Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:12:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080813.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_SRR3080813 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080813.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:12:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080813.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,866,227
Mapped reads	2,700,673 / 94.22%
Unmapped reads	165,554 / 5.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,786 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	127,786 / 4.46%
Duplication rate	3.61%
Clipped reads	702,035 / 24.49%

2.2. ACGT Content

Number/percentage of A's	57,306,388 / 29.78%
Number/percentage of C's	36,511,480 / 18.98%
Number/percentage of T's	60,299,559 / 31.34%
Number/percentage of G's	38,269,573 / 19.89%
Number/percentage of N's	27,322 / 0.01%
GC Percentage	38.86%

2.3. Coverage

Mean	0.0622

Standard Deviation	0.5747

2.4. Mapping Quality

Mean Mapping Quality	48.02

2.5. Mismatches and indels

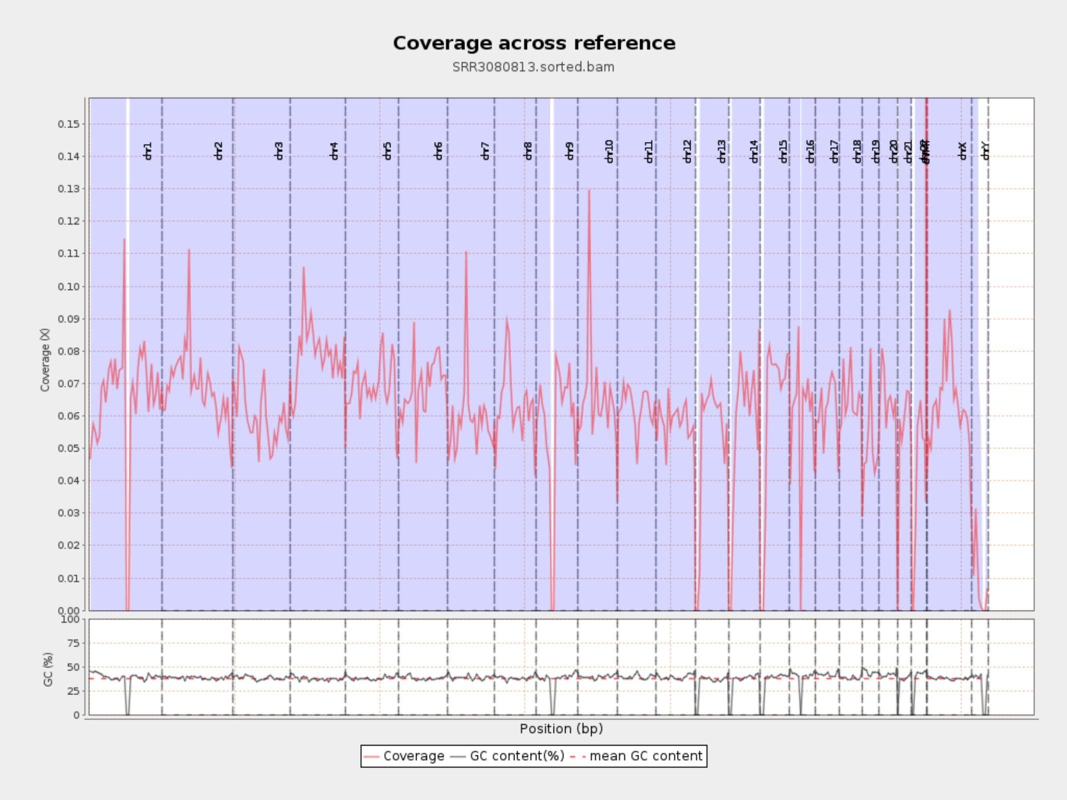
General error rate	0.85%
Mismatches	1,598,766
Insertions	15,383
Mapped reads with at least one insertion	0.56%
Deletions	42,974
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.2%

2.6. Chromosome stats

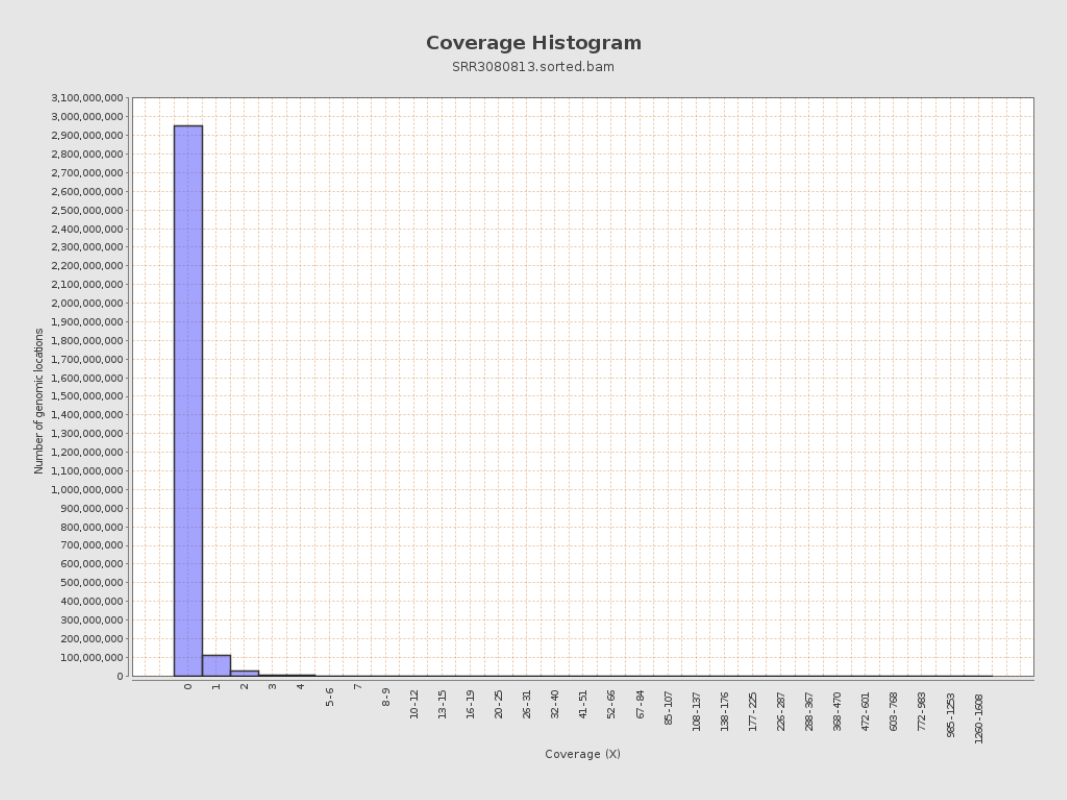
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16289597	0.0654	1.1008
chr2	243199373	16865378	0.0693	0.5386
chr3	198022430	11989255	0.0605	0.3148
chr4	191154276	15142637	0.0792	0.3898
chr5	180915260	12521346	0.0692	0.3352
chr6	171115067	11760475	0.0687	0.4141
chr7	159138663	9485254	0.0596	0.6689

chr8	146364022	9275826	0.0634	1.0617
chr9	141213431	8039902	0.0569	0.4667
chr10	135534747	9032857	0.0666	0.6177
chr11	135006516	8412018	0.0623	0.4072
chr12	133851895	7792739	0.0582	0.3128
chr13	115169878	5945691	0.0516	0.287
chr14	107349540	5974818	0.0557	0.3211
chr15	102531392	6245842	0.0609	0.3085
chr16	90354753	5306770	0.0587	0.3898
chr17	81195210	5036082	0.062	0.3367
chr18	78077248	5080270	0.0651	0.9534
chr19	59128983	3032412	0.0513	0.762
chr20	63025520	4096339	0.065	0.3332
chr21	48129895	2611953	0.0543	0.328
chr22	51304566	1999502	0.039	0.245
chrMT	16571	55938	3.3757	2.7607
chrX	155270560	9985277	0.0643	0.3474
chrY	59373566	513404	0.0086	0.2691

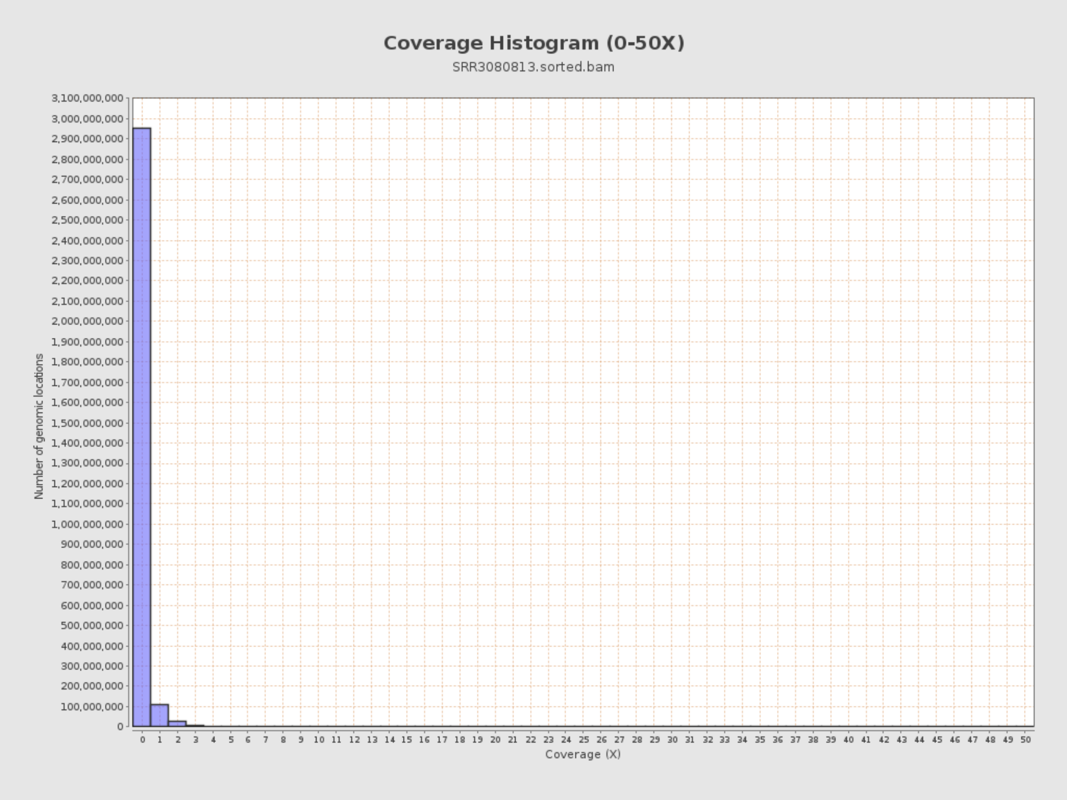
3. Results : Coverage across reference



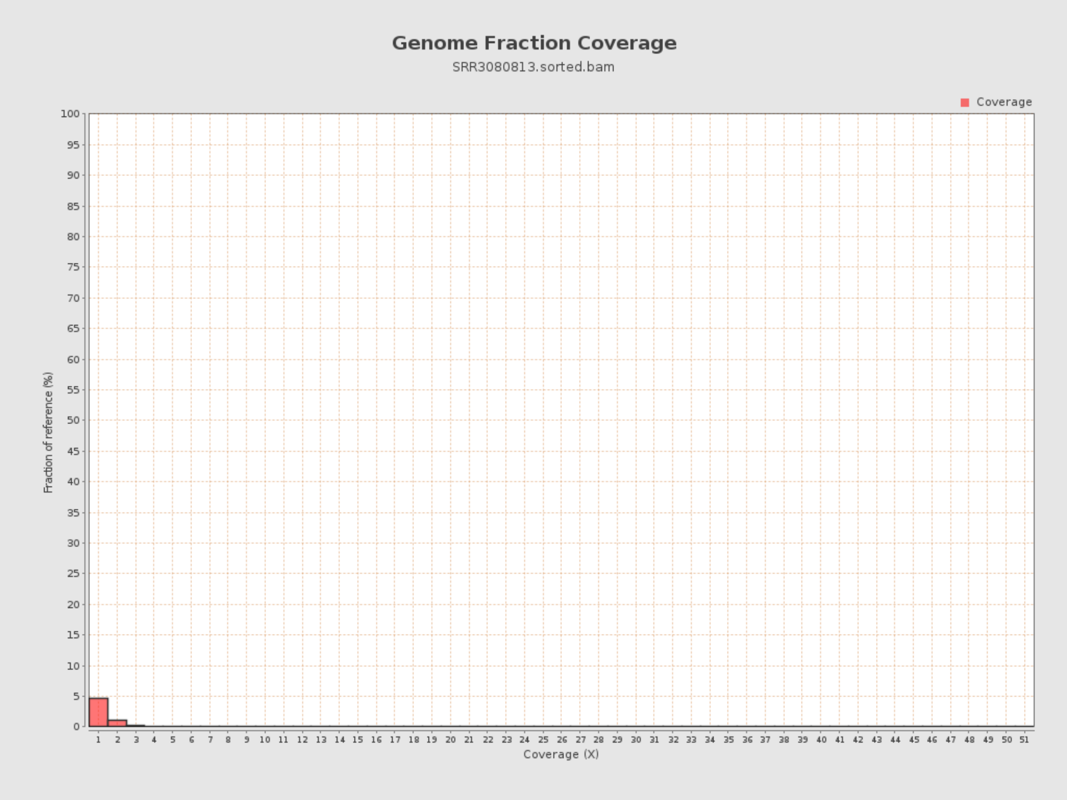
4. Results : Coverage Histogram



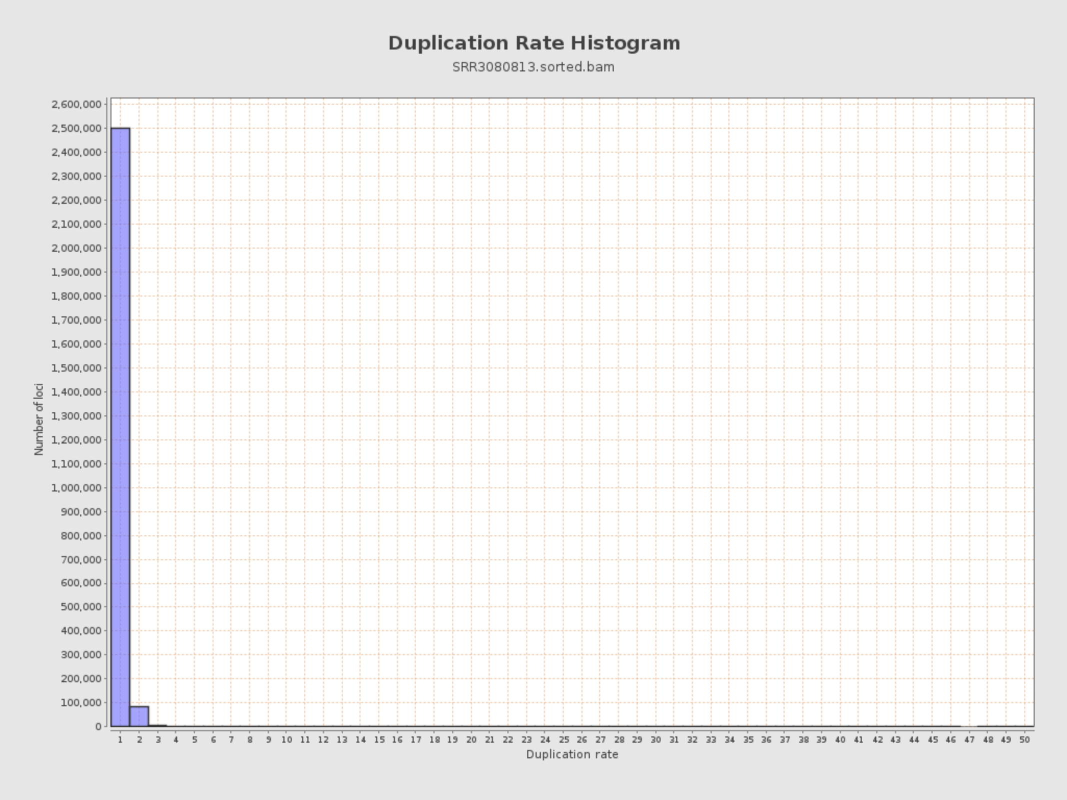
5. Results : Coverage Histogram (0-50X)



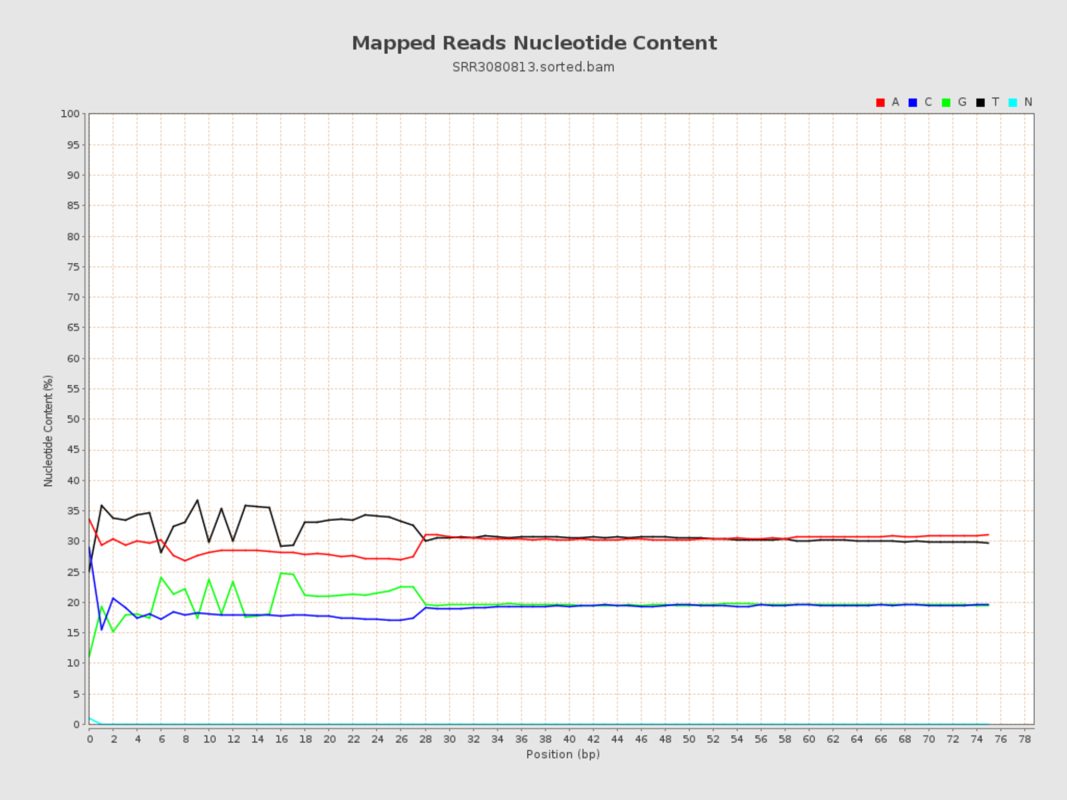
6. Results : Genome Fraction Coverage



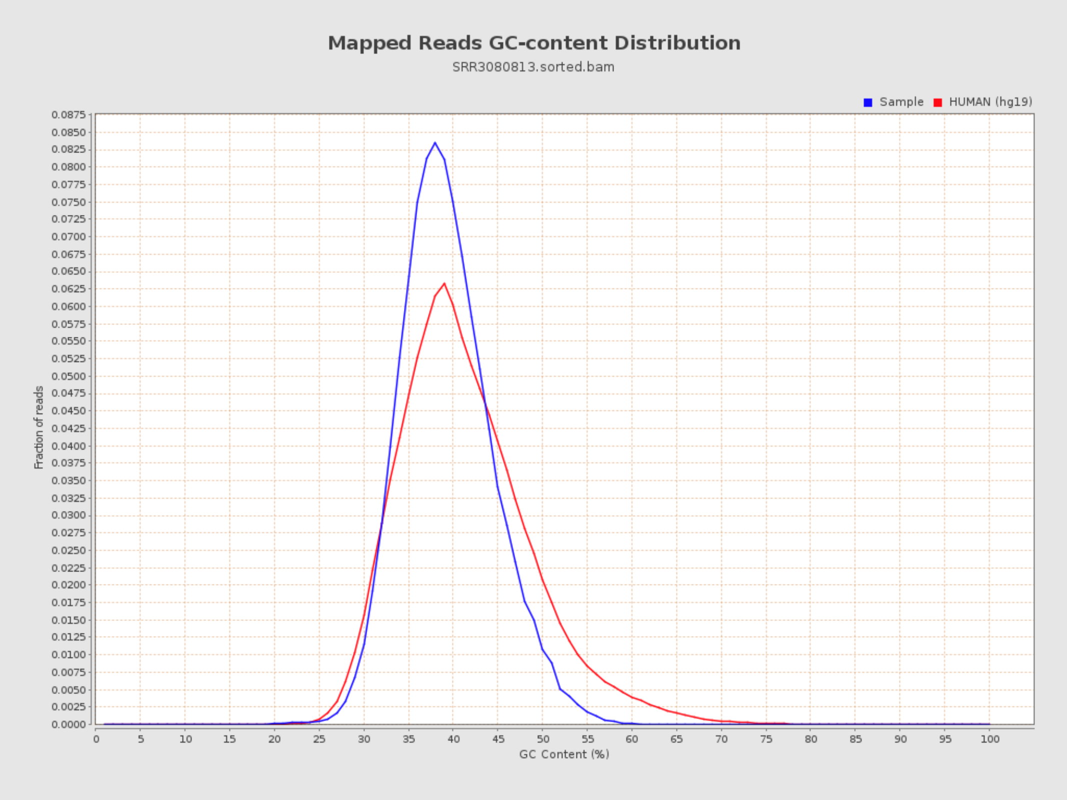
7. Results : Duplication Rate Histogram



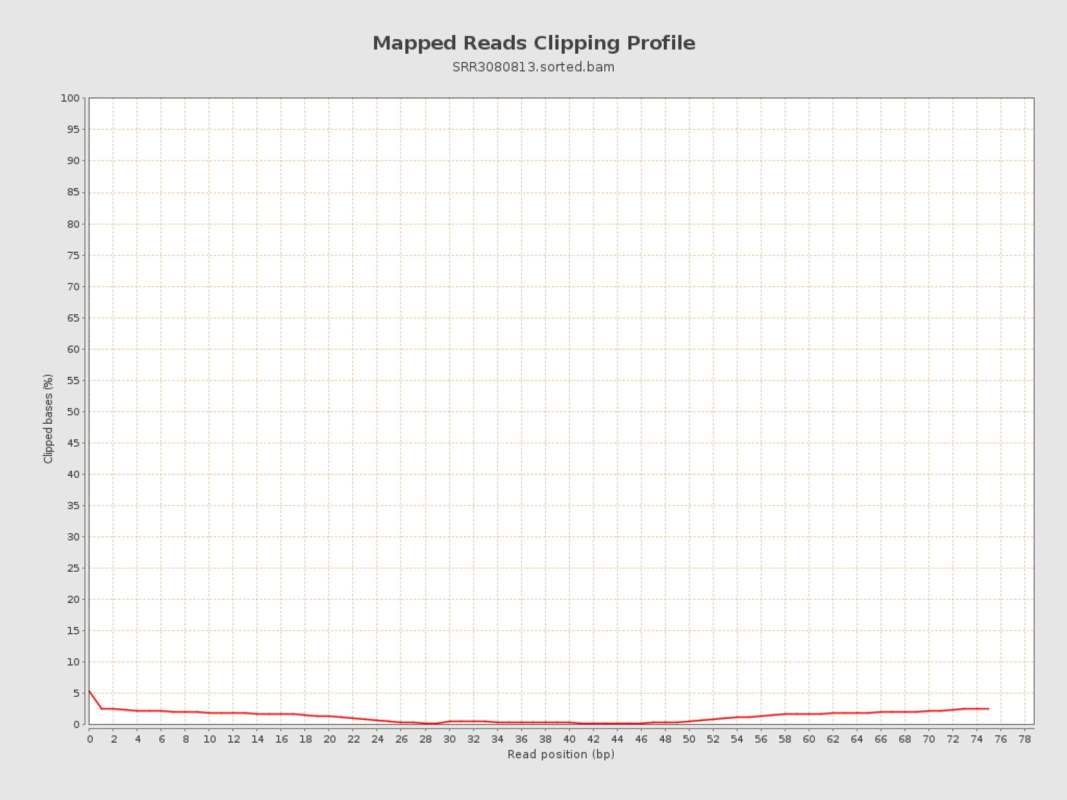
8. Results : Mapped Reads Nucleotide Content



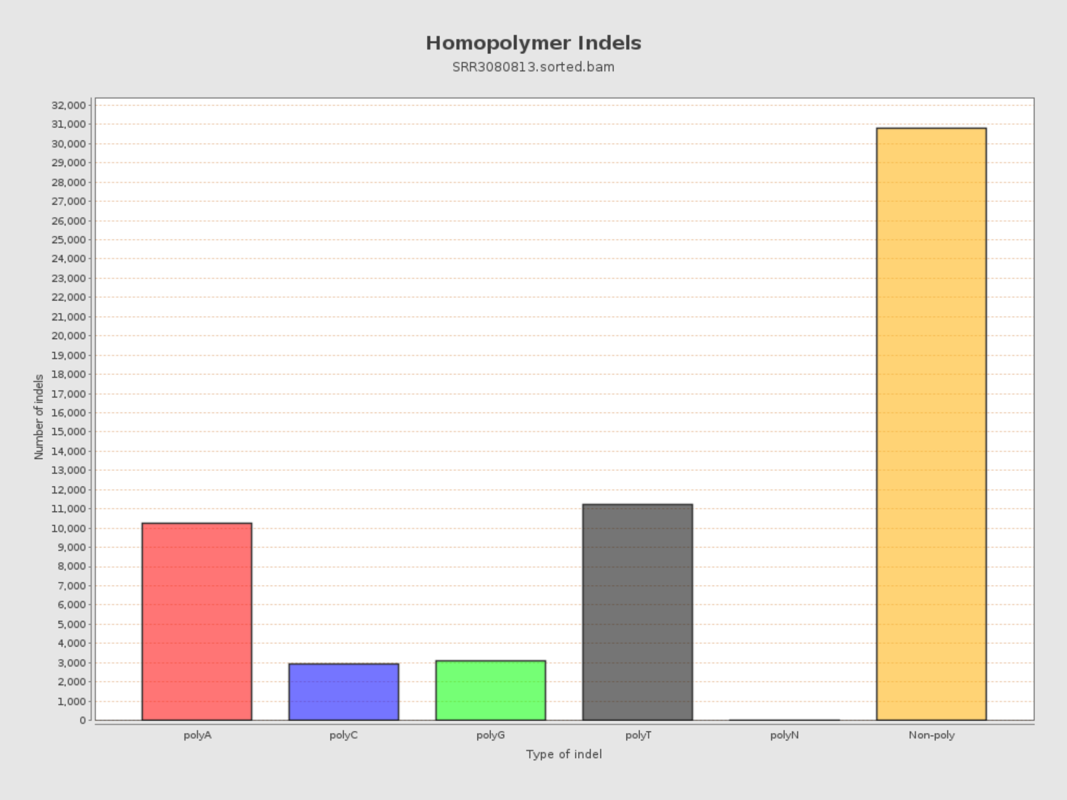
9. Results : Mapped Reads GC-content Distribution



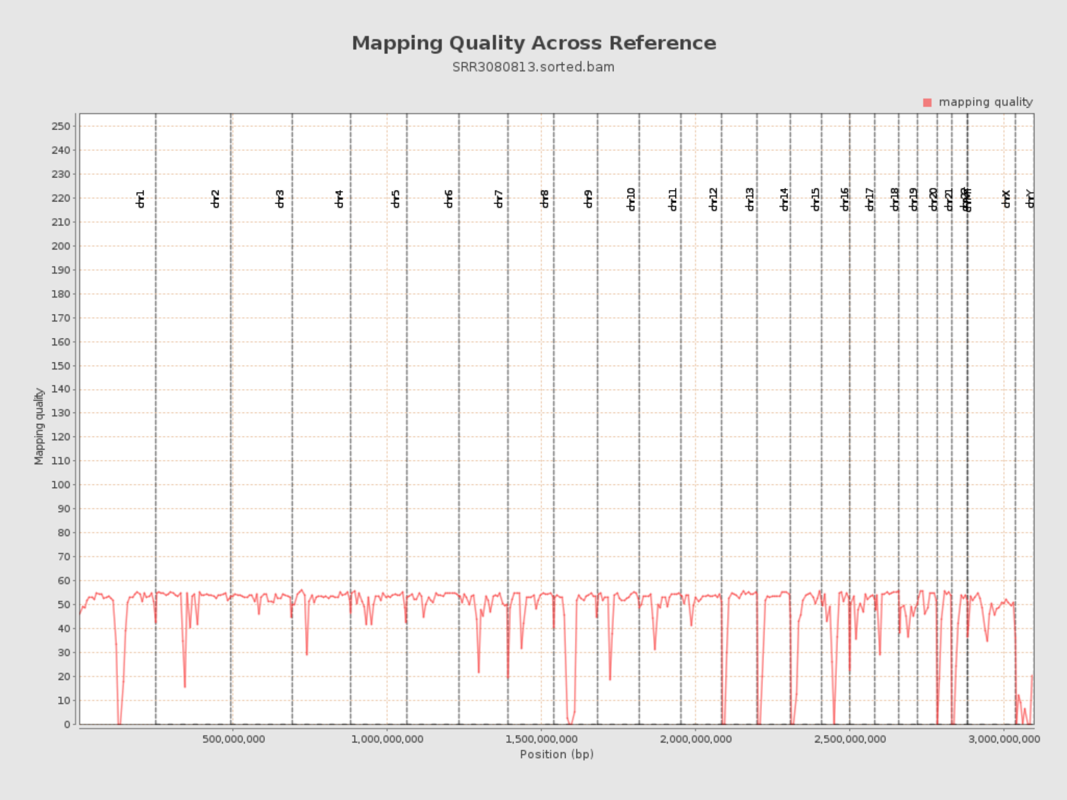
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram