Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:34:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716114.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_SRR9716114 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716114.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:34:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,349,194
Mapped reads	1,164,497 / 86.31%
Unmapped reads	184,697 / 13.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,359 / 0.25%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	25,895 / 1.92%
Duplication rate	1.6%
Clipped reads	1,165,978 / 86.42%

2.2. ACGT Content

Number/percentage of A's	14,845,740 / 22.56%
Number/percentage of C's	13,655,830 / 20.75%
Number/percentage of T's	19,840,788 / 30.15%
Number/percentage of G's	17,463,995 / 26.54%
Number/percentage of N's	1,929 / 0%
GC Percentage	47.29%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.1875

2.4. Mapping Quality

Mean Mapping Quality	40.62

2.5. Mismatches and indels

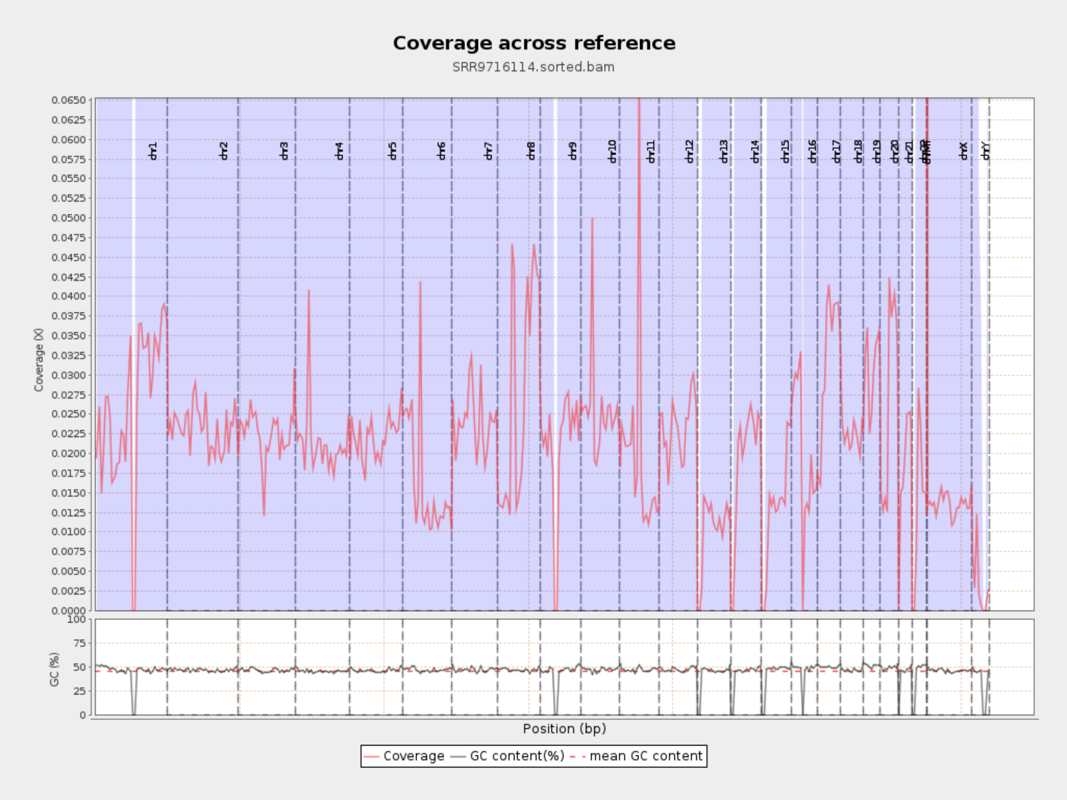
General error rate	0.53%
Mismatches	341,854
Insertions	4,449
Mapped reads with at least one insertion	0.38%
Deletions	10,990
Mapped reads with at least one deletion	0.94%
Homopolymer indels	38.69%

2.6. Chromosome stats

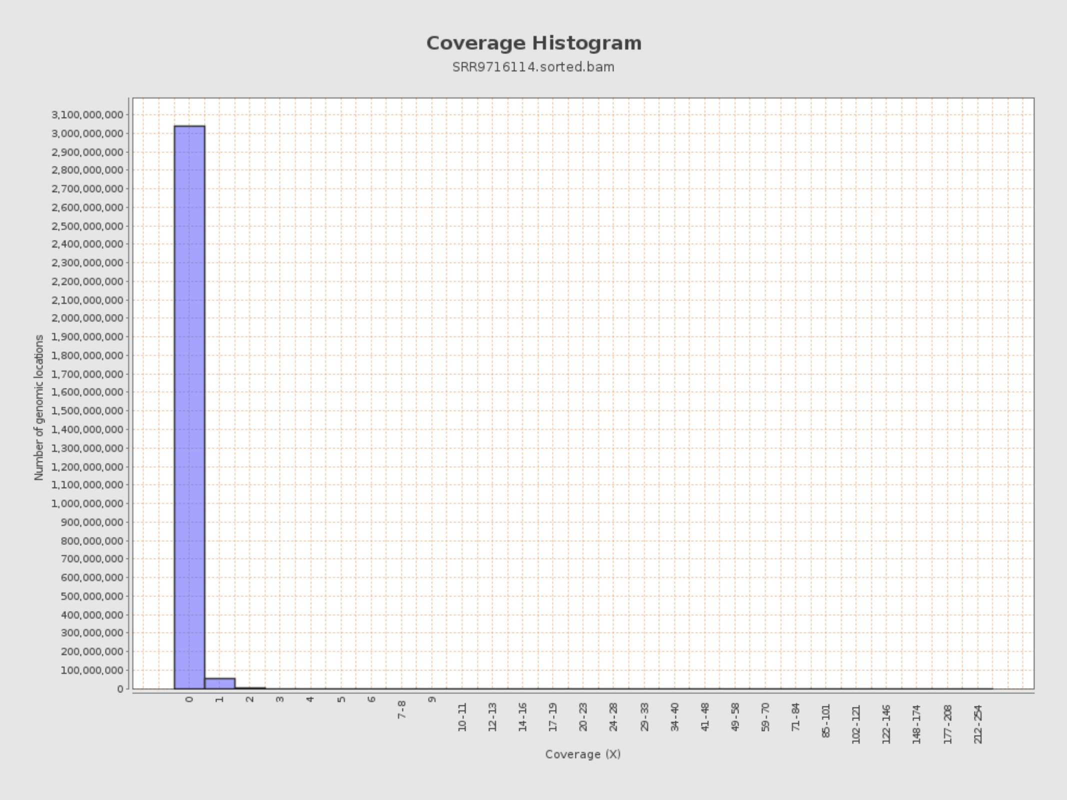
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6503679	0.0261	0.2424
chr2	243199373	5654326	0.0232	0.2173
chr3	198022430	4430833	0.0224	0.1657
chr4	191154276	4112830	0.0215	0.181
chr5	180915260	4021347	0.0222	0.1616
chr6	171115067	2821164	0.0165	0.1434
chr7	159138663	3849892	0.0242	0.2191

chr8	146364022	4046853	0.0276	0.1906
chr9	141213431	2913579	0.0206	0.1697
chr10	135534747	3474783	0.0256	0.2848
chr11	135006516	2714641	0.0201	0.1839
chr12	133851895	3137497	0.0234	0.1679
chr13	115169878	1168782	0.0101	0.1098
chr14	107349540	2043513	0.019	0.153
chr15	102531392	1310084	0.0128	0.1246
chr16	90354753	1762771	0.0195	0.1661
chr17	81195210	2628499	0.0324	0.2058
chr18	78077248	1748687	0.0224	0.2128
chr19	59128983	1805403	0.0305	0.2301
chr20	63025520	1706496	0.0271	0.1869
chr21	48129895	894976	0.0186	0.1647
chr22	51304566	721036	0.0141	0.1299
chrMT	16571	50288	3.0347	2.8581
chrX	155270560	2108927	0.0136	0.1361
chrY	59373566	196039	0.0033	0.1036

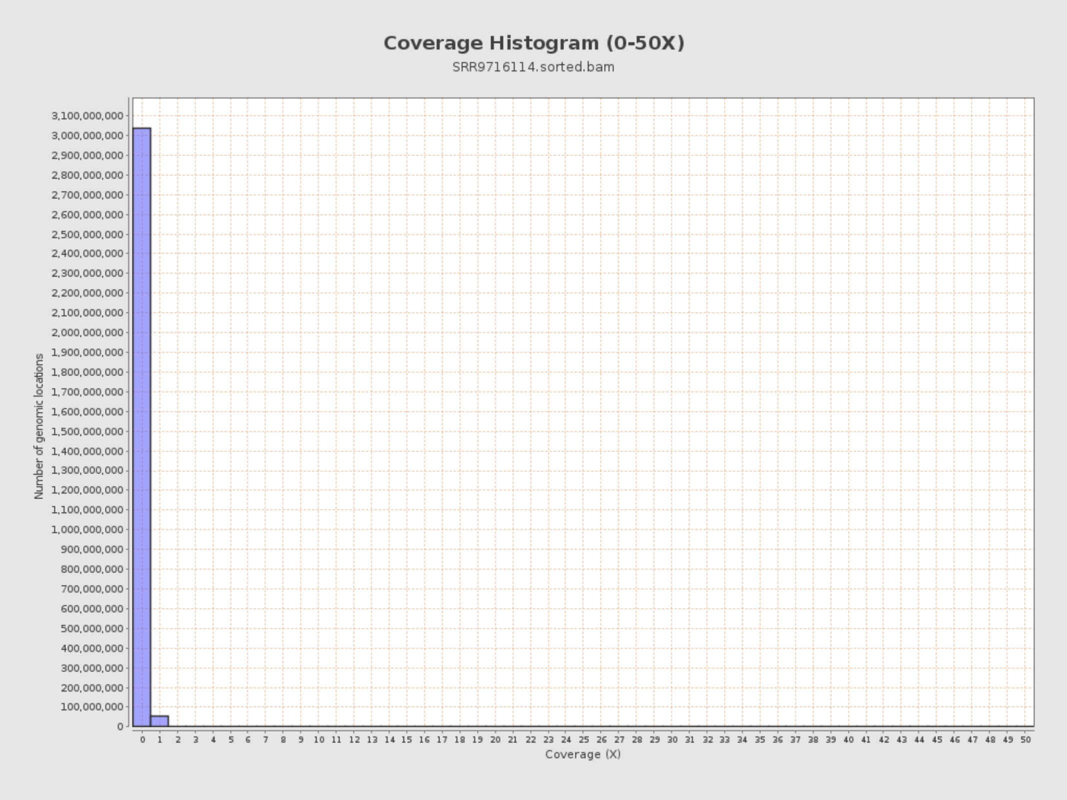
3. Results : Coverage across reference



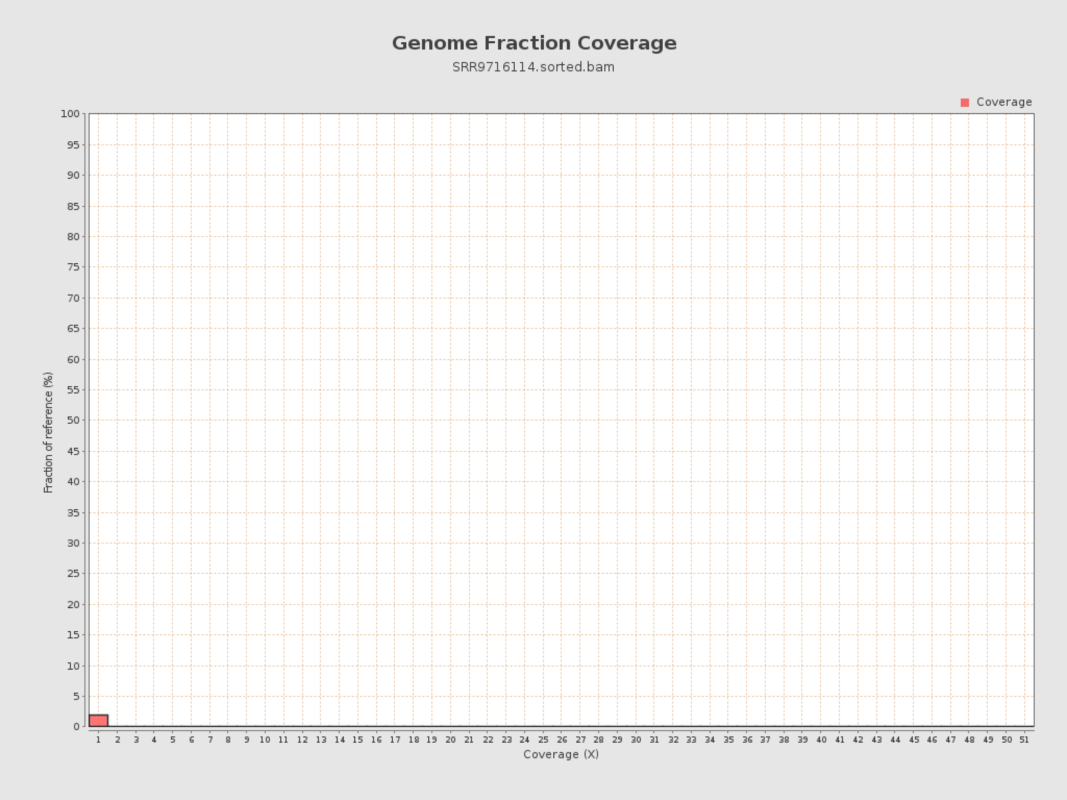
4. Results : Coverage Histogram



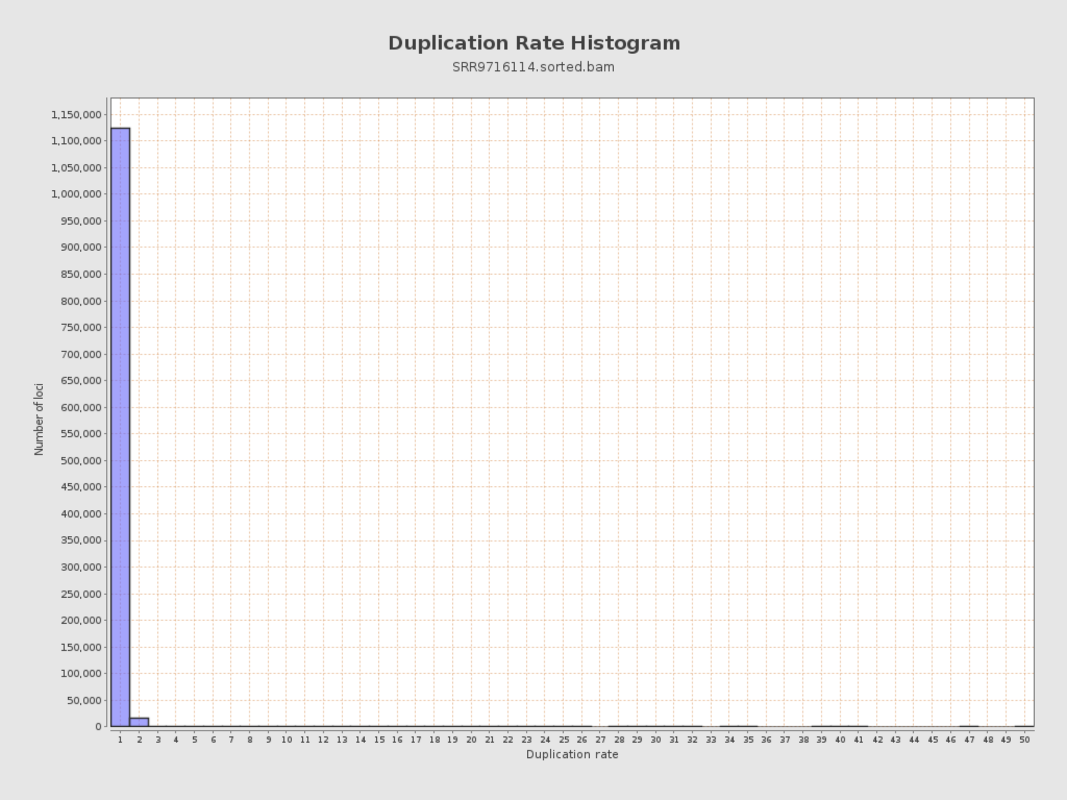
5. Results : Coverage Histogram (0-50X)



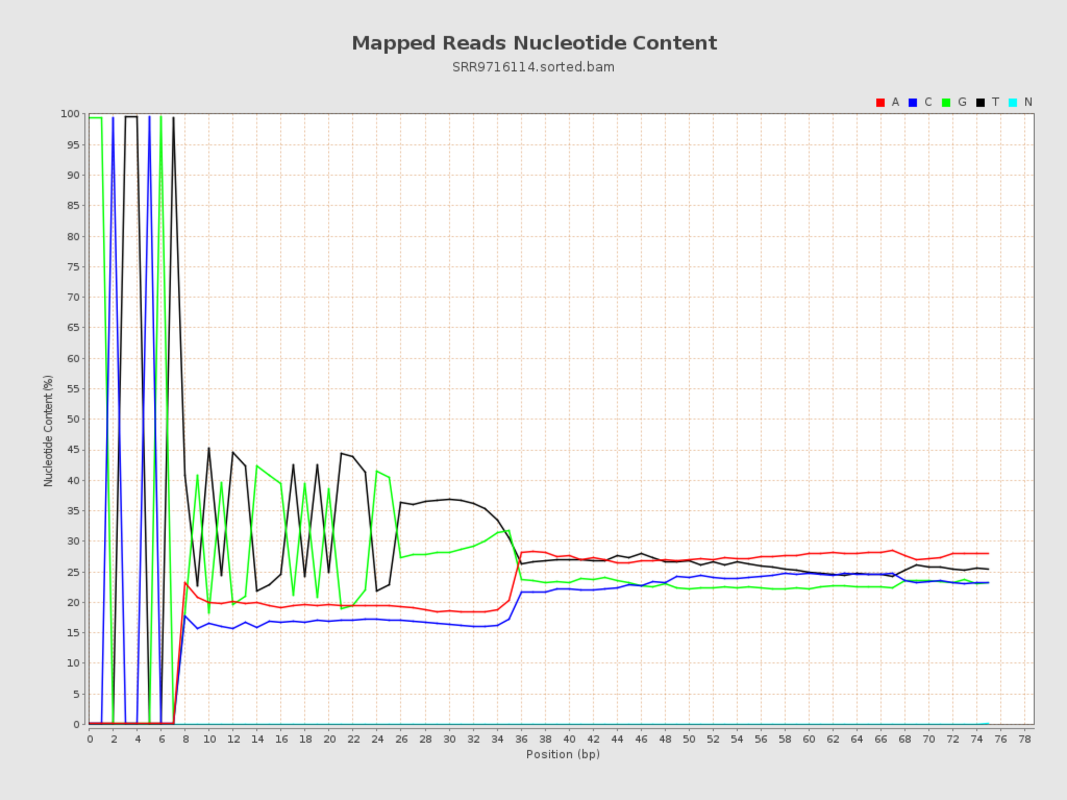
6. Results : Genome Fraction Coverage



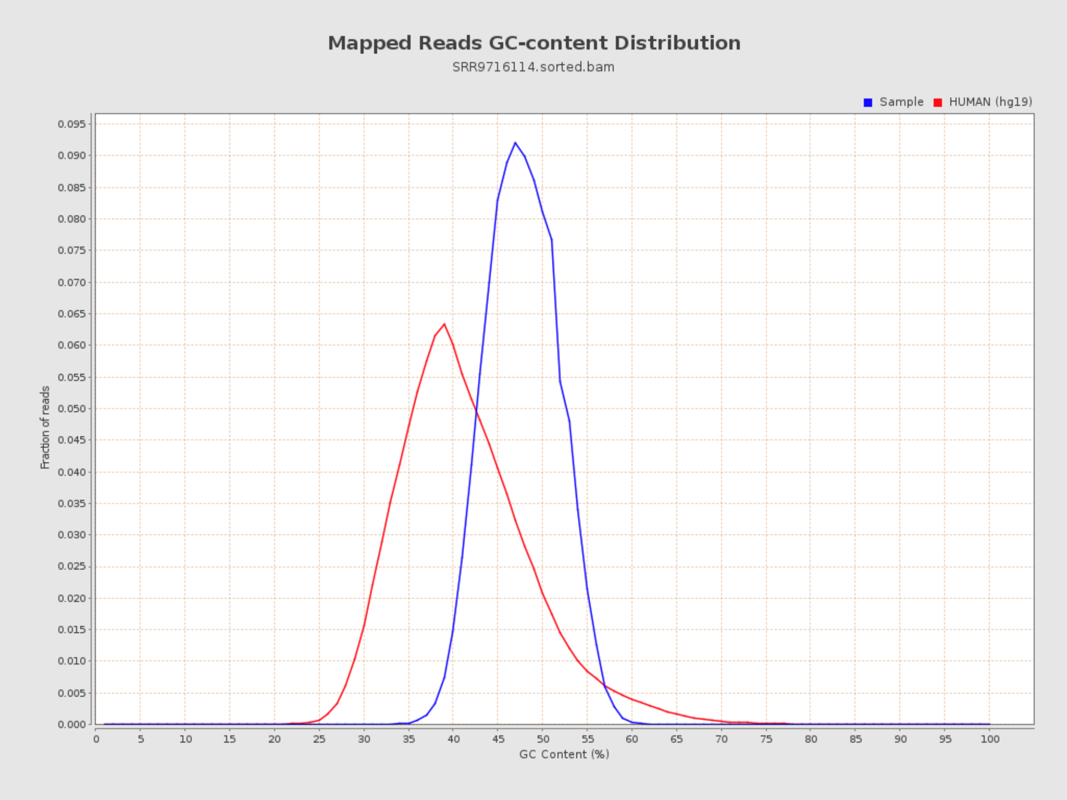
7. Results : Duplication Rate Histogram



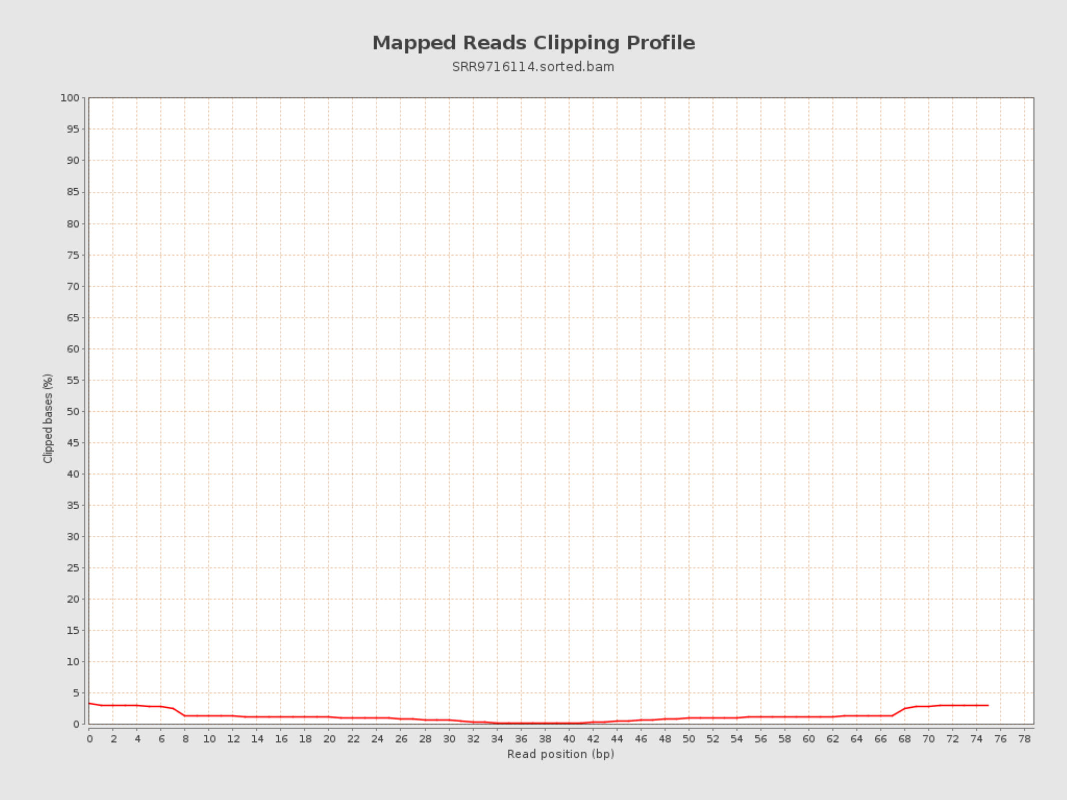
8. Results : Mapped Reads Nucleotide Content



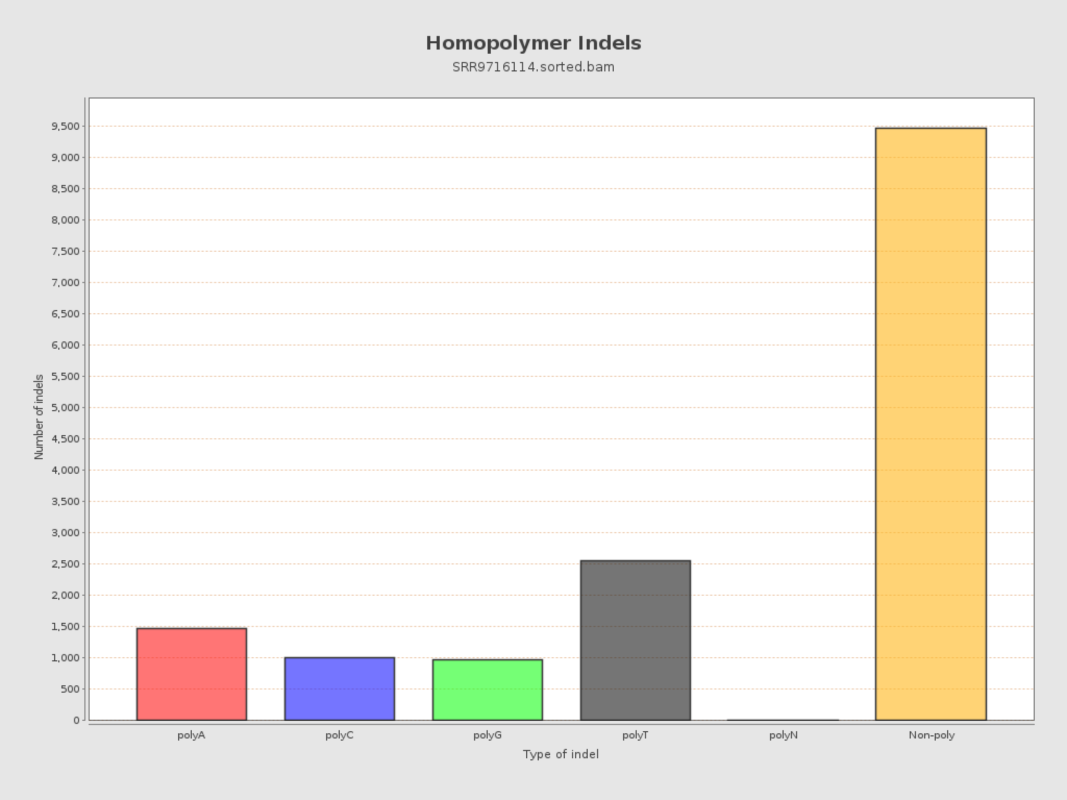
9. Results : Mapped Reads GC-content Distribution



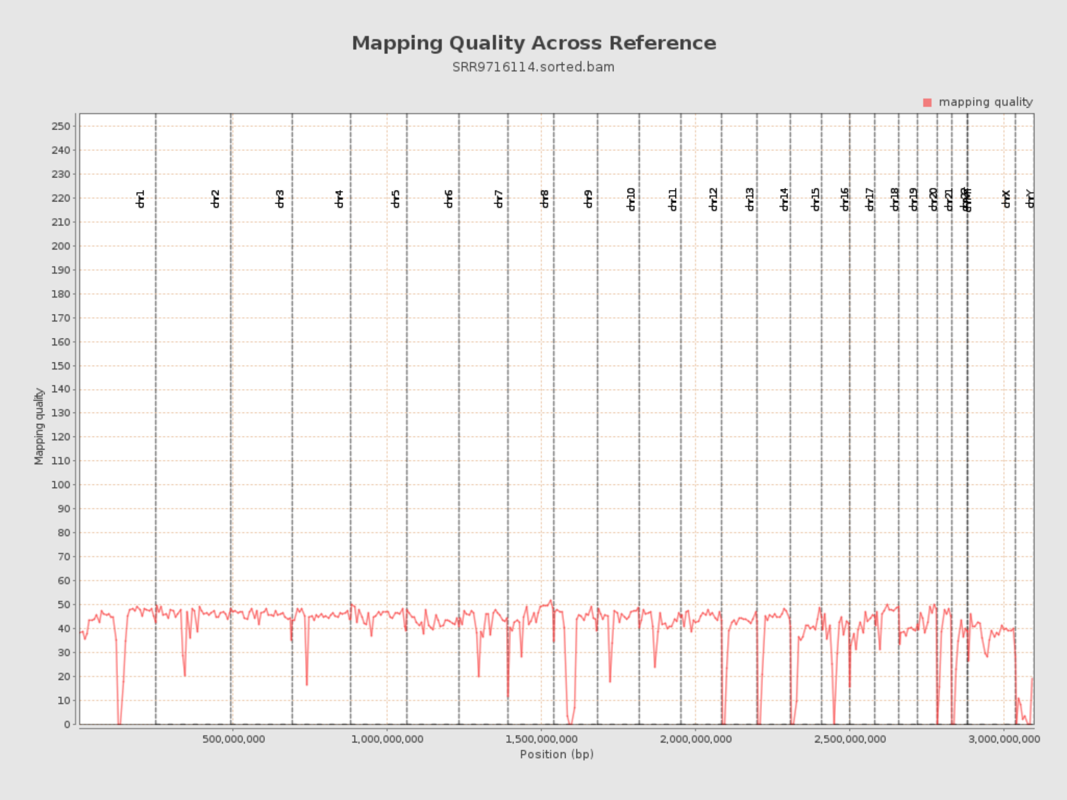
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram