Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:01:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716167.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_SRR9716167 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716167.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:01:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716167.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,545,466
Mapped reads	3,241,750 / 91.43%
Unmapped reads	303,716 / 8.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,186 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	172,145 / 4.86%
Duplication rate	3.95%
Clipped reads	3,252,196 / 91.73%

2.2. ACGT Content

Number/percentage of A's	49,352,554 / 26.21%
Number/percentage of C's	33,835,971 / 17.97%
Number/percentage of T's	58,541,173 / 31.09%
Number/percentage of G's	46,553,806 / 24.72%
Number/percentage of N's	3,088 / 0%
GC Percentage	42.7%

2.3. Coverage

Mean	0.0608

Standard Deviation	0.5101

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

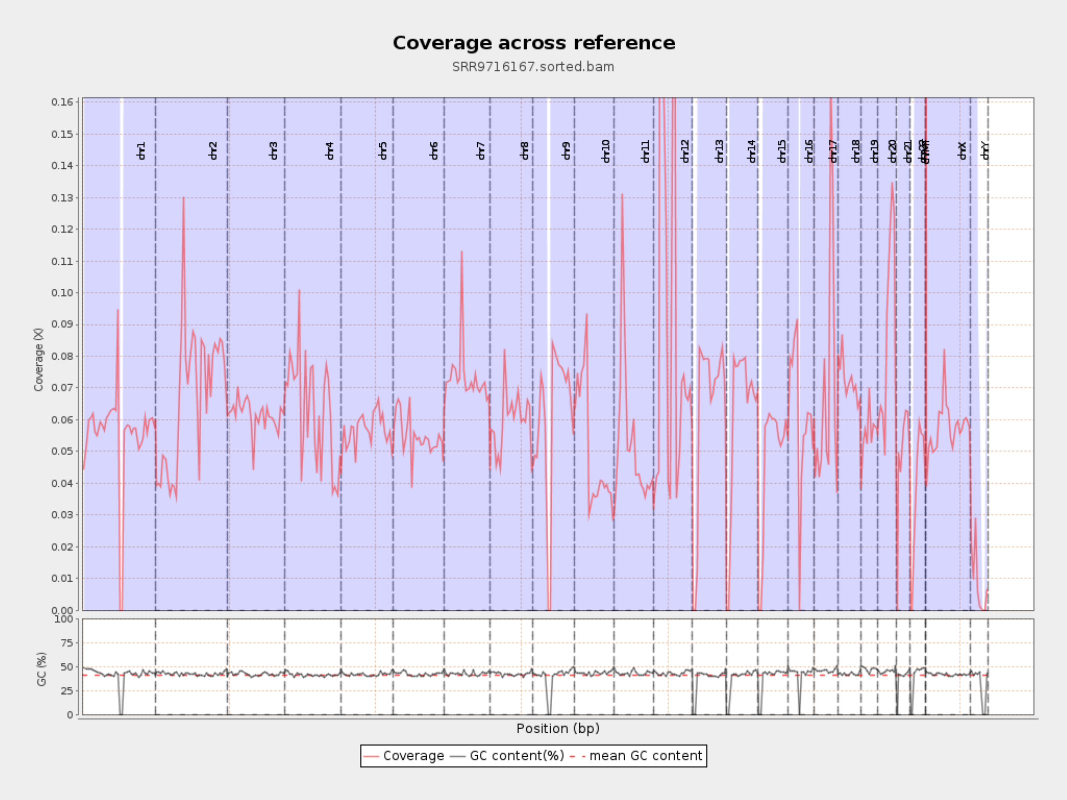
General error rate	0.53%
Mismatches	985,631
Insertions	12,041
Mapped reads with at least one insertion	0.37%
Deletions	30,874
Mapped reads with at least one deletion	0.95%
Homopolymer indels	41.48%

2.6. Chromosome stats

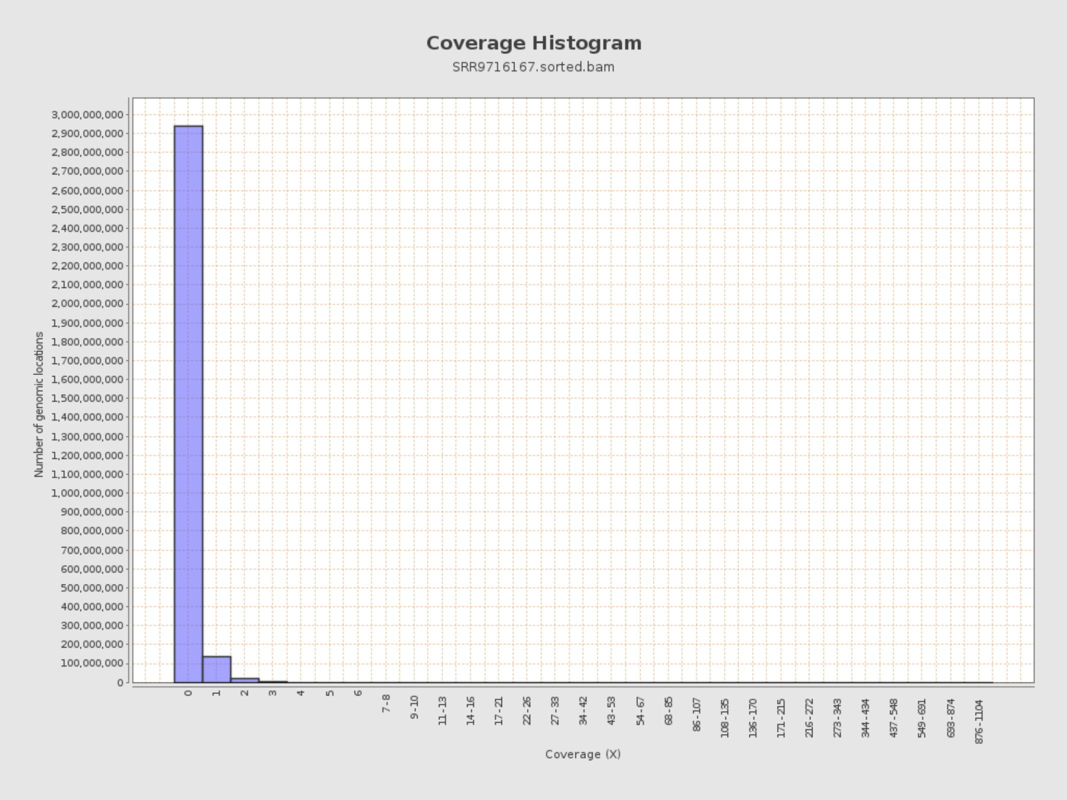
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13775513	0.0553	0.9247
chr2	243199373	16342340	0.0672	0.5663
chr3	198022430	12191724	0.0616	0.2828
chr4	191154276	12048313	0.063	0.3364
chr5	180915260	10257962	0.0567	0.282
chr6	171115067	9393567	0.0549	0.3168
chr7	159138663	11674043	0.0734	0.7085

chr8	146364022	8704976	0.0595	0.5271
chr9	141213431	8651389	0.0613	0.5231
chr10	135534747	6721827	0.0496	0.483
chr11	135006516	7206384	0.0534	0.4186
chr12	133851895	13192877	0.0986	0.4305
chr13	115169878	7307644	0.0635	0.2878
chr14	107349540	6656108	0.062	0.3389
chr15	102531392	4779520	0.0466	0.2488
chr16	90354753	5412796	0.0599	0.3291
chr17	81195210	5704801	0.0703	0.327
chr18	78077248	5658234	0.0725	1.0682
chr19	59128983	3327096	0.0563	0.7087
chr20	63025520	5598062	0.0888	0.361
chr21	48129895	2380134	0.0495	0.3225
chr22	51304566	1933662	0.0377	0.2203
chrMT	16571	11504	0.6942	1.0292
chrX	155270560	8892757	0.0573	0.3753
chrY	59373566	514226	0.0087	0.1977

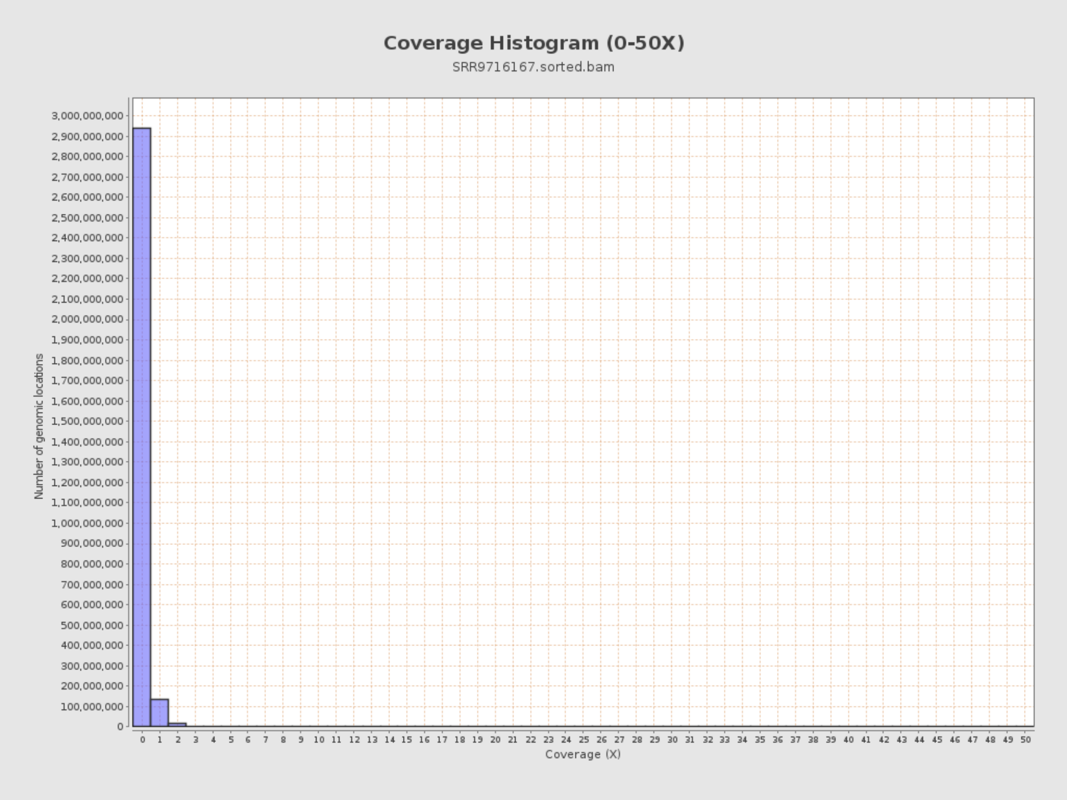
3. Results : Coverage across reference



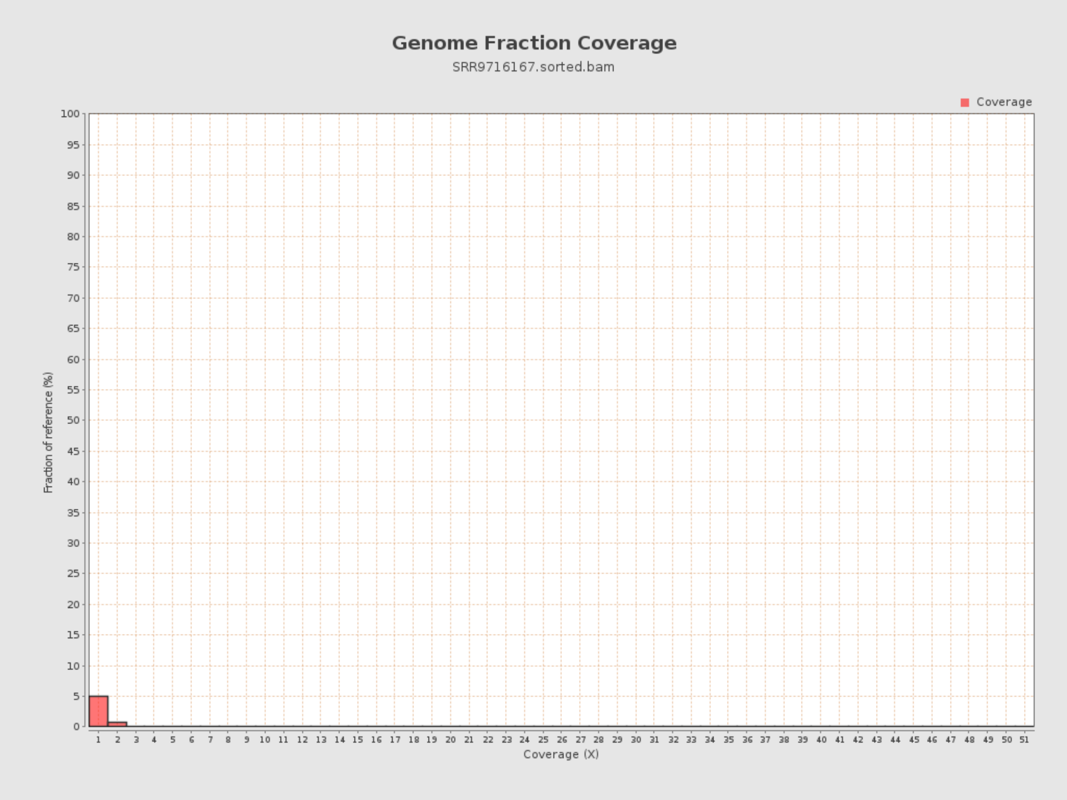
4. Results : Coverage Histogram



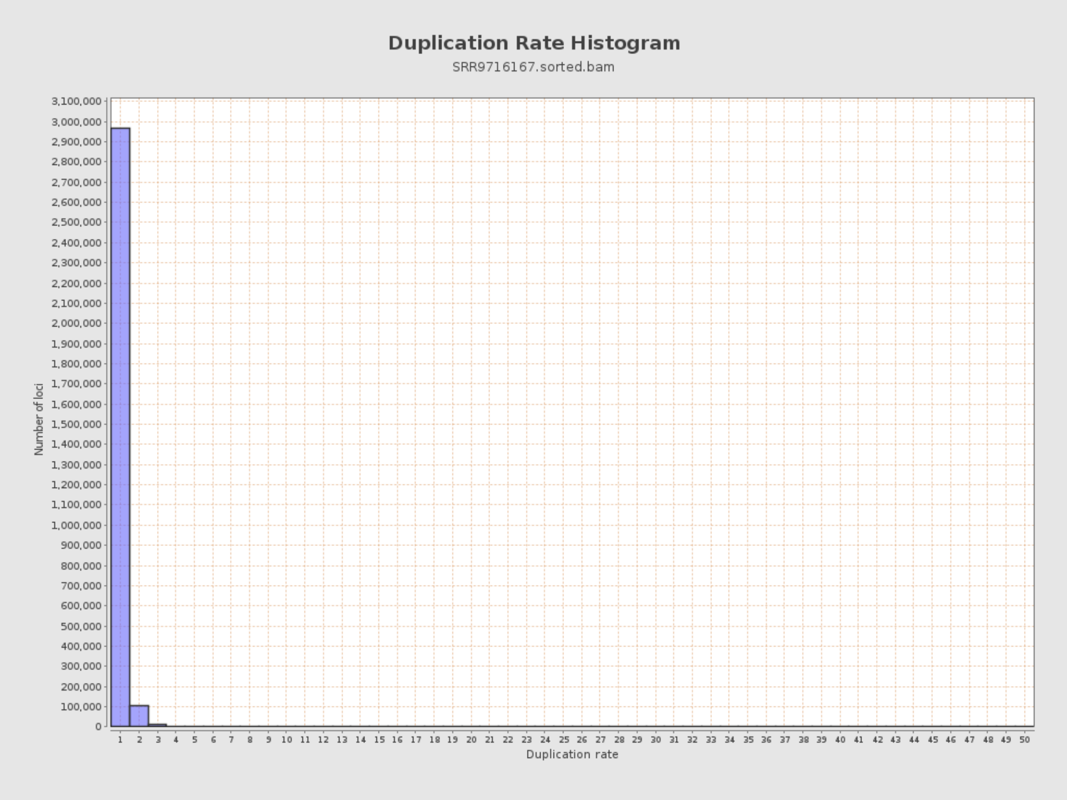
5. Results : Coverage Histogram (0-50X)



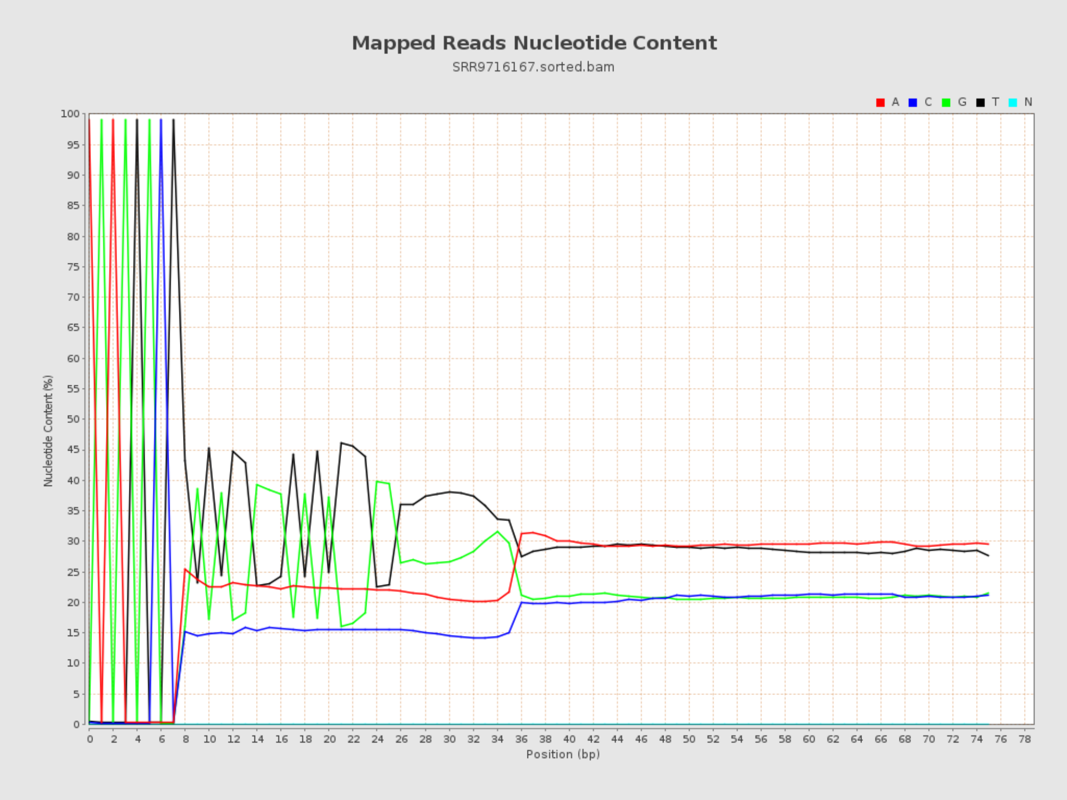
6. Results : Genome Fraction Coverage



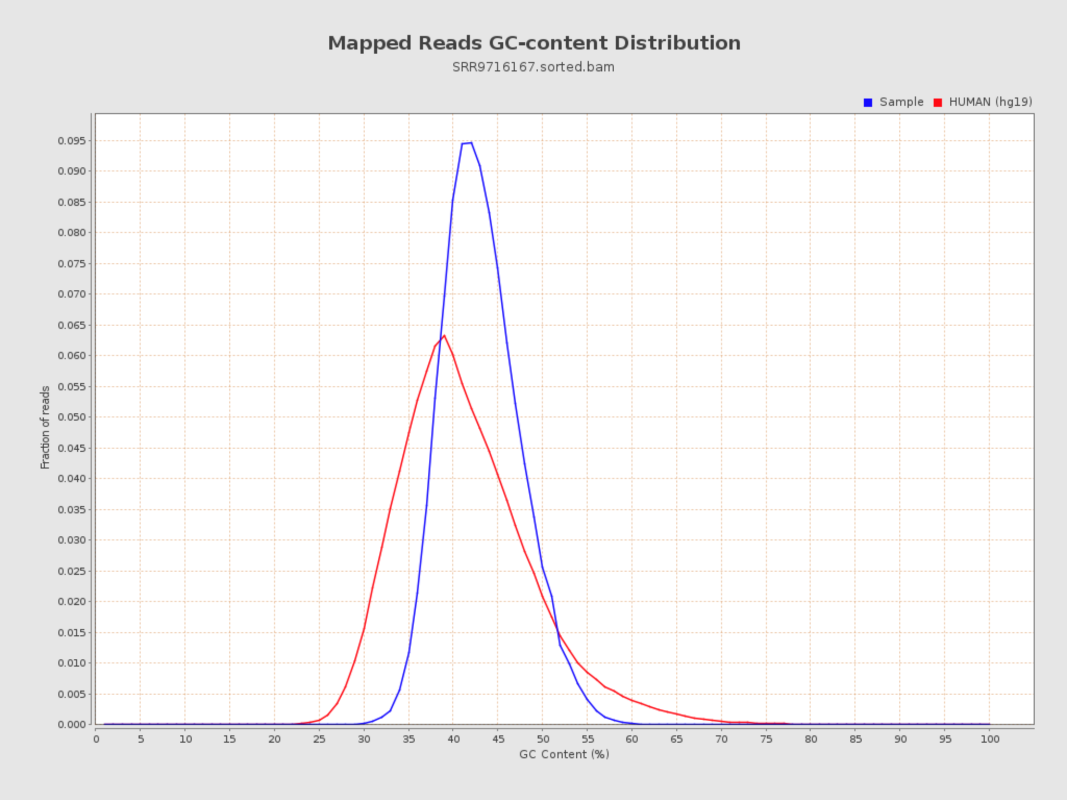
7. Results : Duplication Rate Histogram



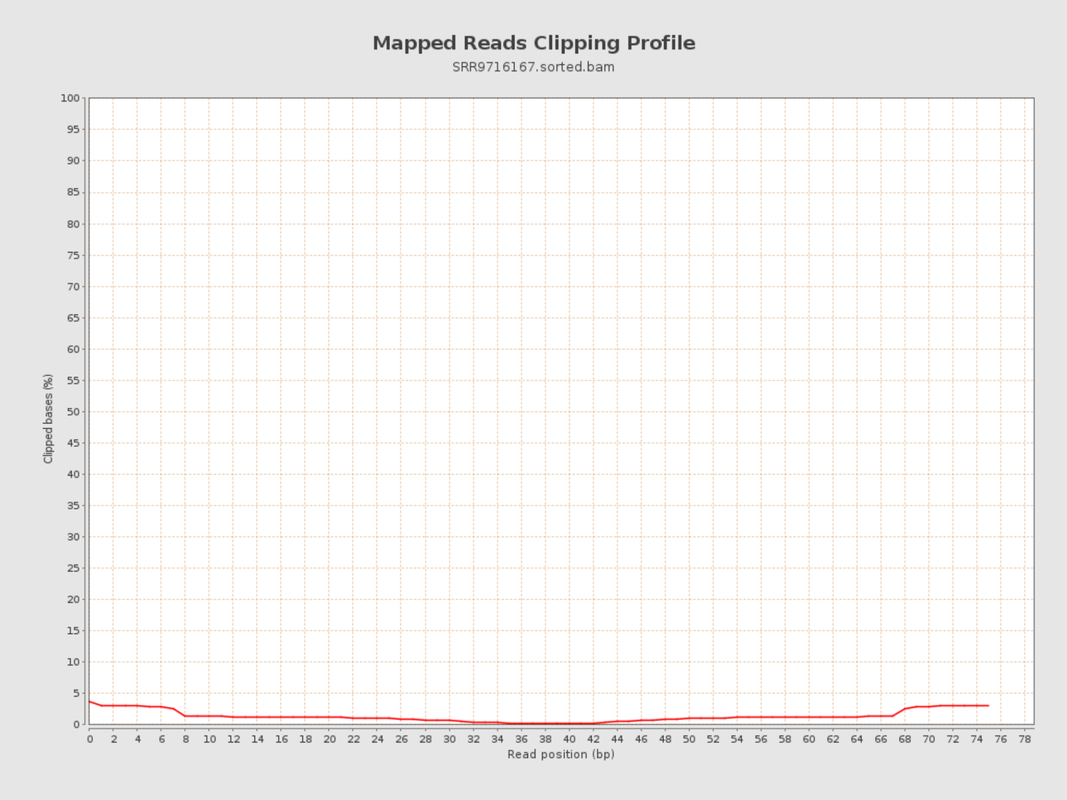
8. Results : Mapped Reads Nucleotide Content



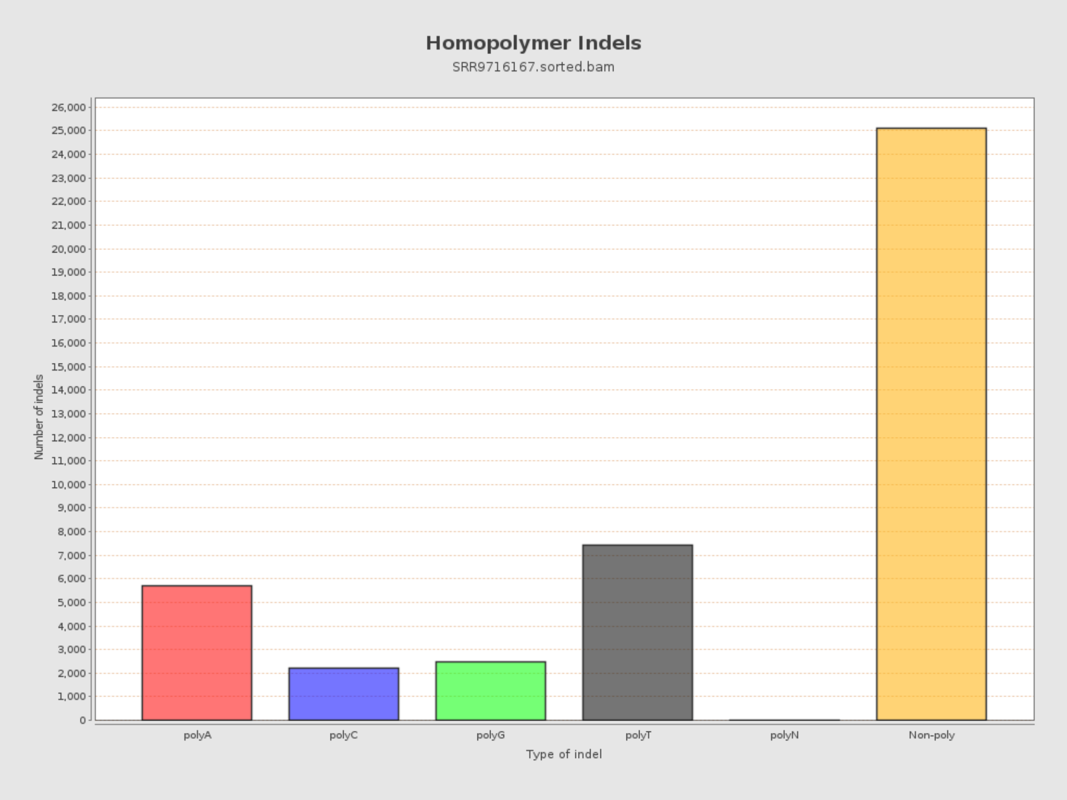
9. Results : Mapped Reads GC-content Distribution



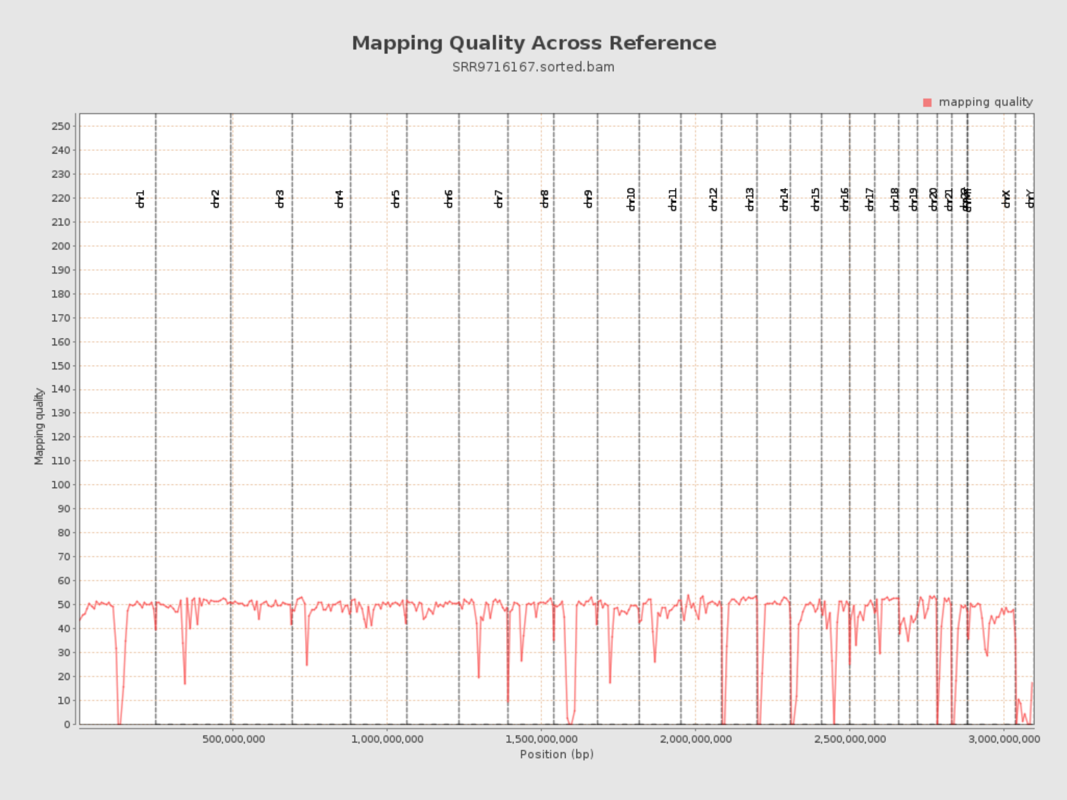
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram