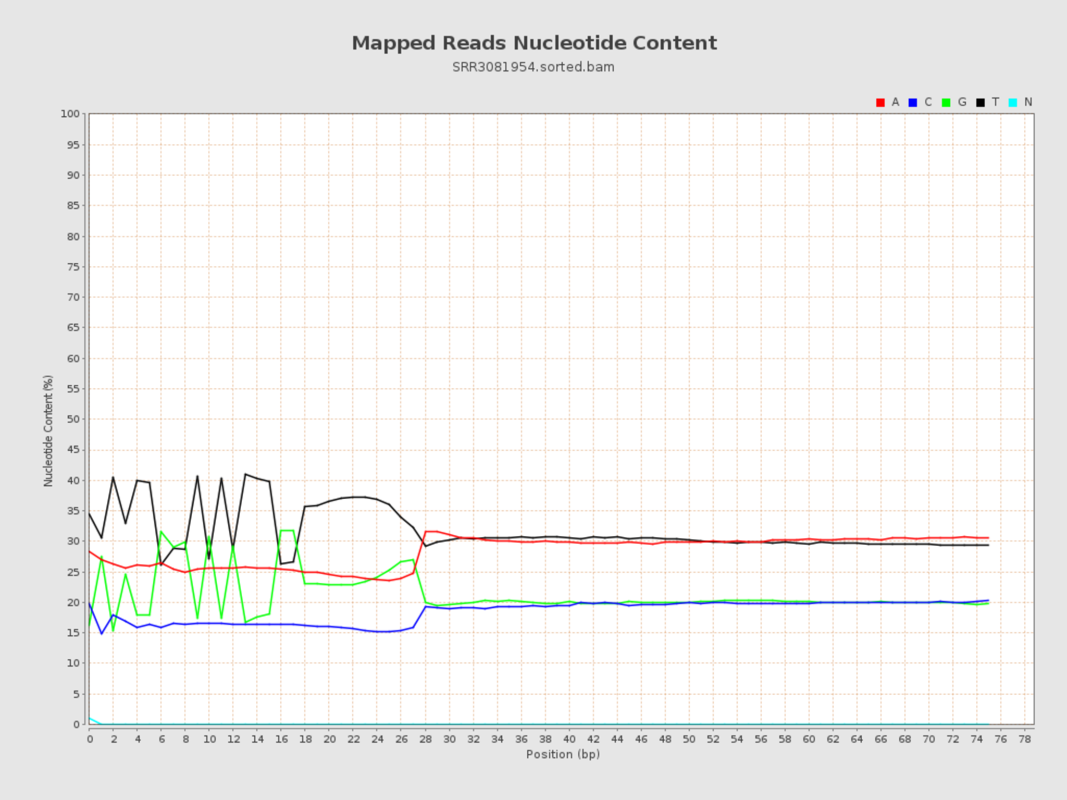
6. Results : Genome Fraction Coverage



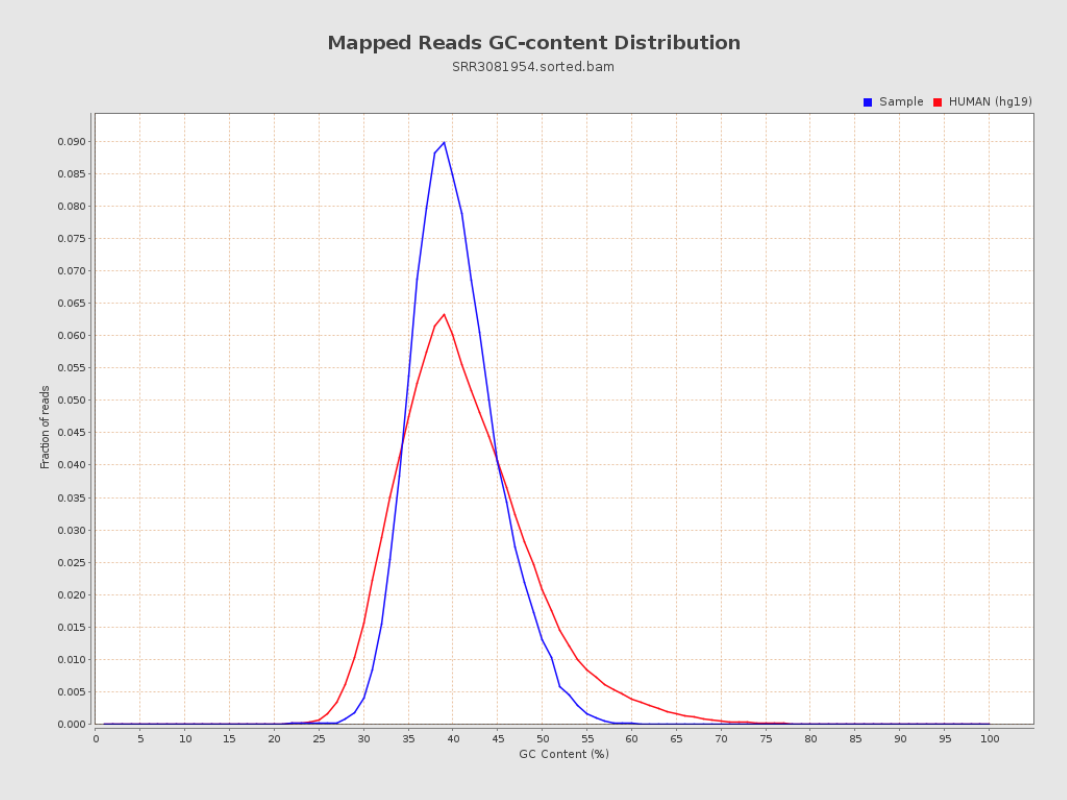
7. Results : Duplication Rate Histogram



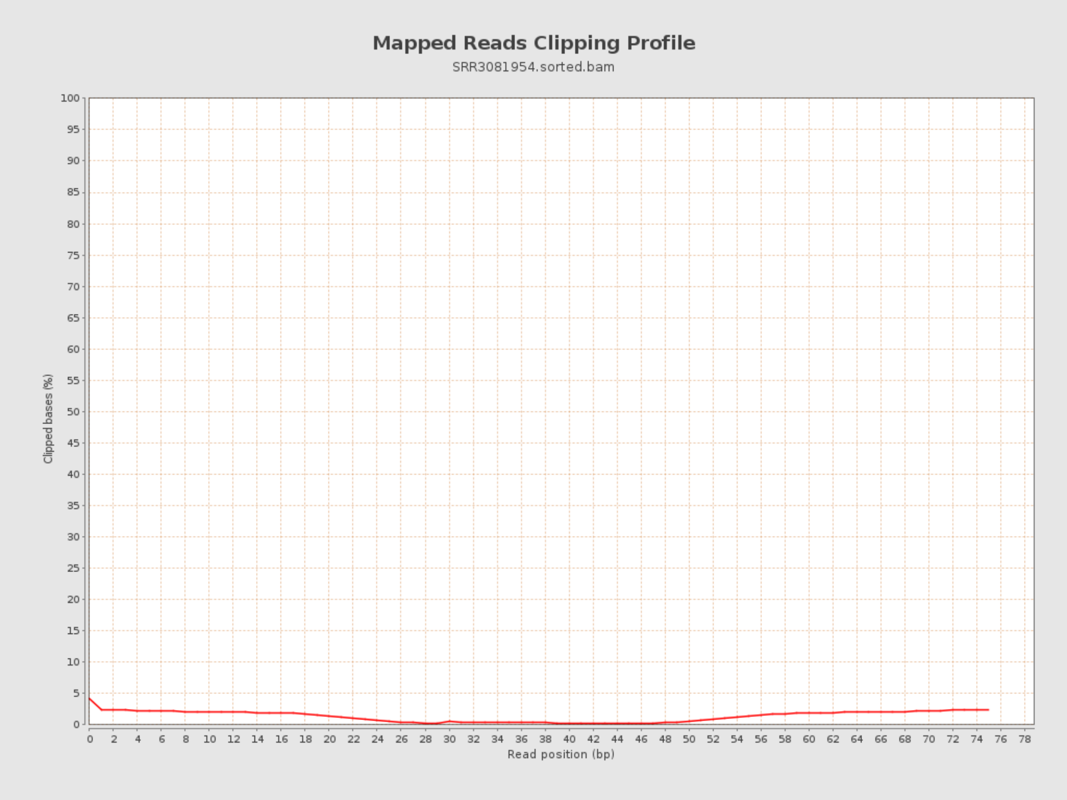
8. Results : Mapped Reads Nucleotide Content



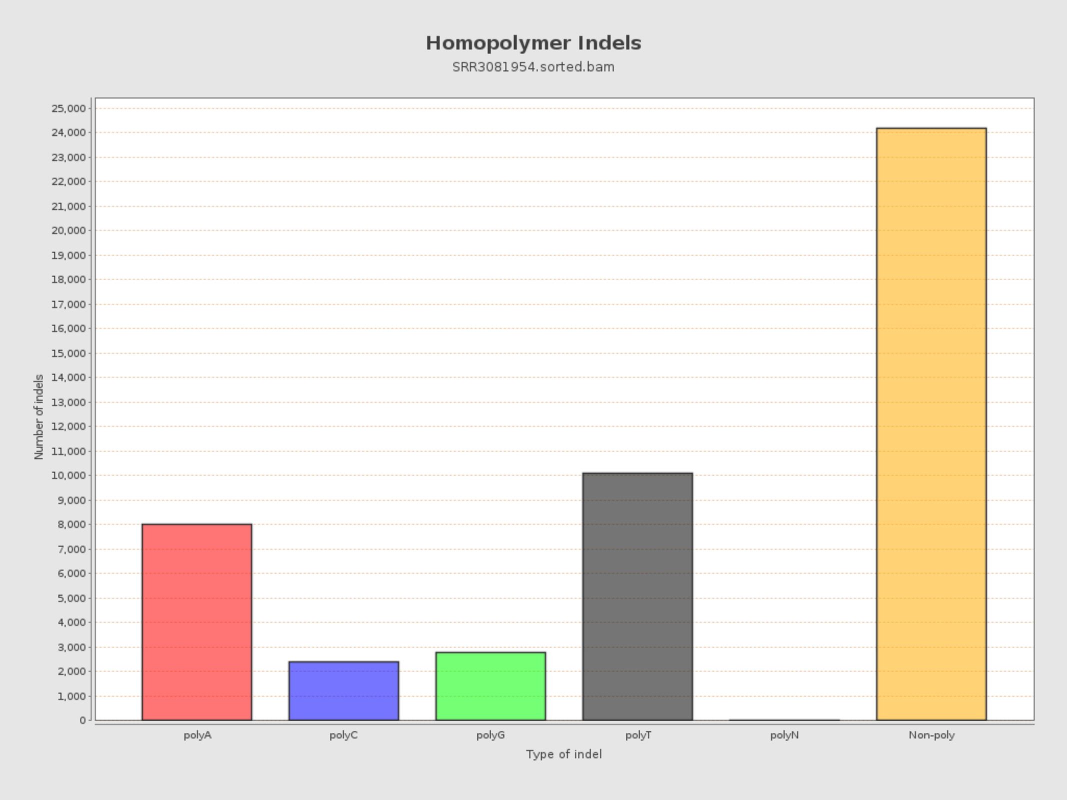
9. Results : Mapped Reads GC-content Distribution



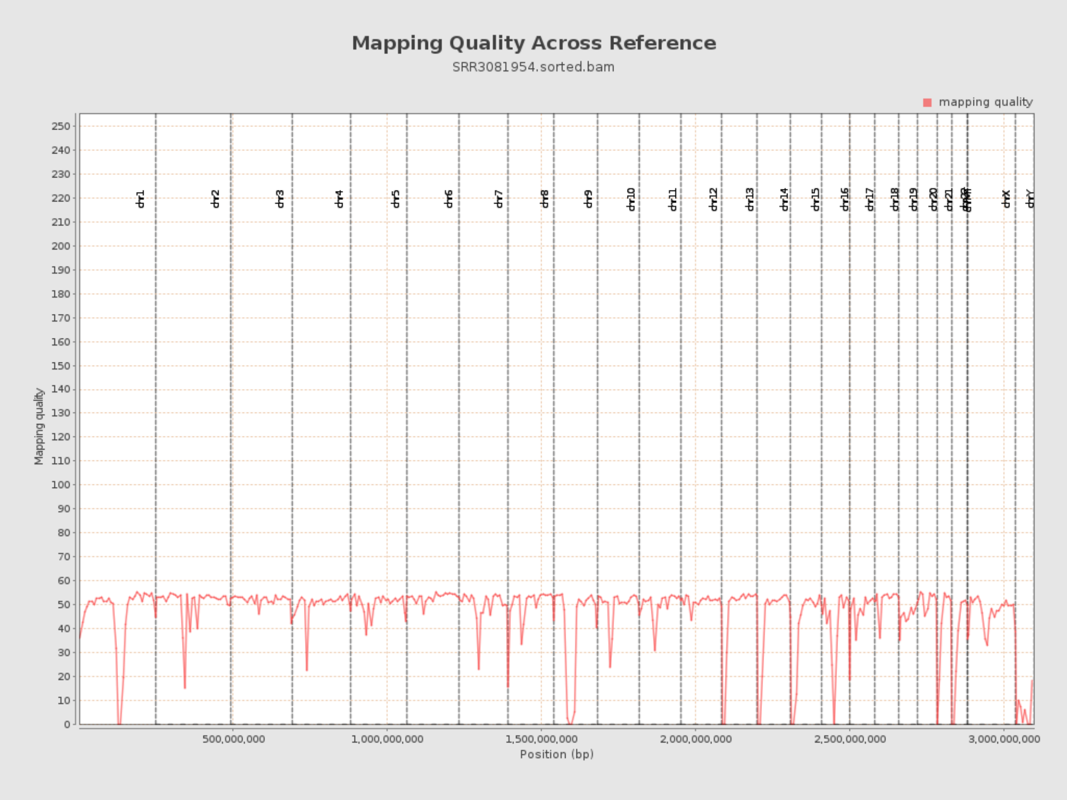
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram