Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:35:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716573.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_SRR9716573 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716573.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:35:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716573.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,874,446
Mapped reads	1,736,170 / 92.62%
Unmapped reads	138,276 / 7.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,812 / 2.28%
Read min/max/mean length	30 / 101 / 101.84
Duplicated reads (estimated)	77,773 / 4.15%
Duplication rate	3.39%
Clipped reads	1,776,081 / 94.75%

2.2. ACGT Content

Number/percentage of A's	33,943,494 / 25.46%
Number/percentage of C's	27,216,783 / 20.41%
Number/percentage of T's	40,024,059 / 30.02%
Number/percentage of G's	32,132,575 / 24.1%
Number/percentage of N's	5,162 / 0%
GC Percentage	44.52%

2.3. Coverage

Mean	0.0431

Standard Deviation	0.3616

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

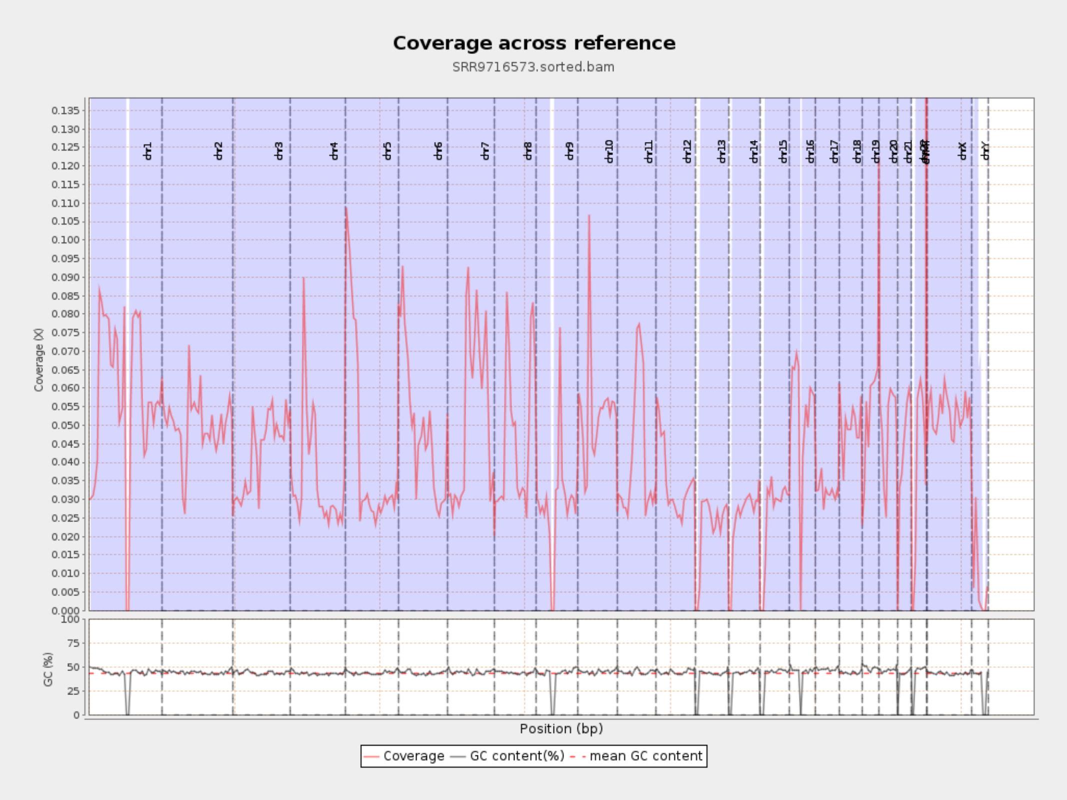
General error rate	0.69%
Mismatches	895,833
Insertions	11,578
Mapped reads with at least one insertion	0.66%
Deletions	25,717
Mapped reads with at least one deletion	1.45%
Homopolymer indels	37.77%

2.6. Chromosome stats

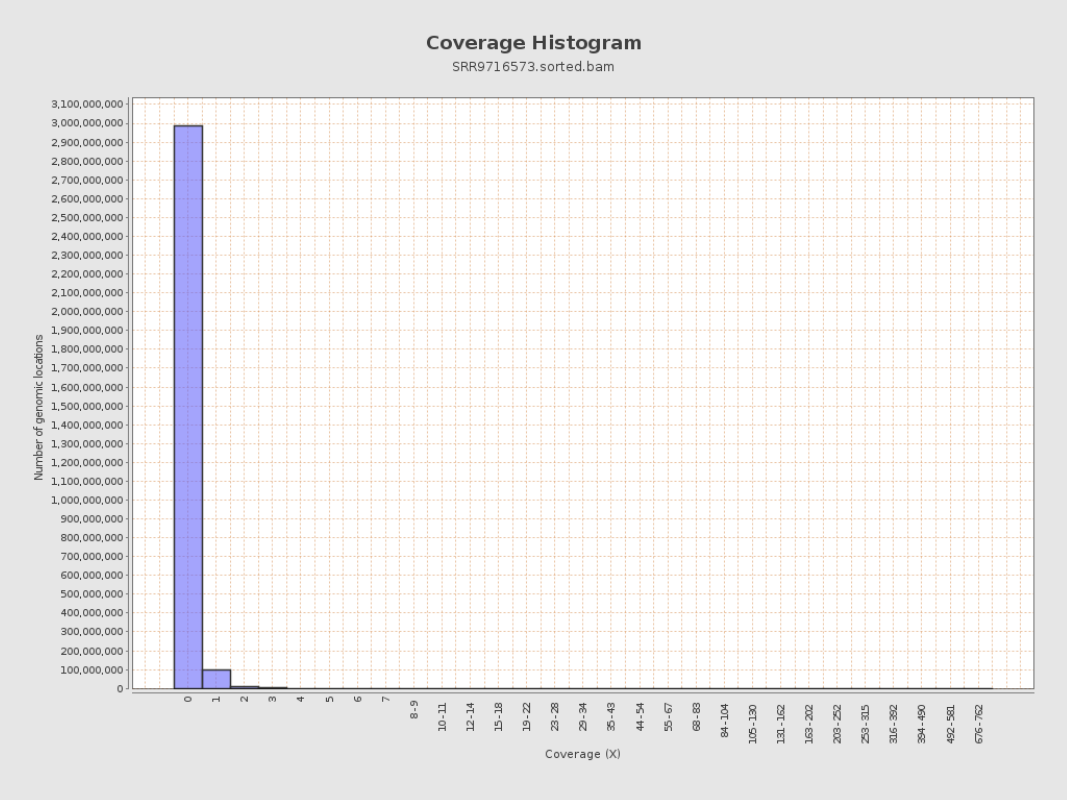
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14489815	0.0581	0.6731
chr2	243199373	12150481	0.05	0.3603
chr3	198022430	8456266	0.0427	0.2395
chr4	191154276	6731489	0.0352	0.3204
chr5	180915260	7904444	0.0437	0.2465
chr6	171115067	8460946	0.0494	0.2727
chr7	159138663	8508684	0.0535	0.514

chr8	146364022	6863834	0.0469	0.3704
chr9	141213431	4035600	0.0286	0.2529
chr10	135534747	7214670	0.0532	0.4936
chr11	135006516	5638835	0.0418	0.3236
chr12	133851895	4681743	0.035	0.216
chr13	115169878	2543769	0.0221	0.1688
chr14	107349540	2605658	0.0243	0.1968
chr15	102531392	2624685	0.0256	0.1843
chr16	90354753	4826202	0.0534	0.2892
chr17	81195210	2604632	0.0321	0.243
chr18	78077248	3873542	0.0496	0.401
chr19	59128983	3284801	0.0556	0.5086
chr20	63025520	3086300	0.049	0.2761
chr21	48129895	2065764	0.0429	0.2975
chr22	51304566	1903582	0.0371	0.2303
chrMT	16571	54525	3.2904	2.871
chrX	155270560	8302893	0.0535	0.2823
chrY	59373566	462154	0.0078	0.2941

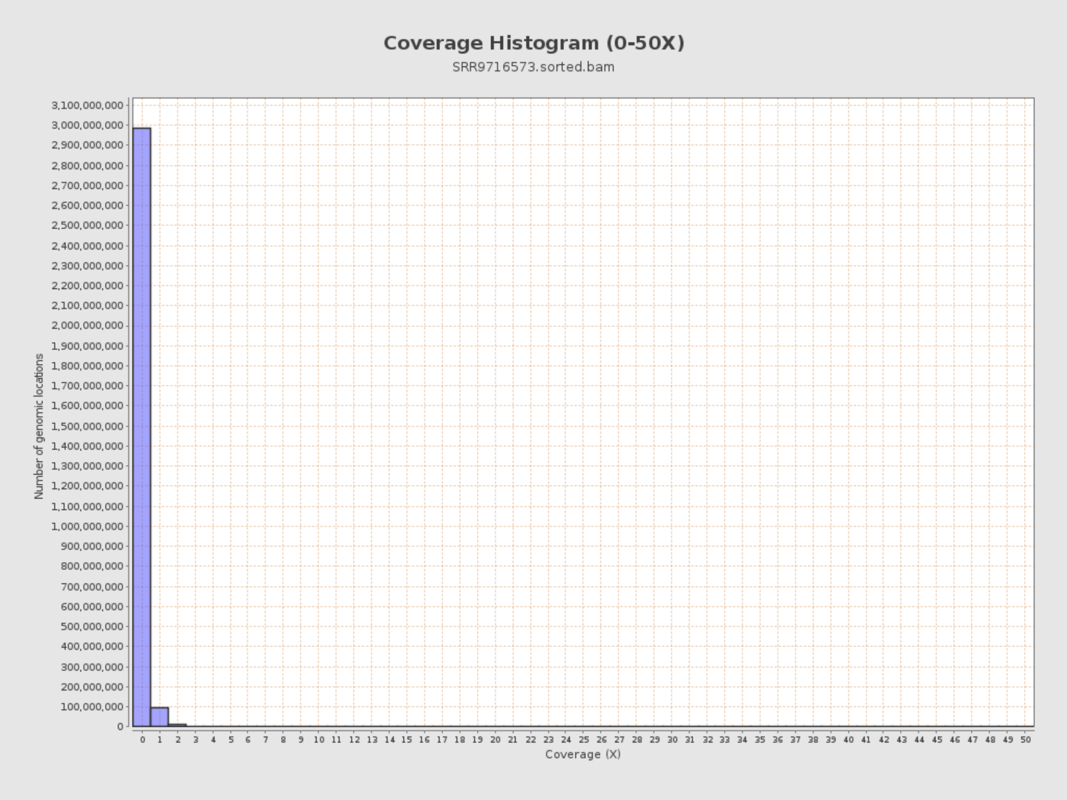
3. Results : Coverage across reference



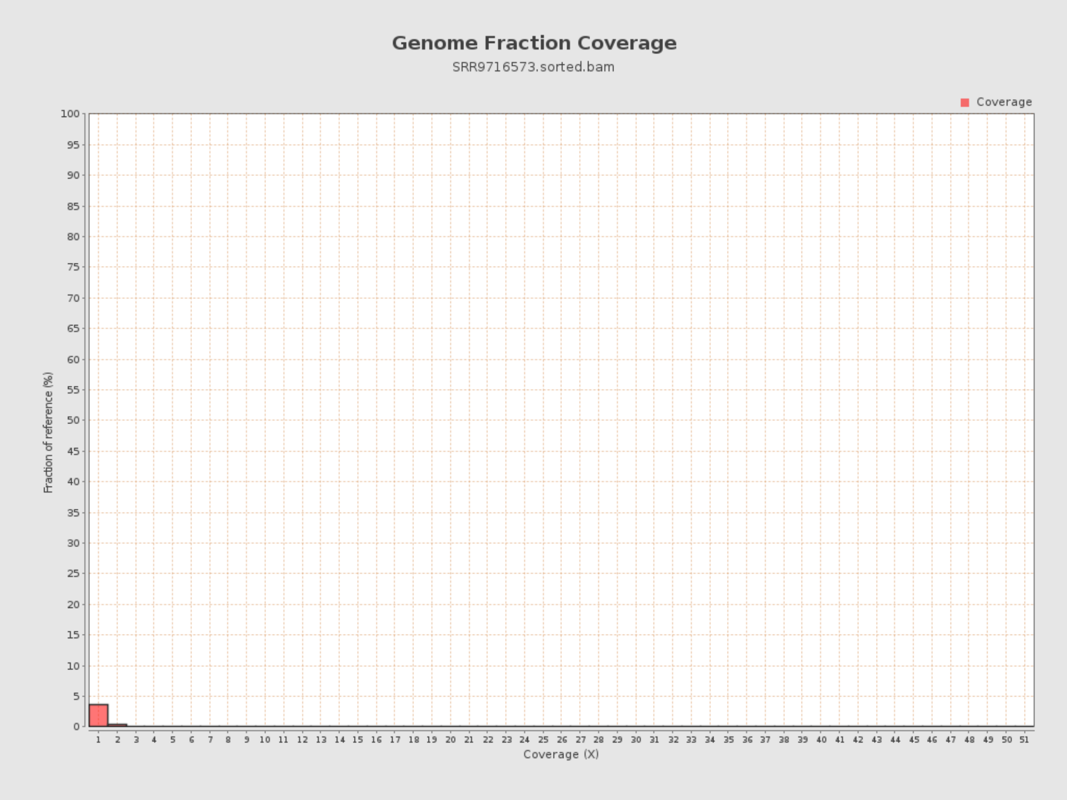
4. Results : Coverage Histogram



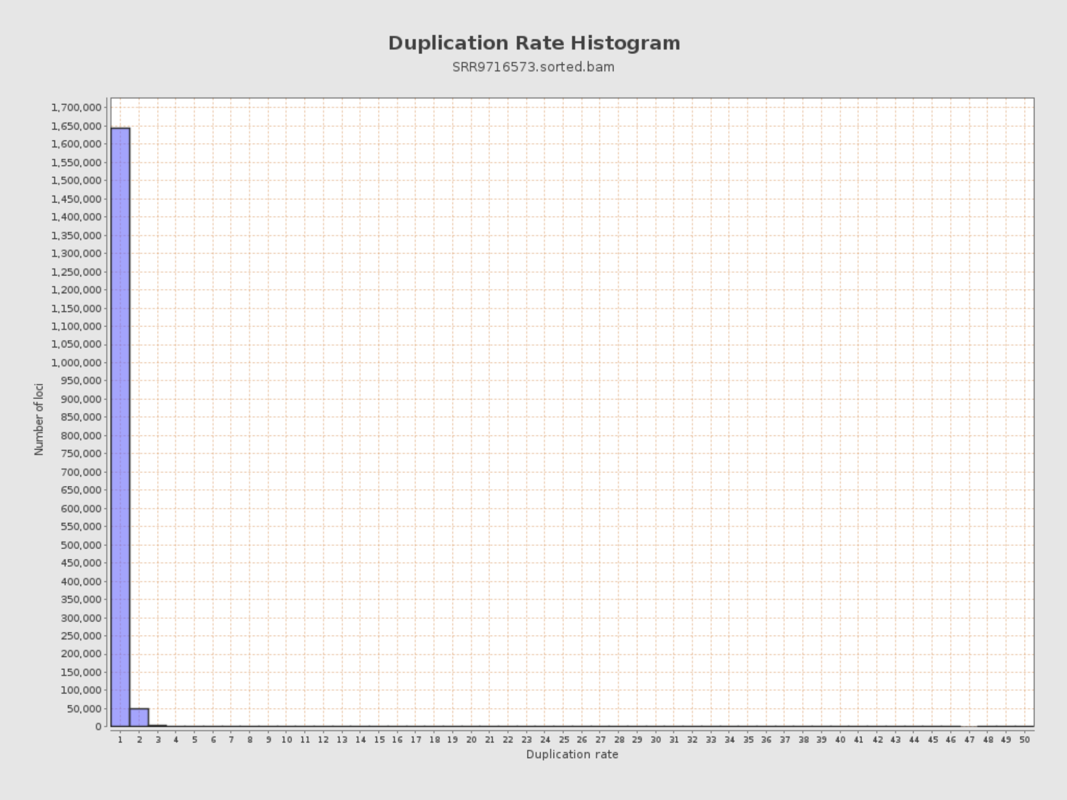
5. Results : Coverage Histogram (0-50X)



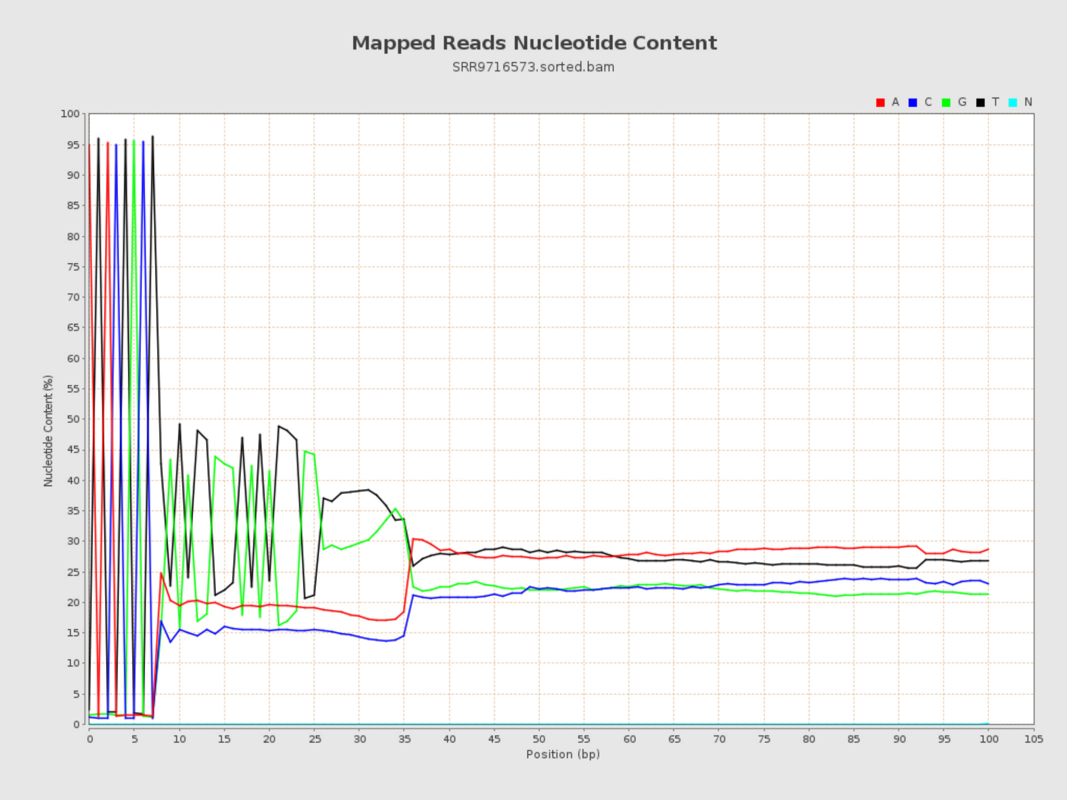
6. Results : Genome Fraction Coverage



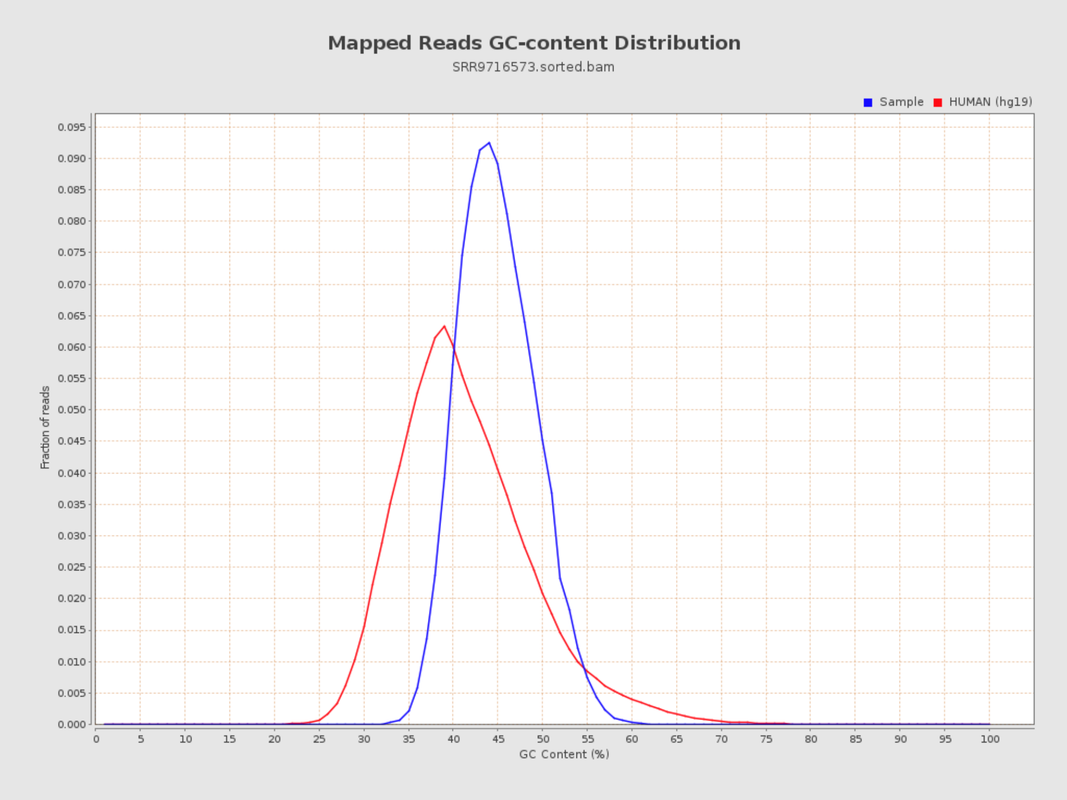
7. Results : Duplication Rate Histogram



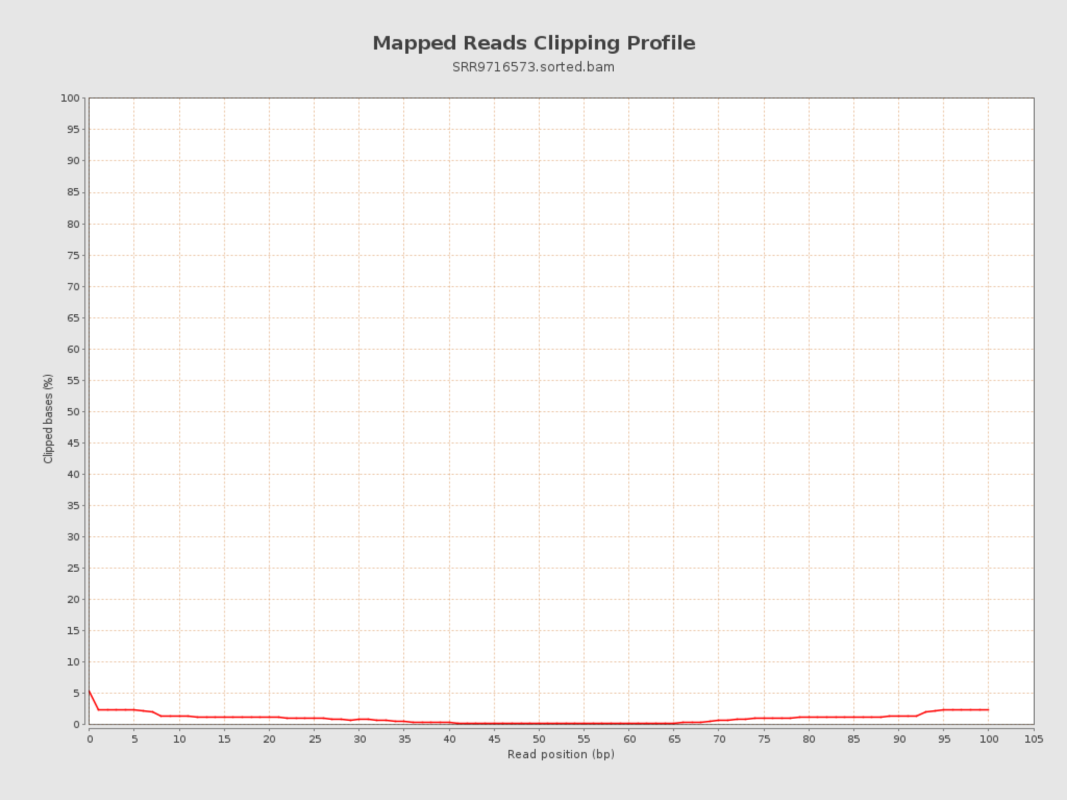
8. Results : Mapped Reads Nucleotide Content



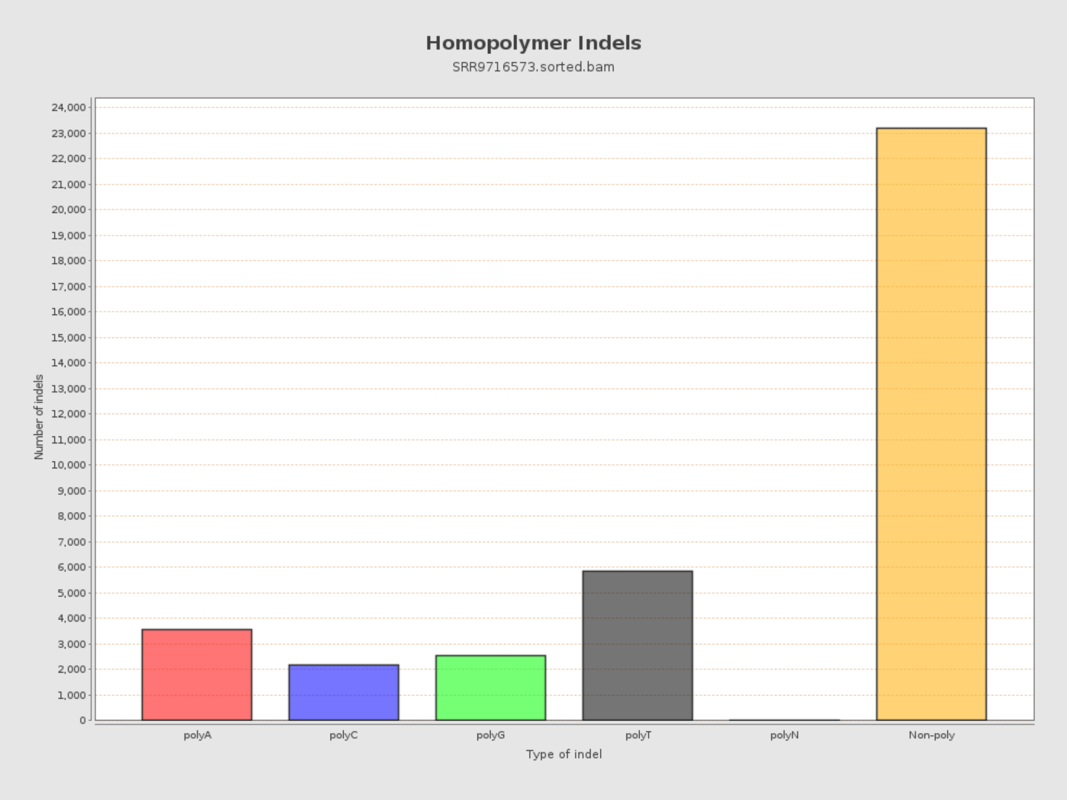
9. Results : Mapped Reads GC-content Distribution



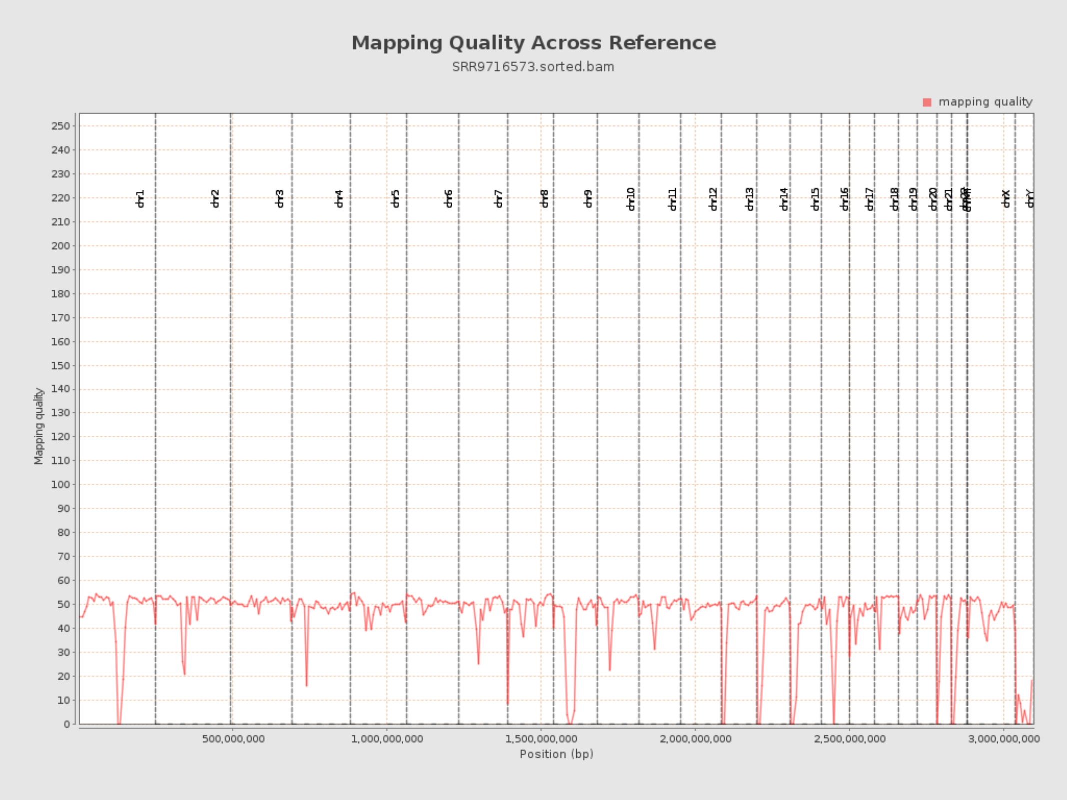
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram