Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 03:10:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716660.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_SRR9716660 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716660.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 03:10:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716660.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	639,777
Mapped reads	549,284 / 85.86%
Unmapped reads	90,493 / 14.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,187 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	9,203 / 1.44%
Duplication rate	1.17%
Clipped reads	550,057 / 85.98%

2.2. ACGT Content

Number/percentage of A's	7,329,965 / 23.69%
Number/percentage of C's	5,935,305 / 19.18%
Number/percentage of T's	9,761,989 / 31.55%
Number/percentage of G's	7,918,067 / 25.59%
Number/percentage of N's	513 / 0%
GC Percentage	44.77%

2.3. Coverage

Mean	0.01

Standard Deviation	0.1226

2.4. Mapping Quality

Mean Mapping Quality	41.58

2.5. Mismatches and indels

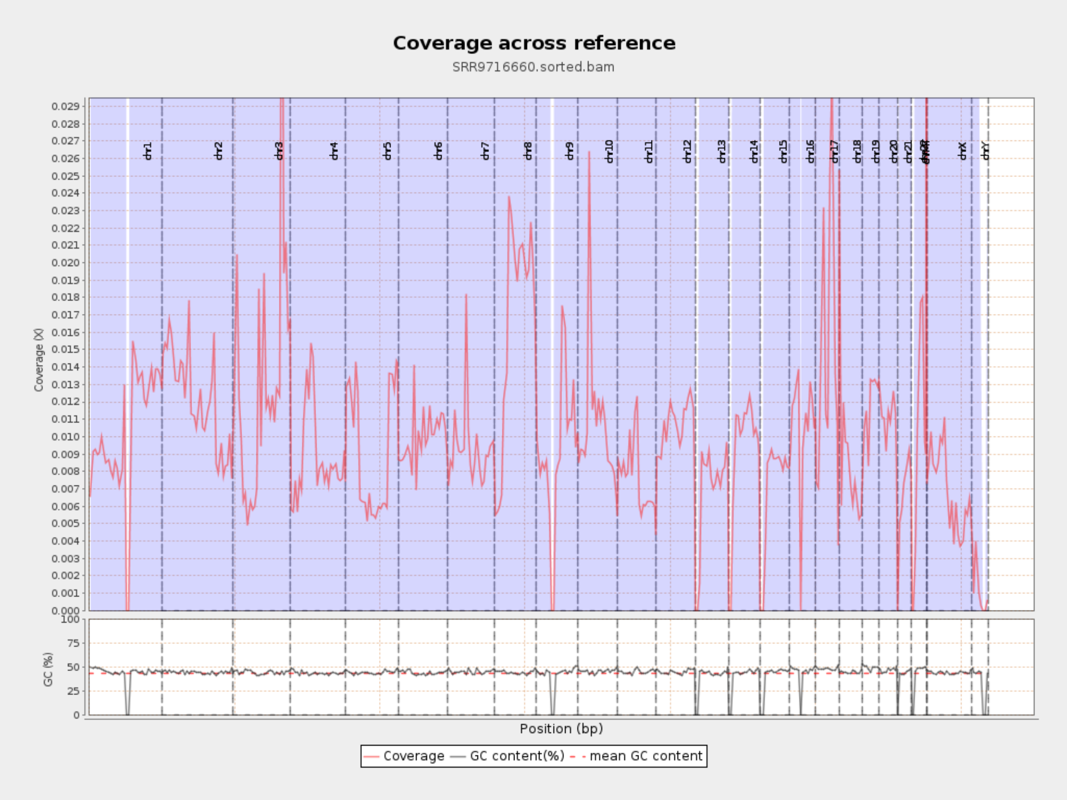
General error rate	0.55%
Mismatches	167,268
Insertions	2,232
Mapped reads with at least one insertion	0.4%
Deletions	5,922
Mapped reads with at least one deletion	1.07%
Homopolymer indels	40.89%

2.6. Chromosome stats

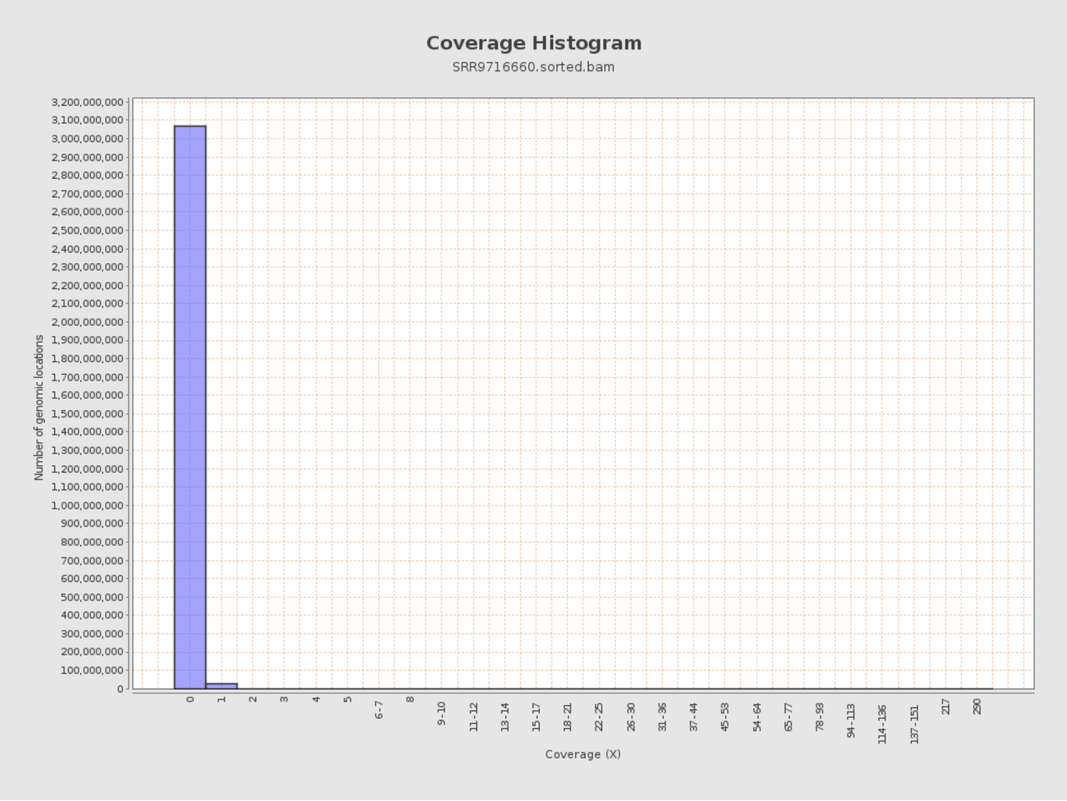
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2520211	0.0101	0.1481
chr2	243199373	2979292	0.0123	0.1647
chr3	198022430	2616047	0.0132	0.1241
chr4	191154276	1690325	0.0088	0.0997
chr5	180915260	1640758	0.0091	0.0985
chr6	171115067	1706137	0.01	0.11
chr7	159138663	1489131	0.0094	0.1491

chr8	146364022	2439658	0.0167	0.1432
chr9	141213431	1269934	0.009	0.1032
chr10	135534747	1470633	0.0109	0.1623
chr11	135006516	1031668	0.0076	0.1004
chr12	133851895	1430220	0.0107	0.1126
chr13	115169878	788170	0.0068	0.0852
chr14	107349540	985644	0.0092	0.1
chr15	102531392	720204	0.007	0.0873
chr16	90354753	959862	0.0106	0.1122
chr17	81195210	1223640	0.0151	0.1299
chr18	78077248	656069	0.0084	0.1249
chr19	59128983	690258	0.0117	0.1496
chr20	63025520	697528	0.0111	0.1166
chr21	48129895	315240	0.0065	0.0862
chr22	51304566	477268	0.0093	0.1
chrMT	16571	1251	0.0755	0.2928
chrX	155270560	1083753	0.007	0.0955
chrY	59373566	72383	0.0012	0.0453

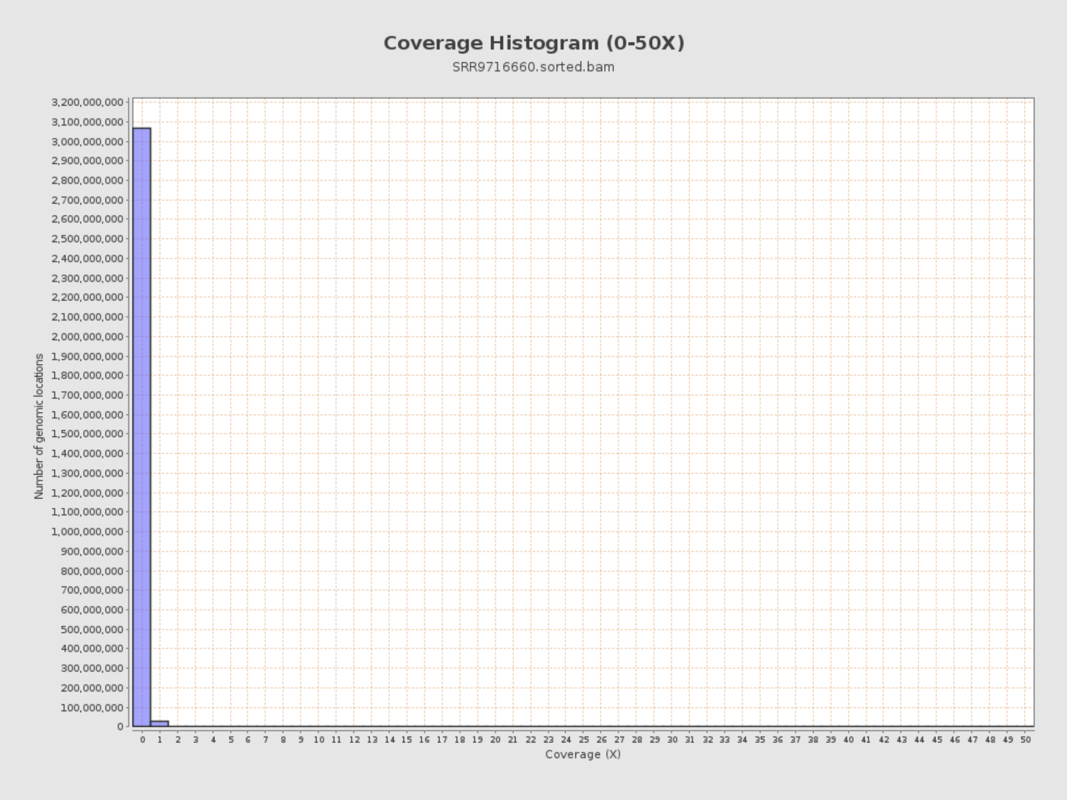
3. Results : Coverage across reference



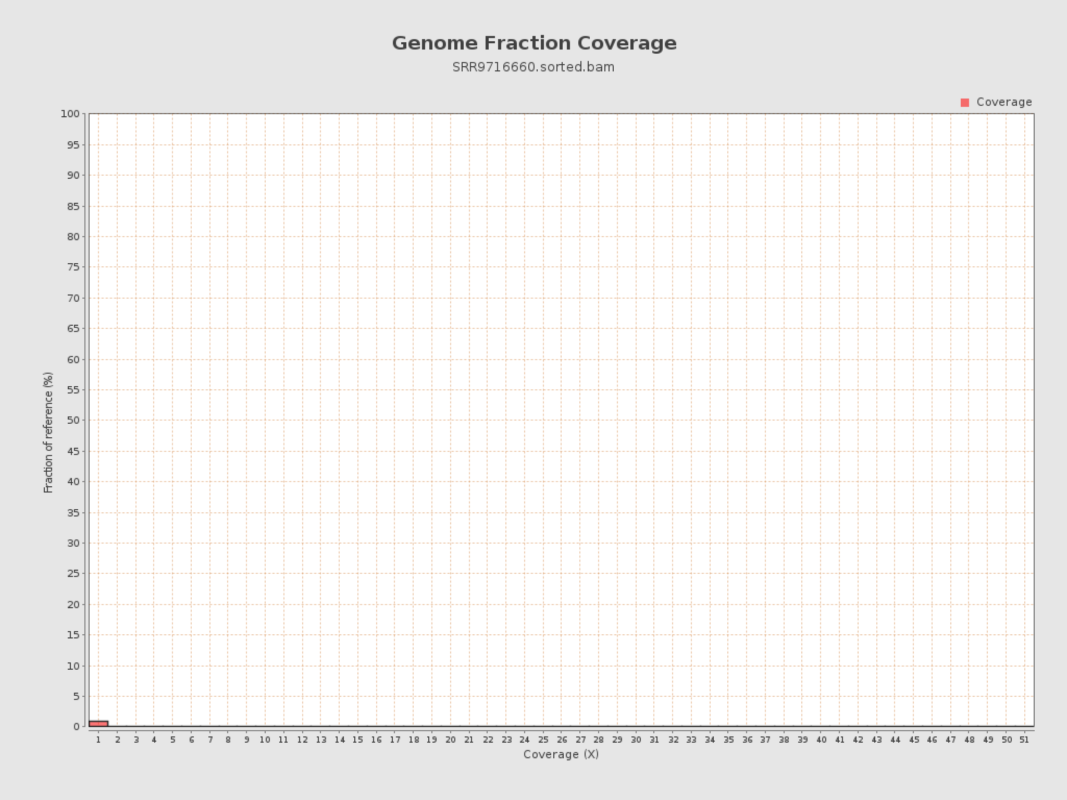
4. Results : Coverage Histogram



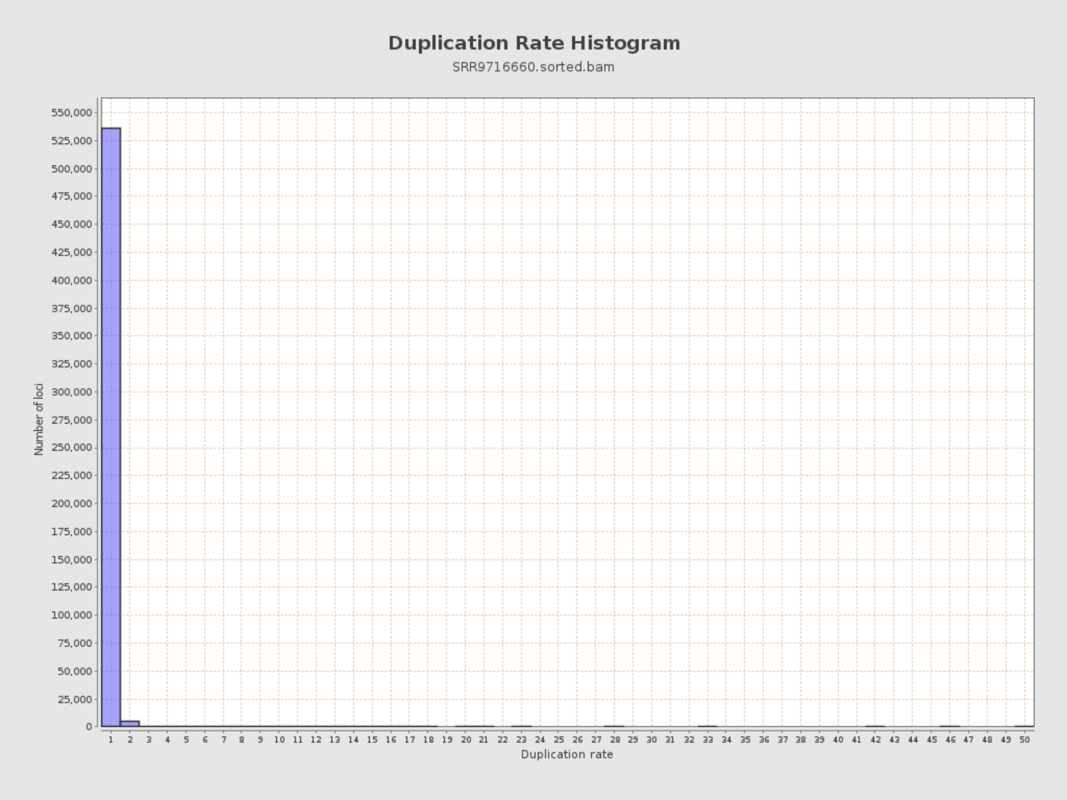
5. Results : Coverage Histogram (0-50X)



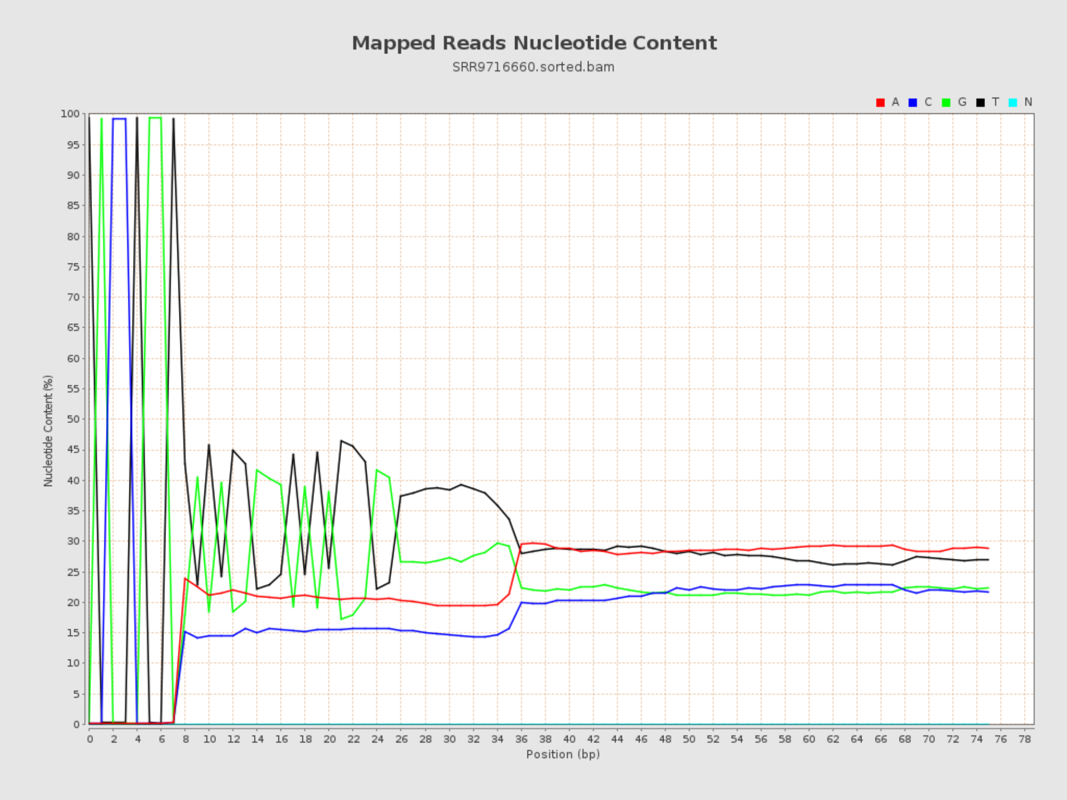
6. Results : Genome Fraction Coverage



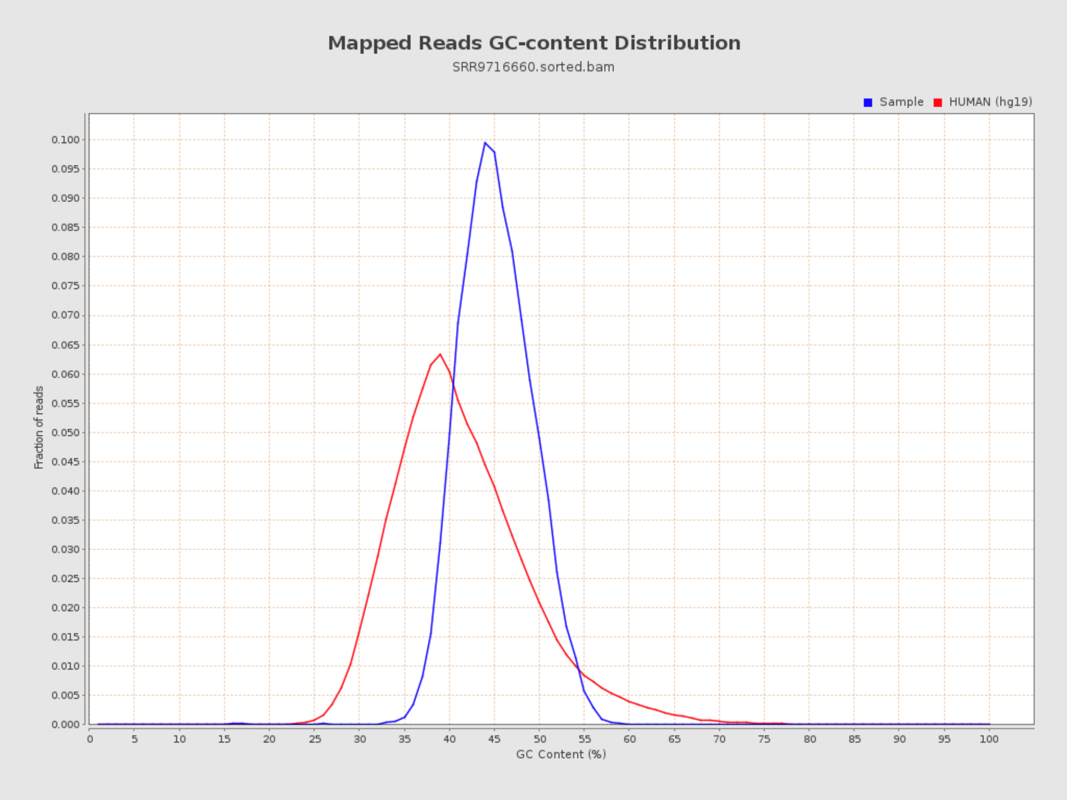
7. Results : Duplication Rate Histogram



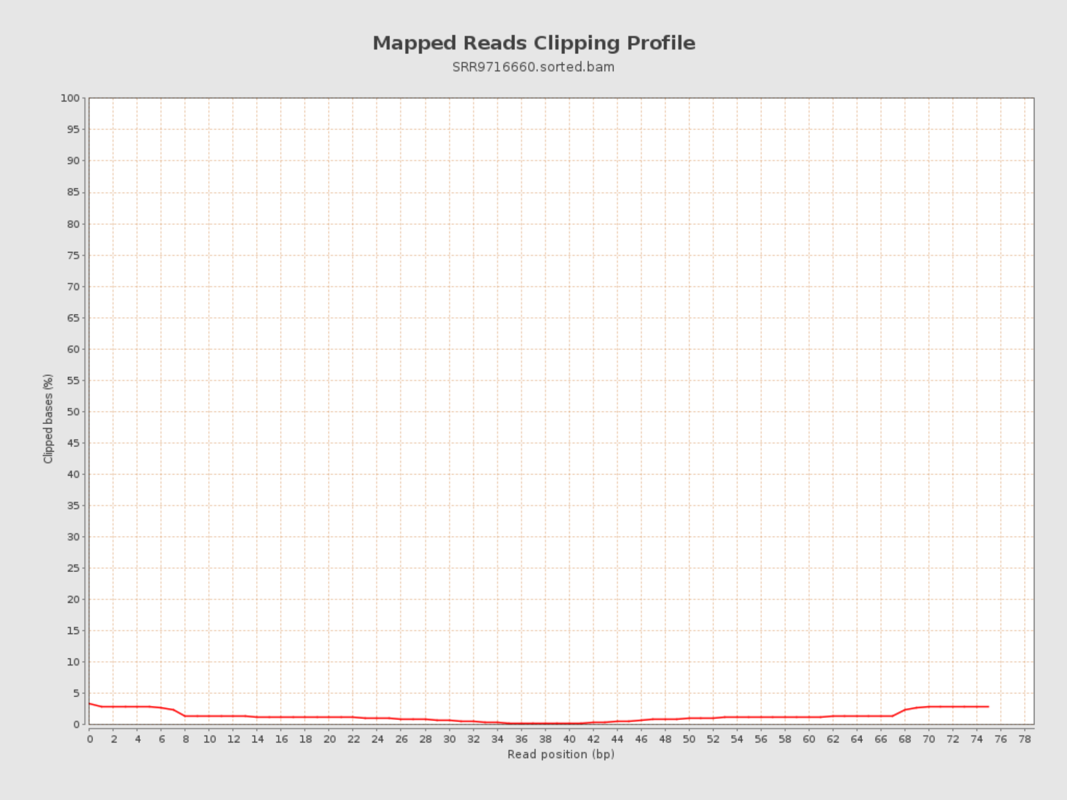
8. Results : Mapped Reads Nucleotide Content



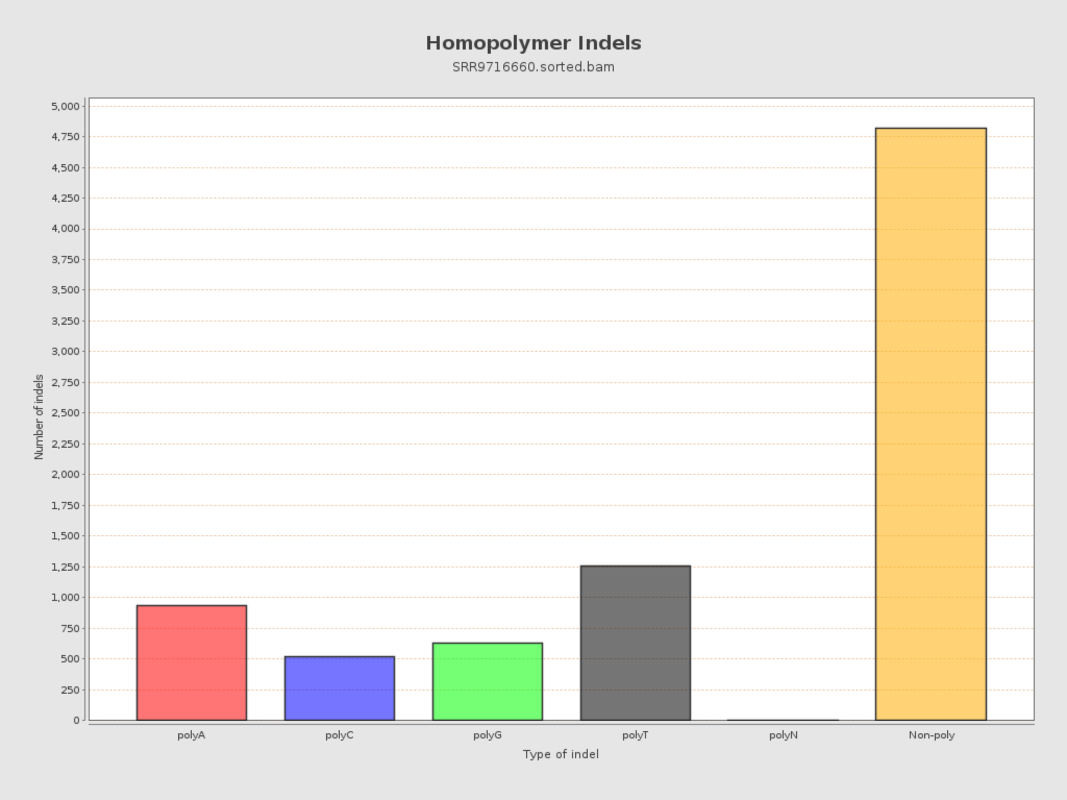
9. Results : Mapped Reads GC-content Distribution



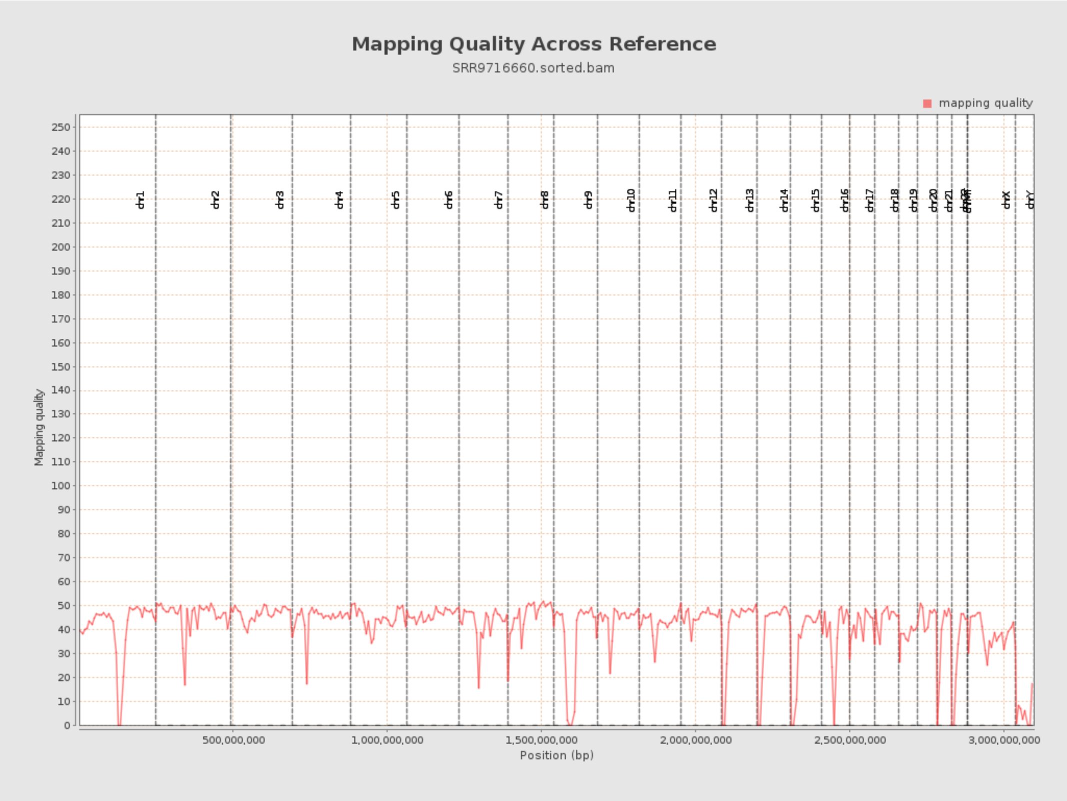
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram