Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:55:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716329.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_SRR9716329 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716329.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:55:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716329.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	490,552
Mapped reads	443,890 / 90.49%
Unmapped reads	46,662 / 9.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,613 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	9,115 / 1.86%
Duplication rate	1.67%
Clipped reads	444,306 / 90.57%

2.2. ACGT Content

Number/percentage of A's	6,531,909 / 25.42%
Number/percentage of C's	4,734,788 / 18.43%
Number/percentage of T's	8,274,092 / 32.2%
Number/percentage of G's	6,151,447 / 23.94%
Number/percentage of N's	405 / 0%
GC Percentage	42.37%

2.3. Coverage

Mean	0.0083

Standard Deviation	0.1091

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

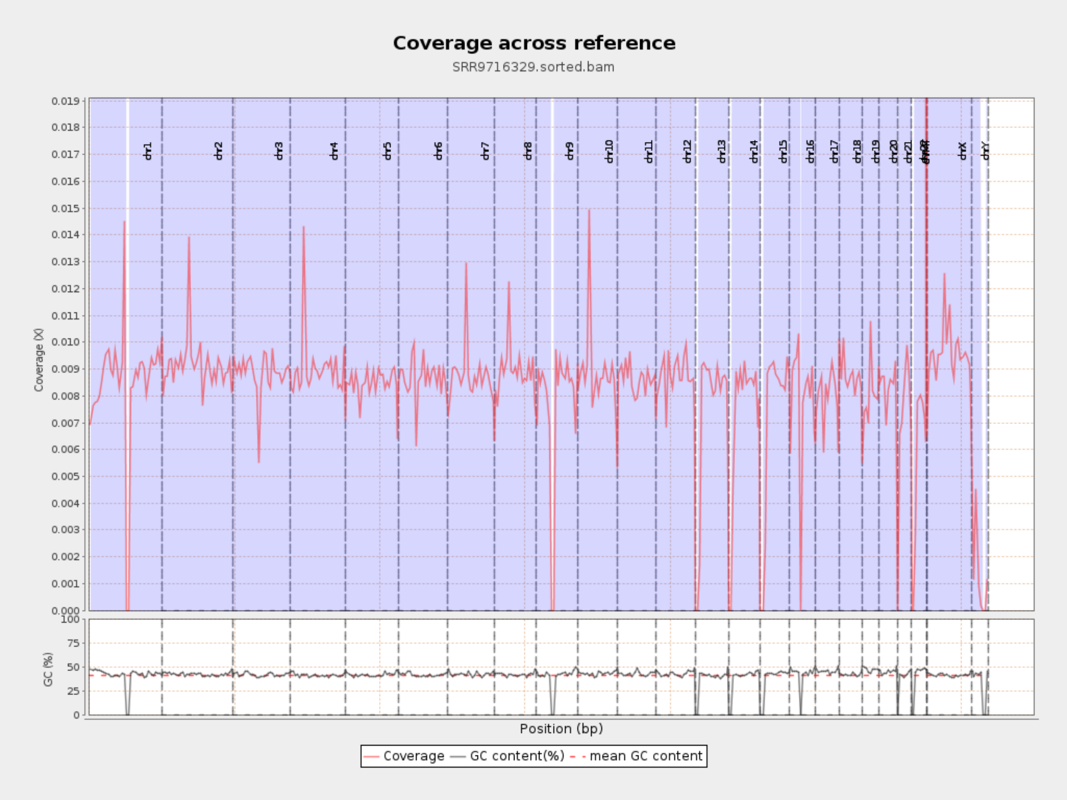
General error rate	0.54%
Mismatches	136,427
Insertions	1,611
Mapped reads with at least one insertion	0.36%
Deletions	4,335
Mapped reads with at least one deletion	0.97%
Homopolymer indels	43.36%

2.6. Chromosome stats

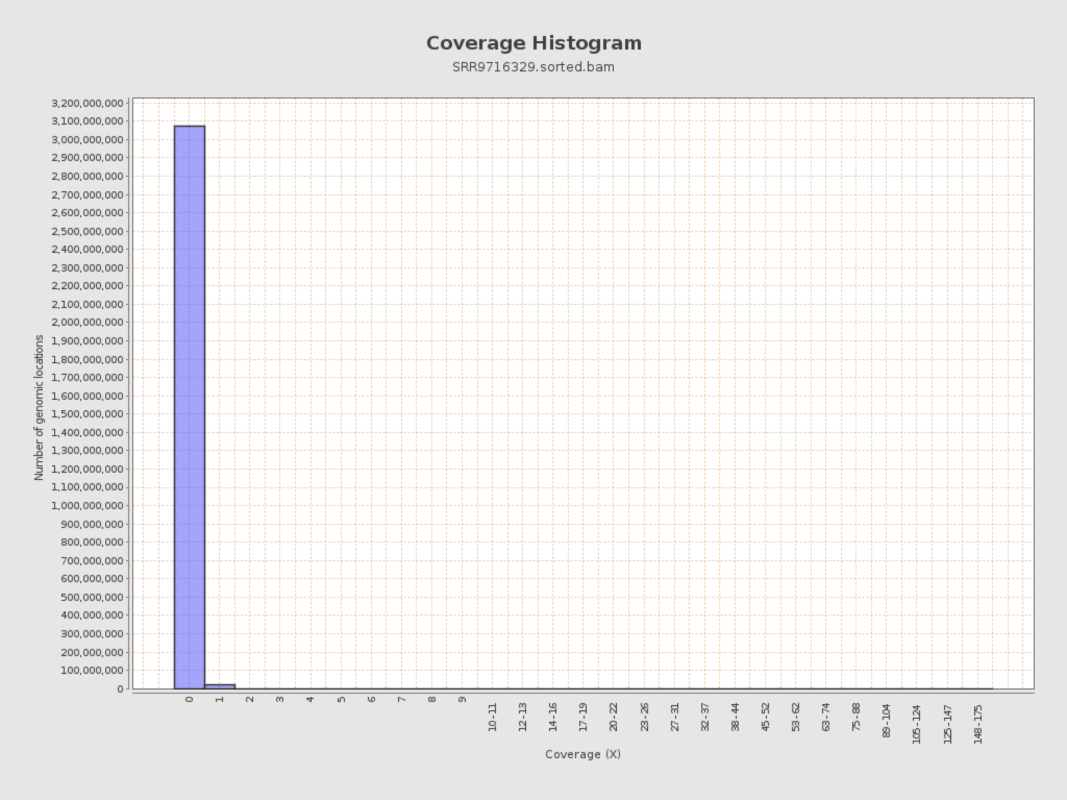
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2096936	0.0084	0.1626
chr2	243199373	2231964	0.0092	0.116
chr3	198022430	1747053	0.0088	0.0969
chr4	191154276	1728386	0.009	0.1013
chr5	180915260	1538054	0.0085	0.0952
chr6	171115067	1485406	0.0087	0.0989
chr7	159138663	1402108	0.0088	0.1187

chr8	146364022	1311694	0.009	0.117
chr9	141213431	1072527	0.0076	0.1003
chr10	135534747	1210591	0.0089	0.1099
chr11	135006516	1159236	0.0086	0.1063
chr12	133851895	1172147	0.0088	0.0974
chr13	115169878	832526	0.0072	0.0875
chr14	107349540	768852	0.0072	0.088
chr15	102531392	727200	0.0071	0.0867
chr16	90354753	701436	0.0078	0.0932
chr17	81195210	645253	0.0079	0.0938
chr18	78077248	687718	0.0088	0.1474
chr19	59128983	474116	0.008	0.1333
chr20	63025520	521510	0.0083	0.0943
chr21	48129895	345824	0.0072	0.0897
chr22	51304566	271870	0.0053	0.0747
chrMT	16571	2989	0.1804	0.4196
chrX	155270560	1484830	0.0096	0.1043
chrY	59373566	79644	0.0013	0.0459

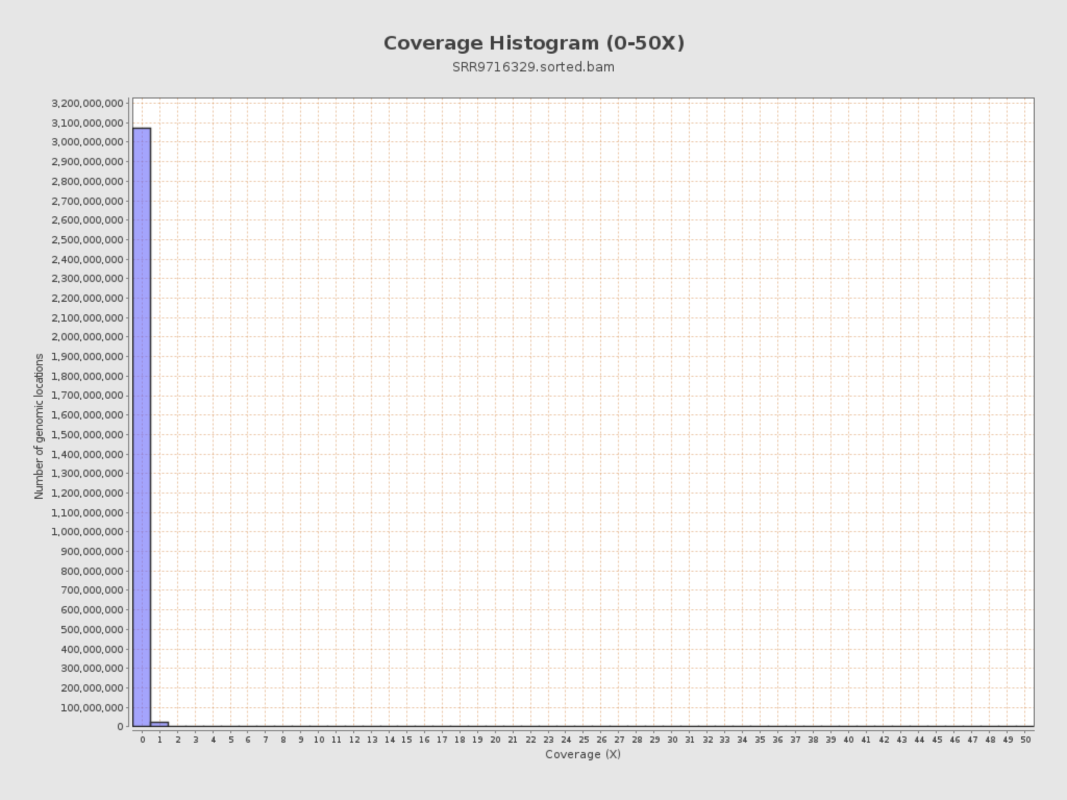
3. Results : Coverage across reference



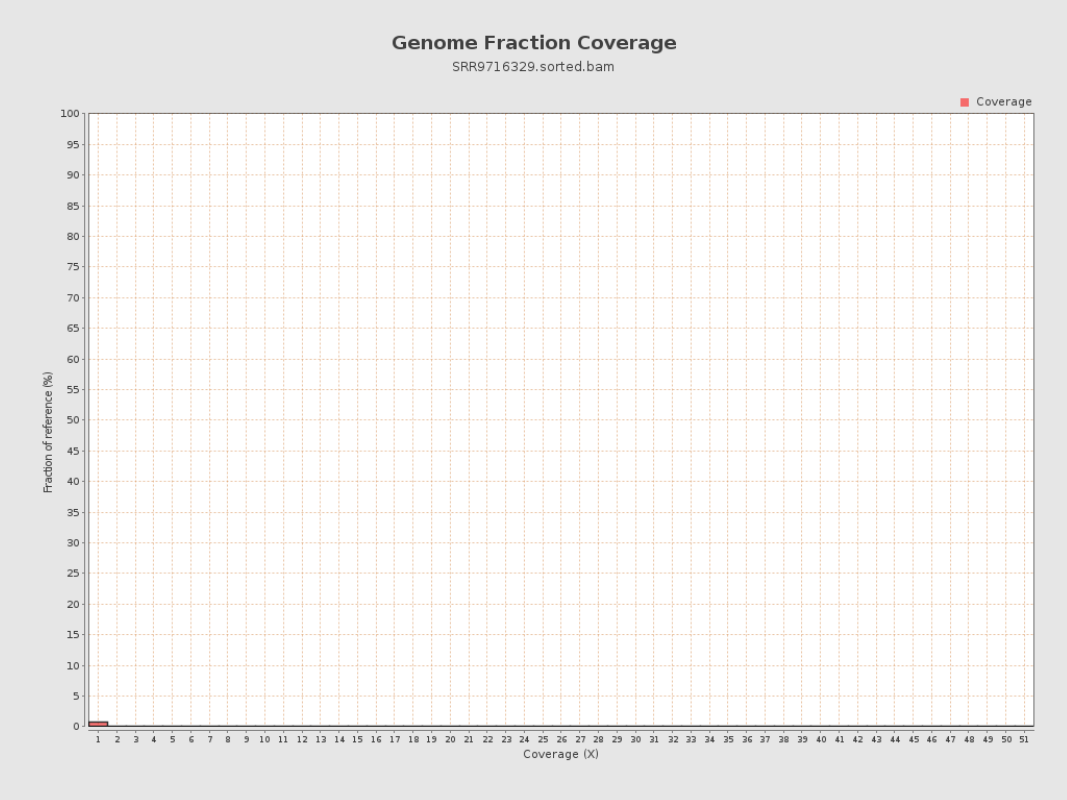
4. Results : Coverage Histogram



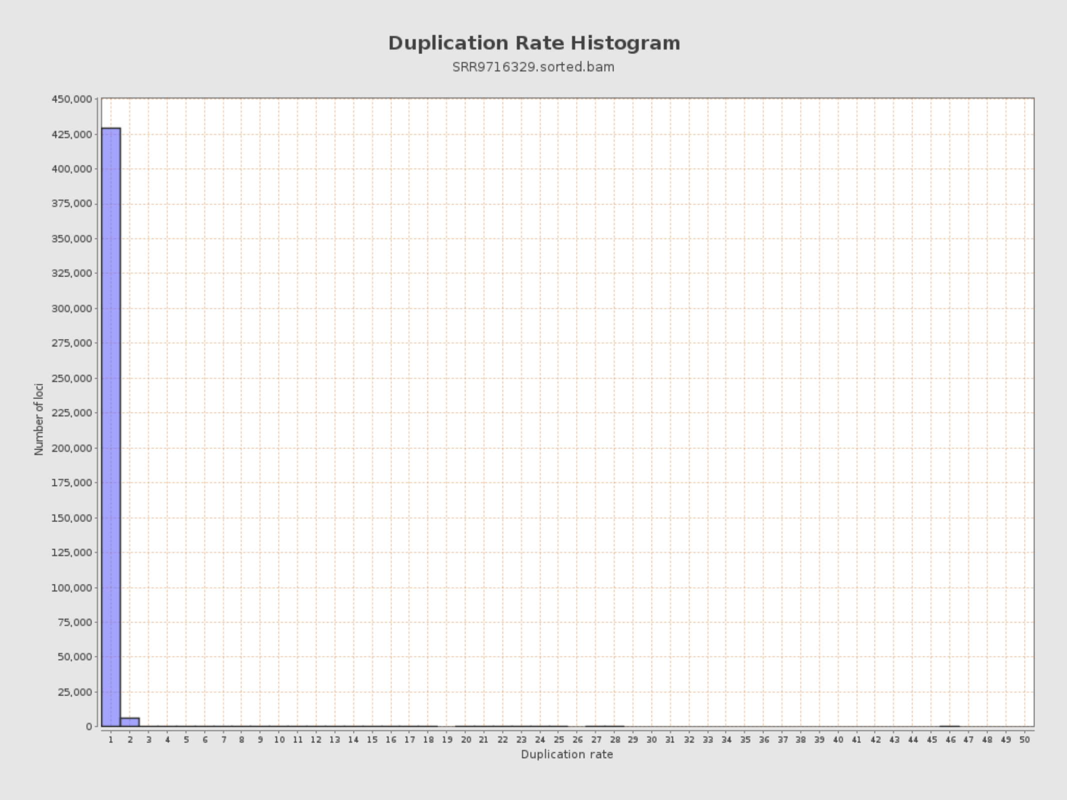
5. Results : Coverage Histogram (0-50X)



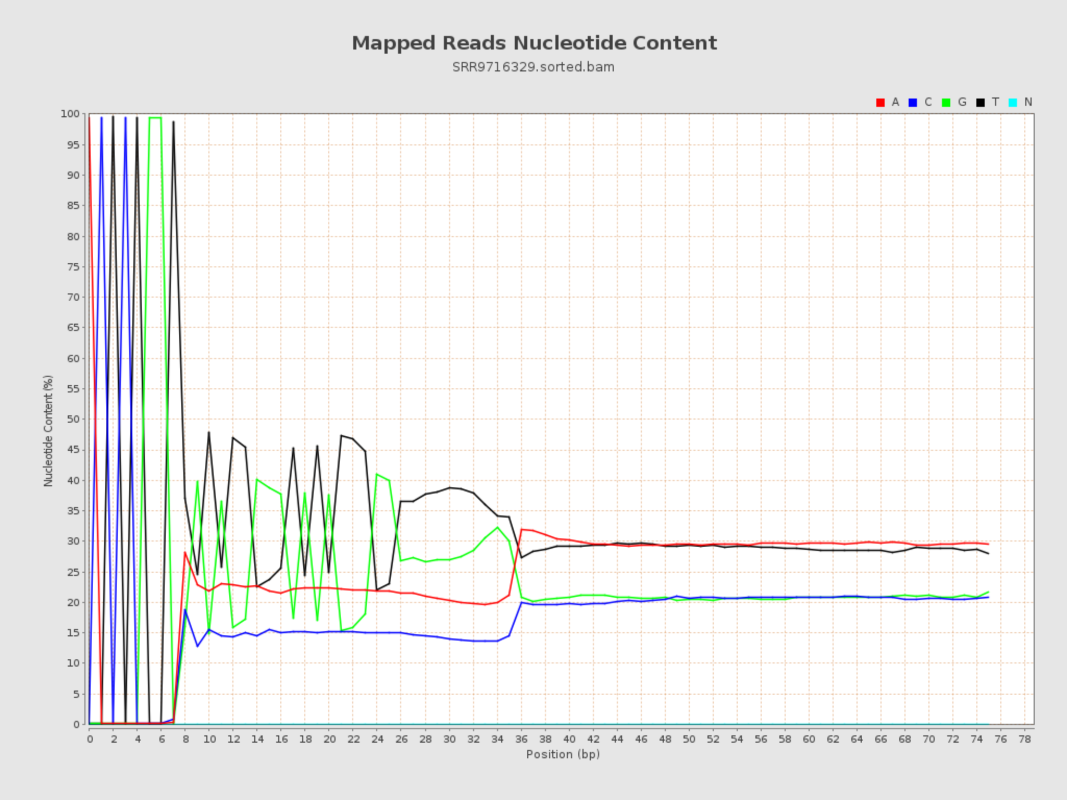
6. Results : Genome Fraction Coverage



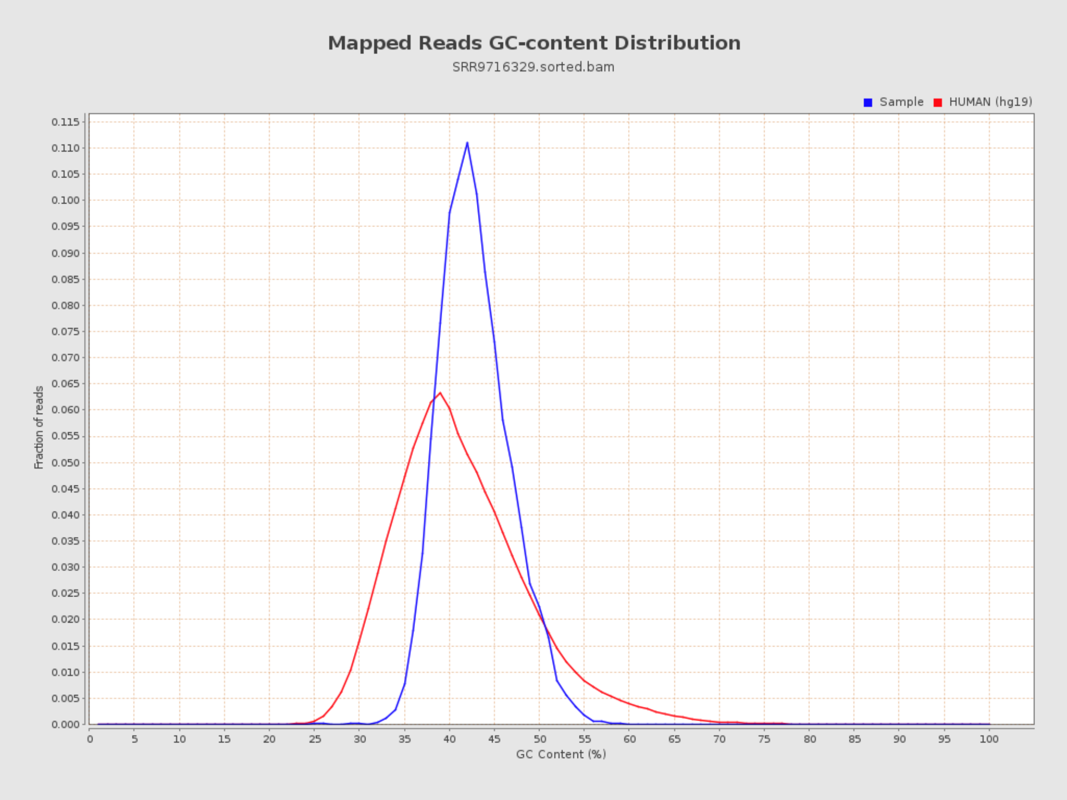
7. Results : Duplication Rate Histogram



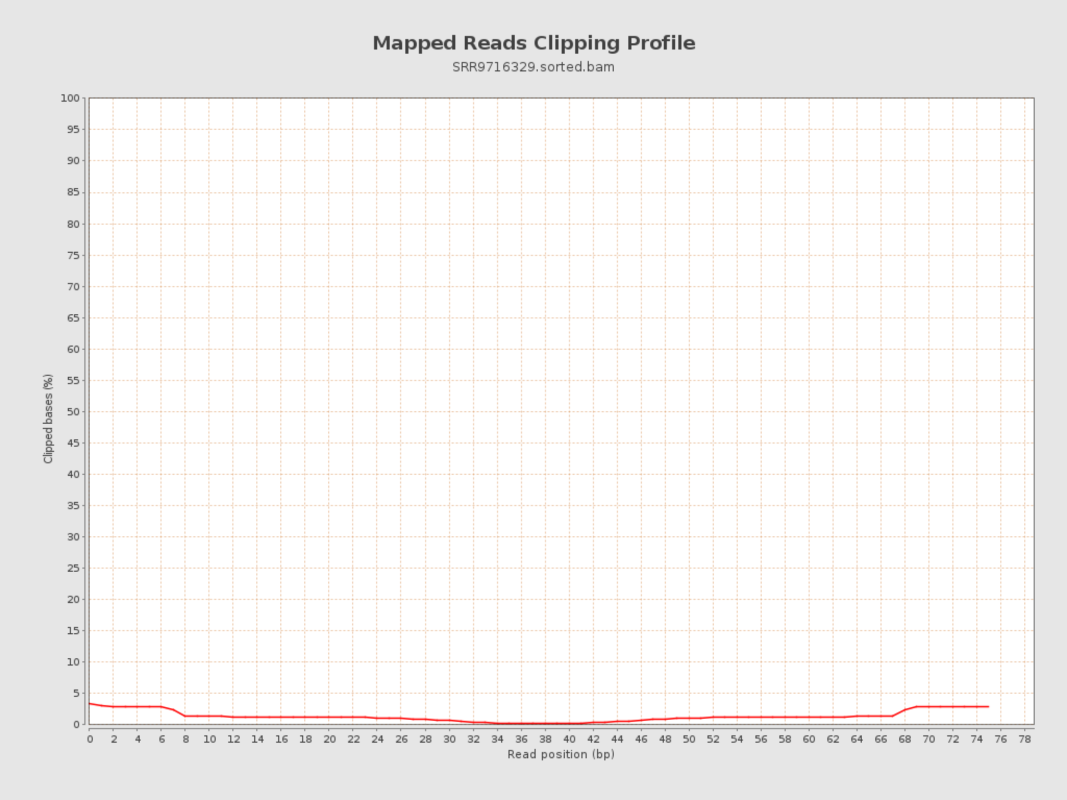
8. Results : Mapped Reads Nucleotide Content



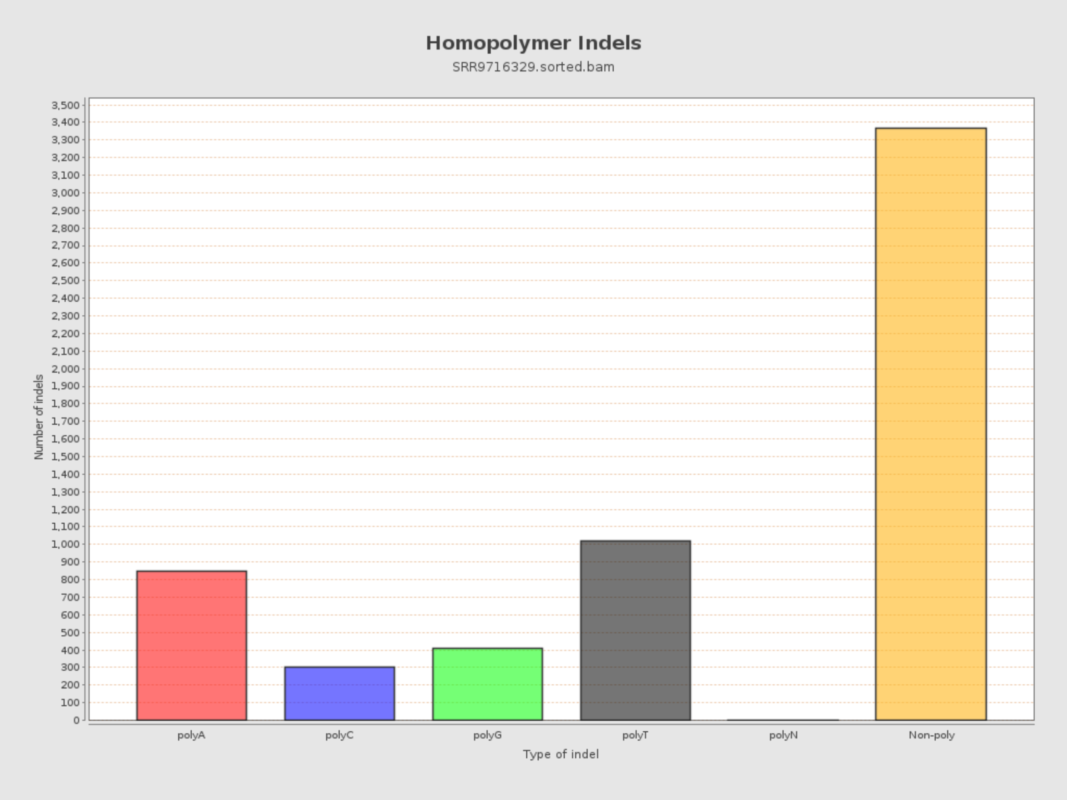
9. Results : Mapped Reads GC-content Distribution



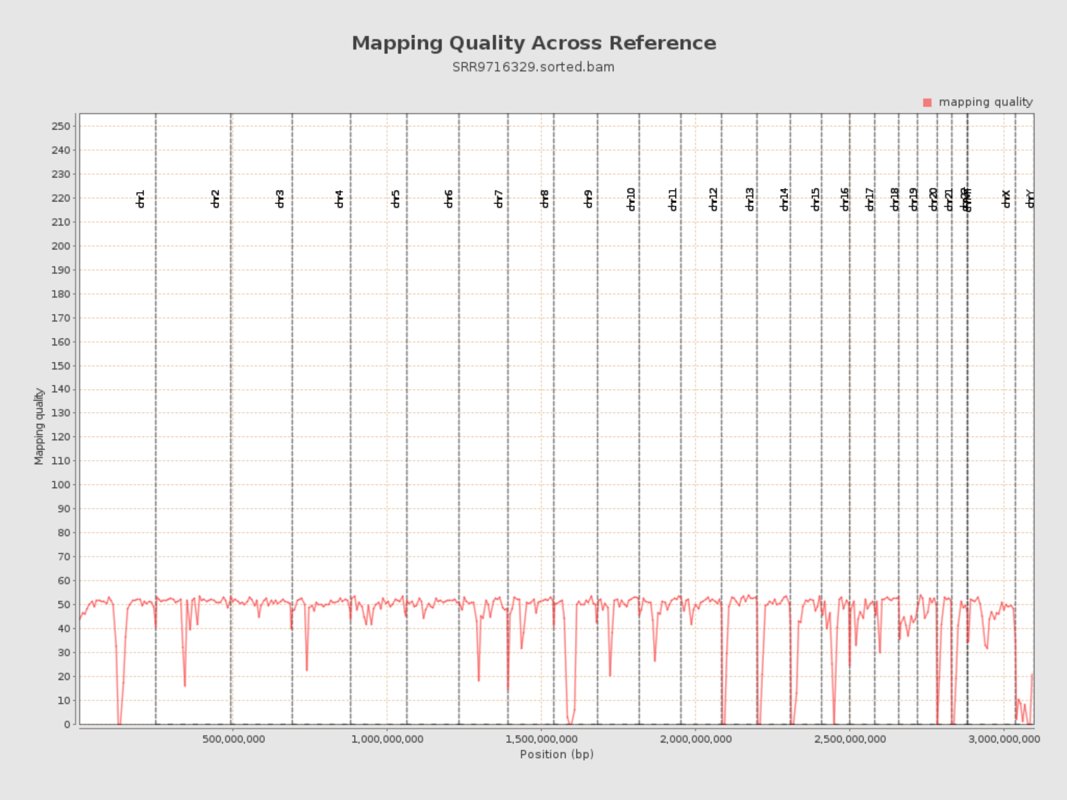
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram