Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:53:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525222.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_SRR10525222 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525222.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:53:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525222.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,209,676
Mapped reads	1,096,885 / 90.68%
Unmapped reads	112,791 / 9.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,121 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	30,566 / 2.53%
Duplication rate	2.04%
Clipped reads	1,097,048 / 90.69%

2.2. ACGT Content

Number/percentage of A's	15,064,487 / 23.73%
Number/percentage of C's	11,135,741 / 17.54%
Number/percentage of T's	21,025,893 / 33.12%
Number/percentage of G's	16,262,953 / 25.61%
Number/percentage of N's	1,387 / 0%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0205

Standard Deviation	0.2087

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

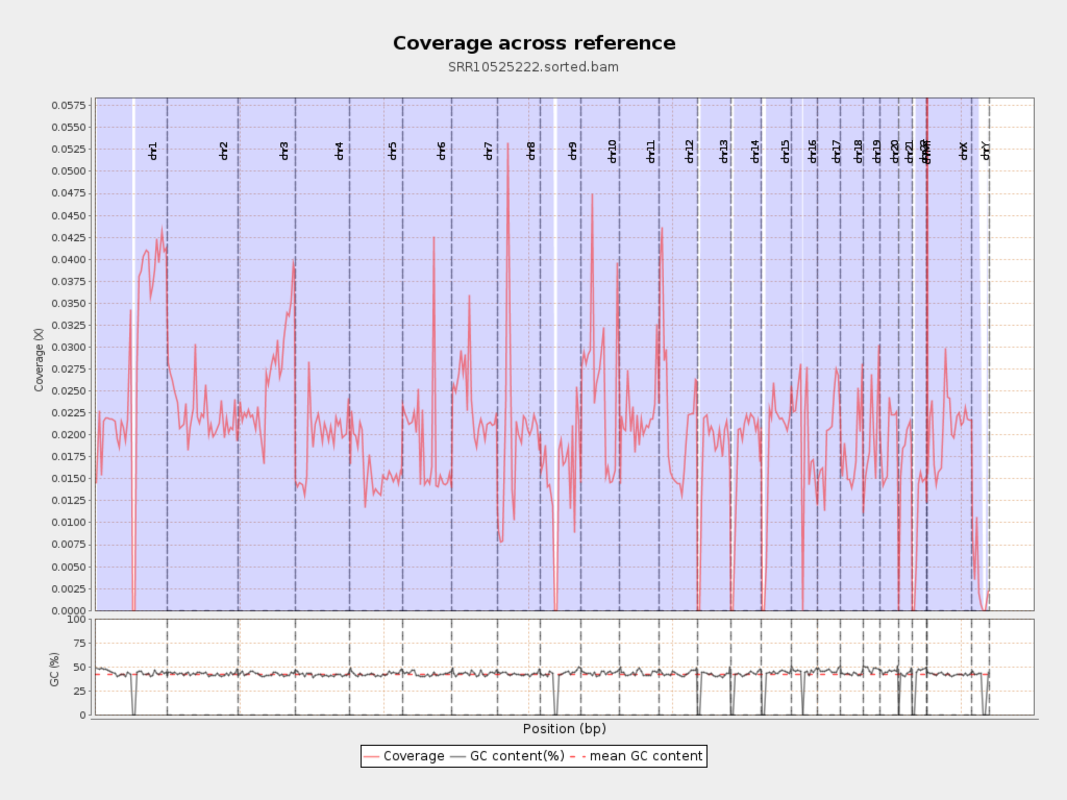
General error rate	0.53%
Mismatches	329,206
Insertions	4,320
Mapped reads with at least one insertion	0.39%
Deletions	12,783
Mapped reads with at least one deletion	1.16%
Homopolymer indels	43.96%

2.6. Chromosome stats

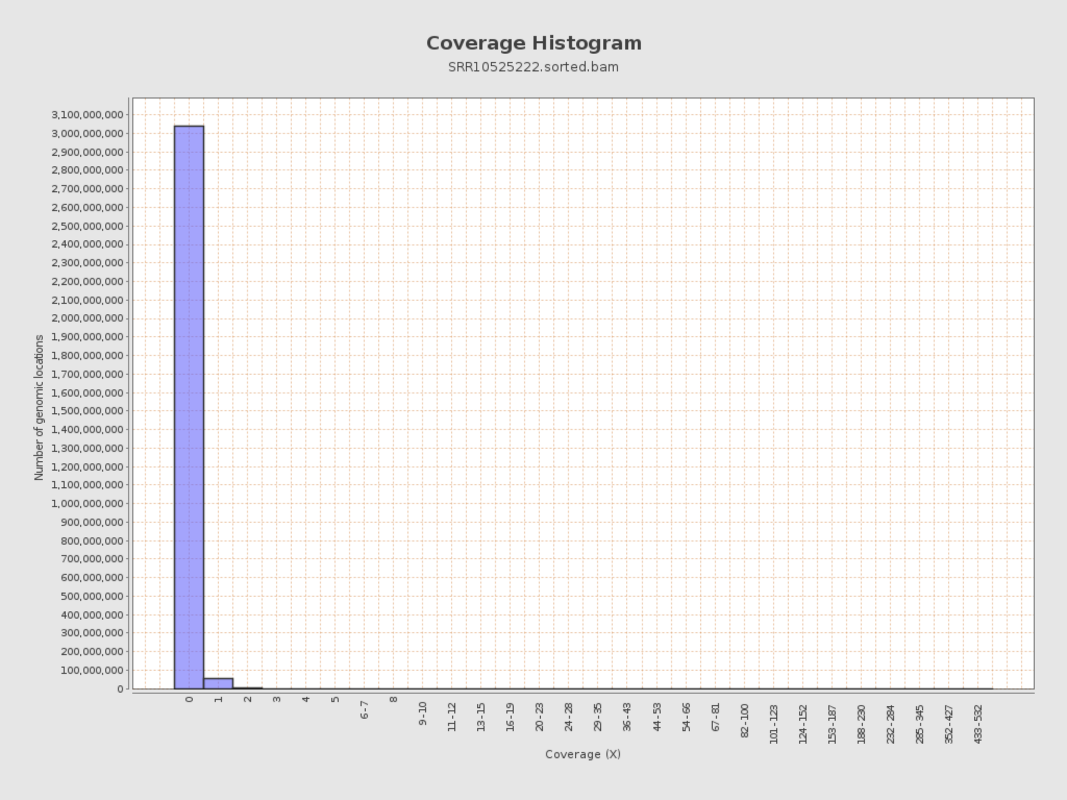
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6898919	0.0277	0.3605
chr2	243199373	5445957	0.0224	0.2698
chr3	198022430	5179849	0.0262	0.1748
chr4	191154276	3740404	0.0196	0.1569
chr5	180915260	2944080	0.0163	0.1351
chr6	171115067	3250659	0.019	0.1616
chr7	159138663	3784975	0.0238	0.2871

chr8	146364022	2974009	0.0203	0.1892
chr9	141213431	2124892	0.015	0.1514
chr10	135534747	3554820	0.0262	0.2526
chr11	135006516	2972148	0.022	0.1814
chr12	133851895	2951638	0.0221	0.1591
chr13	115169878	2010292	0.0175	0.1422
chr14	107349540	1859174	0.0173	0.1425
chr15	102531392	1833306	0.0179	0.1442
chr16	90354753	1756736	0.0194	0.1626
chr17	81195210	1632388	0.0201	0.1537
chr18	78077248	1402118	0.018	0.2534
chr19	59128983	1173370	0.0198	0.2674
chr20	63025520	1204291	0.0191	0.1491
chr21	48129895	828022	0.0172	0.146
chr22	51304566	532353	0.0104	0.1086
chrMT	16571	4290	0.2589	0.5774
chrX	155270560	3261784	0.021	0.1658
chrY	59373566	190229	0.0032	0.0929

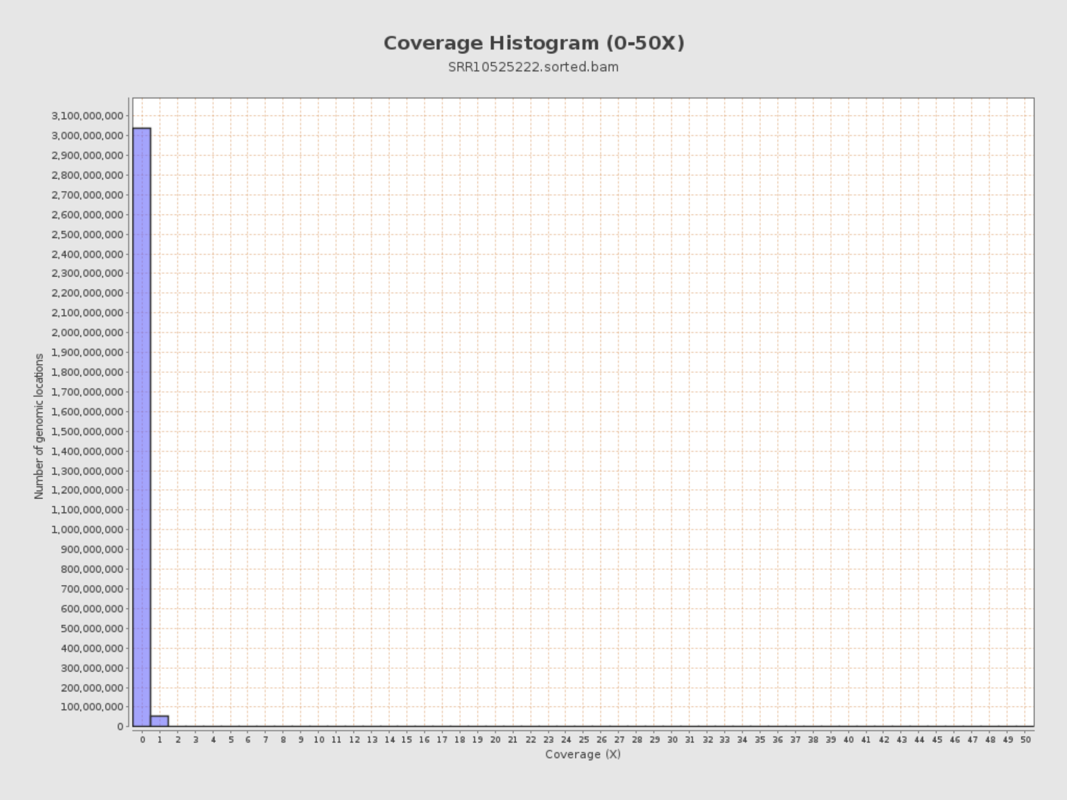
3. Results : Coverage across reference



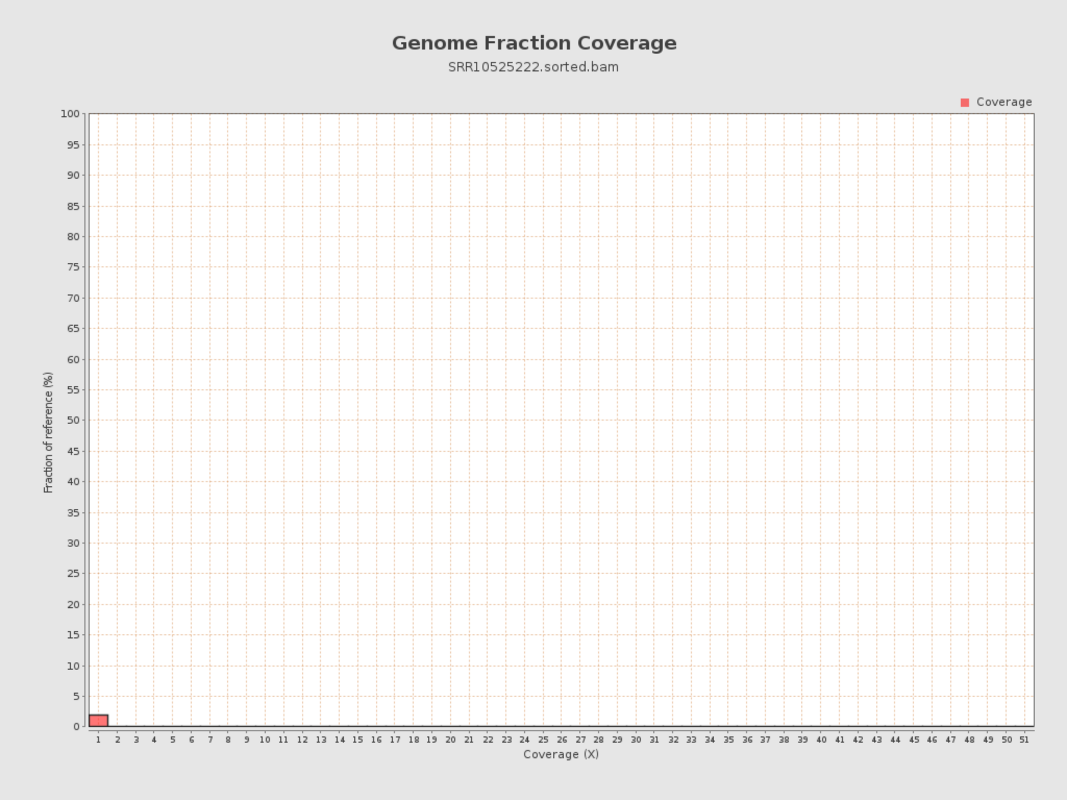
4. Results : Coverage Histogram



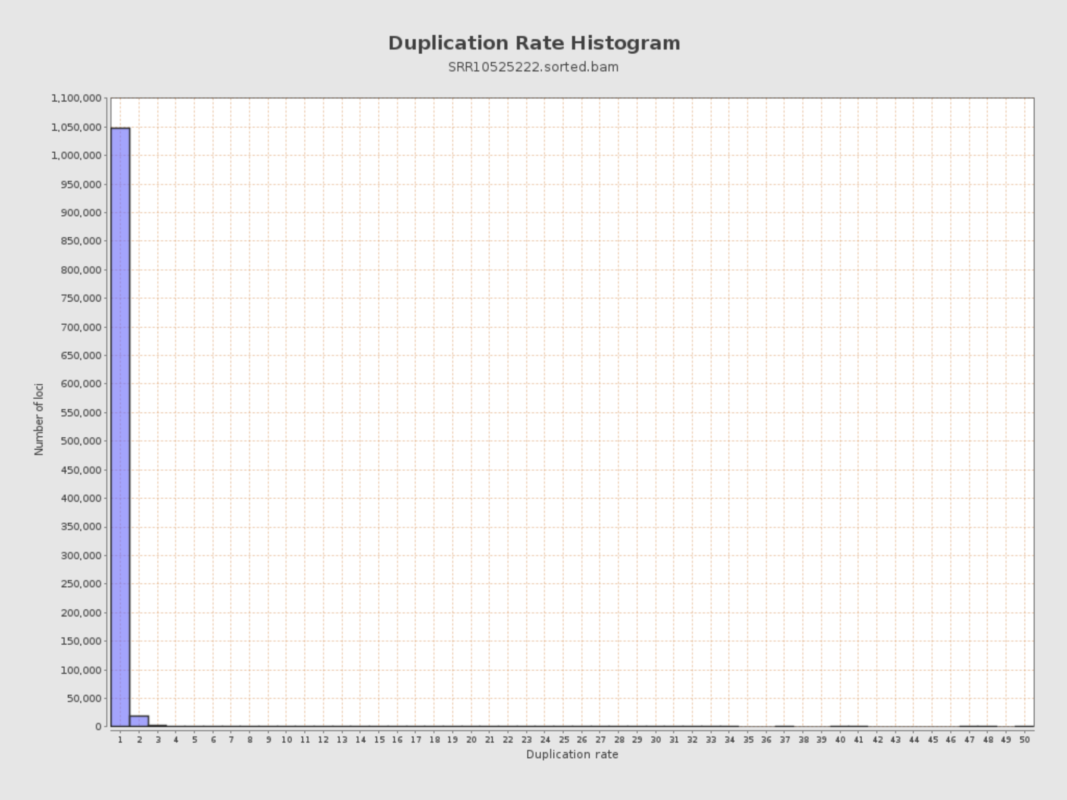
5. Results : Coverage Histogram (0-50X)



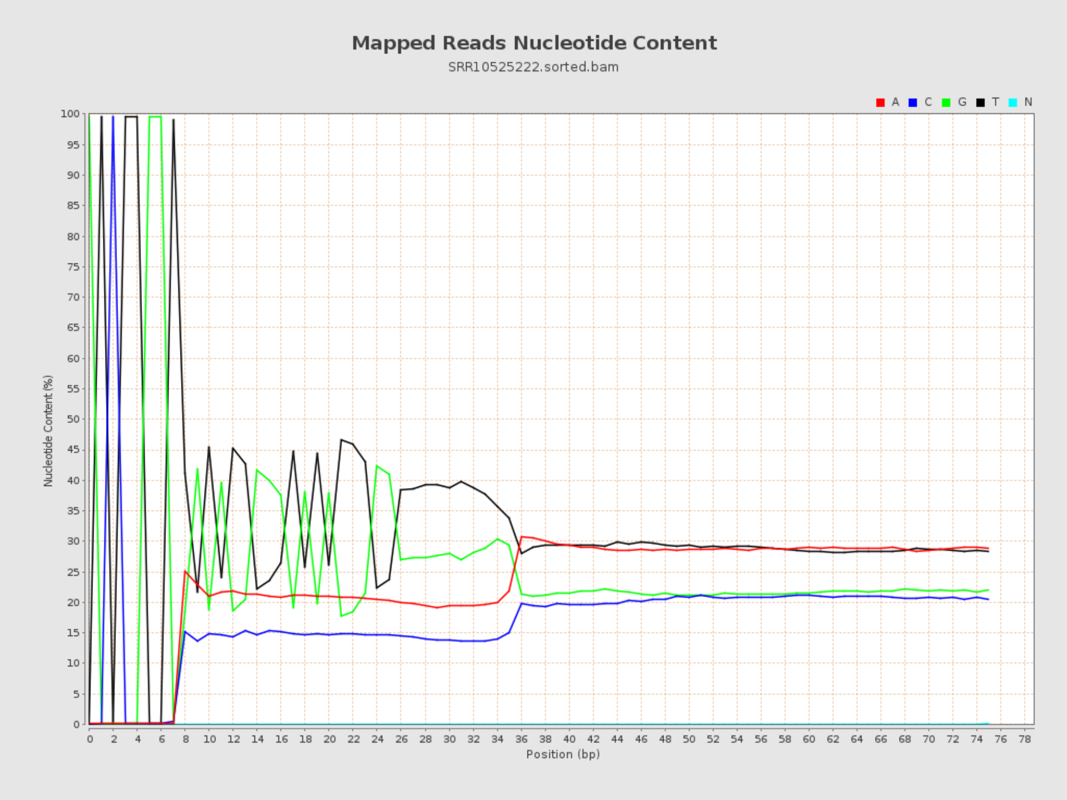
6. Results : Genome Fraction Coverage



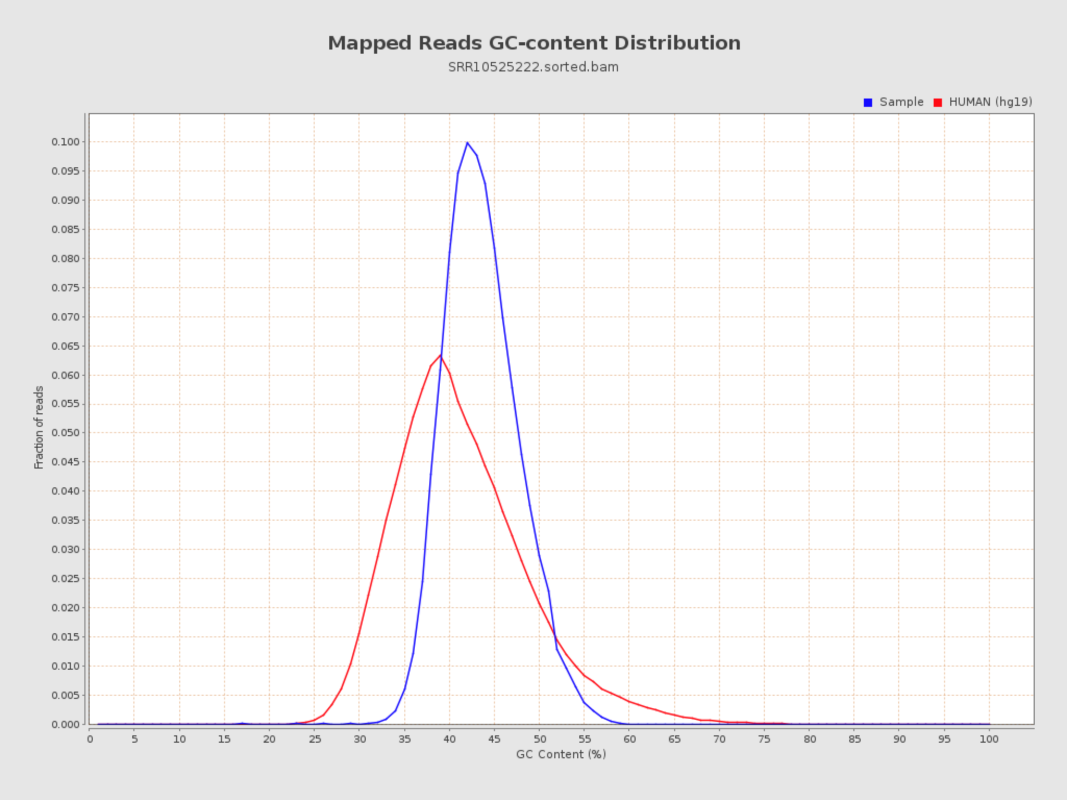
7. Results : Duplication Rate Histogram



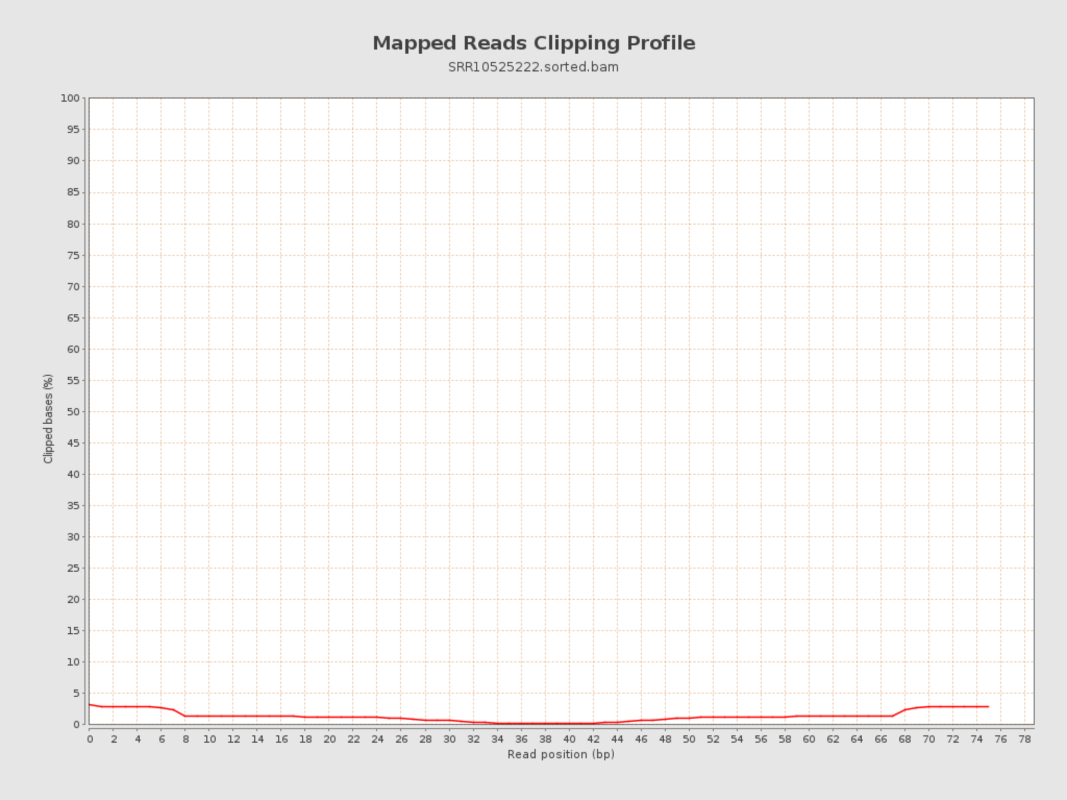
8. Results : Mapped Reads Nucleotide Content



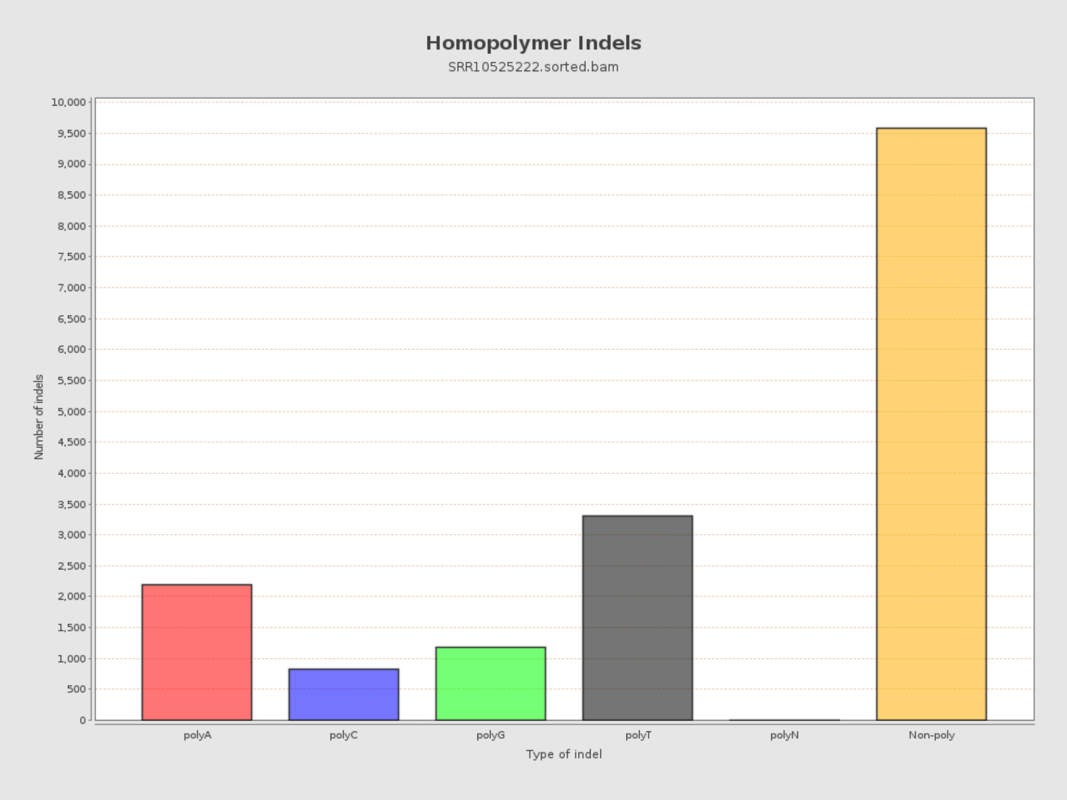
9. Results : Mapped Reads GC-content Distribution



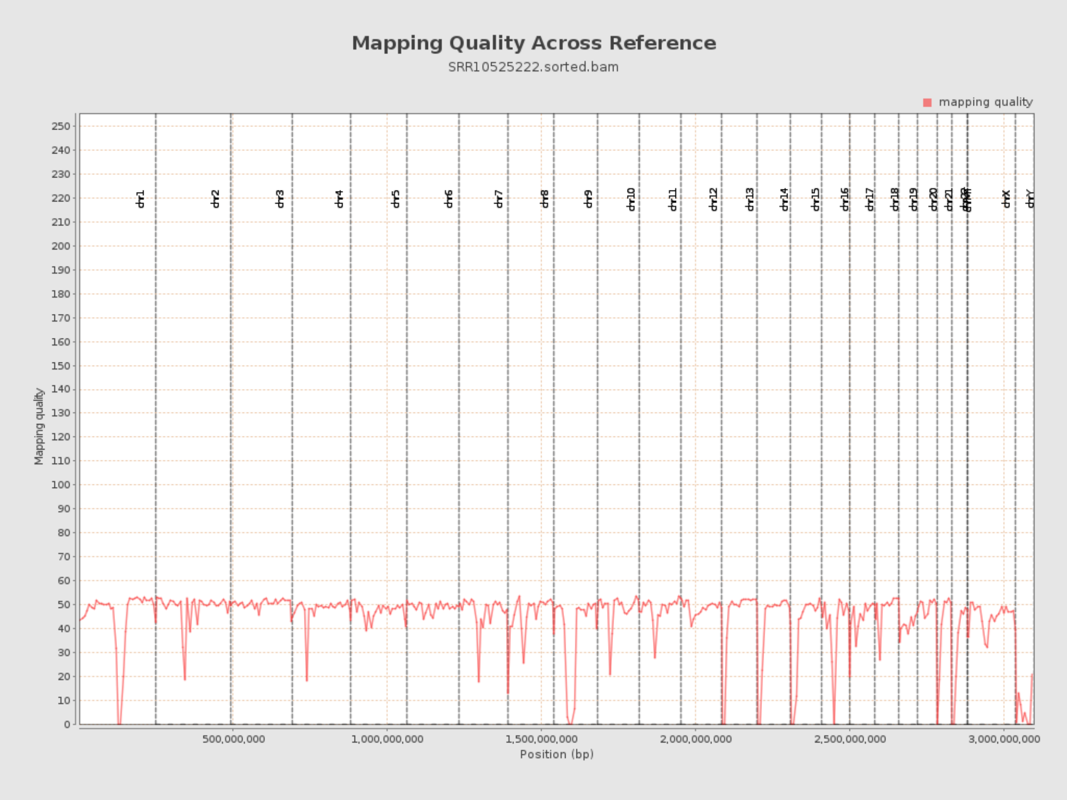
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram