Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:00:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525266.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_SRR10525266 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525266.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:00:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525266.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	636,089
Mapped reads	585,318 / 92.02%
Unmapped reads	50,771 / 7.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,508 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	12,156 / 1.91%
Duplication rate	1.53%
Clipped reads	585,971 / 92.12%

2.2. ACGT Content

Number/percentage of A's	8,901,413 / 26.39%
Number/percentage of C's	6,638,242 / 19.68%
Number/percentage of T's	10,550,036 / 31.28%
Number/percentage of G's	7,637,530 / 22.64%
Number/percentage of N's	710 / 0%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0109

Standard Deviation	0.1352

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

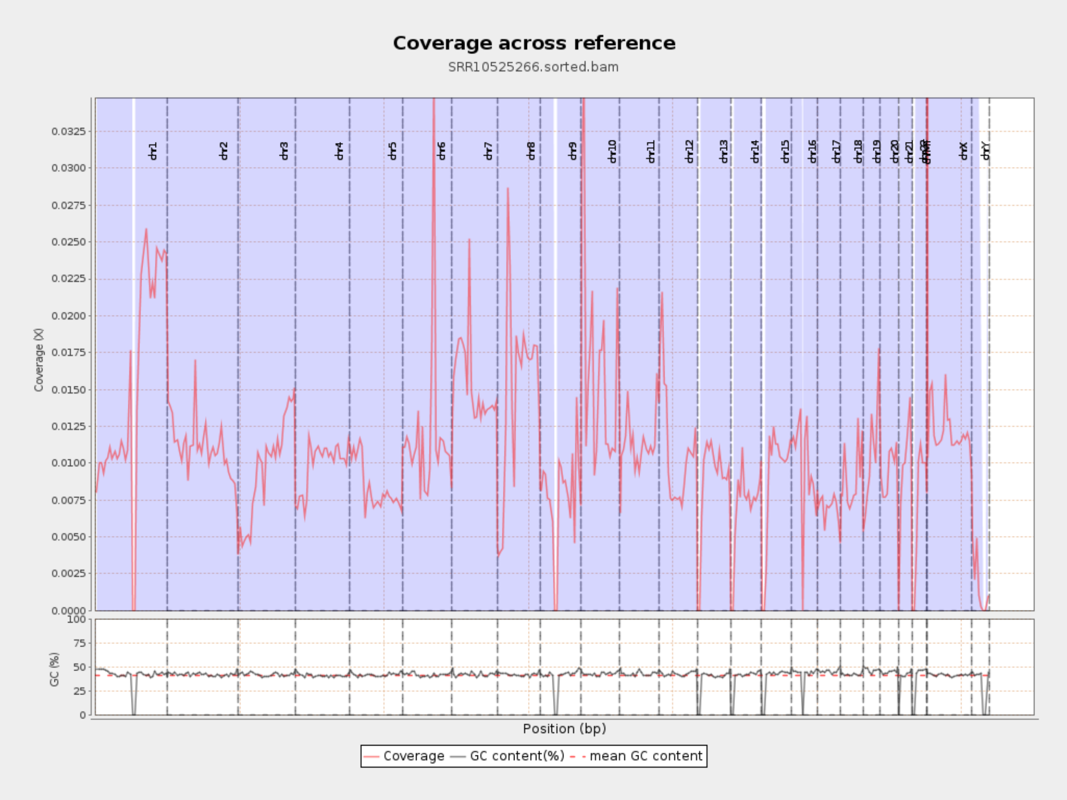
General error rate	0.52%
Mismatches	169,073
Insertions	2,638
Mapped reads with at least one insertion	0.45%
Deletions	7,059
Mapped reads with at least one deletion	1.2%
Homopolymer indels	43.39%

2.6. Chromosome stats

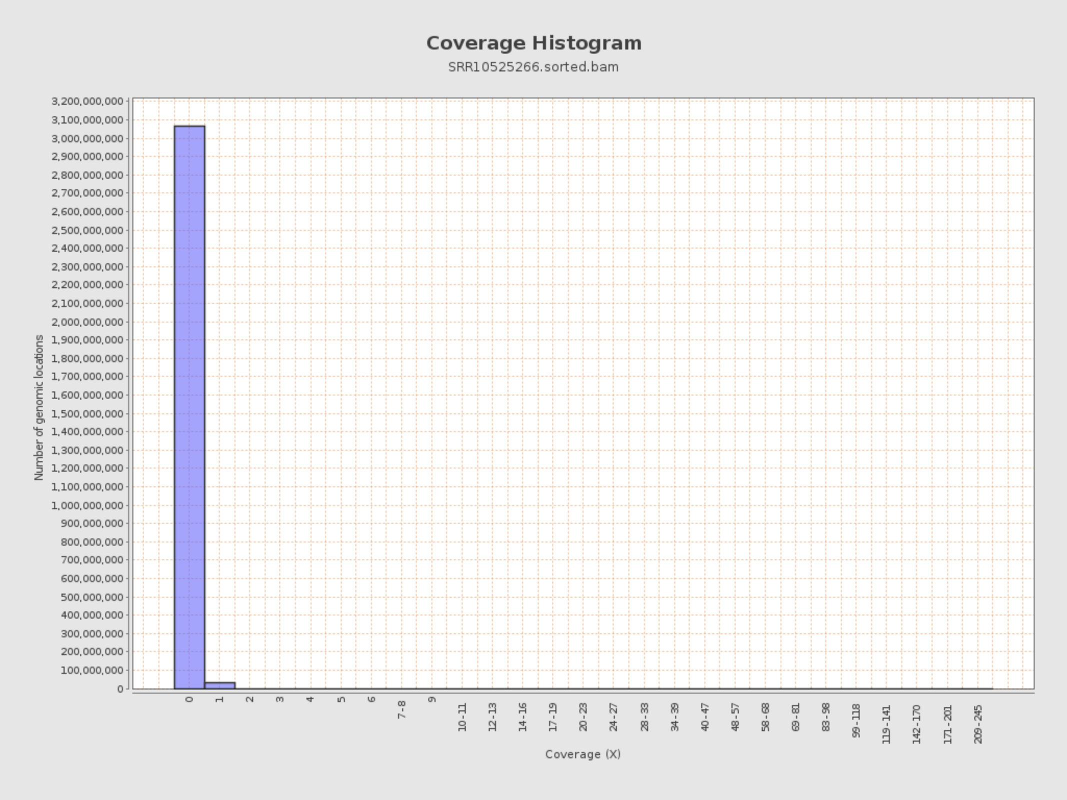
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3796573	0.0152	0.2122
chr2	243199373	2694399	0.0111	0.1503
chr3	198022430	1899902	0.0096	0.103
chr4	191154276	1898488	0.0099	0.1051
chr5	180915260	1516658	0.0084	0.095
chr6	171115067	2068308	0.0121	0.1198
chr7	159138663	2461416	0.0155	0.2215

chr8	146364022	2222356	0.0152	0.1454
chr9	141213431	1089011	0.0077	0.1039
chr10	135534747	2244108	0.0166	0.1577
chr11	135006516	1524050	0.0113	0.1221
chr12	133851895	1469080	0.011	0.1091
chr13	115169878	1003248	0.0087	0.0966
chr14	107349540	748666	0.007	0.0878
chr15	102531392	903323	0.0088	0.0988
chr16	90354753	875921	0.0097	0.107
chr17	81195210	563167	0.0069	0.0877
chr18	78077248	695910	0.0089	0.1718
chr19	59128983	630991	0.0107	0.1523
chr20	63025520	590414	0.0094	0.1009
chr21	48129895	463458	0.0096	0.1029
chr22	51304566	367338	0.0072	0.0872
chrMT	16571	18552	1.1195	1.2436
chrX	155270560	1896208	0.0122	0.1188
chrY	59373566	97410	0.0016	0.0499

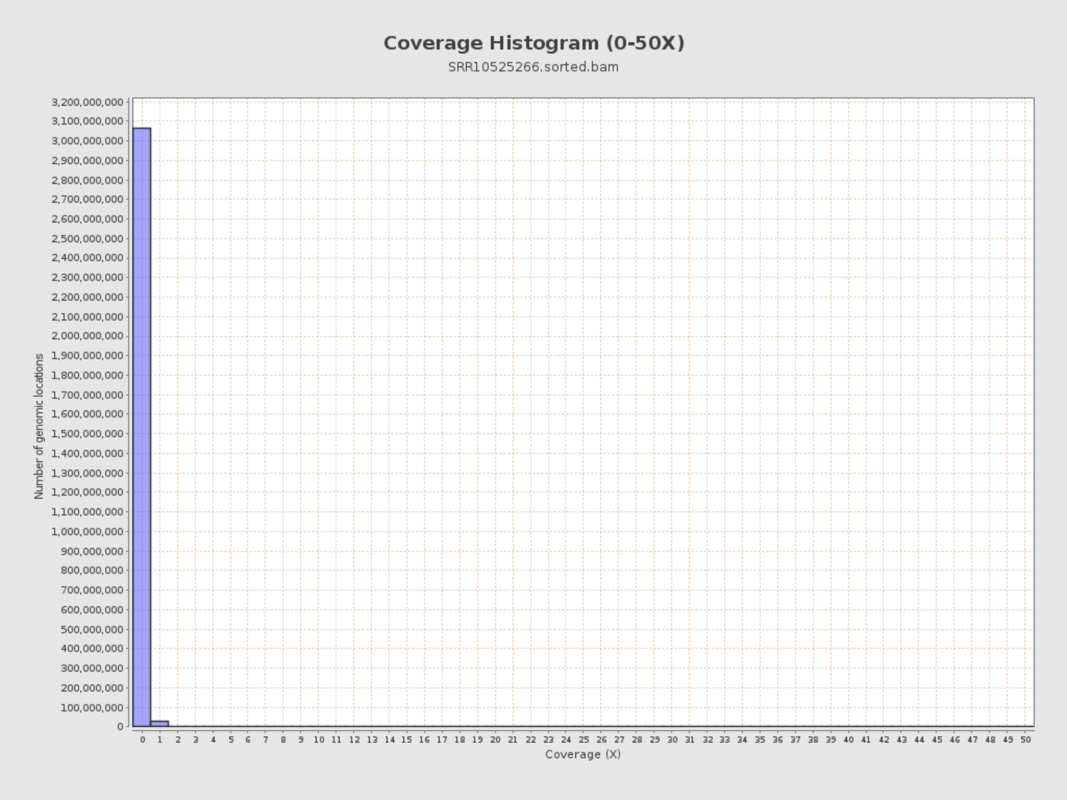
3. Results : Coverage across reference



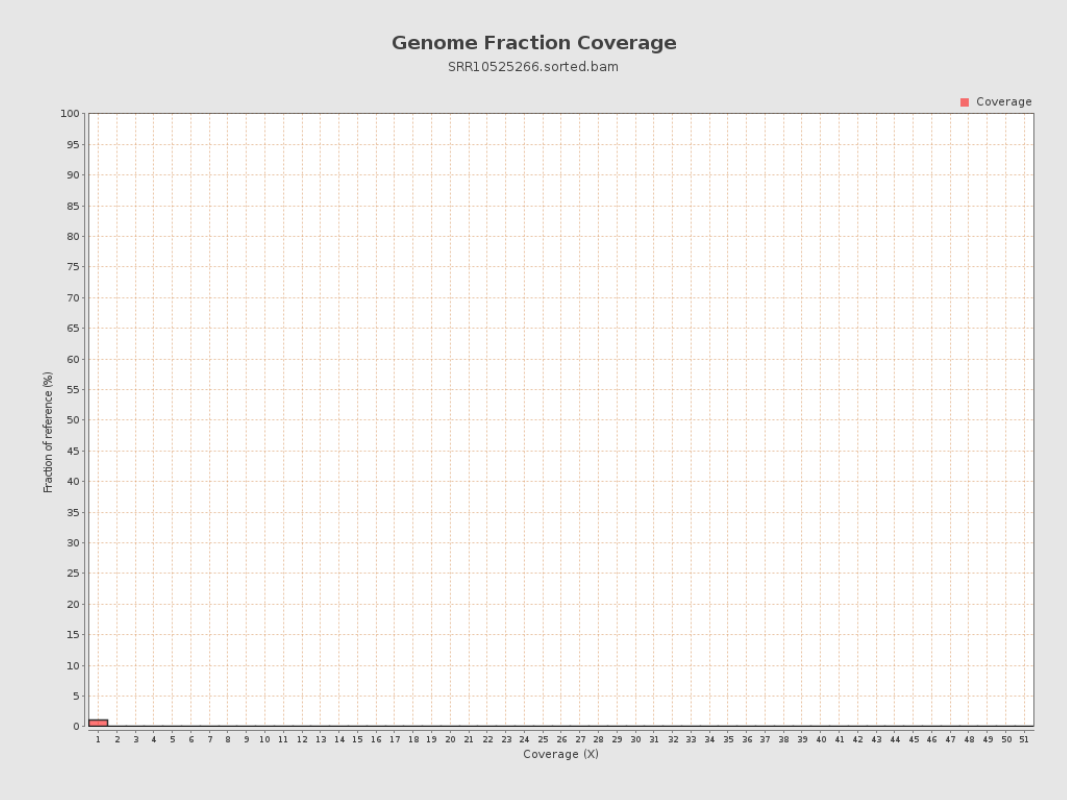
4. Results : Coverage Histogram



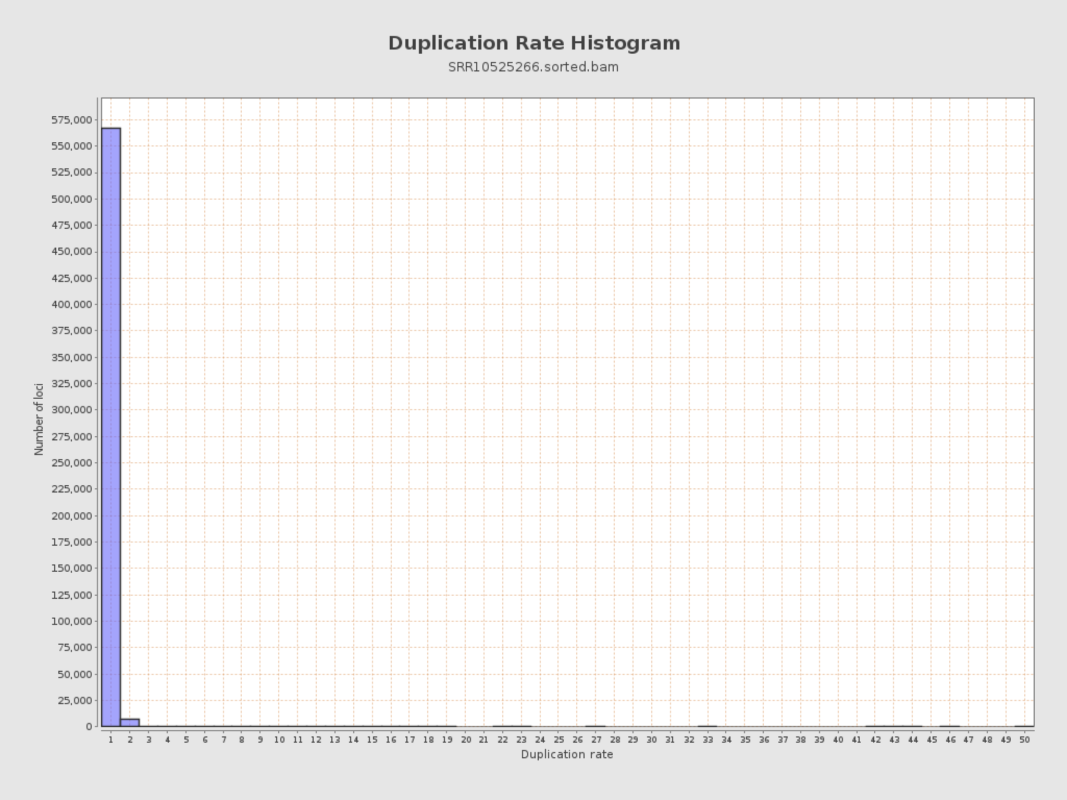
5. Results : Coverage Histogram (0-50X)



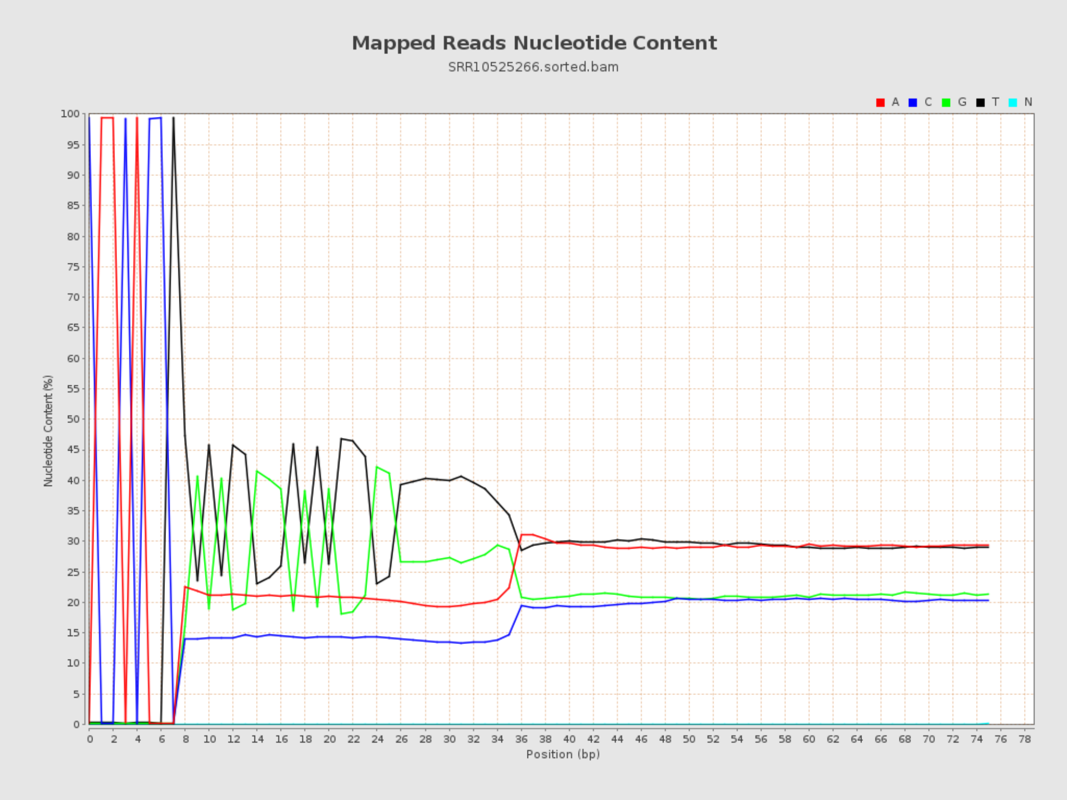
6. Results : Genome Fraction Coverage



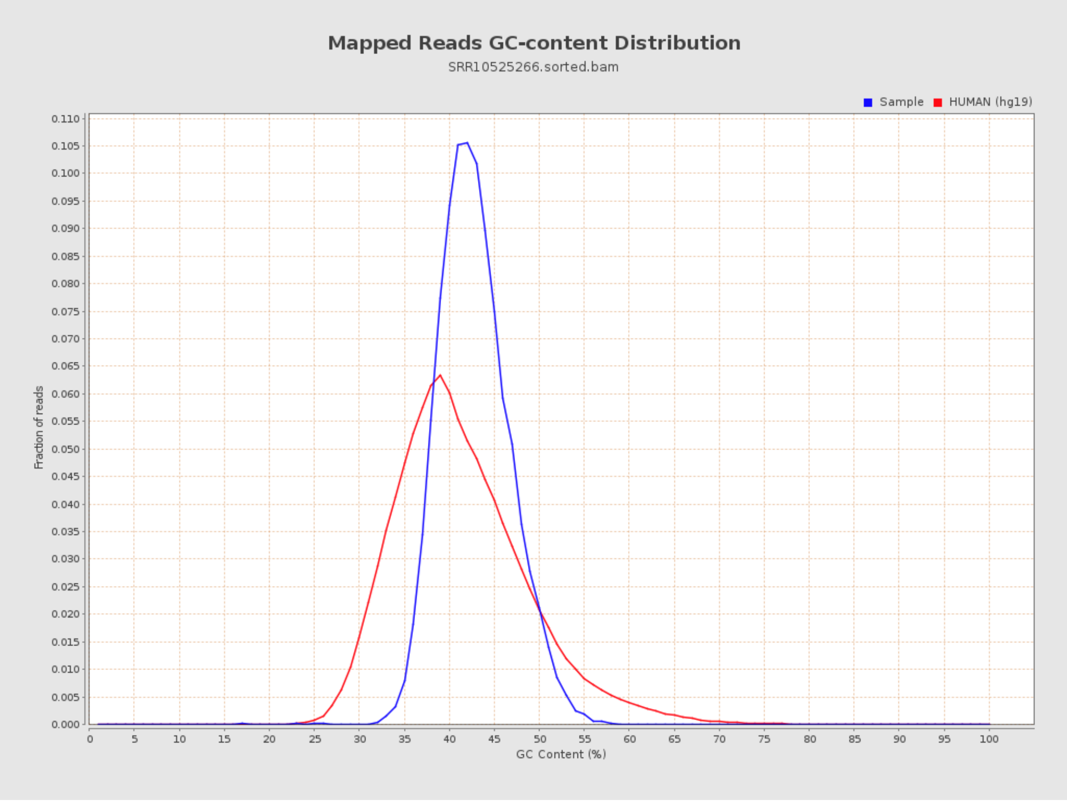
7. Results : Duplication Rate Histogram



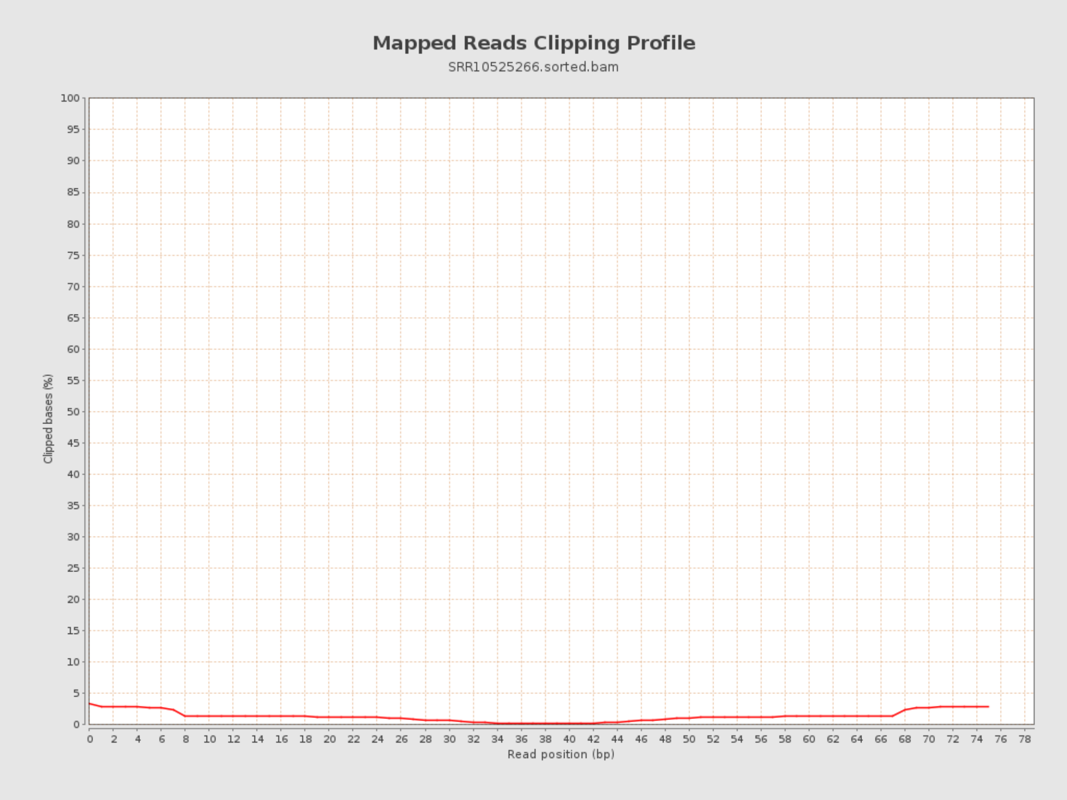
8. Results : Mapped Reads Nucleotide Content



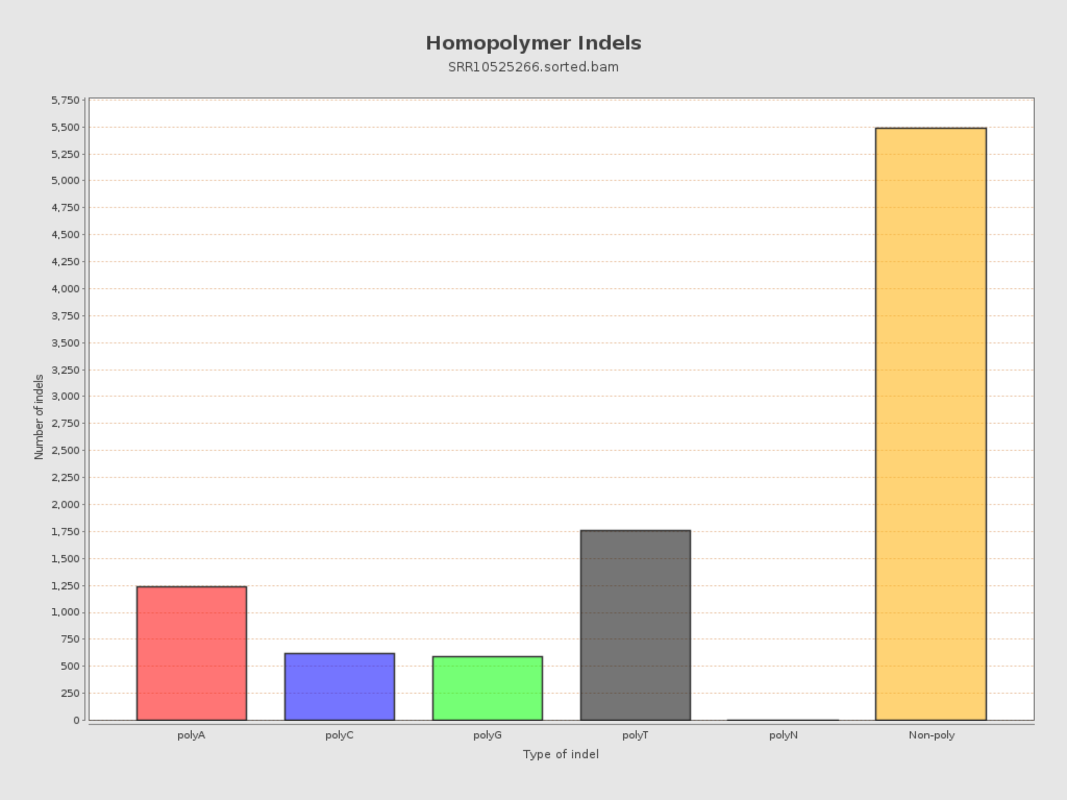
9. Results : Mapped Reads GC-content Distribution



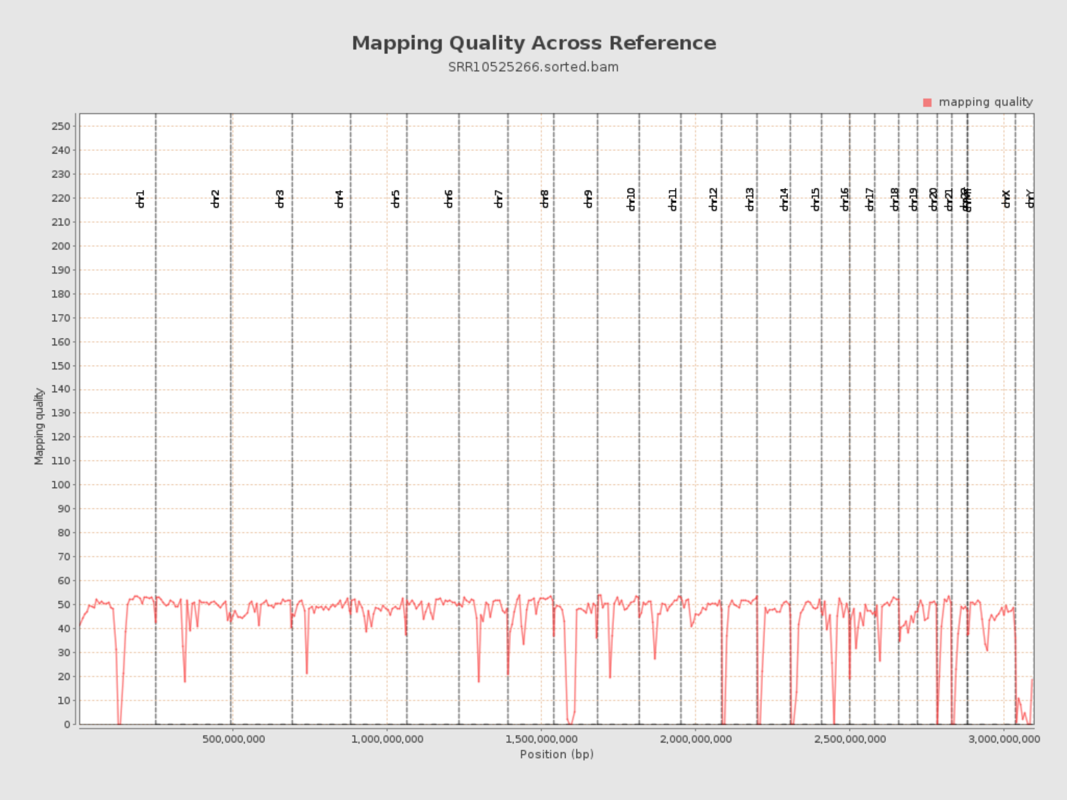
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram