Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:09:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716625.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_SRR9716625 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716625.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:09:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716625.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	876,056
Mapped reads	653,625 / 74.61%
Unmapped reads	222,431 / 25.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,939 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	15,664 / 1.79%
Duplication rate	1.85%
Clipped reads	654,865 / 74.75%

2.2. ACGT Content

Number/percentage of A's	9,984,888 / 26.52%
Number/percentage of C's	6,756,768 / 17.94%
Number/percentage of T's	11,707,325 / 31.09%
Number/percentage of G's	9,203,299 / 24.44%
Number/percentage of N's	1,109 / 0%
GC Percentage	42.39%

2.3. Coverage

Mean	0.0122

Standard Deviation	0.1424

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

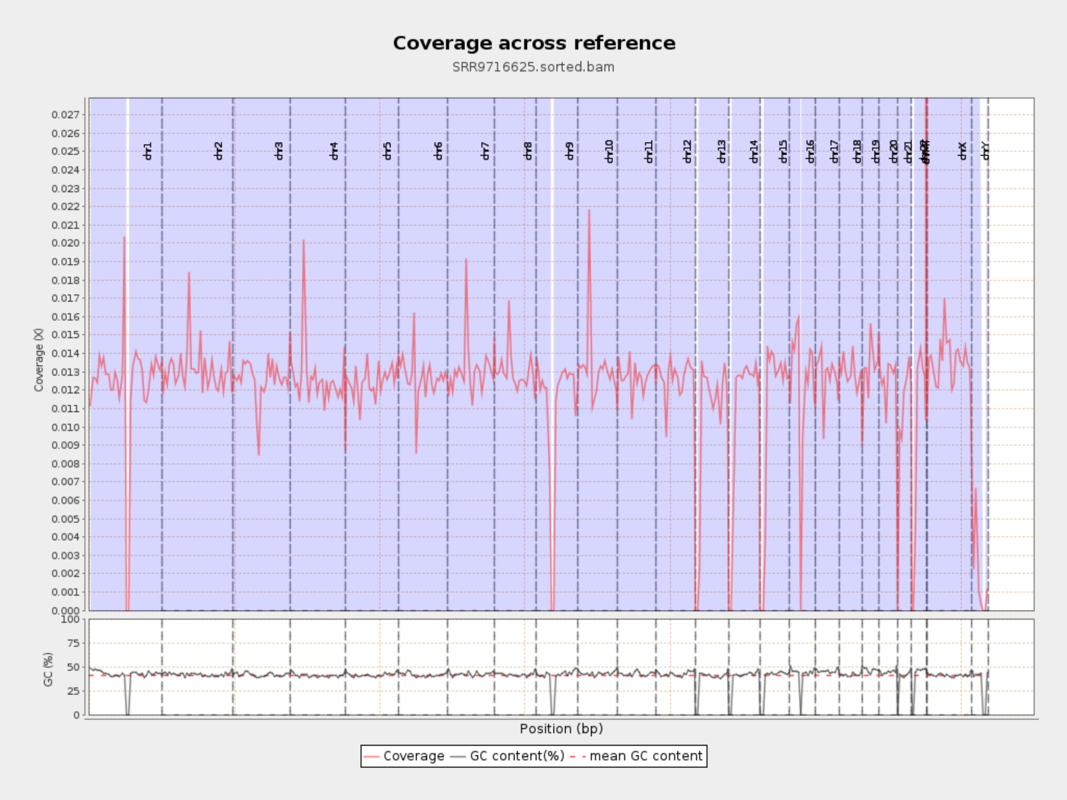
General error rate	0.53%
Mismatches	193,762
Insertions	2,601
Mapped reads with at least one insertion	0.4%
Deletions	7,040
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.25%

2.6. Chromosome stats

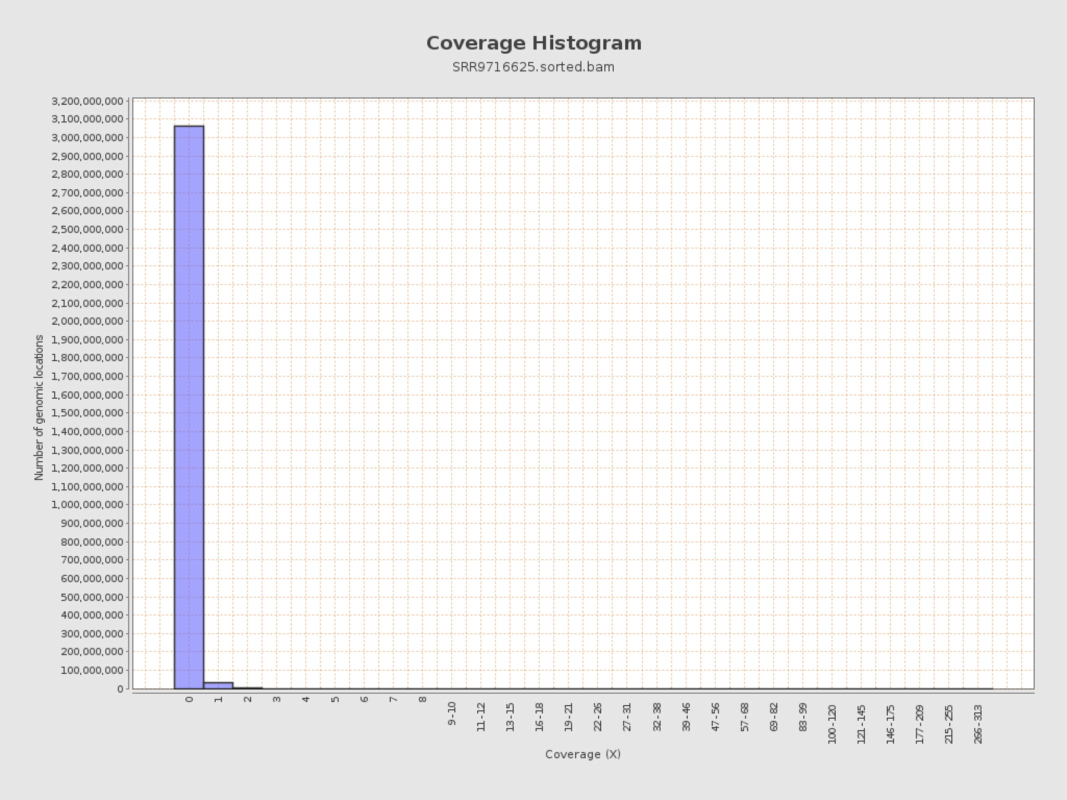
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3045291	0.0122	0.2254
chr2	243199373	3198347	0.0132	0.1771
chr3	198022430	2487794	0.0126	0.1181
chr4	191154276	2421060	0.0127	0.1224
chr5	180915260	2251730	0.0124	0.1167
chr6	171115067	2177225	0.0127	0.1276
chr7	159138663	2088469	0.0131	0.1636

chr8	146364022	1905760	0.013	0.1381
chr9	141213431	1527421	0.0108	0.1271
chr10	135534747	1801167	0.0133	0.1405
chr11	135006516	1719879	0.0127	0.1296
chr12	133851895	1696949	0.0127	0.119
chr13	115169878	1165721	0.0101	0.105
chr14	107349540	1145700	0.0107	0.1112
chr15	102531392	1104053	0.0108	0.1094
chr16	90354753	1104469	0.0122	0.1202
chr17	81195210	1035527	0.0128	0.1202
chr18	78077248	1015334	0.013	0.1868
chr19	59128983	789718	0.0134	0.1677
chr20	63025520	787076	0.0125	0.1176
chr21	48129895	506948	0.0105	0.1114
chr22	51304566	465660	0.0091	0.1002
chrMT	16571	2747	0.1658	0.4408
chrX	155270560	2106956	0.0136	0.1267
chrY	59373566	113731	0.0019	0.0626

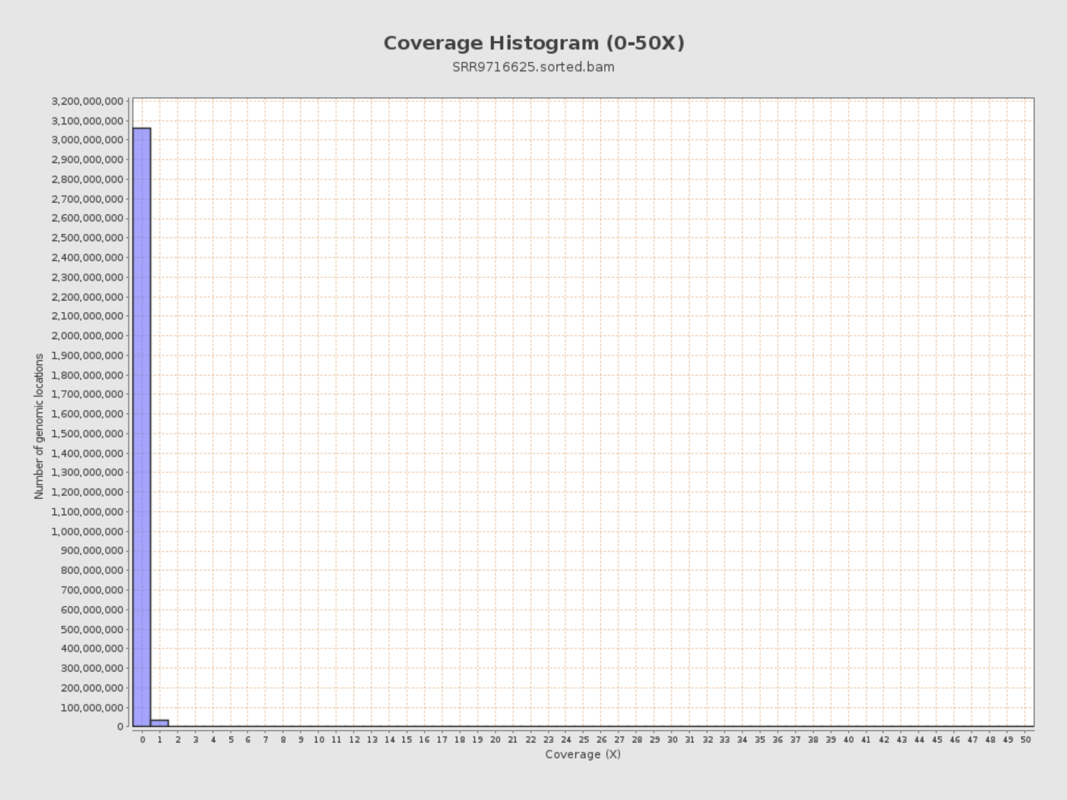
3. Results : Coverage across reference



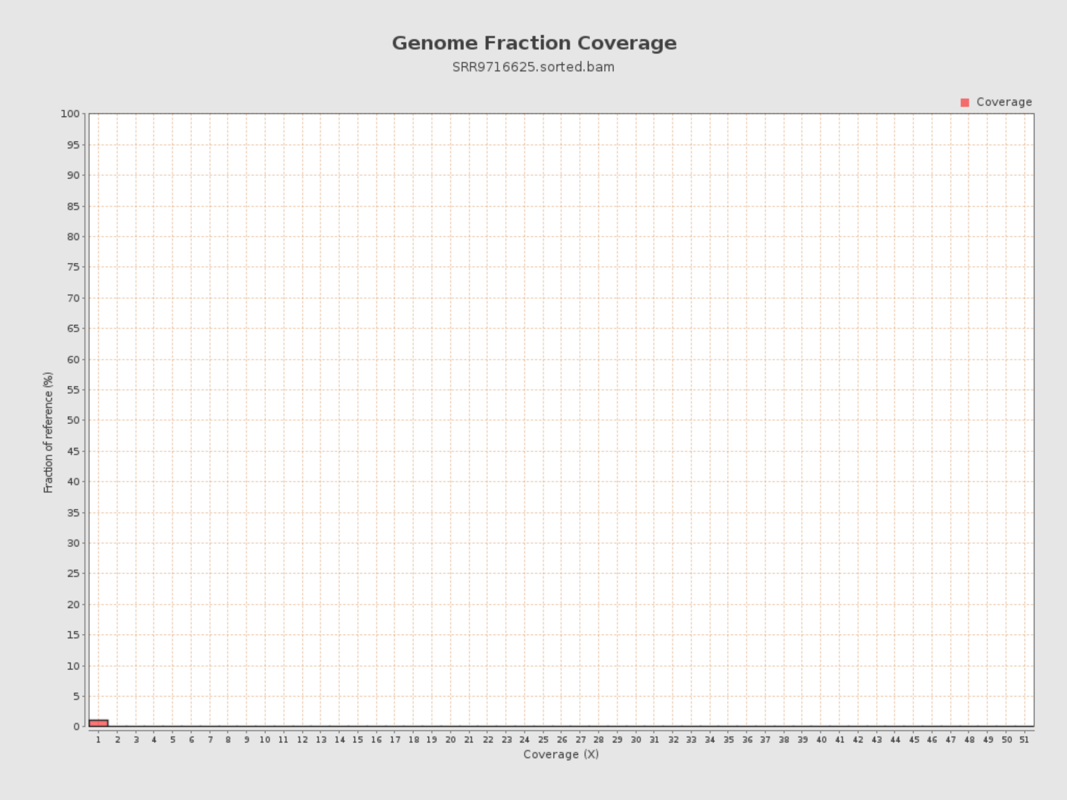
4. Results : Coverage Histogram



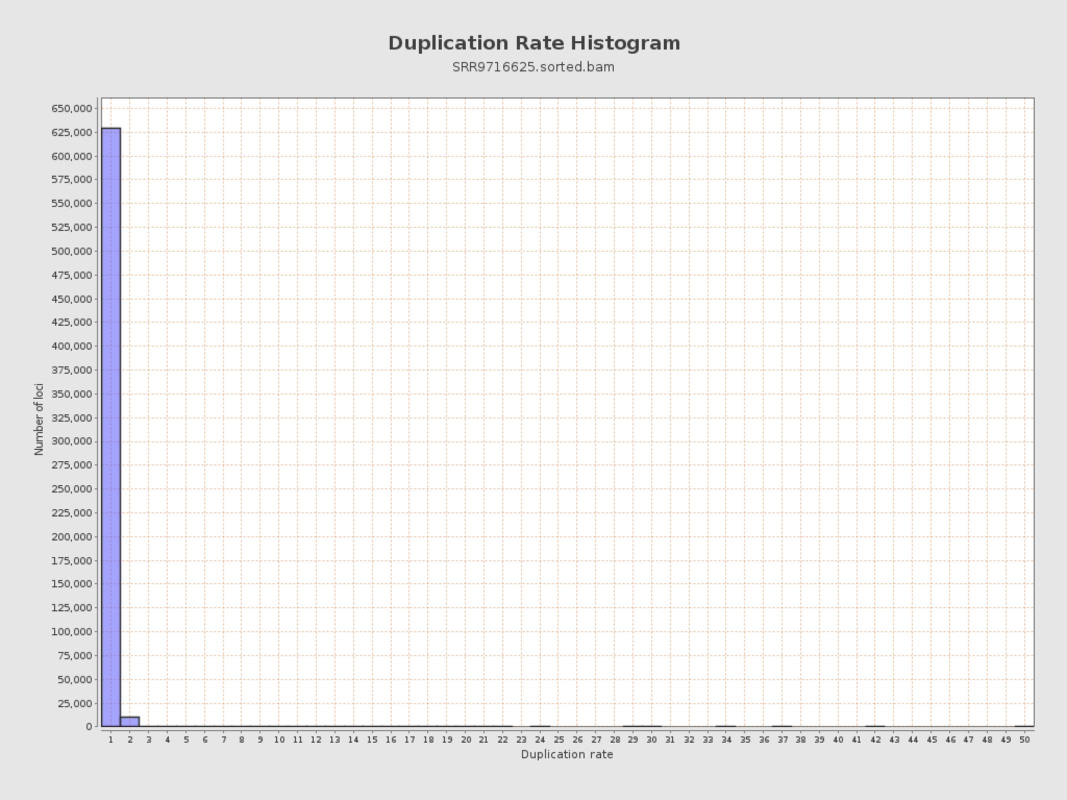
5. Results : Coverage Histogram (0-50X)



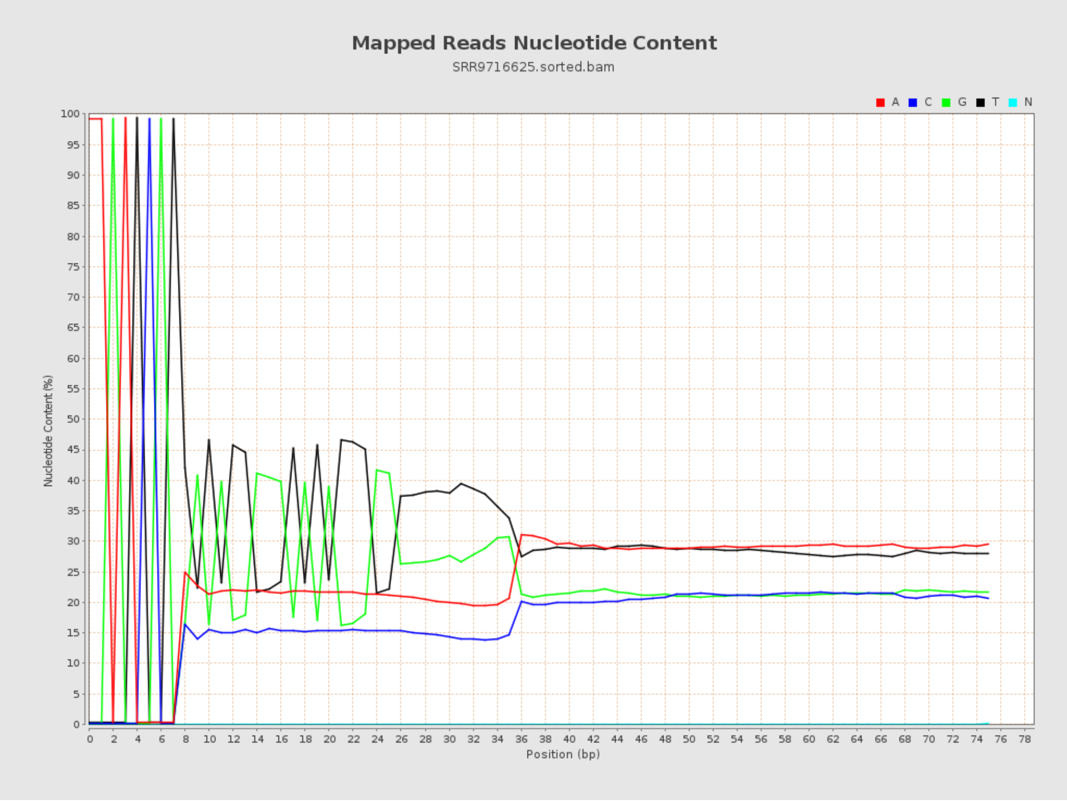
6. Results : Genome Fraction Coverage



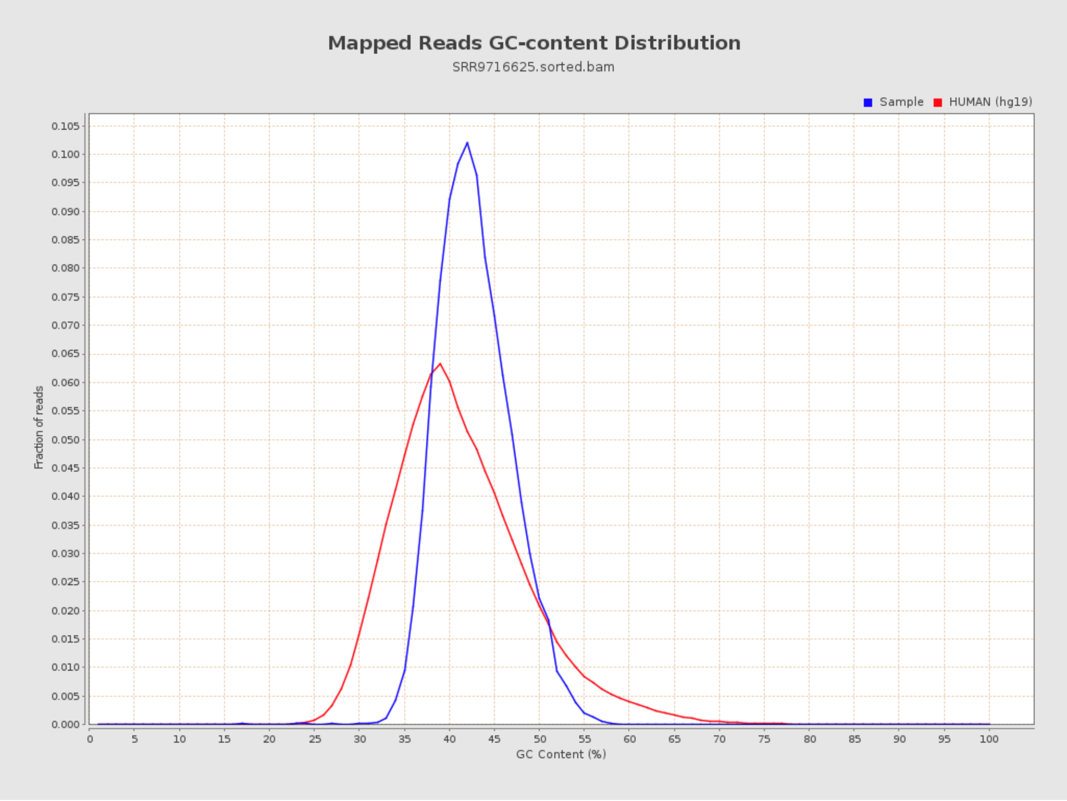
7. Results : Duplication Rate Histogram



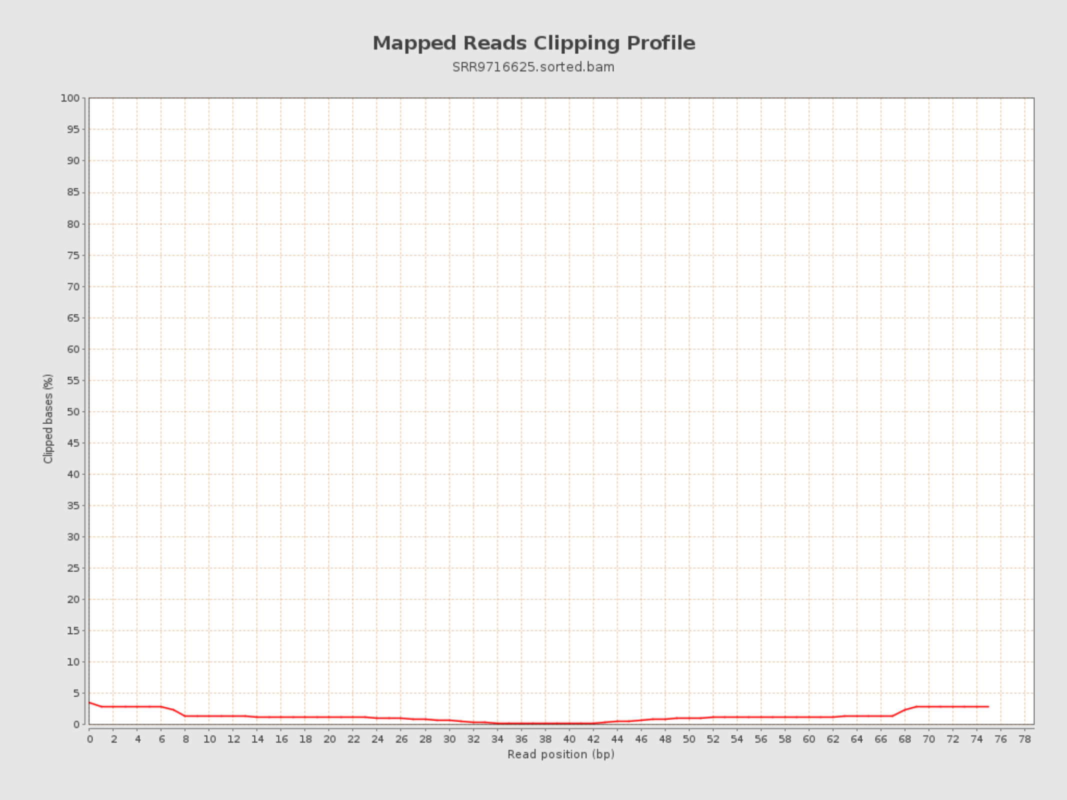
8. Results : Mapped Reads Nucleotide Content



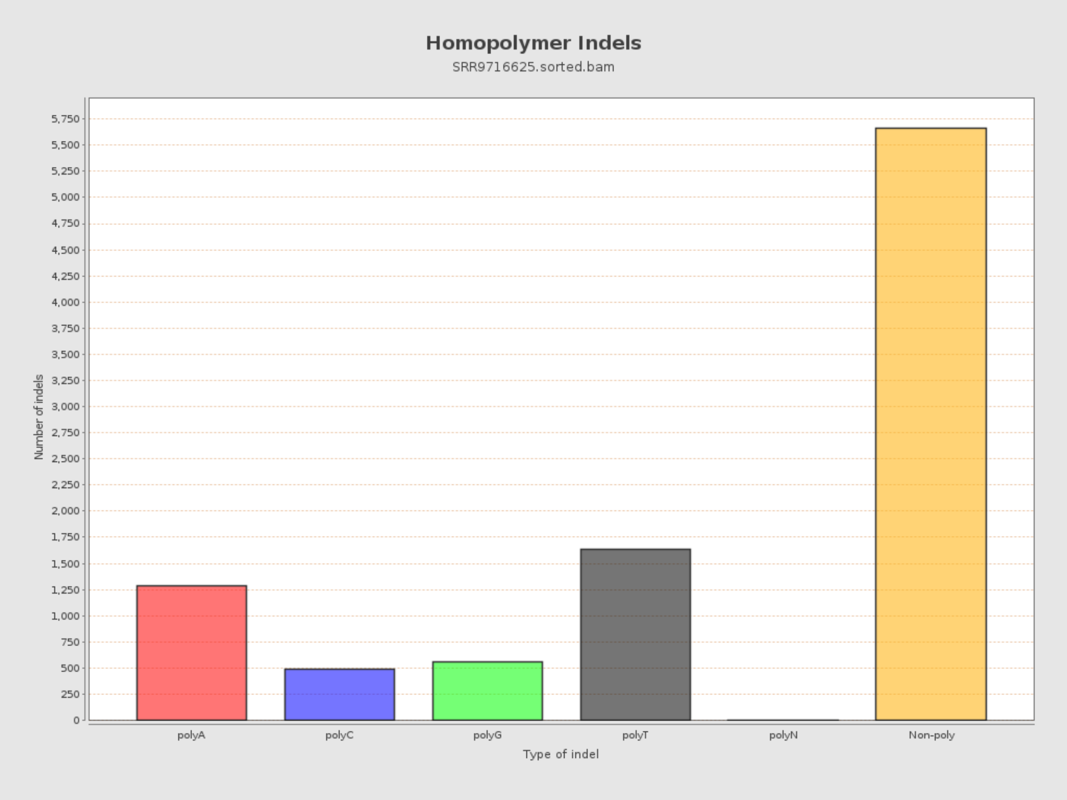
9. Results : Mapped Reads GC-content Distribution



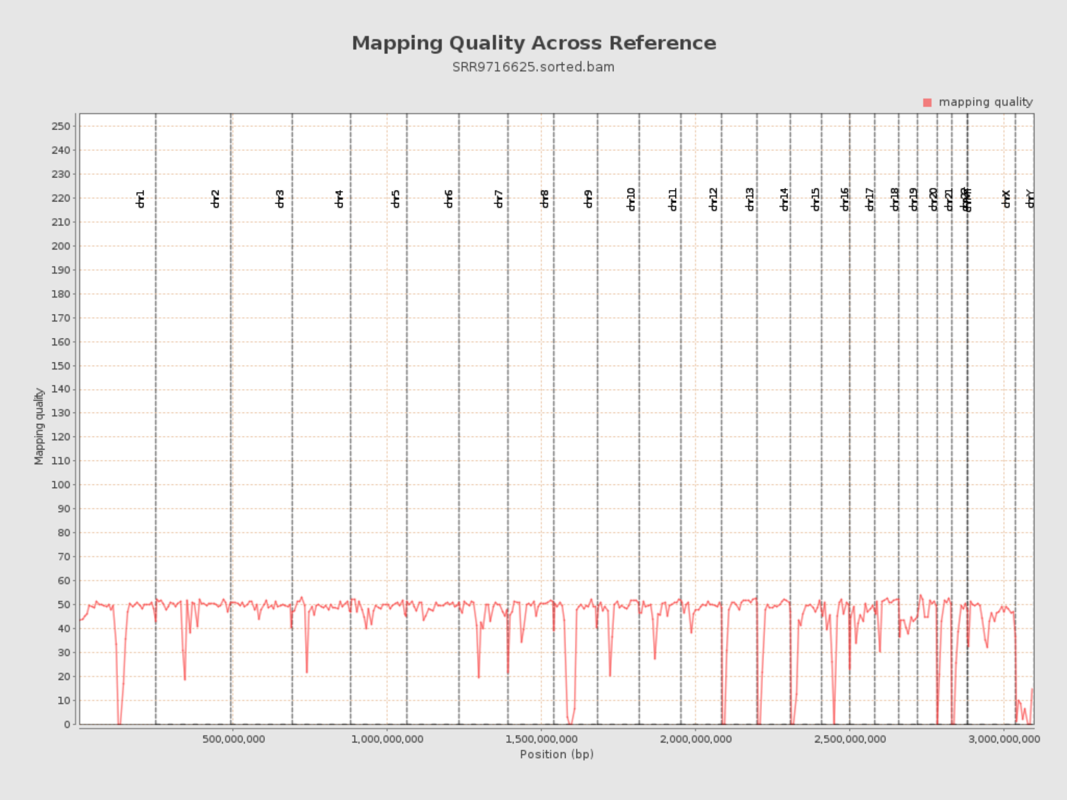
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram