Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 04:03:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083677.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_SRR3083677 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083677.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 04:03:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083677.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,738,850
Mapped reads	1,400,571 / 80.55%
Unmapped reads	338,279 / 19.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,372 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	35,663 / 2.05%
Duplication rate	2.11%
Clipped reads	834,071 / 47.97%

2.2. ACGT Content

Number/percentage of A's	25,986,975 / 29.65%
Number/percentage of C's	16,143,776 / 18.42%
Number/percentage of T's	26,062,646 / 29.73%
Number/percentage of G's	19,445,957 / 22.19%
Number/percentage of N's	11,086 / 0.01%
GC Percentage	40.6%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.245

2.4. Mapping Quality

Mean Mapping Quality	45.78

2.5. Mismatches and indels

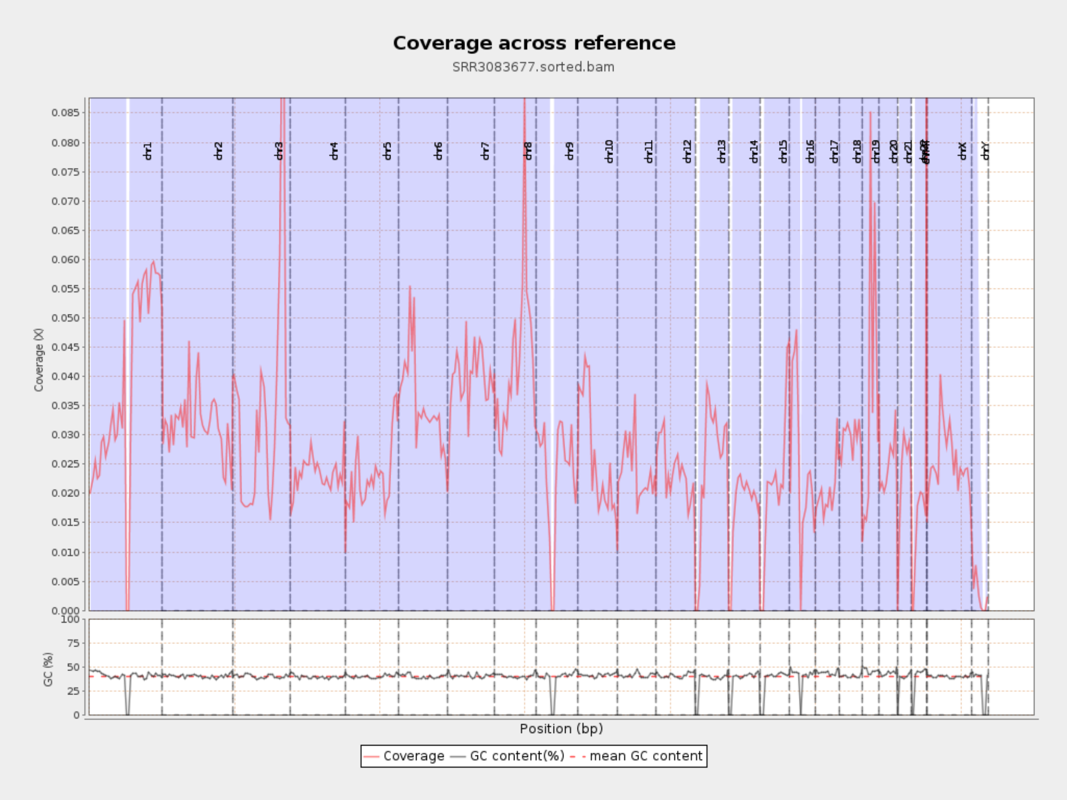
General error rate	0.9%
Mismatches	777,746
Insertions	6,122
Mapped reads with at least one insertion	0.43%
Deletions	18,232
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.27%

2.6. Chromosome stats

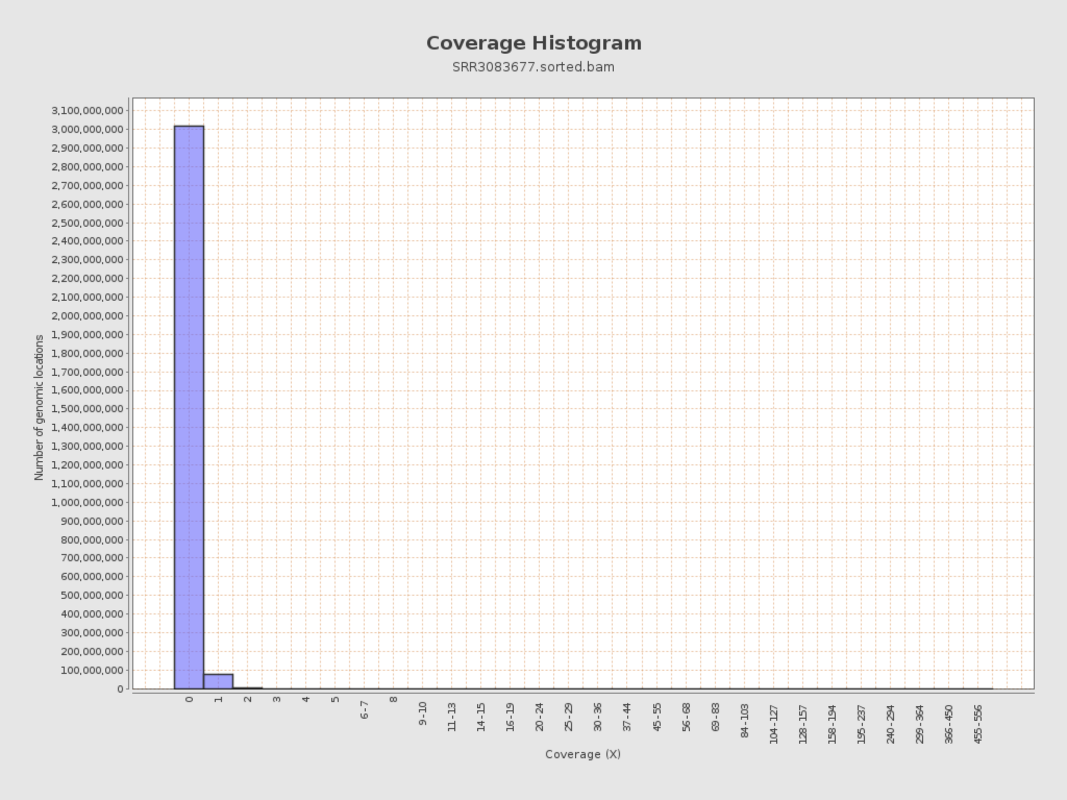
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9591677	0.0385	0.4967
chr2	243199373	7770281	0.032	0.2264
chr3	198022430	6789888	0.0343	0.1984
chr4	191154276	4483640	0.0235	0.164
chr5	180915260	4186201	0.0231	0.1628
chr6	171115067	6091085	0.0356	0.2346
chr7	159138663	6343270	0.0399	0.3435

chr8	146364022	6261638	0.0428	0.2877
chr9	141213431	3296325	0.0233	0.183
chr10	135534747	3633044	0.0268	0.2176
chr11	135006516	3185501	0.0236	0.1799
chr12	133851895	3188461	0.0238	0.164
chr13	115169878	2876311	0.025	0.1672
chr14	107349540	1878773	0.0175	0.1416
chr15	102531392	2158025	0.021	0.155
chr16	90354753	2261455	0.025	0.1725
chr17	81195210	1662016	0.0205	0.155
chr18	78077248	2317830	0.0297	0.2714
chr19	59128983	2189004	0.037	0.352
chr20	63025520	1563759	0.0248	0.1676
chr21	48129895	1095667	0.0228	0.1615
chr22	51304566	692219	0.0135	0.122
chrMT	16571	2613	0.1577	0.4025
chrX	155270560	3989849	0.0257	0.1772
chrY	59373566	170874	0.0029	0.0633

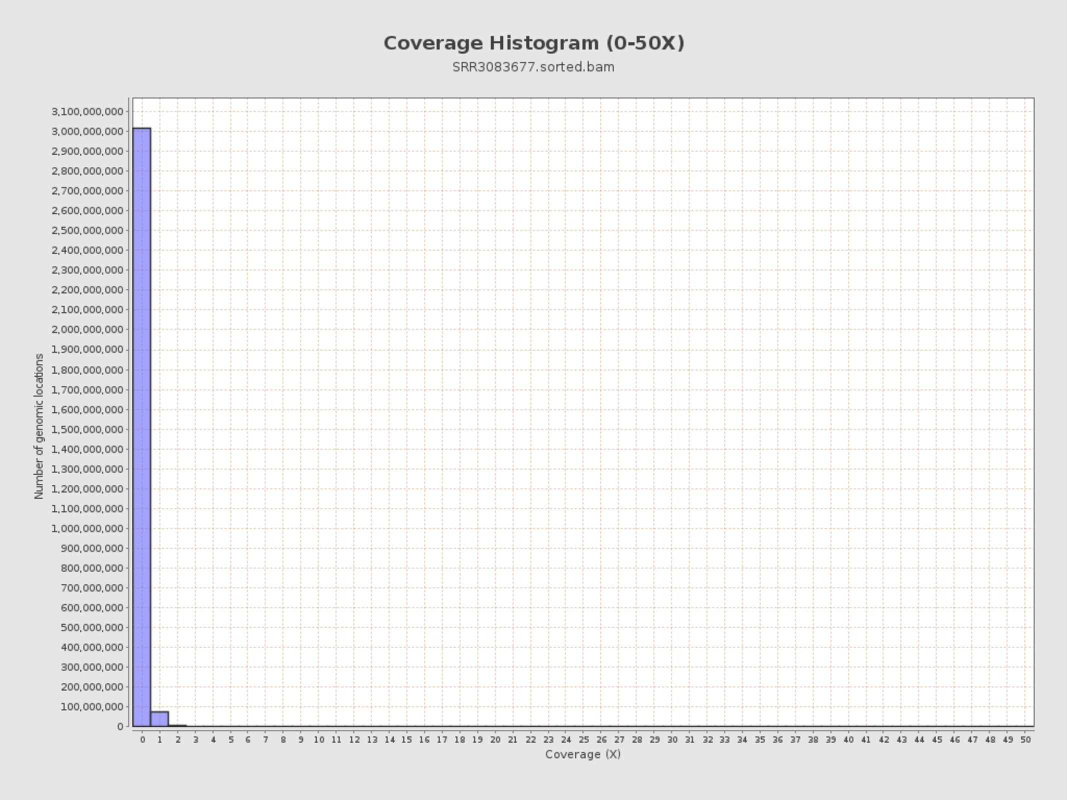
3. Results : Coverage across reference



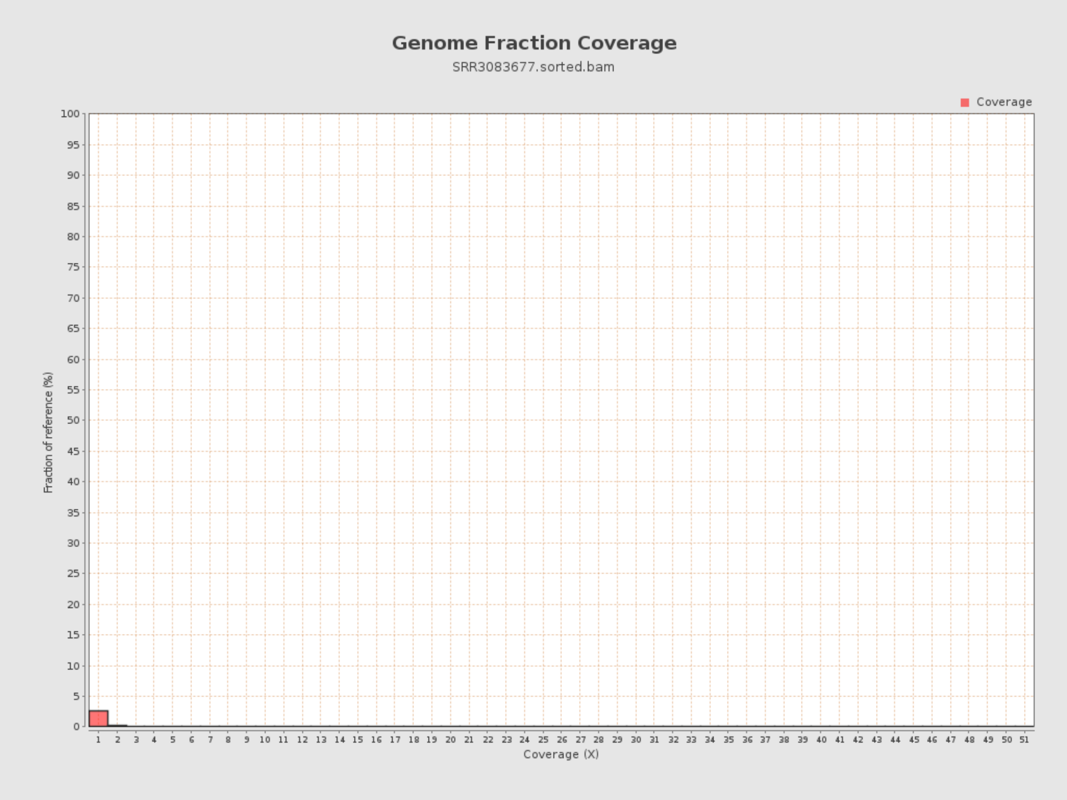
4. Results : Coverage Histogram



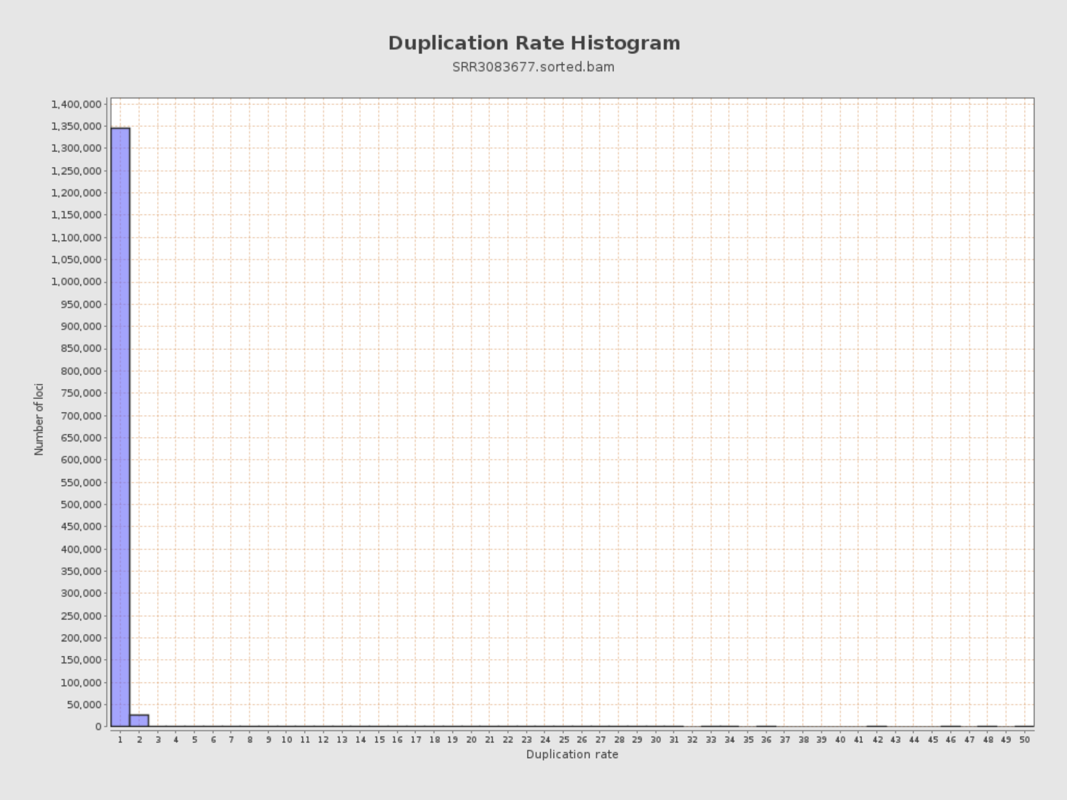
5. Results : Coverage Histogram (0-50X)



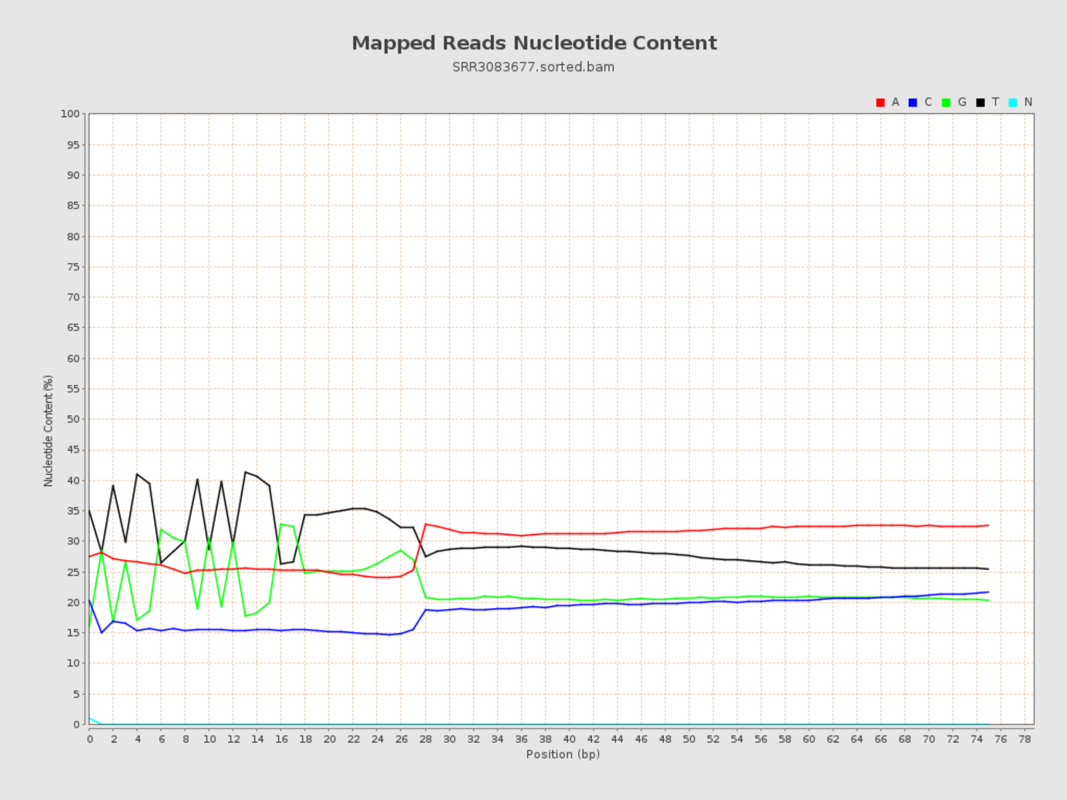
6. Results : Genome Fraction Coverage



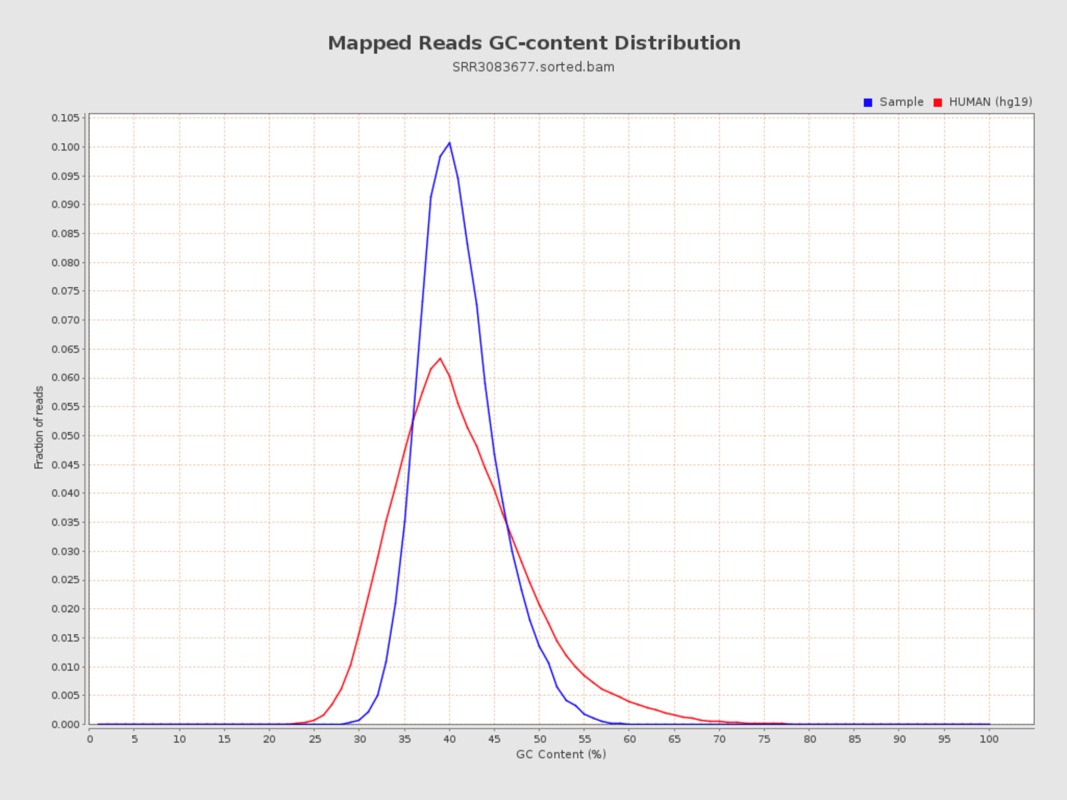
7. Results : Duplication Rate Histogram



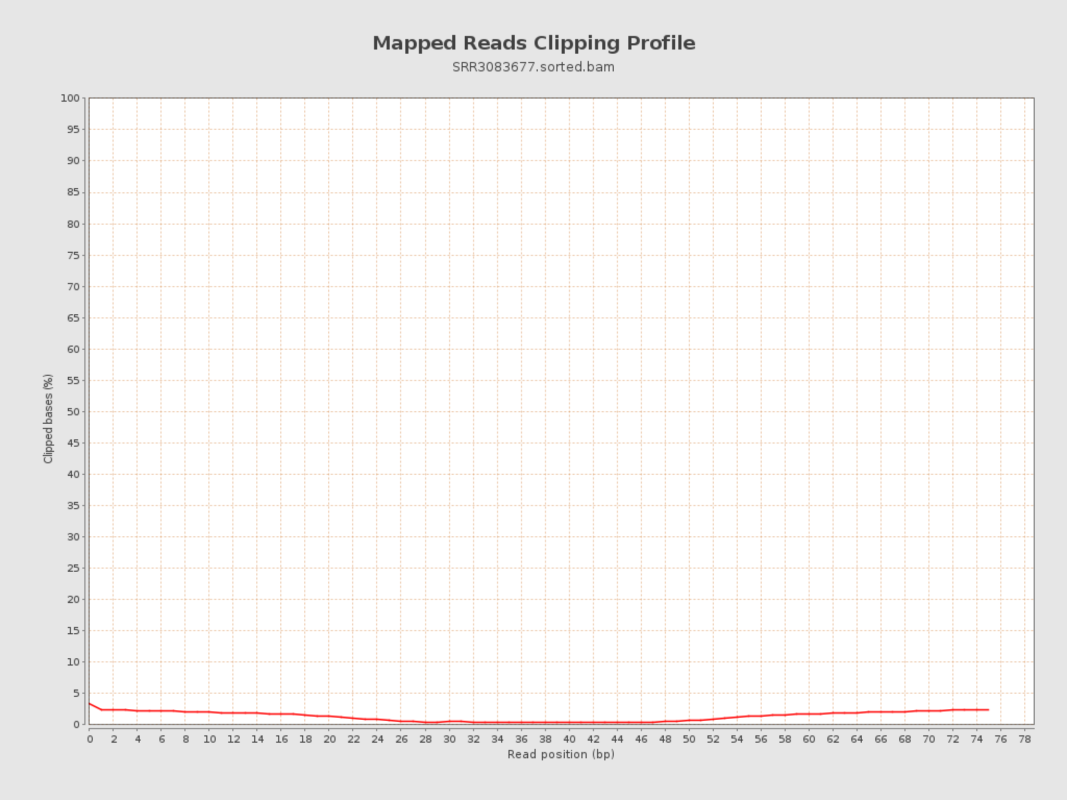
8. Results : Mapped Reads Nucleotide Content



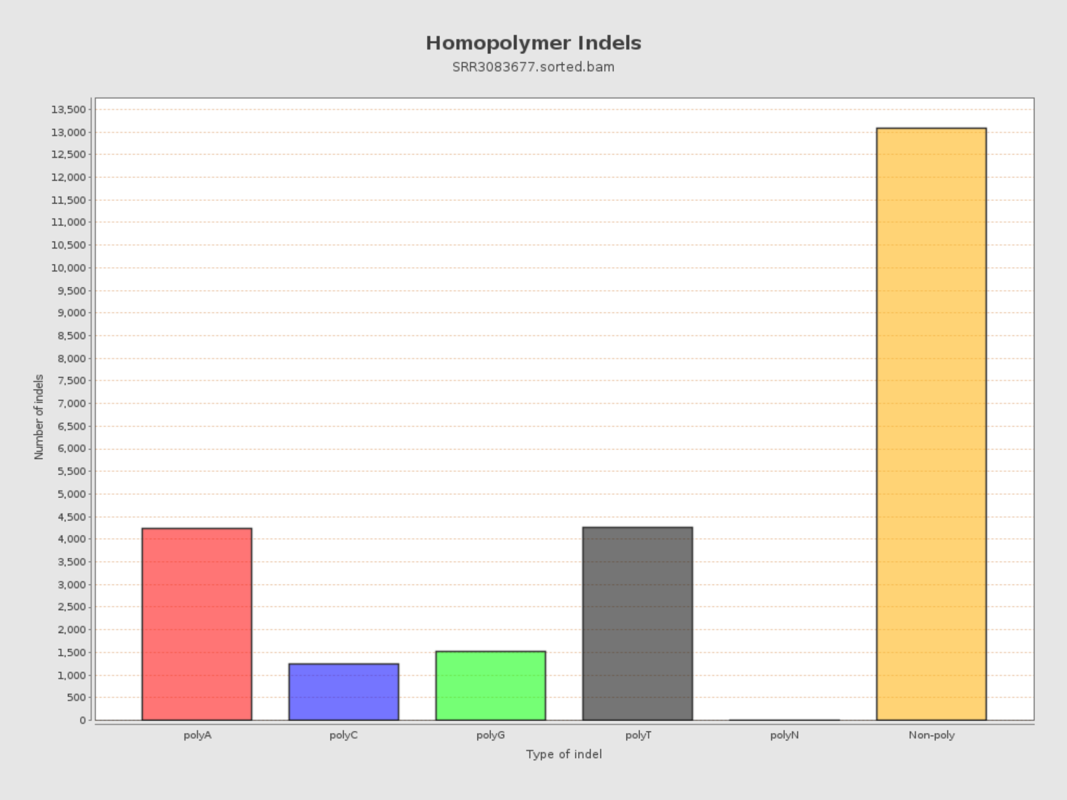
9. Results : Mapped Reads GC-content Distribution



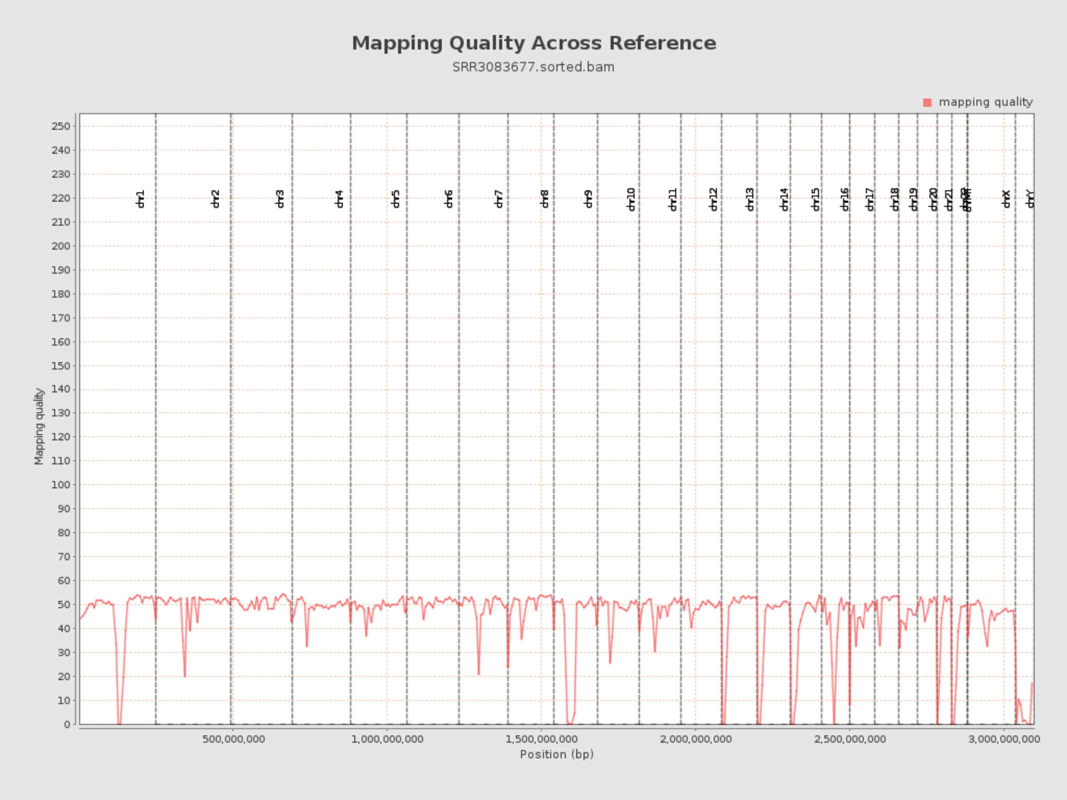
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram