Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:51:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716289.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_SRR9716289 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716289.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:51:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716289.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,153,432
Mapped reads	946,296 / 82.04%
Unmapped reads	207,136 / 17.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,129 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	18,904 / 1.64%
Duplication rate	1.4%
Clipped reads	947,103 / 82.11%

2.2. ACGT Content

Number/percentage of A's	12,815,835 / 24.69%
Number/percentage of C's	11,634,952 / 22.41%
Number/percentage of T's	14,799,670 / 28.51%
Number/percentage of G's	12,655,603 / 24.38%
Number/percentage of N's	1,530 / 0%
GC Percentage	46.8%

2.3. Coverage

Mean	0.0168

Standard Deviation	0.156

2.4. Mapping Quality

Mean Mapping Quality	38.81

2.5. Mismatches and indels

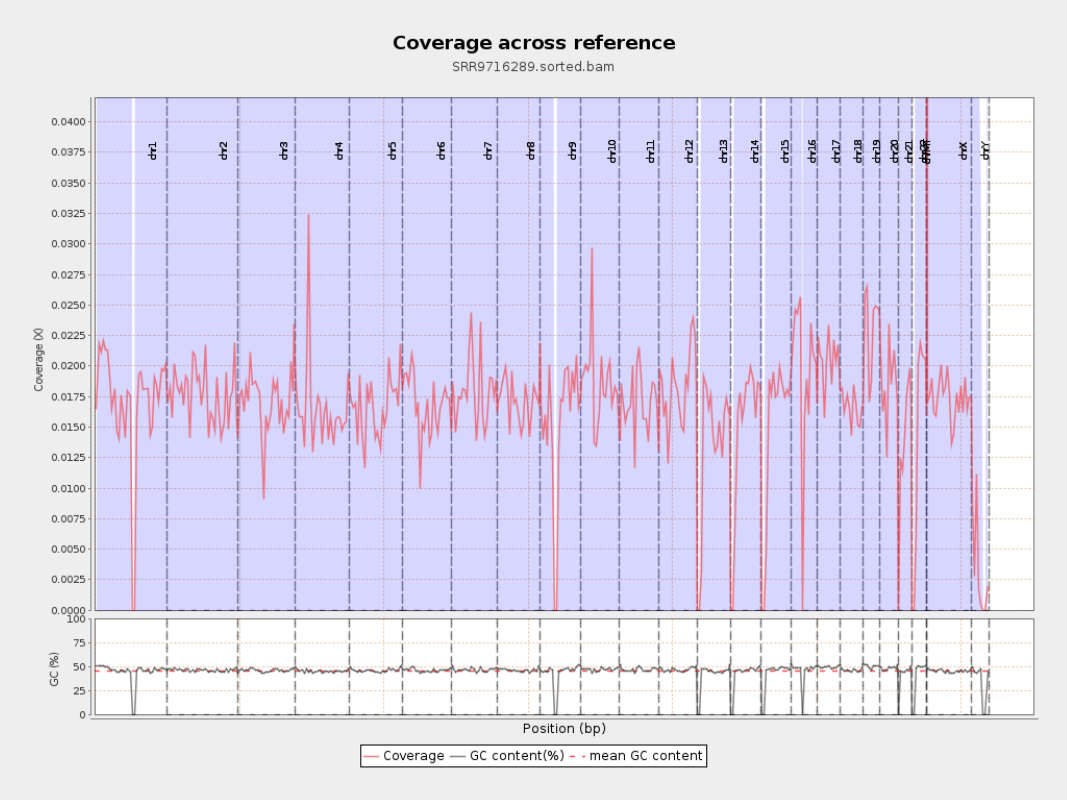
General error rate	0.55%
Mismatches	275,340
Insertions	4,320
Mapped reads with at least one insertion	0.45%
Deletions	8,698
Mapped reads with at least one deletion	0.91%
Homopolymer indels	33.4%

2.6. Chromosome stats

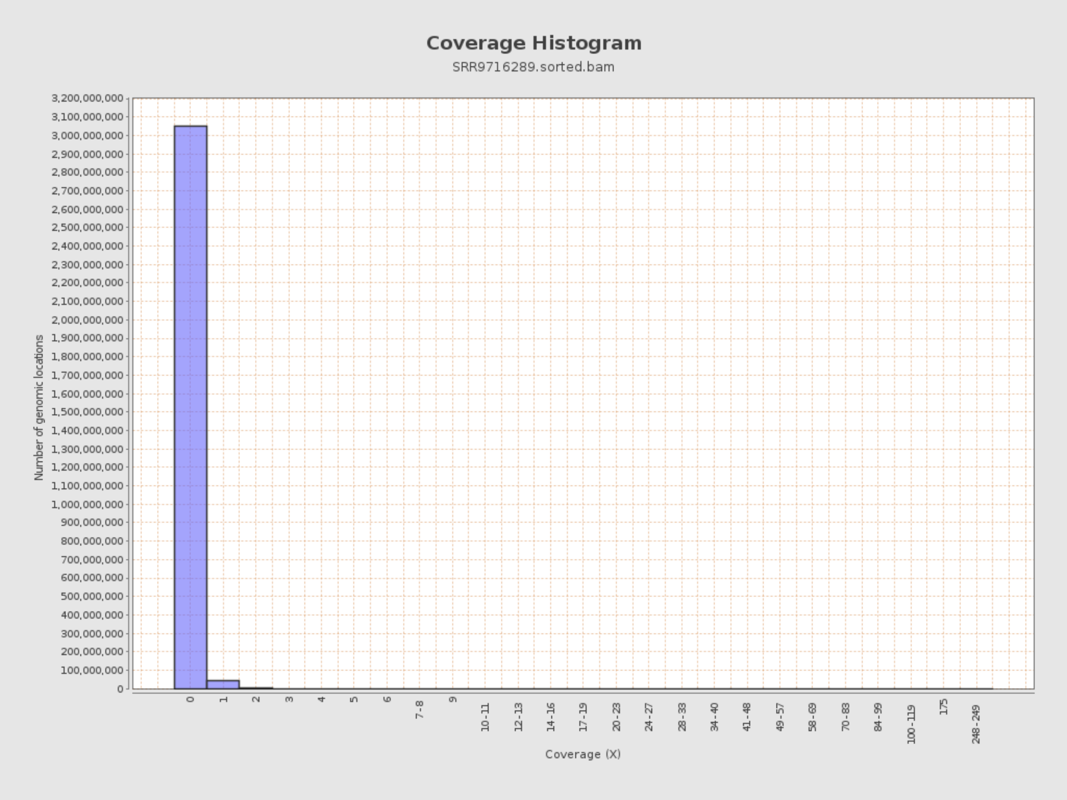
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4229077	0.017	0.1626
chr2	243199373	4298547	0.0177	0.1897
chr3	198022430	3368368	0.017	0.1478
chr4	191154276	3180625	0.0166	0.1561
chr5	180915260	3028147	0.0167	0.1404
chr6	171115067	2872746	0.0168	0.1434
chr7	159138663	2858311	0.018	0.1698

chr8	146364022	2502863	0.0171	0.147
chr9	141213431	2140560	0.0152	0.1397
chr10	135534747	2535608	0.0187	0.1888
chr11	135006516	2317337	0.0172	0.1646
chr12	133851895	2446874	0.0183	0.1464
chr13	115169878	1532045	0.0133	0.1255
chr14	107349540	1578950	0.0147	0.134
chr15	102531392	1506730	0.0147	0.1339
chr16	90354753	1748692	0.0194	0.1607
chr17	81195210	1662838	0.0205	0.1603
chr18	78077248	1296542	0.0166	0.1742
chr19	59128983	1355229	0.0229	0.1868
chr20	63025520	1168923	0.0185	0.1532
chr21	48129895	669461	0.0139	0.143
chr22	51304566	725806	0.0141	0.1314
chrMT	16571	14759	0.8907	1.1682
chrX	155270560	2696570	0.0174	0.1533
chrY	59373566	186525	0.0031	0.1

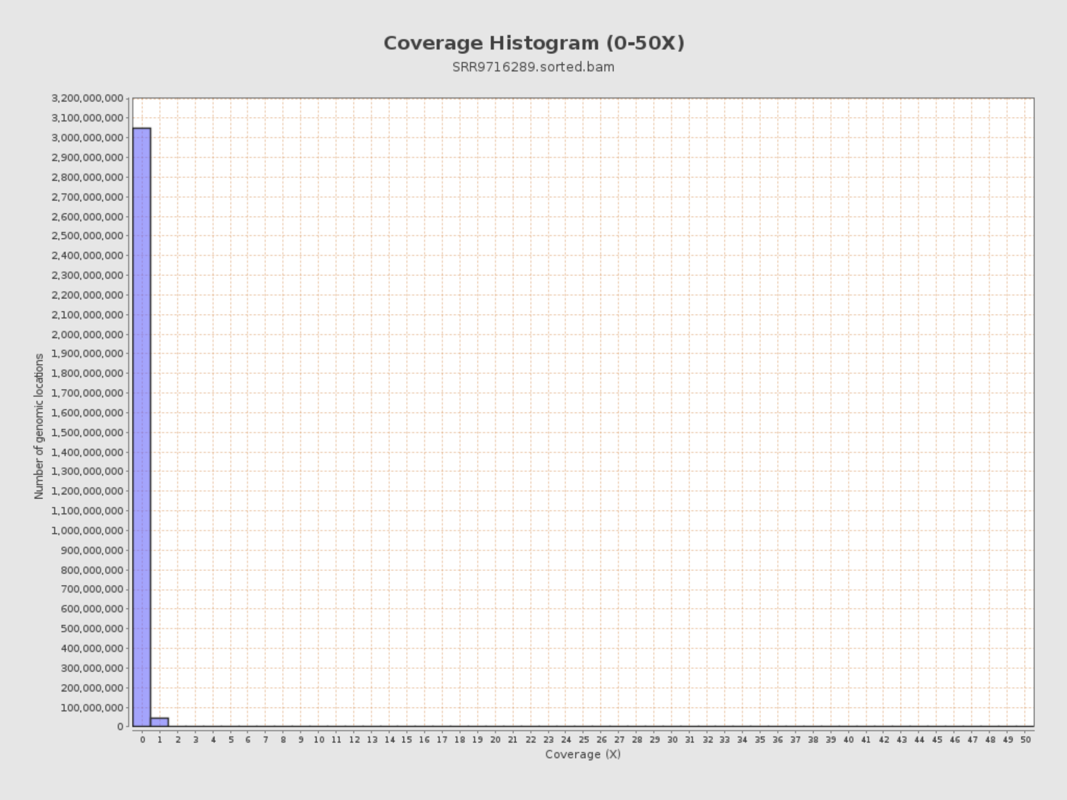
3. Results : Coverage across reference



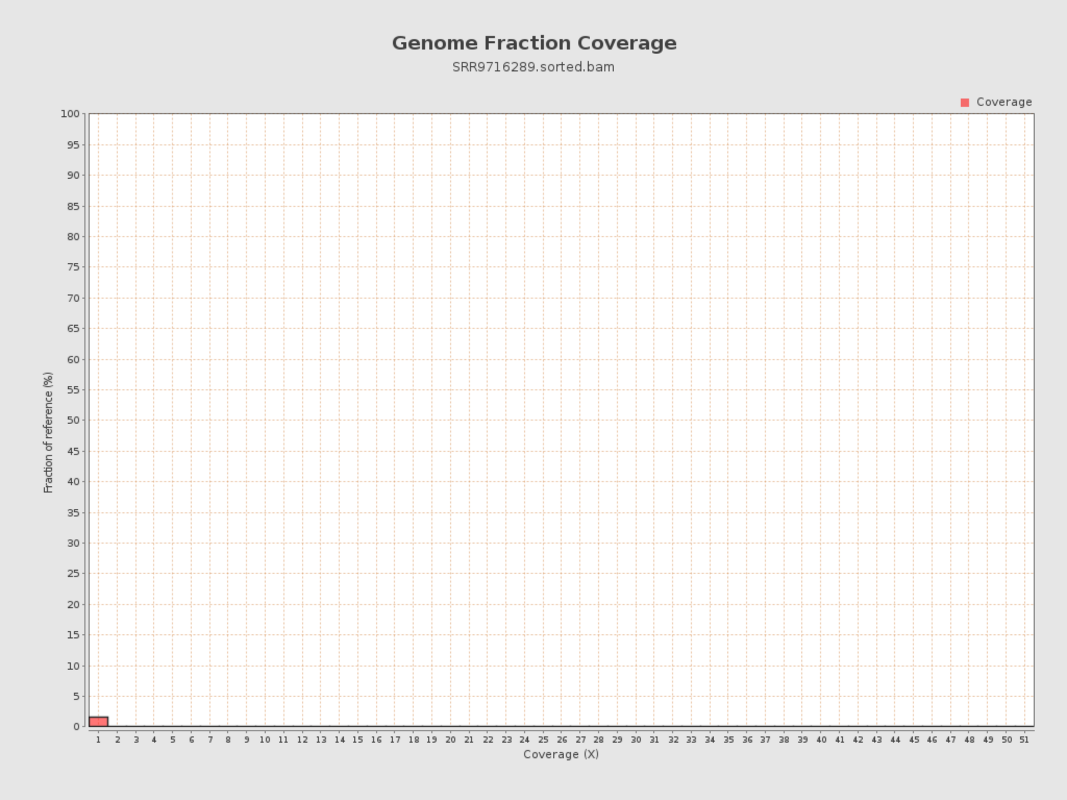
4. Results : Coverage Histogram



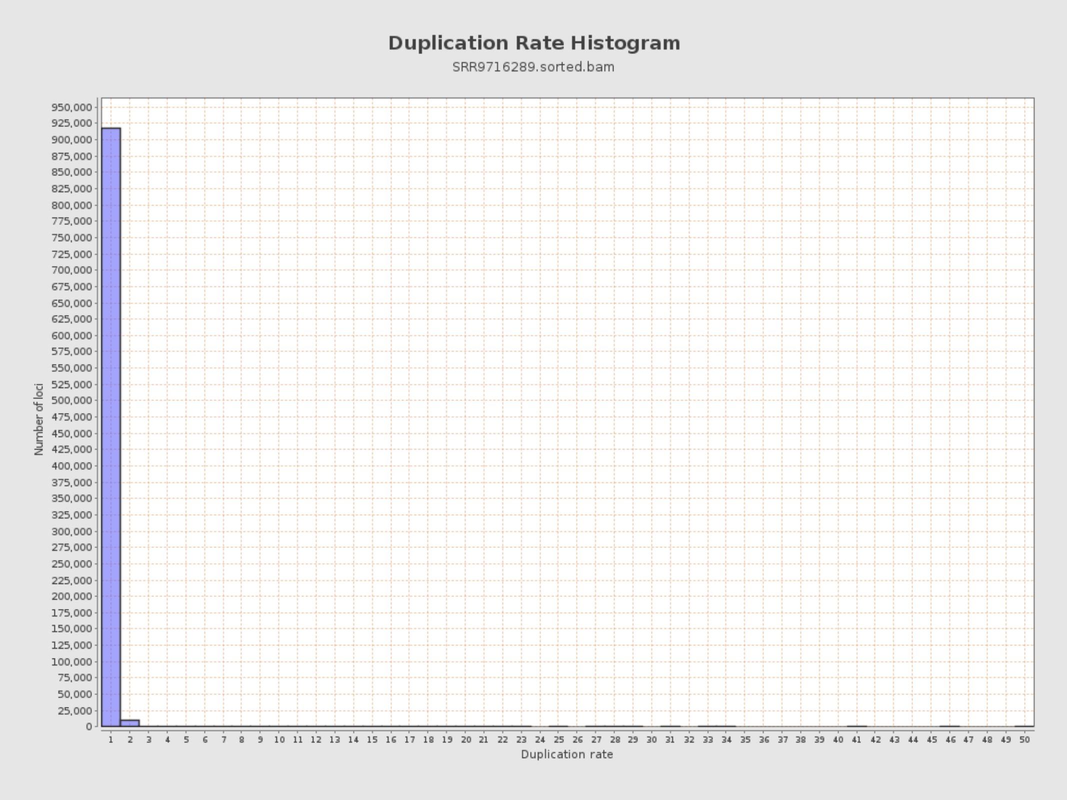
5. Results : Coverage Histogram (0-50X)



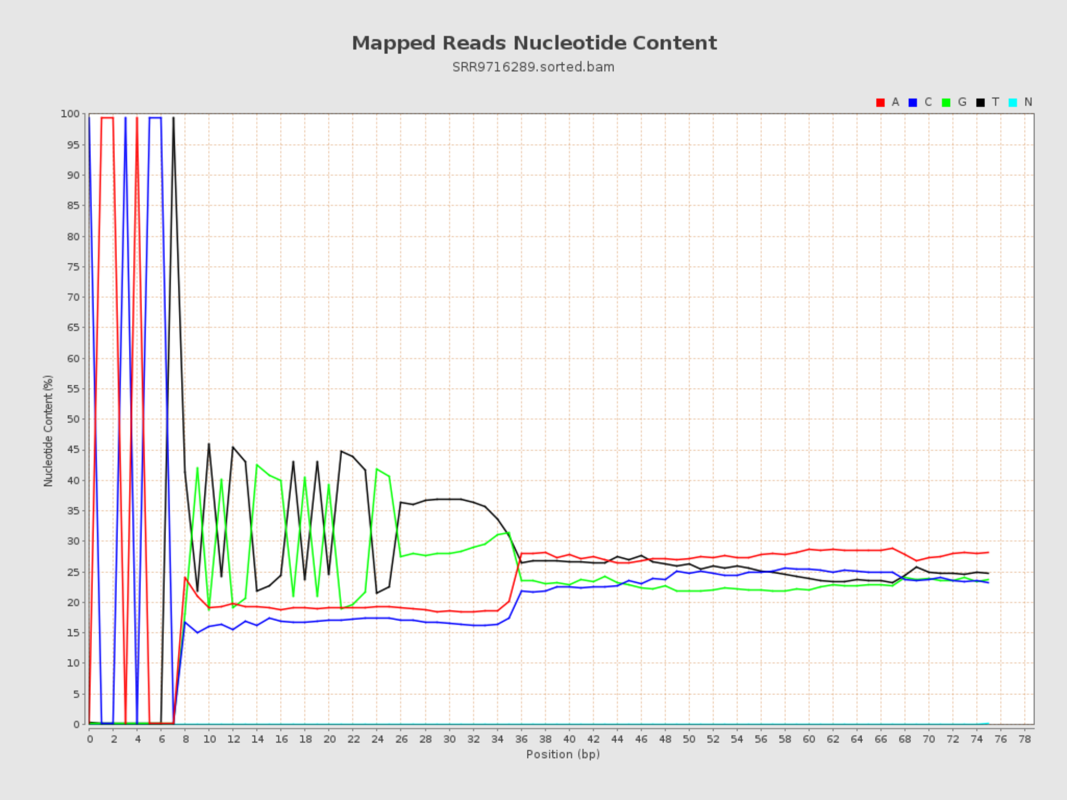
6. Results : Genome Fraction Coverage



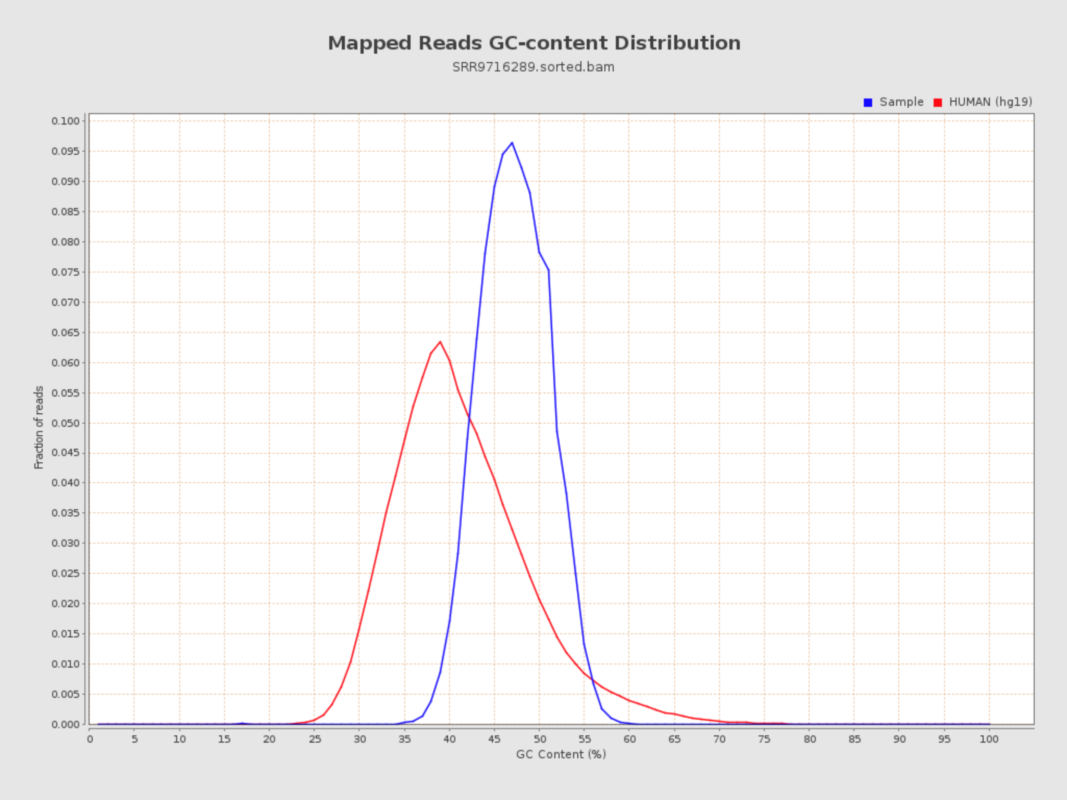
7. Results : Duplication Rate Histogram



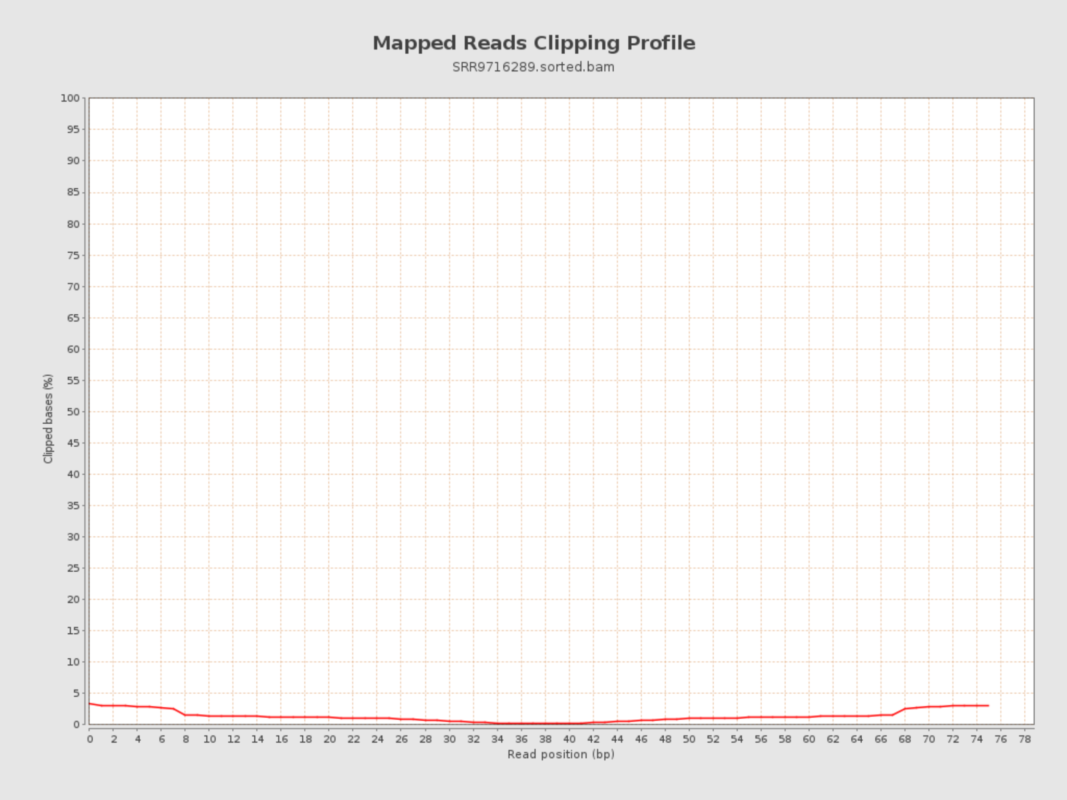
8. Results : Mapped Reads Nucleotide Content



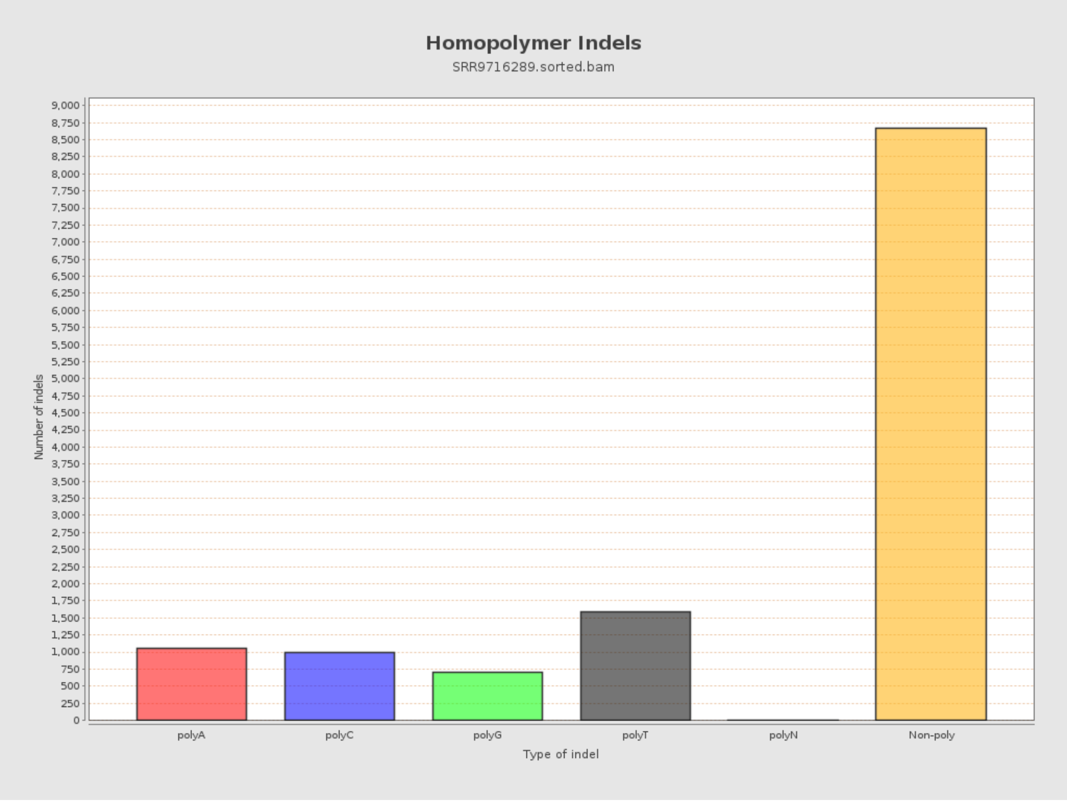
9. Results : Mapped Reads GC-content Distribution



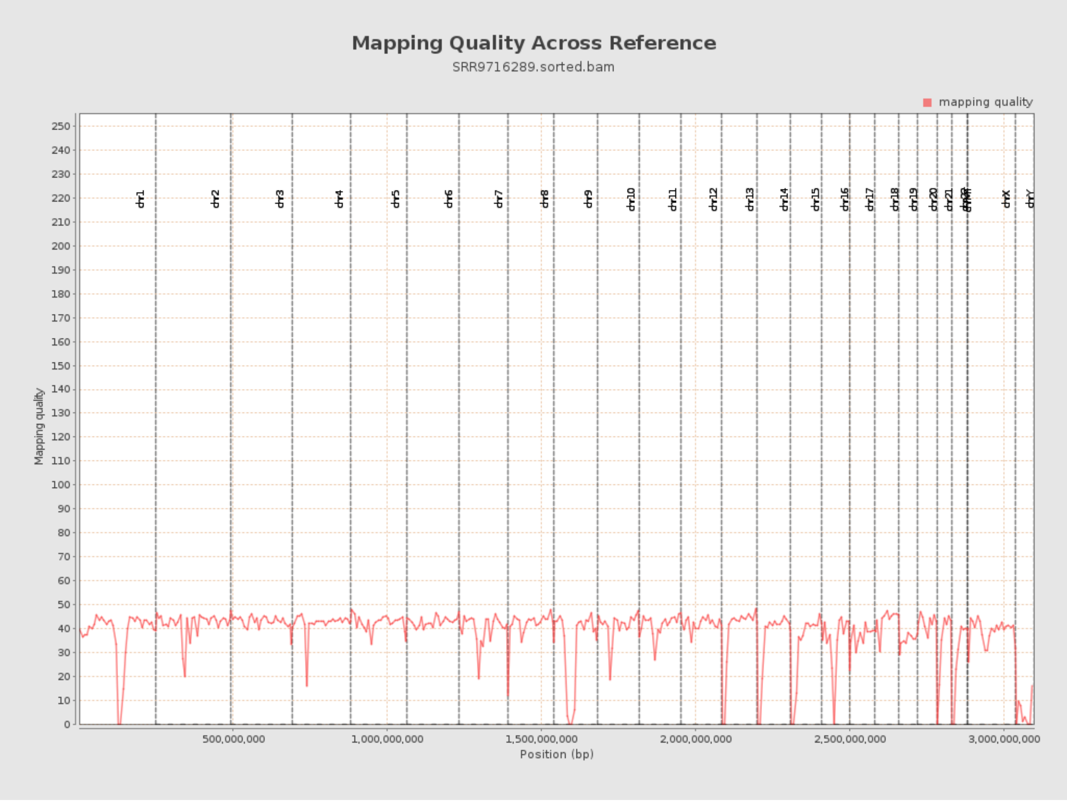
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram