Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:52:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004152.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_SRR6004152 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004152.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:52:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004152.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,623,082
Mapped reads	1,401,393 / 86.34%
Unmapped reads	221,689 / 13.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,594 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	44,030 / 2.71%
Duplication rate	2.19%
Clipped reads	671,566 / 41.38%

2.2. ACGT Content

Number/percentage of A's	26,029,512 / 28.21%
Number/percentage of C's	17,075,052 / 18.5%
Number/percentage of T's	28,130,251 / 30.48%
Number/percentage of G's	20,987,830 / 22.74%
Number/percentage of N's	61,614 / 0.07%
GC Percentage	41.25%

2.3. Coverage

Mean	0.0298

Standard Deviation	0.3127

2.4. Mapping Quality

Mean Mapping Quality	43.53

2.5. Mismatches and indels

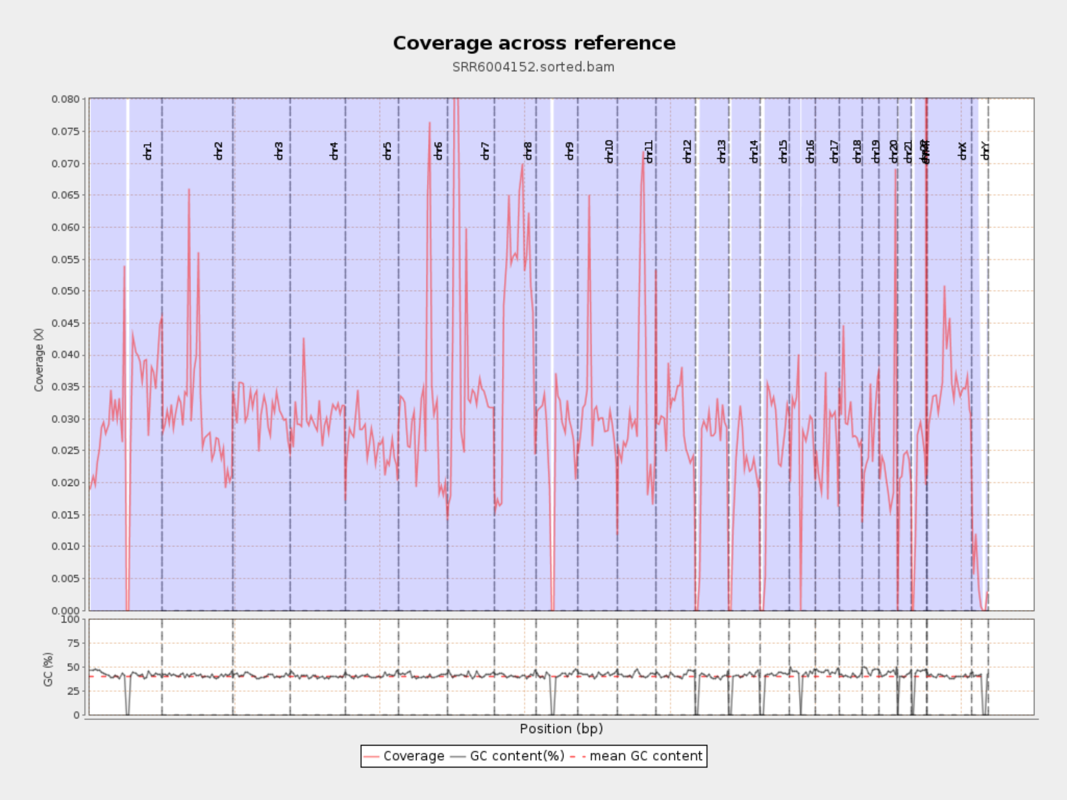
General error rate	0.96%
Mismatches	872,298
Insertions	7,563
Mapped reads with at least one insertion	0.54%
Deletions	26,132
Mapped reads with at least one deletion	1.84%
Homopolymer indels	44.91%

2.6. Chromosome stats

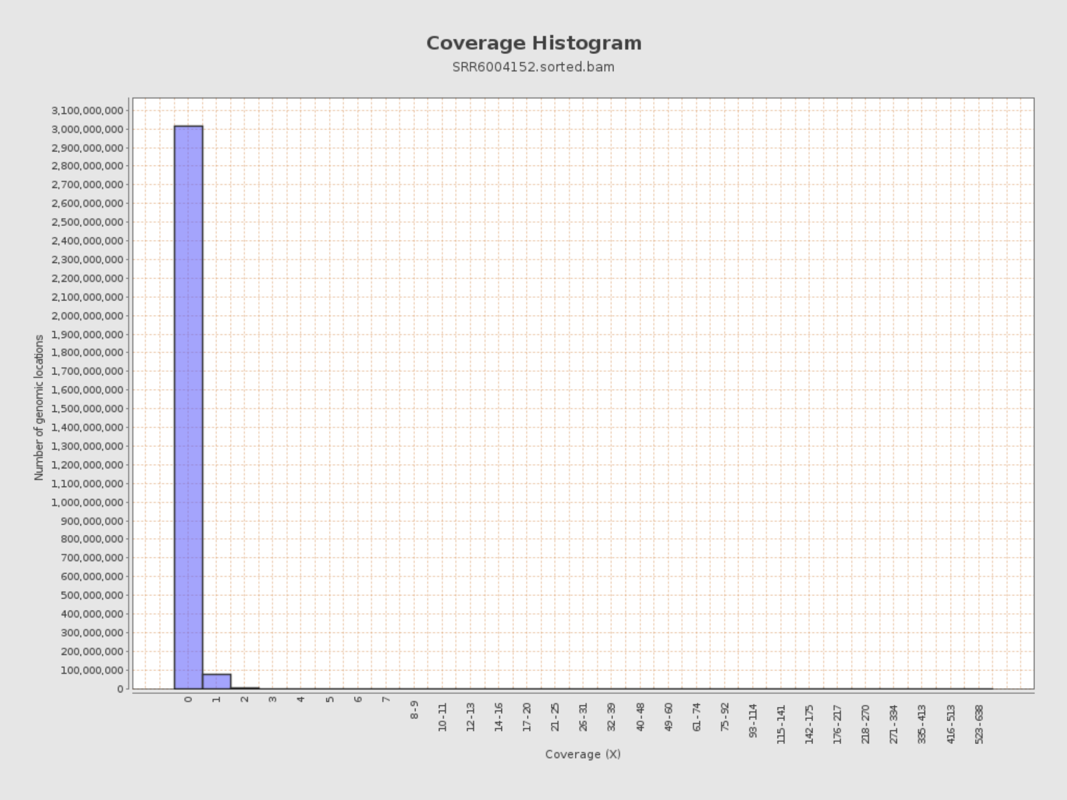
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7725968	0.031	0.569
chr2	243199373	7457316	0.0307	0.3511
chr3	198022430	6233013	0.0315	0.1928
chr4	191154276	5810259	0.0304	0.1973
chr5	180915260	4743485	0.0262	0.176
chr6	171115067	5354488	0.0313	0.211
chr7	159138663	6473096	0.0407	0.4566

chr8	146364022	6822705	0.0466	0.361
chr9	141213431	3750509	0.0266	0.3098
chr10	135534747	4264702	0.0315	0.3411
chr11	135006516	4396481	0.0326	0.2777
chr12	133851895	4005066	0.0299	0.1925
chr13	115169878	2778706	0.0241	0.166
chr14	107349540	2196190	0.0205	0.1898
chr15	102531392	2445580	0.0239	0.1725
chr16	90354753	2466896	0.0273	0.2278
chr17	81195210	2085808	0.0257	0.1861
chr18	78077248	2371428	0.0304	0.5868
chr19	59128983	1617610	0.0274	0.3844
chr20	63025520	1681330	0.0267	0.1901
chr21	48129895	984573	0.0205	0.1767
chr22	51304566	959716	0.0187	0.1458
chrMT	16571	16380	0.9885	1.2959
chrX	155270560	5440422	0.035	0.2286
chrY	59373566	247185	0.0042	0.101

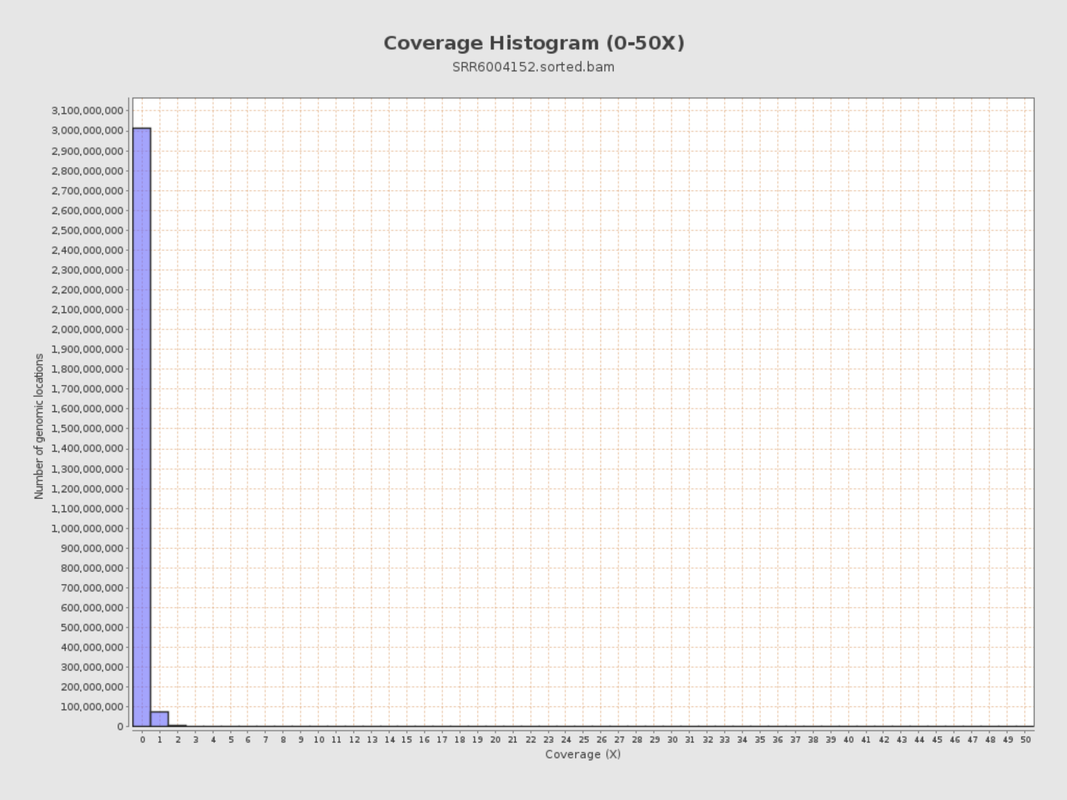
3. Results : Coverage across reference



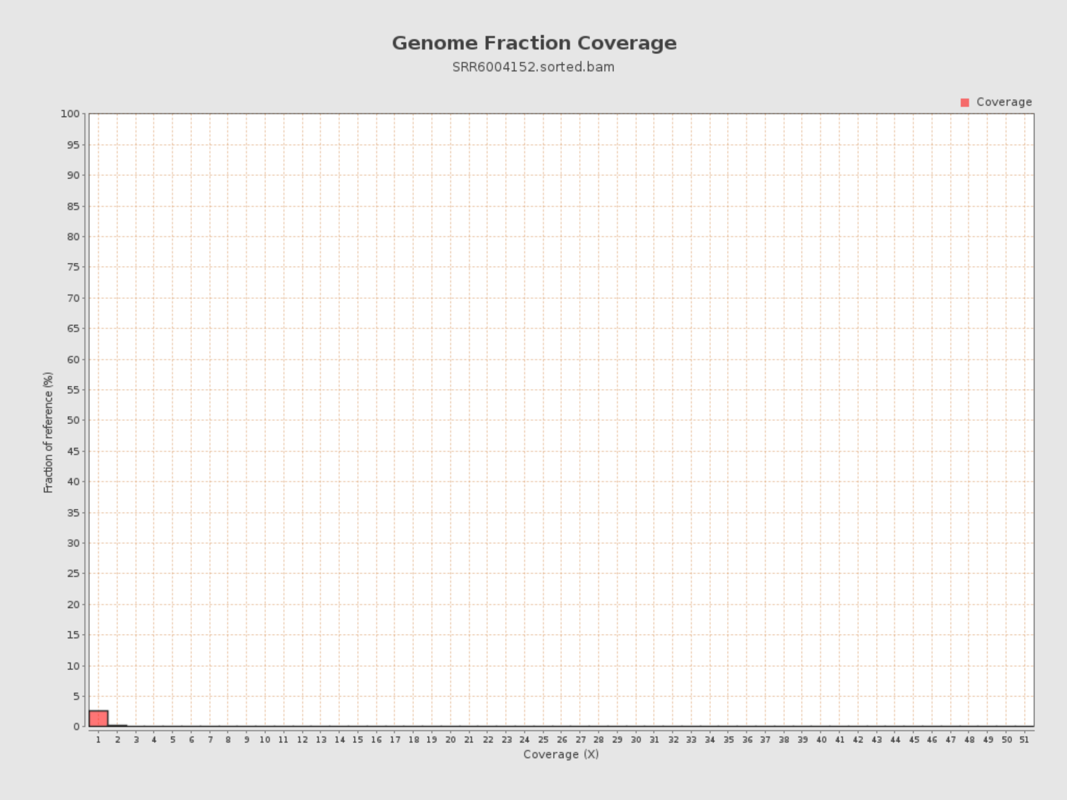
4. Results : Coverage Histogram



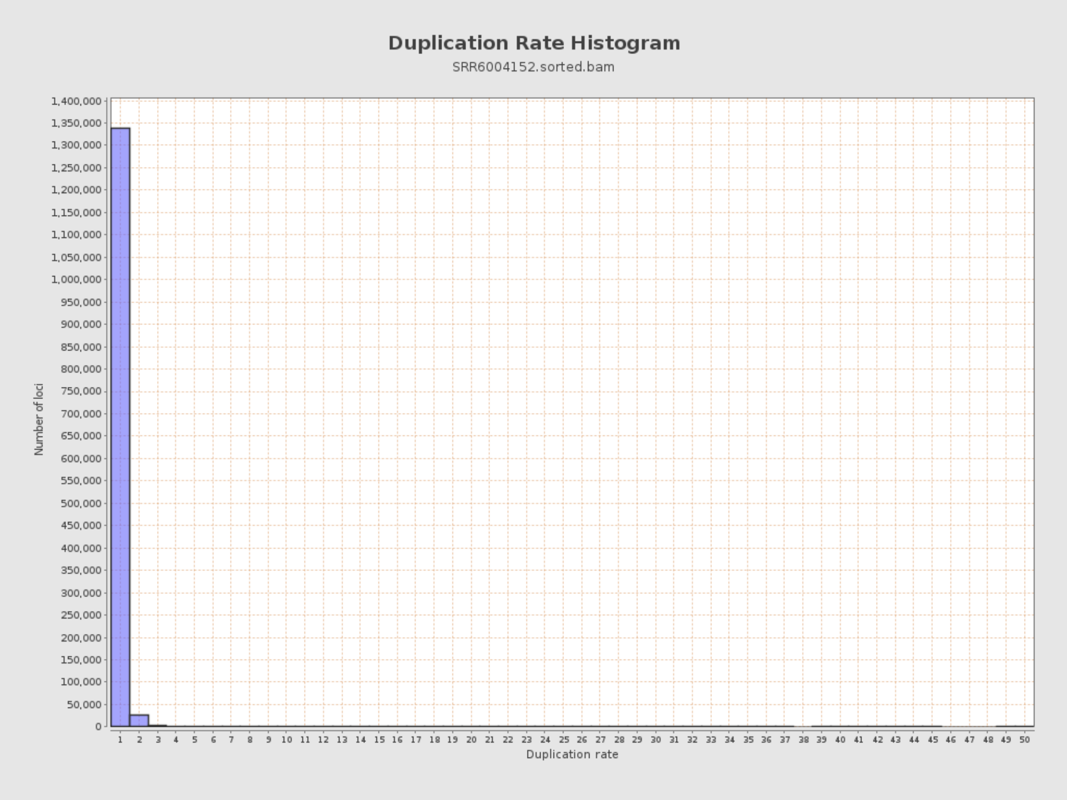
5. Results : Coverage Histogram (0-50X)



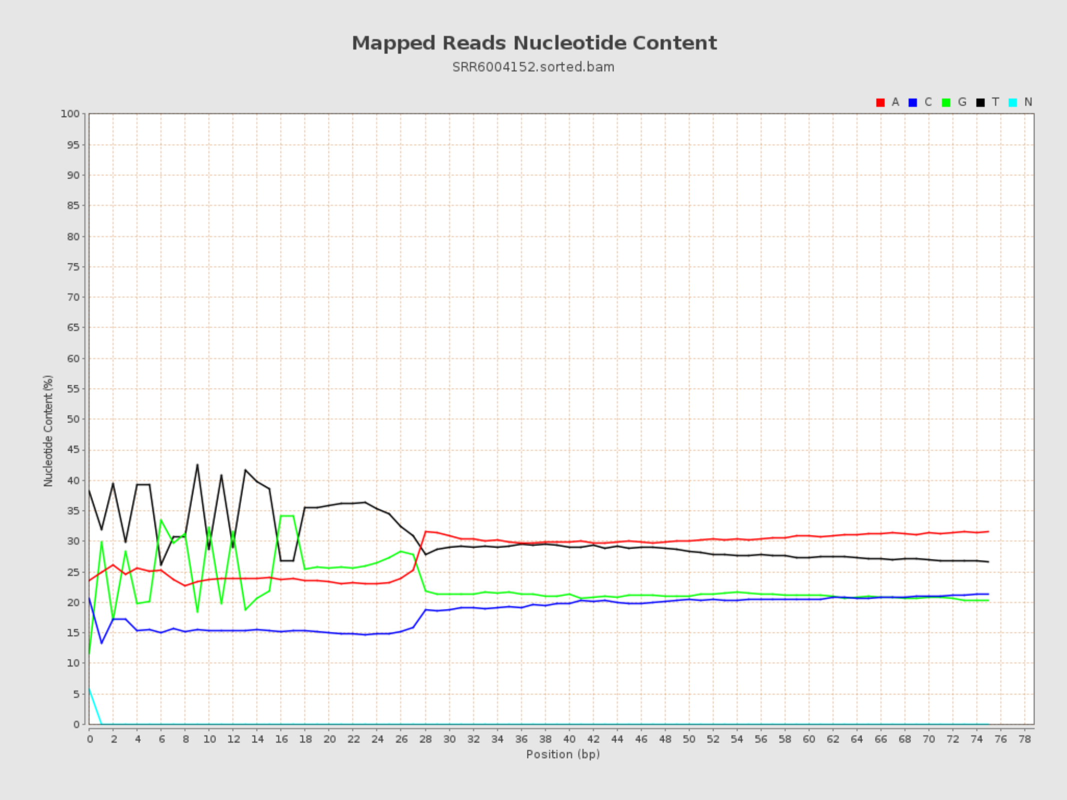
6. Results : Genome Fraction Coverage



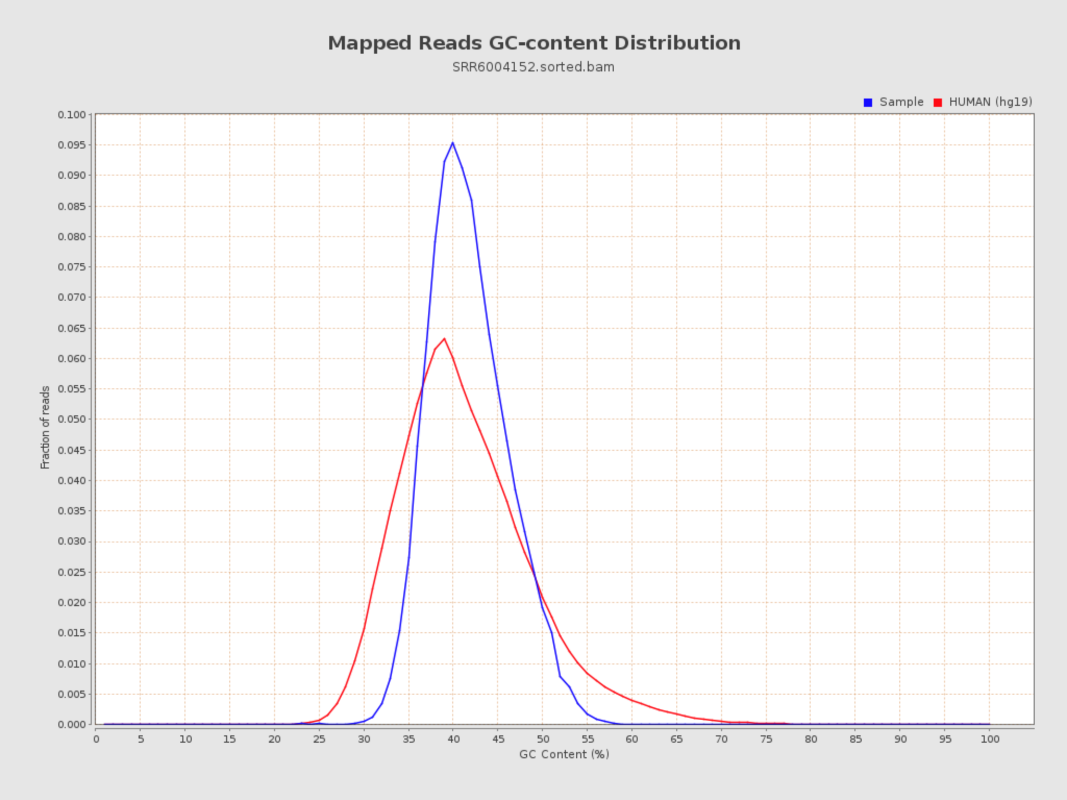
7. Results : Duplication Rate Histogram



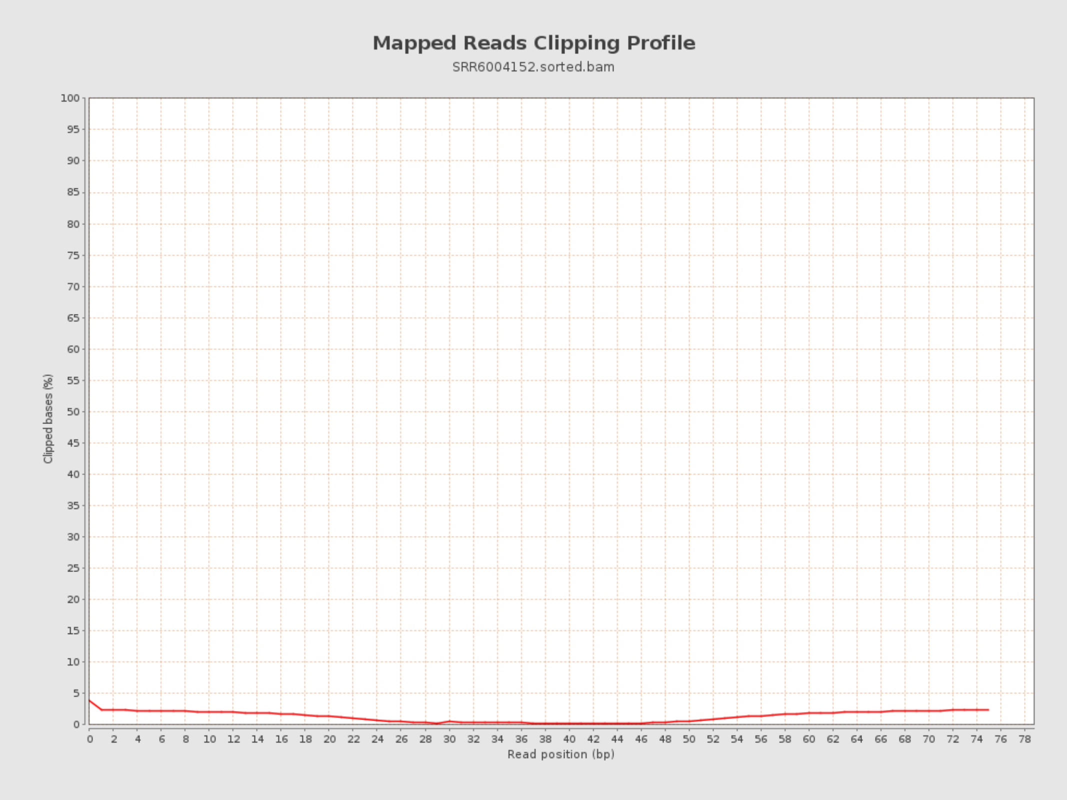
8. Results : Mapped Reads Nucleotide Content



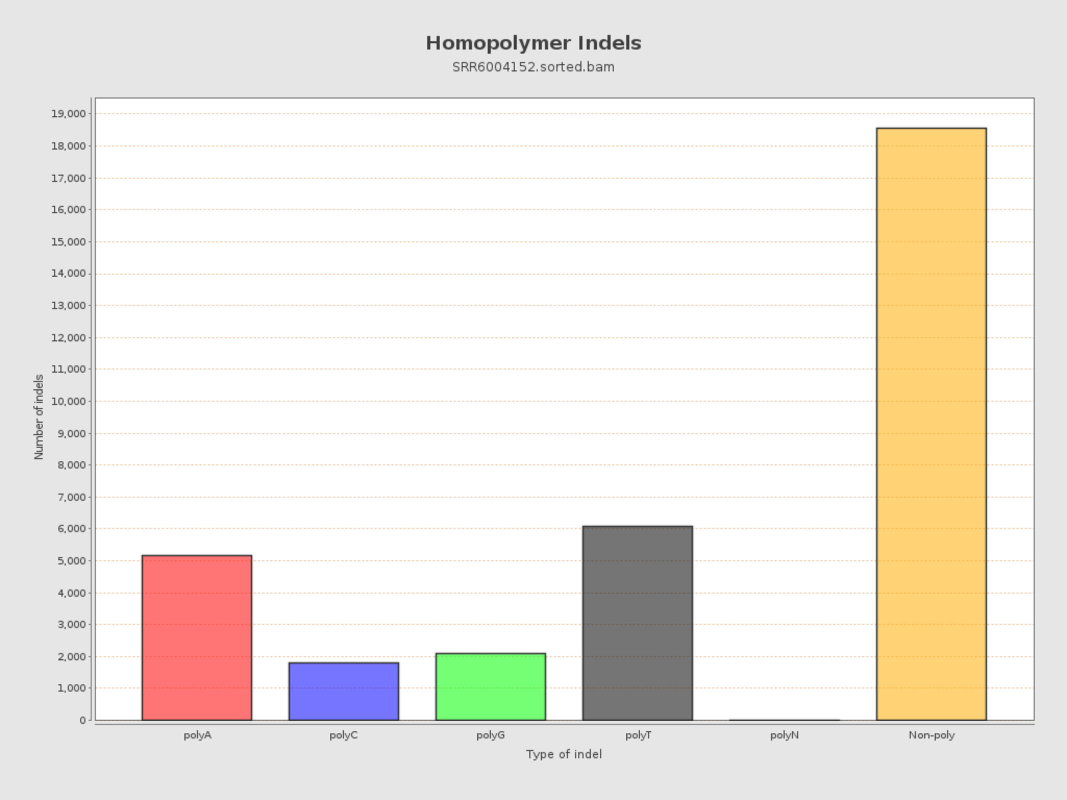
9. Results : Mapped Reads GC-content Distribution



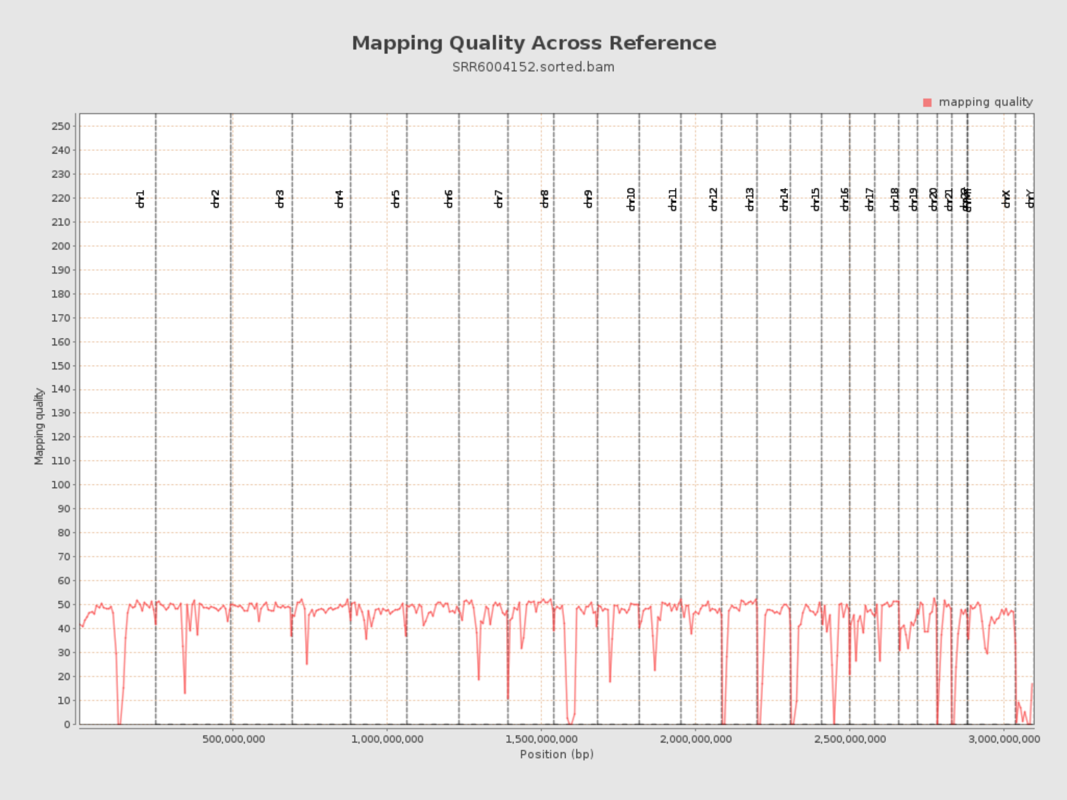
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram