Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:31:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081950.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_SRR3081950 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081950.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:31:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081950.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,864,894
Mapped reads	2,648,374 / 92.44%
Unmapped reads	216,520 / 7.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,794 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	123,456 / 4.31%
Duplication rate	3.68%
Clipped reads	979,277 / 34.18%

2.2. ACGT Content

Number/percentage of A's	51,279,634 / 28.36%
Number/percentage of C's	33,403,388 / 18.47%
Number/percentage of T's	57,181,030 / 31.62%
Number/percentage of G's	38,931,280 / 21.53%
Number/percentage of N's	23,500 / 0.01%
GC Percentage	40%

2.3. Coverage

Mean	0.0584

Standard Deviation	0.4586

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

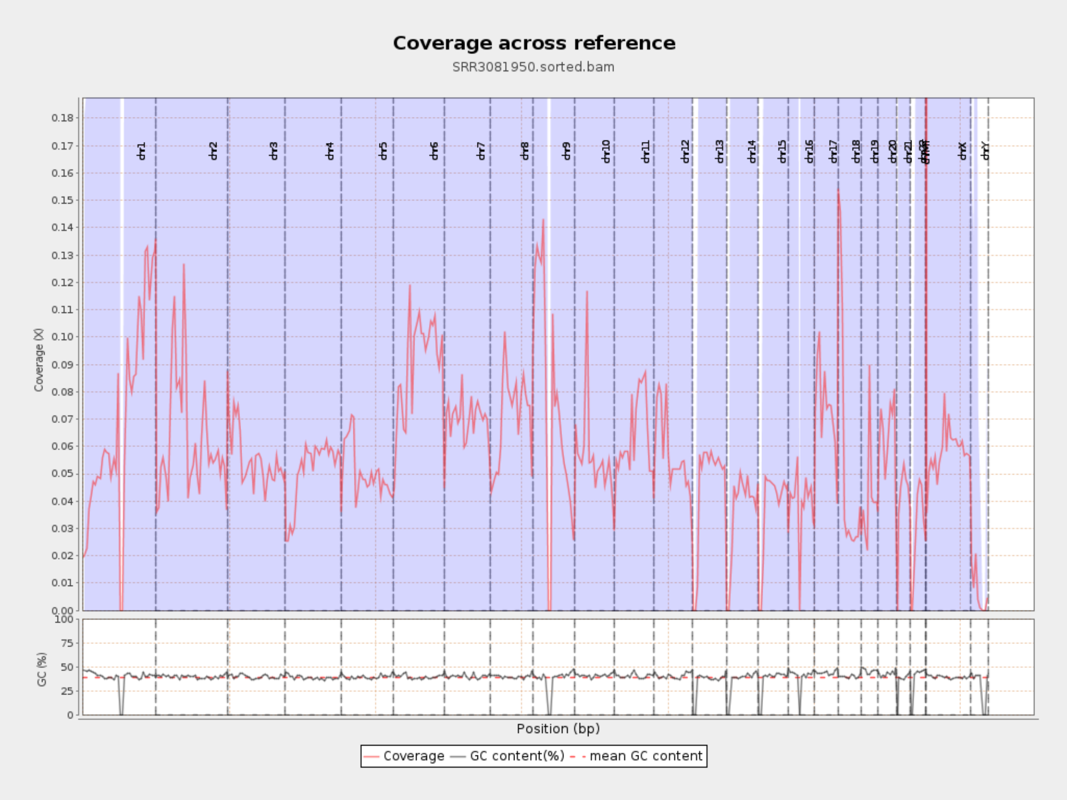
General error rate	0.77%
Mismatches	1,362,558
Insertions	12,808
Mapped reads with at least one insertion	0.48%
Deletions	39,033
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.04%

2.6. Chromosome stats

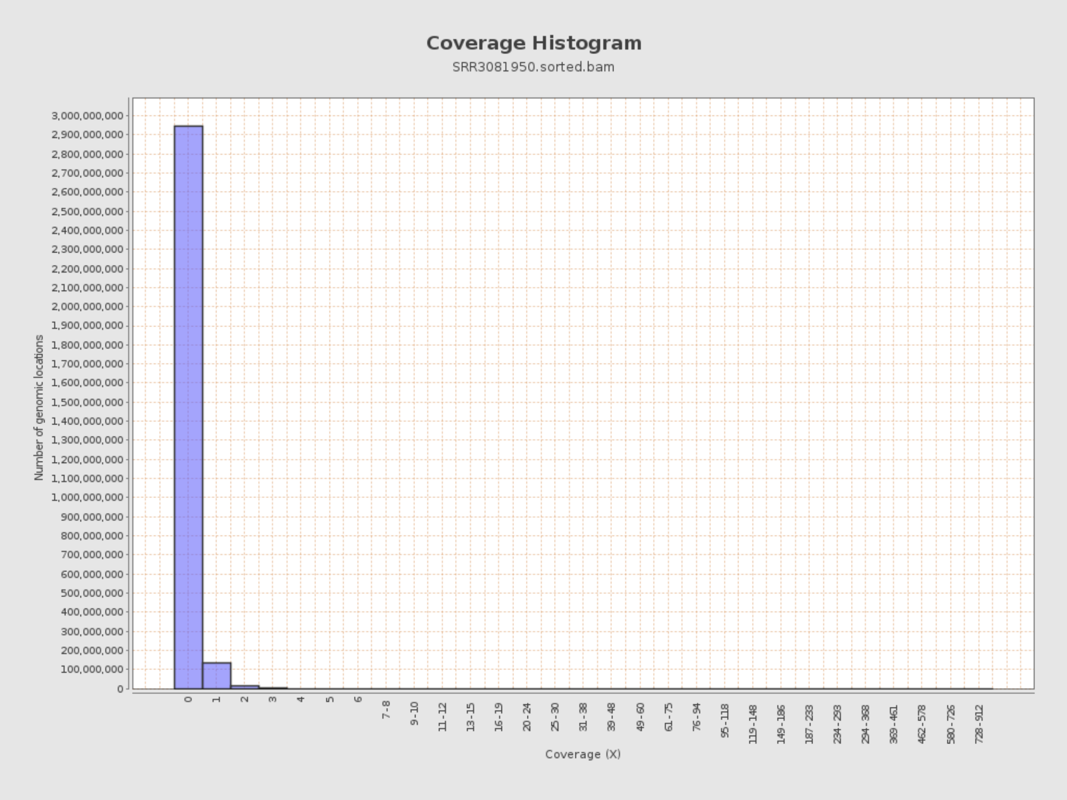
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17454884	0.07	0.7557
chr2	243199373	15388801	0.0633	0.6176
chr3	198022430	11036469	0.0557	0.2759
chr4	191154276	9790504	0.0512	0.2789
chr5	180915260	9139483	0.0505	0.2598
chr6	171115067	15660798	0.0915	0.4246
chr7	159138663	11125955	0.0699	0.477

chr8	146364022	10362894	0.0708	0.6737
chr9	141213431	10682403	0.0756	0.5351
chr10	135534747	7687991	0.0567	0.5188
chr11	135006516	8654875	0.0641	0.3793
chr12	133851895	7681376	0.0574	0.283
chr13	115169878	5239047	0.0455	0.2407
chr14	107349540	3930444	0.0366	0.2639
chr15	102531392	3776811	0.0368	0.2202
chr16	90354753	3449190	0.0382	0.272
chr17	81195210	6125439	0.0754	0.3693
chr18	78077248	4227545	0.0541	0.7716
chr19	59128983	2456049	0.0415	0.5844
chr20	63025520	4133276	0.0656	0.2996
chr21	48129895	1945305	0.0404	0.2675
chr22	51304566	1485982	0.029	0.1898
chrMT	16571	41042	2.4767	2.0906
chrX	155270560	9021988	0.0581	0.3242
chrY	59373566	389391	0.0066	0.166

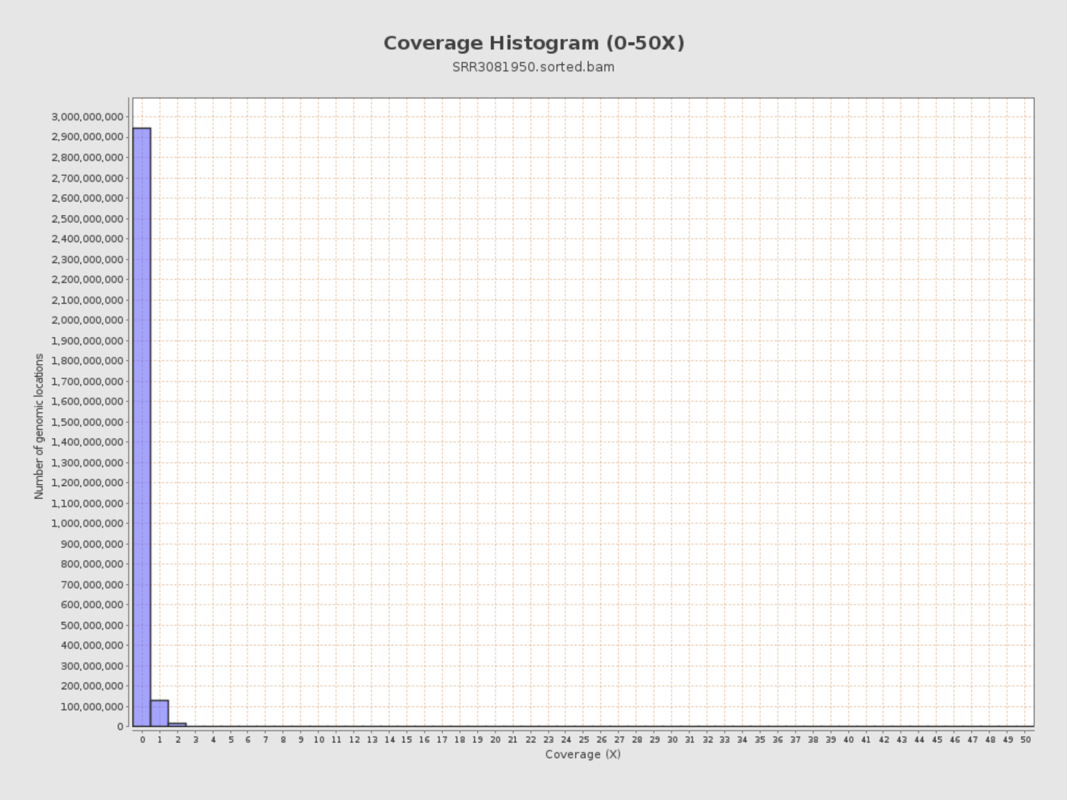
3. Results : Coverage across reference



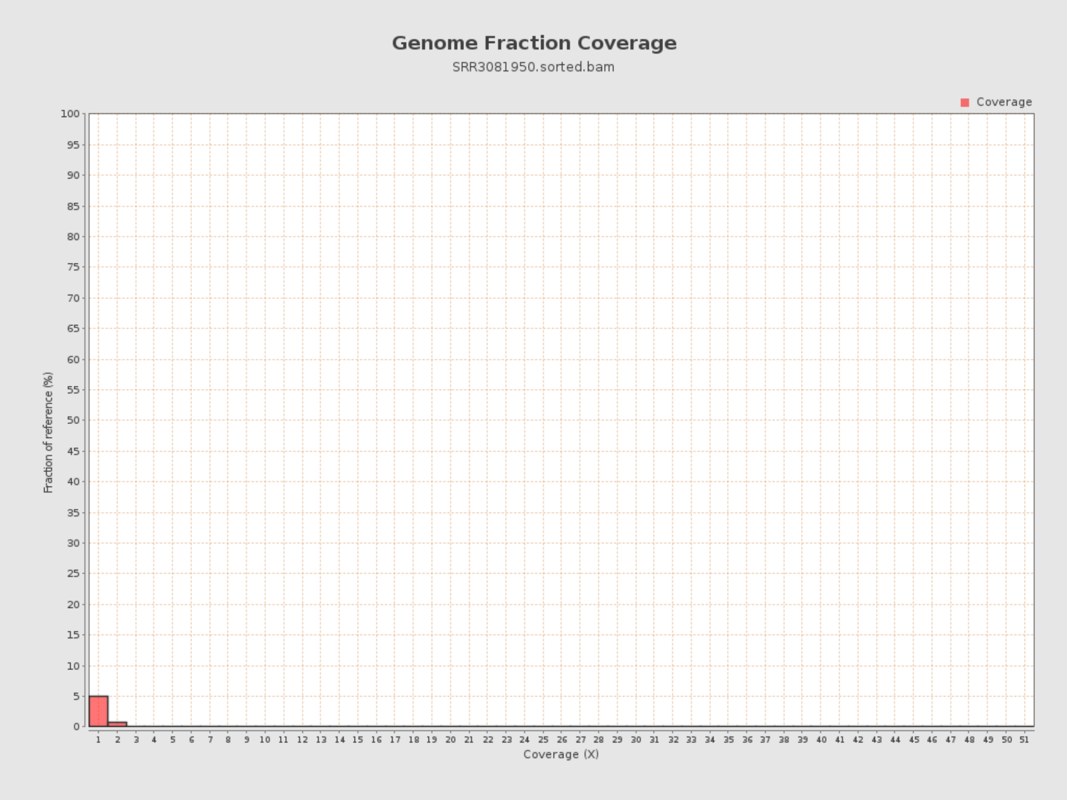
4. Results : Coverage Histogram



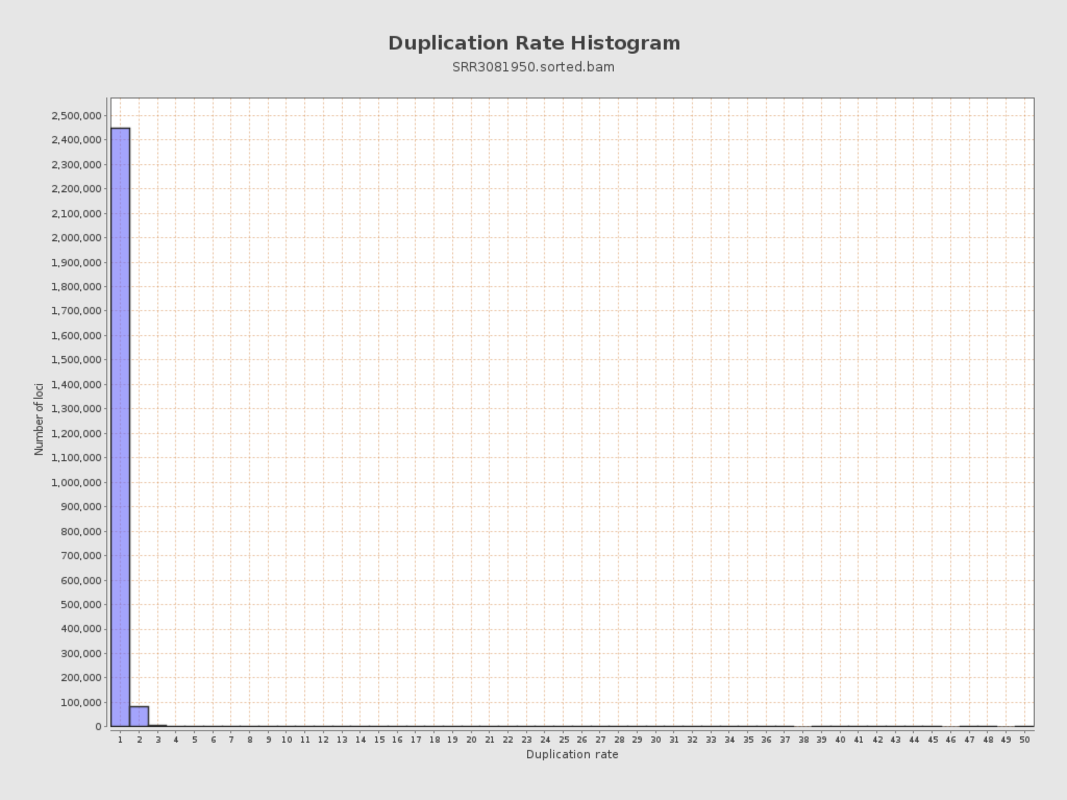
5. Results : Coverage Histogram (0-50X)



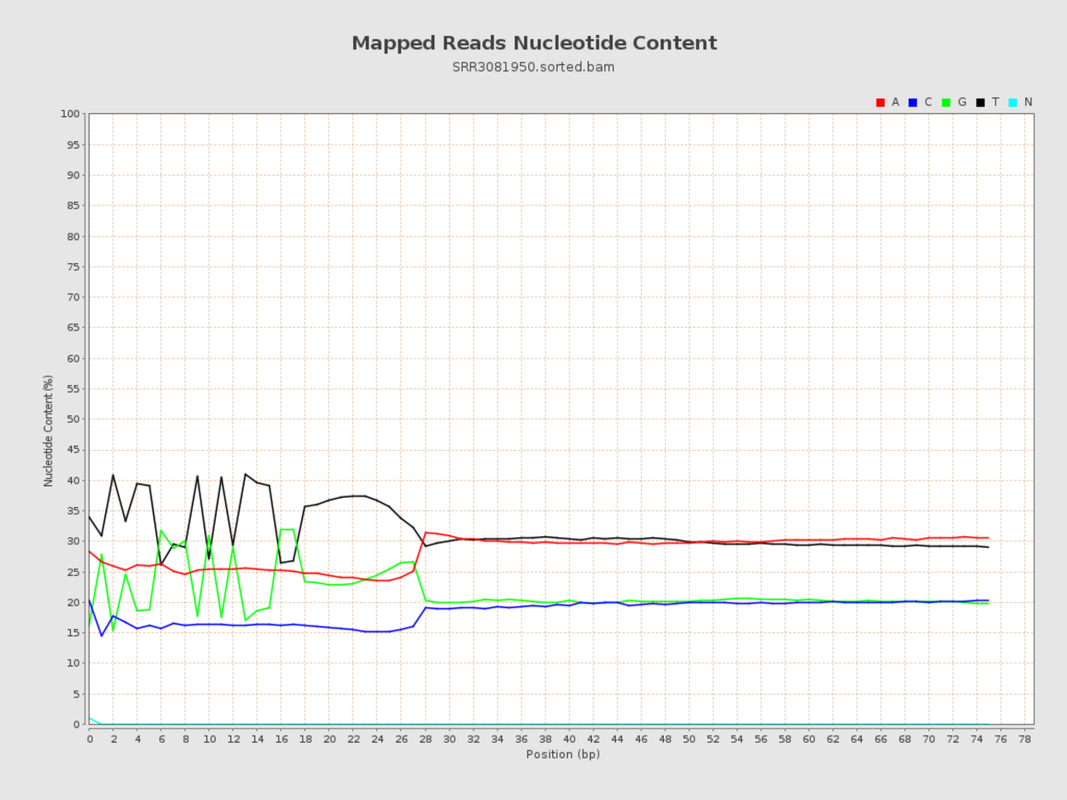
6. Results : Genome Fraction Coverage



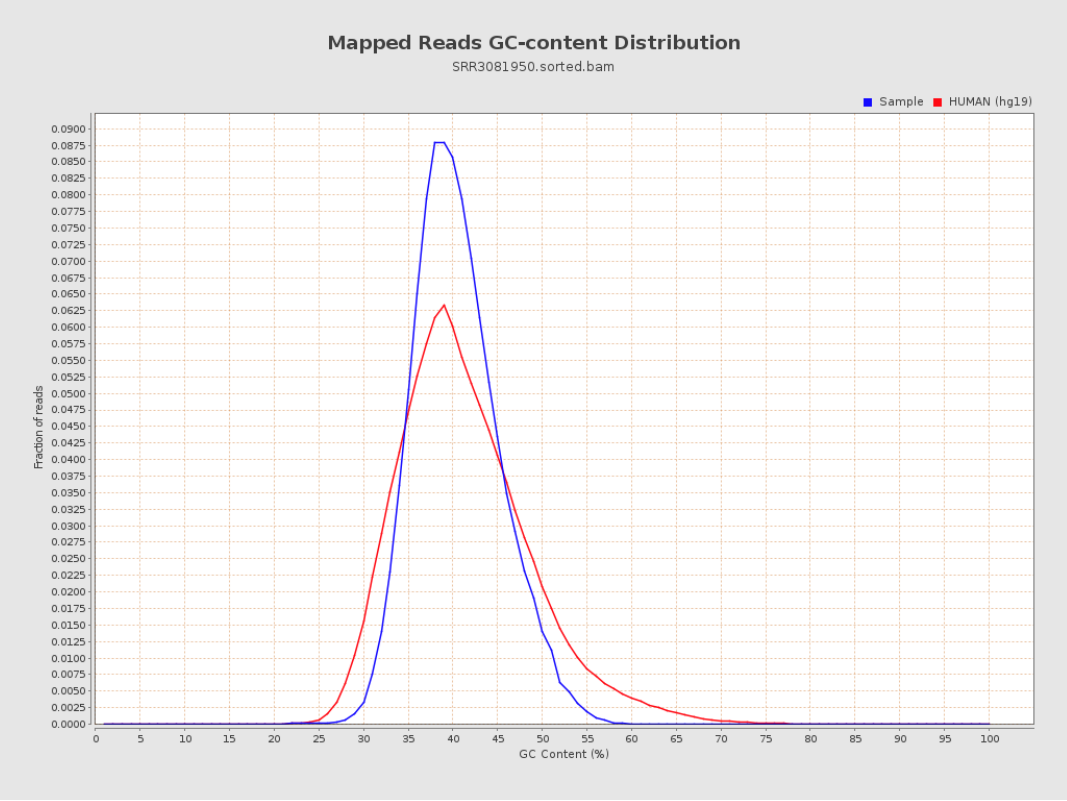
7. Results : Duplication Rate Histogram



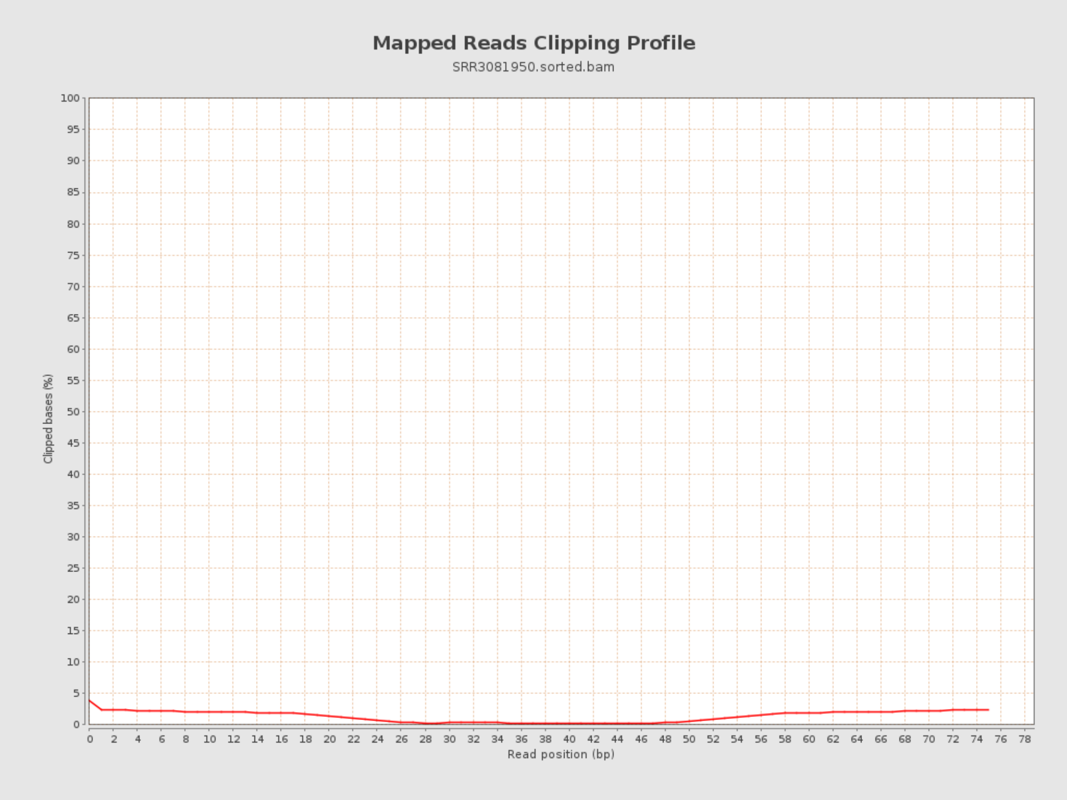
8. Results : Mapped Reads Nucleotide Content



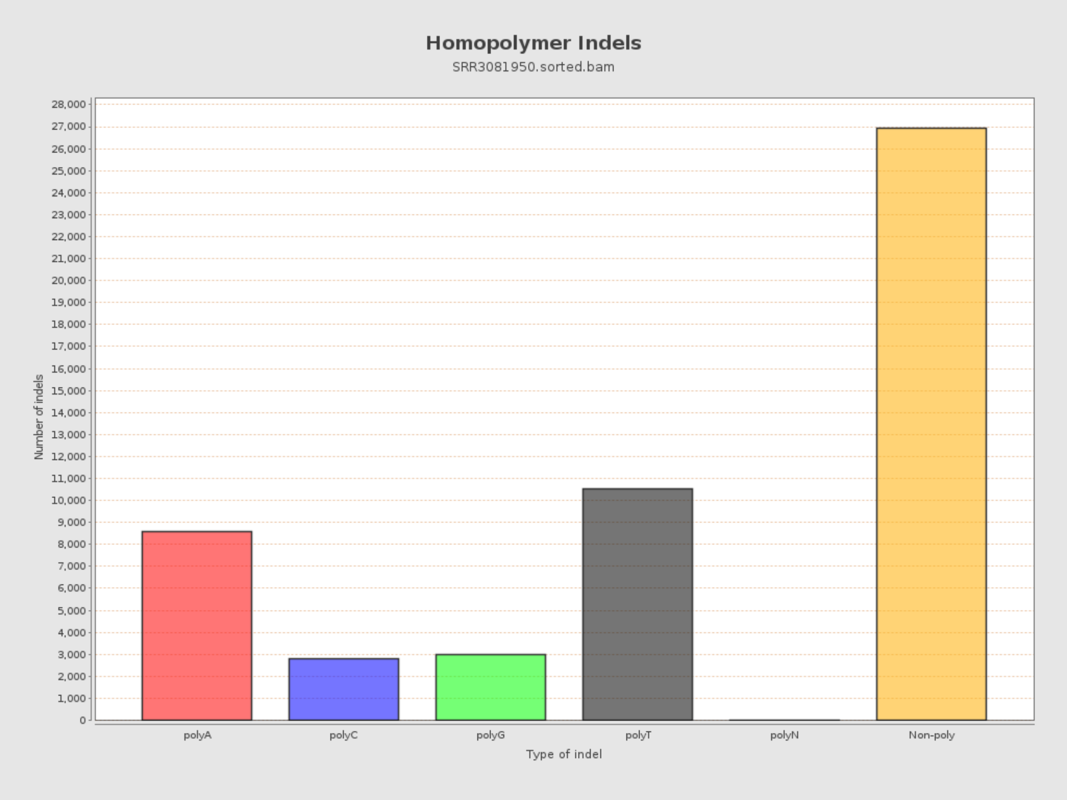
9. Results : Mapped Reads GC-content Distribution



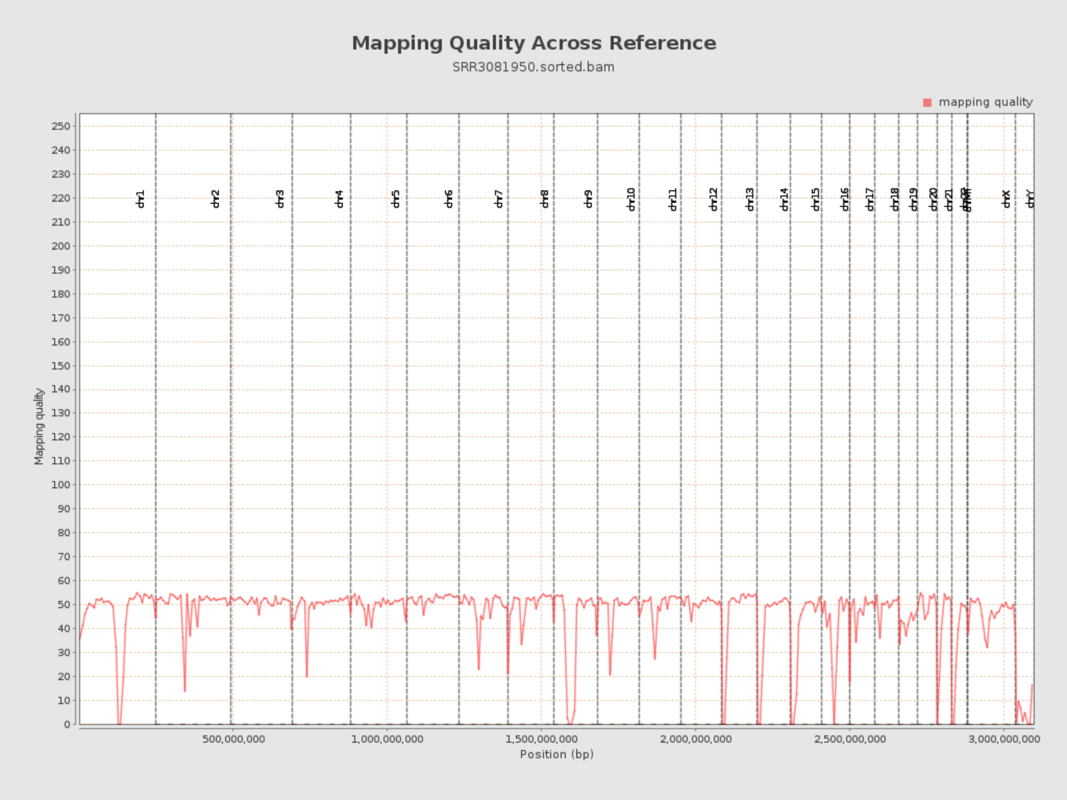
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram