Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:34:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716819.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_SRR9716819 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716819.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:34:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716819.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	483,082
Mapped reads	389,353 / 80.6%
Unmapped reads	93,729 / 19.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,861 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	10,378 / 2.15%
Duplication rate	2.19%
Clipped reads	390,022 / 80.74%

2.2. ACGT Content

Number/percentage of A's	5,234,597 / 23.53%
Number/percentage of C's	4,606,033 / 20.7%
Number/percentage of T's	7,039,667 / 31.64%
Number/percentage of G's	5,368,591 / 24.13%
Number/percentage of N's	161 / 0%
GC Percentage	44.83%

2.3. Coverage

Mean	0.0072

Standard Deviation	0.0995

2.4. Mapping Quality

Mean Mapping Quality	44.7

2.5. Mismatches and indels

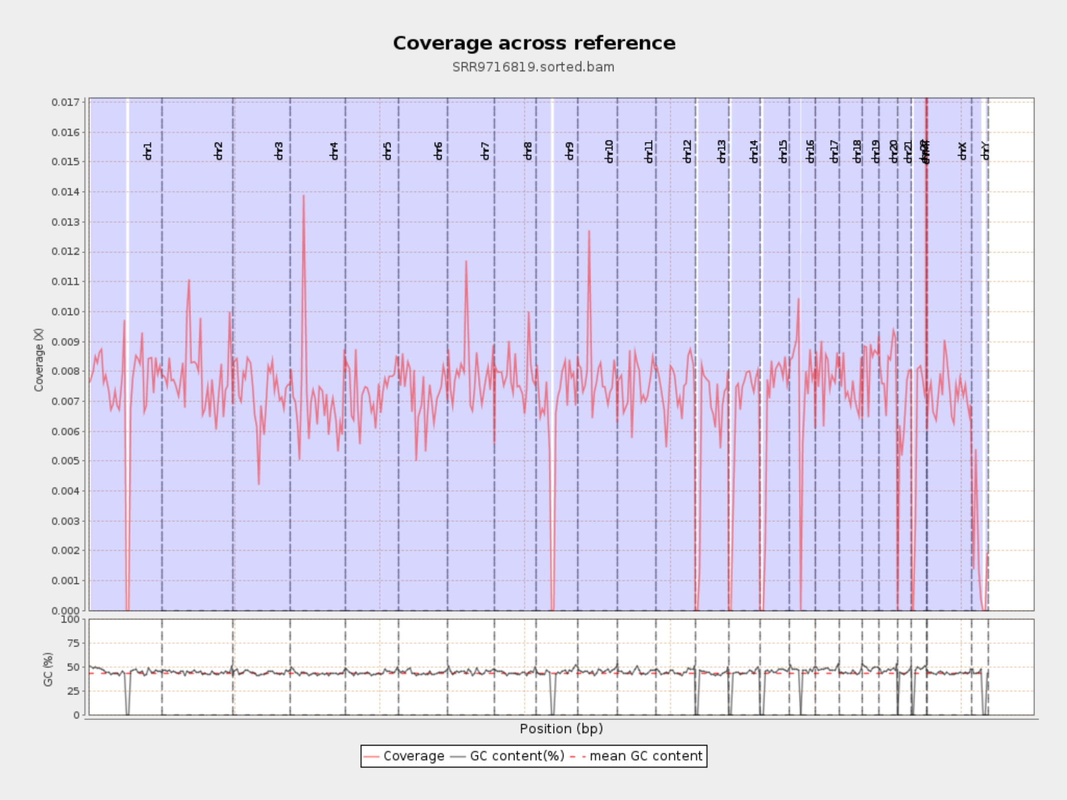
General error rate	0.55%
Mismatches	118,710
Insertions	1,718
Mapped reads with at least one insertion	0.44%
Deletions	4,212
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.4%

2.6. Chromosome stats

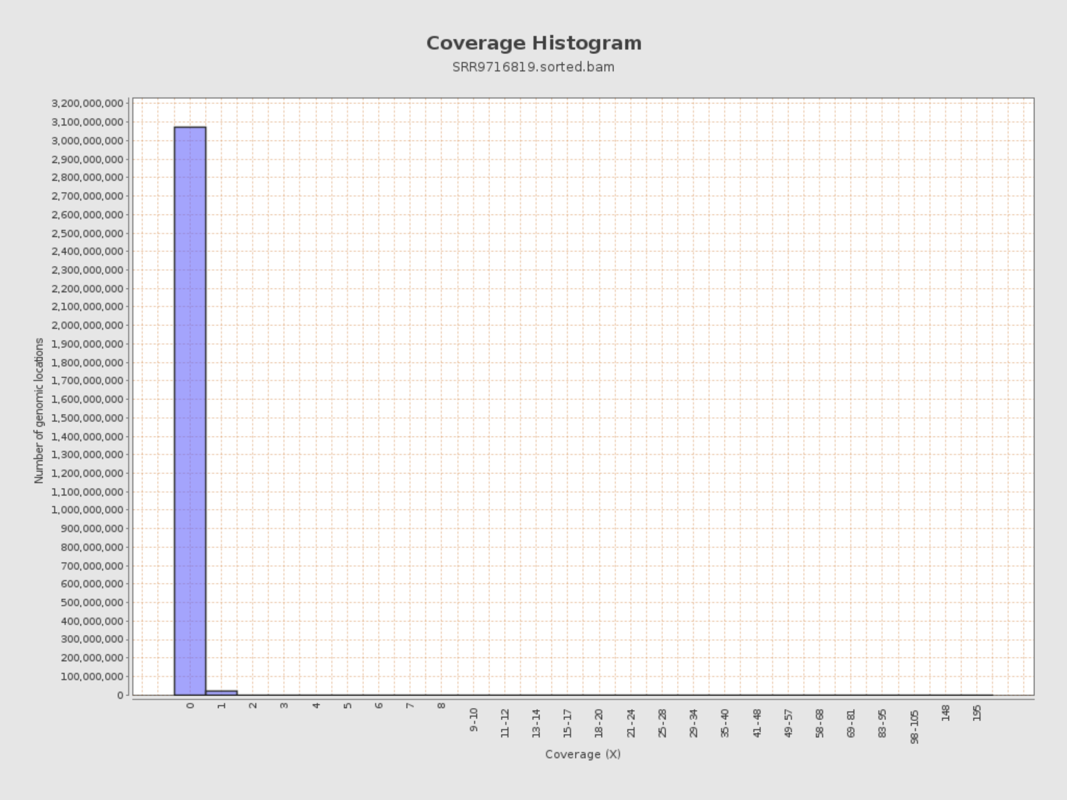
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1840341	0.0074	0.1165
chr2	243199373	1907327	0.0078	0.127
chr3	198022430	1450329	0.0073	0.0901
chr4	191154276	1348370	0.0071	0.0947
chr5	180915260	1325565	0.0073	0.0901
chr6	171115067	1238917	0.0072	0.0922
chr7	159138663	1264565	0.0079	0.1153

chr8	146364022	1152076	0.0079	0.1059
chr9	141213431	912254	0.0065	0.0885
chr10	135534747	1072628	0.0079	0.1061
chr11	135006516	1014888	0.0075	0.0998
chr12	133851895	1003209	0.0075	0.0915
chr13	115169878	689205	0.006	0.0814
chr14	107349540	679558	0.0063	0.0846
chr15	102531392	650673	0.0063	0.0839
chr16	90354753	678359	0.0075	0.092
chr17	81195210	648366	0.008	0.0959
chr18	78077248	578423	0.0074	0.1166
chr19	59128983	493024	0.0083	0.1072
chr20	63025520	509462	0.0081	0.0962
chr21	48129895	295456	0.0061	0.0868
chr22	51304566	278606	0.0054	0.078
chrMT	16571	3345	0.2019	0.4579
chrX	155270560	1124574	0.0072	0.092
chrY	59373566	96237	0.0016	0.0536

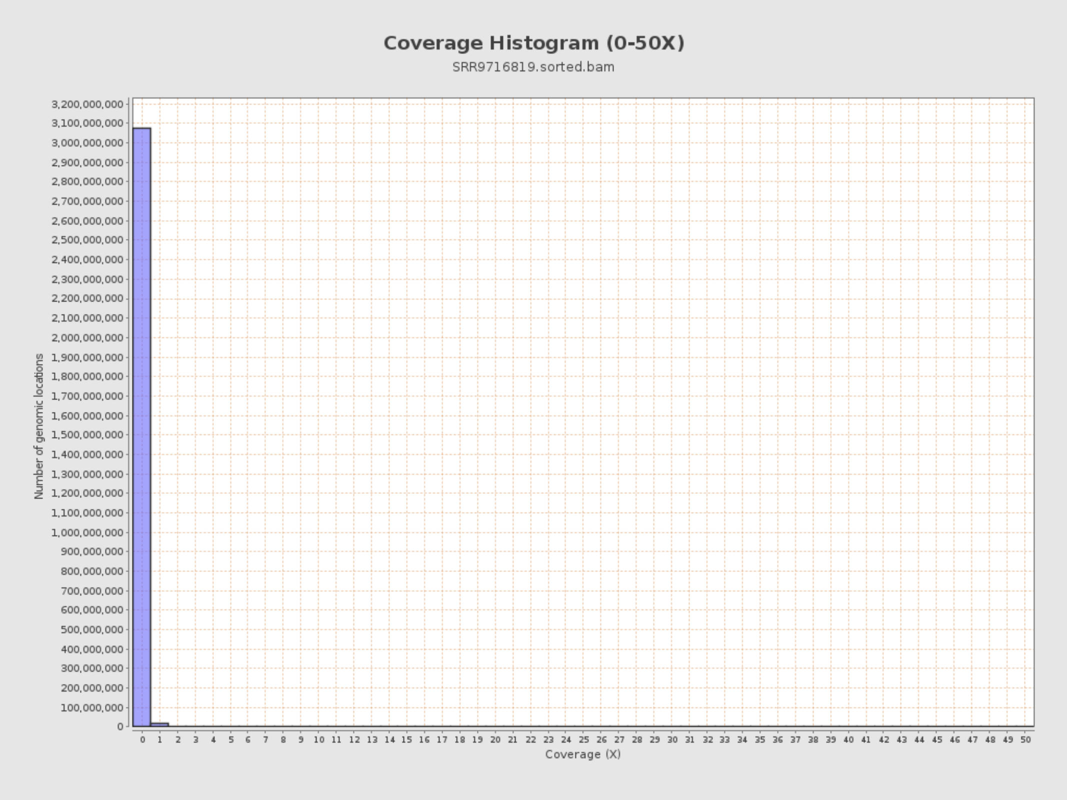
3. Results : Coverage across reference



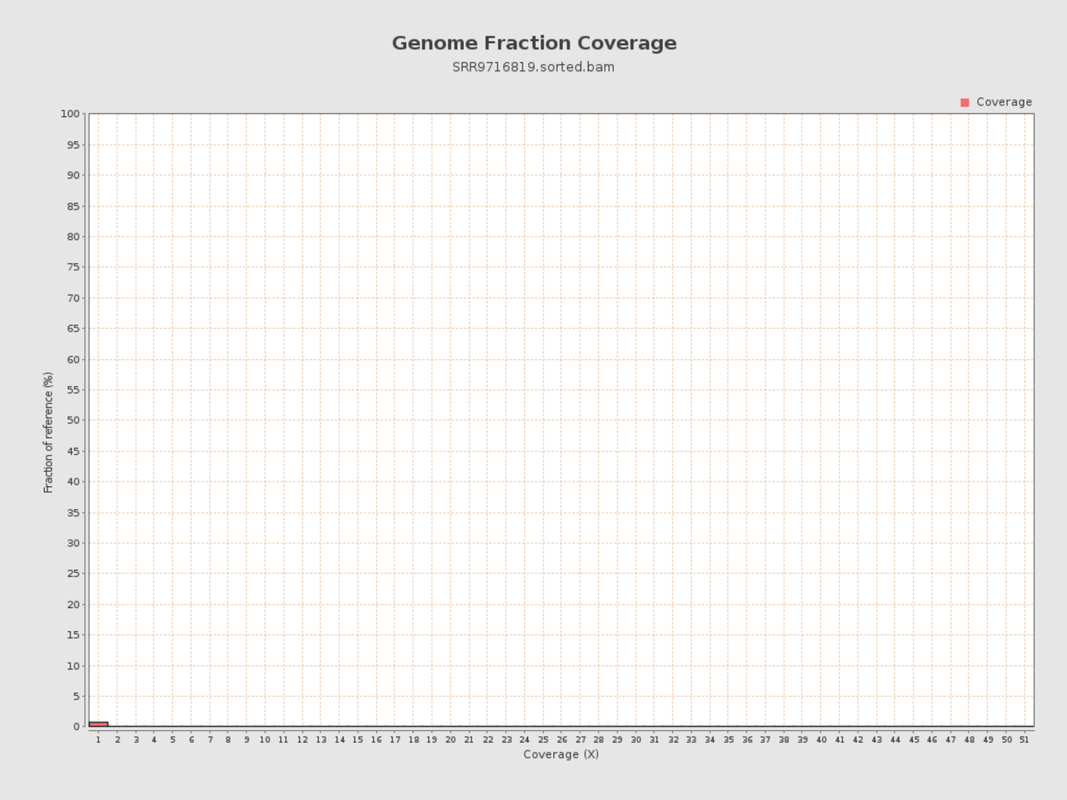
4. Results : Coverage Histogram



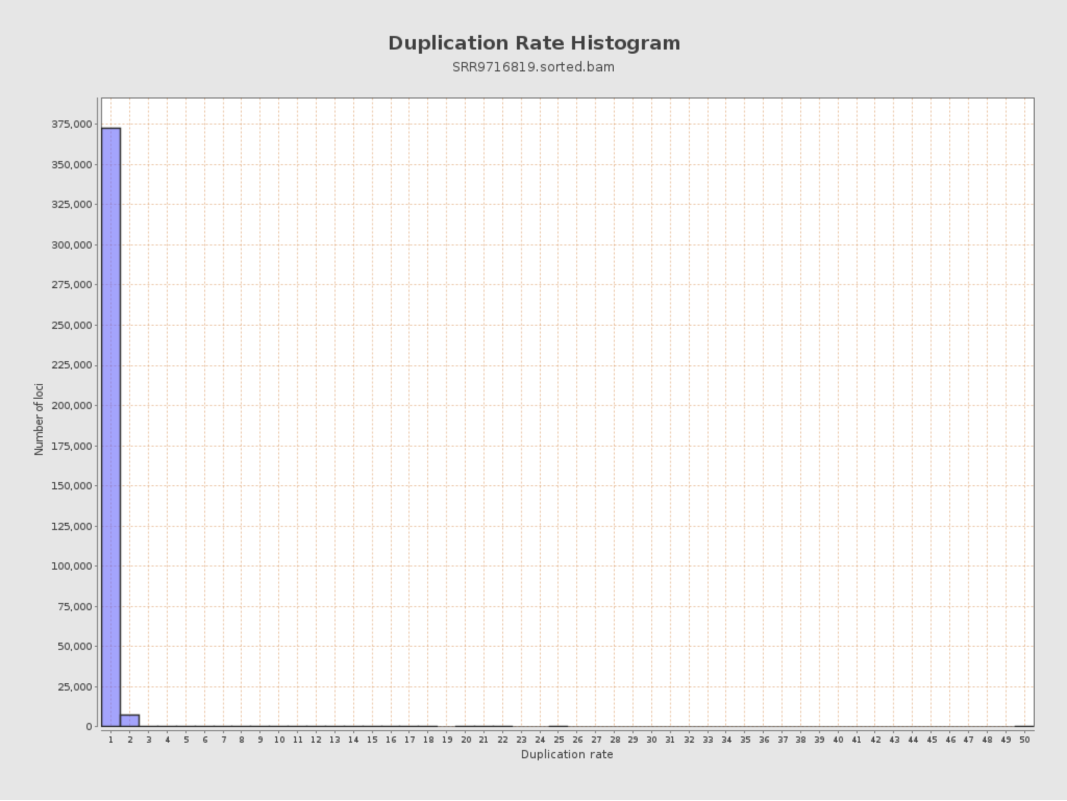
5. Results : Coverage Histogram (0-50X)



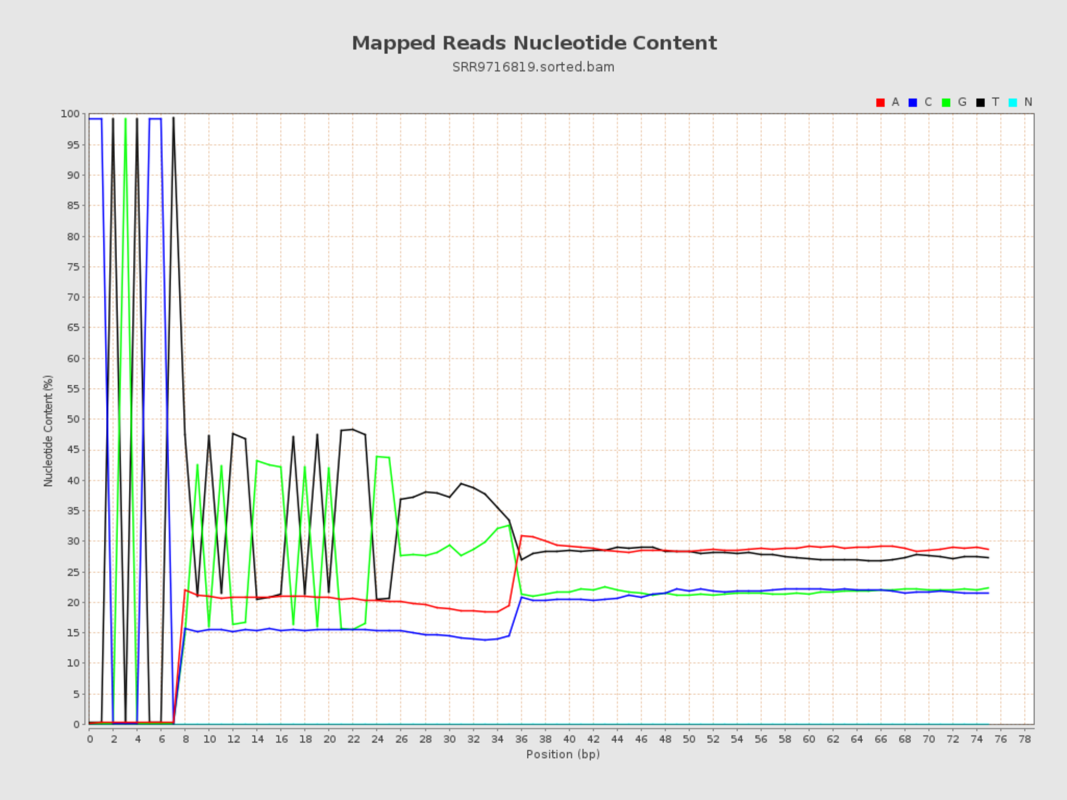
6. Results : Genome Fraction Coverage



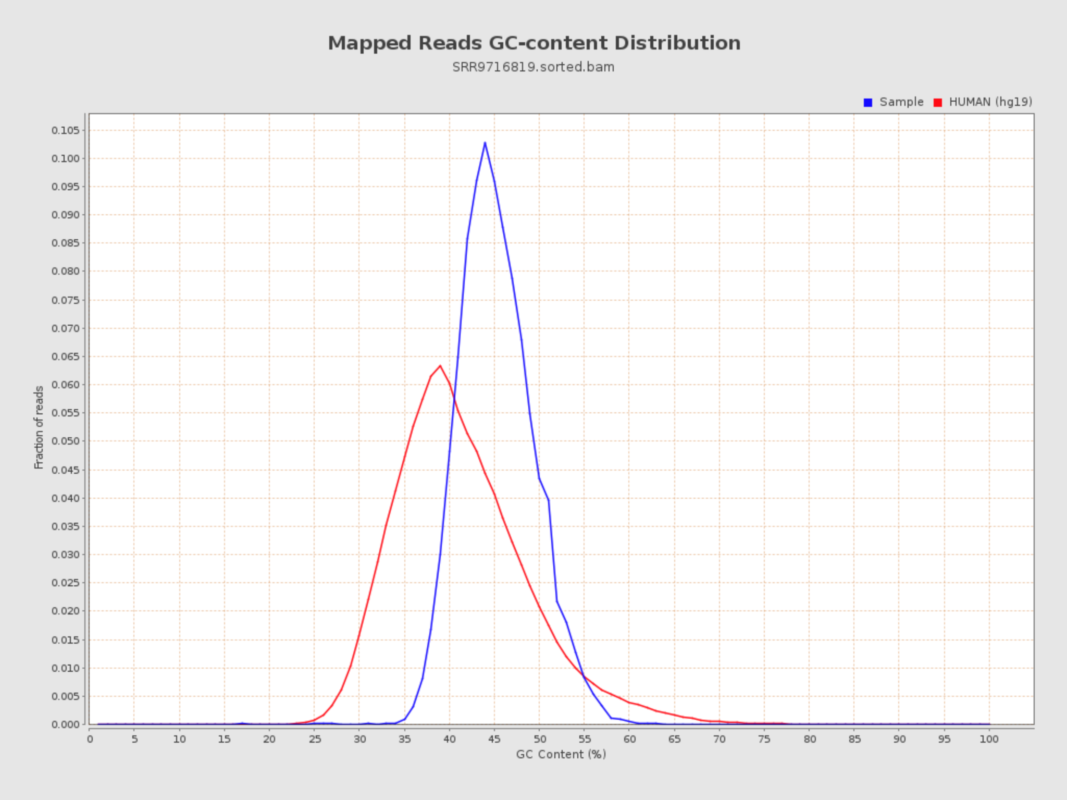
7. Results : Duplication Rate Histogram



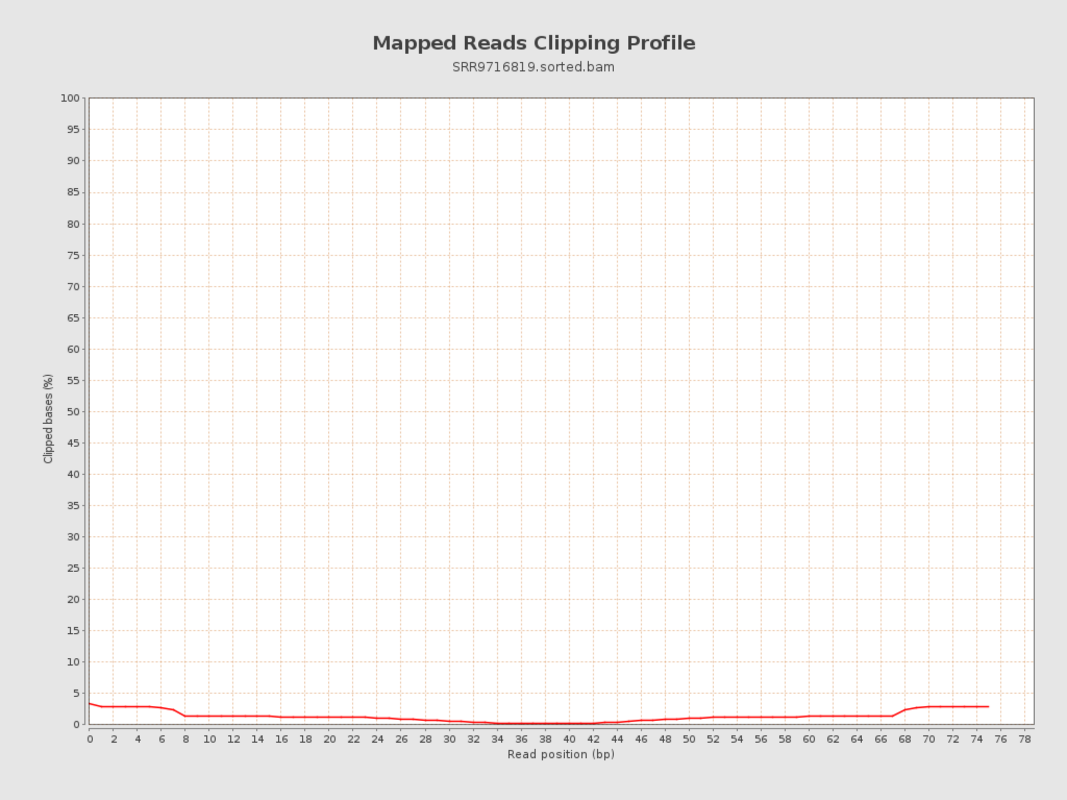
8. Results : Mapped Reads Nucleotide Content



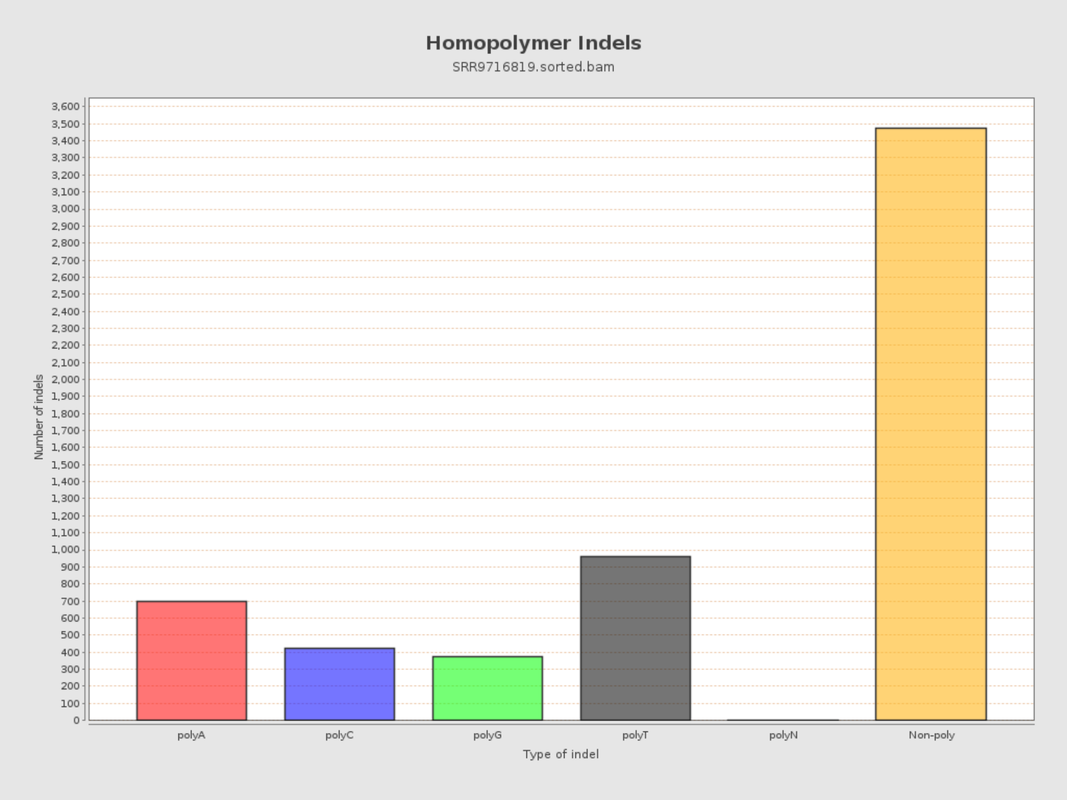
9. Results : Mapped Reads GC-content Distribution



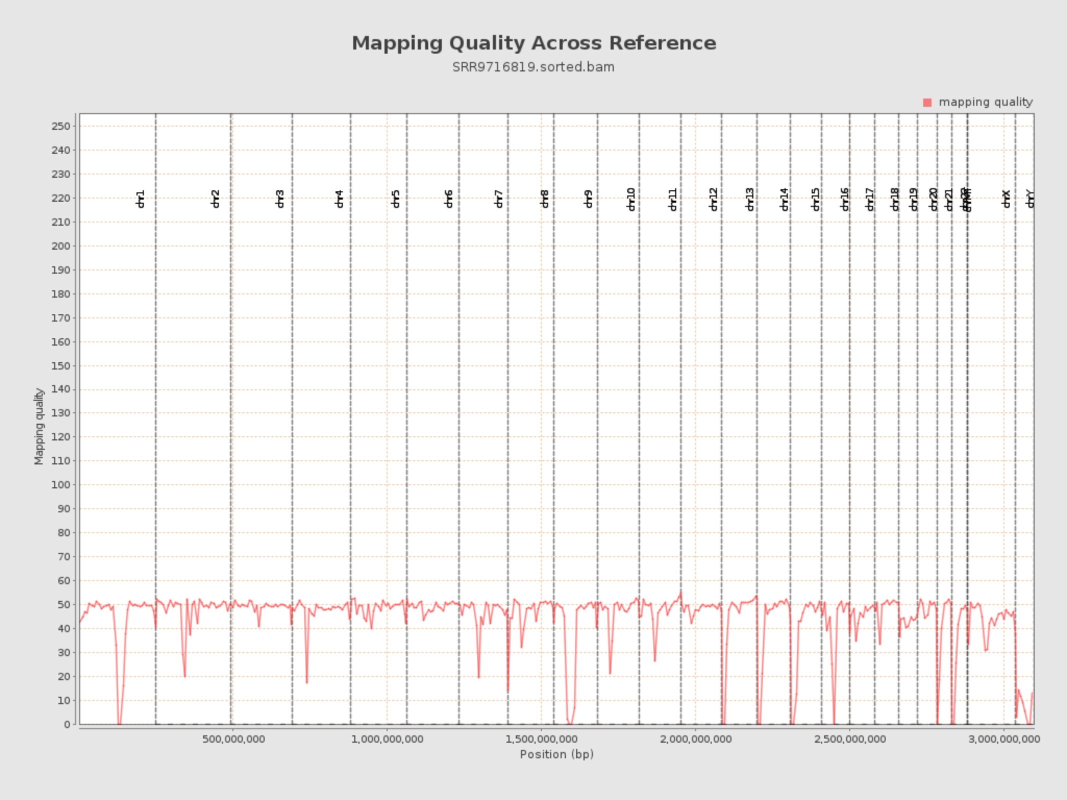
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram