Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:25:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716692.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_SRR9716692 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716692.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:25:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716692.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	682,617
Mapped reads	618,314 / 90.58%
Unmapped reads	64,303 / 9.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,202 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	16,045 / 2.35%
Duplication rate	1.88%
Clipped reads	618,867 / 90.66%

2.2. ACGT Content

Number/percentage of A's	8,951,365 / 25.26%
Number/percentage of C's	6,485,544 / 18.3%
Number/percentage of T's	11,613,400 / 32.77%
Number/percentage of G's	8,383,334 / 23.66%
Number/percentage of N's	663 / 0%
GC Percentage	41.96%

2.3. Coverage

Mean	0.0115

Standard Deviation	0.1402

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Mismatches and indels

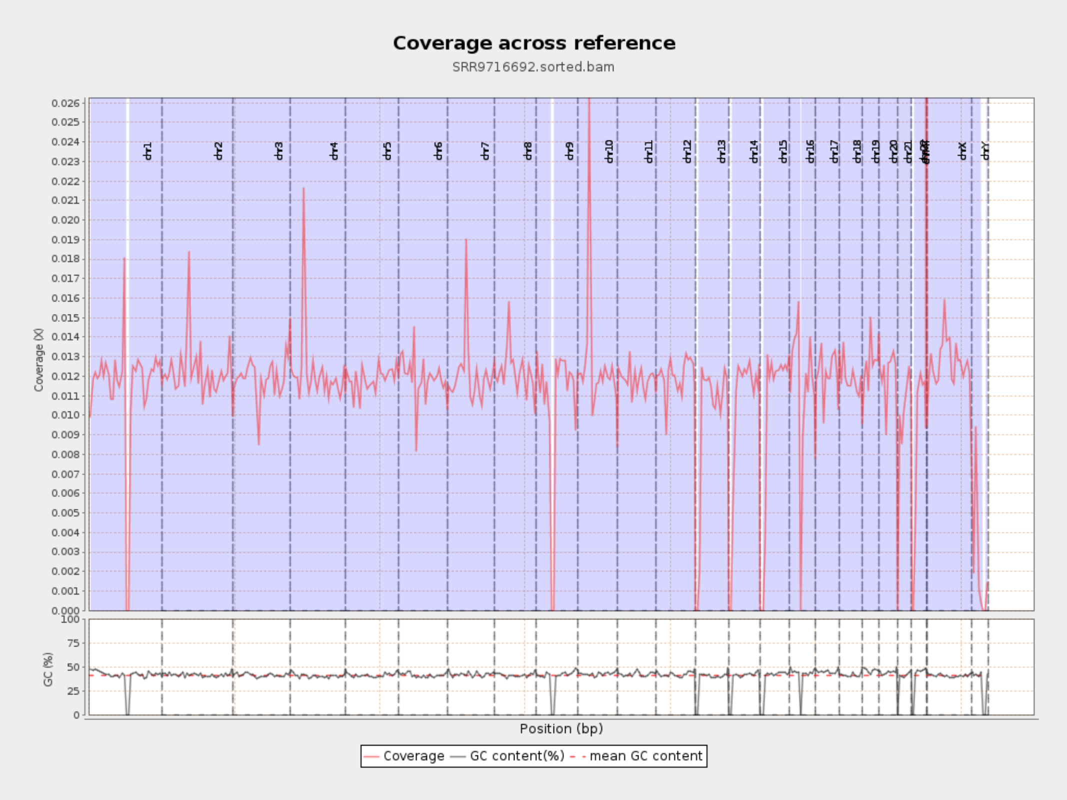
General error rate	0.54%
Mismatches	185,213
Insertions	2,576
Mapped reads with at least one insertion	0.41%
Deletions	7,127
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41%

2.6. Chromosome stats

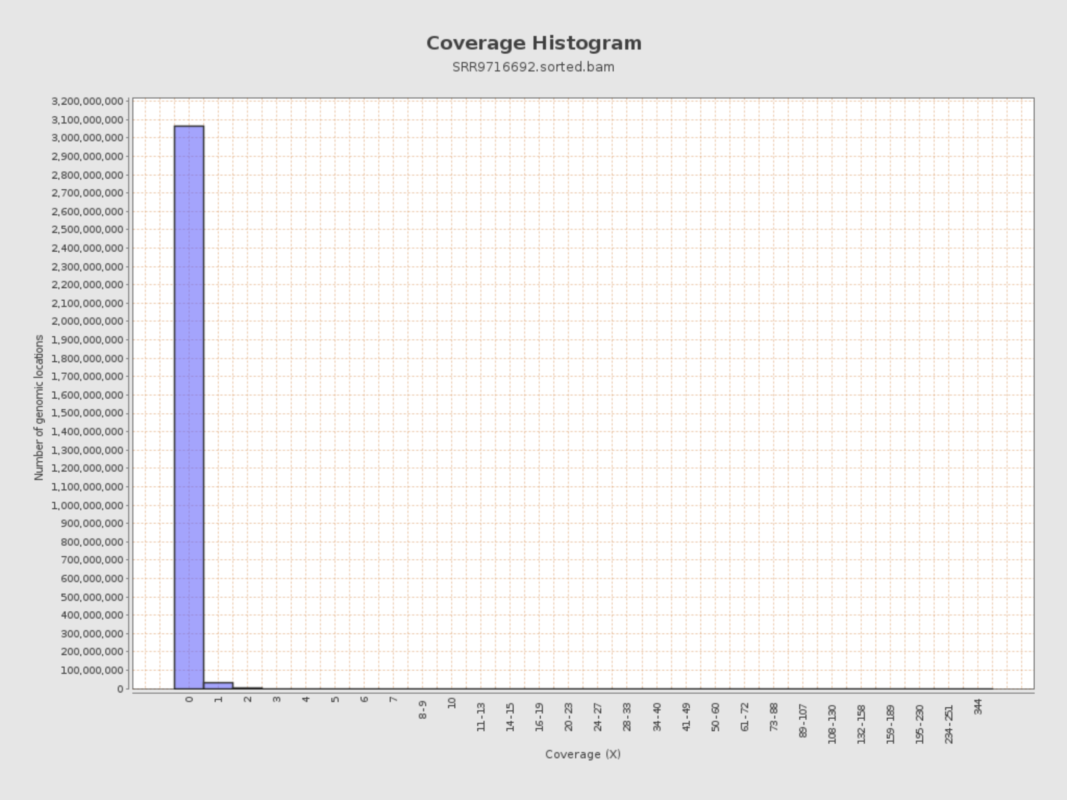
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2839318	0.0114	0.1992
chr2	243199373	3001663	0.0123	0.1888
chr3	198022430	2348584	0.0119	0.115
chr4	191154276	2324462	0.0122	0.1255
chr5	180915260	2141414	0.0118	0.1132
chr6	171115067	2041380	0.0119	0.1236
chr7	159138663	1922302	0.0121	0.157

chr8	146364022	1790338	0.0122	0.1601
chr9	141213431	1478042	0.0105	0.1211
chr10	135534747	1721113	0.0127	0.1573
chr11	135006516	1589639	0.0118	0.1279
chr12	133851895	1609687	0.012	0.1155
chr13	115169878	1099751	0.0095	0.103
chr14	107349540	1073717	0.01	0.1048
chr15	102531392	1027523	0.01	0.1052
chr16	90354753	1036067	0.0115	0.1156
chr17	81195210	979973	0.0121	0.1186
chr18	78077248	930931	0.0119	0.1728
chr19	59128983	747071	0.0126	0.1609
chr20	63025520	756129	0.012	0.1157
chr21	48129895	463935	0.0096	0.1143
chr22	51304566	413585	0.0081	0.0938
chrMT	16571	6989	0.4218	0.7314
chrX	155270560	1964526	0.0127	0.1218
chrY	59373566	137648	0.0023	0.104

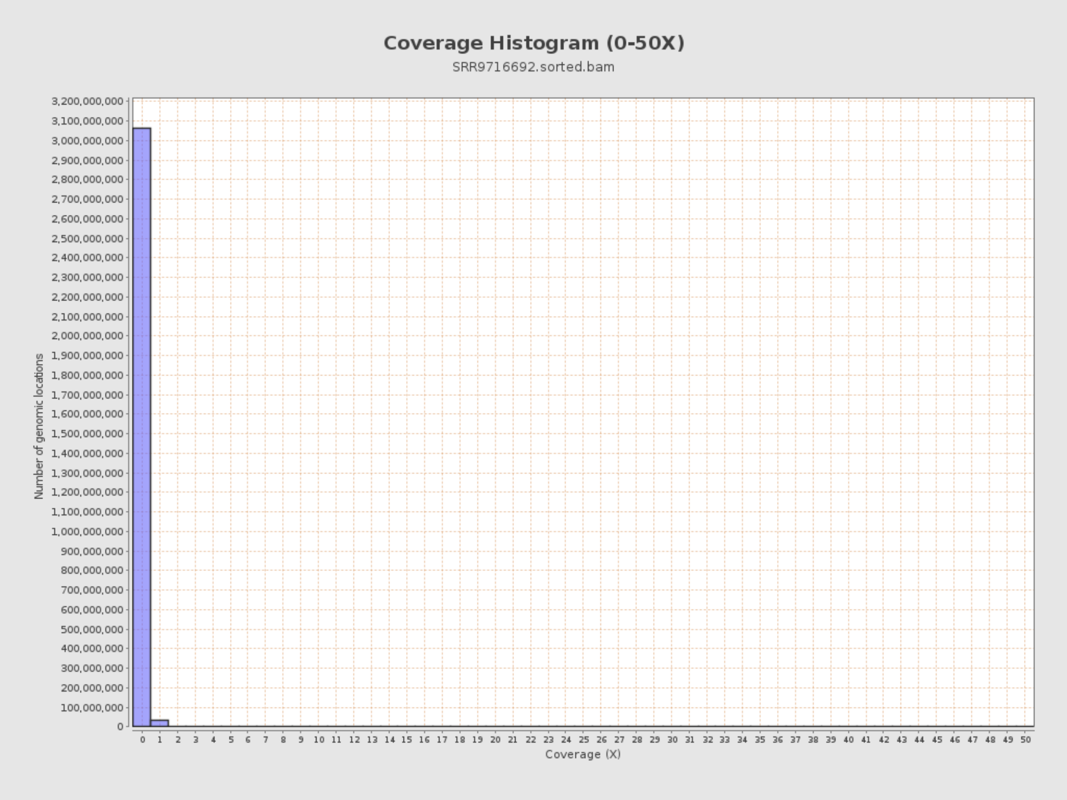
3. Results : Coverage across reference



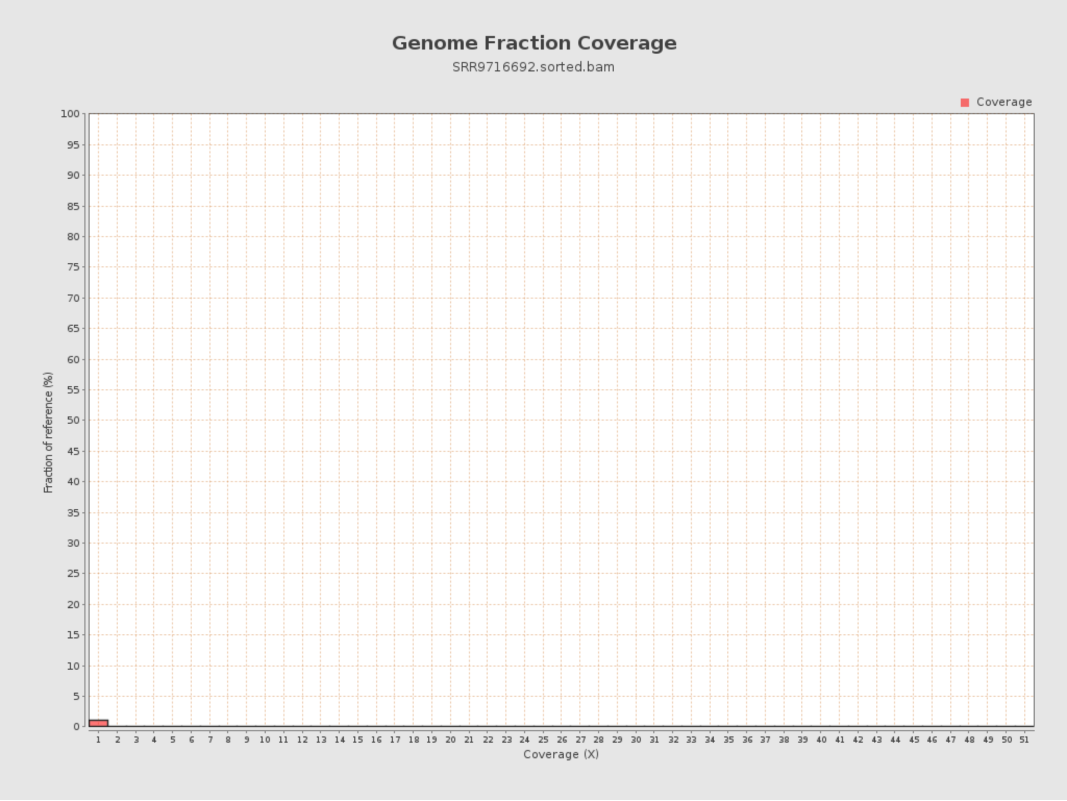
4. Results : Coverage Histogram



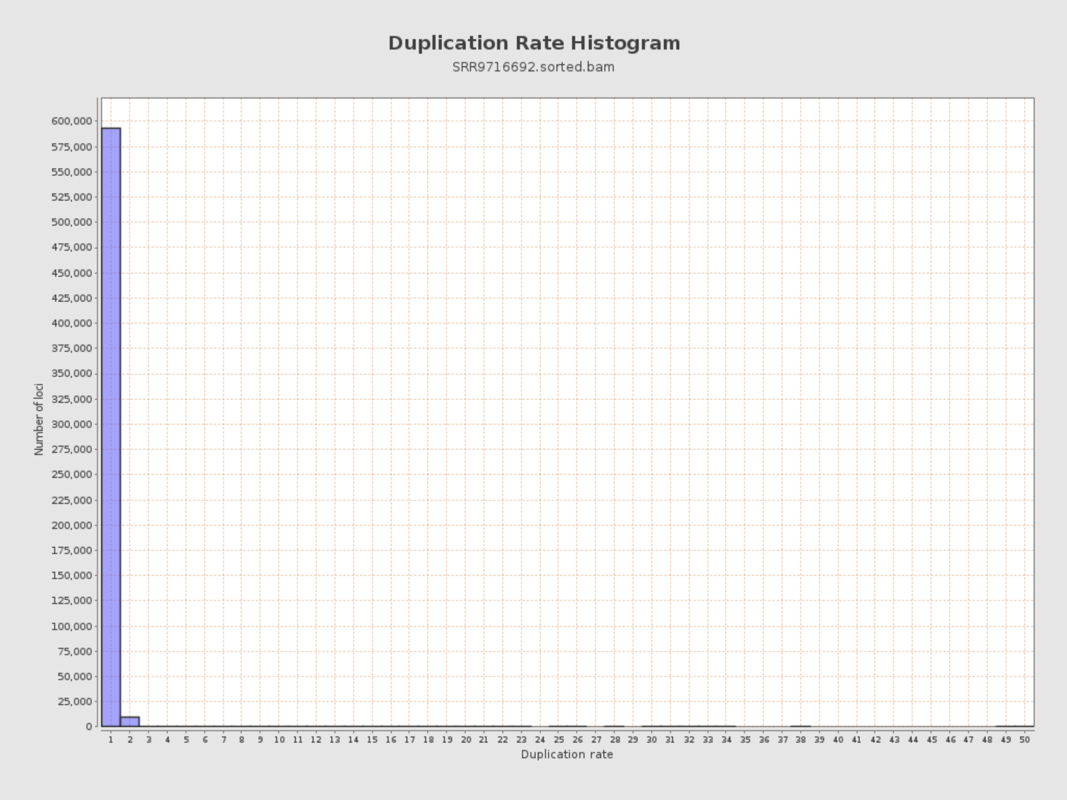
5. Results : Coverage Histogram (0-50X)



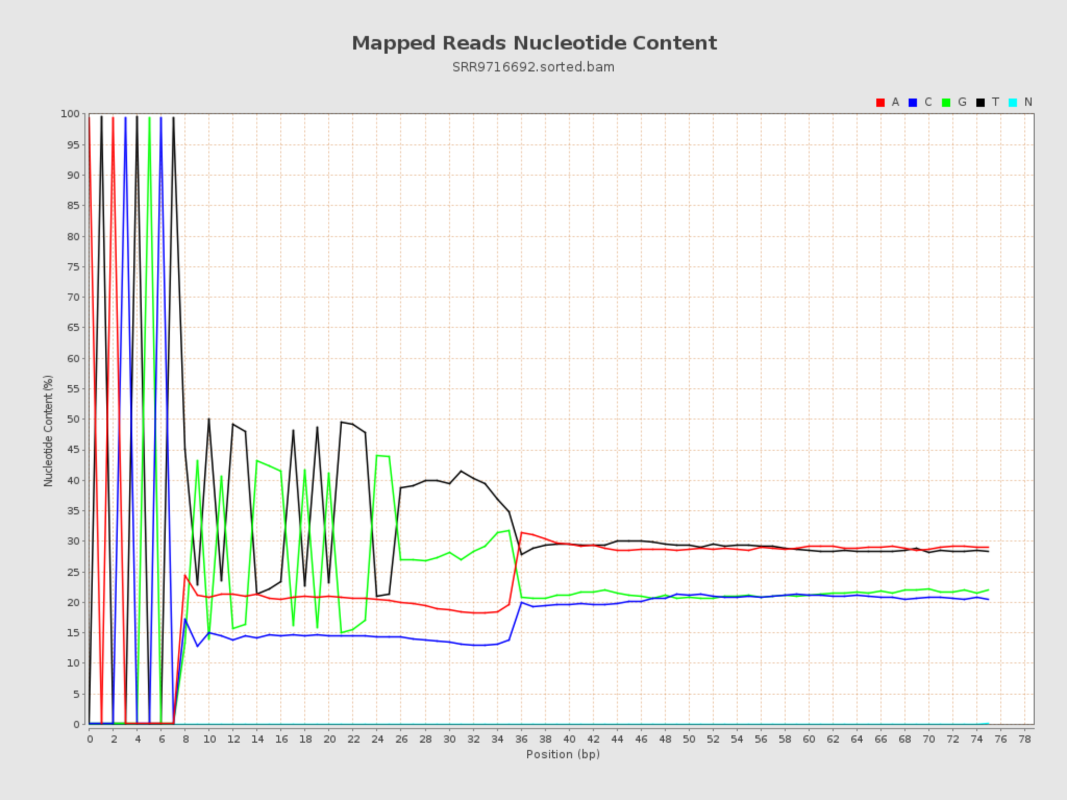
6. Results : Genome Fraction Coverage



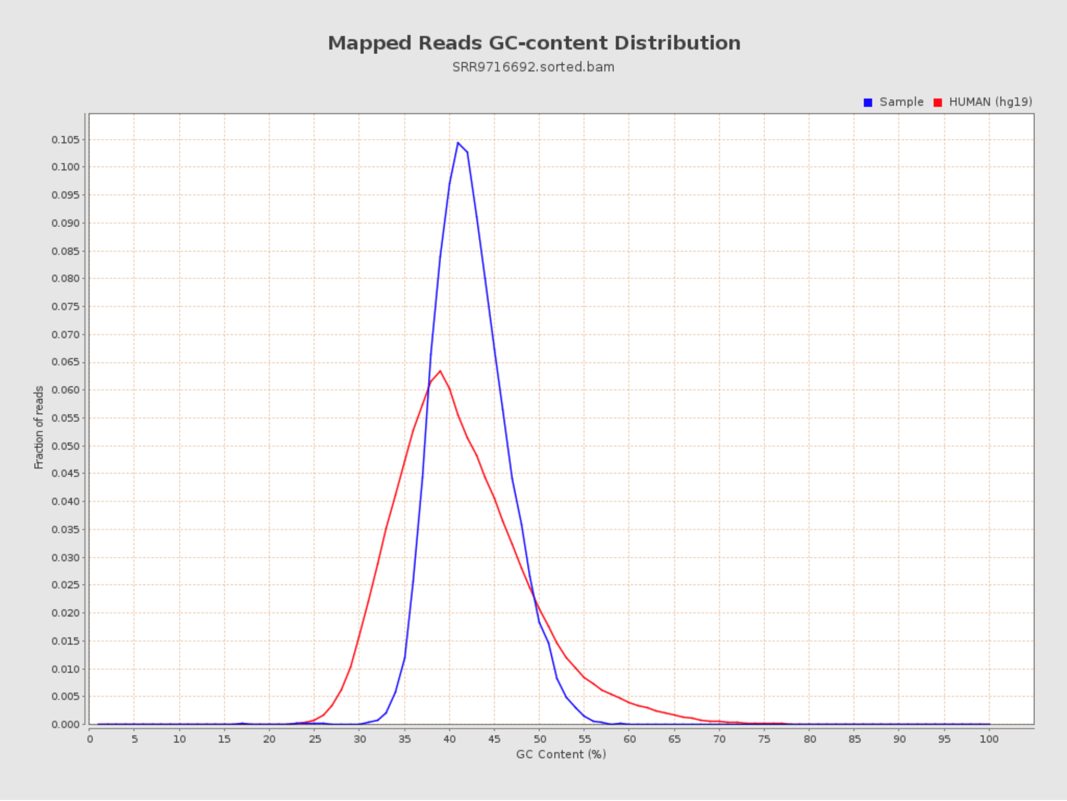
7. Results : Duplication Rate Histogram



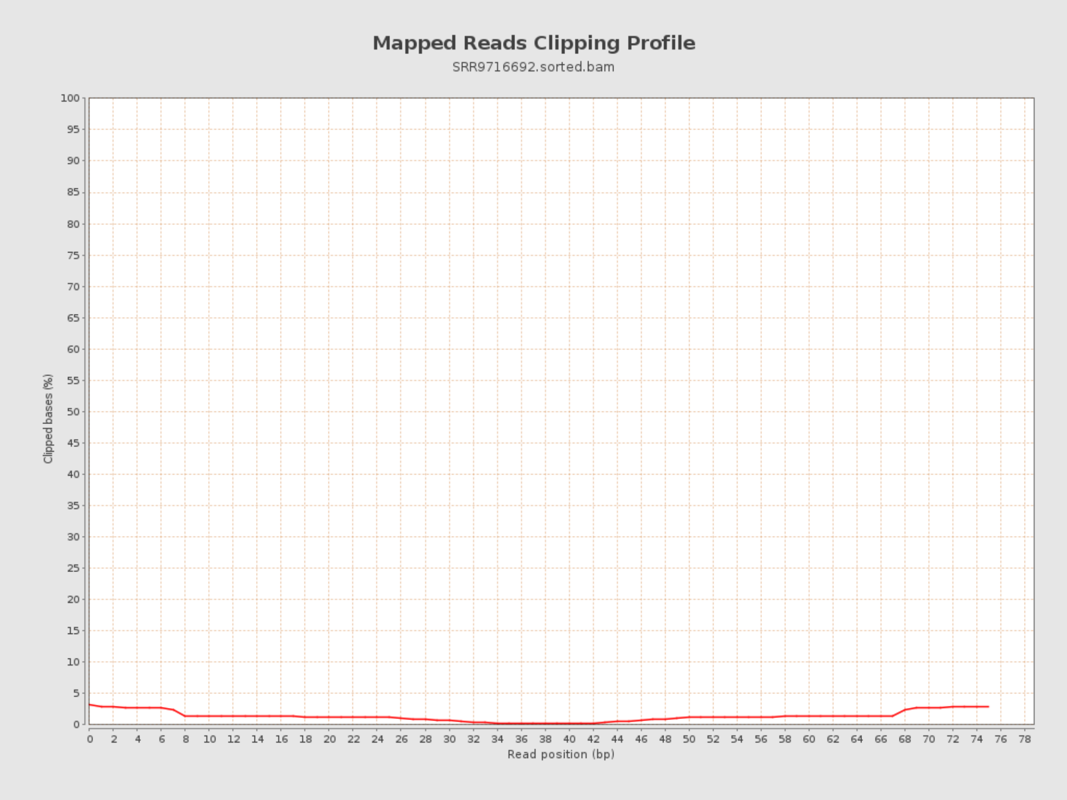
8. Results : Mapped Reads Nucleotide Content



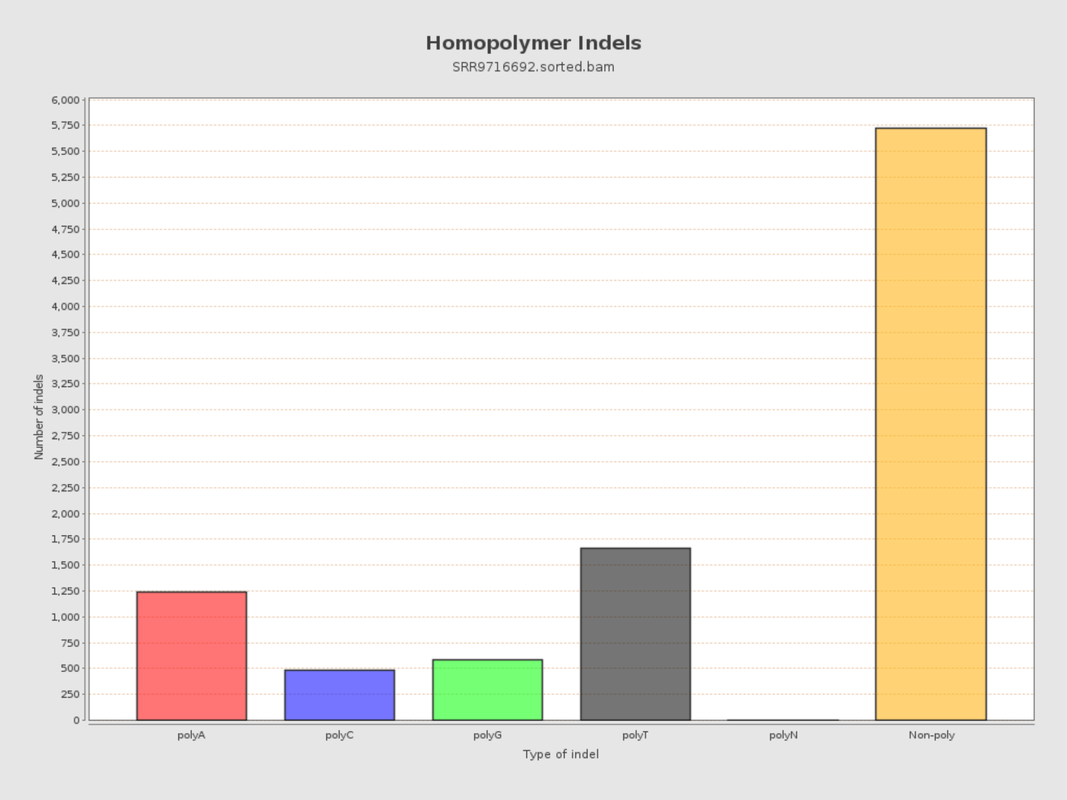
9. Results : Mapped Reads GC-content Distribution



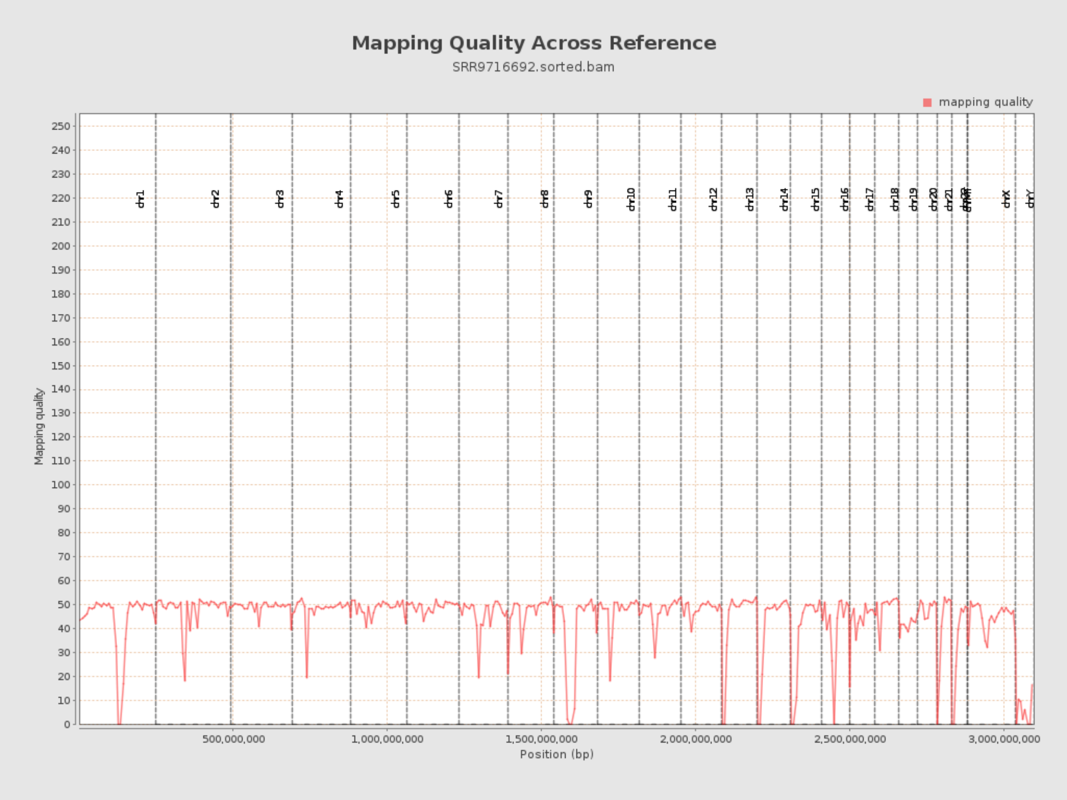
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram