Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:27:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716860.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_SRR9716860 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716860.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:27:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716860.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,017,782
Mapped reads	1,894,901 / 93.91%
Unmapped reads	122,881 / 6.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,922 / 2.18%
Read min/max/mean length	30 / 101 / 101.79
Duplicated reads (estimated)	92,205 / 4.57%
Duplication rate	3.68%
Clipped reads	1,934,641 / 95.88%

2.2. ACGT Content

Number/percentage of A's	35,473,081 / 24.23%
Number/percentage of C's	30,028,622 / 20.51%
Number/percentage of T's	43,805,562 / 29.92%
Number/percentage of G's	37,113,713 / 25.35%
Number/percentage of N's	5,581 / 0%
GC Percentage	45.85%

2.3. Coverage

Mean	0.0473

Standard Deviation	0.3975

2.4. Mapping Quality

Mean Mapping Quality	46.13

2.5. Mismatches and indels

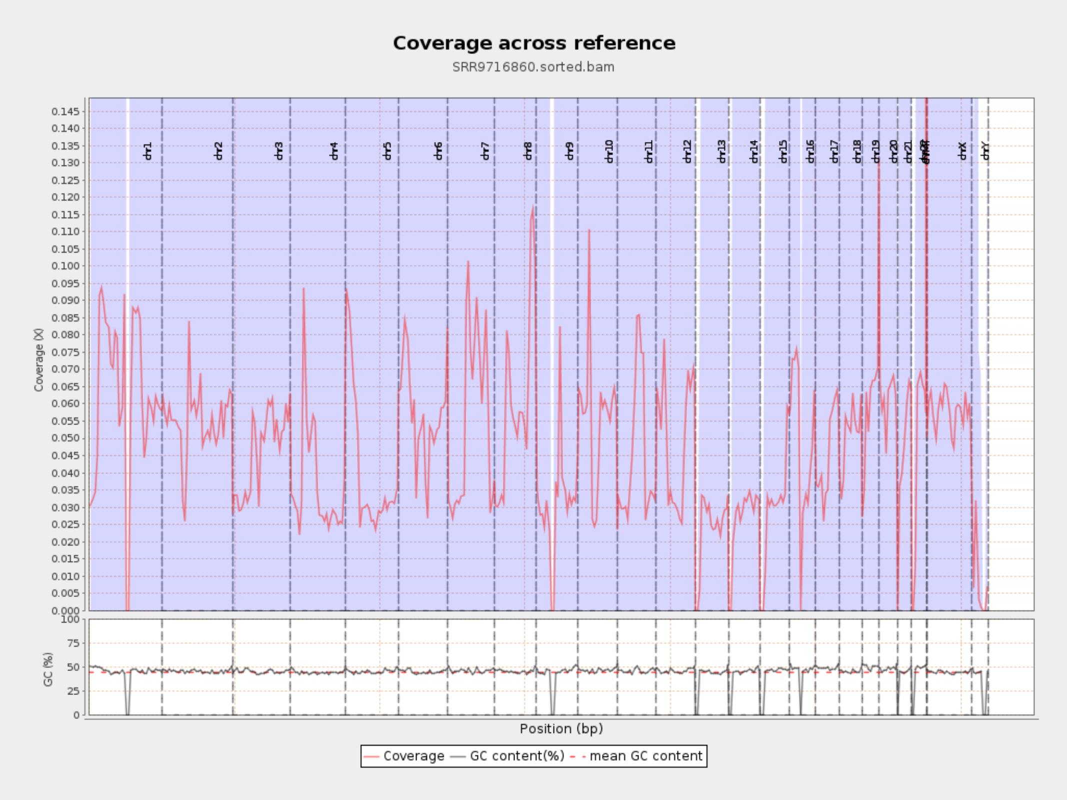
General error rate	0.7%
Mismatches	992,786
Insertions	12,925
Mapped reads with at least one insertion	0.67%
Deletions	29,178
Mapped reads with at least one deletion	1.51%
Homopolymer indels	38.83%

2.6. Chromosome stats

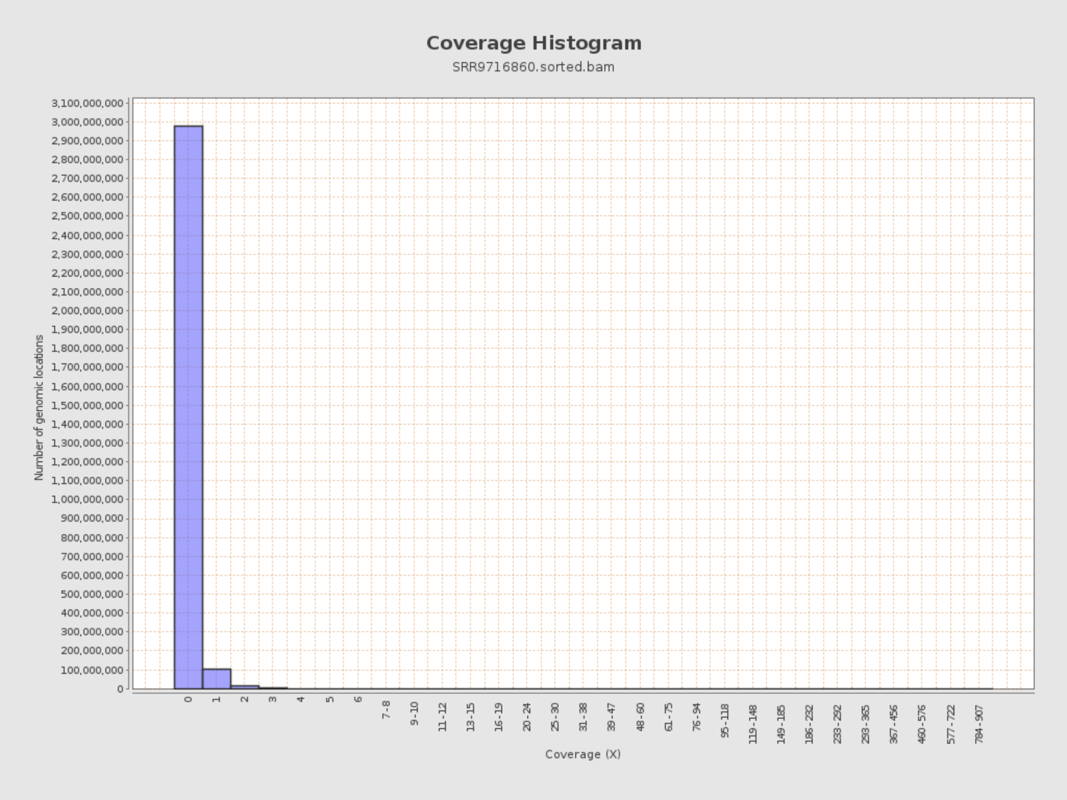
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15621916	0.0627	0.7964
chr2	243199373	13344852	0.0549	0.4057
chr3	198022430	9102381	0.046	0.2512
chr4	191154276	6898032	0.0361	0.3367
chr5	180915260	7343985	0.0406	0.2371
chr6	171115067	9713443	0.0568	0.2976
chr7	159138663	8957710	0.0563	0.5062

chr8	146364022	8840719	0.0604	0.4058
chr9	141213431	4350193	0.0308	0.2758
chr10	135534747	7608764	0.0561	0.5339
chr11	135006516	6058959	0.0449	0.3247
chr12	133851895	6580609	0.0492	0.2617
chr13	115169878	2676139	0.0232	0.1741
chr14	107349540	2813558	0.0262	0.2081
chr15	102531392	2935518	0.0286	0.195
chr16	90354753	4460892	0.0494	0.2795
chr17	81195210	3689444	0.0454	0.2844
chr18	78077248	3971506	0.0509	0.4253
chr19	59128983	3597945	0.0608	0.571
chr20	63025520	3846218	0.061	0.3073
chr21	48129895	2248392	0.0467	0.3129
chr22	51304566	2262860	0.0441	0.2679
chrMT	16571	68043	4.1061	3.5605
chrX	155270560	8992153	0.0579	0.2991
chrY	59373566	502889	0.0085	0.3043

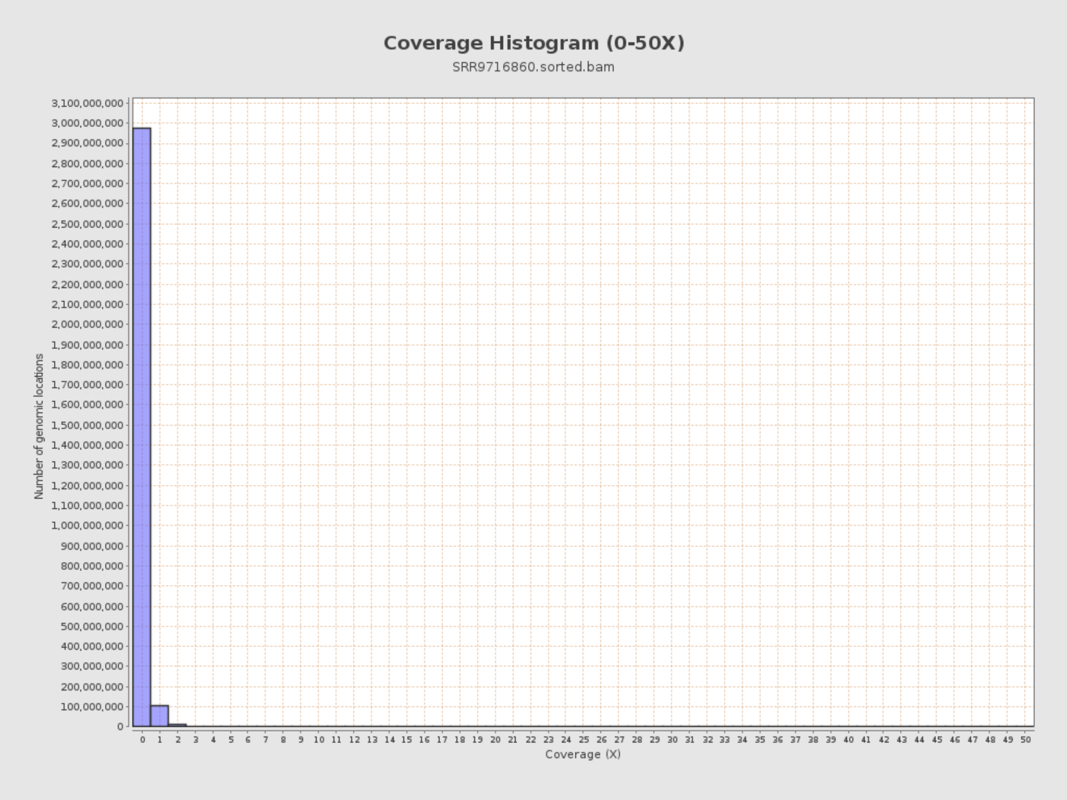
3. Results : Coverage across reference



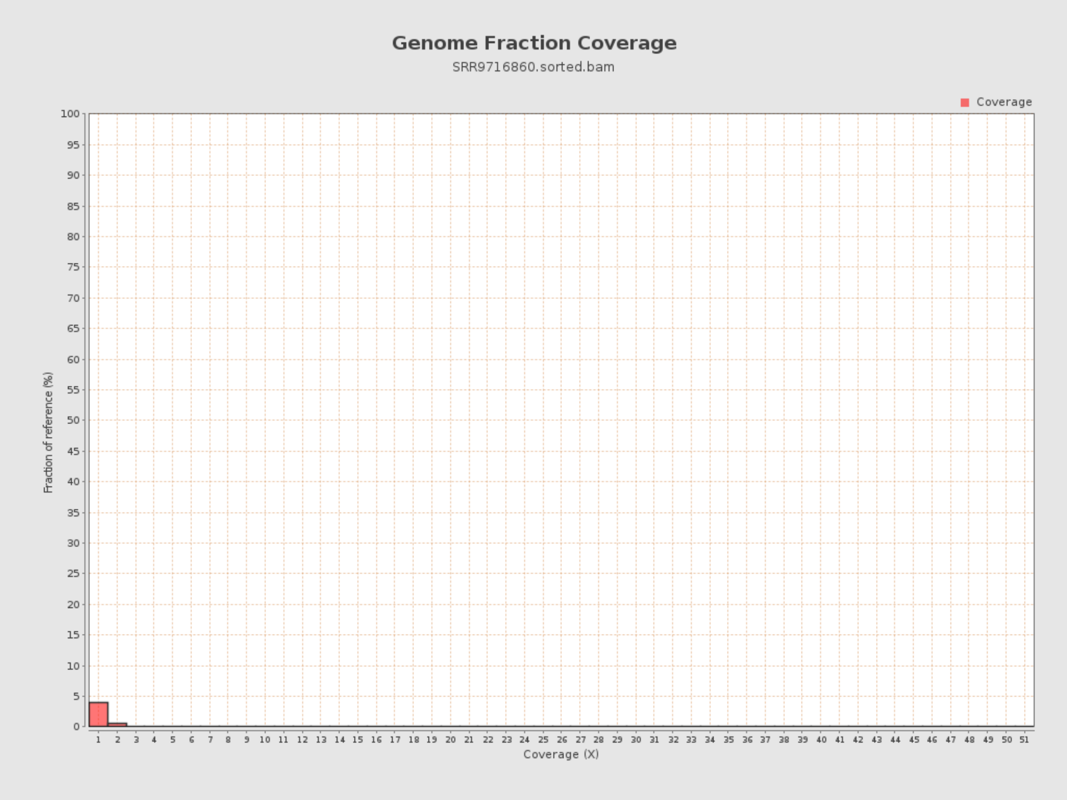
4. Results : Coverage Histogram



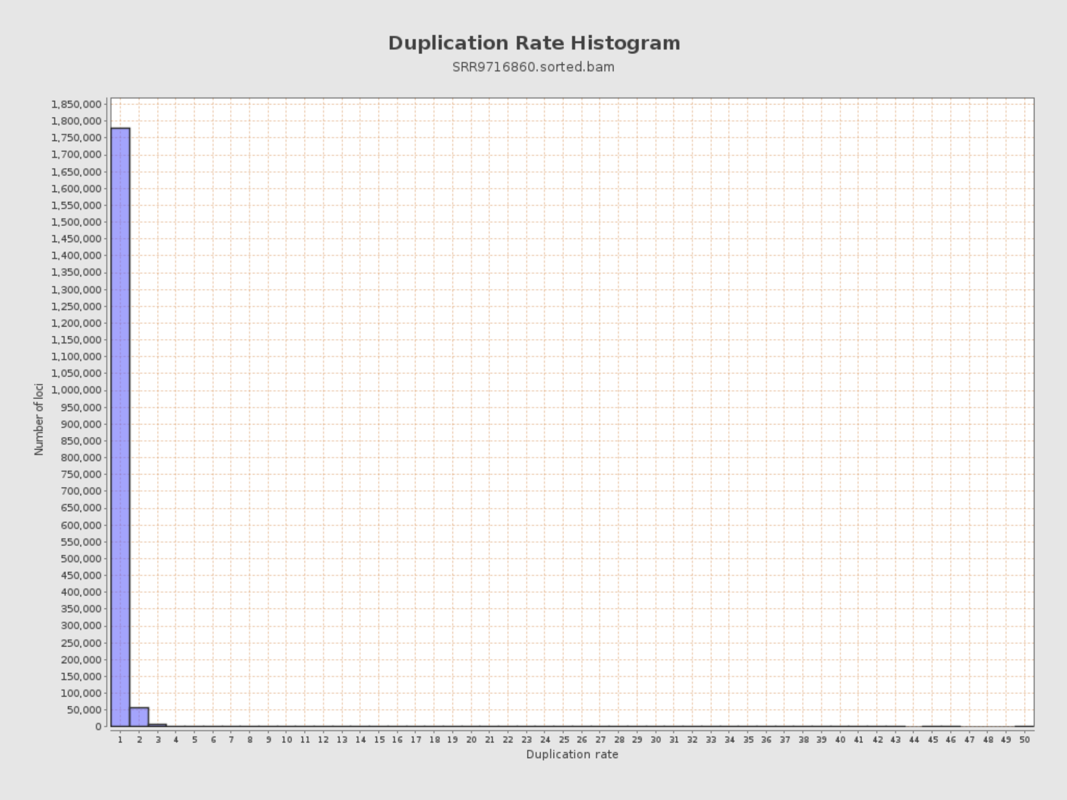
5. Results : Coverage Histogram (0-50X)



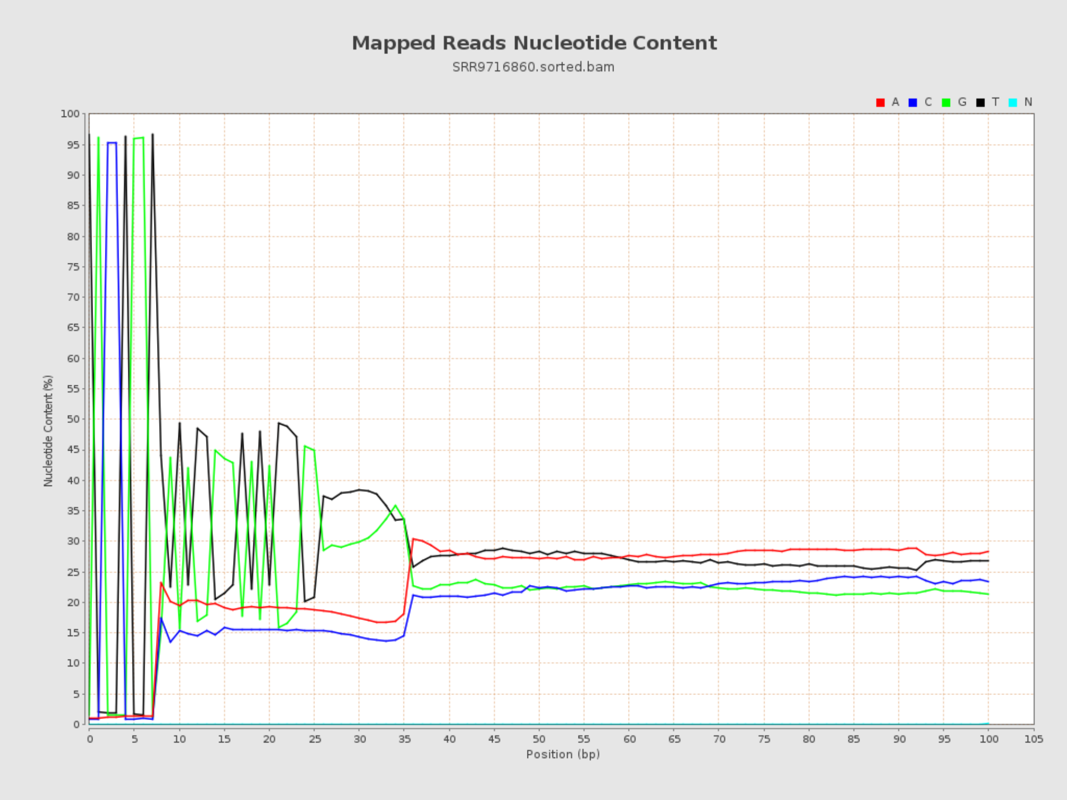
6. Results : Genome Fraction Coverage



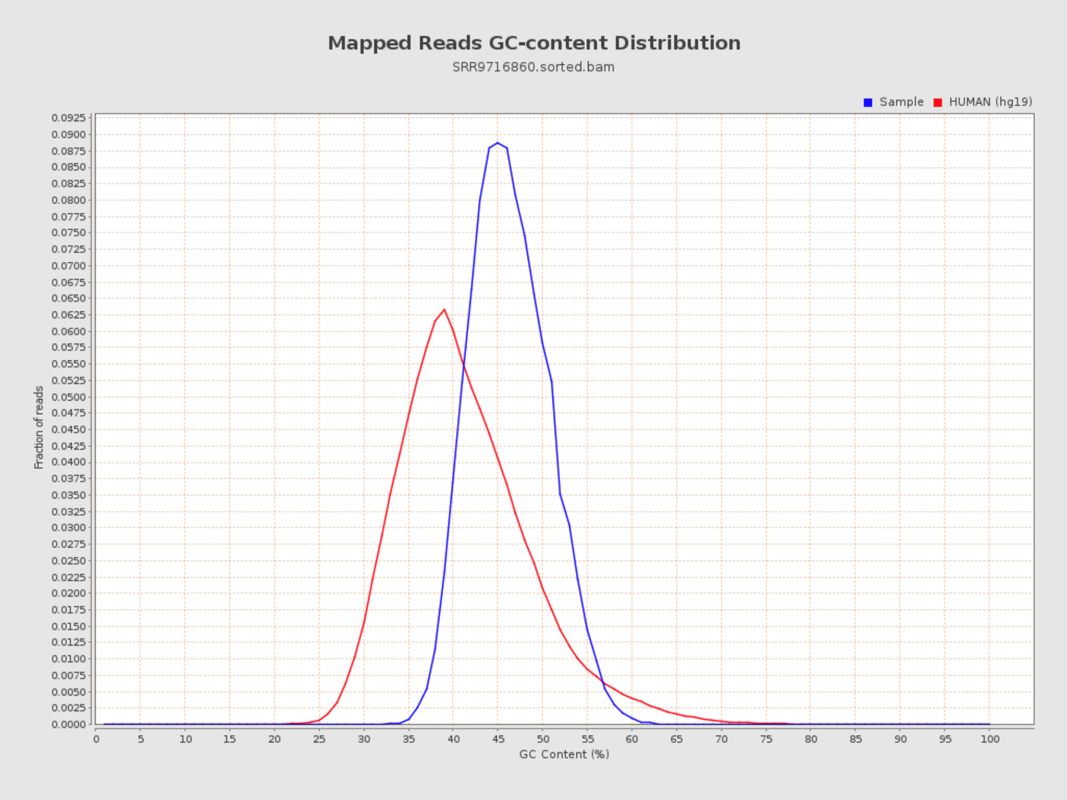
7. Results : Duplication Rate Histogram



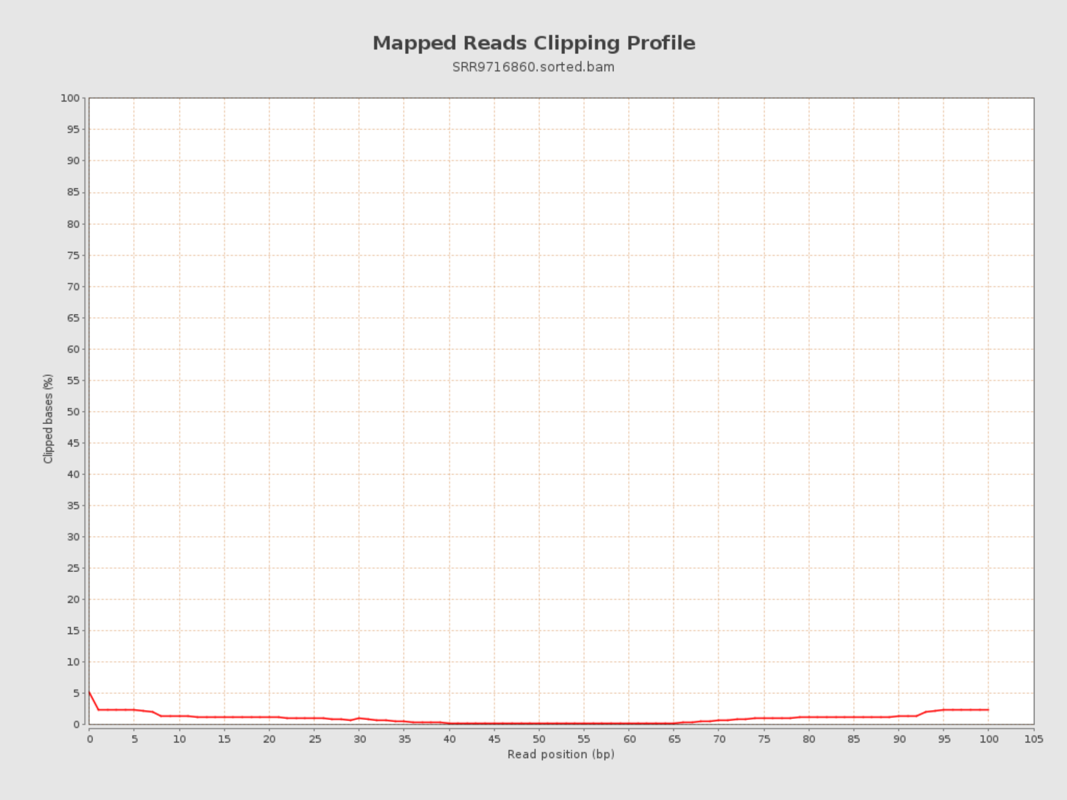
8. Results : Mapped Reads Nucleotide Content



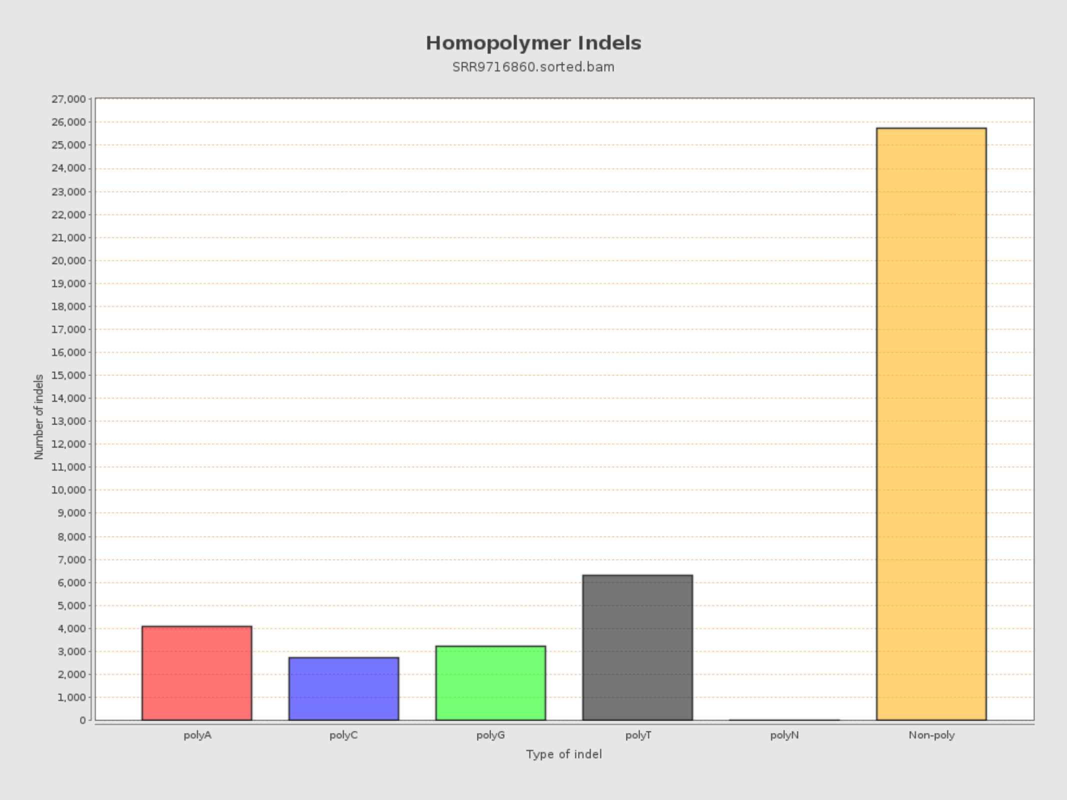
9. Results : Mapped Reads GC-content Distribution



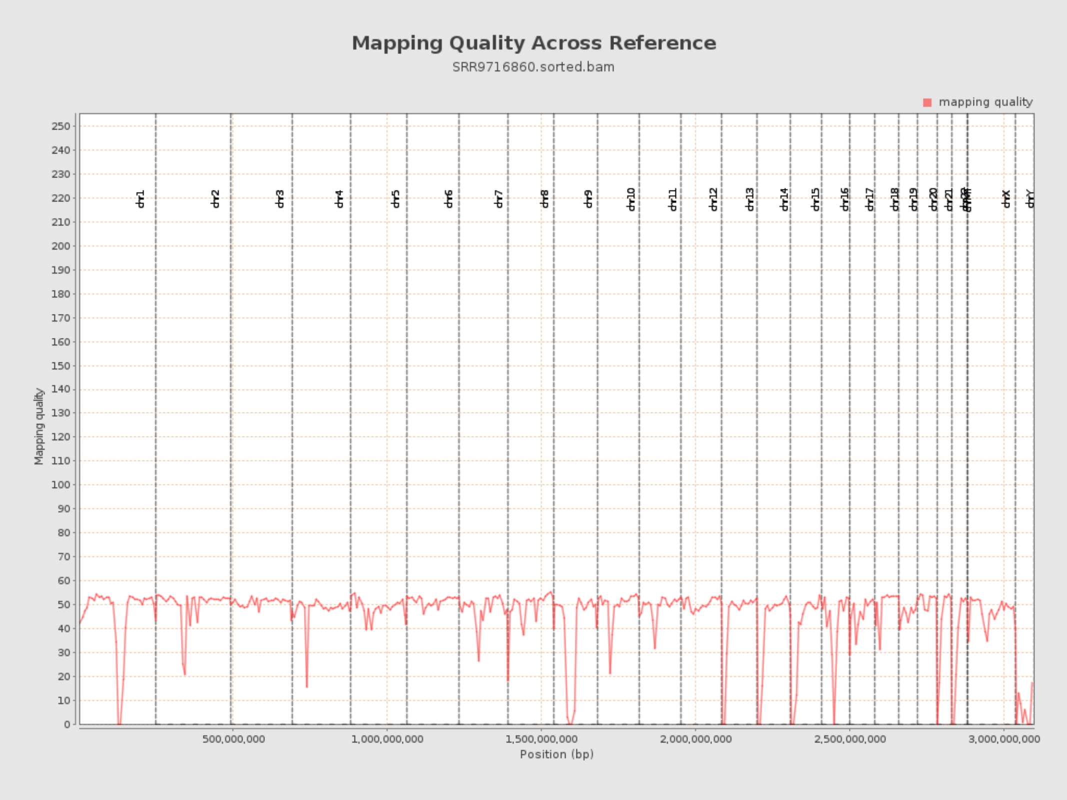
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram