Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:48:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081100.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_SRR3081100 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081100.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:48:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081100.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,293,716
Mapped reads	2,099,351 / 91.53%
Unmapped reads	194,365 / 8.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,023 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	91,409 / 3.99%
Duplication rate	3.45%
Clipped reads	910,252 / 39.68%

2.2. ACGT Content

Number/percentage of A's	39,092,276 / 27.71%
Number/percentage of C's	26,478,995 / 18.77%
Number/percentage of T's	44,175,308 / 31.31%
Number/percentage of G's	31,333,281 / 22.21%
Number/percentage of N's	1,542 / 0%
GC Percentage	40.98%

2.3. Coverage

Mean	0.0456

Standard Deviation	0.379

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

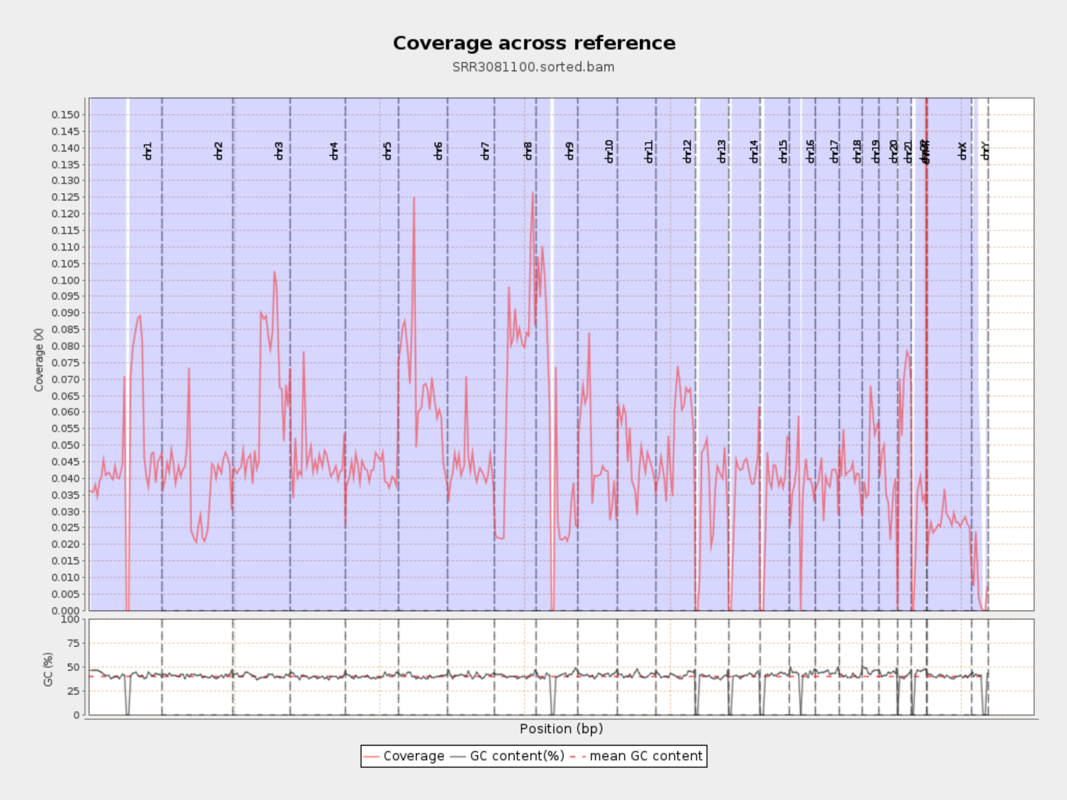
General error rate	0.91%
Mismatches	1,263,498
Insertions	11,222
Mapped reads with at least one insertion	0.53%
Deletions	31,959
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.68%

2.6. Chromosome stats

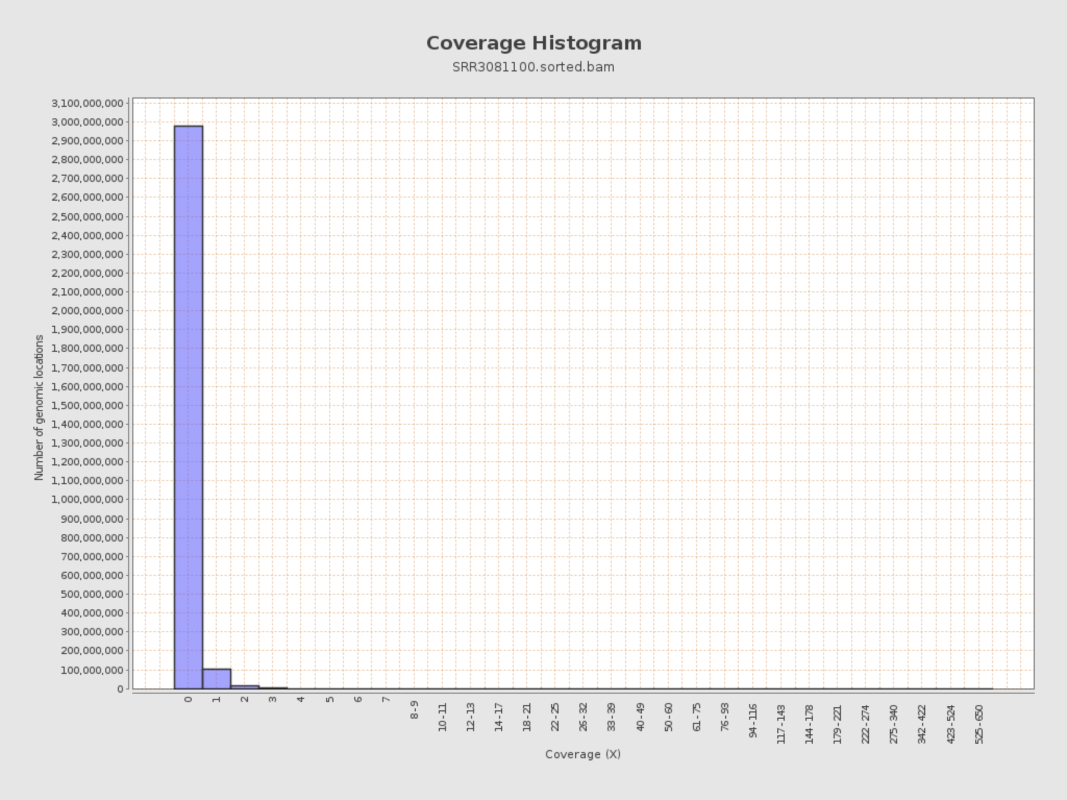
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11815797	0.0474	0.6096
chr2	243199373	9445550	0.0388	0.4009
chr3	198022430	12297242	0.0621	0.2832
chr4	191154276	8680933	0.0454	0.2696
chr5	180915260	7624459	0.0421	0.2338
chr6	171115067	11731870	0.0686	0.4858
chr7	159138663	6976147	0.0438	0.4125

chr8	146364022	10383854	0.0709	0.4599
chr9	141213431	6896374	0.0488	0.4142
chr10	135534747	6401687	0.0472	0.386
chr11	135006516	6295749	0.0466	0.2943
chr12	133851895	7125661	0.0532	0.272
chr13	115169878	3842100	0.0334	0.2058
chr14	107349540	3853252	0.0359	0.2627
chr15	102531392	3563607	0.0348	0.2105
chr16	90354753	3288305	0.0364	0.2651
chr17	81195210	3135726	0.0386	0.2268
chr18	78077248	3319471	0.0425	0.687
chr19	59128983	2887878	0.0488	0.4741
chr20	63025520	2335781	0.0371	0.2288
chr21	48129895	3036718	0.0631	0.3188
chr22	51304566	1294485	0.0252	0.1771
chrMT	16571	414593	25.0192	12.3906
chrX	155270560	4107663	0.0265	0.2072
chrY	59373566	378643	0.0064	0.1606

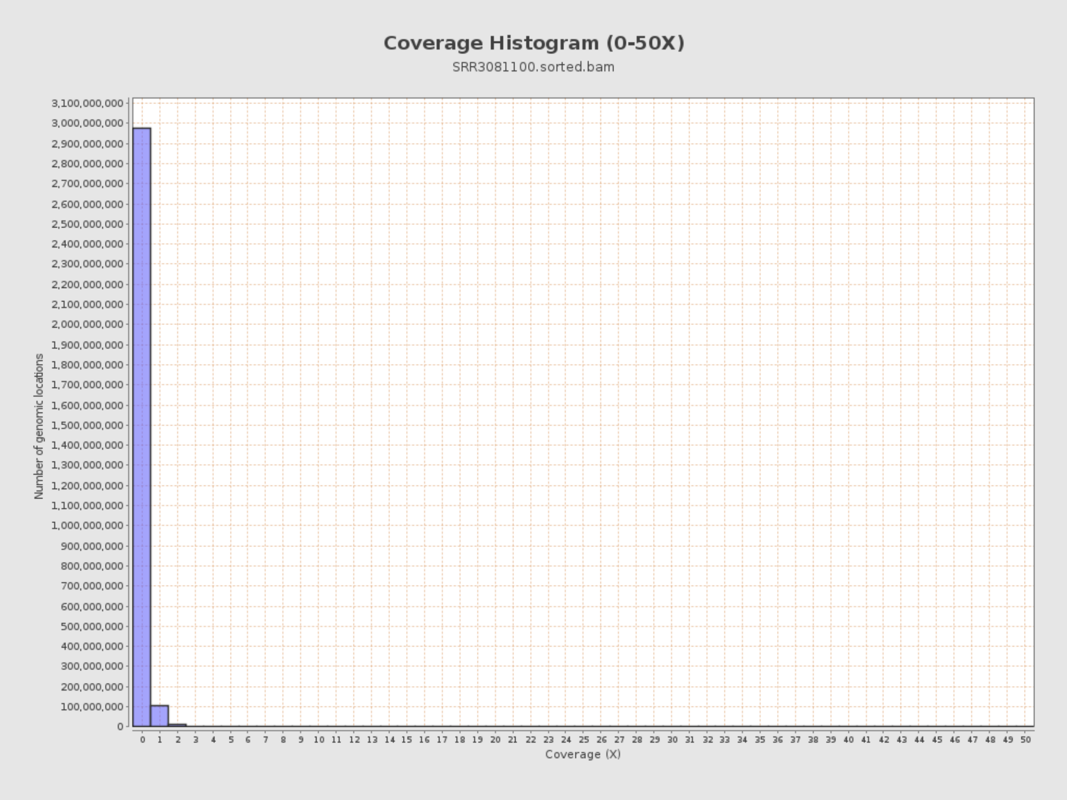
3. Results : Coverage across reference



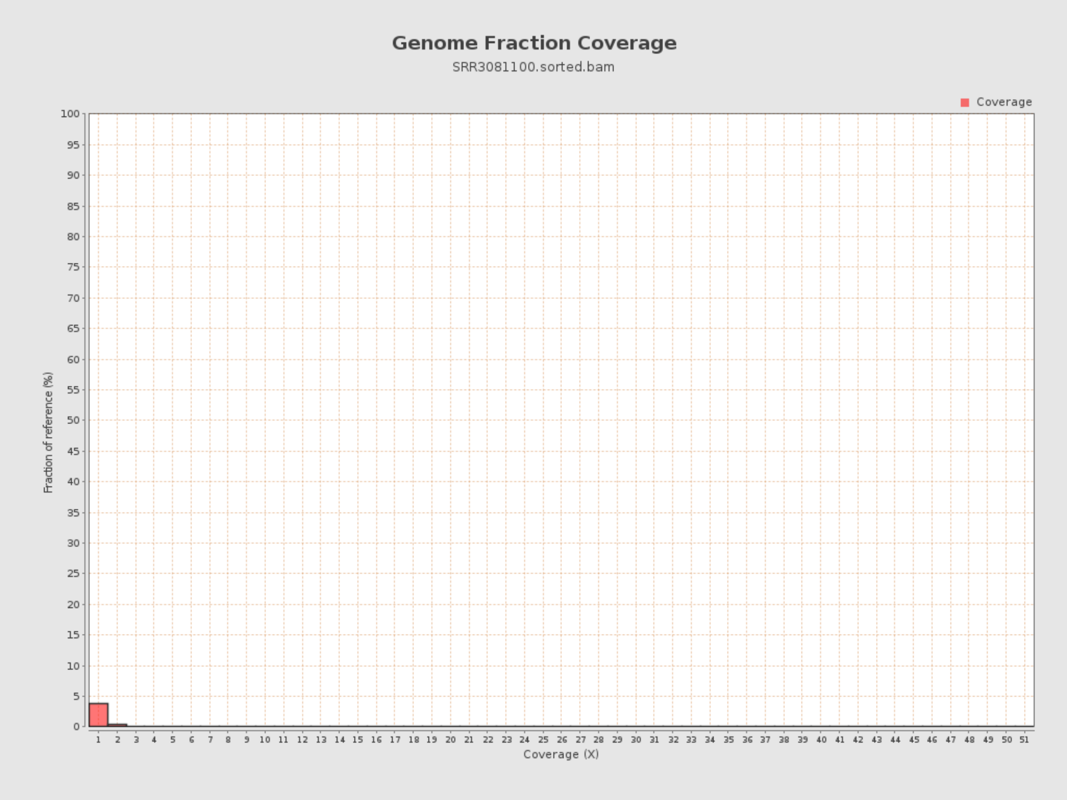
4. Results : Coverage Histogram



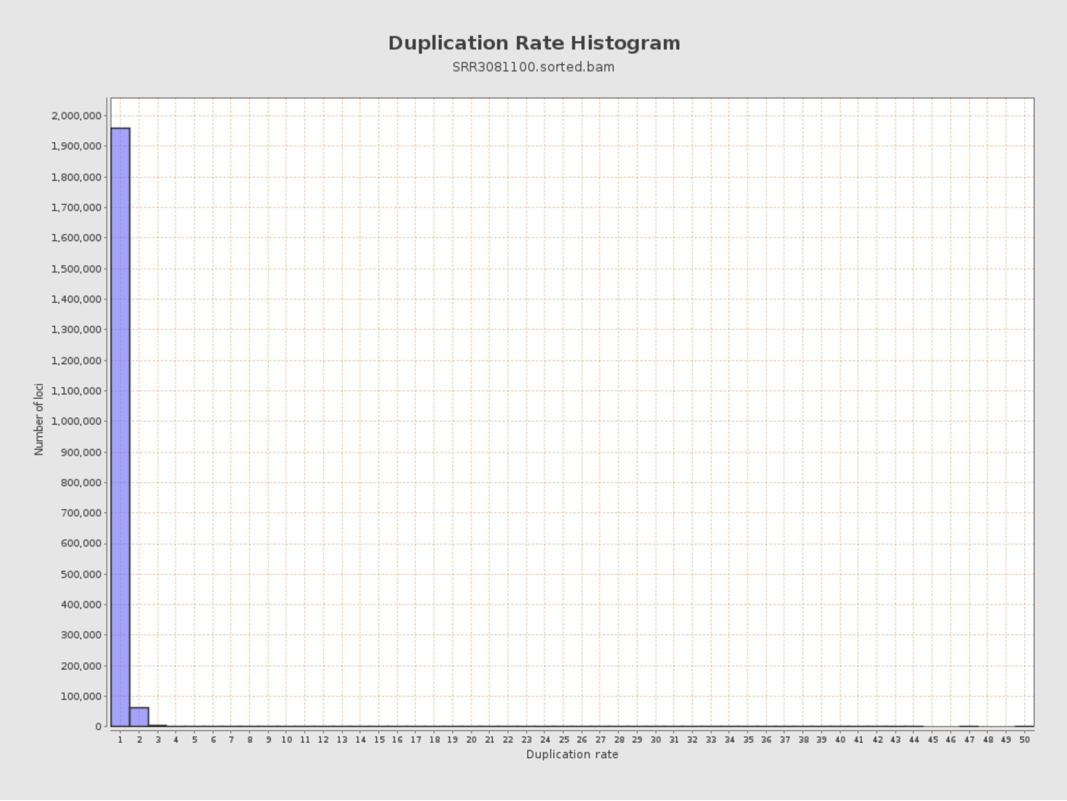
5. Results : Coverage Histogram (0-50X)



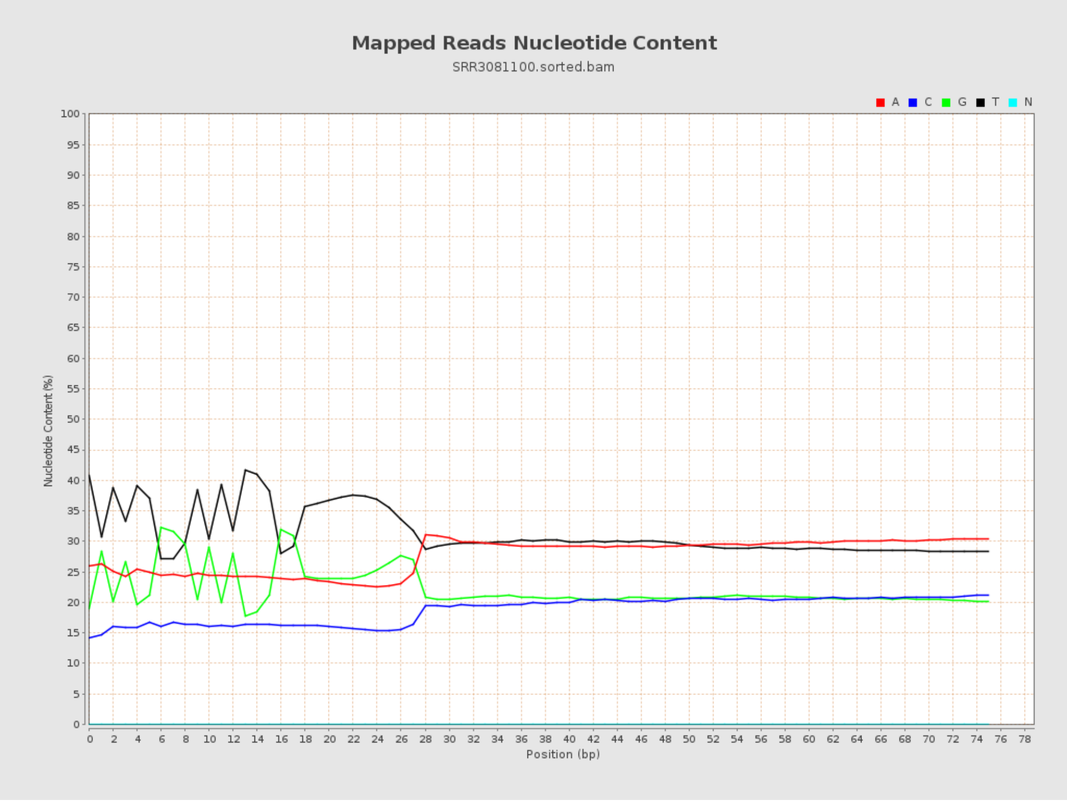
6. Results : Genome Fraction Coverage



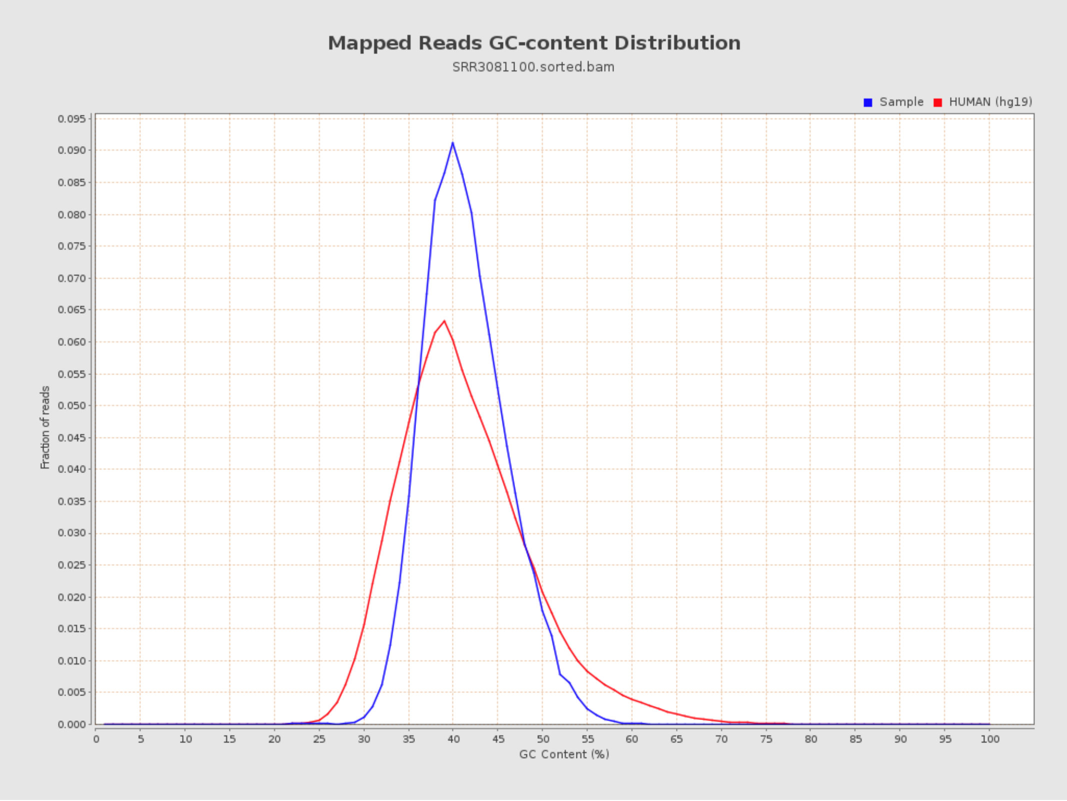
7. Results : Duplication Rate Histogram



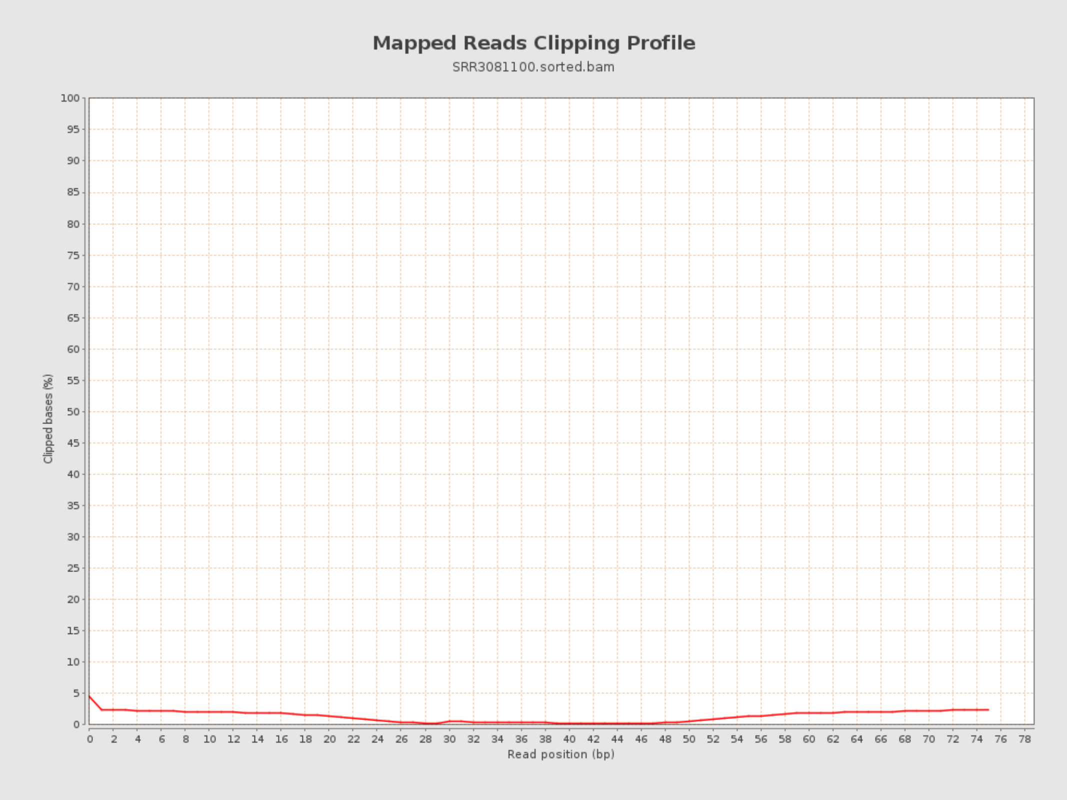
8. Results : Mapped Reads Nucleotide Content



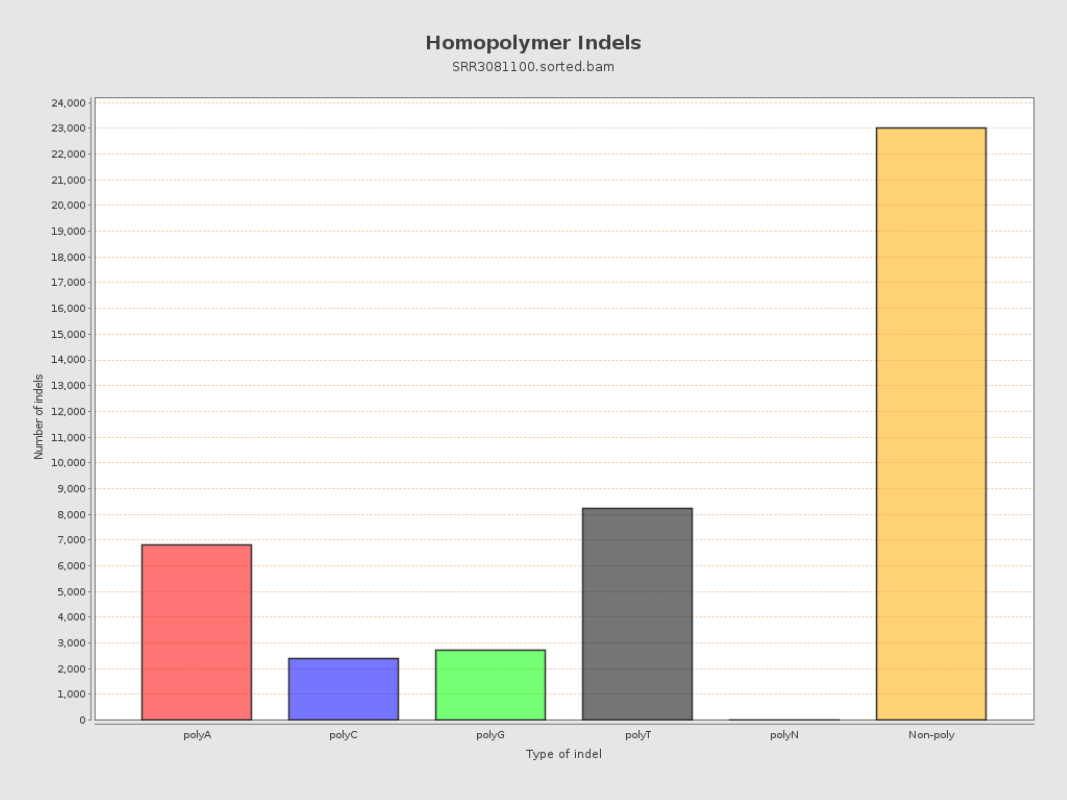
9. Results : Mapped Reads GC-content Distribution



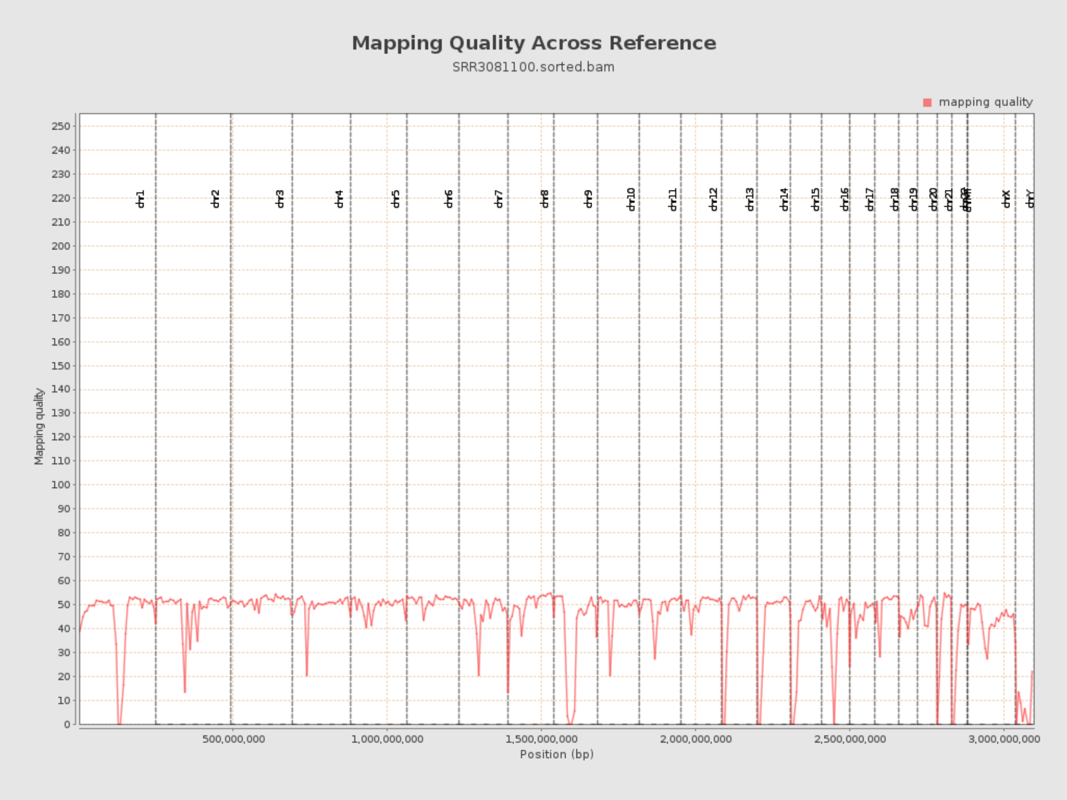
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram