Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:15:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004143.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_SRR6004143 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004143.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:15:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004143.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,991,597
Mapped reads	4,035,571 / 80.85%
Unmapped reads	956,026 / 19.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,071 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	228,479 / 4.58%
Duplication rate	4.08%
Clipped reads	1,739,273 / 34.84%

2.2. ACGT Content

Number/percentage of A's	75,384,608 / 27.81%
Number/percentage of C's	49,019,774 / 18.08%
Number/percentage of T's	87,006,844 / 32.09%
Number/percentage of G's	59,661,907 / 22.01%
Number/percentage of N's	29,424 / 0.01%
GC Percentage	40.09%

2.3. Coverage

Mean	0.0876

Standard Deviation	0.8445

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

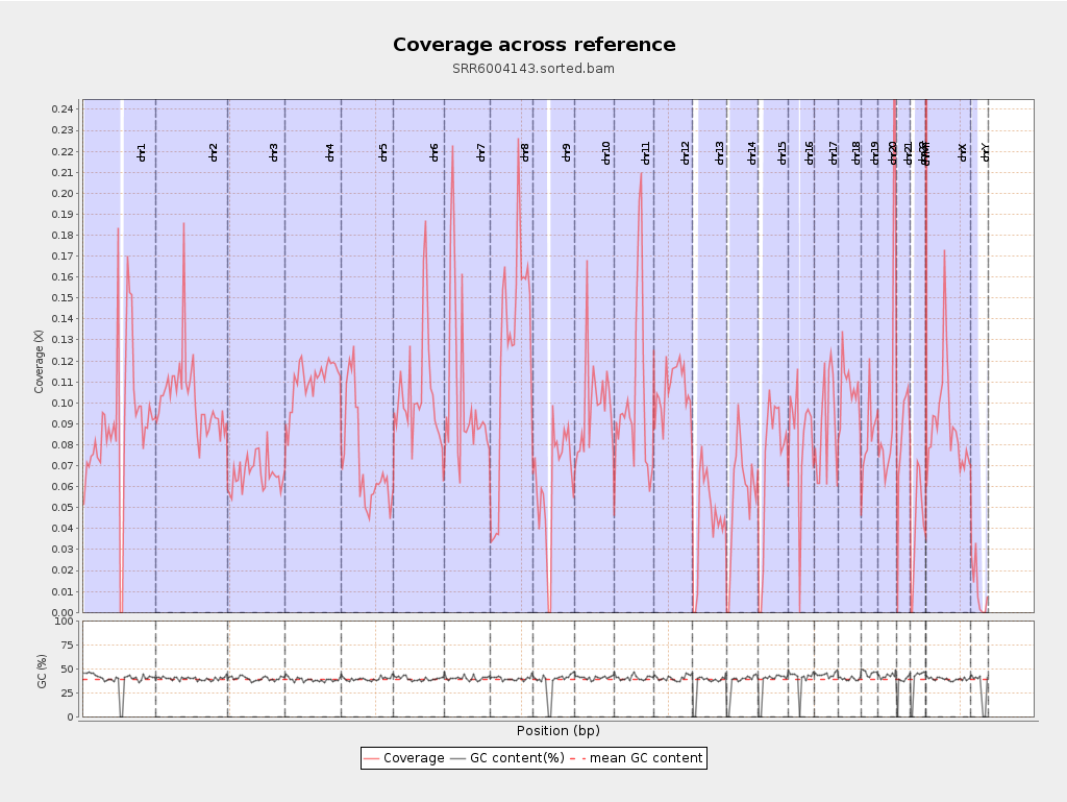
General error rate	0.99%
Mismatches	2,634,377
Insertions	24,913
Mapped reads with at least one insertion	0.61%
Deletions	77,745
Mapped reads with at least one deletion	1.9%
Homopolymer indels	47.02%

2.6. Chromosome stats

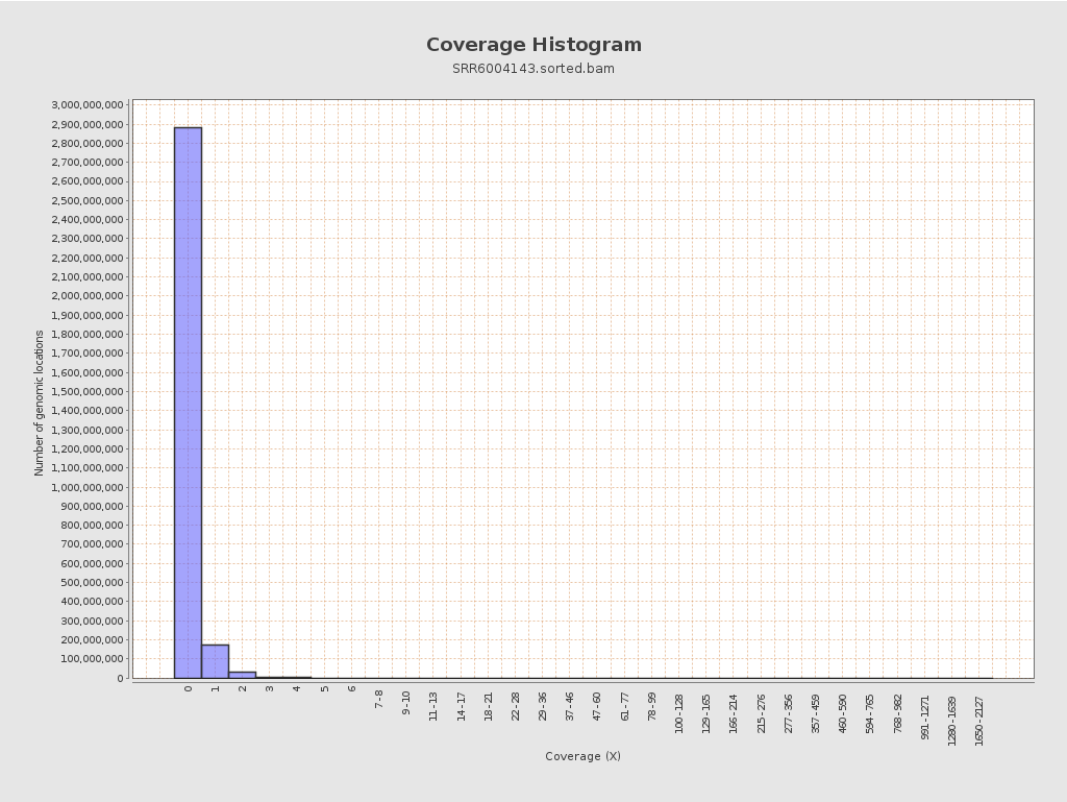
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22298066	0.0895	1.8036
chr2	243199373	24741614	0.1017	0.9569
chr3	198022430	13144976	0.0664	0.323
chr4	191154276	21117282	0.1105	0.433
chr5	180915260	13077924	0.0723	0.3414
chr6	171115067	17893343	0.1046	0.532
chr7	159138663	16316639	0.1025	1.0938

chr8	146364022	18226722	0.1245	1.2349
chr9	141213431	8832102	0.0625	0.7192
chr10	135534747	13327951	0.0983	0.7946
chr11	135006516	13698303	0.1015	0.6374
chr12	133851895	14229180	0.1063	0.4073
chr13	115169878	5111346	0.0444	0.2534
chr14	107349540	6175180	0.0575	0.373
chr15	102531392	7334006	0.0715	0.3273
chr16	90354753	7406103	0.082	0.4635
chr17	81195210	7303723	0.09	0.4285
chr18	78077248	8313926	0.1065	1.5
chr19	59128983	5037917	0.0852	1.2234
chr20	63025520	6856294	0.1088	0.4372
chr21	48129895	3922632	0.0815	0.4029
chr22	51304566	2110612	0.0411	0.2383
chrMT	16571	139261	8.4039	5.6015
chrX	155270560	13981064	0.09	0.4936
chrY	59373566	638012	0.0107	0.2383

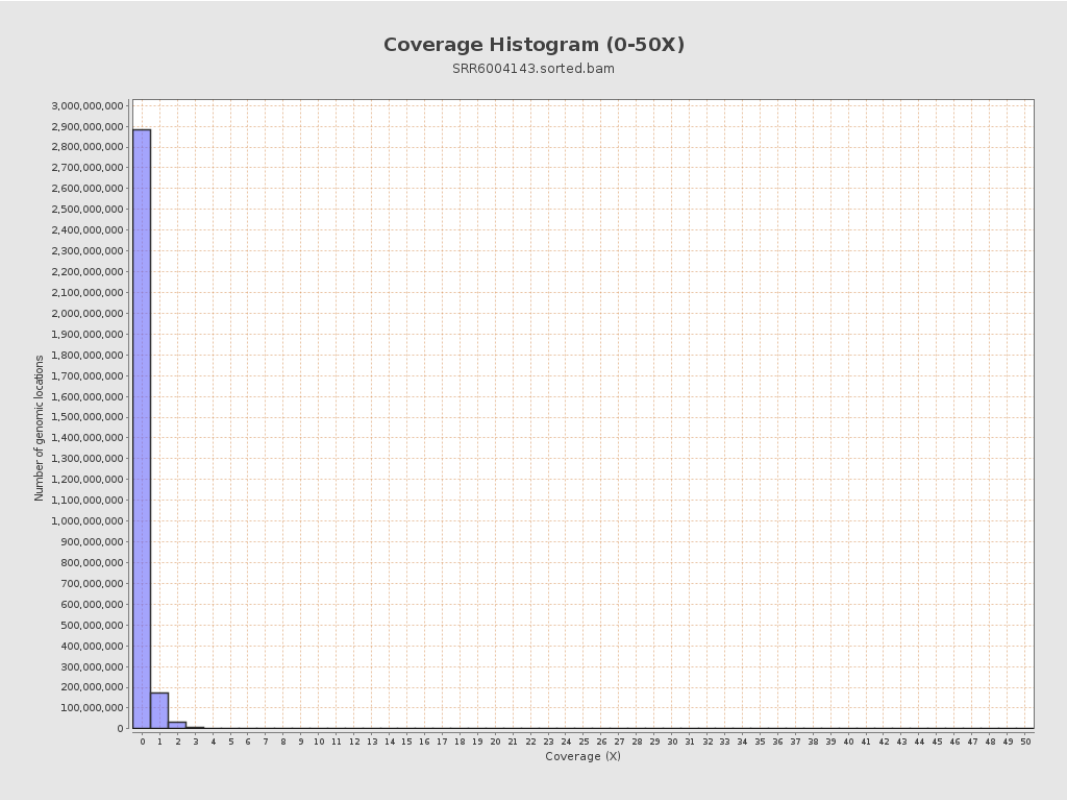
3. Results : Coverage across reference



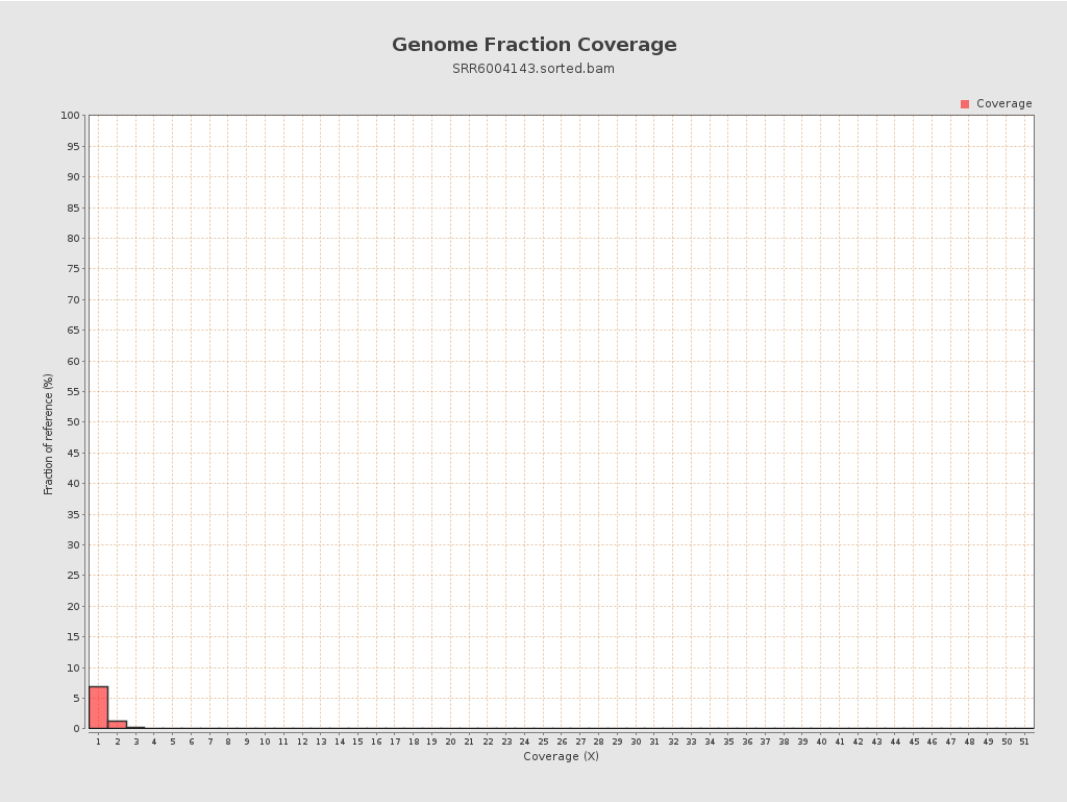
4. Results : Coverage Histogram



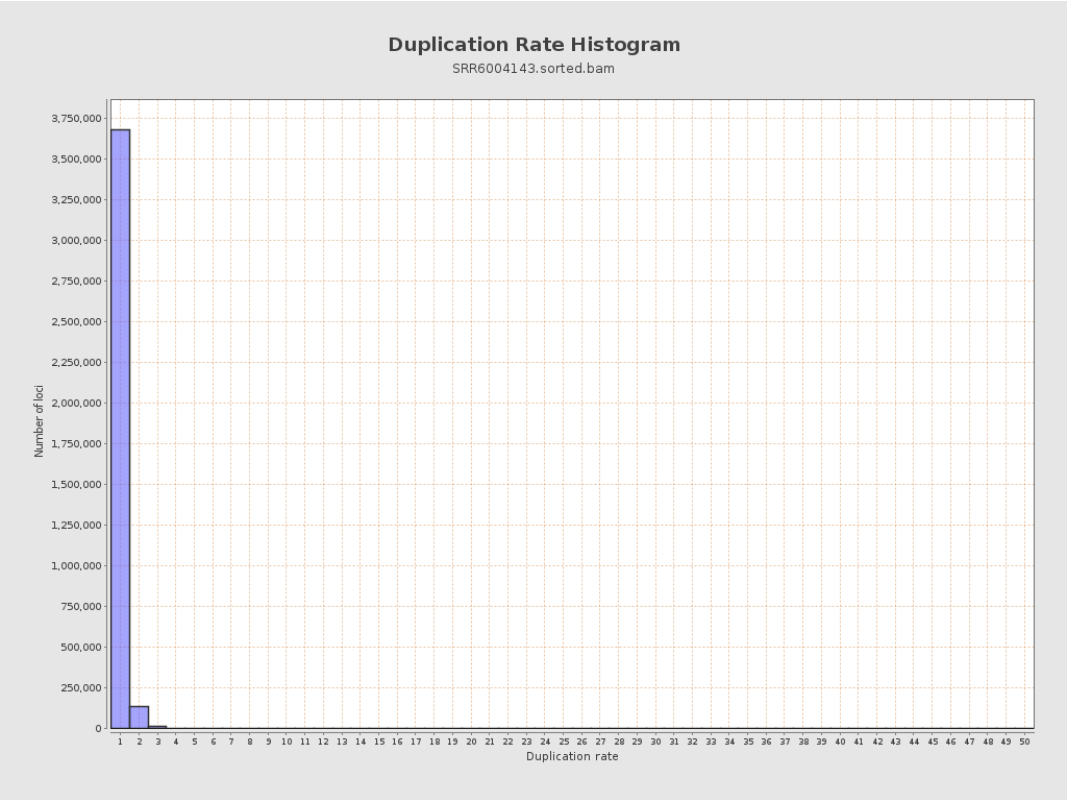
5. Results : Coverage Histogram (0-50X)



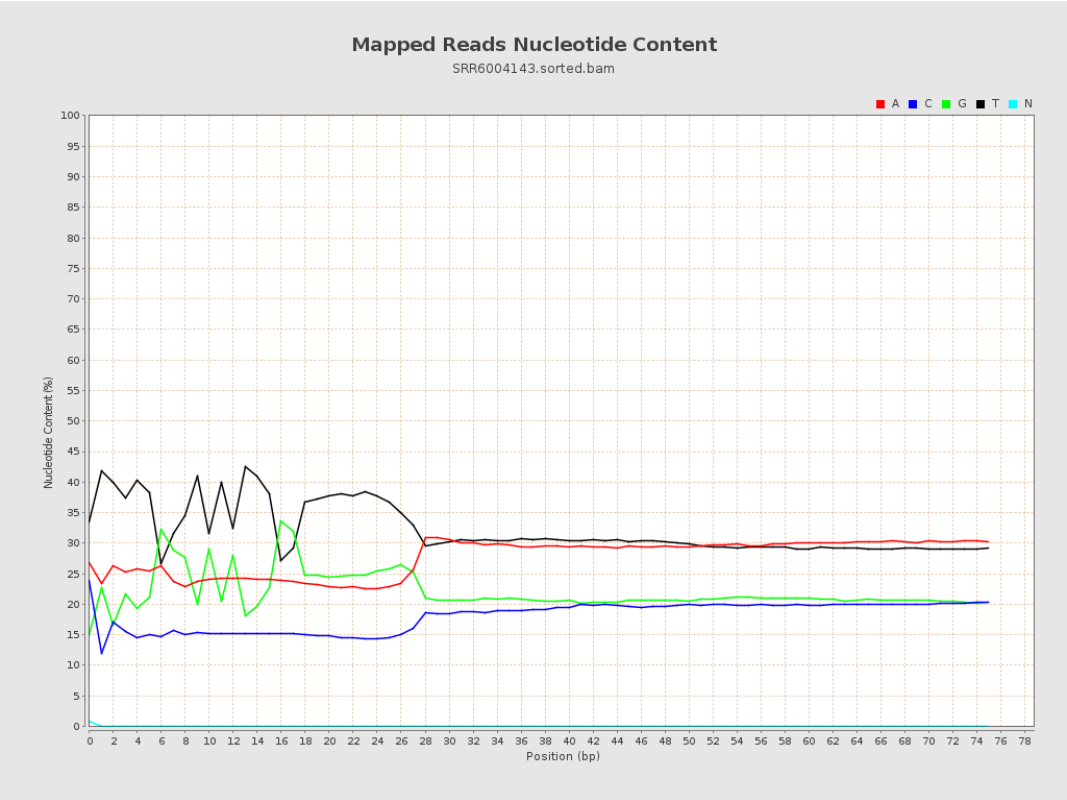
6. Results : Genome Fraction Coverage



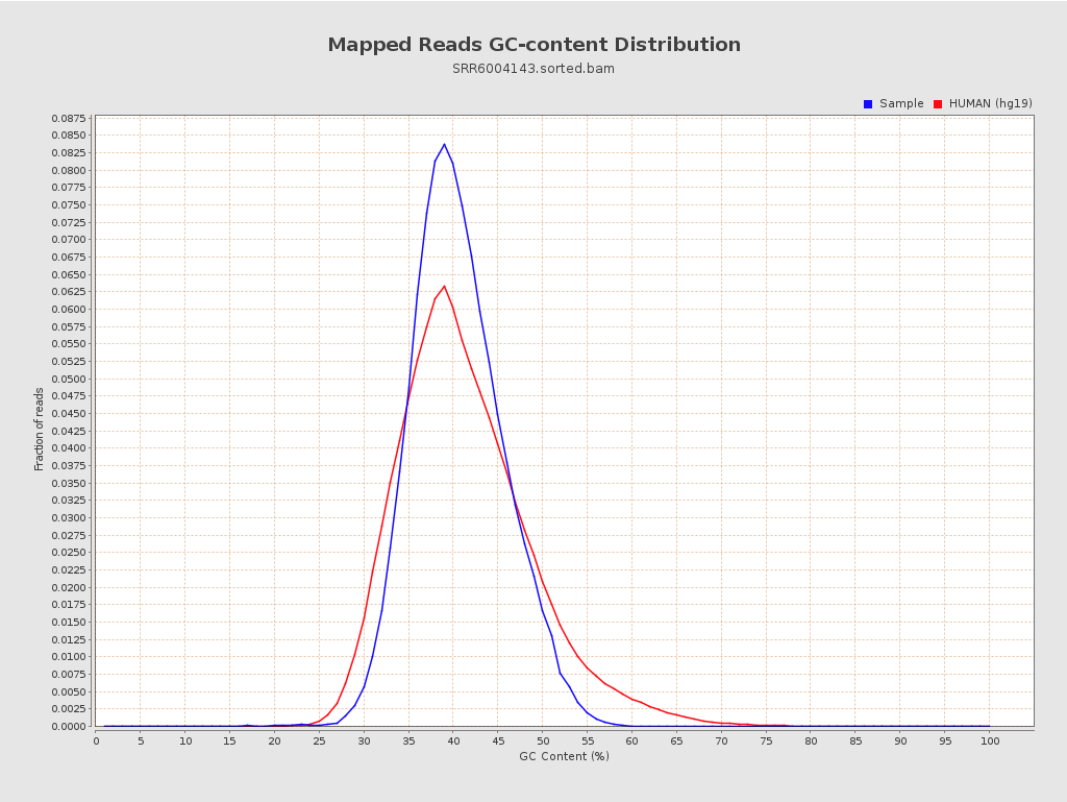
7. Results : Duplication Rate Histogram



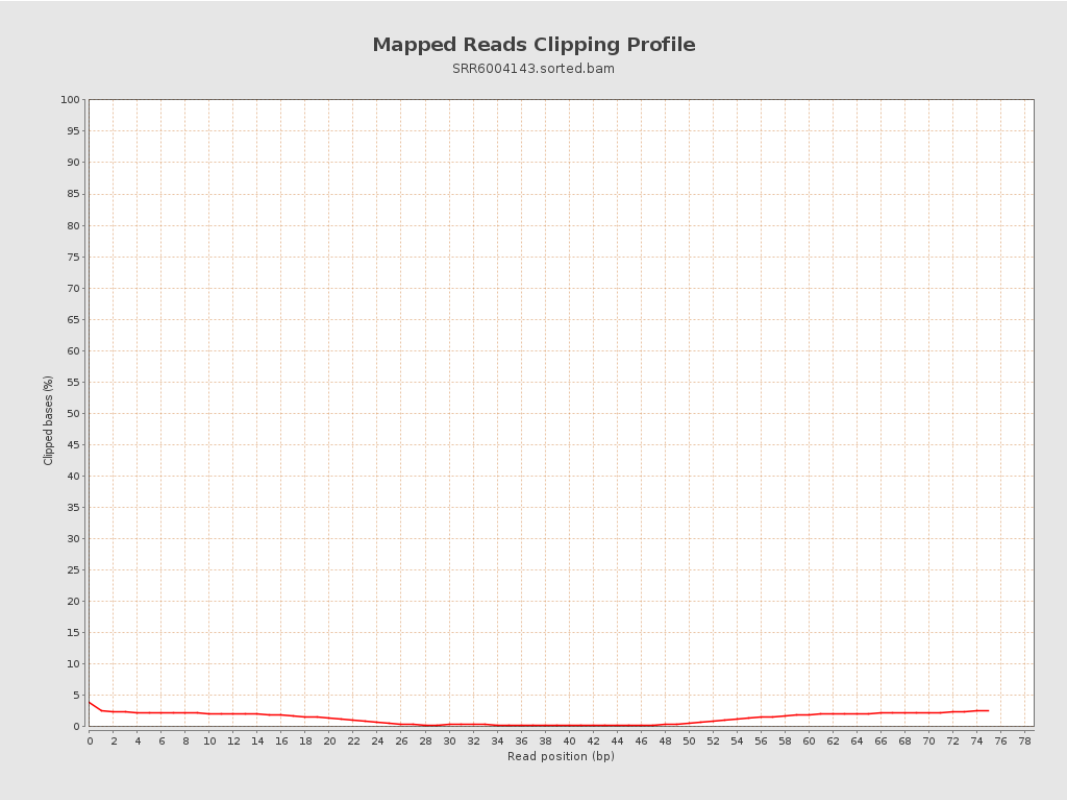
8. Results : Mapped Reads Nucleotide Content



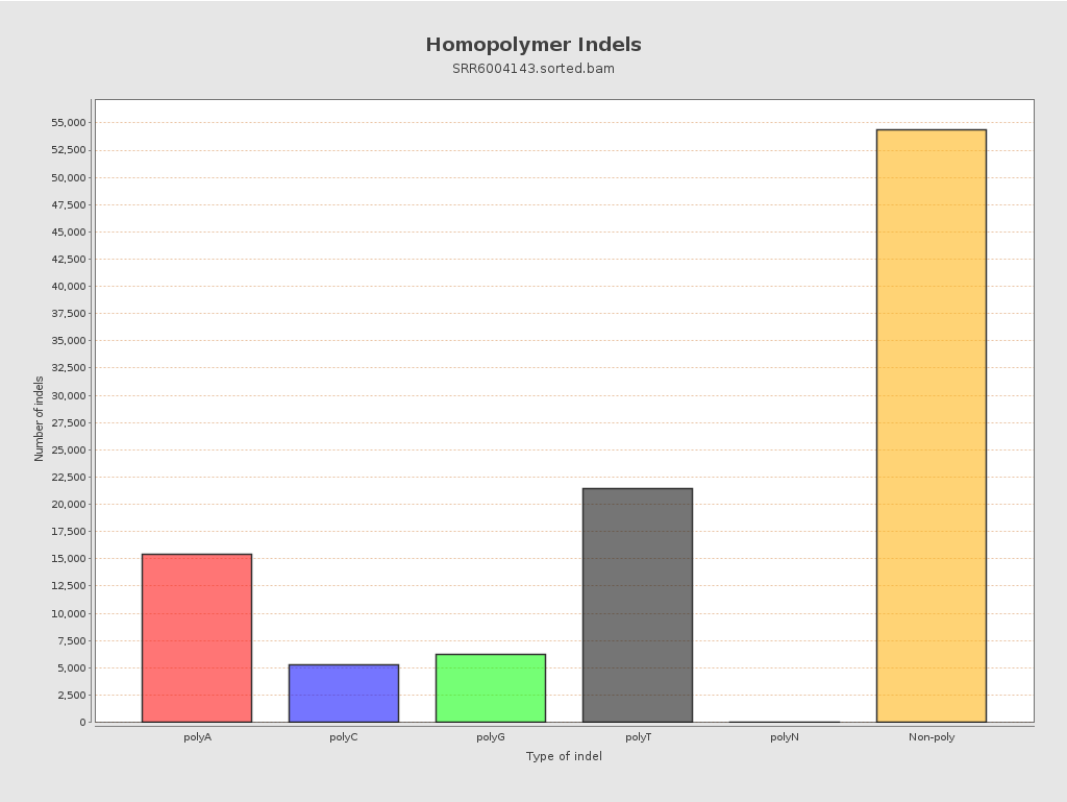
9. Results : Mapped Reads GC-content Distribution



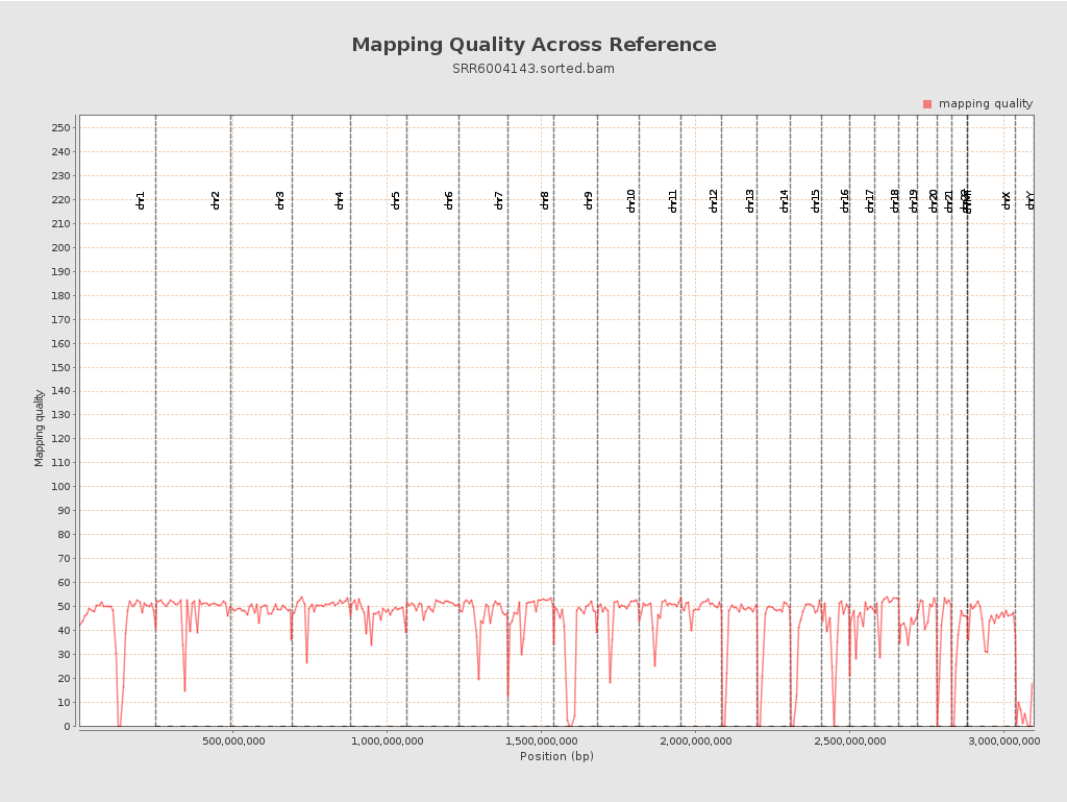
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram