Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:14:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716627.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_SRR9716627 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716627.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:14:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716627.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	894,326
Mapped reads	807,717 / 90.32%
Unmapped reads	86,609 / 9.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,434 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	22,640 / 2.53%
Duplication rate	2.19%
Clipped reads	808,167 / 90.37%

2.2. ACGT Content

Number/percentage of A's	12,107,439 / 25.75%
Number/percentage of C's	8,872,907 / 18.87%
Number/percentage of T's	14,998,694 / 31.9%
Number/percentage of G's	11,043,883 / 23.49%
Number/percentage of N's	1,509 / 0%
GC Percentage	42.35%

2.3. Coverage

Mean	0.0152

Standard Deviation	0.1658

2.4. Mapping Quality

Mean Mapping Quality	45.28

2.5. Mismatches and indels

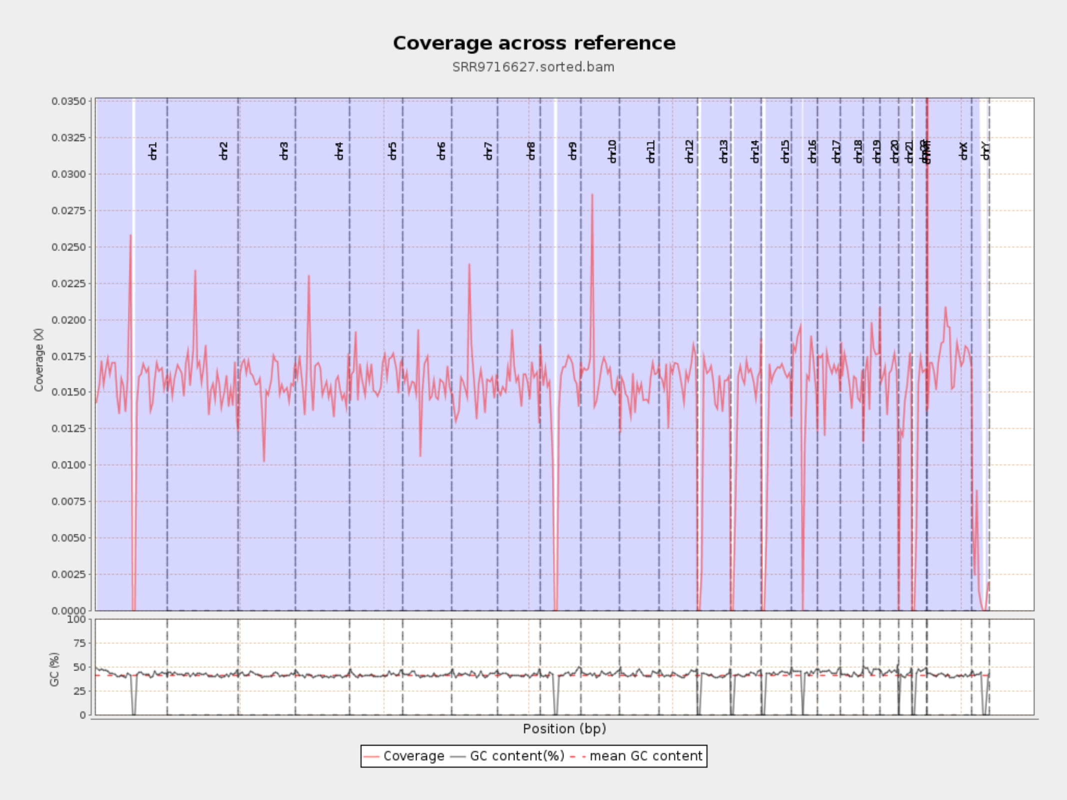
General error rate	0.51%
Mismatches	233,263
Insertions	3,857
Mapped reads with at least one insertion	0.48%
Deletions	8,701
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.86%

2.6. Chromosome stats

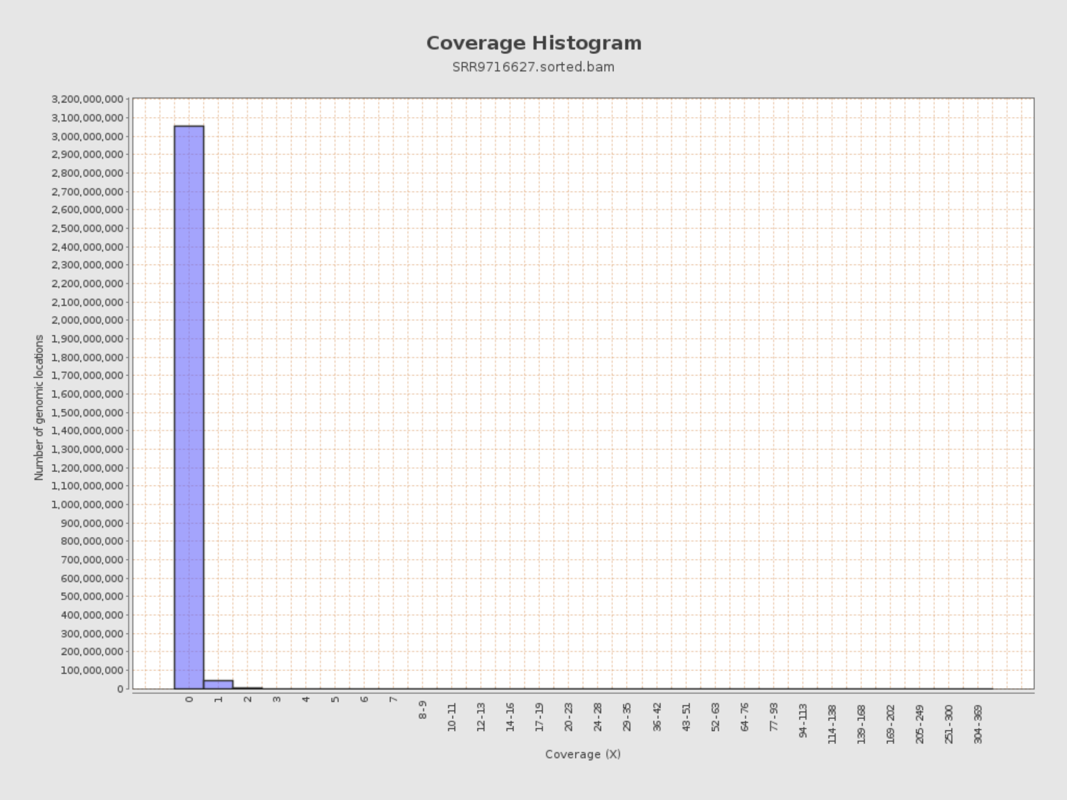
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3771101	0.0151	0.2788
chr2	243199373	3904986	0.0161	0.2063
chr3	198022430	3094970	0.0156	0.1329
chr4	191154276	3032656	0.0159	0.1391
chr5	180915260	2954691	0.0163	0.1355
chr6	171115067	2657793	0.0155	0.1445
chr7	159138663	2486755	0.0156	0.1824

chr8	146364022	2314045	0.0158	0.1537
chr9	141213431	1986009	0.0141	0.1418
chr10	135534747	2276761	0.0168	0.1671
chr11	135006516	2055438	0.0152	0.1459
chr12	133851895	2159811	0.0161	0.1352
chr13	115169878	1505381	0.0131	0.1212
chr14	107349540	1439908	0.0134	0.1246
chr15	102531392	1357055	0.0132	0.1228
chr16	90354753	1378811	0.0153	0.135
chr17	81195210	1338600	0.0165	0.1403
chr18	78077248	1234906	0.0158	0.2184
chr19	59128983	1012130	0.0171	0.2047
chr20	63025520	1007360	0.016	0.1343
chr21	48129895	635592	0.0132	0.126
chr22	51304566	579630	0.0113	0.1124
chrMT	16571	3985	0.2405	0.5175
chrX	155270560	2705684	0.0174	0.1471
chrY	59373566	144181	0.0024	0.0726

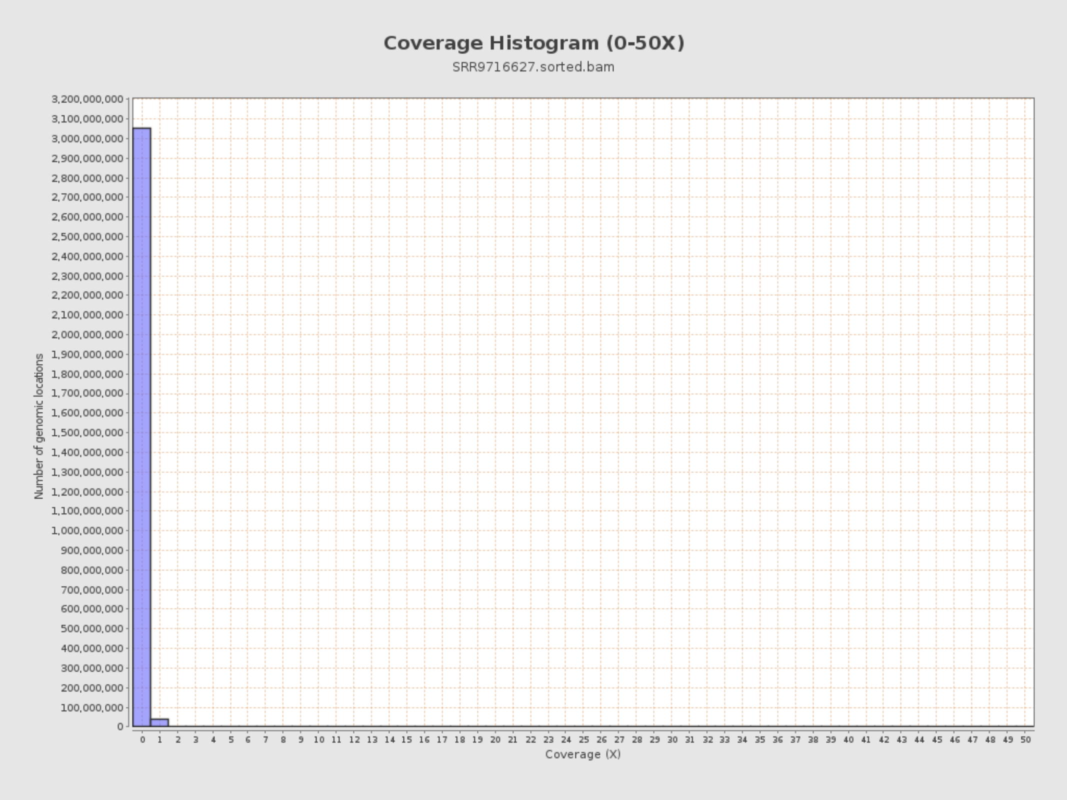
3. Results : Coverage across reference



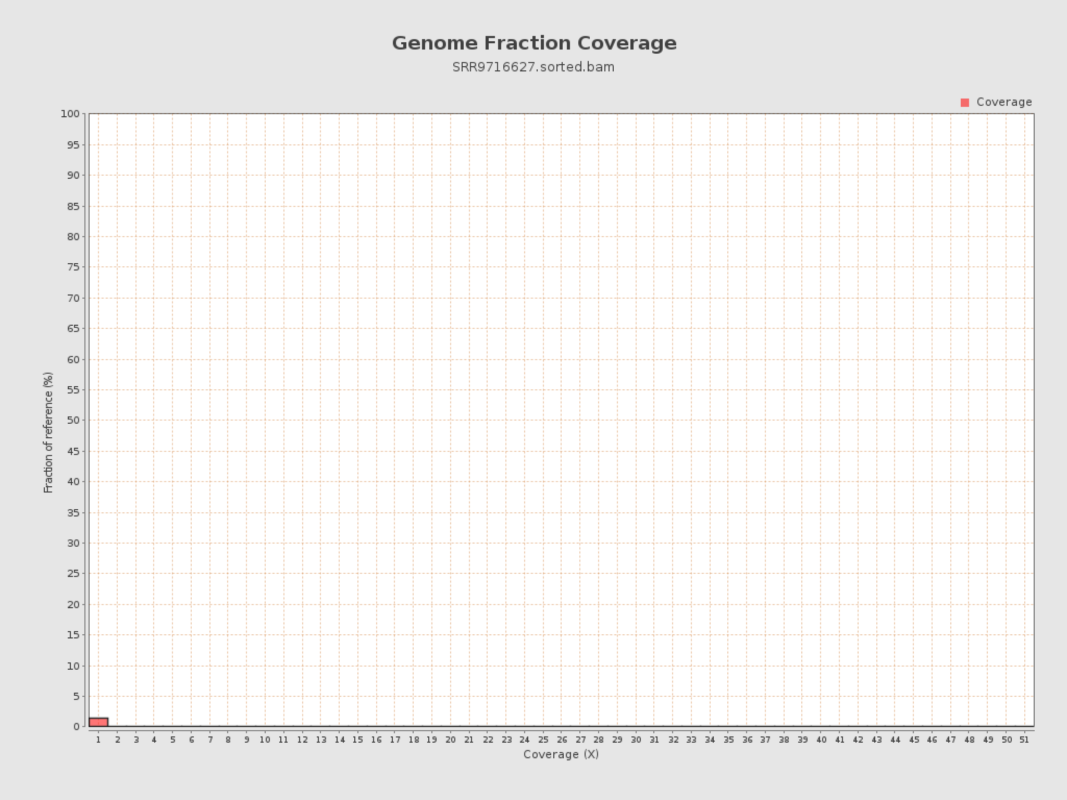
4. Results : Coverage Histogram



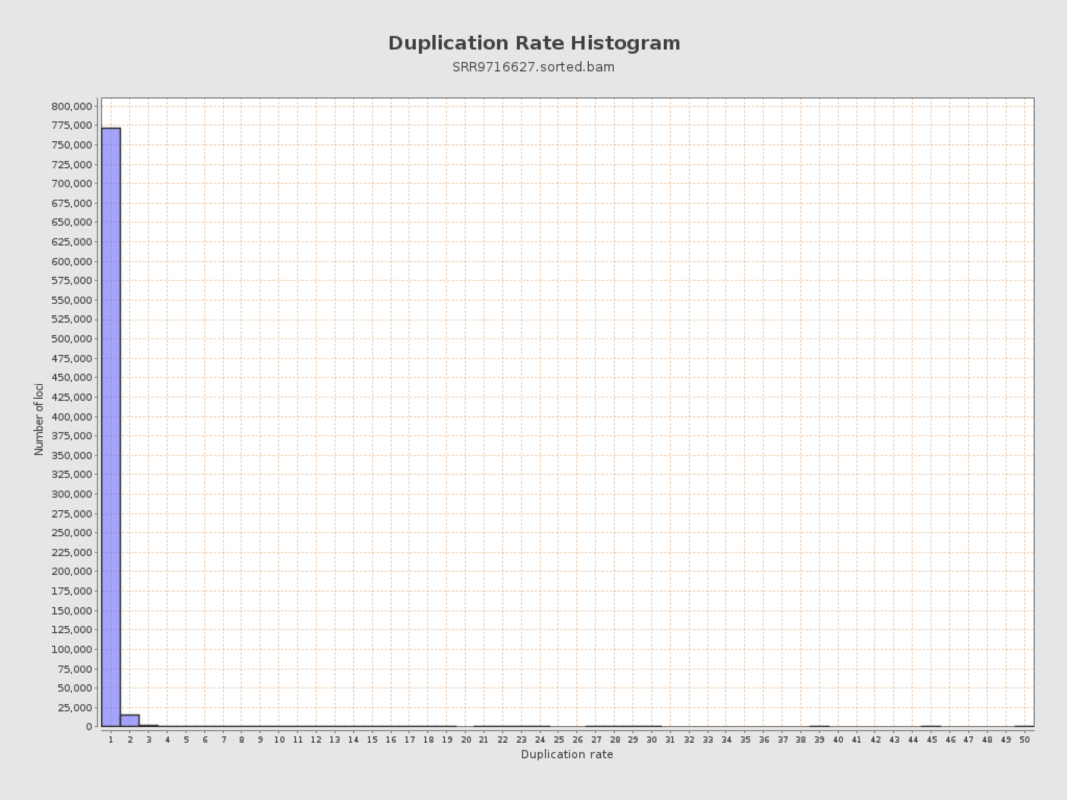
5. Results : Coverage Histogram (0-50X)



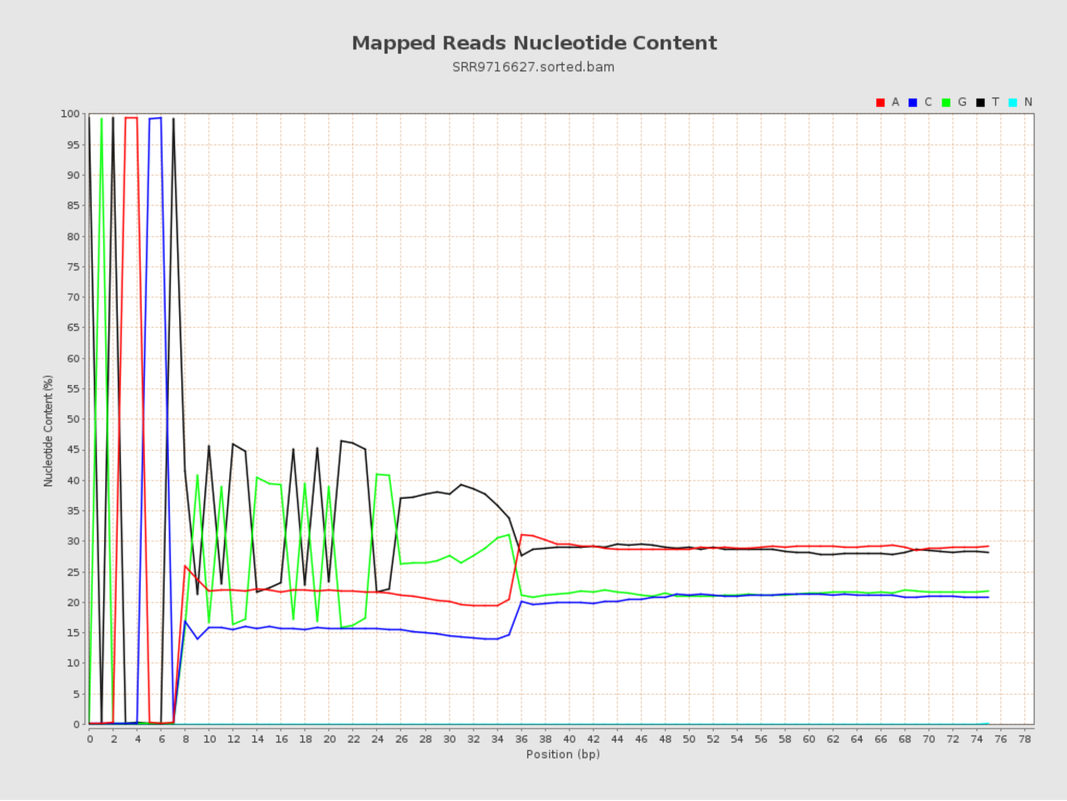
6. Results : Genome Fraction Coverage



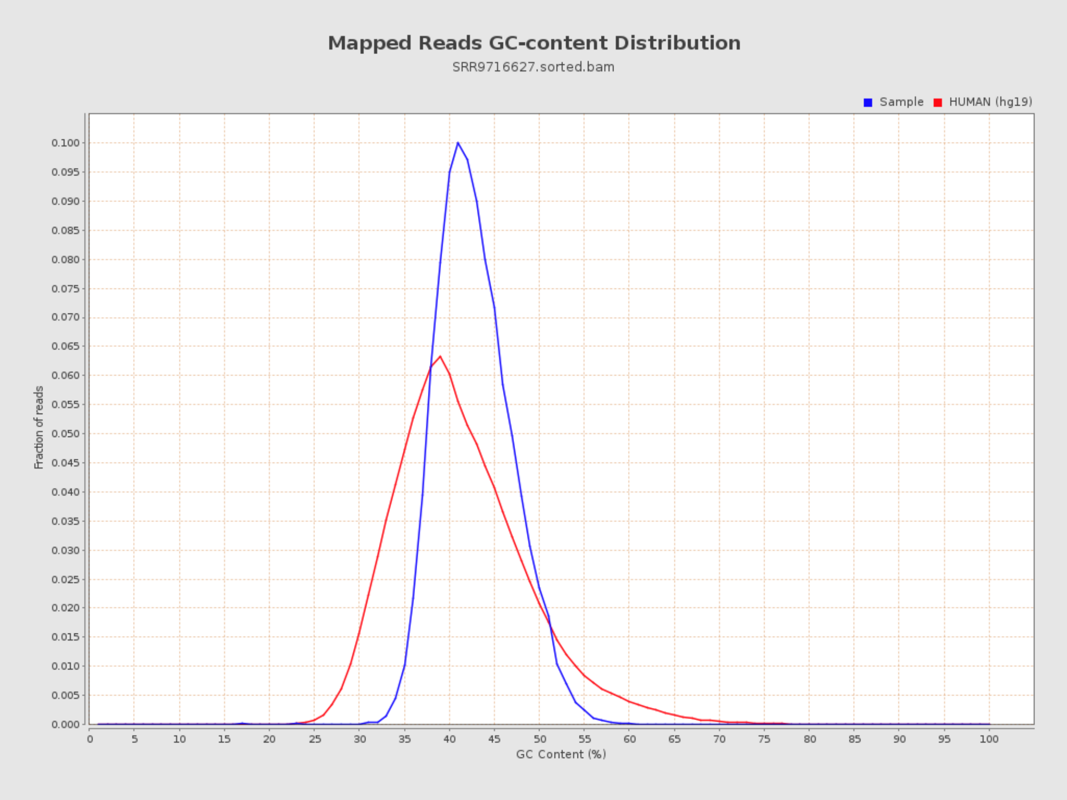
7. Results : Duplication Rate Histogram



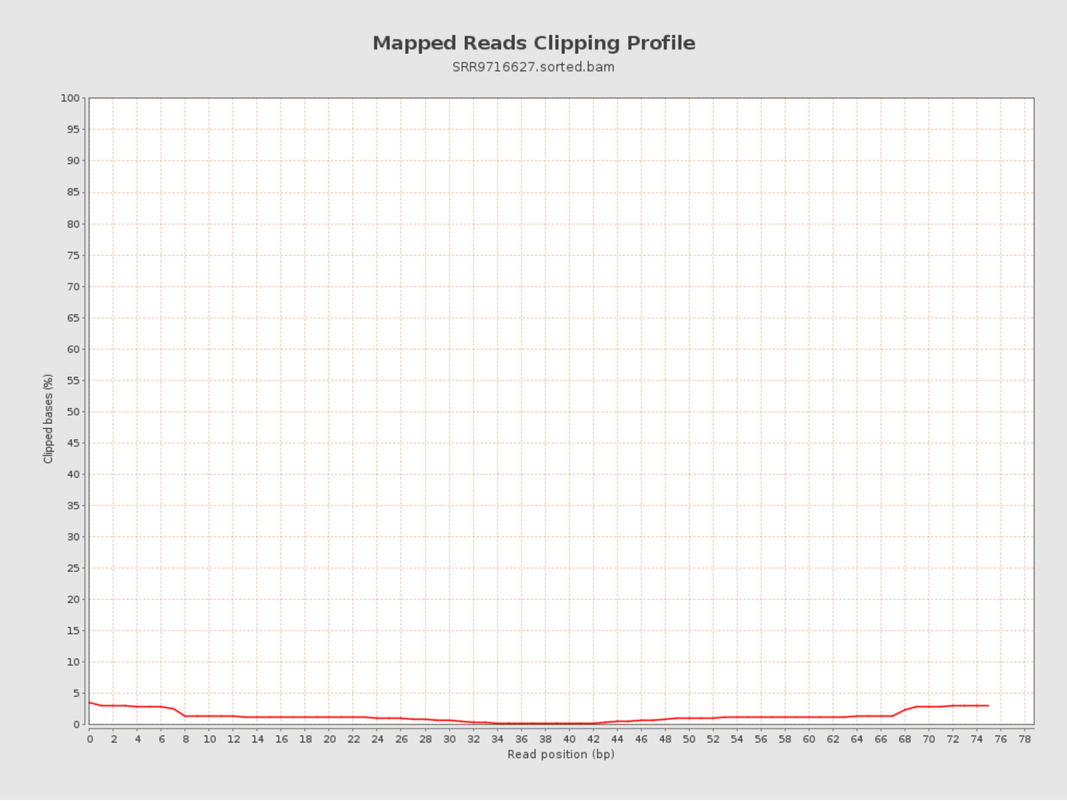
8. Results : Mapped Reads Nucleotide Content



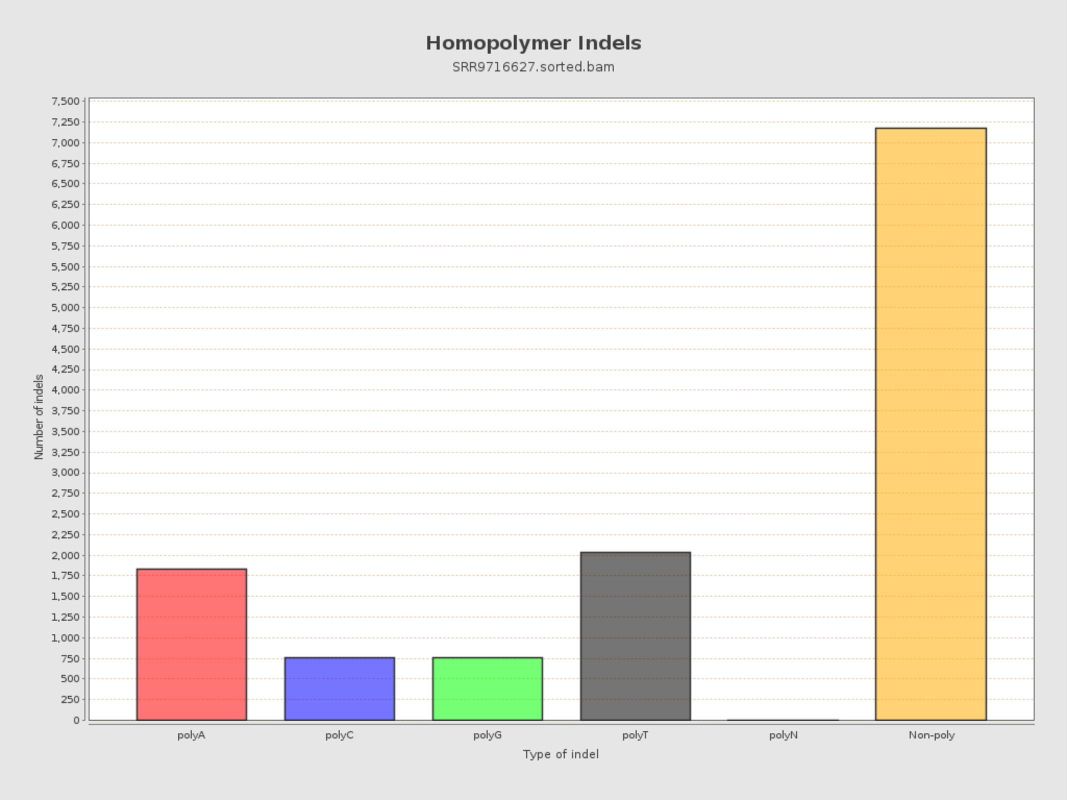
9. Results : Mapped Reads GC-content Distribution



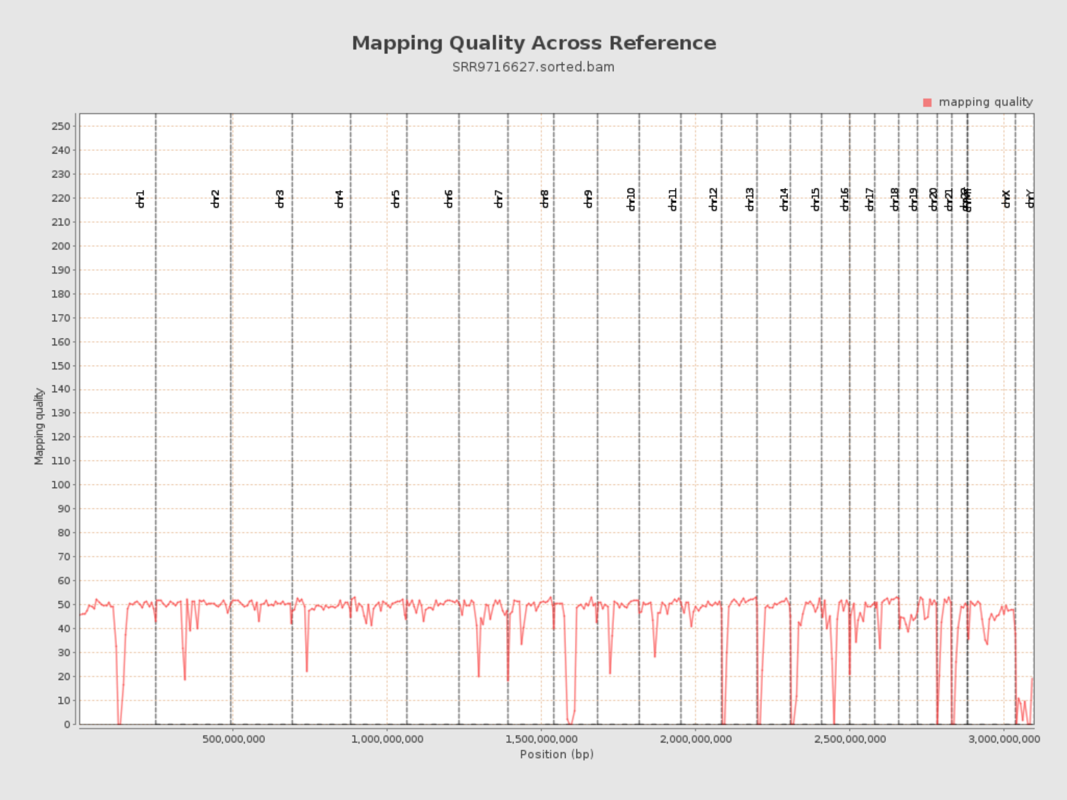
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram