Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:24:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525236.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_SRR10525236 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525236.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:24:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525236.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	632,553
Mapped reads	583,113 / 92.18%
Unmapped reads	49,440 / 7.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,965 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	12,374 / 1.96%
Duplication rate	1.59%
Clipped reads	583,436 / 92.24%

2.2. ACGT Content

Number/percentage of A's	8,439,280 / 24.94%
Number/percentage of C's	6,128,053 / 18.11%
Number/percentage of T's	11,108,796 / 32.83%
Number/percentage of G's	8,156,942 / 24.11%
Number/percentage of N's	626 / 0%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0109

Standard Deviation	0.1363

2.4. Mapping Quality

Mean Mapping Quality	45.3

2.5. Mismatches and indels

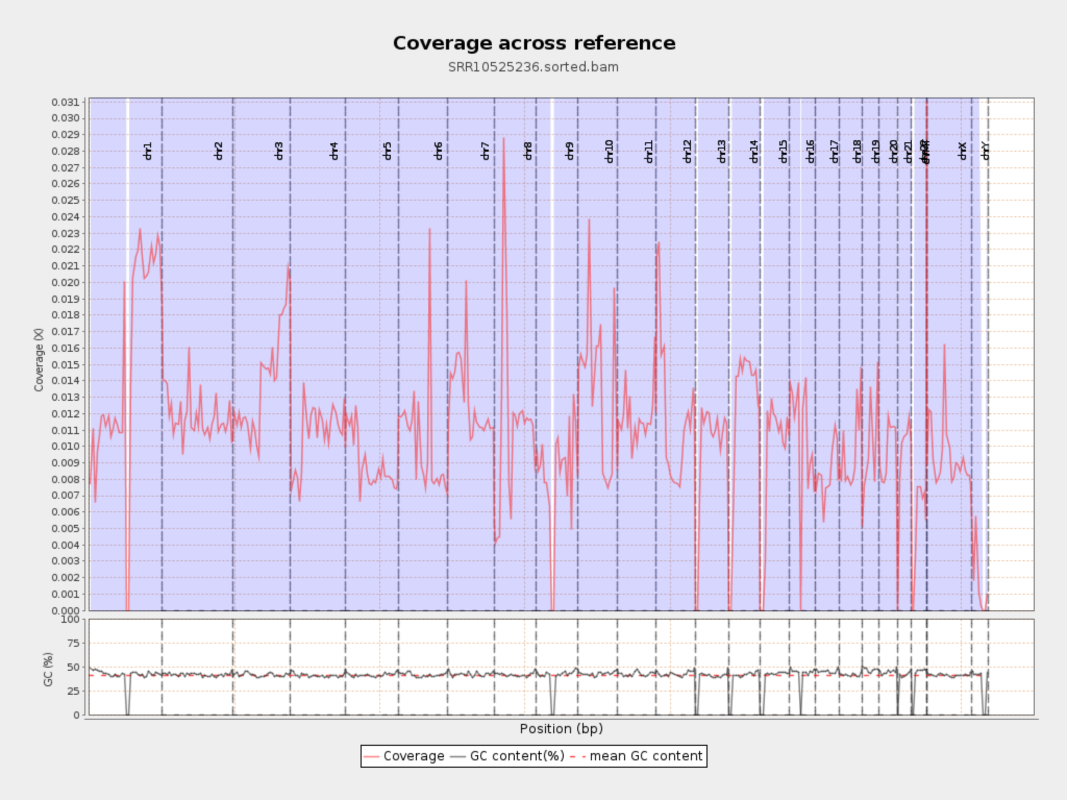
General error rate	0.51%
Mismatches	167,073
Insertions	2,707
Mapped reads with at least one insertion	0.46%
Deletions	6,777
Mapped reads with at least one deletion	1.15%
Homopolymer indels	42.68%

2.6. Chromosome stats

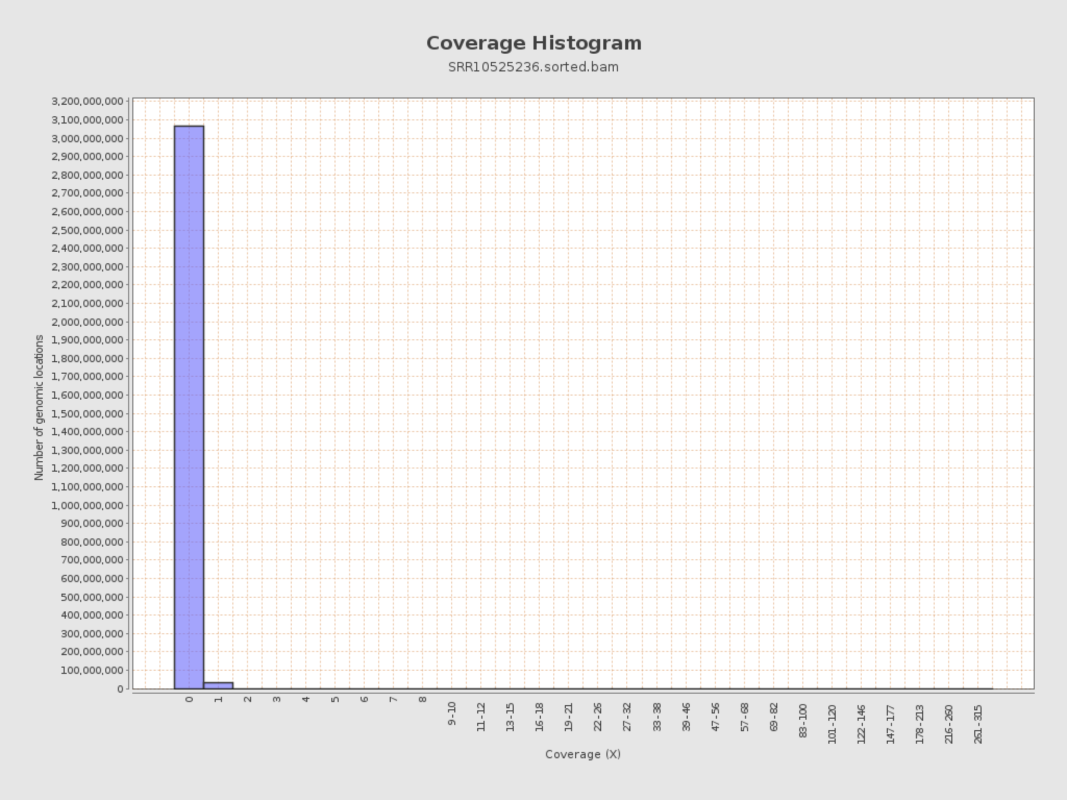
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3691694	0.0148	0.2286
chr2	243199373	2890188	0.0119	0.1674
chr3	198022430	2738869	0.0138	0.122
chr4	191154276	2054118	0.0107	0.1102
chr5	180915260	1622028	0.009	0.0983
chr6	171115067	1761601	0.0103	0.1119
chr7	159138663	2050884	0.0129	0.1808

chr8	146364022	1638399	0.0112	0.1341
chr9	141213431	1143057	0.0081	0.104
chr10	135534747	1876639	0.0138	0.1479
chr11	135006516	1589043	0.0118	0.1224
chr12	133851895	1582006	0.0118	0.1133
chr13	115169878	1120533	0.0097	0.1027
chr14	107349540	1295044	0.0121	0.1151
chr15	102531392	936614	0.0091	0.1004
chr16	90354753	931875	0.0103	0.1096
chr17	81195210	676762	0.0083	0.0959
chr18	78077248	751958	0.0096	0.1641
chr19	59128983	598985	0.0101	0.1563
chr20	63025520	612826	0.0097	0.1026
chr21	48129895	447195	0.0093	0.1031
chr22	51304566	261222	0.0051	0.0735
chrMT	16571	515	0.0311	0.1735
chrX	155270560	1473611	0.0095	0.1062
chrY	59373566	98753	0.0017	0.0567

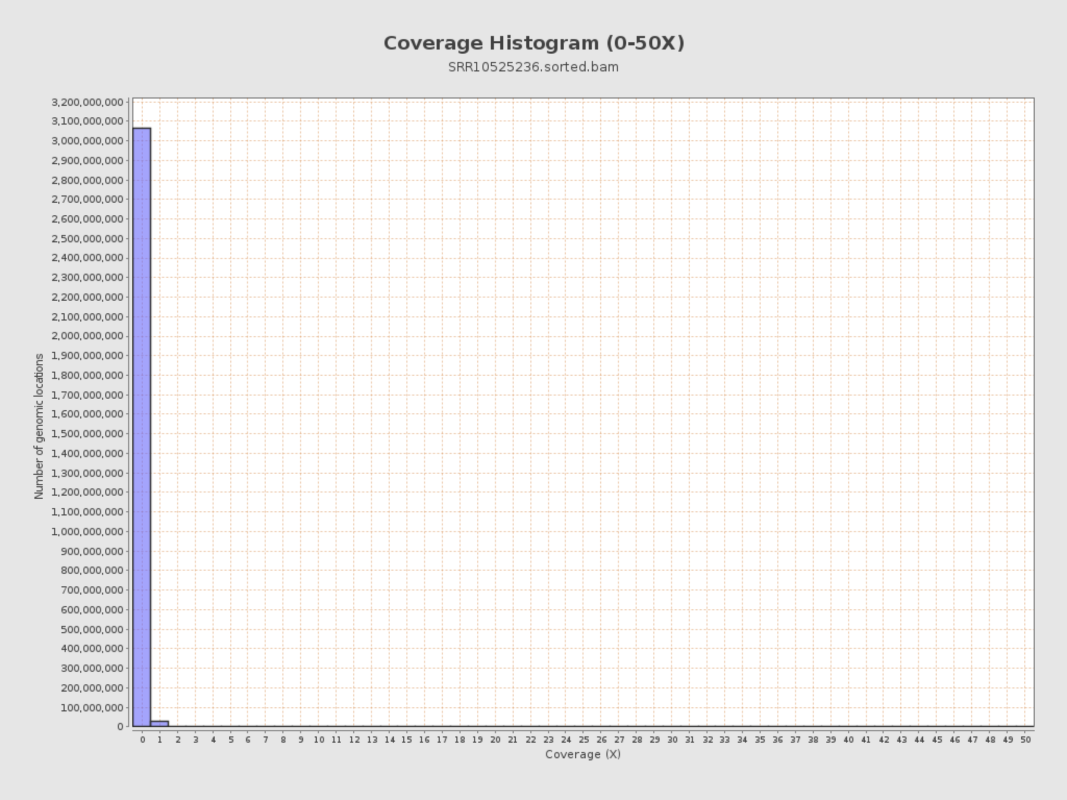
3. Results : Coverage across reference



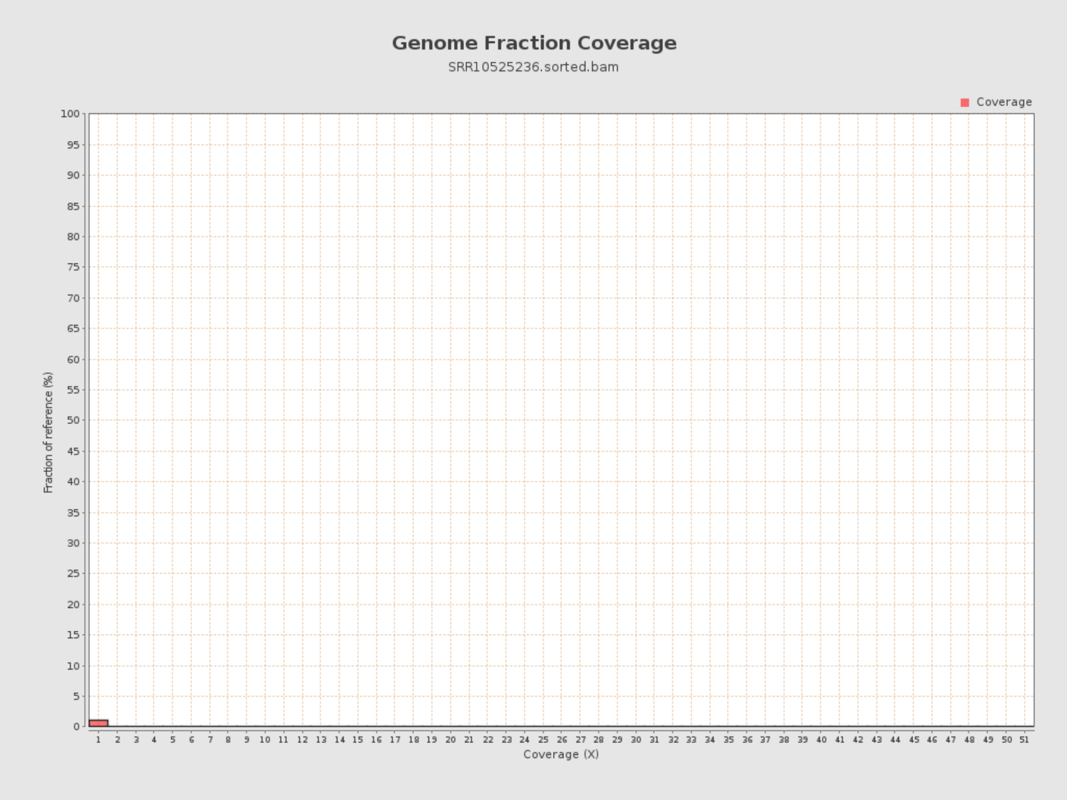
4. Results : Coverage Histogram



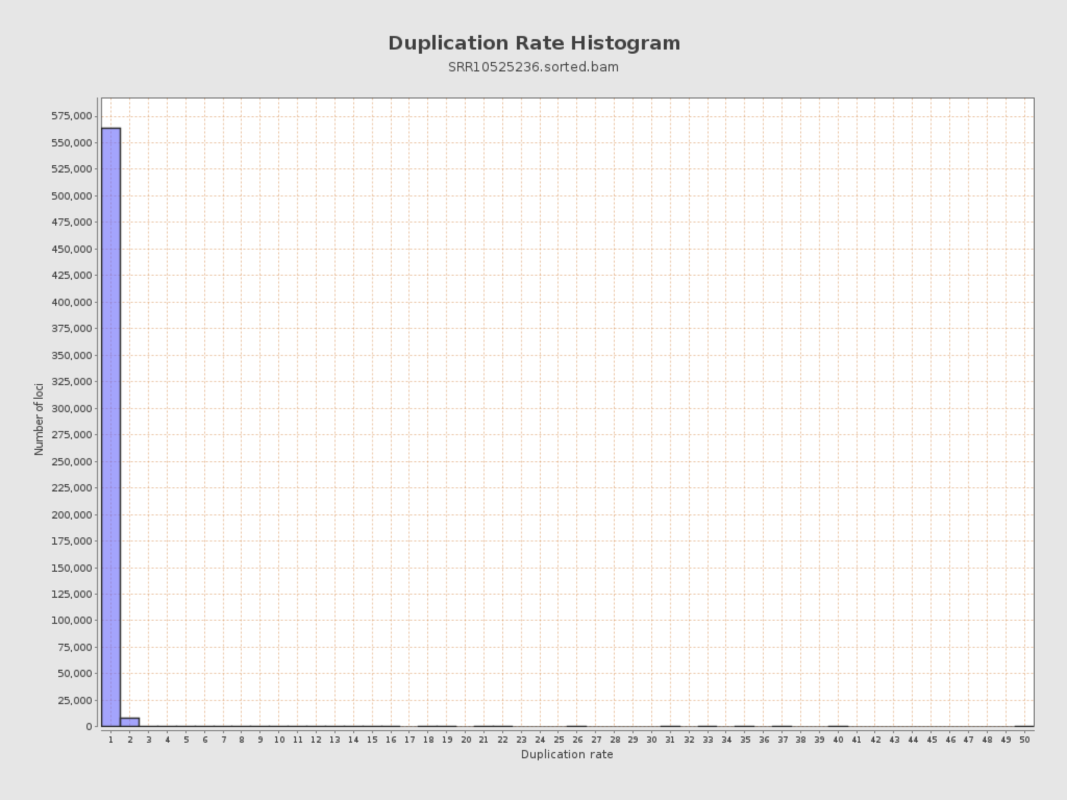
5. Results : Coverage Histogram (0-50X)



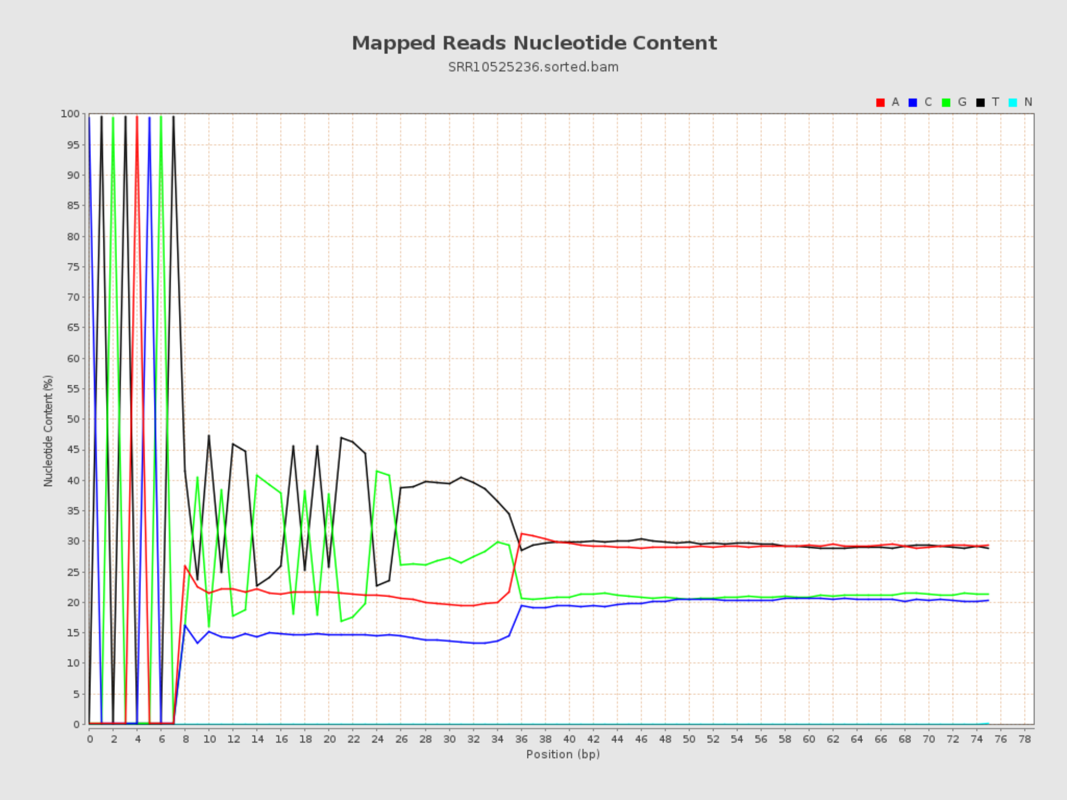
6. Results : Genome Fraction Coverage



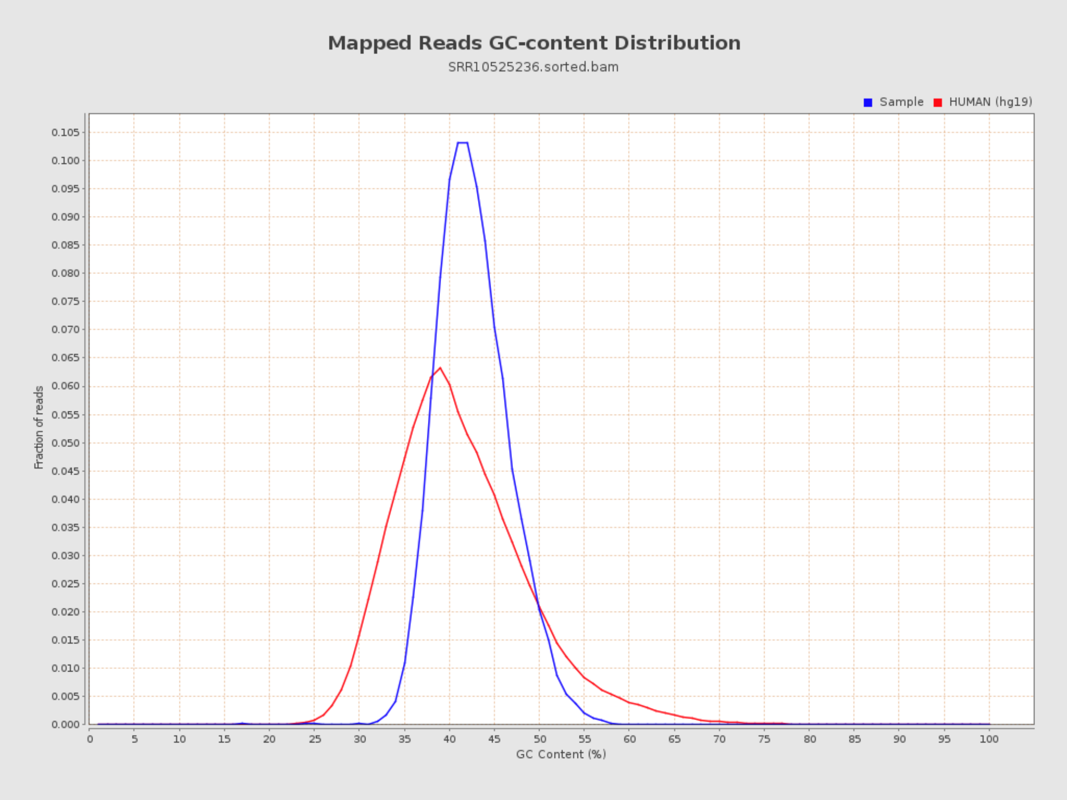
7. Results : Duplication Rate Histogram



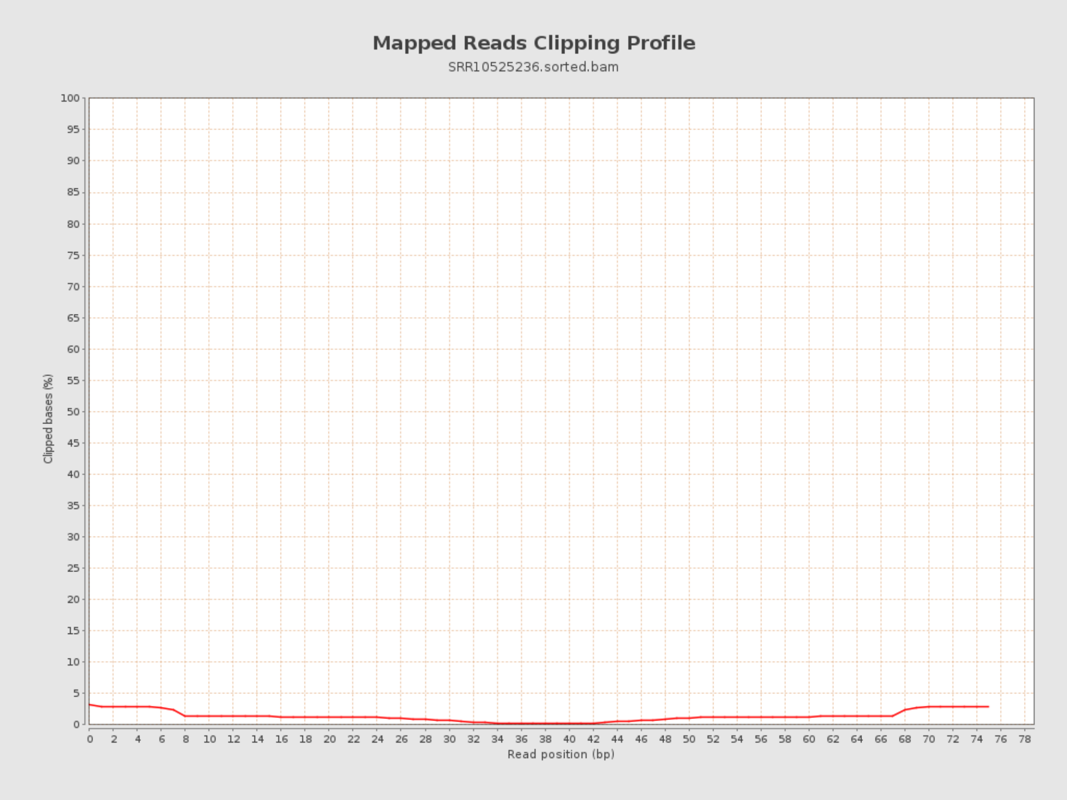
8. Results : Mapped Reads Nucleotide Content



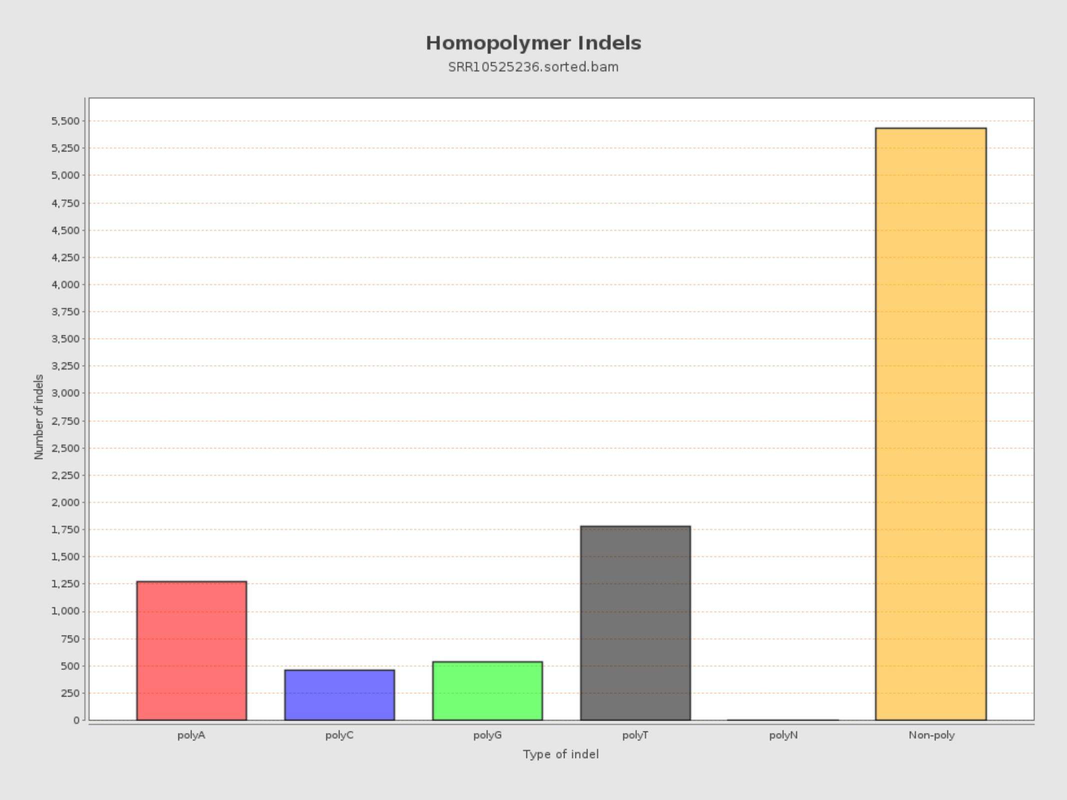
9. Results : Mapped Reads GC-content Distribution



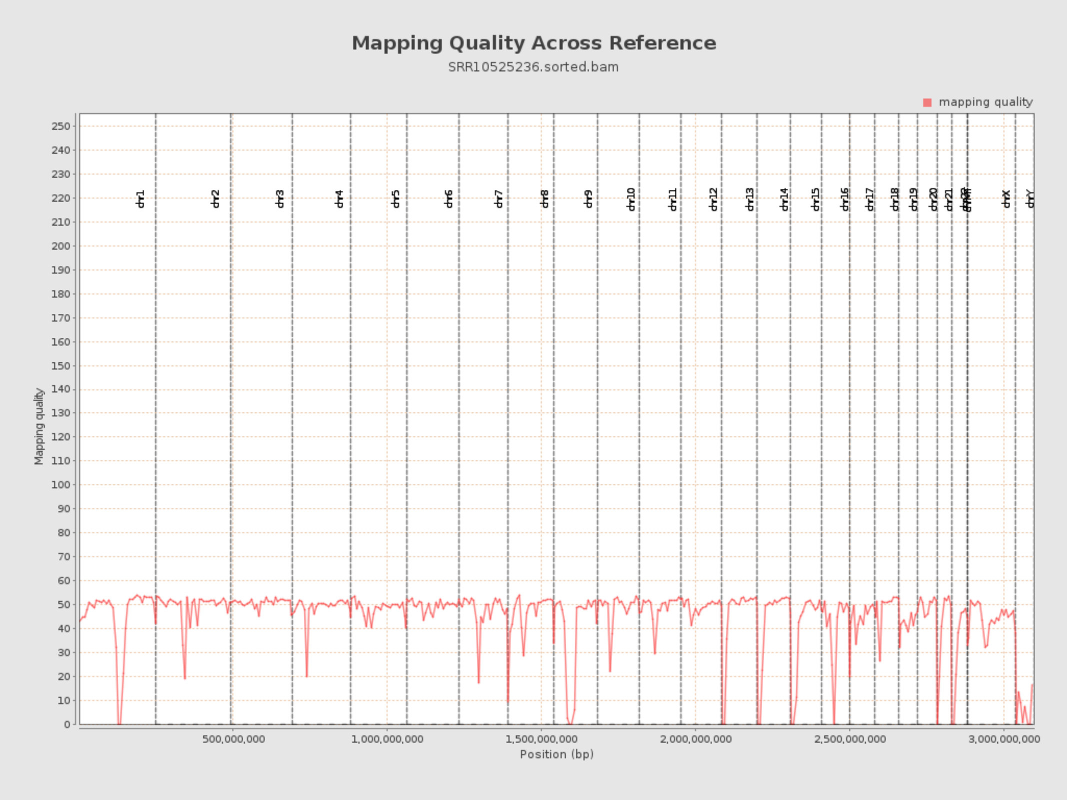
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram