Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:29:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716139.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_SRR9716139 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716139.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:29:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716139.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	440,427
Mapped reads	403,763 / 91.68%
Unmapped reads	36,664 / 8.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,159 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	6,495 / 1.47%
Duplication rate	1.26%
Clipped reads	404,393 / 91.82%

2.2. ACGT Content

Number/percentage of A's	5,512,834 / 23.61%
Number/percentage of C's	4,352,516 / 18.64%
Number/percentage of T's	7,526,047 / 32.23%
Number/percentage of G's	5,962,790 / 25.53%
Number/percentage of N's	145 / 0%
GC Percentage	44.17%

2.3. Coverage

Mean	0.0075

Standard Deviation	0.0997

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

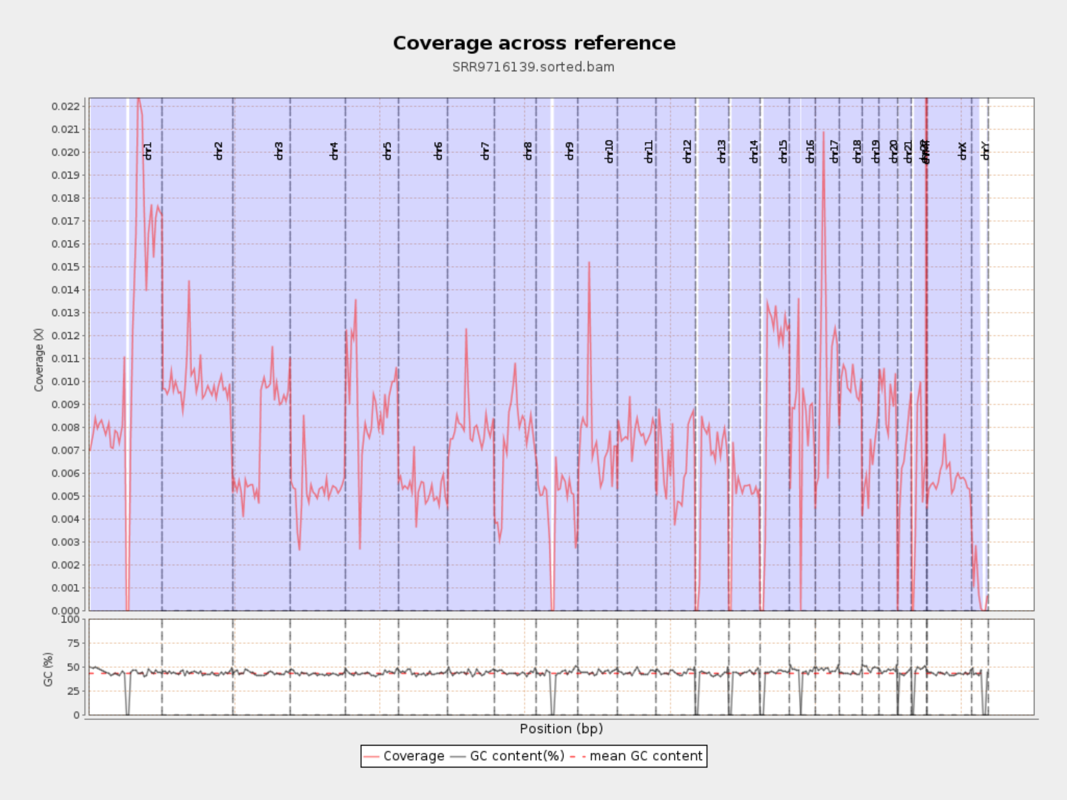
General error rate	0.5%
Mismatches	113,927
Insertions	1,361
Mapped reads with at least one insertion	0.33%
Deletions	4,308
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.09%

2.6. Chromosome stats

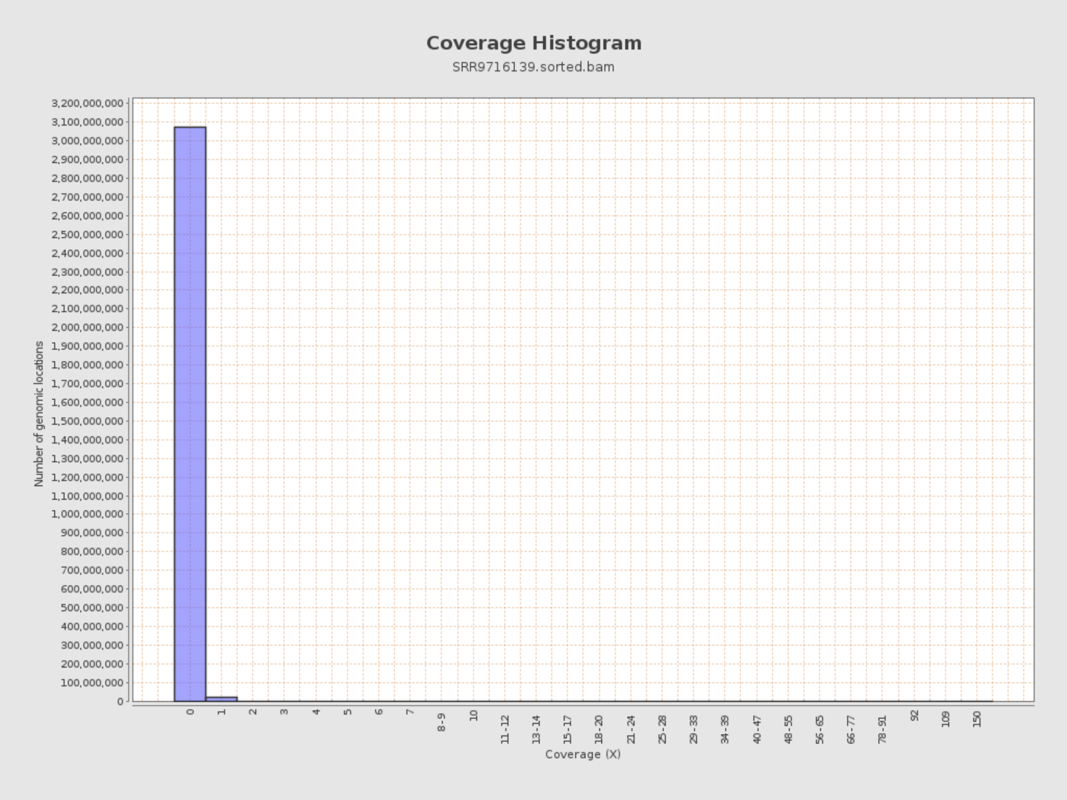
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2842805	0.0114	0.1346
chr2	243199373	2403978	0.0099	0.1259
chr3	198022430	1495754	0.0076	0.0899
chr4	191154276	993459	0.0052	0.0757
chr5	180915260	1643030	0.0091	0.0979
chr6	171115067	903240	0.0053	0.0785
chr7	159138663	1289638	0.0081	0.1164

chr8	146364022	1072630	0.0073	0.0932
chr9	141213431	642402	0.0045	0.0799
chr10	135534747	1010525	0.0075	0.1099
chr11	135006516	1044457	0.0077	0.0979
chr12	133851895	851950	0.0064	0.0825
chr13	115169878	717219	0.0062	0.081
chr14	107349540	515232	0.0048	0.0721
chr15	102531392	1033286	0.0101	0.1034
chr16	90354753	737128	0.0082	0.0966
chr17	81195210	894643	0.011	0.1111
chr18	78077248	773885	0.0099	0.1374
chr19	59128983	383412	0.0065	0.1053
chr20	63025520	587137	0.0093	0.0998
chr21	48129895	308097	0.0064	0.0834
chr22	51304566	269459	0.0053	0.0745
chrMT	16571	2784	0.168	0.4093
chrX	155270560	891948	0.0057	0.0814
chrY	59373566	53274	0.0009	0.0348

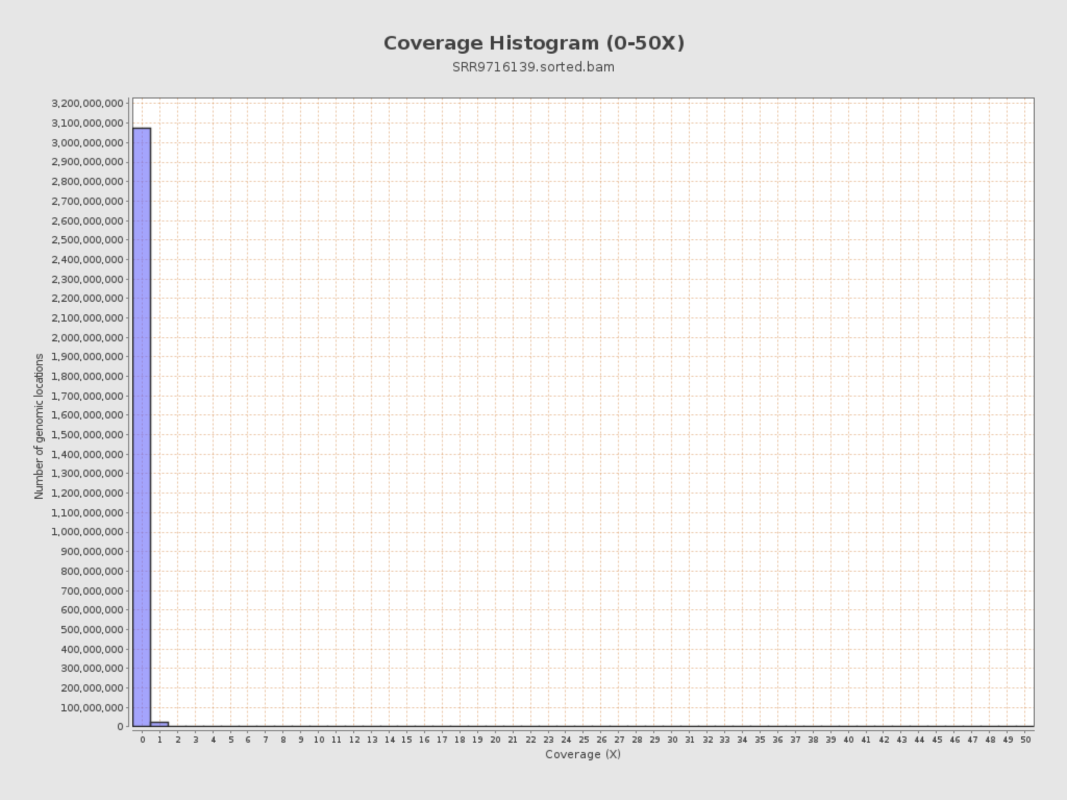
3. Results : Coverage across reference



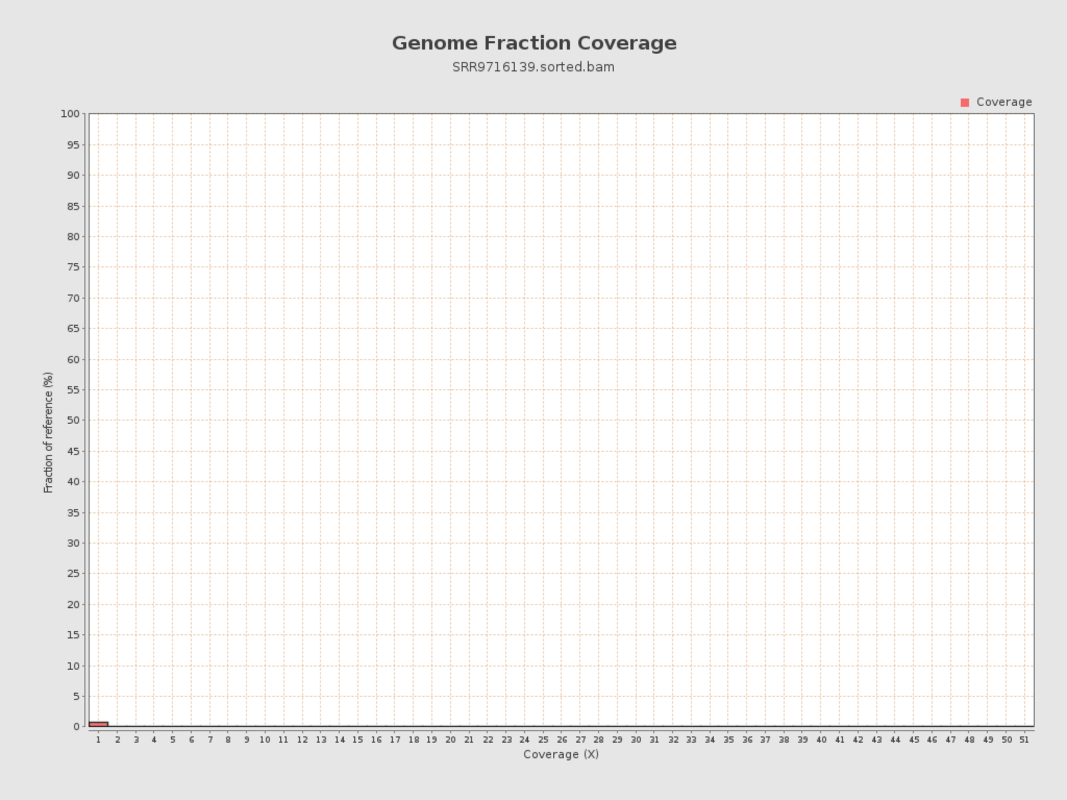
4. Results : Coverage Histogram



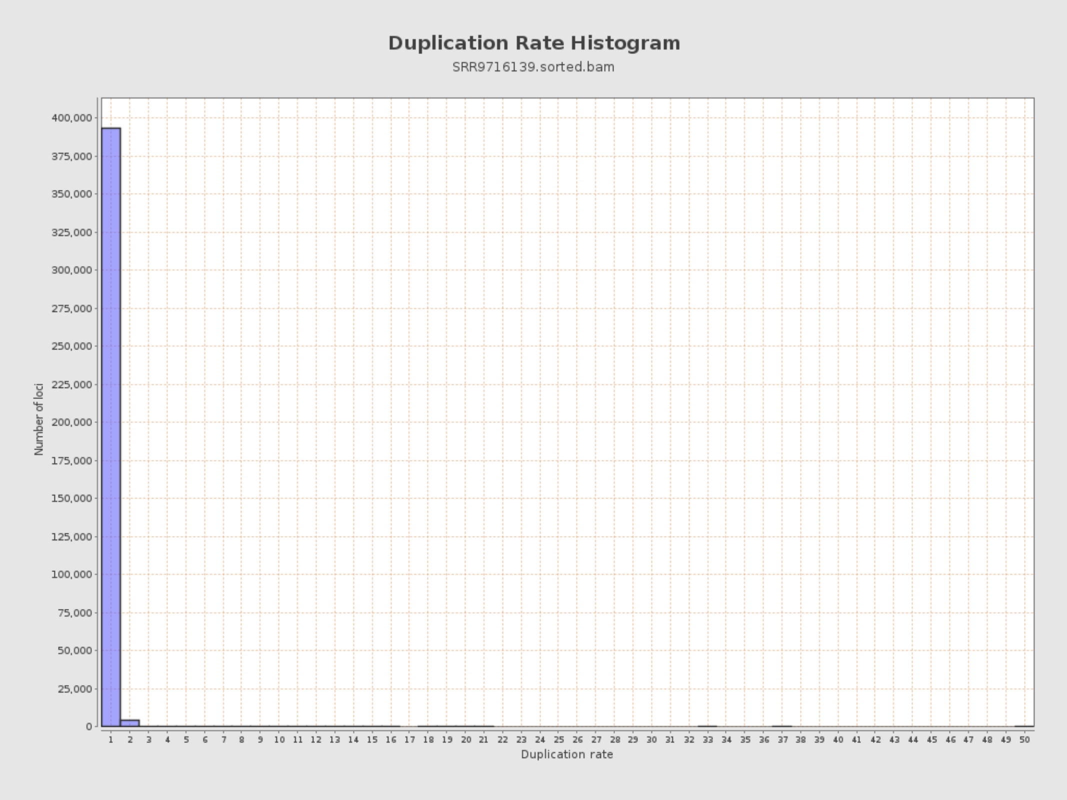
5. Results : Coverage Histogram (0-50X)



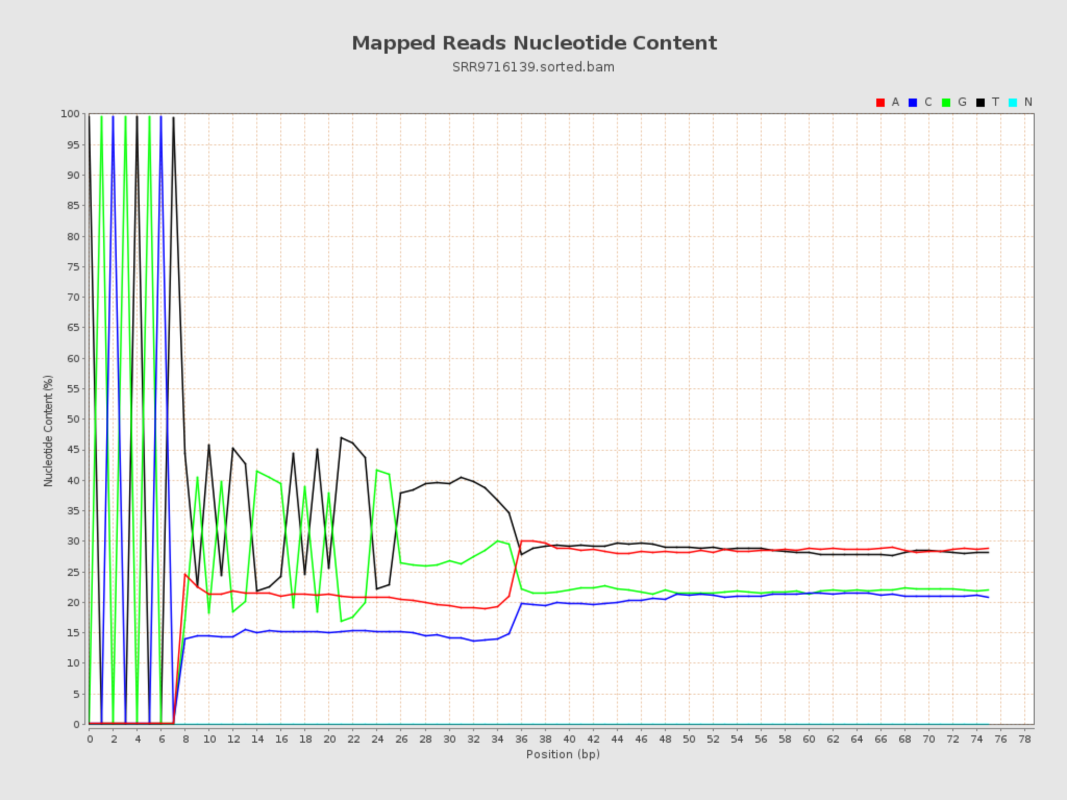
6. Results : Genome Fraction Coverage



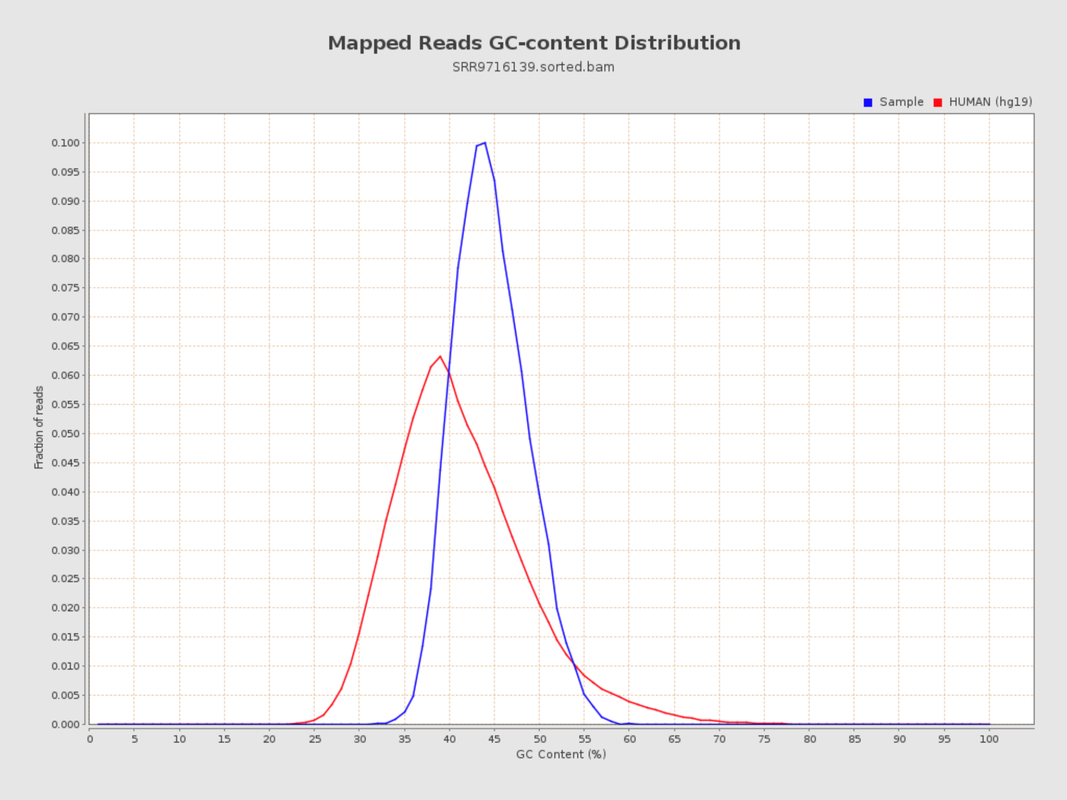
7. Results : Duplication Rate Histogram



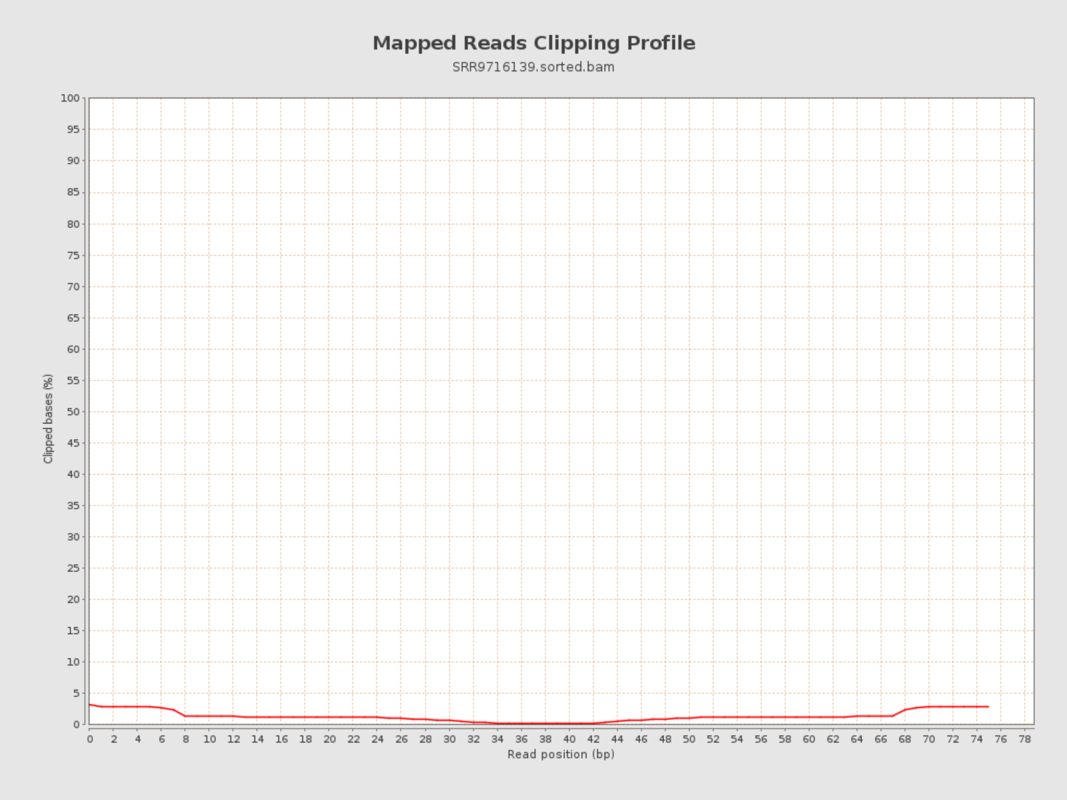
8. Results : Mapped Reads Nucleotide Content



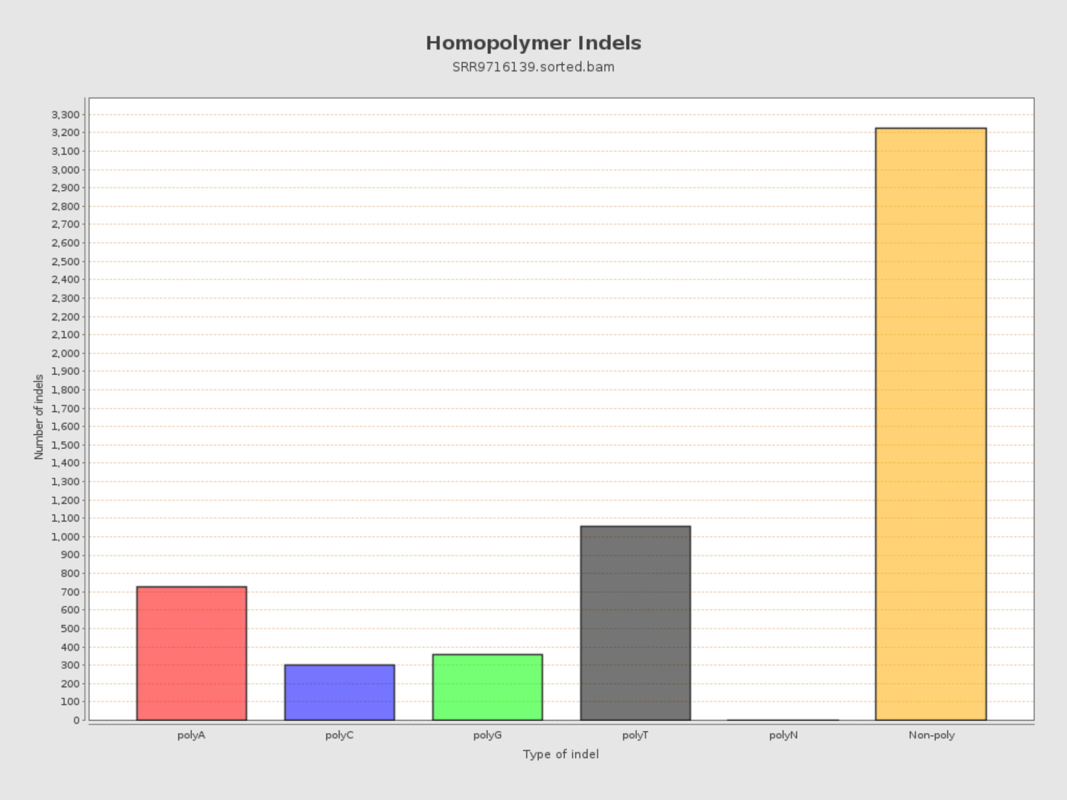
9. Results : Mapped Reads GC-content Distribution



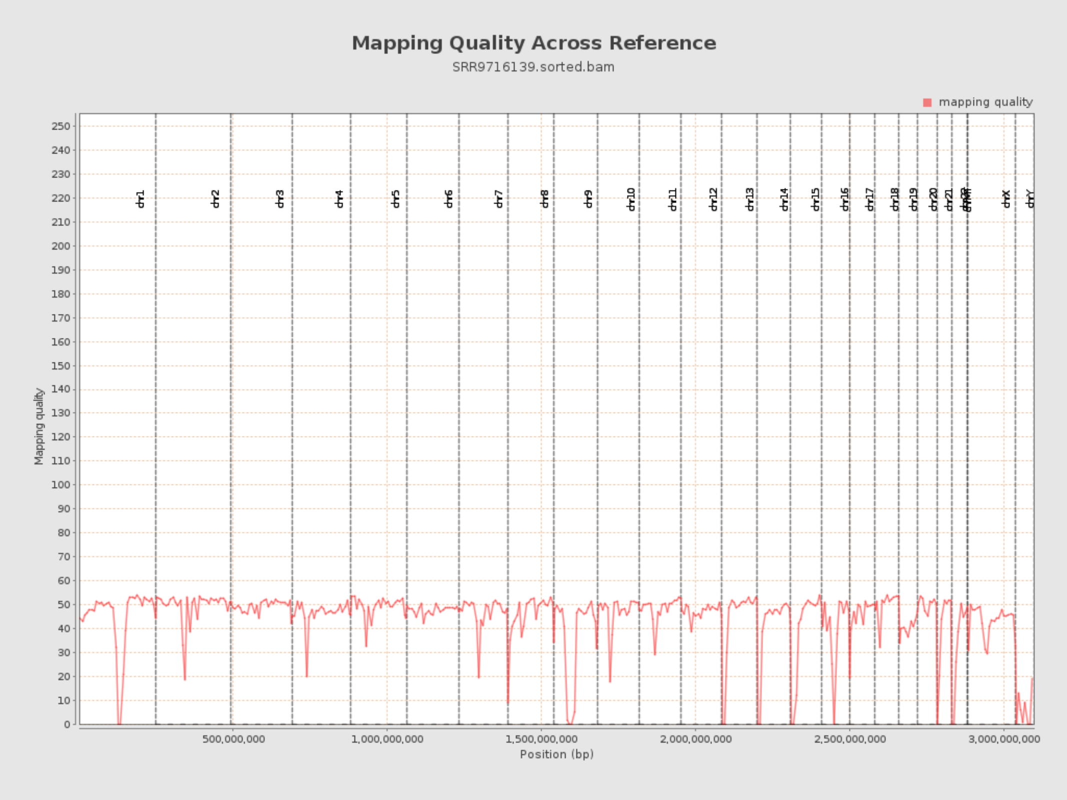
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram