Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:15:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525172.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_SRR10525172 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525172.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:15:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525172.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,229,288
Mapped reads	2,049,835 / 91.95%
Unmapped reads	179,453 / 8.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,686 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	77,449 / 3.47%
Duplication rate	2.7%
Clipped reads	2,049,491 / 91.93%

2.2. ACGT Content

Number/percentage of A's	30,962,612 / 25.76%
Number/percentage of C's	22,362,124 / 18.6%
Number/percentage of T's	38,460,883 / 32%
Number/percentage of G's	28,415,175 / 23.64%
Number/percentage of N's	2,815 / 0%
GC Percentage	42.24%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.3548

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

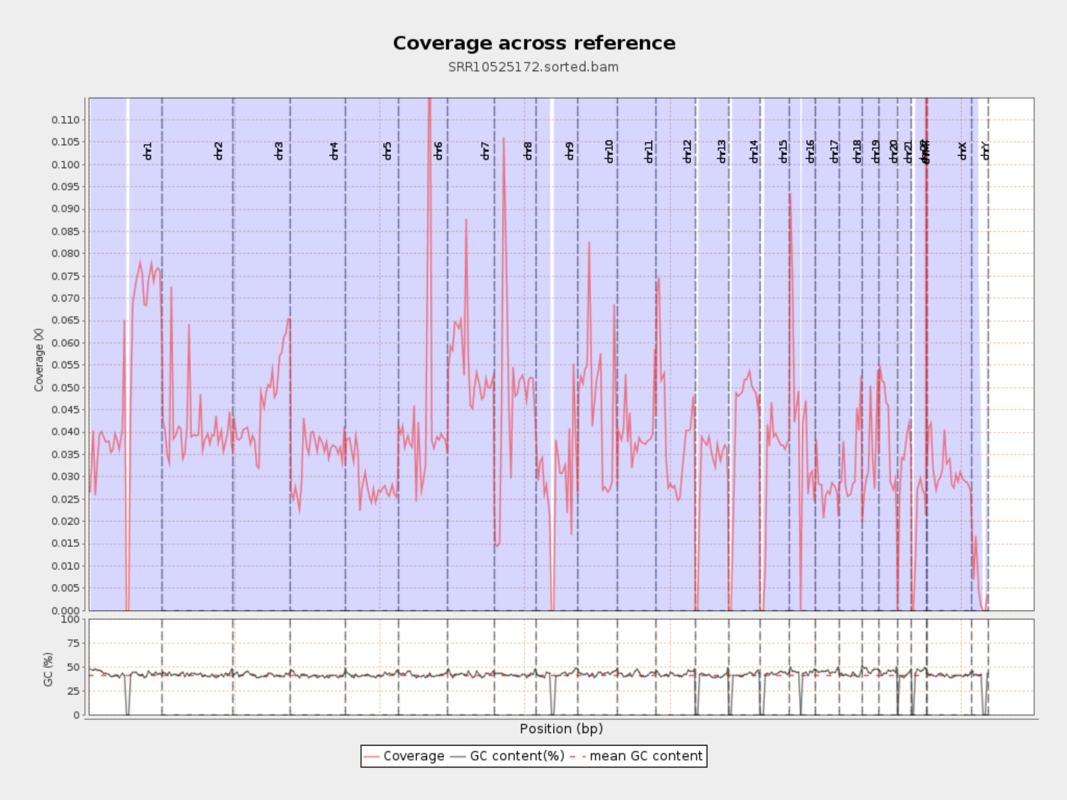
General error rate	0.51%
Mismatches	603,094
Insertions	8,625
Mapped reads with at least one insertion	0.42%
Deletions	23,303
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.18%

2.6. Chromosome stats

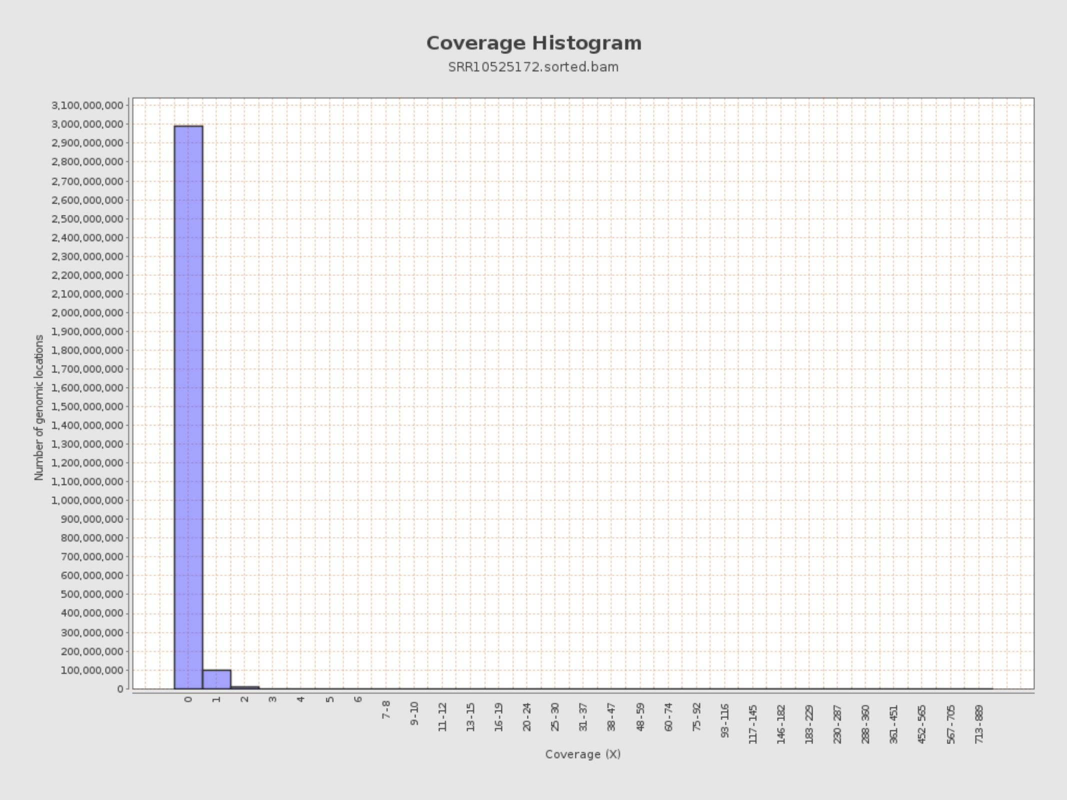
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12648260	0.0507	0.6316
chr2	243199373	9958664	0.0409	0.4652
chr3	198022430	9177491	0.0463	0.2416
chr4	191154276	6622127	0.0346	0.2185
chr5	180915260	5286090	0.0292	0.1893
chr6	171115067	7482149	0.0437	0.2585
chr7	159138663	8883161	0.0558	0.655

chr8	146364022	6896073	0.0471	0.3189
chr9	141213431	4036469	0.0286	0.2665
chr10	135534747	6369313	0.047	0.3903
chr11	135006516	5411483	0.0401	0.2731
chr12	133851895	5346640	0.0399	0.2231
chr13	115169878	3609437	0.0313	0.1971
chr14	107349540	4406786	0.0411	0.2282
chr15	102531392	3201621	0.0312	0.1997
chr16	90354753	3678040	0.0407	0.2498
chr17	81195210	2216963	0.0273	0.1902
chr18	78077248	2600011	0.0333	0.4844
chr19	59128983	2088857	0.0353	0.4541
chr20	63025520	2545181	0.0404	0.2256
chr21	48129895	1537444	0.0319	0.2084
chr22	51304566	974751	0.019	0.1513
chrMT	16571	41613	2.5112	2.1852
chrX	155270560	4897729	0.0315	0.2166
chrY	59373566	324332	0.0055	0.1338

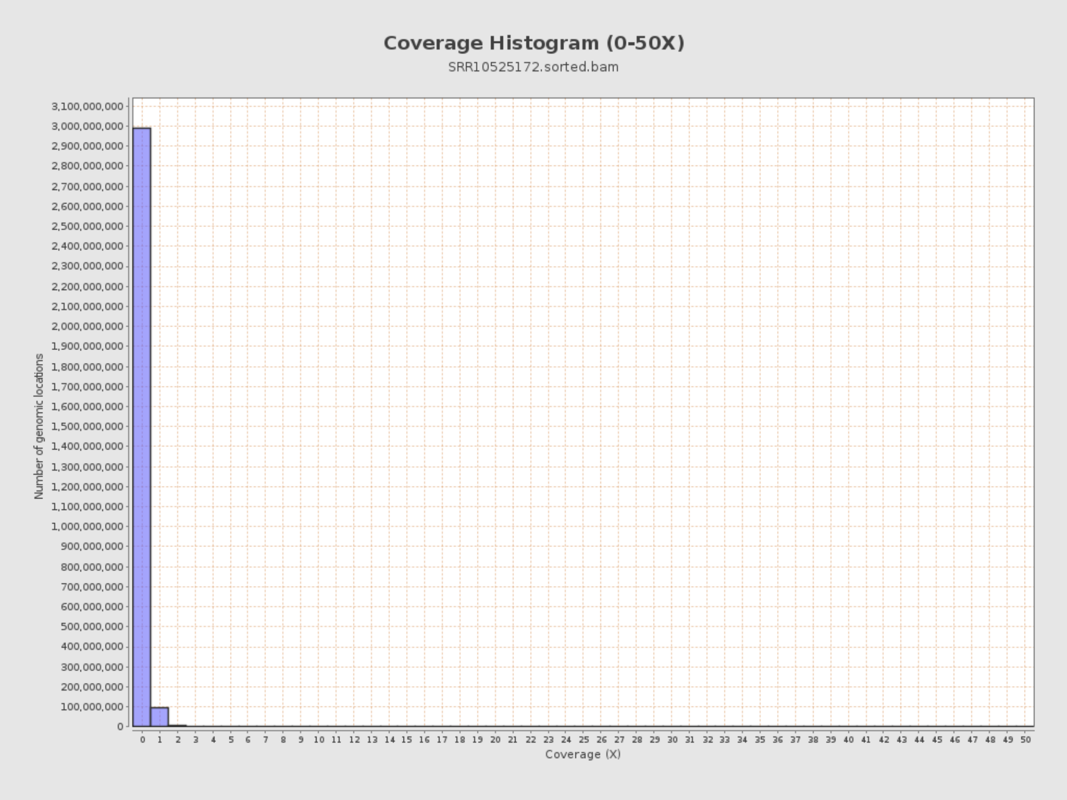
3. Results : Coverage across reference



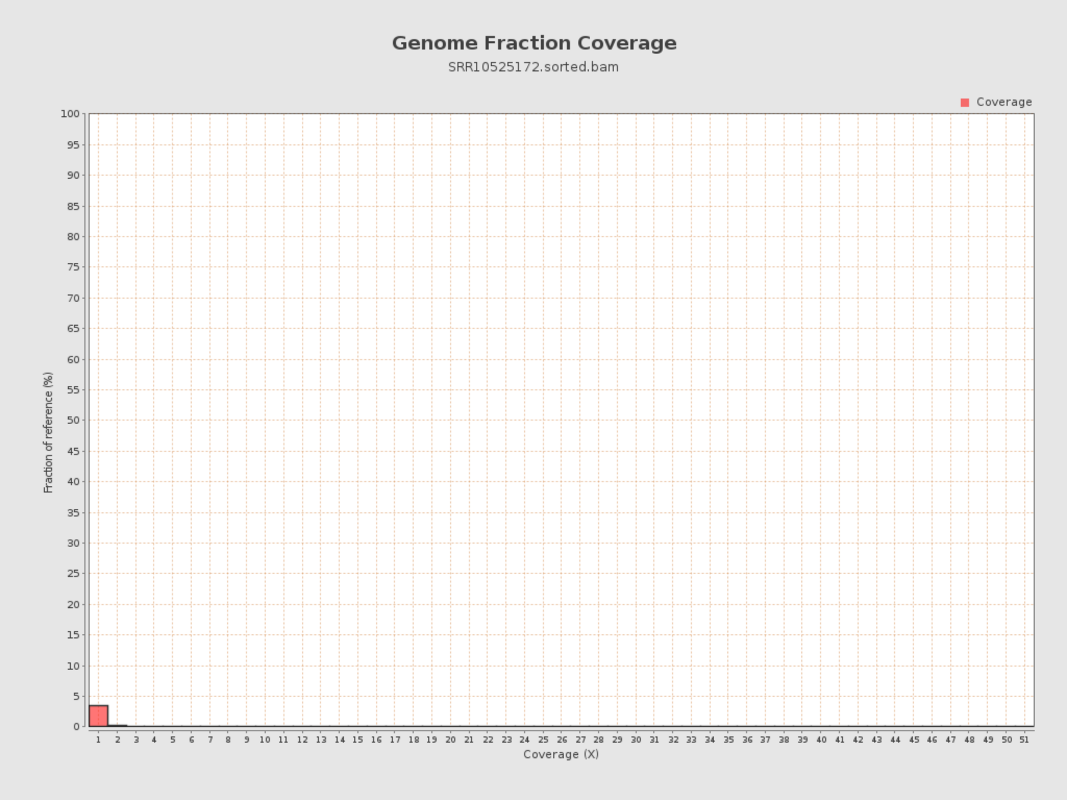
4. Results : Coverage Histogram



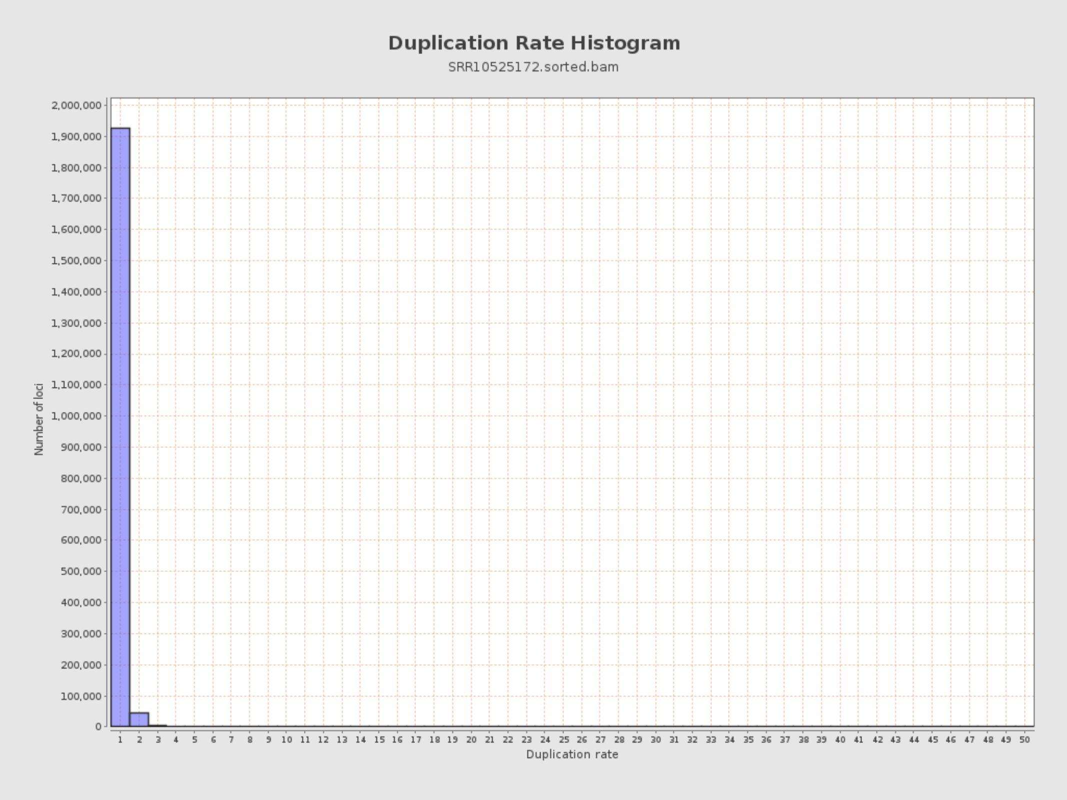
5. Results : Coverage Histogram (0-50X)



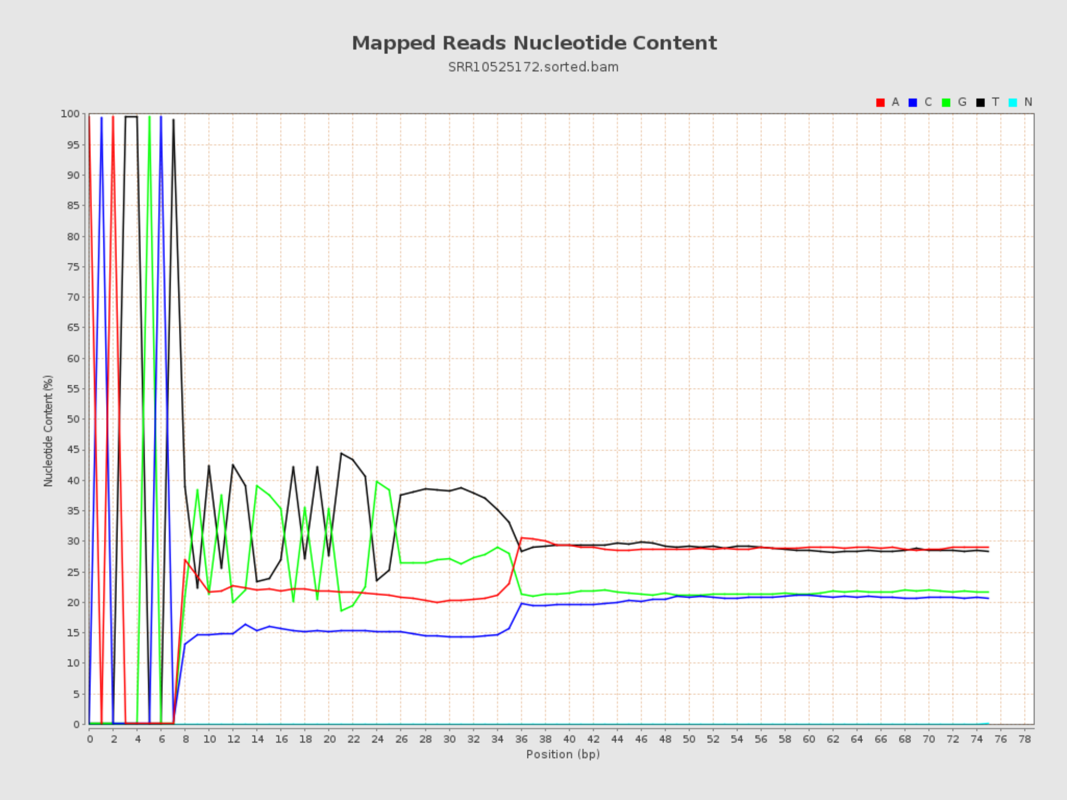
6. Results : Genome Fraction Coverage



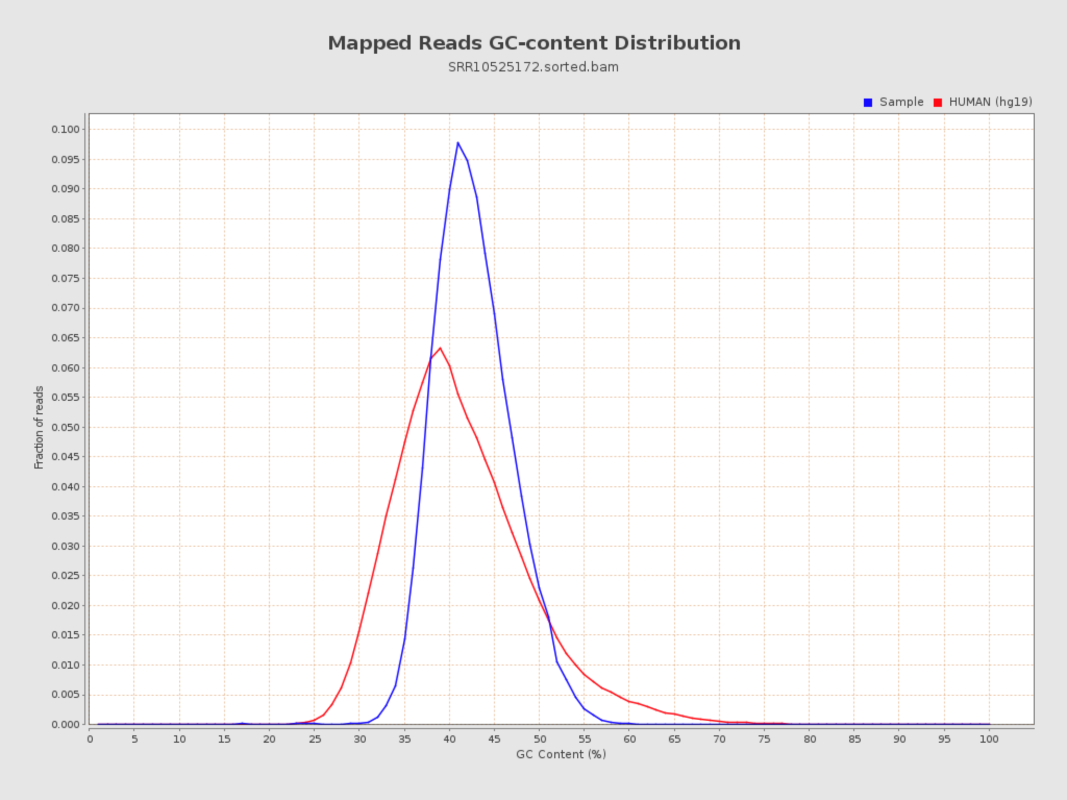
7. Results : Duplication Rate Histogram



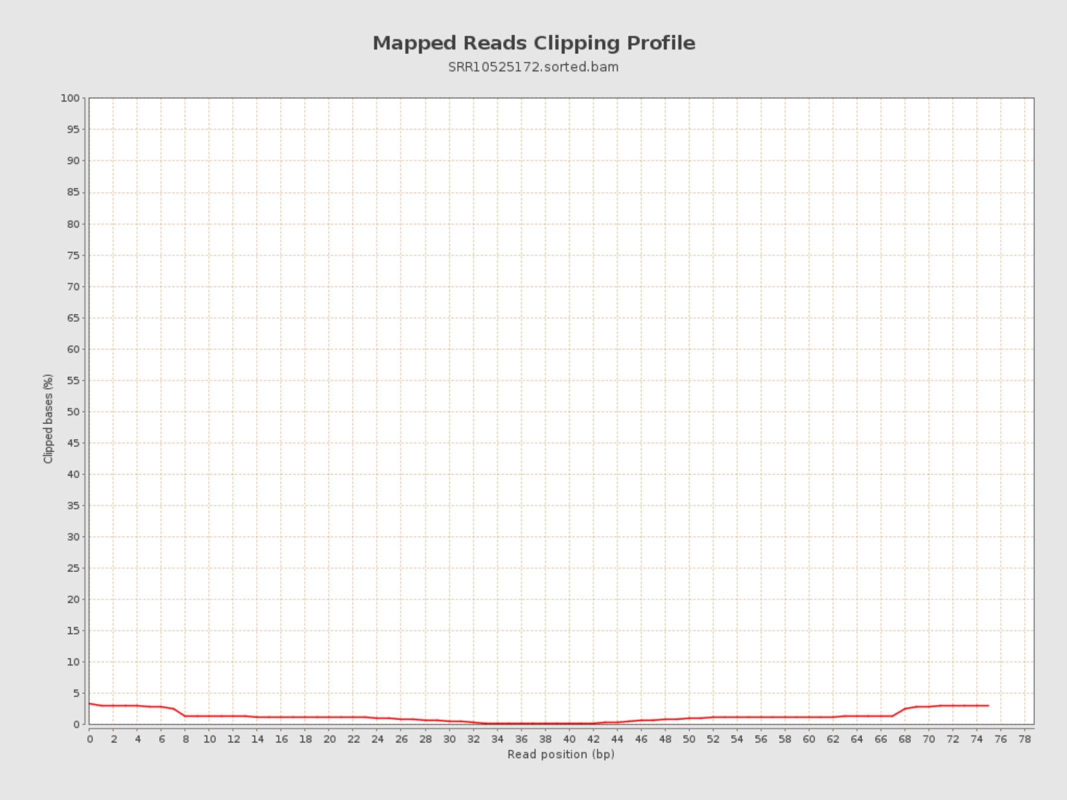
8. Results : Mapped Reads Nucleotide Content



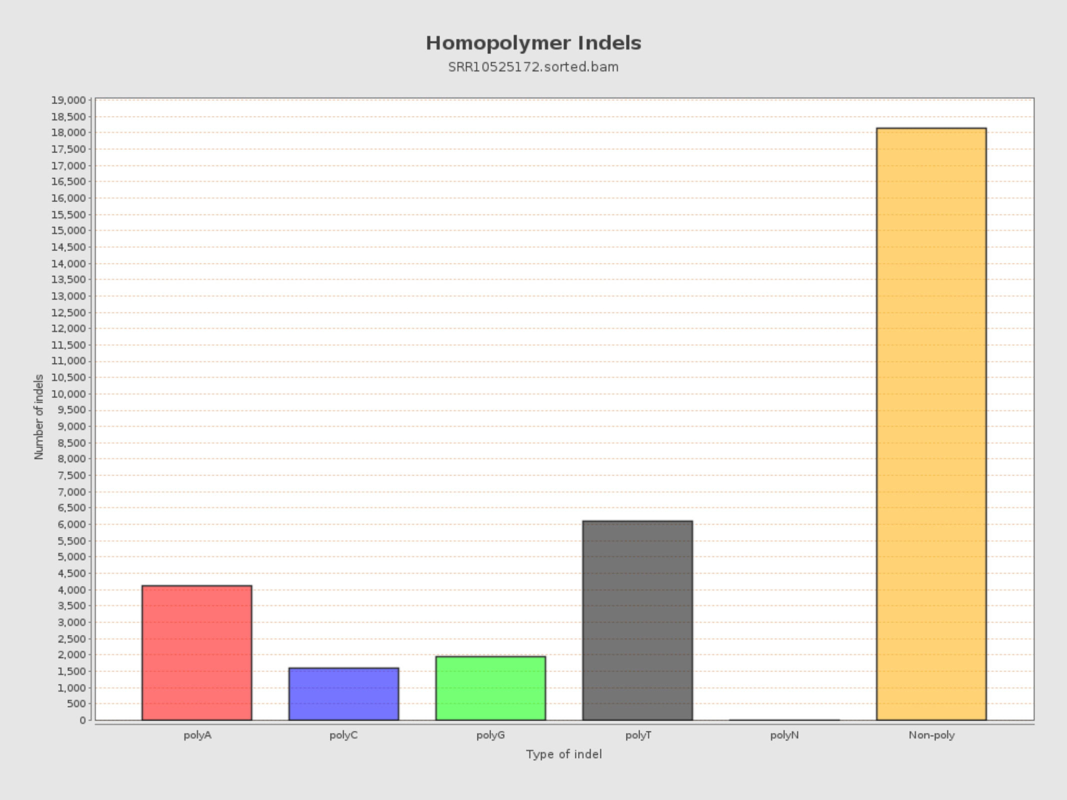
9. Results : Mapped Reads GC-content Distribution



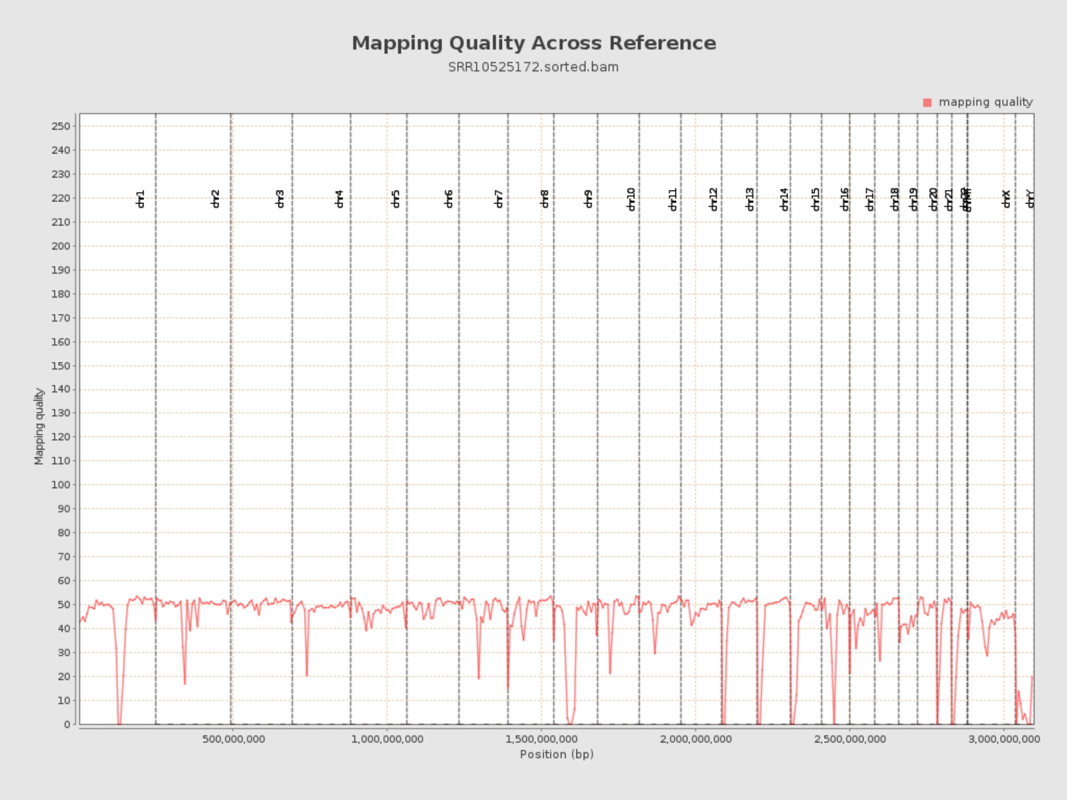
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram