Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:09:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716129.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_SRR9716129 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716129.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:09:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716129.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	603,934
Mapped reads	562,959 / 93.22%
Unmapped reads	40,975 / 6.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,795 / 1.95%
Read min/max/mean length	30 / 101 / 101.7
Duplicated reads (estimated)	11,554 / 1.91%
Duplication rate	1.38%
Clipped reads	573,585 / 94.97%

2.2. ACGT Content

Number/percentage of A's	11,925,229 / 26.71%
Number/percentage of C's	8,966,216 / 20.08%
Number/percentage of T's	13,504,969 / 30.25%
Number/percentage of G's	10,247,881 / 22.95%
Number/percentage of N's	3,232 / 0.01%
GC Percentage	43.04%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1752

2.4. Mapping Quality

Mean Mapping Quality	47.32

2.5. Mismatches and indels

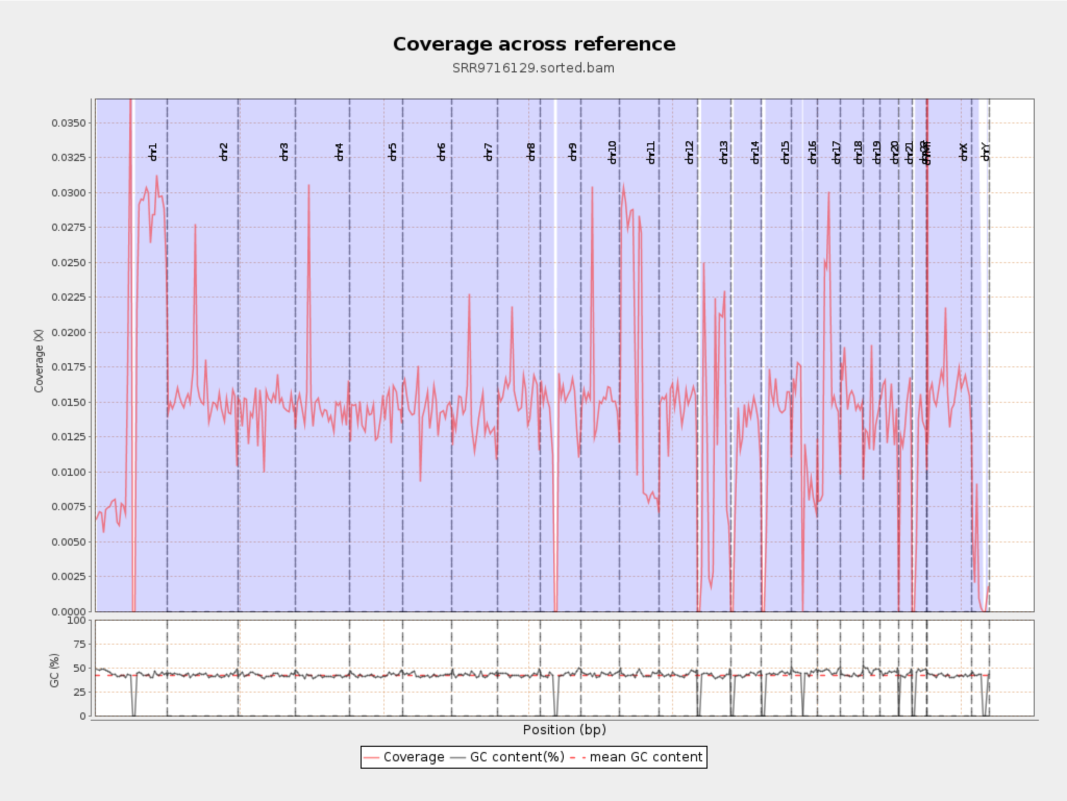
General error rate	0.66%
Mismatches	286,567
Insertions	4,009
Mapped reads with at least one insertion	0.7%
Deletions	10,940
Mapped reads with at least one deletion	1.91%
Homopolymer indels	42.28%

2.6. Chromosome stats

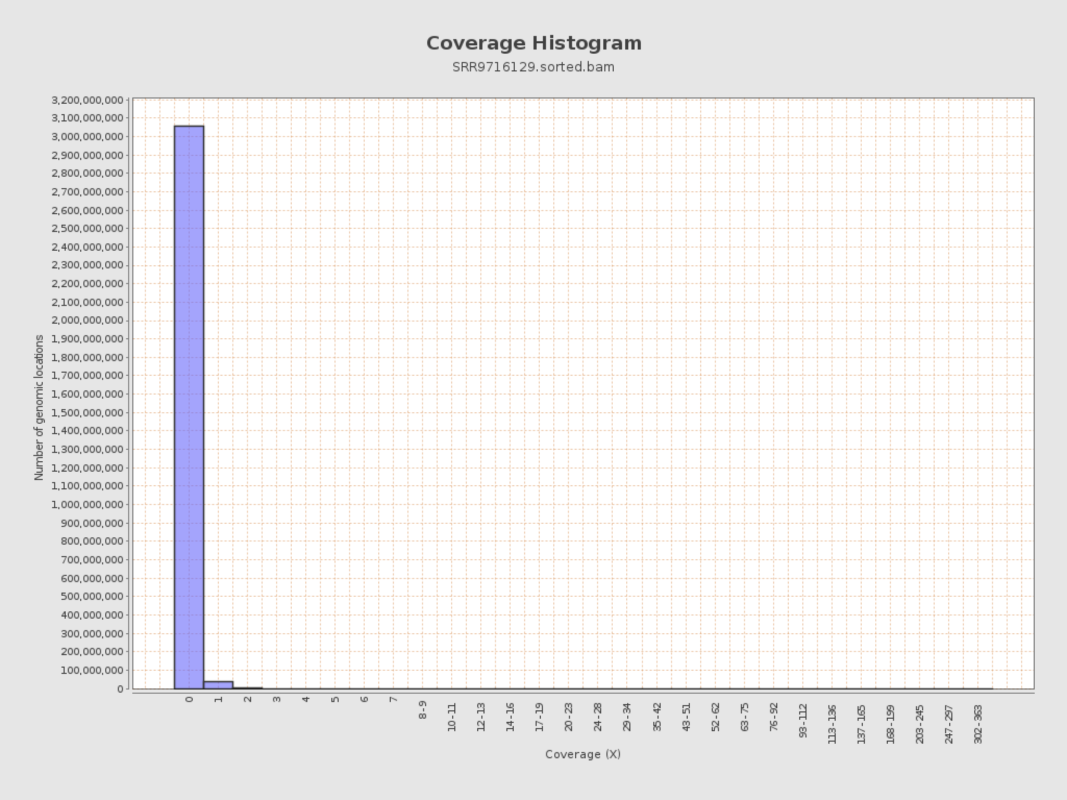
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4320004	0.0173	0.3467
chr2	243199373	3749809	0.0154	0.1815
chr3	198022430	2887890	0.0146	0.1262
chr4	191154276	2886138	0.0151	0.143
chr5	180915260	2584403	0.0143	0.1247
chr6	171115067	2494662	0.0146	0.1305
chr7	159138663	2241850	0.0141	0.1833

chr8	146364022	2291552	0.0157	0.1897
chr9	141213431	1885344	0.0134	0.1496
chr10	135534747	2130994	0.0157	0.1787
chr11	135006516	2491264	0.0185	0.1878
chr12	133851895	2006393	0.015	0.1273
chr13	115169878	1256614	0.0109	0.1091
chr14	107349540	1226771	0.0114	0.114
chr15	102531392	1278804	0.0125	0.1156
chr16	90354753	1008420	0.0112	0.1144
chr17	81195210	1300911	0.016	0.1399
chr18	78077248	1222249	0.0157	0.2088
chr19	59128983	801407	0.0136	0.2295
chr20	63025520	904320	0.0143	0.1261
chr21	48129895	596523	0.0124	0.1232
chr22	51304566	490467	0.0096	0.1018
chrMT	16571	3898	0.2352	0.4941
chrX	155270560	2469403	0.0159	0.1398
chrY	59373566	138228	0.0023	0.0945

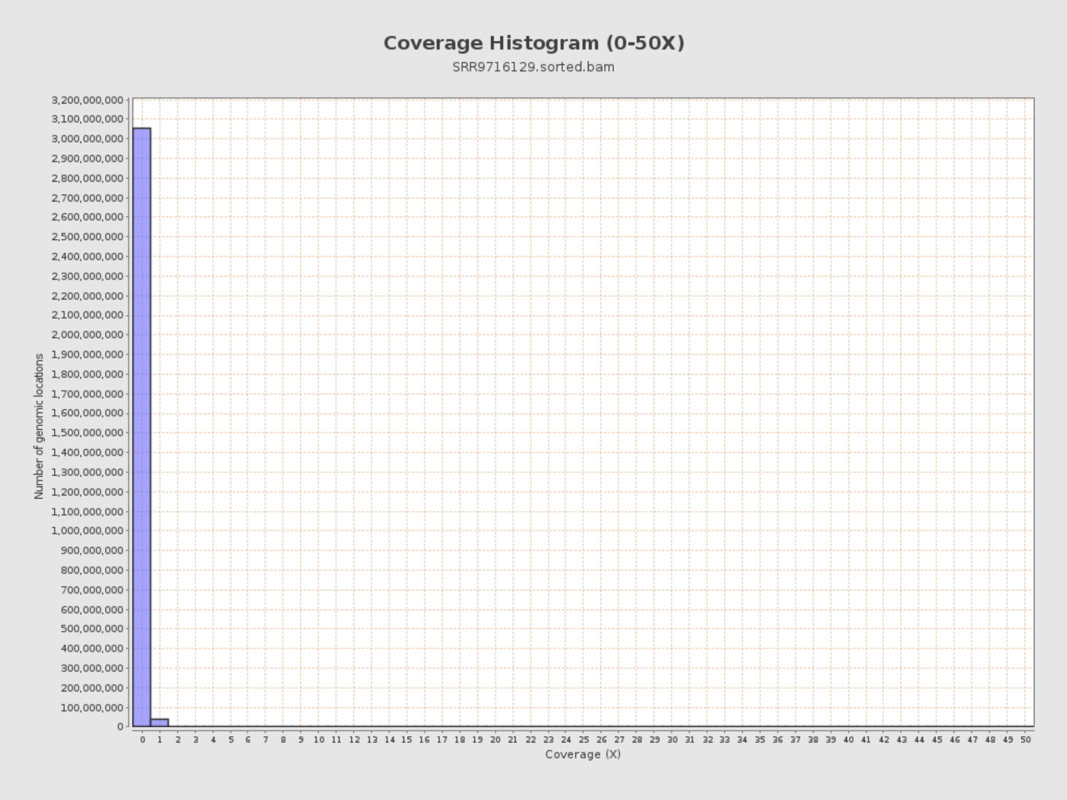
3. Results : Coverage across reference



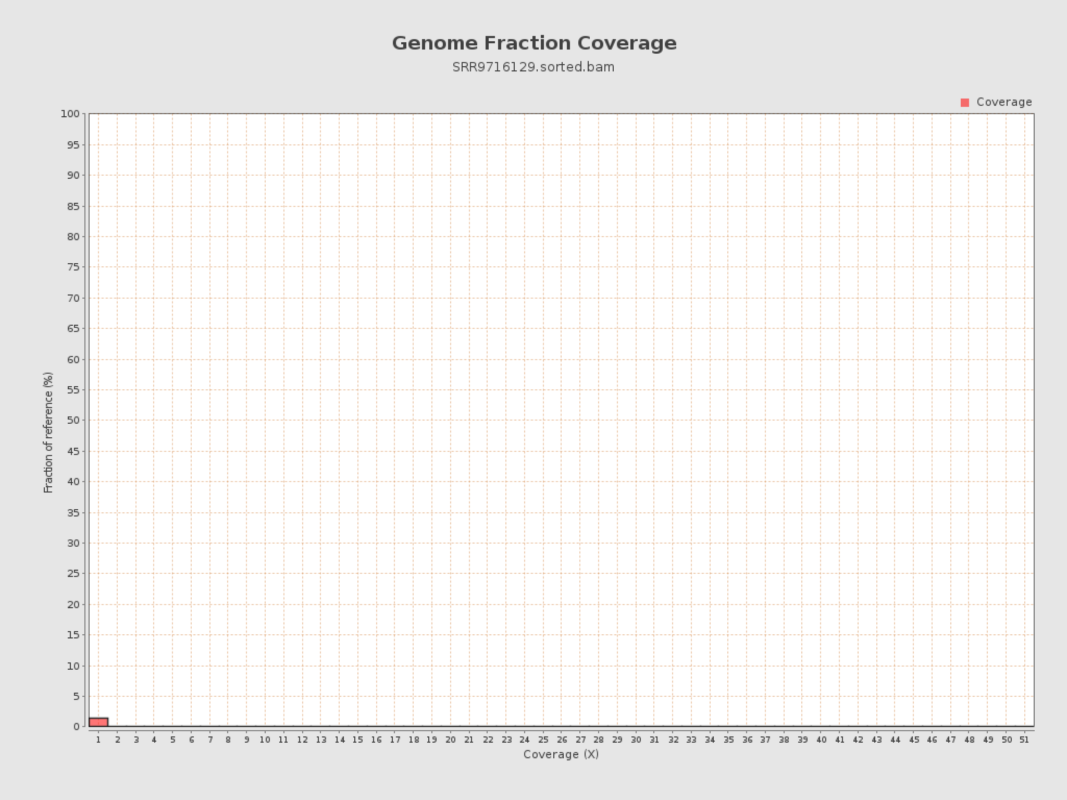
4. Results : Coverage Histogram



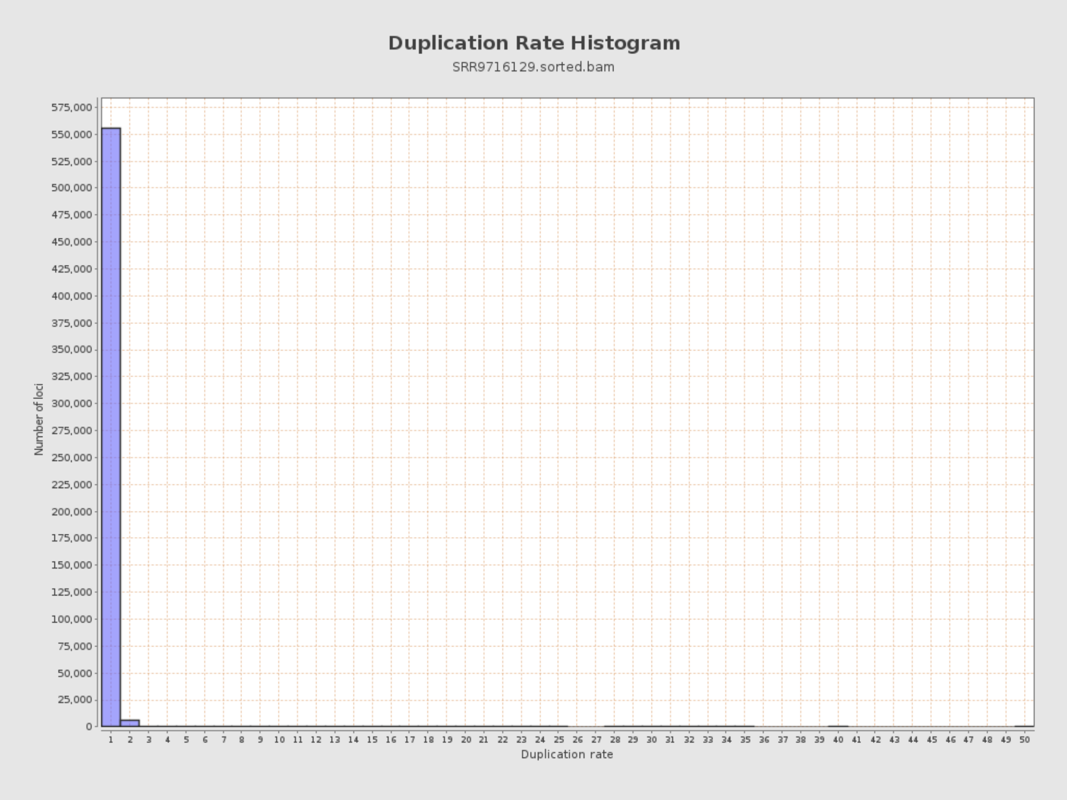
5. Results : Coverage Histogram (0-50X)



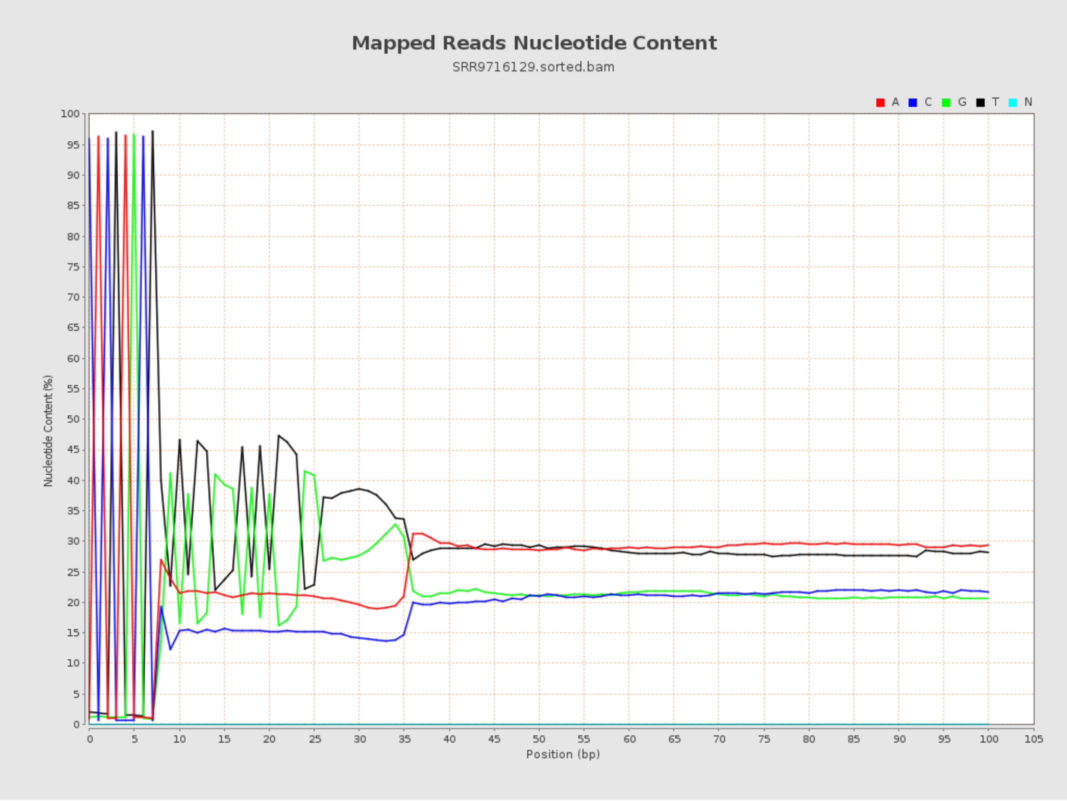
6. Results : Genome Fraction Coverage



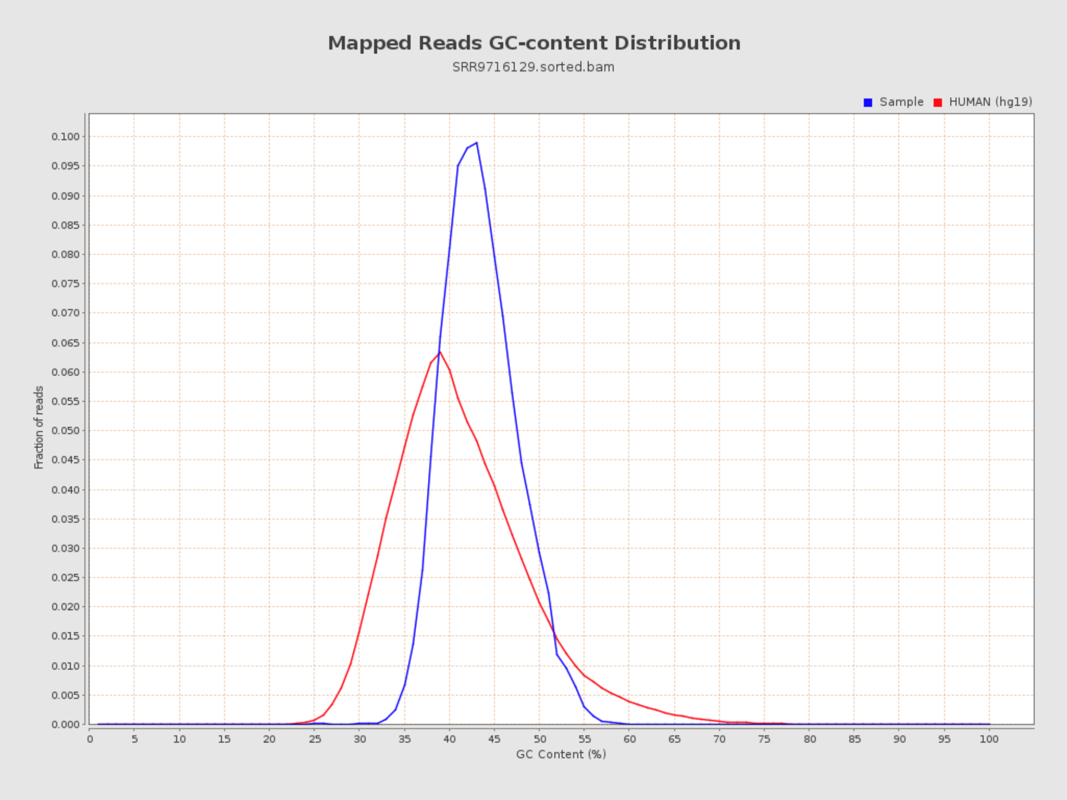
7. Results : Duplication Rate Histogram



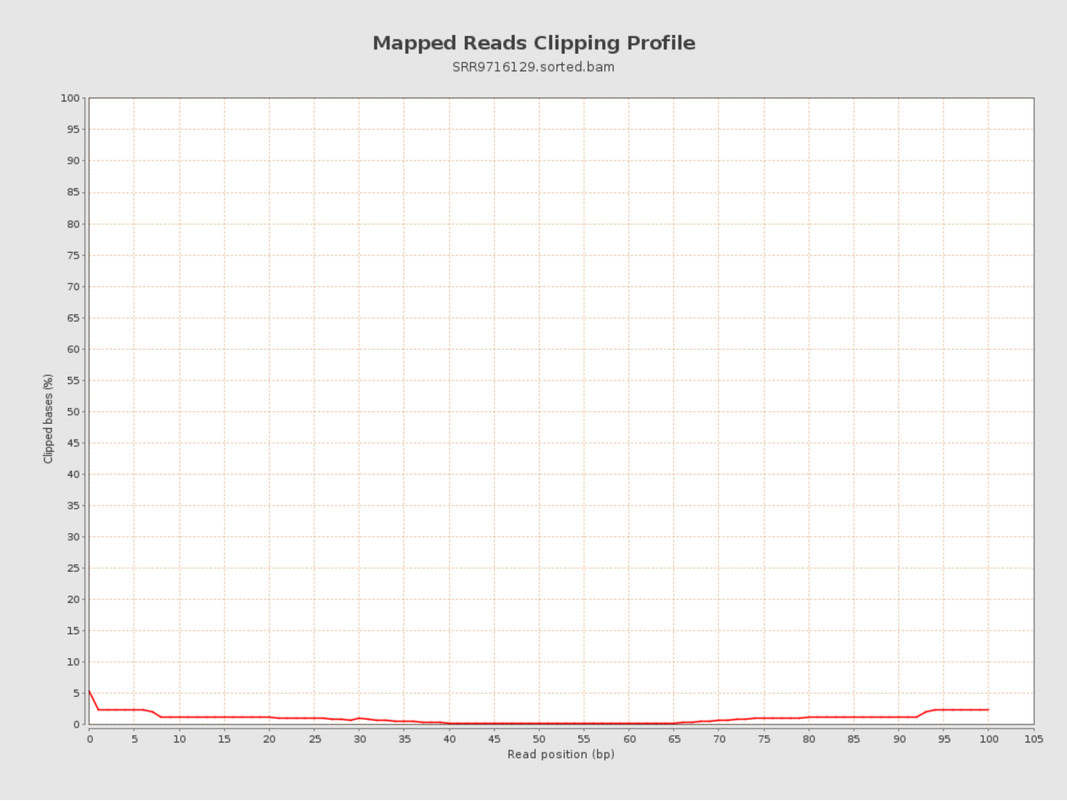
8. Results : Mapped Reads Nucleotide Content



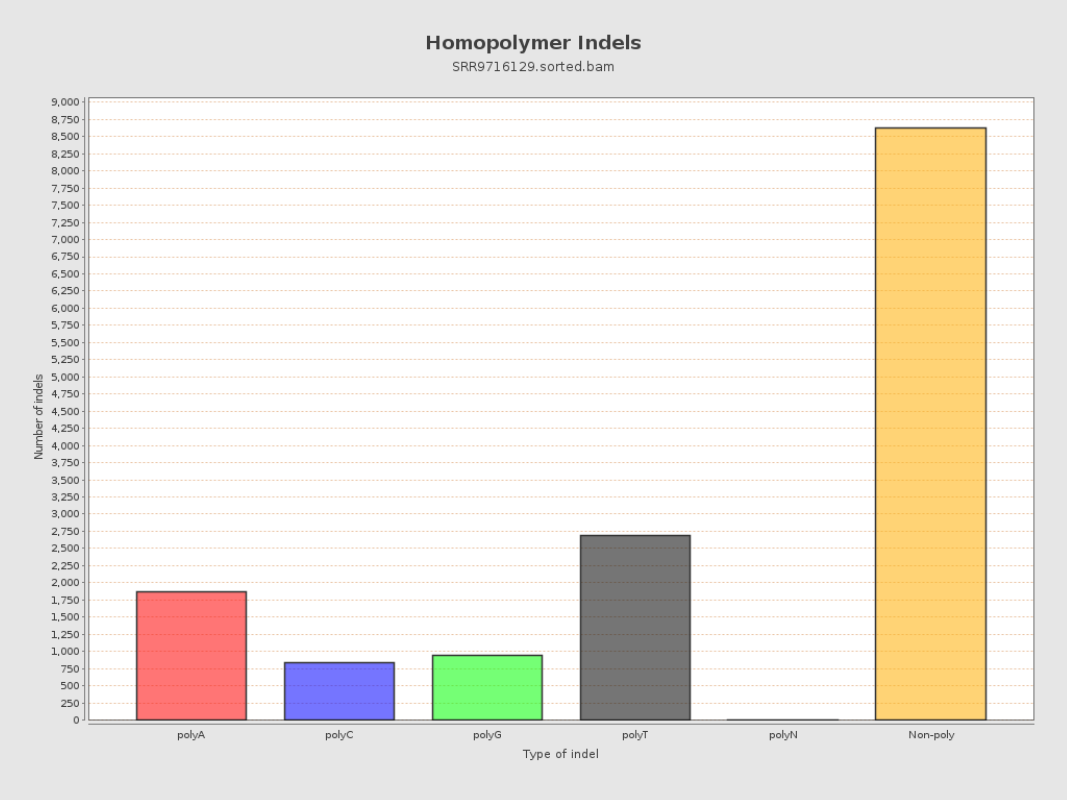
9. Results : Mapped Reads GC-content Distribution



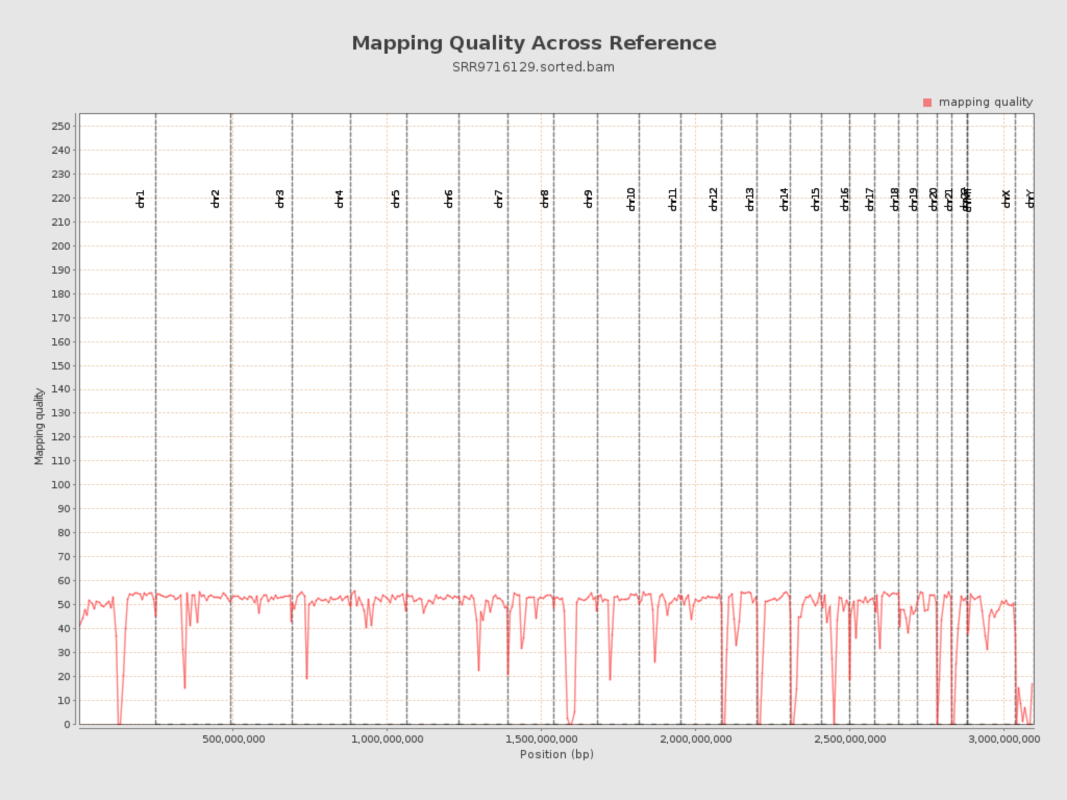
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram