Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 00:31:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716211.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_SRR9716211 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716211.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 00:31:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716211.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,357,344
Mapped reads	5,796,255 / 91.17%
Unmapped reads	561,089 / 8.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	137,601 / 2.16%
Read min/max/mean length	30 / 101 / 101.78
Duplicated reads (estimated)	416,015 / 6.54%
Duplication rate	5.26%
Clipped reads	5,931,357 / 93.3%

2.2. ACGT Content

Number/percentage of A's	111,552,306 / 26.34%
Number/percentage of C's	89,838,100 / 21.21%
Number/percentage of T's	123,260,966 / 29.1%
Number/percentage of G's	98,808,844 / 23.33%
Number/percentage of N's	49,445 / 0.01%
GC Percentage	44.54%

2.3. Coverage

Mean	0.1369

Standard Deviation	0.9087

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

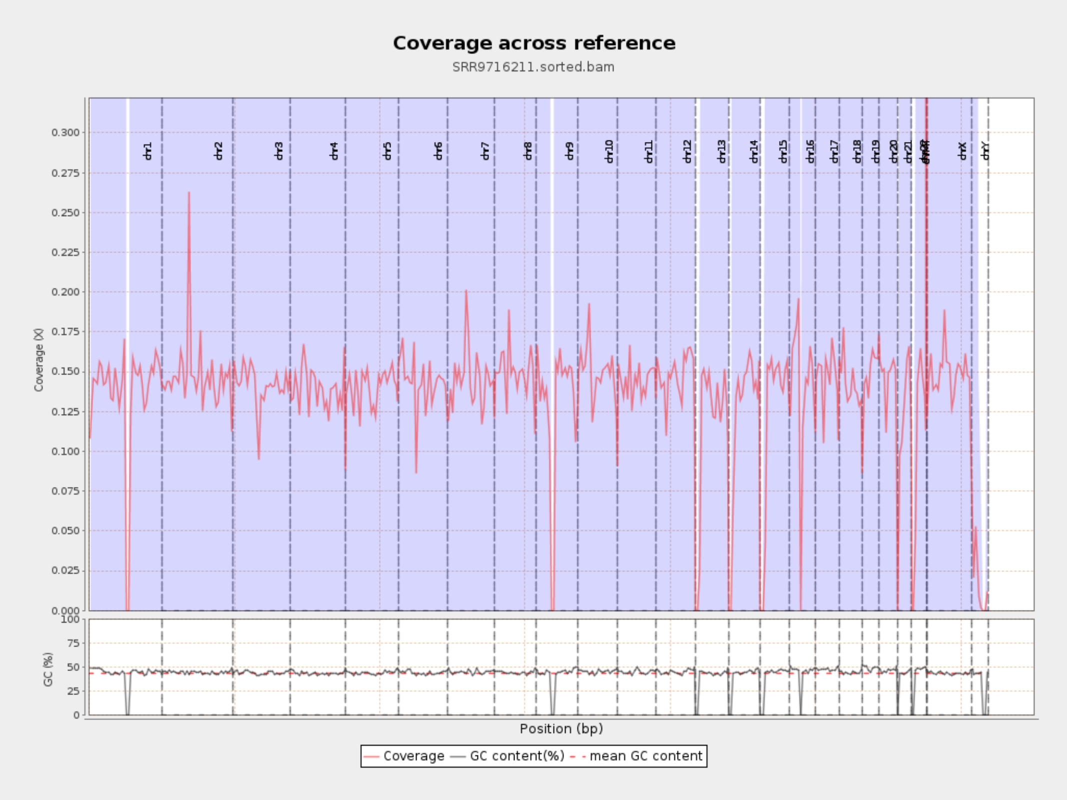
General error rate	0.75%
Mismatches	3,119,840
Insertions	31,415
Mapped reads with at least one insertion	0.54%
Deletions	79,614
Mapped reads with at least one deletion	1.36%
Homopolymer indels	40.46%

2.6. Chromosome stats

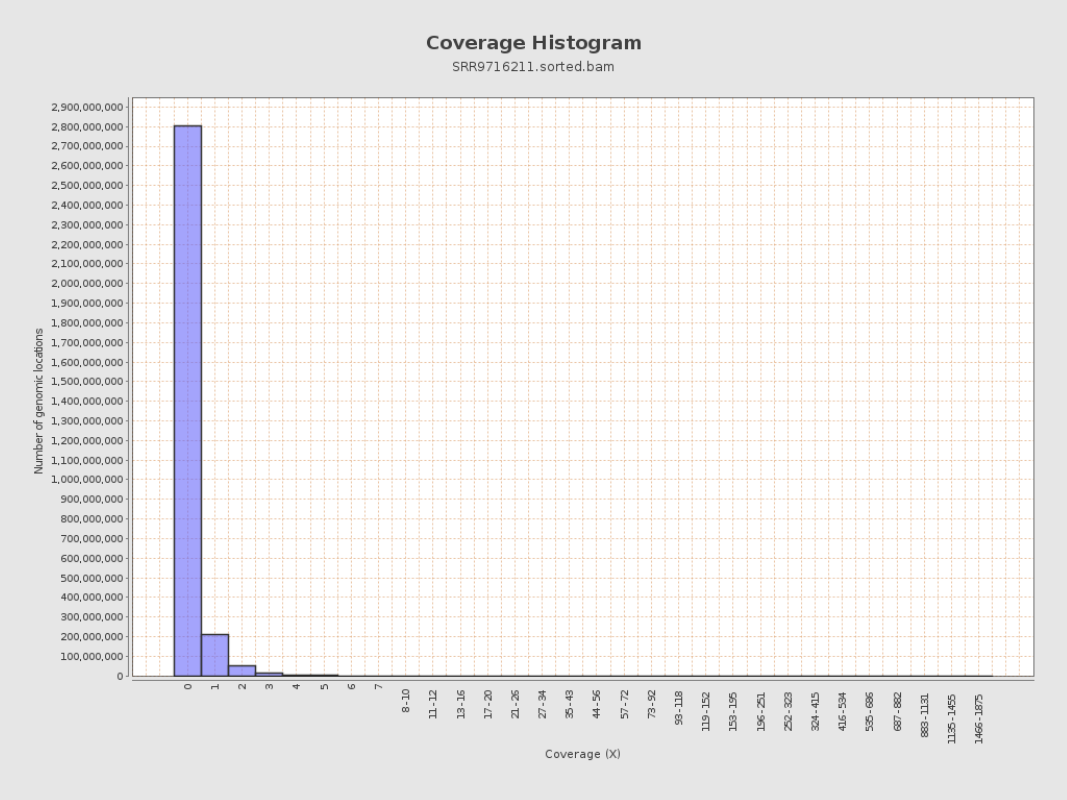
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33839066	0.1358	1.0905
chr2	243199373	36033620	0.1482	1.4567
chr3	198022430	27996117	0.1414	0.5171
chr4	191154276	26578264	0.139	0.5772
chr5	180915260	25352640	0.1401	0.5263
chr6	171115067	24495296	0.1432	0.6543
chr7	159138663	23184503	0.1457	1.2041

chr8	146364022	21921699	0.1498	1.2377
chr9	141213431	17920031	0.1269	0.9856
chr10	135534747	20374340	0.1503	0.8555
chr11	135006516	19383970	0.1436	1.0128
chr12	133851895	19725630	0.1474	0.5482
chr13	115169878	13097893	0.1137	0.4657
chr14	107349540	12876453	0.1199	0.6336
chr15	102531392	12316621	0.1201	0.4903
chr16	90354753	12730605	0.1409	0.6198
chr17	81195210	11800979	0.1453	0.6218
chr18	78077248	11206312	0.1435	1.8448
chr19	59128983	8804829	0.1489	0.9822
chr20	63025520	9111049	0.1446	0.5687
chr21	48129895	5639254	0.1172	0.5393
chr22	51304566	5126825	0.0999	0.4489
chrMT	16571	75376	4.5487	5.0091
chrX	155270560	23044866	0.1484	0.7872
chrY	59373566	1009778	0.017	0.3978

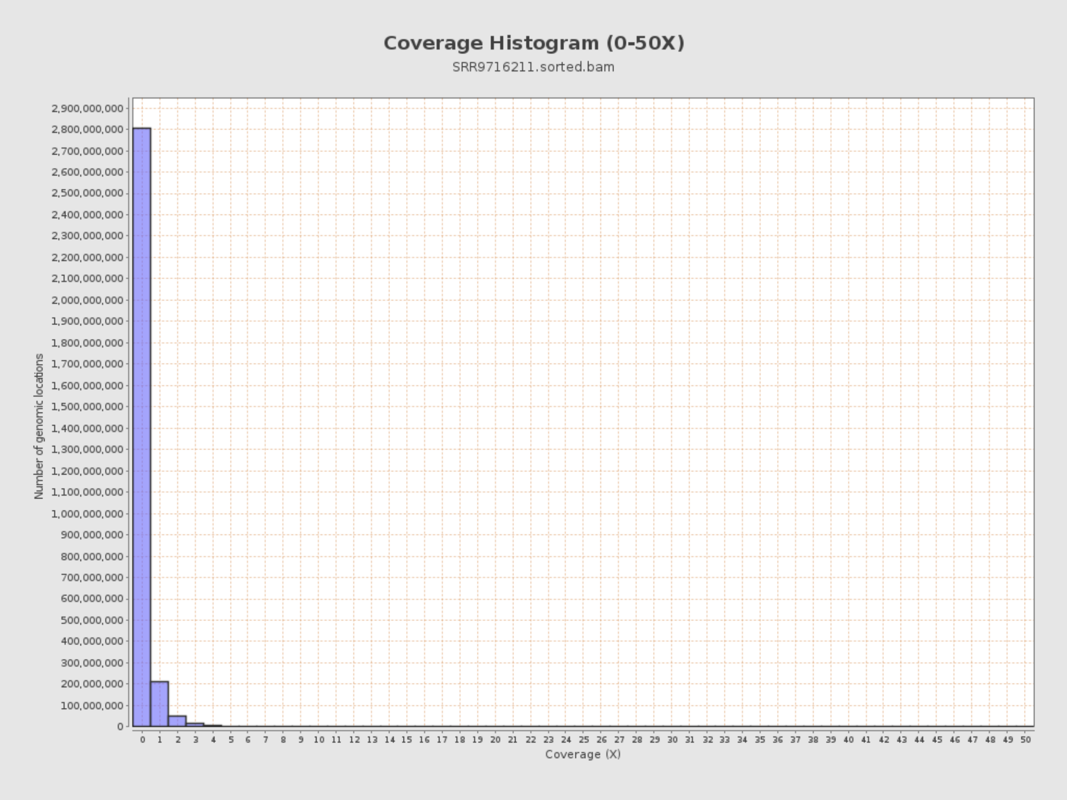
3. Results : Coverage across reference



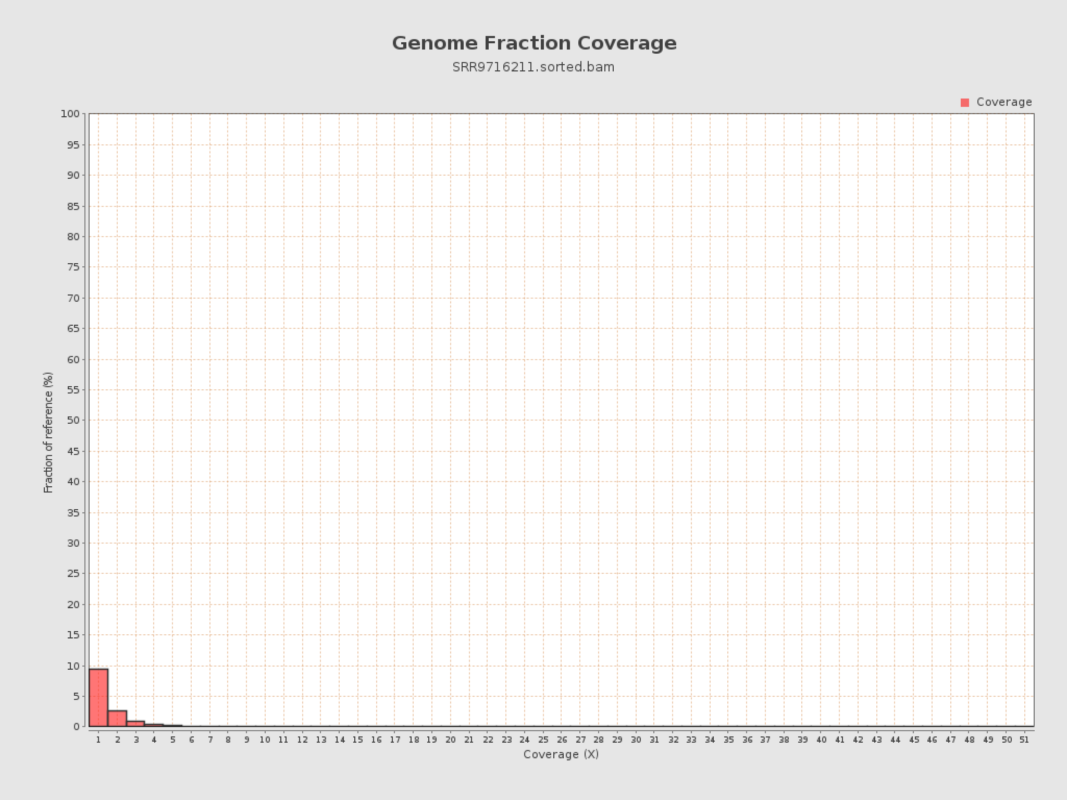
4. Results : Coverage Histogram



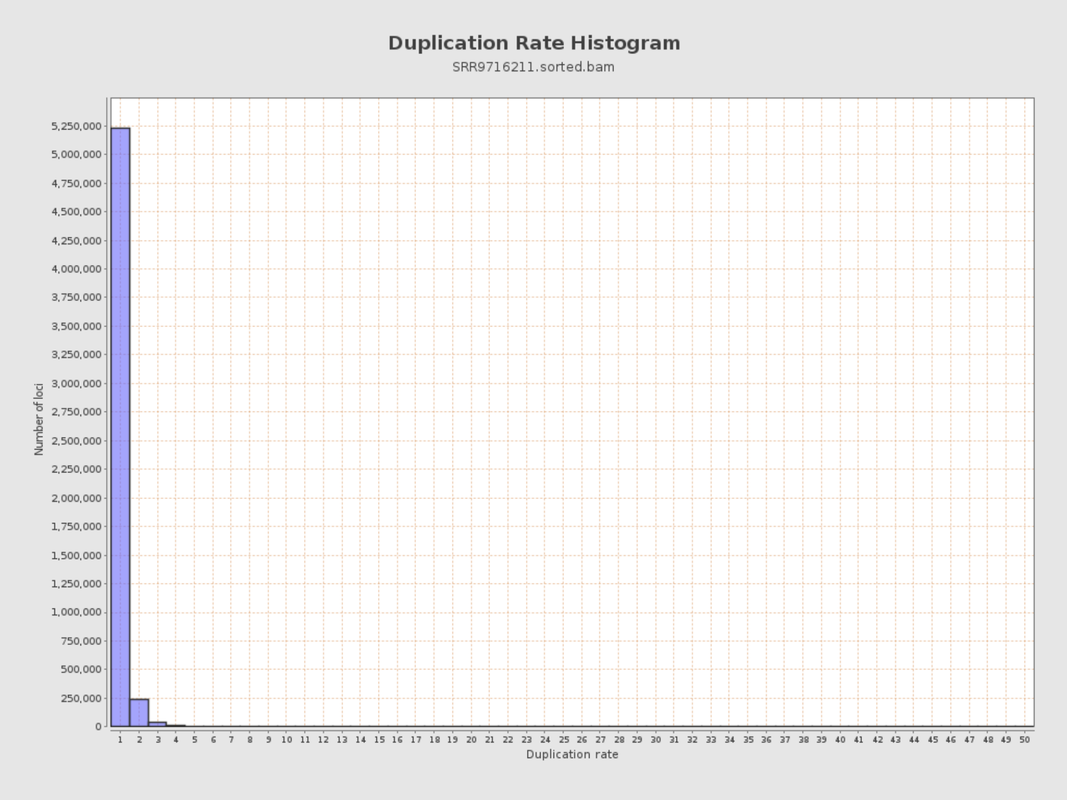
5. Results : Coverage Histogram (0-50X)



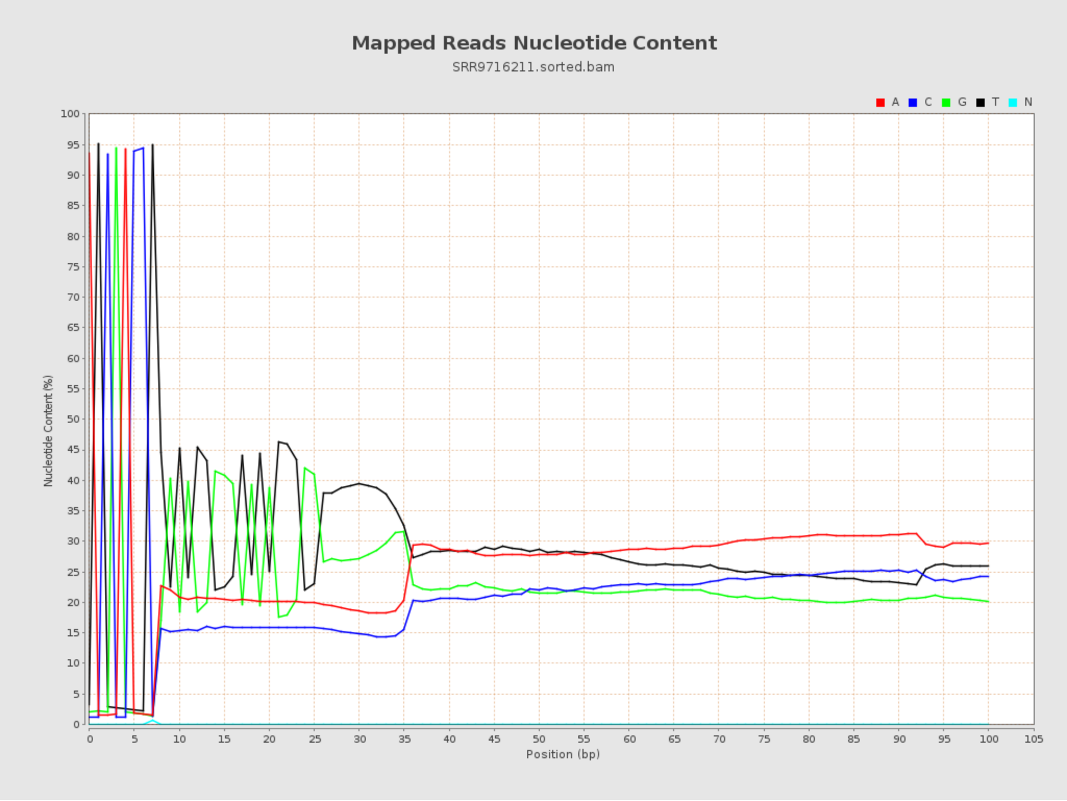
6. Results : Genome Fraction Coverage



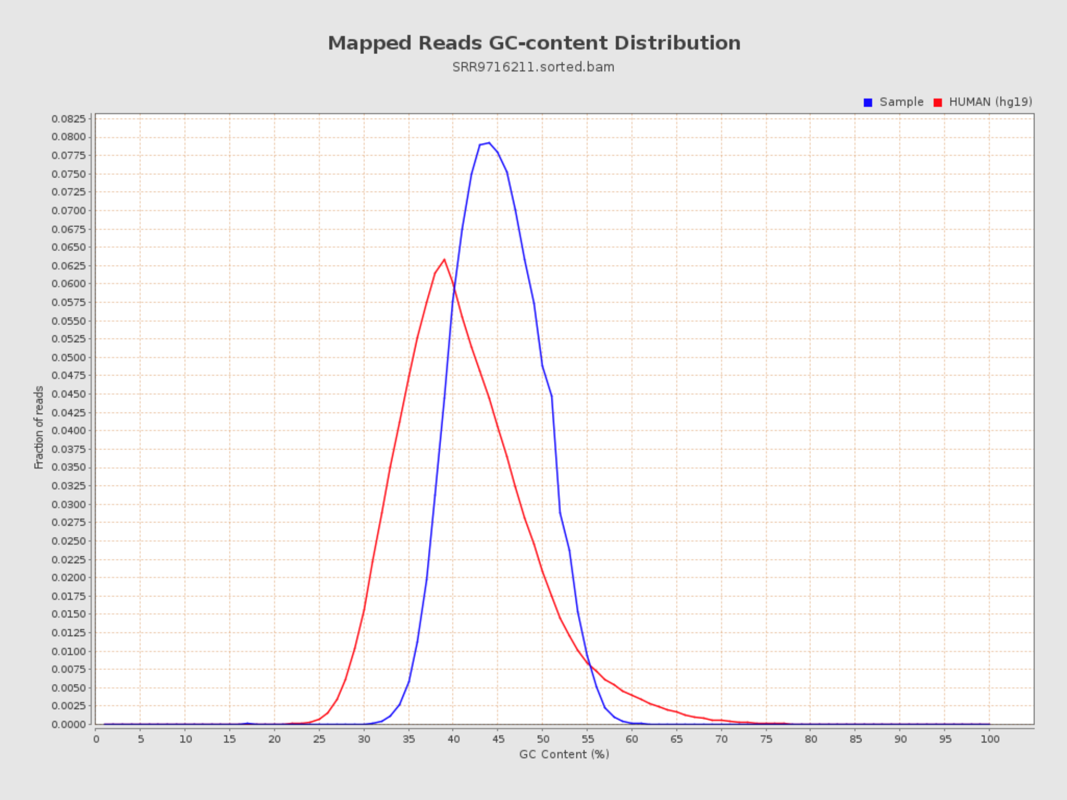
7. Results : Duplication Rate Histogram



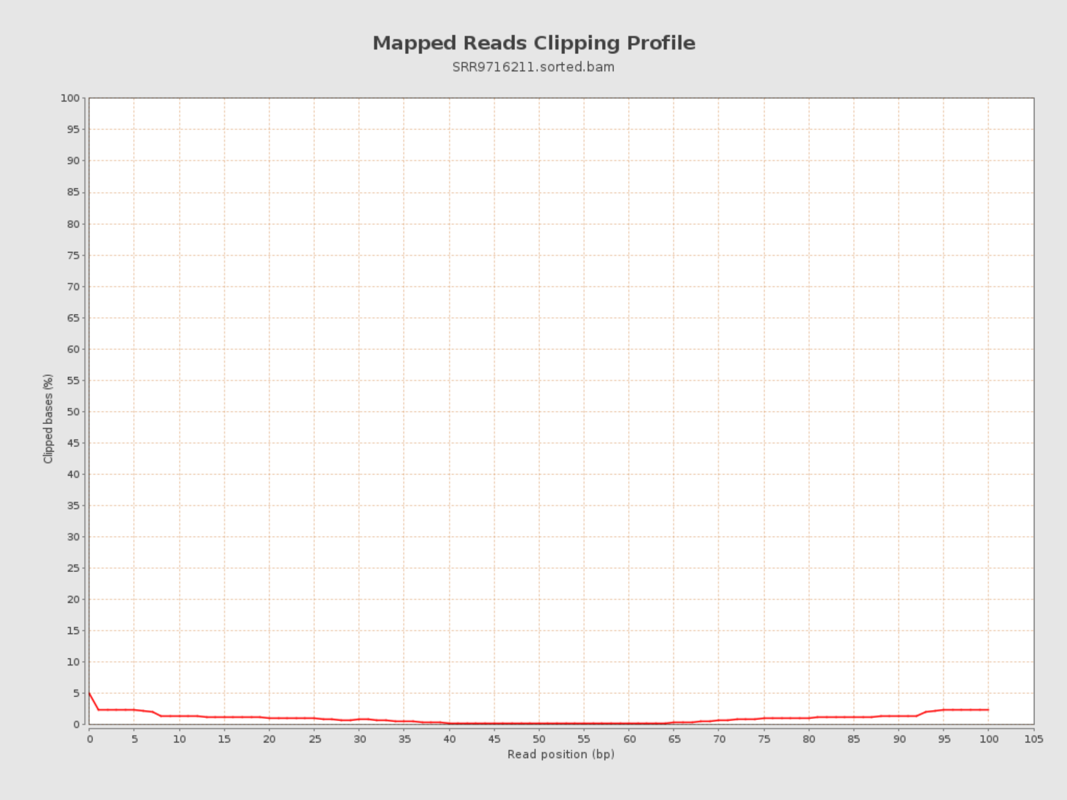
8. Results : Mapped Reads Nucleotide Content



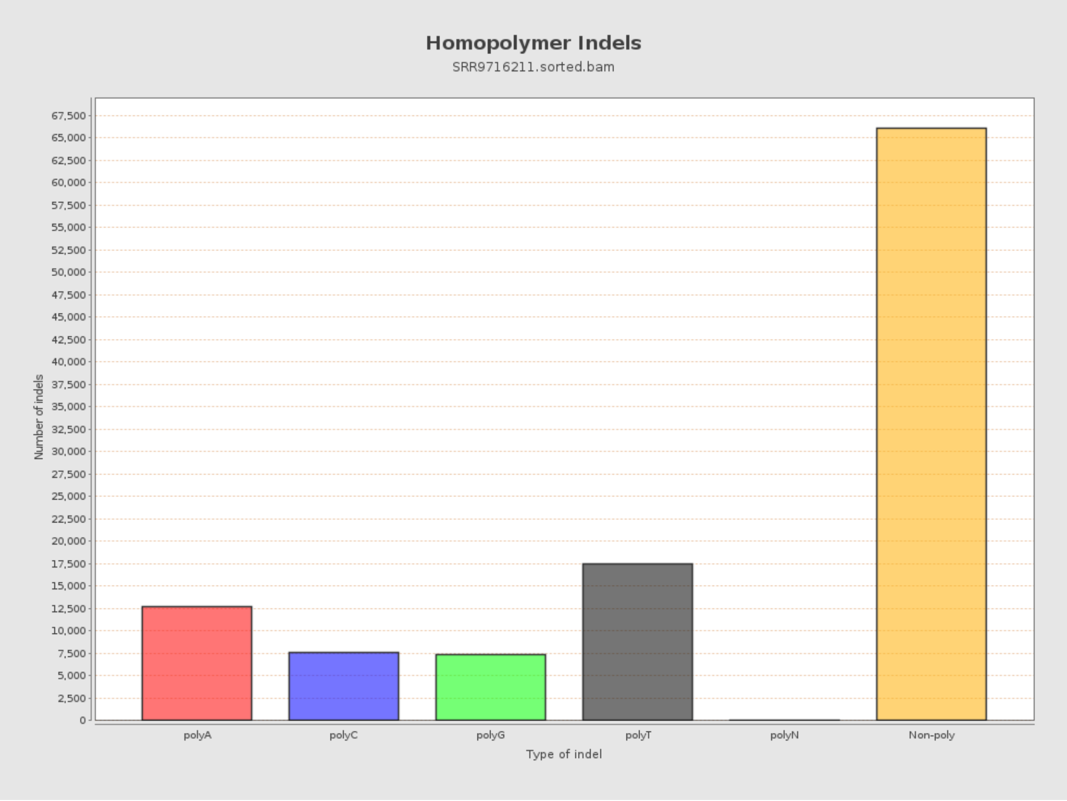
9. Results : Mapped Reads GC-content Distribution



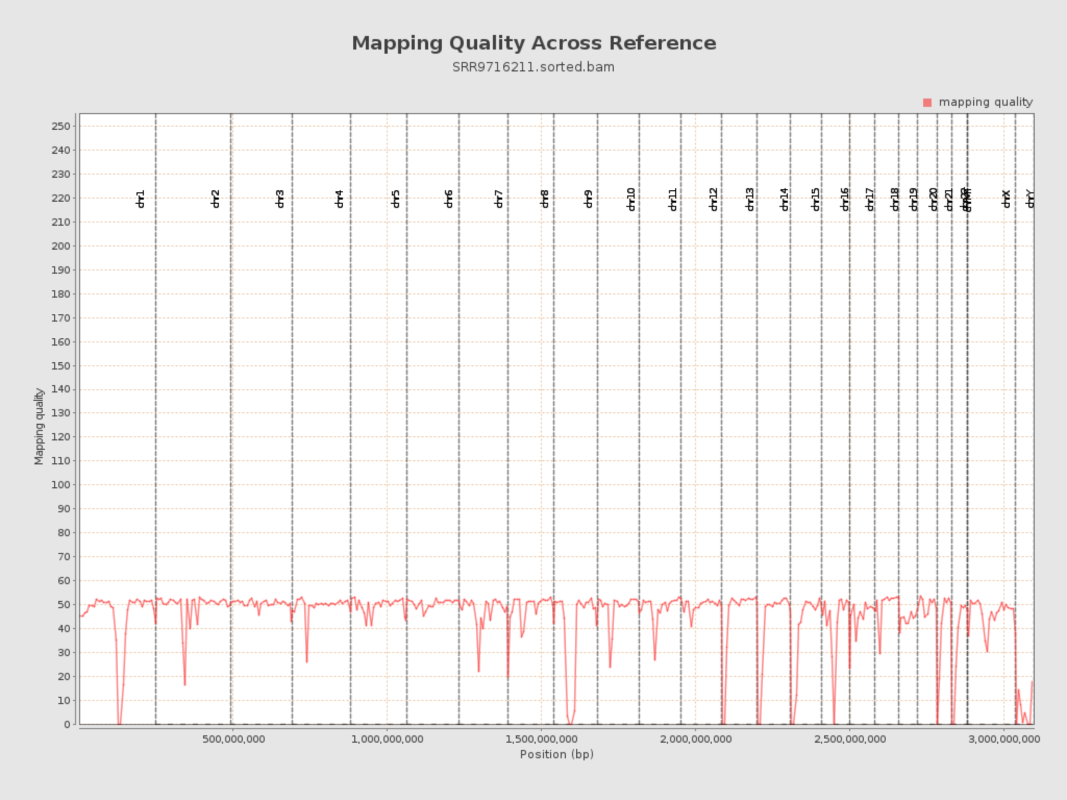
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram