Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:05:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525104.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_SRR10525104 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525104.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:05:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525104.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,655,370
Mapped reads	2,433,843 / 91.66%
Unmapped reads	221,527 / 8.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,363 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	103,159 / 3.88%
Duplication rate	3.19%
Clipped reads	2,443,962 / 92.04%

2.2. ACGT Content

Number/percentage of A's	36,573,902 / 26.07%
Number/percentage of C's	27,951,636 / 19.93%
Number/percentage of T's	43,058,072 / 30.69%
Number/percentage of G's	32,689,033 / 23.3%
Number/percentage of N's	4,525 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0453

Standard Deviation	0.3698

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

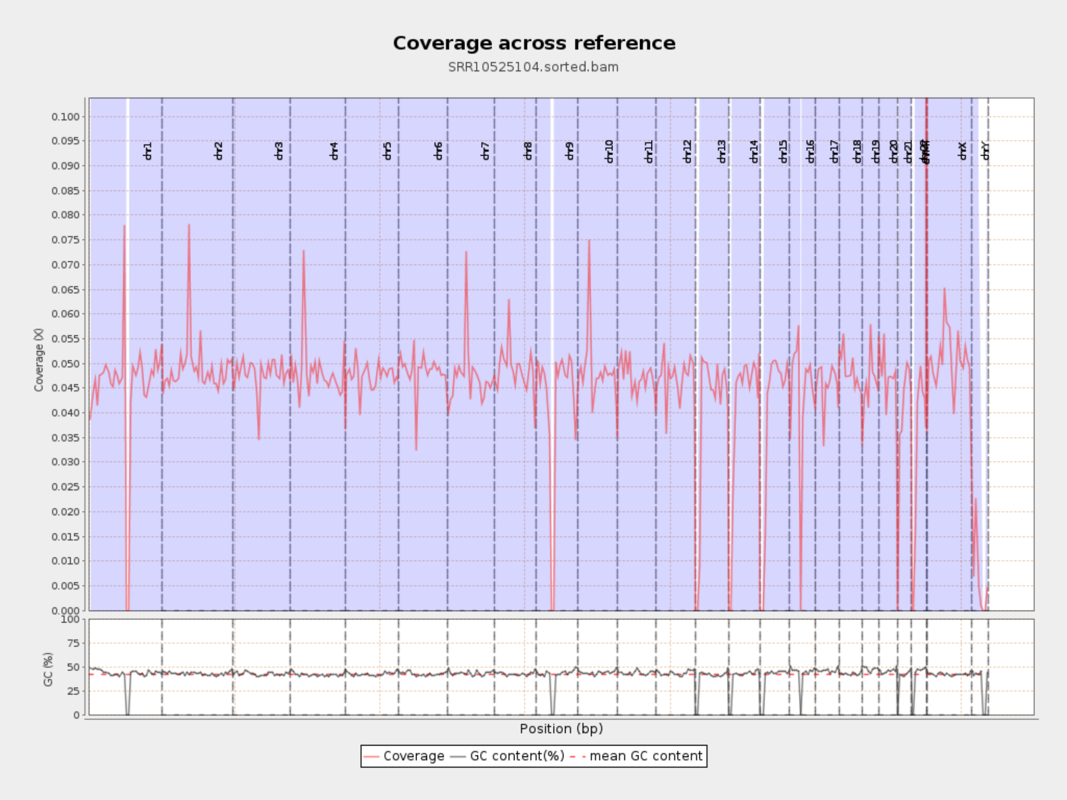
General error rate	0.49%
Mismatches	670,174
Insertions	7,629
Mapped reads with at least one insertion	0.31%
Deletions	21,260
Mapped reads with at least one deletion	0.87%
Homopolymer indels	43%

2.6. Chromosome stats

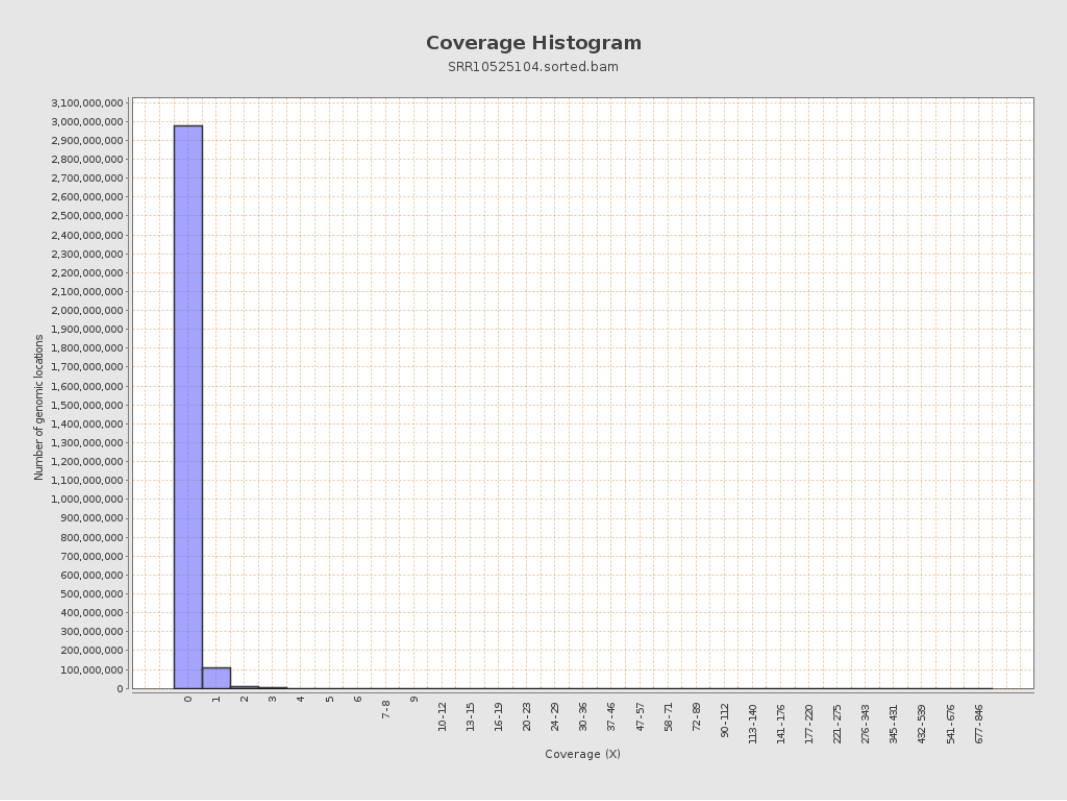
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11241195	0.0451	0.6939
chr2	243199373	11955545	0.0492	0.3949
chr3	198022430	9487809	0.0479	0.2466
chr4	191154276	9219905	0.0482	0.2768
chr5	180915260	8601084	0.0475	0.2479
chr6	171115067	8281092	0.0484	0.2767
chr7	159138663	7575408	0.0476	0.4332

chr8	146364022	7136428	0.0488	0.4046
chr9	141213431	5880622	0.0416	0.3546
chr10	135534747	6619500	0.0488	0.3538
chr11	135006516	6373202	0.0472	0.3452
chr12	133851895	6296820	0.047	0.2543
chr13	115169878	4519929	0.0392	0.2213
chr14	107349540	4271772	0.0398	0.2551
chr15	102531392	3962306	0.0386	0.2218
chr16	90354753	3944984	0.0437	0.2617
chr17	81195210	3696137	0.0455	0.2595
chr18	78077248	3792353	0.0486	0.6399
chr19	59128983	2755427	0.0466	0.5163
chr20	63025520	2976442	0.0472	0.2576
chr21	48129895	1887162	0.0392	0.2531
chr22	51304566	1581172	0.0308	0.1974
chrMT	16571	8734	0.5271	0.8136
chrX	155270560	7844168	0.0505	0.2918
chrY	59373566	403425	0.0068	0.1621

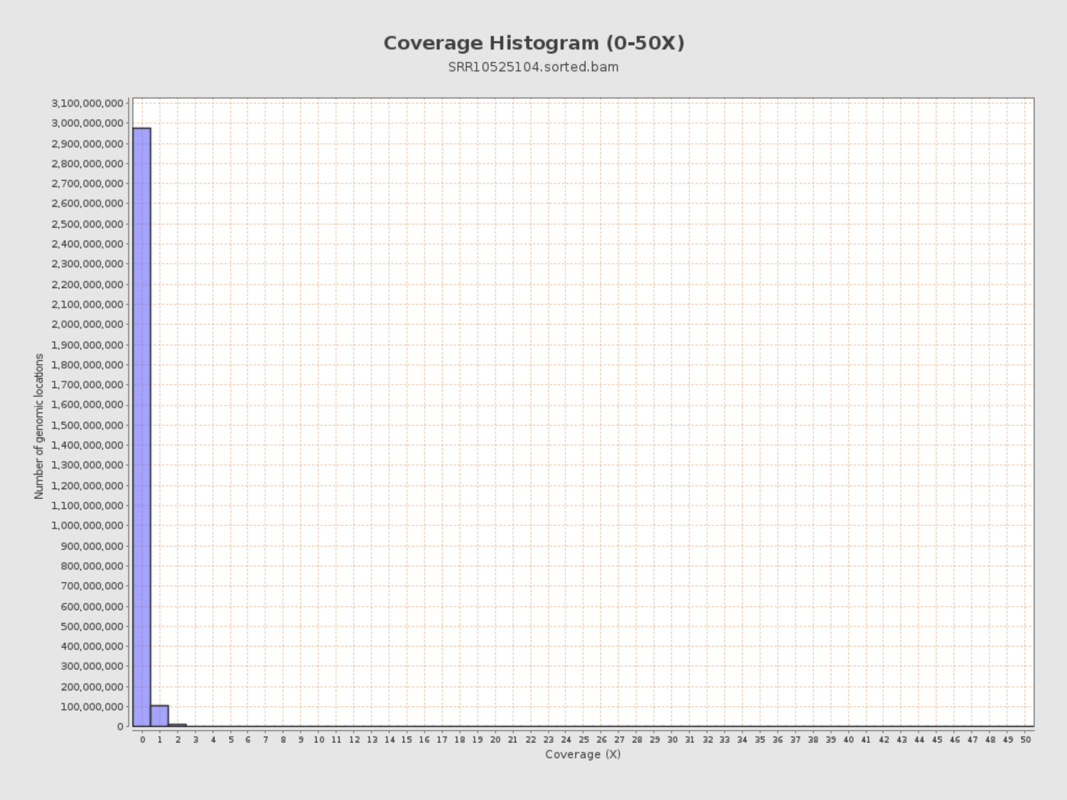
3. Results : Coverage across reference



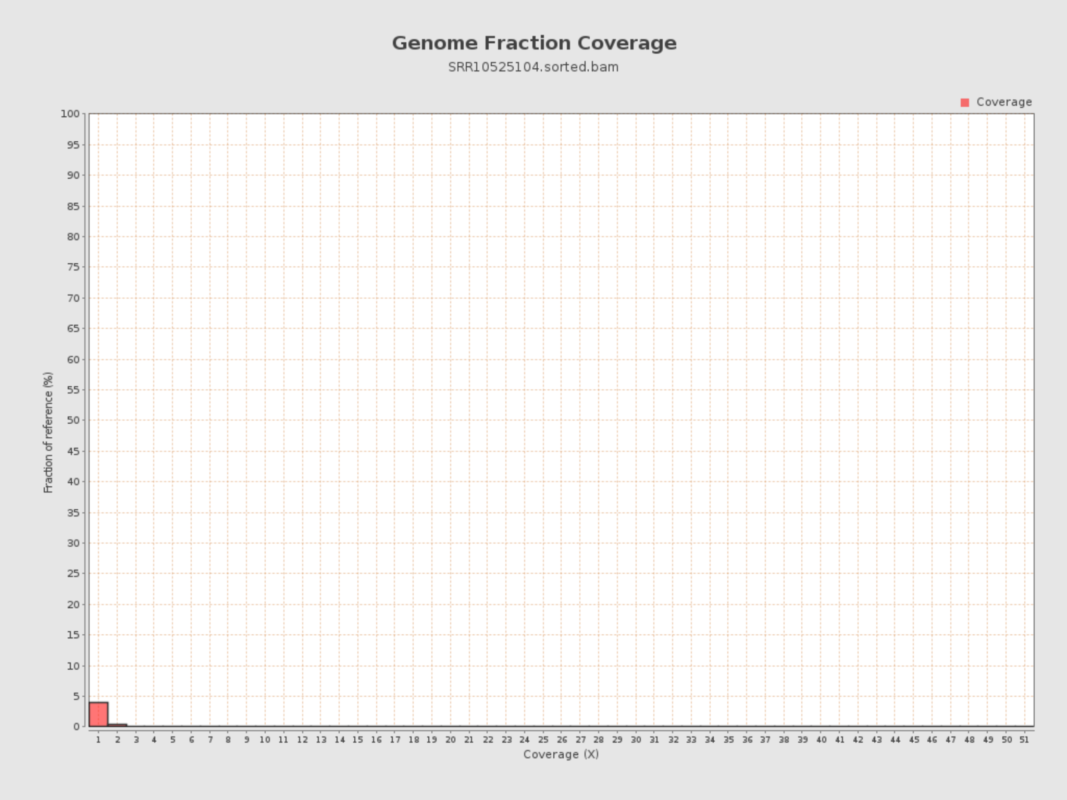
4. Results : Coverage Histogram



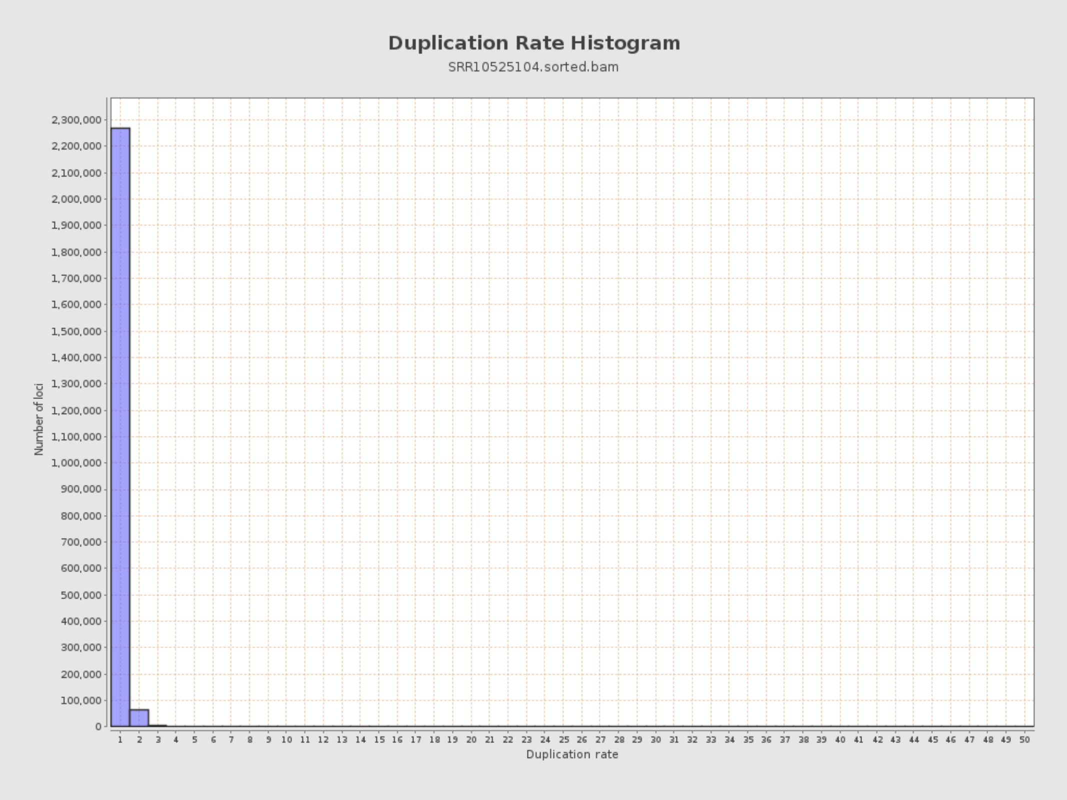
5. Results : Coverage Histogram (0-50X)



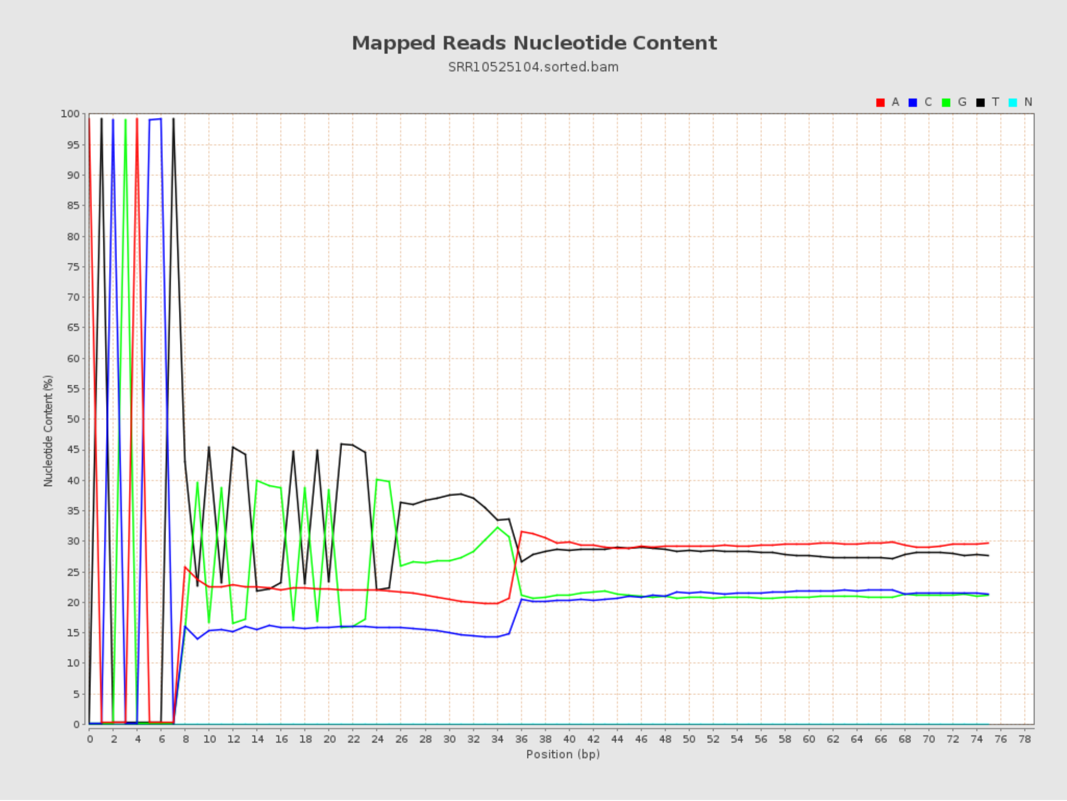
6. Results : Genome Fraction Coverage



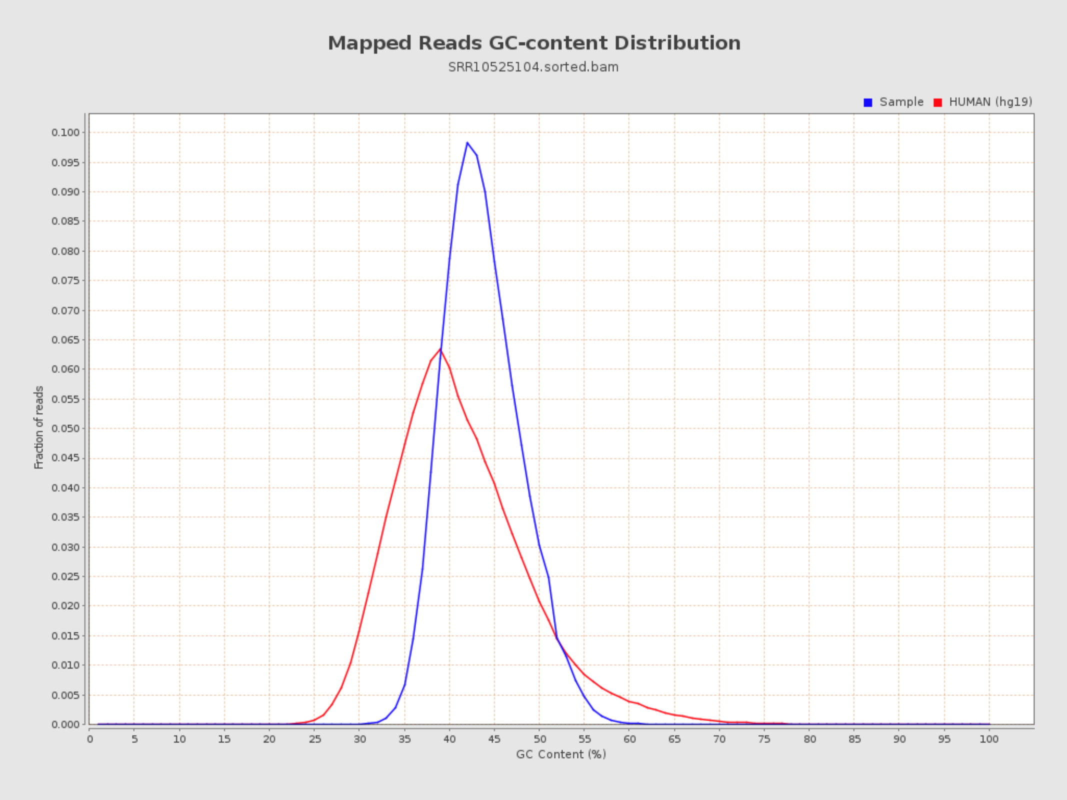
7. Results : Duplication Rate Histogram



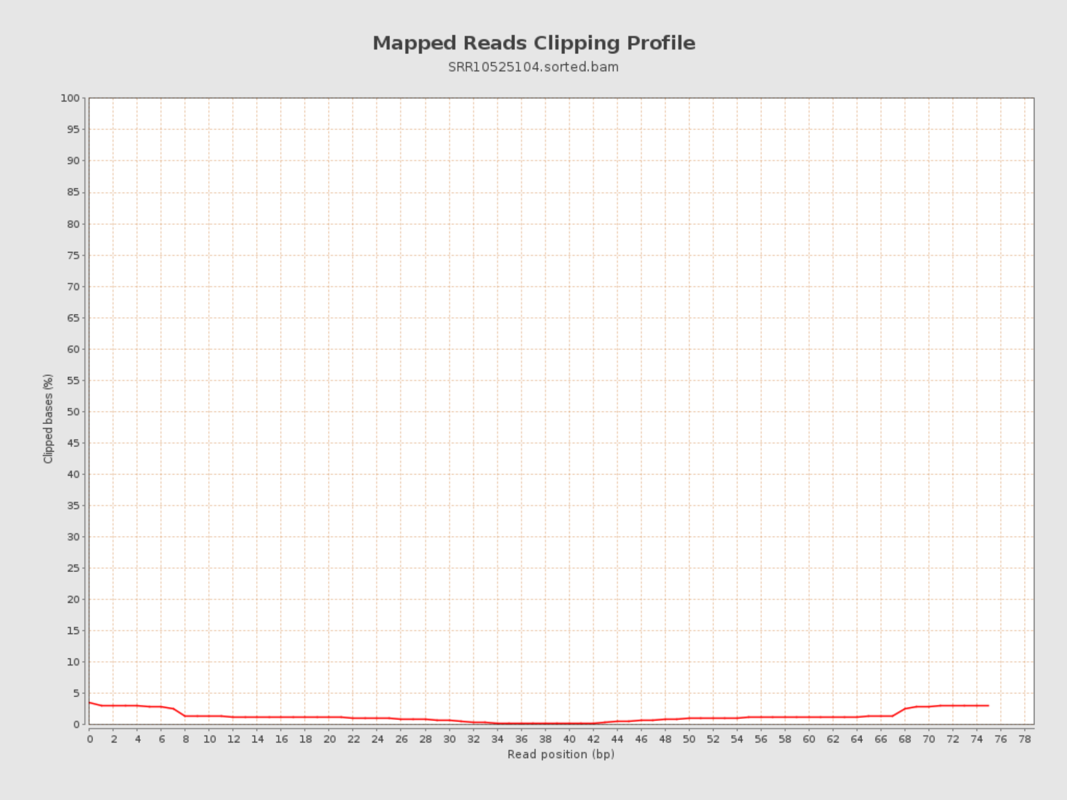
8. Results : Mapped Reads Nucleotide Content



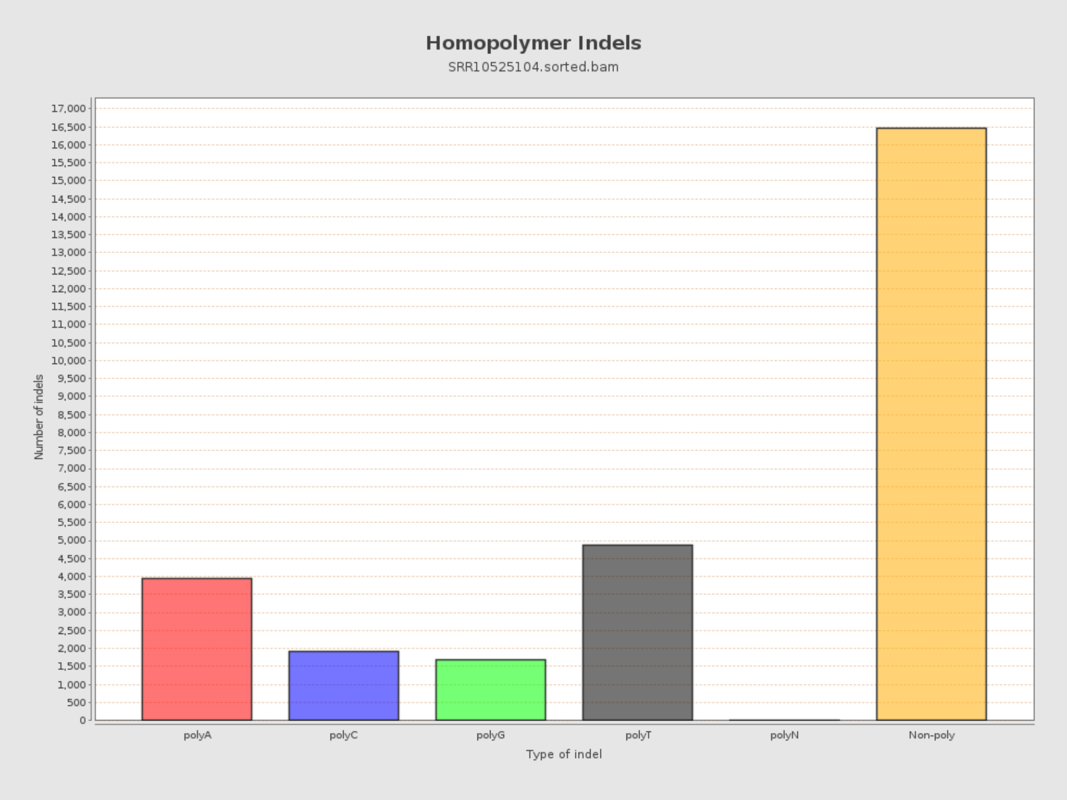
9. Results : Mapped Reads GC-content Distribution



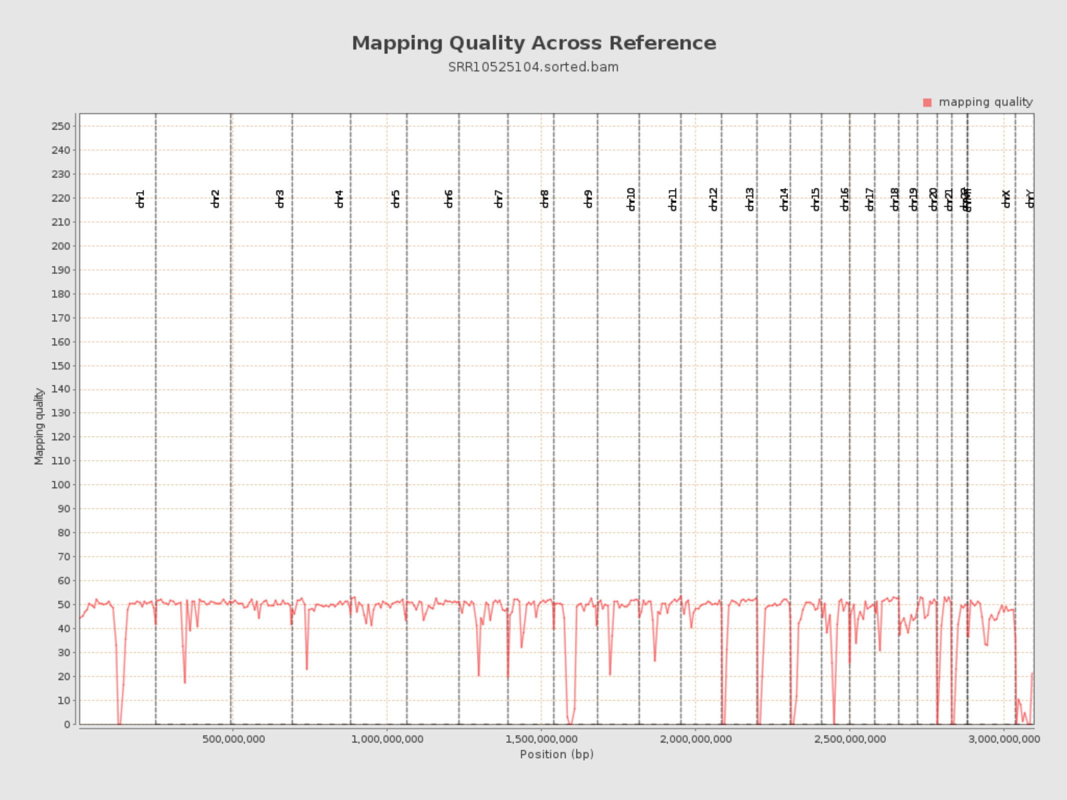
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram