Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:03:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081957.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_SRR3081957 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081957.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:03:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081957.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,704,699
Mapped reads	2,463,977 / 91.1%
Unmapped reads	240,722 / 8.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,209 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	109,361 / 4.04%
Duplication rate	3.1%
Clipped reads	808,364 / 29.89%

2.2. ACGT Content

Number/percentage of A's	49,315,080 / 28.84%
Number/percentage of C's	31,999,846 / 18.72%
Number/percentage of T's	53,565,751 / 31.33%
Number/percentage of G's	36,071,860 / 21.1%
Number/percentage of N's	22,127 / 0.01%
GC Percentage	39.81%

2.3. Coverage

Mean	0.0553

Standard Deviation	0.5488

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

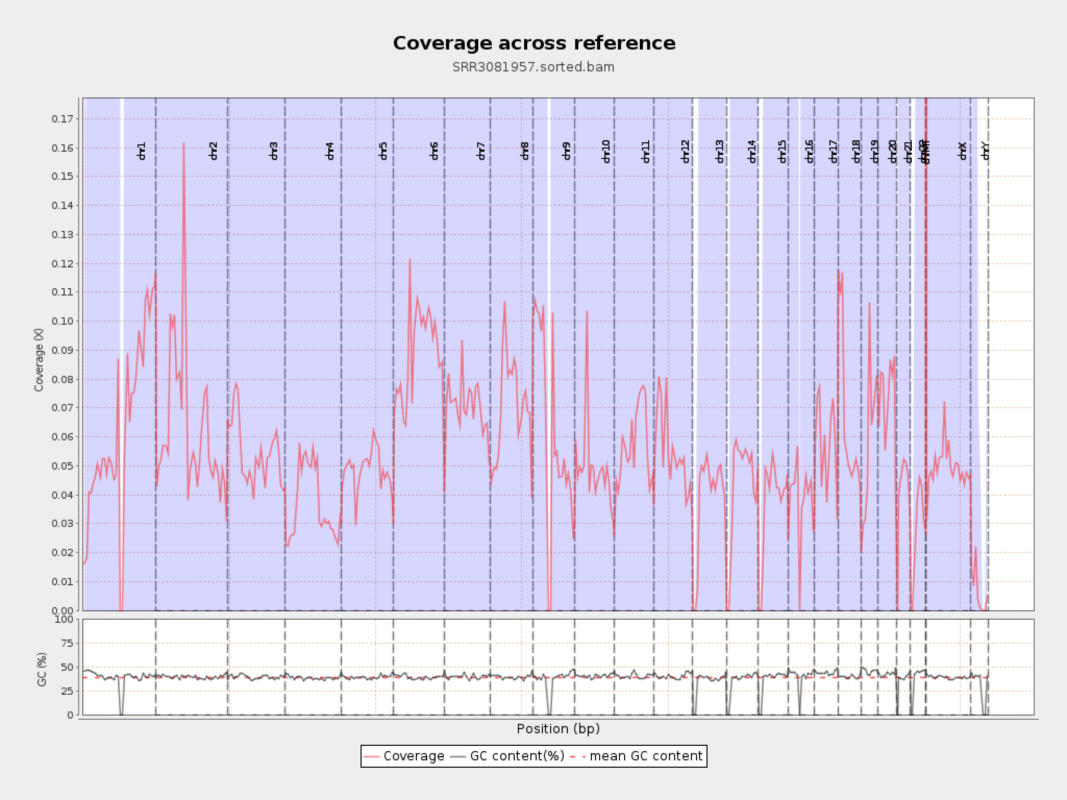
General error rate	0.81%
Mismatches	1,365,052
Insertions	13,100
Mapped reads with at least one insertion	0.53%
Deletions	39,726
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.39%

2.6. Chromosome stats

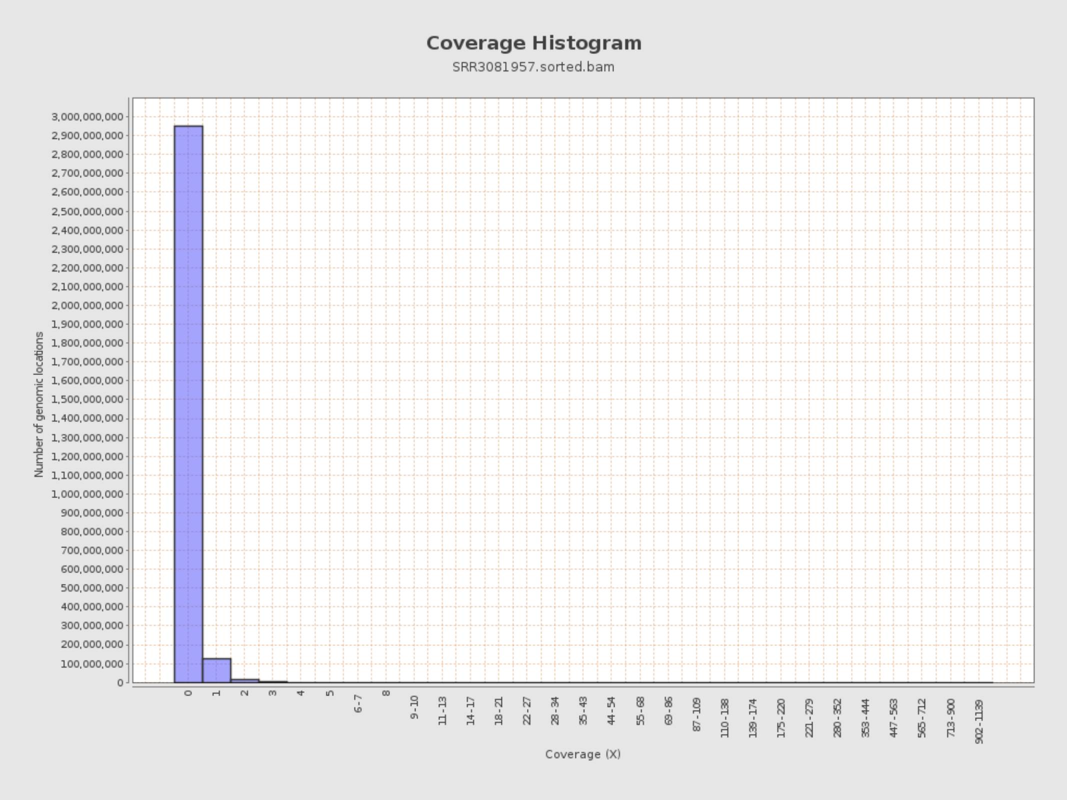
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15610288	0.0626	0.9631
chr2	243199373	15476798	0.0636	0.8475
chr3	198022430	10813931	0.0546	0.2648
chr4	191154276	7123897	0.0373	0.252
chr5	180915260	8728218	0.0482	0.2554
chr6	171115067	15310676	0.0895	0.4258
chr7	159138663	11162410	0.0701	0.5779

chr8	146364022	10285337	0.0703	0.804
chr9	141213431	8669449	0.0614	0.6682
chr10	135534747	6702851	0.0495	0.474
chr11	135006516	7710630	0.0571	0.4341
chr12	133851895	7353121	0.0549	0.2838
chr13	115169878	4418924	0.0384	0.219
chr14	107349540	4680891	0.0436	0.284
chr15	102531392	3763370	0.0367	0.2159
chr16	90354753	3392653	0.0375	0.2967
chr17	81195210	4783311	0.0589	0.3081
chr18	78077248	5161456	0.0661	1.044
chr19	59128983	3511040	0.0594	0.651
chr20	63025520	4692129	0.0744	0.3184
chr21	48129895	1978833	0.0411	0.2788
chr22	51304566	1414192	0.0276	0.1842
chrMT	16571	214925	12.9699	7.8252
chrX	155270560	7696420	0.0496	0.3288
chrY	59373566	389739	0.0066	0.1855

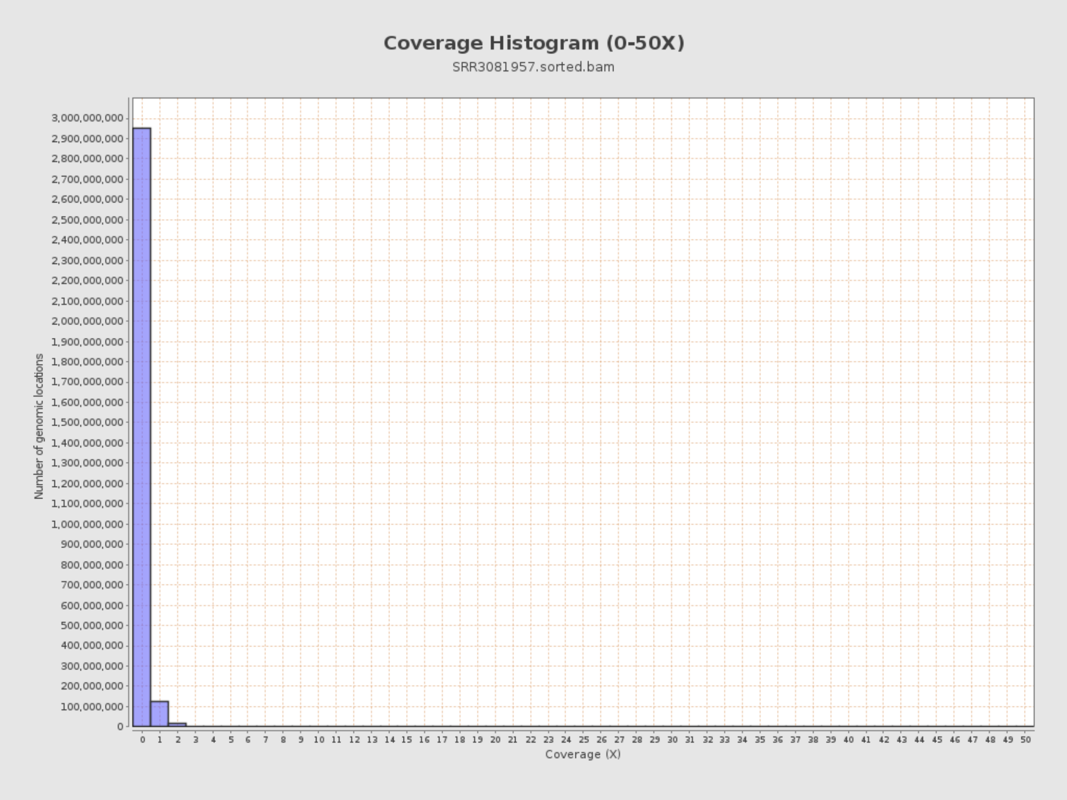
3. Results : Coverage across reference



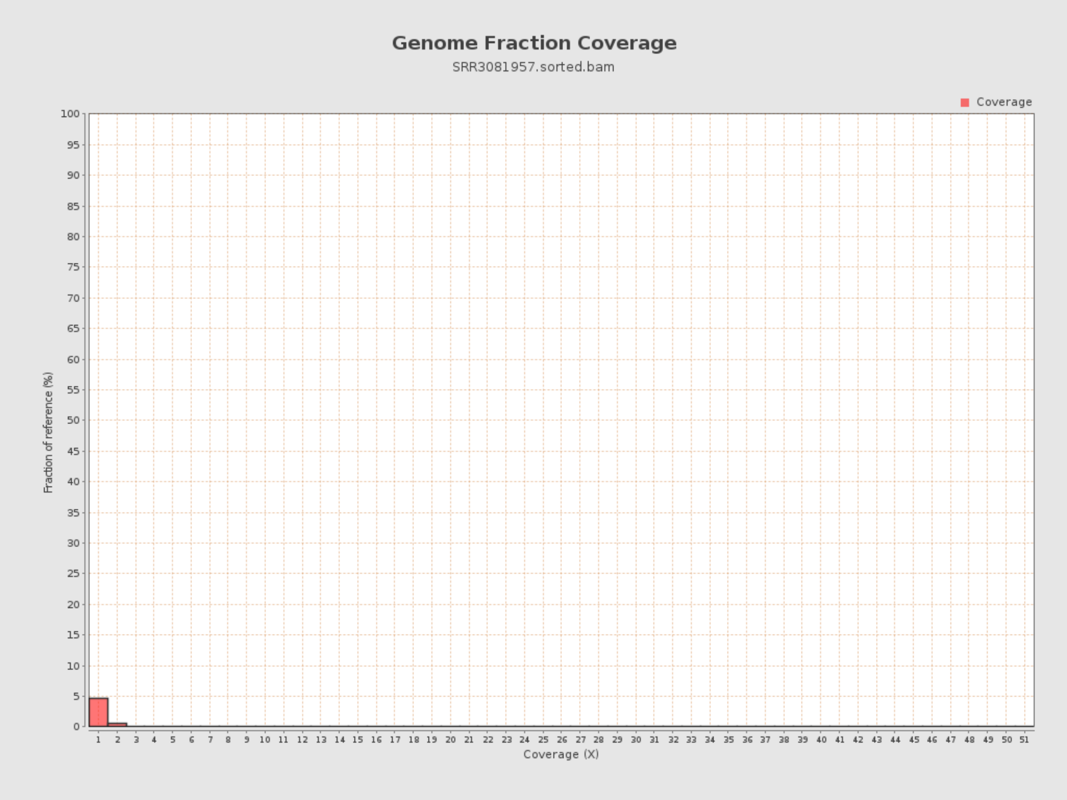
4. Results : Coverage Histogram



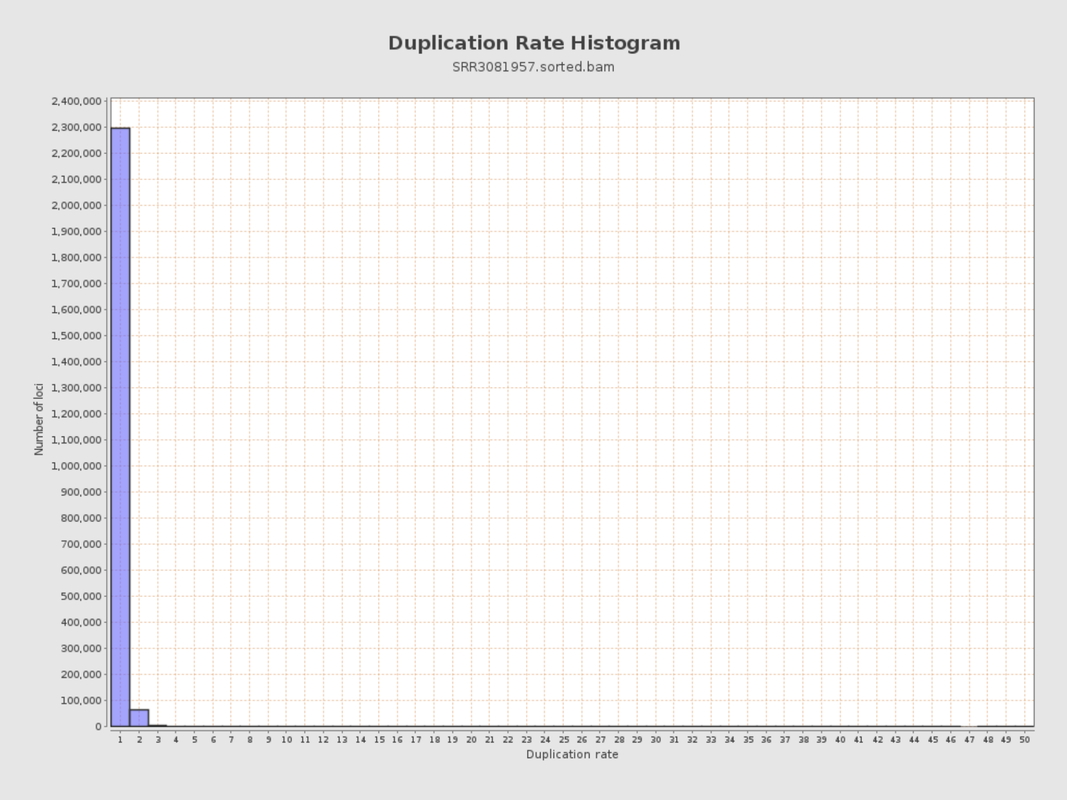
5. Results : Coverage Histogram (0-50X)



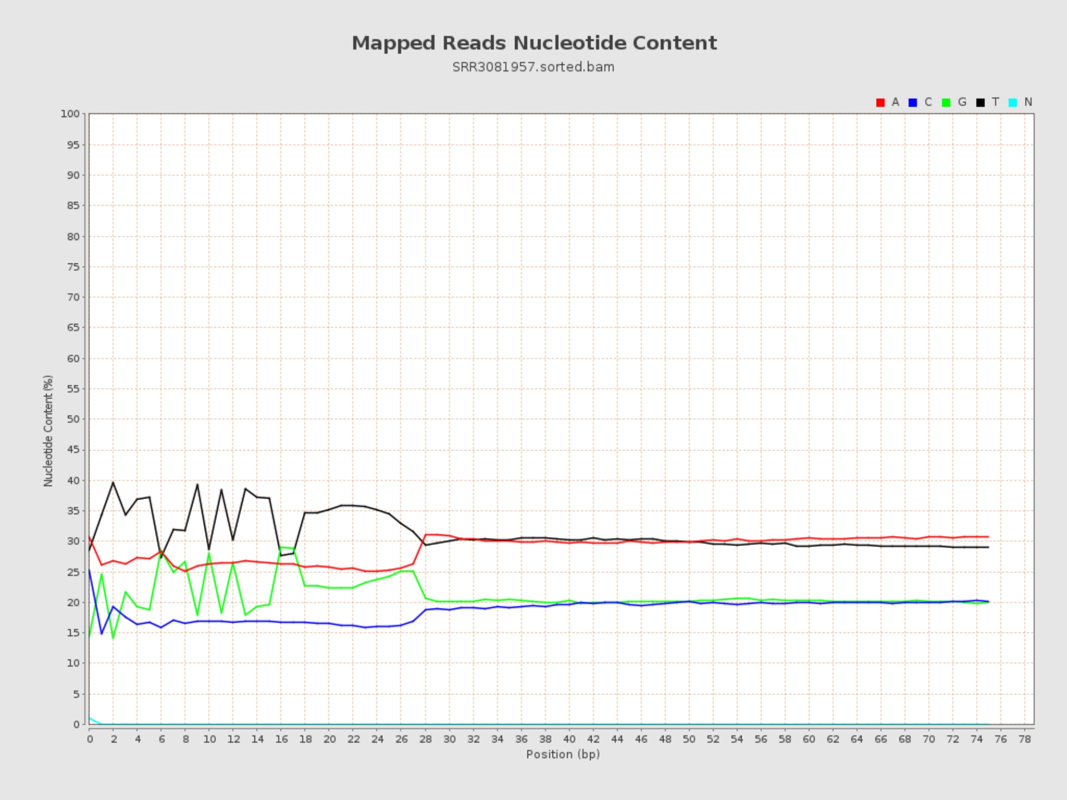
6. Results : Genome Fraction Coverage



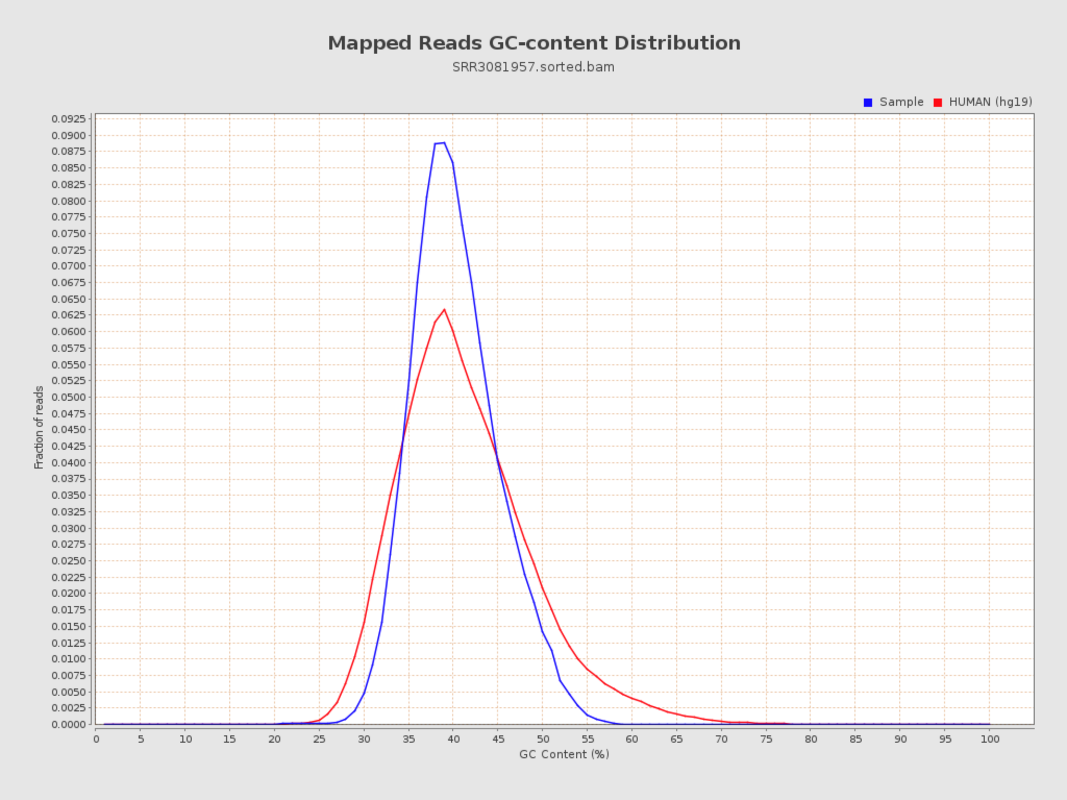
7. Results : Duplication Rate Histogram



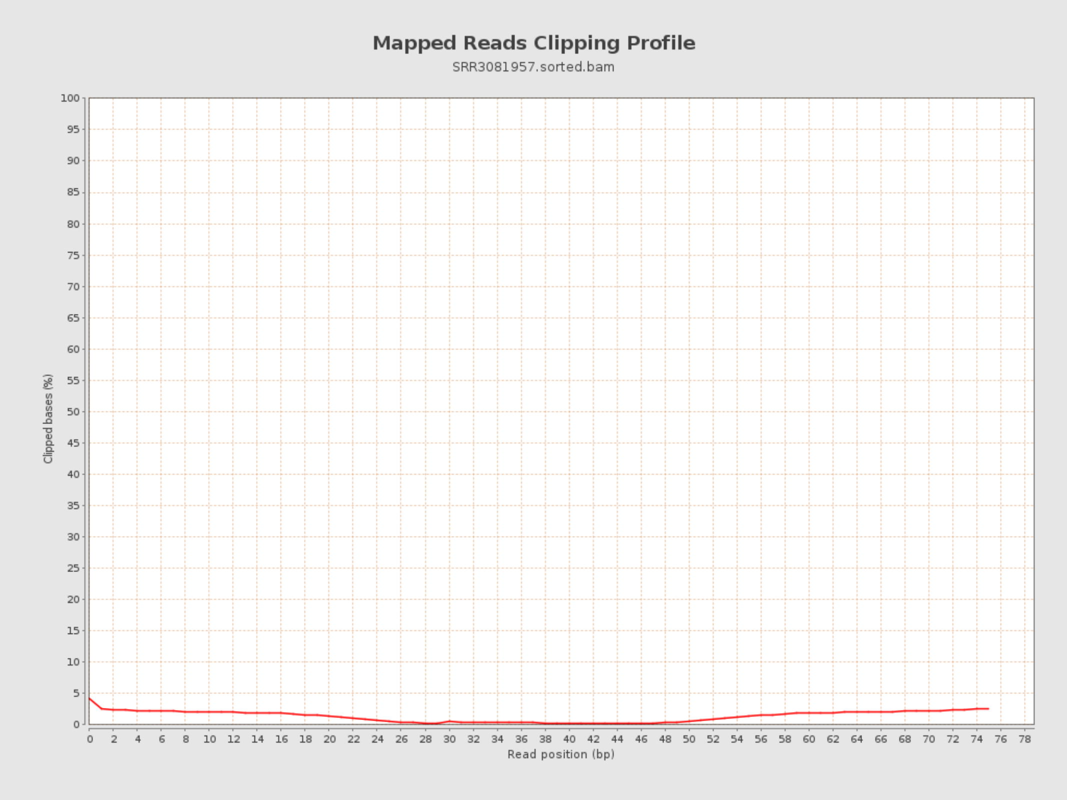
8. Results : Mapped Reads Nucleotide Content



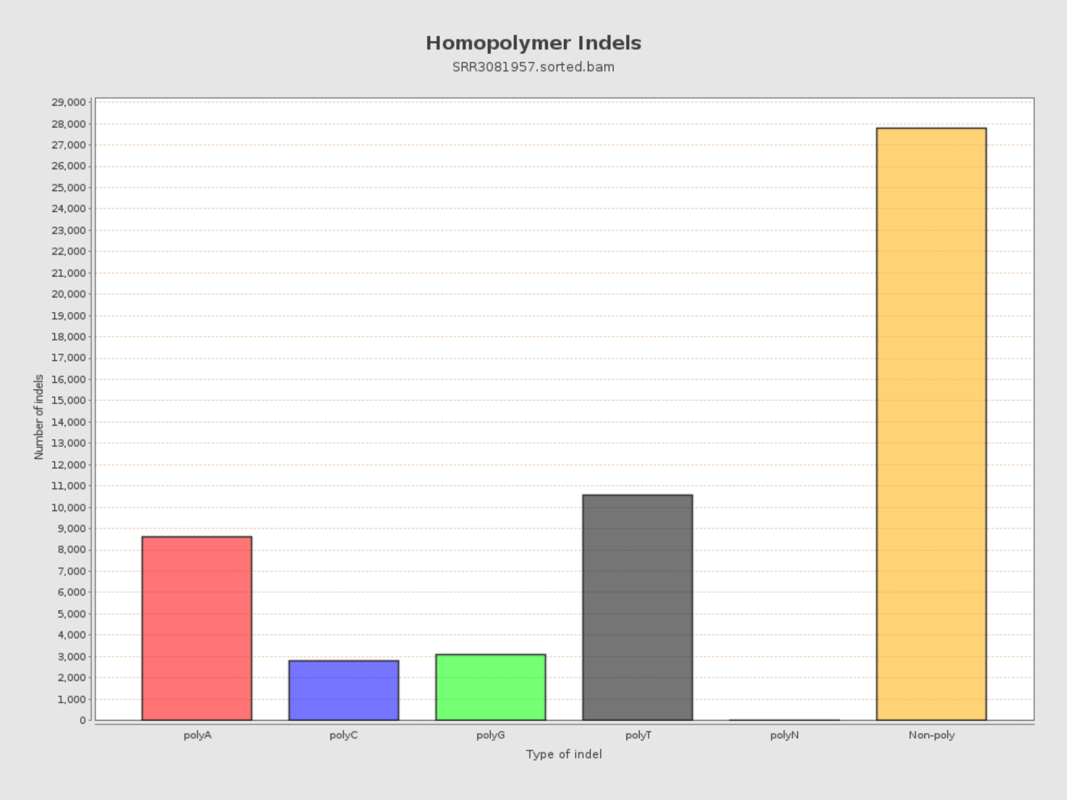
9. Results : Mapped Reads GC-content Distribution



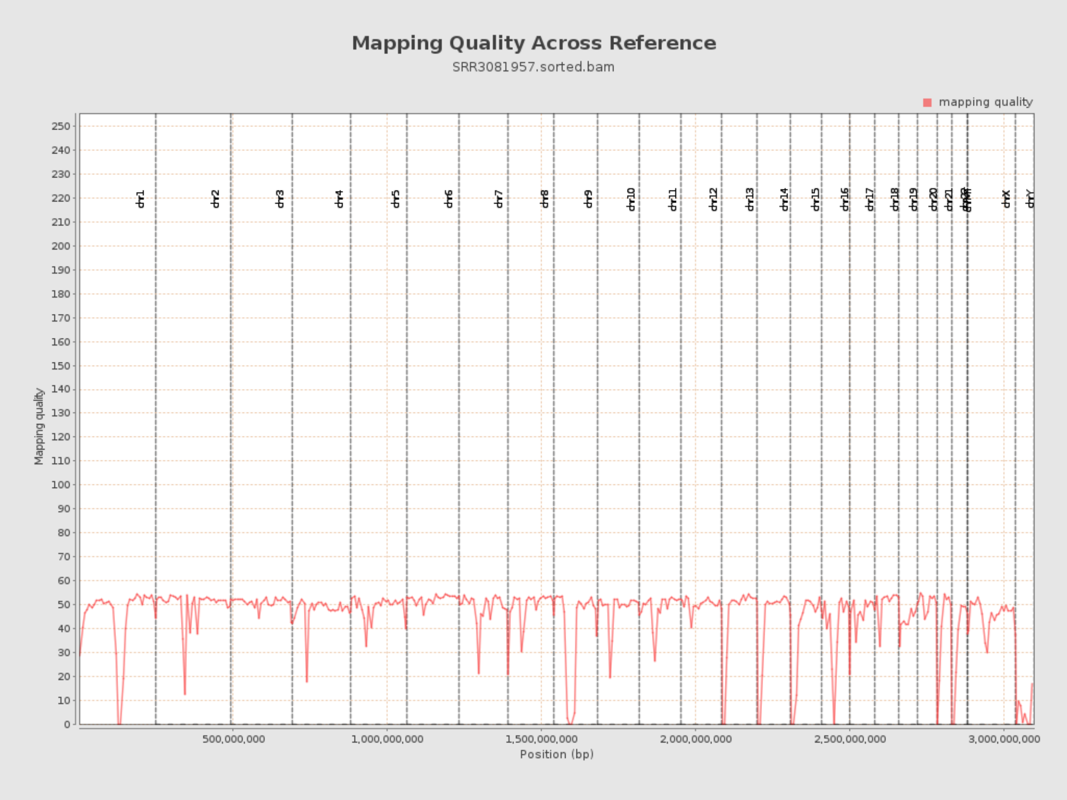
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram