Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:12:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004041.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_SRR6004041 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004041.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:12:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,919,478
Mapped reads	2,578,616 / 88.32%
Unmapped reads	340,862 / 11.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,580 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	142,886 / 4.89%
Duplication rate	4.45%
Clipped reads	1,203,199 / 41.21%

2.2. ACGT Content

Number/percentage of A's	47,350,753 / 27.66%
Number/percentage of C's	32,372,107 / 18.91%
Number/percentage of T's	53,147,265 / 31.05%
Number/percentage of G's	38,299,995 / 22.37%
Number/percentage of N's	20,660 / 0.01%
GC Percentage	41.28%

2.3. Coverage

Mean	0.0553

Standard Deviation	0.43

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

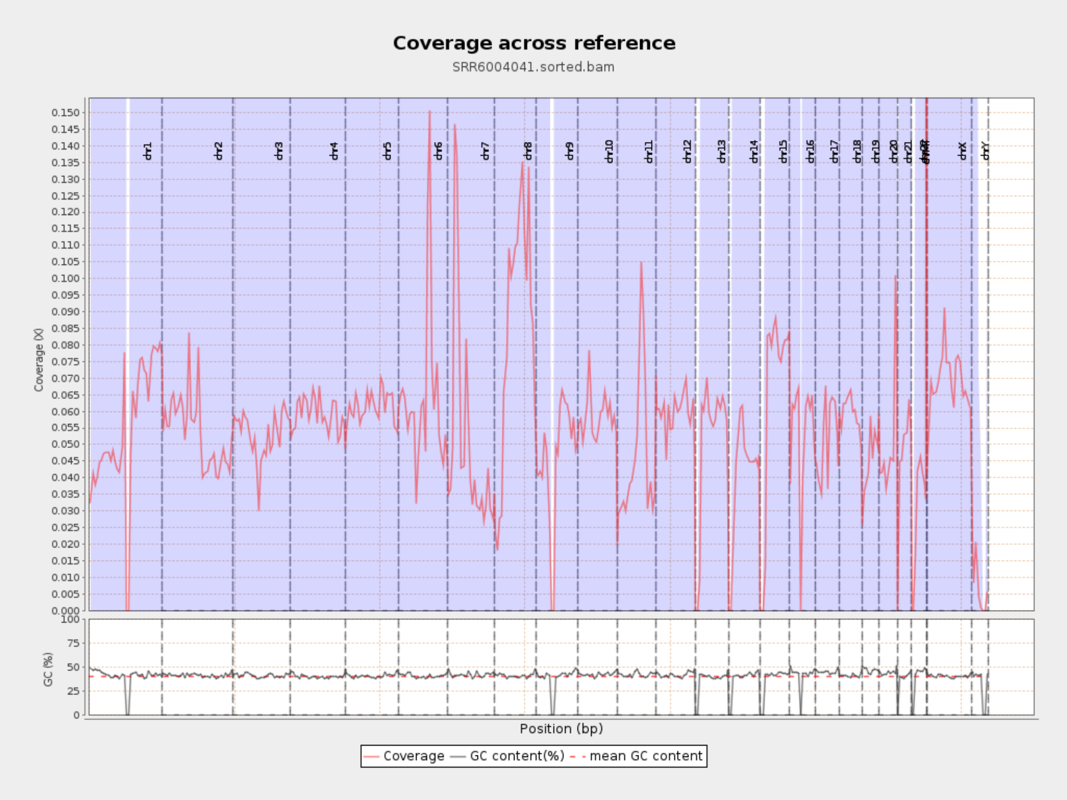
General error rate	0.75%
Mismatches	1,258,319
Insertions	12,042
Mapped reads with at least one insertion	0.46%
Deletions	43,693
Mapped reads with at least one deletion	1.68%
Homopolymer indels	47.14%

2.6. Chromosome stats

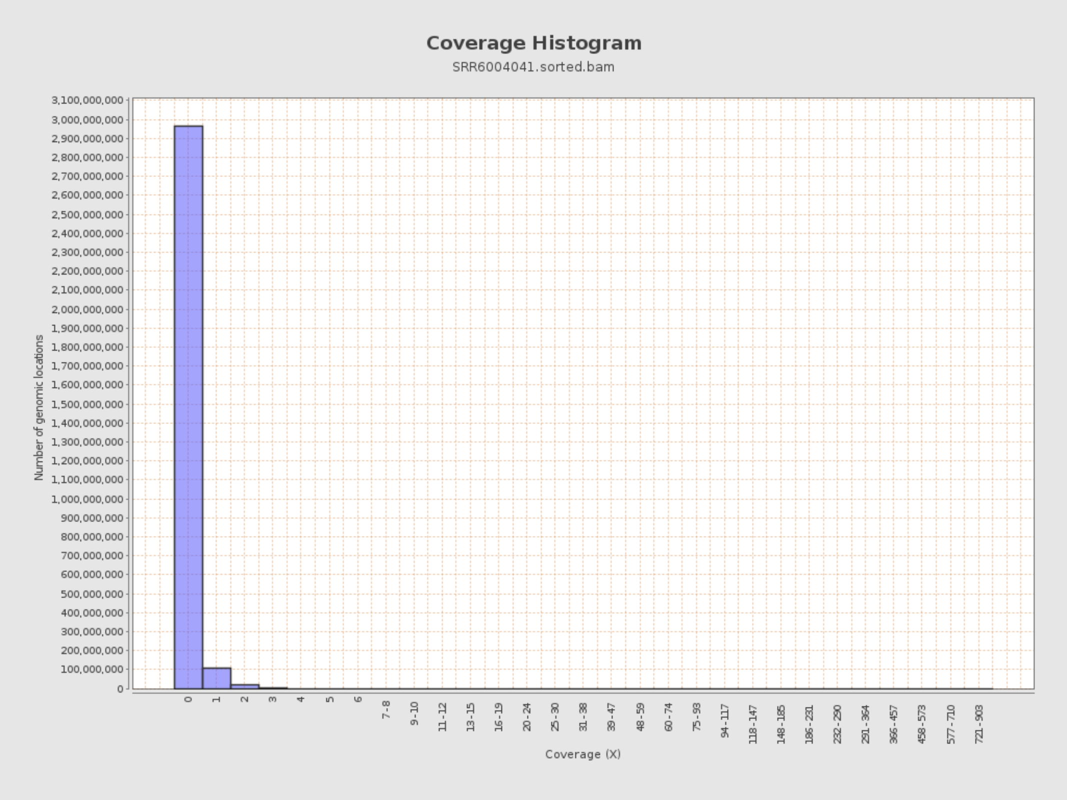
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13491743	0.0541	0.7318
chr2	243199373	13082807	0.0538	0.4736
chr3	198022430	10530966	0.0532	0.282
chr4	191154276	11278859	0.059	0.318
chr5	180915260	11115282	0.0614	0.3064
chr6	171115067	11000417	0.0643	0.3508
chr7	159138663	8321069	0.0523	0.557

chr8	146364022	12455863	0.0851	0.6596
chr9	141213431	6419602	0.0455	0.3777
chr10	135534747	7910997	0.0584	0.3977
chr11	135006516	6354243	0.0471	0.35
chr12	133851895	8023581	0.0599	0.3072
chr13	115169878	5801242	0.0504	0.2758
chr14	107349540	4364977	0.0407	0.2733
chr15	102531392	6638161	0.0647	0.316
chr16	90354753	4816695	0.0533	0.3078
chr17	81195210	4208736	0.0518	0.3032
chr18	78077248	4654776	0.0596	0.6539
chr19	59128983	2709422	0.0458	0.5512
chr20	63025520	3269068	0.0519	0.293
chr21	48129895	2278303	0.0473	0.2872
chr22	51304566	1491933	0.0291	0.206
chrMT	16571	10020	0.6047	1.0725
chrX	155270560	10633938	0.0685	0.3562
chrY	59373566	404247	0.0068	0.1452

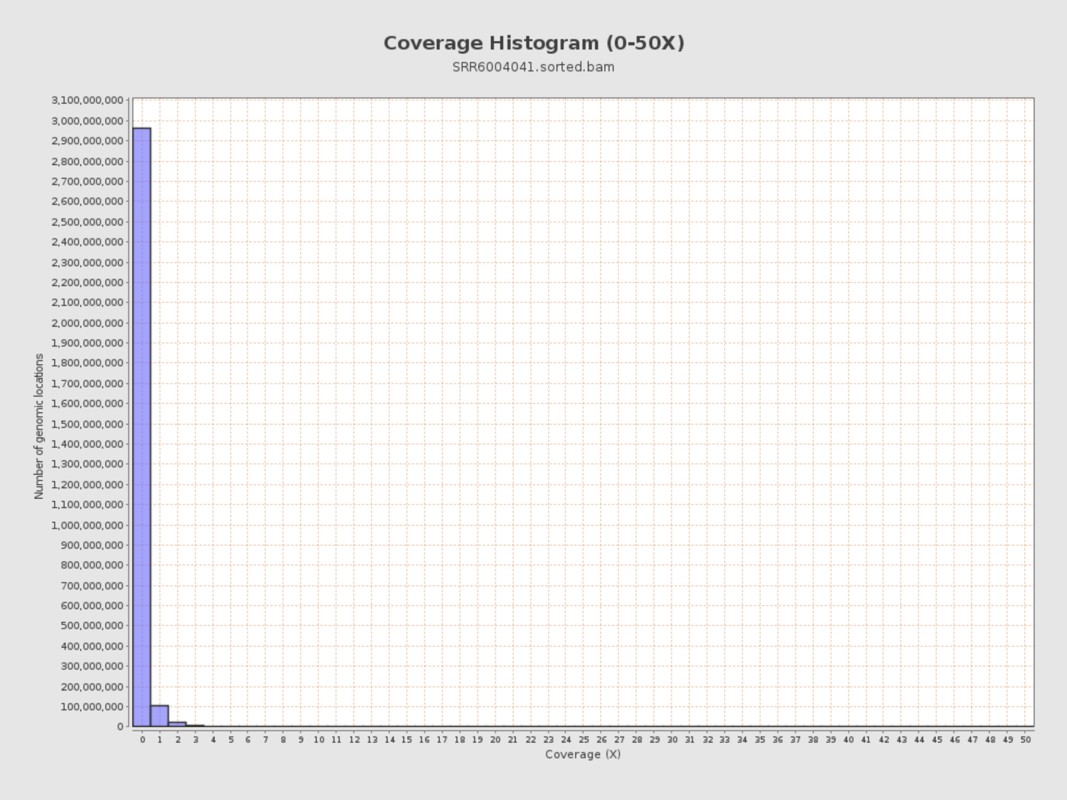
3. Results : Coverage across reference



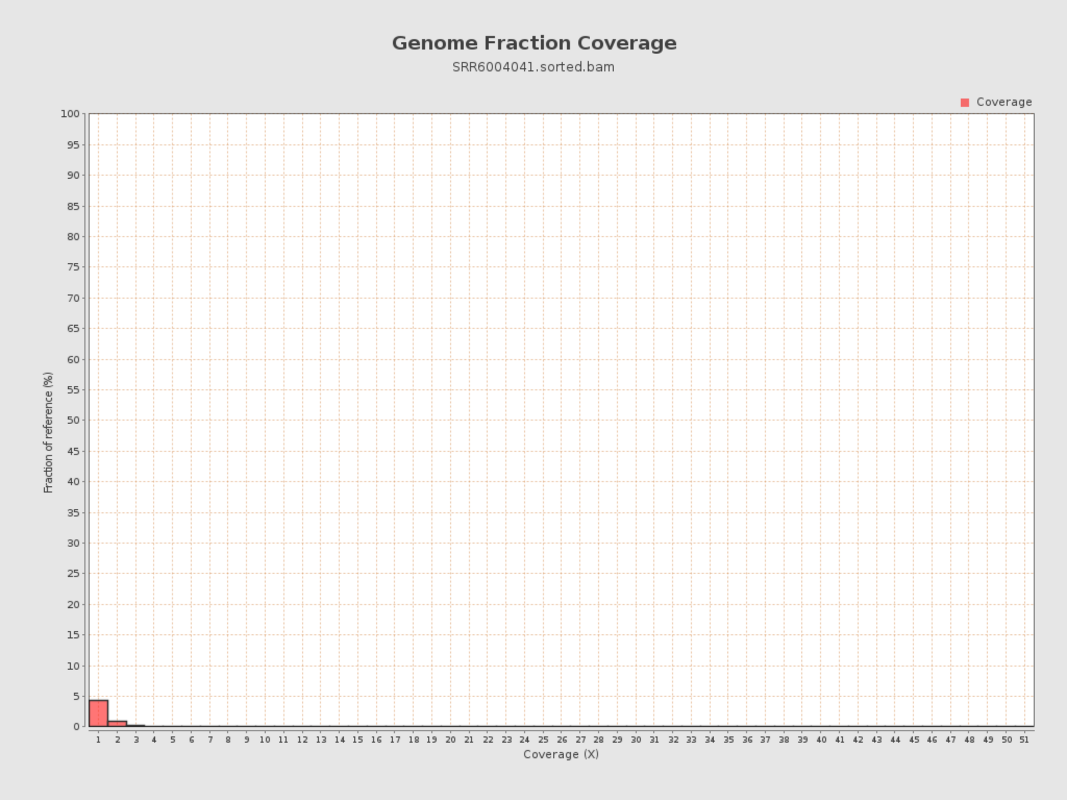
4. Results : Coverage Histogram



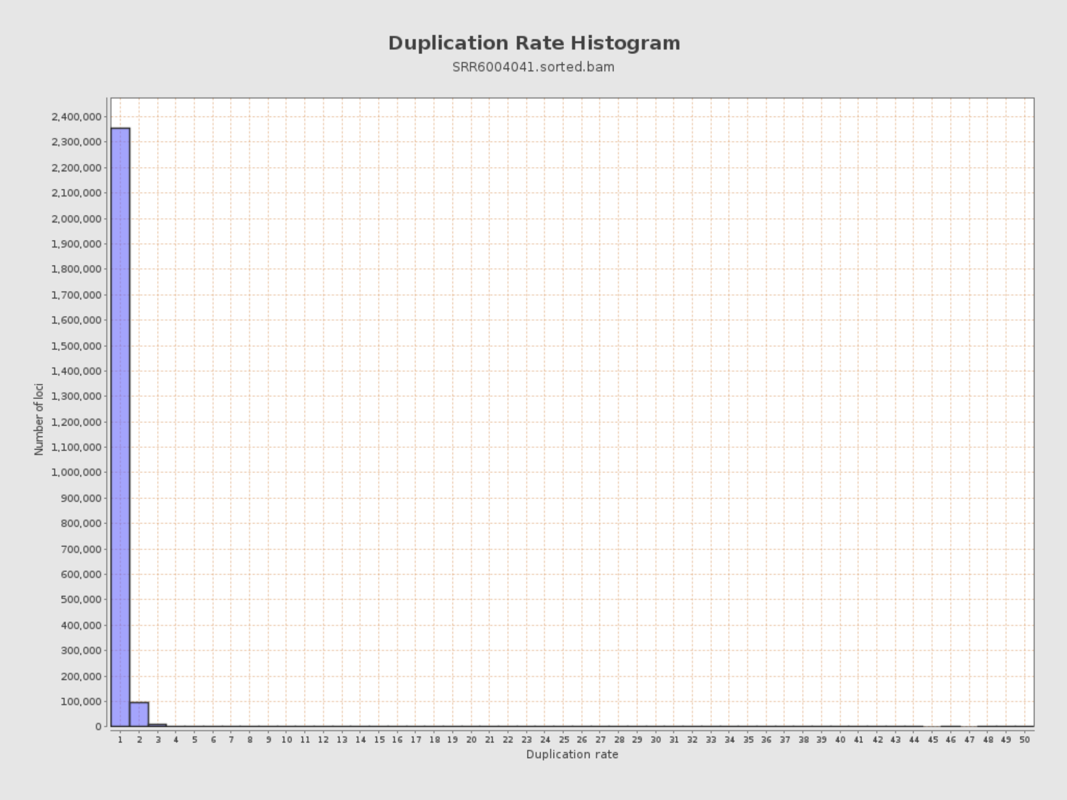
5. Results : Coverage Histogram (0-50X)



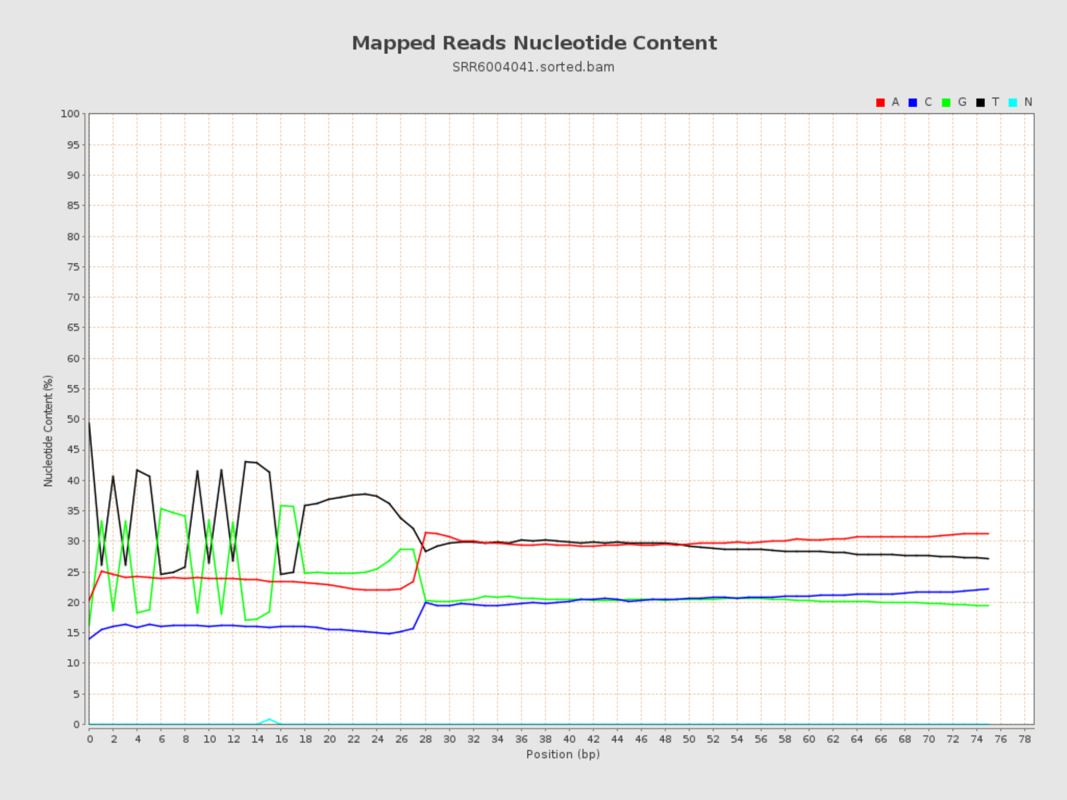
6. Results : Genome Fraction Coverage



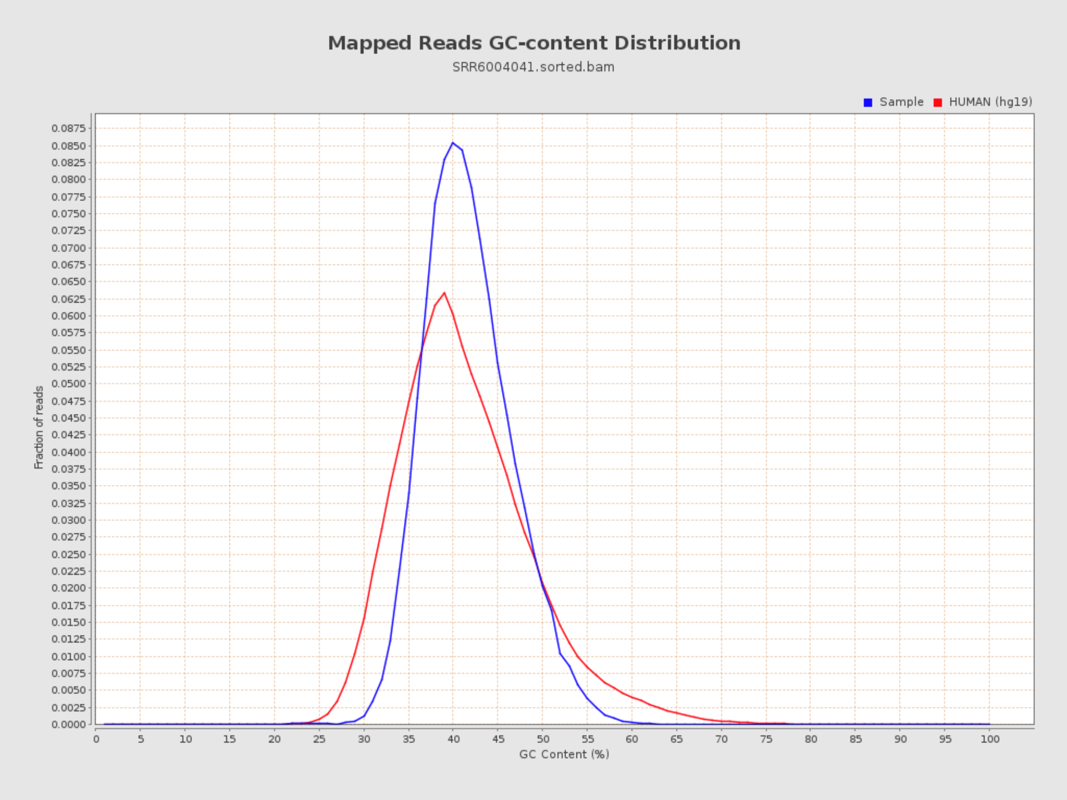
7. Results : Duplication Rate Histogram



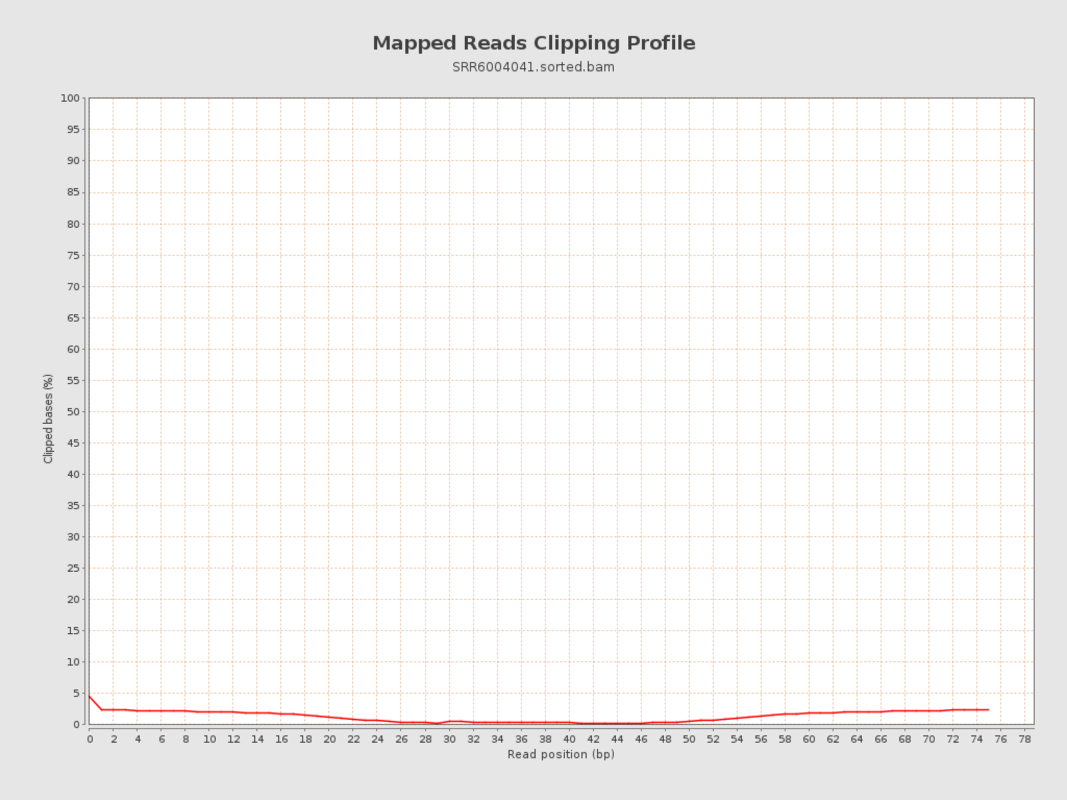
8. Results : Mapped Reads Nucleotide Content



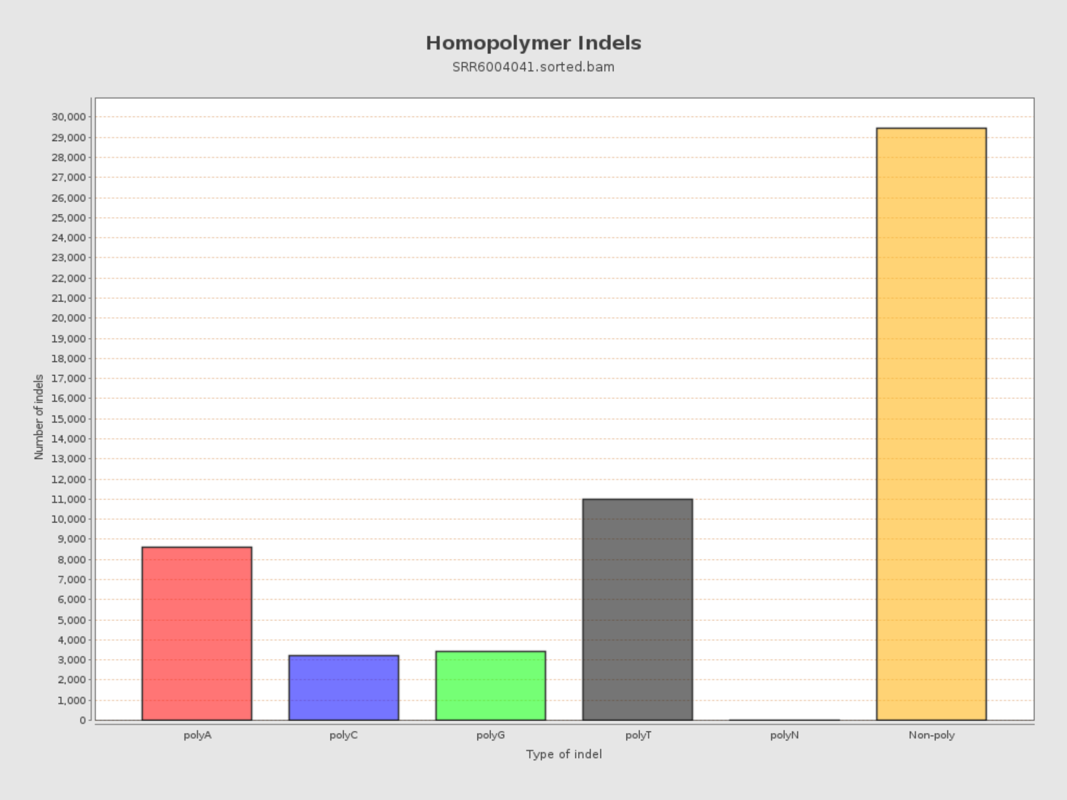
9. Results : Mapped Reads GC-content Distribution



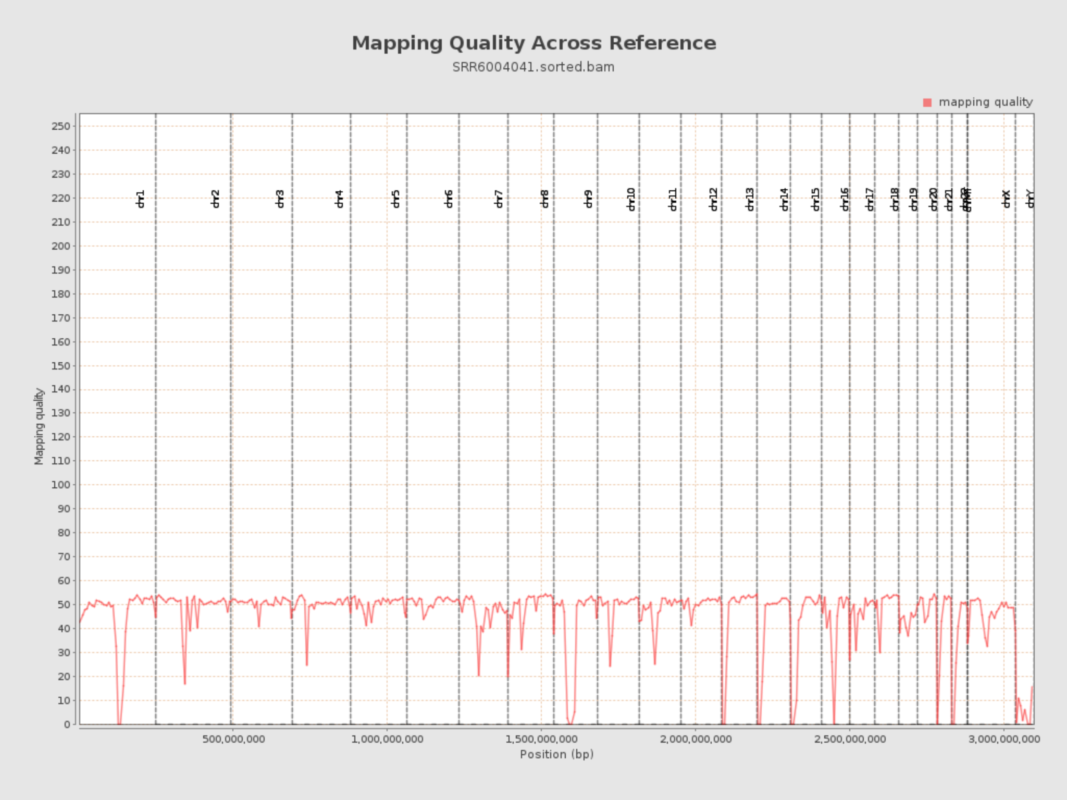
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram