Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:45:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080802.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_SRR3080802 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080802.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:45:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080802.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,094,650
Mapped reads	2,567,754 / 82.97%
Unmapped reads	526,896 / 17.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,675 / 0.96%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	175,684 / 5.68%
Duplication rate	5.74%
Clipped reads	789,348 / 25.51%

2.2. ACGT Content

Number/percentage of A's	55,187,524 / 30.53%
Number/percentage of C's	33,011,856 / 18.26%
Number/percentage of T's	56,830,527 / 31.44%
Number/percentage of G's	35,730,694 / 19.76%
Number/percentage of N's	26,419 / 0.01%
GC Percentage	38.02%

2.3. Coverage

Mean	0.0584

Standard Deviation	0.6391

2.4. Mapping Quality

Mean Mapping Quality	48.01

2.5. Mismatches and indels

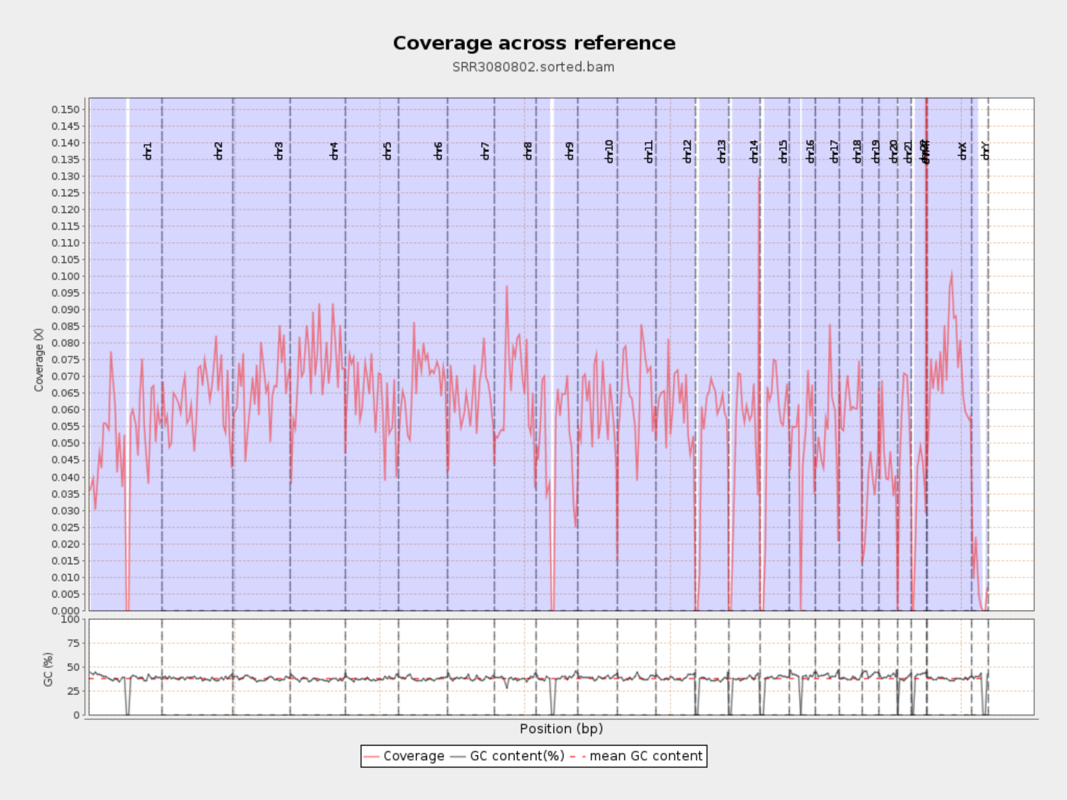
General error rate	0.79%
Mismatches	1,404,449
Insertions	14,018
Mapped reads with at least one insertion	0.54%
Deletions	36,775
Mapped reads with at least one deletion	1.42%
Homopolymer indels	47.84%

2.6. Chromosome stats

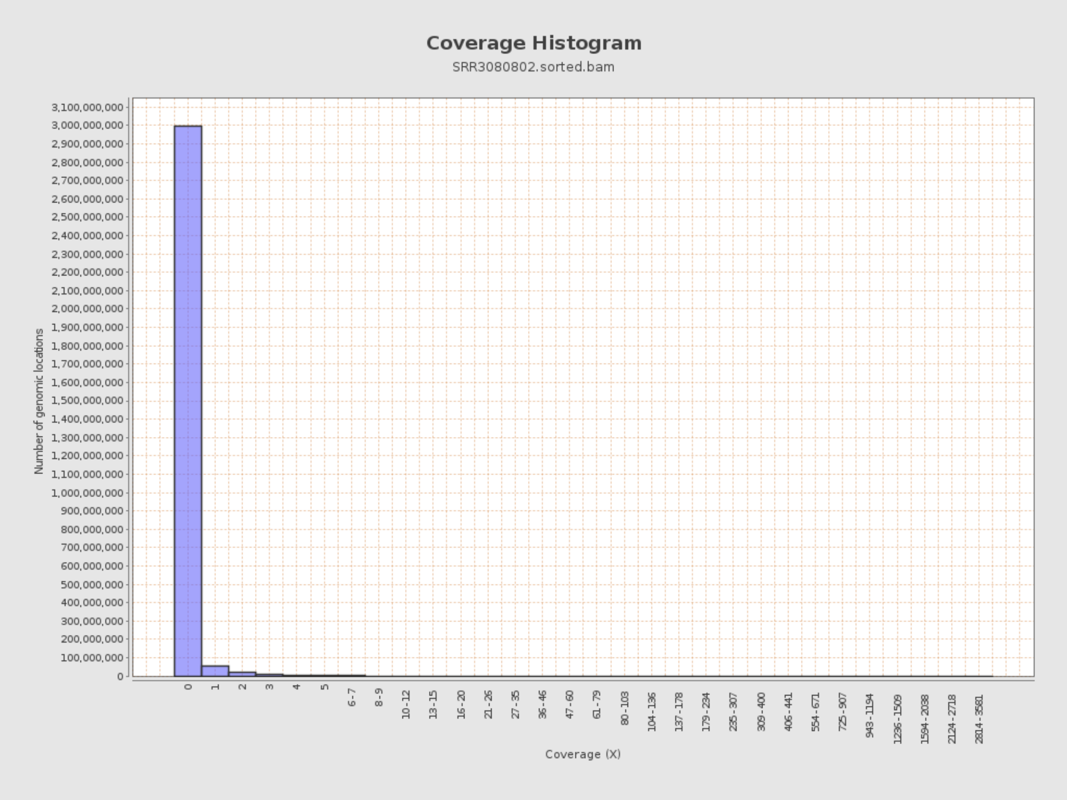
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12439451	0.0499	0.4517
chr2	243199373	15322318	0.063	0.4617
chr3	198022430	13218614	0.0668	0.4243
chr4	191154276	13992576	0.0732	0.4524
chr5	180915260	11468611	0.0634	0.4135
chr6	171115067	11673410	0.0682	0.4493
chr7	159138663	10212630	0.0642	0.461

chr8	146364022	9648484	0.0659	2.2497
chr9	141213431	6691086	0.0474	0.3939
chr10	135534747	8346927	0.0616	0.4361
chr11	135006516	8785056	0.0651	0.4342
chr12	133851895	8147103	0.0609	0.4022
chr13	115169878	5979066	0.0519	0.3786
chr14	107349540	5285628	0.0492	0.3704
chr15	102531392	5303058	0.0517	0.3686
chr16	90354753	4540027	0.0502	0.3645
chr17	81195210	4273848	0.0526	0.3711
chr18	78077248	4838646	0.062	0.5678
chr19	59128983	2154446	0.0364	0.3473
chr20	63025520	2758508	0.0438	0.341
chr21	48129895	2545166	0.0529	0.3832
chr22	51304566	1550511	0.0302	0.2693
chrMT	16571	17200	1.038	1.5649
chrX	155270560	11217021	0.0722	0.4465
chrY	59373566	443332	0.0075	0.1725

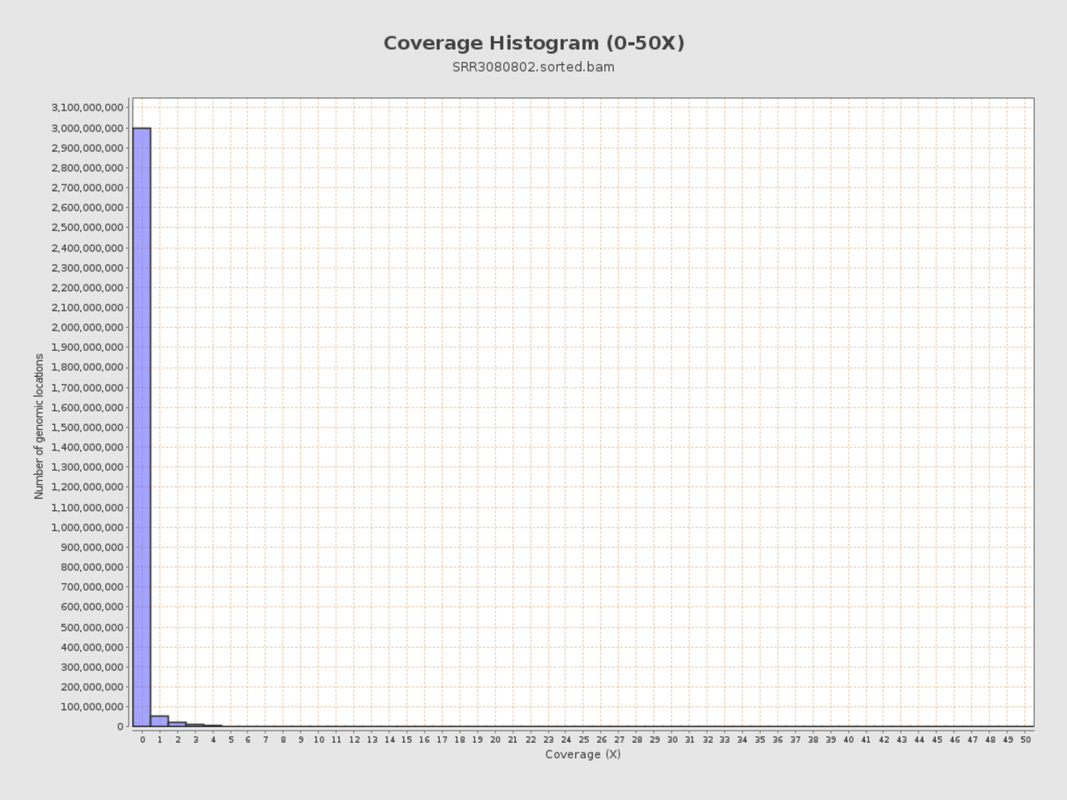
3. Results : Coverage across reference



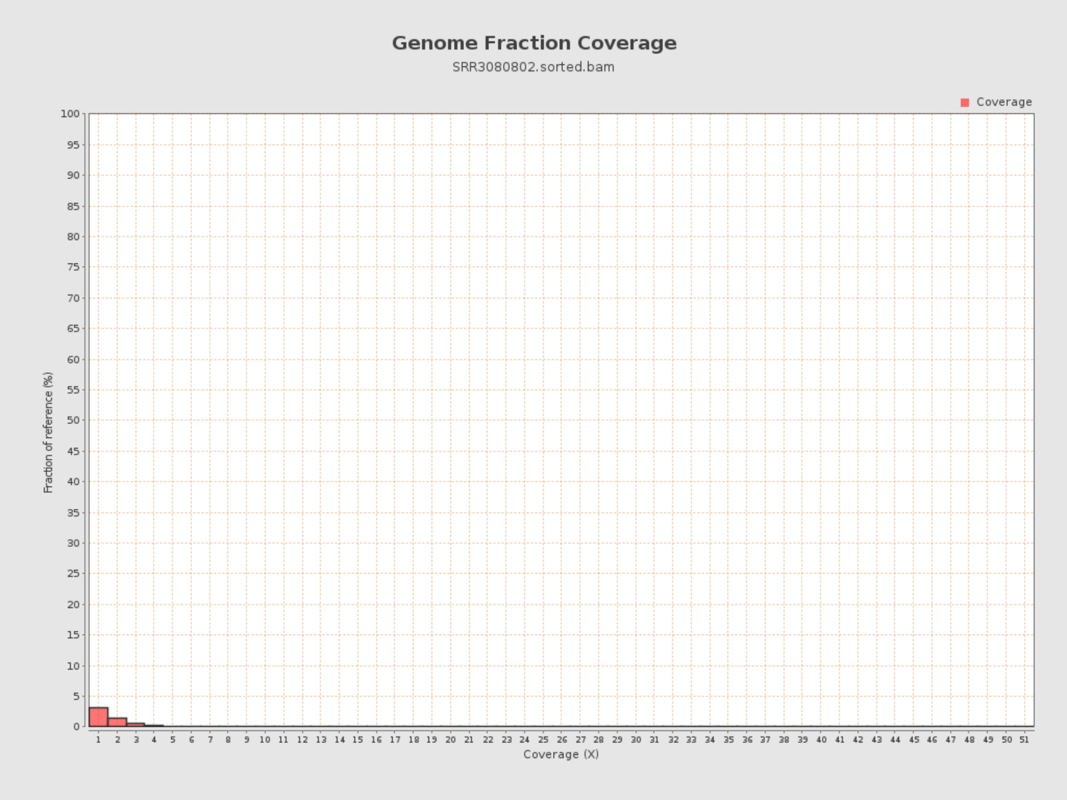
4. Results : Coverage Histogram



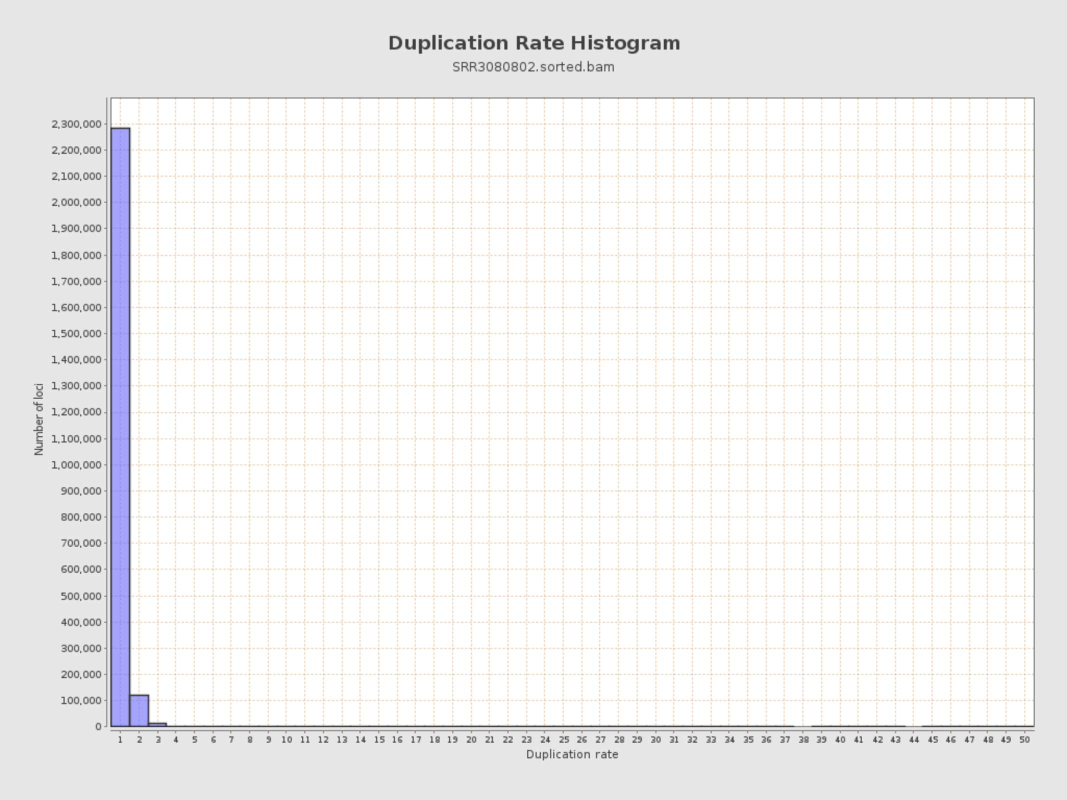
5. Results : Coverage Histogram (0-50X)



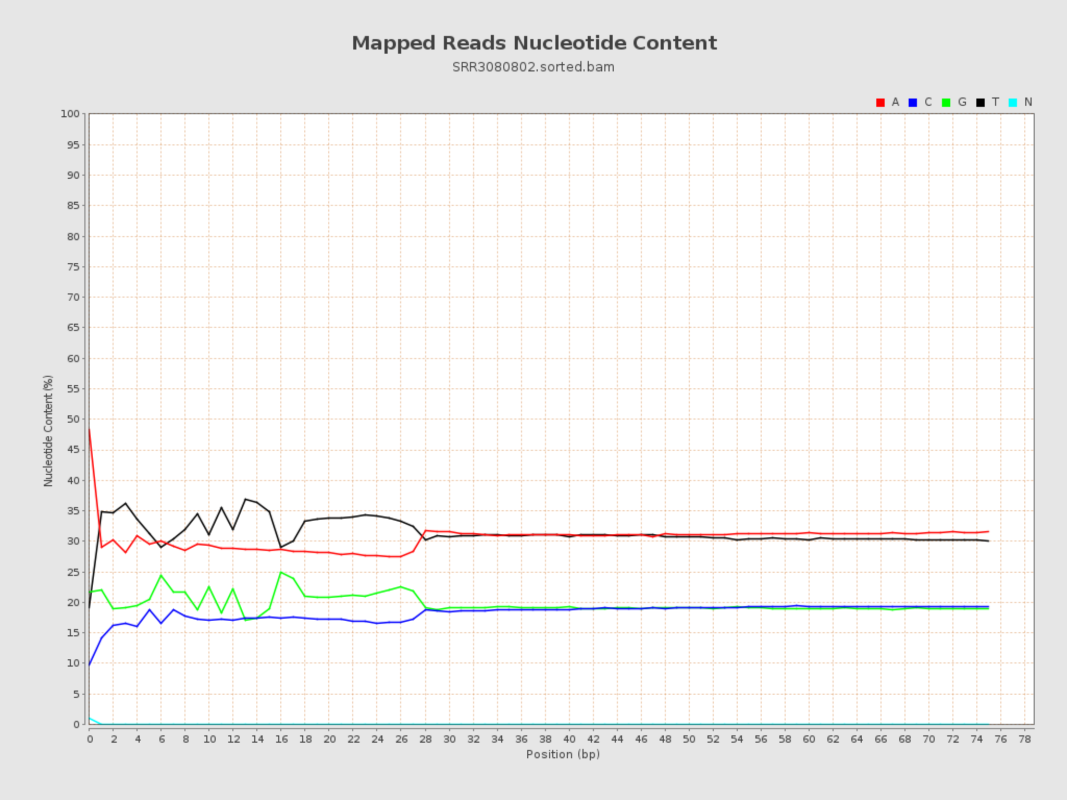
6. Results : Genome Fraction Coverage



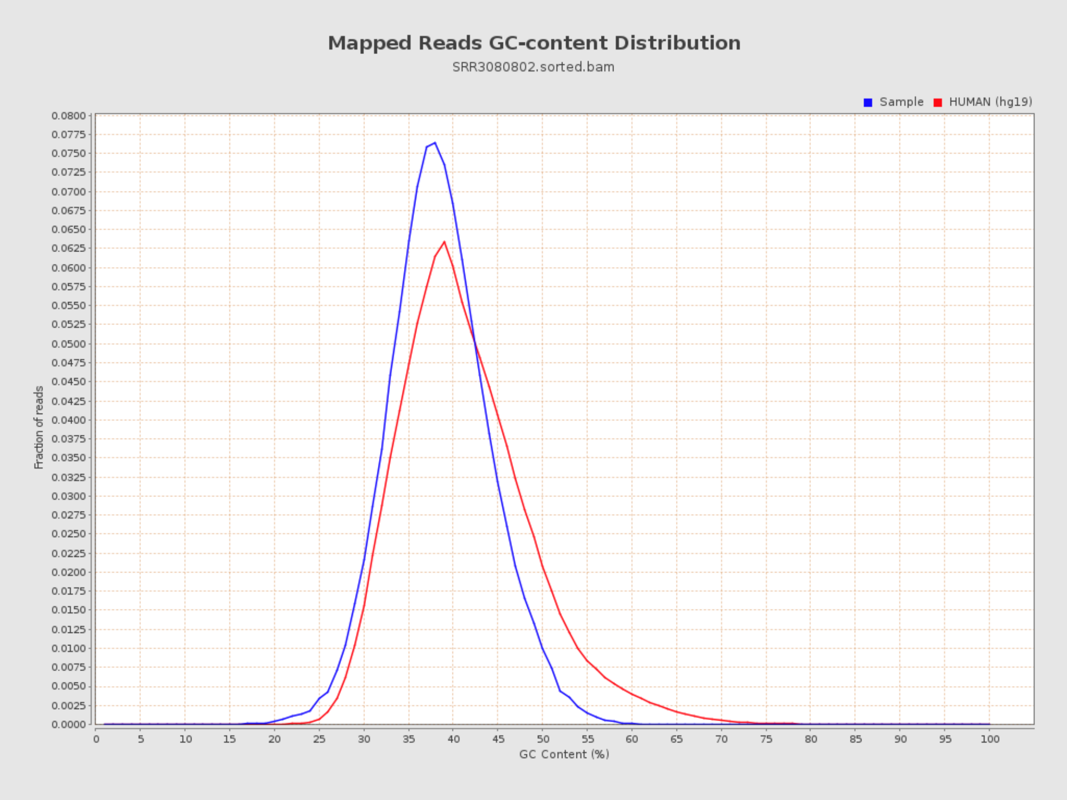
7. Results : Duplication Rate Histogram



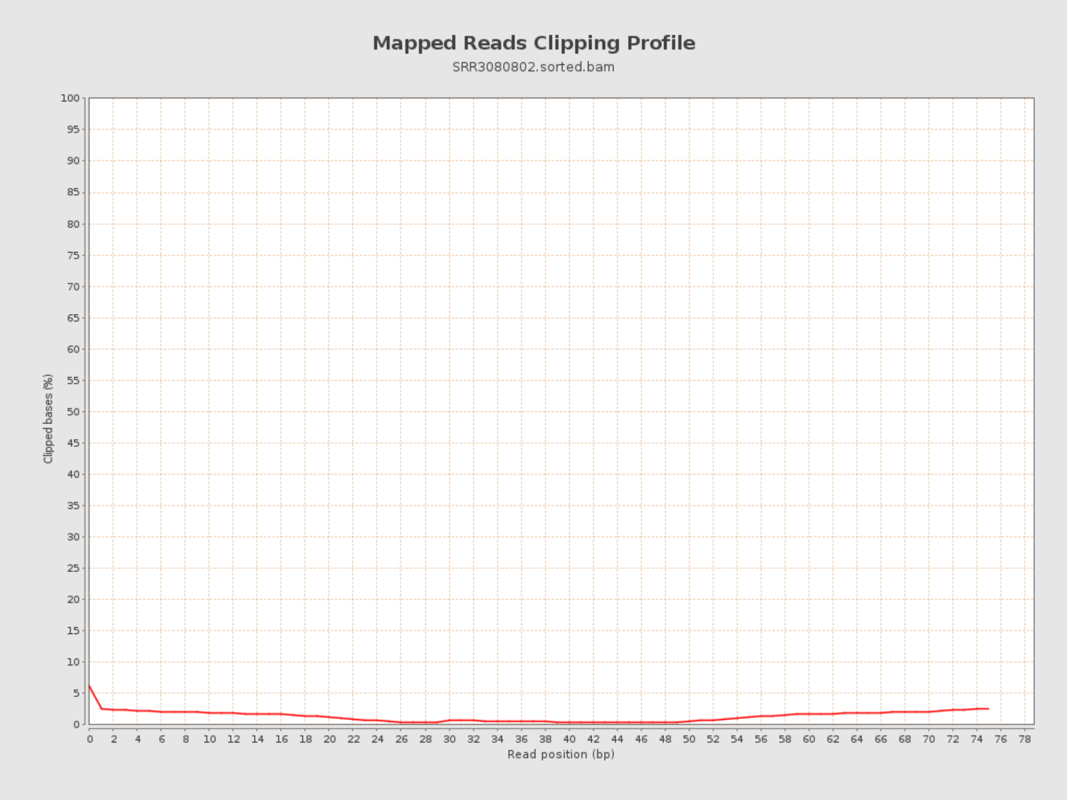
8. Results : Mapped Reads Nucleotide Content



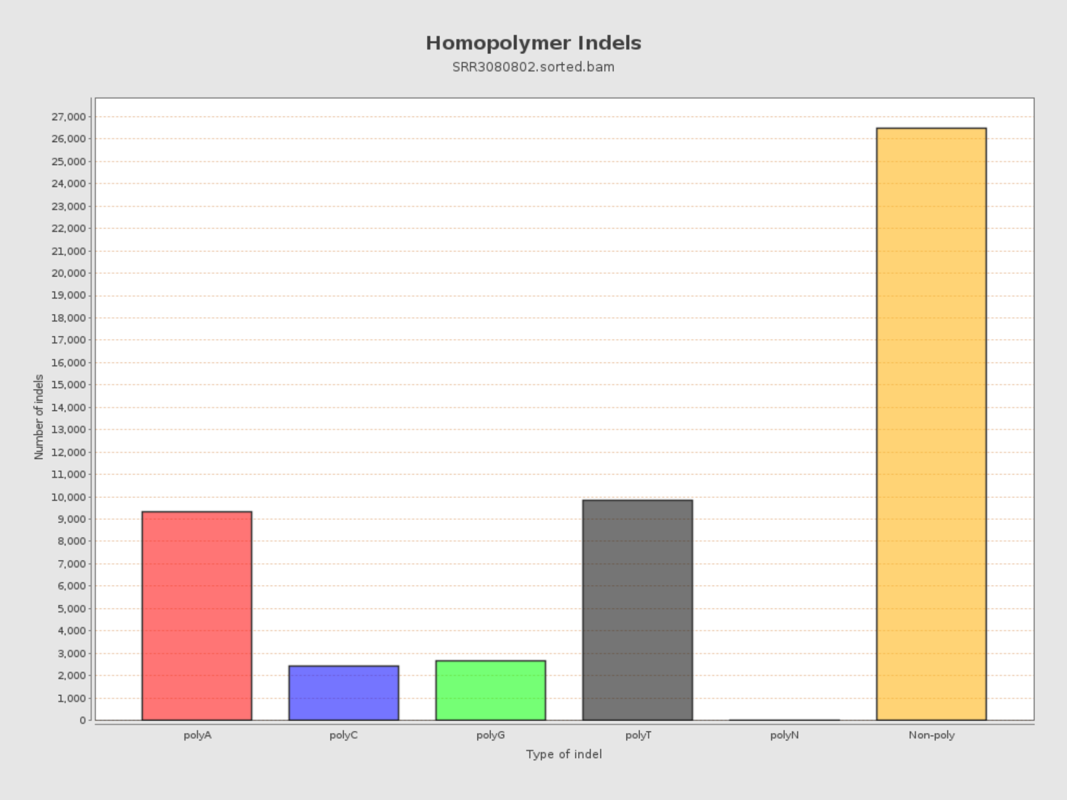
9. Results : Mapped Reads GC-content Distribution



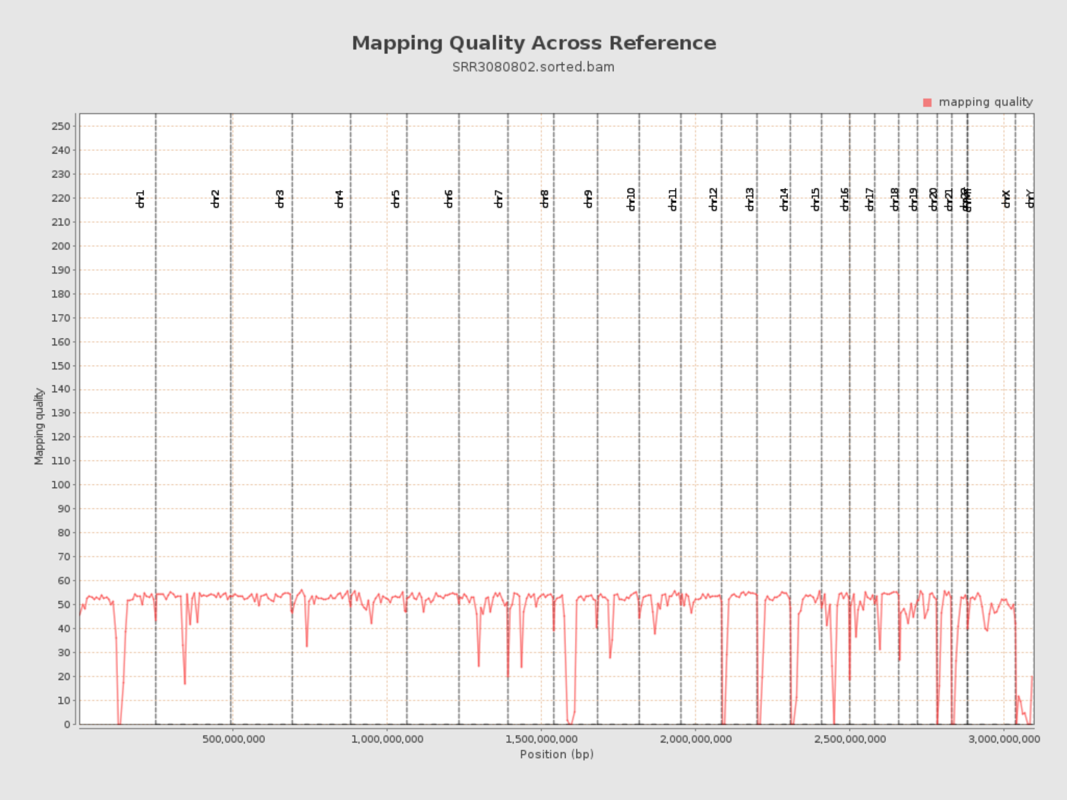
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram