Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:06:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013253.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_SRR6013253 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013253.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:06:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013253.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,307,513
Mapped reads	2,089,225 / 90.54%
Unmapped reads	218,288 / 9.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,841 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	71,476 / 3.1%
Duplication rate	2.09%
Clipped reads	969,130 / 42%

2.2. ACGT Content

Number/percentage of A's	38,181,027 / 27.61%
Number/percentage of C's	25,572,311 / 18.49%
Number/percentage of T's	42,832,403 / 30.97%
Number/percentage of G's	31,703,283 / 22.93%
Number/percentage of N's	2,007 / 0%
GC Percentage	41.42%

2.3. Coverage

Mean	0.0447

Standard Deviation	0.4888

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

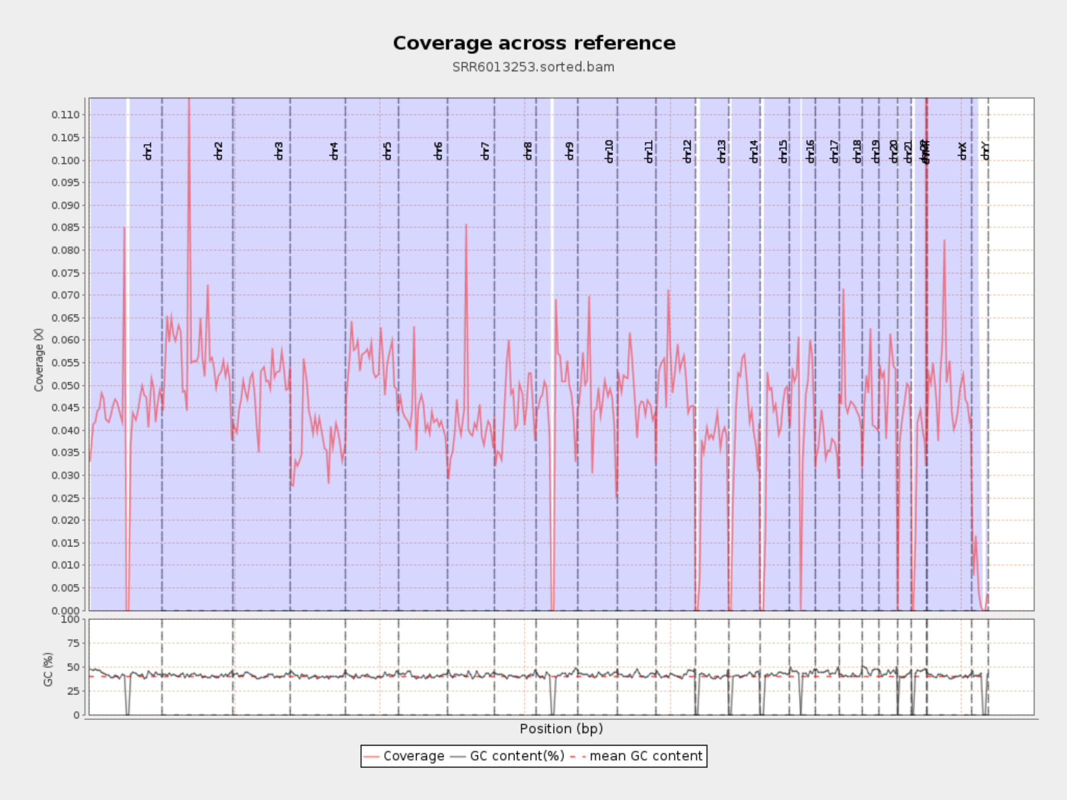
General error rate	0.74%
Mismatches	1,000,888
Insertions	10,702
Mapped reads with at least one insertion	0.51%
Deletions	32,509
Mapped reads with at least one deletion	1.54%
Homopolymer indels	46.39%

2.6. Chromosome stats

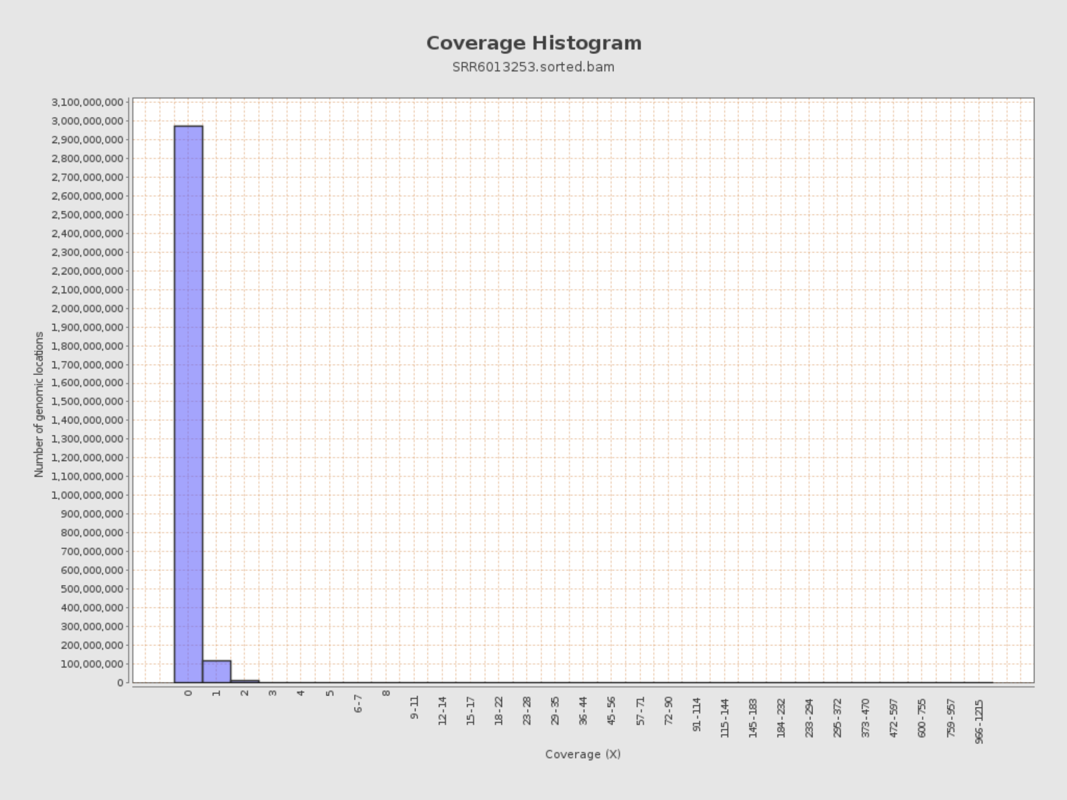
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10732663	0.0431	1.0244
chr2	243199373	13988144	0.0575	0.5793
chr3	198022430	9732704	0.0491	0.2413
chr4	191154276	7281829	0.0381	0.2436
chr5	180915260	10020011	0.0554	0.2638
chr6	171115067	7385392	0.0432	0.3119
chr7	159138663	6678841	0.042	0.6318

chr8	146364022	6525312	0.0446	0.4964
chr9	141213431	6222777	0.0441	0.5018
chr10	135534747	6421500	0.0474	0.3829
chr11	135006516	6442597	0.0477	0.4613
chr12	133851895	7000227	0.0523	0.2625
chr13	115169878	3719934	0.0323	0.1961
chr14	107349540	4166158	0.0388	0.2611
chr15	102531392	3848923	0.0375	0.2373
chr16	90354753	4150330	0.0459	0.2845
chr17	81195210	2968655	0.0366	0.2587
chr18	78077248	3713864	0.0476	0.9564
chr19	59128983	2743253	0.0464	0.6407
chr20	63025520	3198496	0.0507	0.259
chr21	48129895	1921189	0.0399	0.2565
chr22	51304566	1447076	0.0282	0.1807
chrMT	16571	27392	1.653	1.5055
chrX	155270560	7676087	0.0494	0.3107
chrY	59373566	334060	0.0056	0.1298

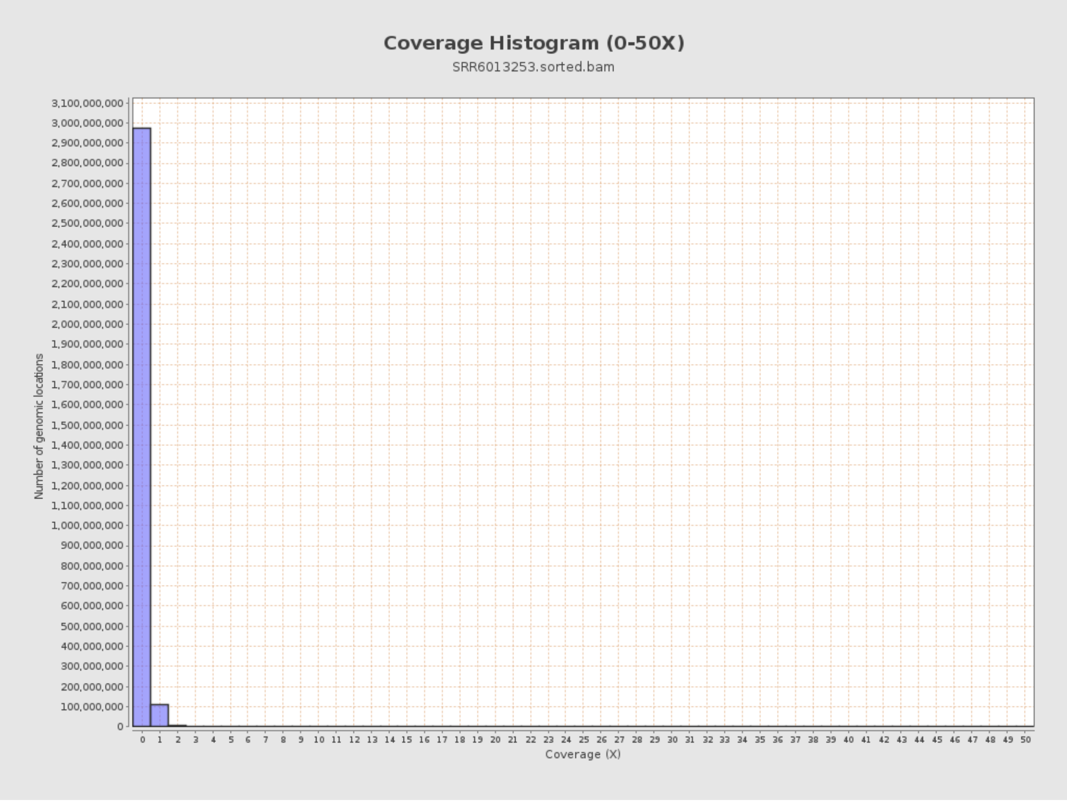
3. Results : Coverage across reference



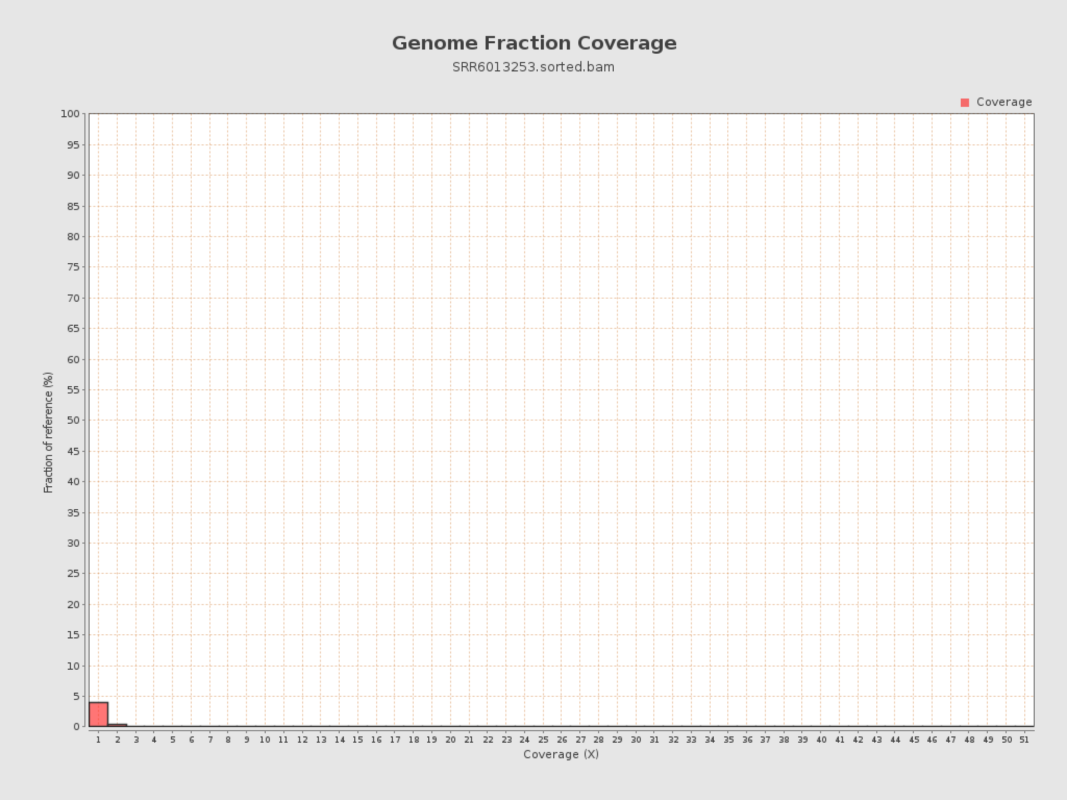
4. Results : Coverage Histogram



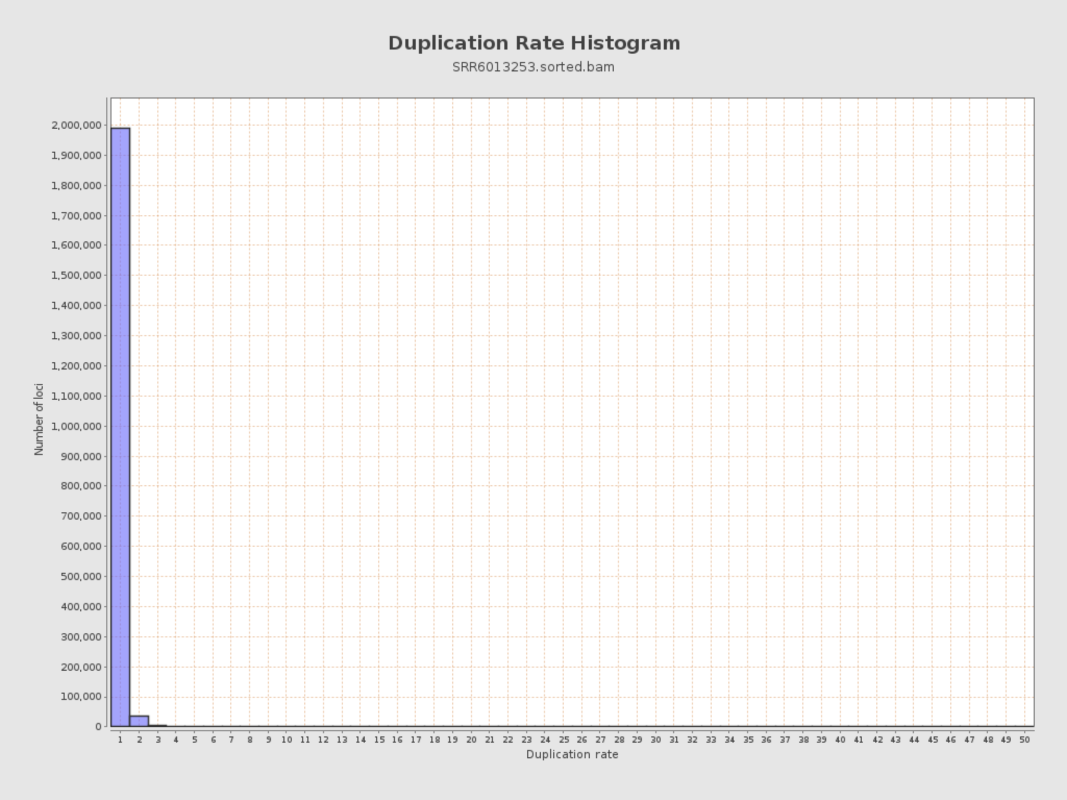
5. Results : Coverage Histogram (0-50X)



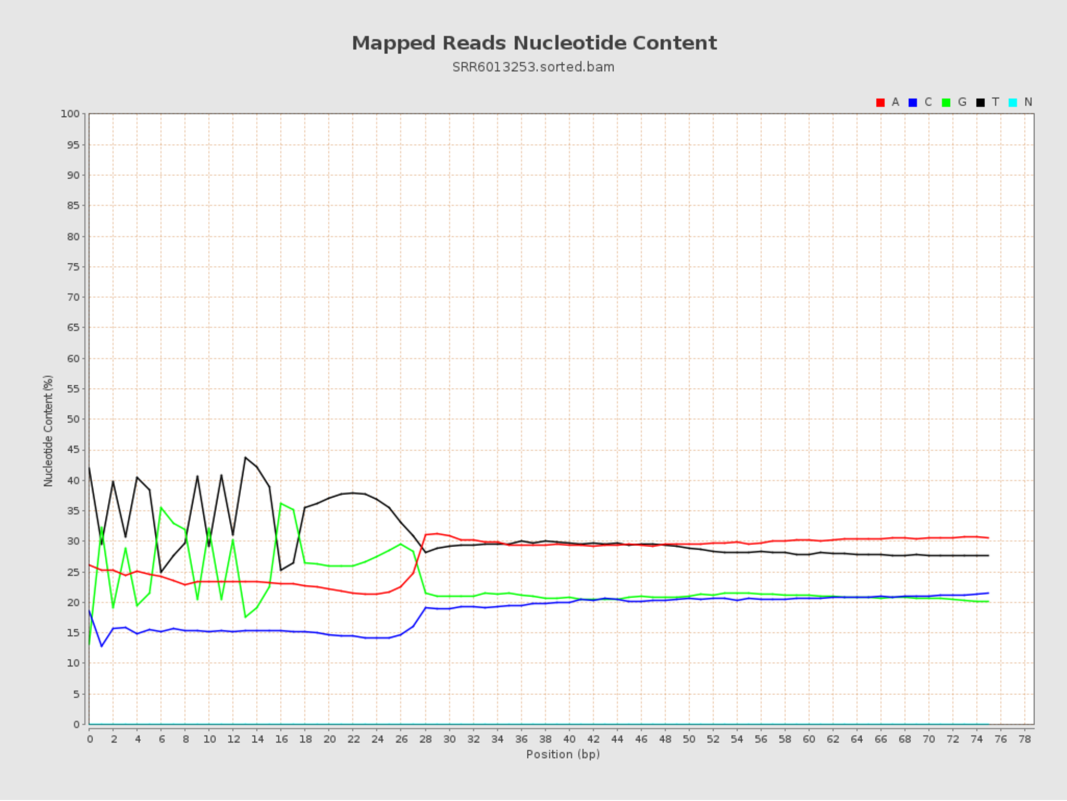
6. Results : Genome Fraction Coverage



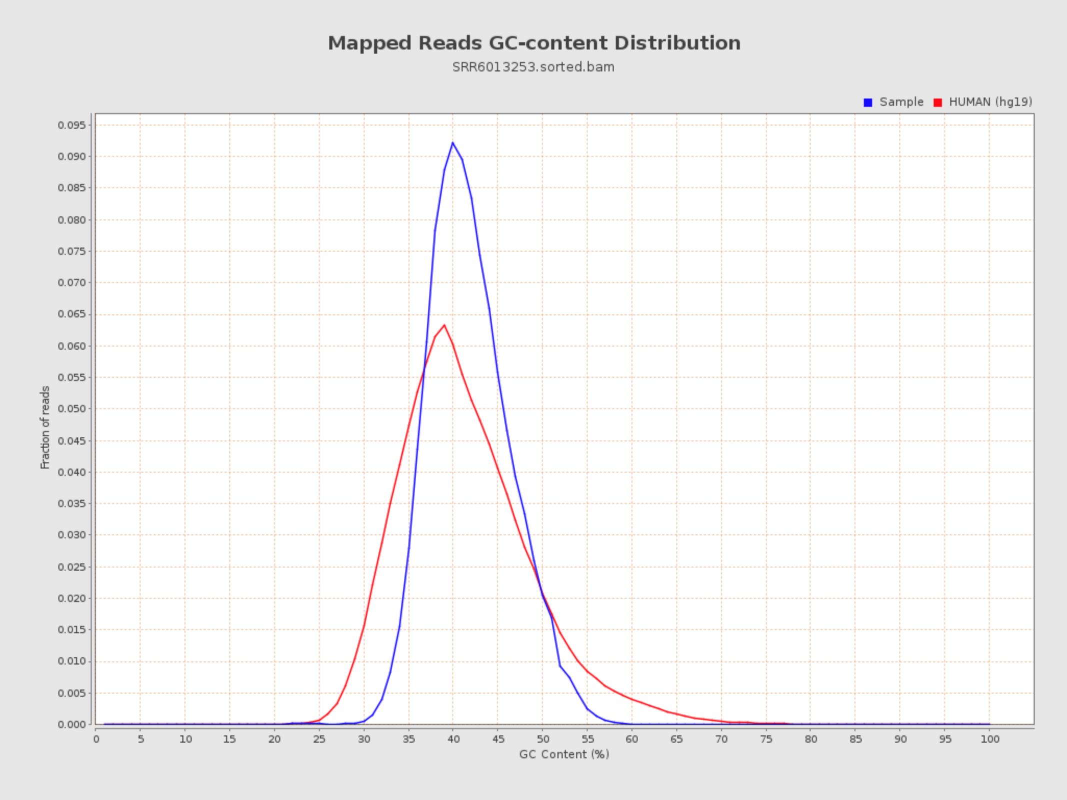
7. Results : Duplication Rate Histogram



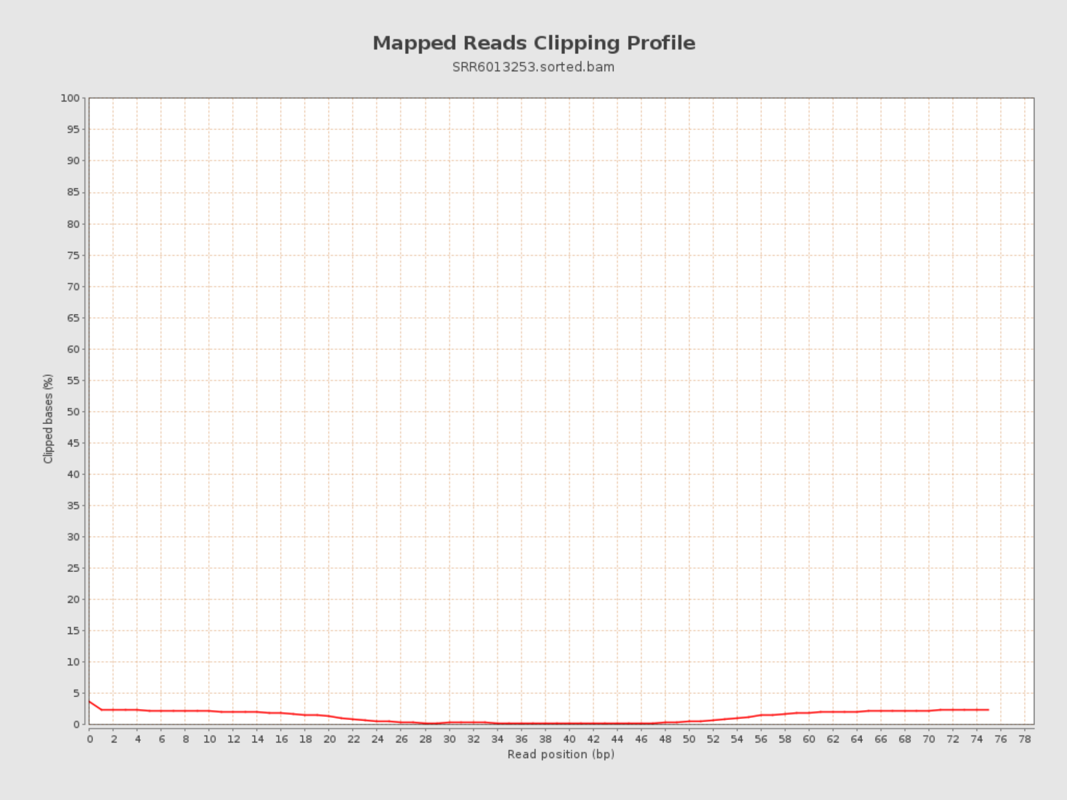
8. Results : Mapped Reads Nucleotide Content



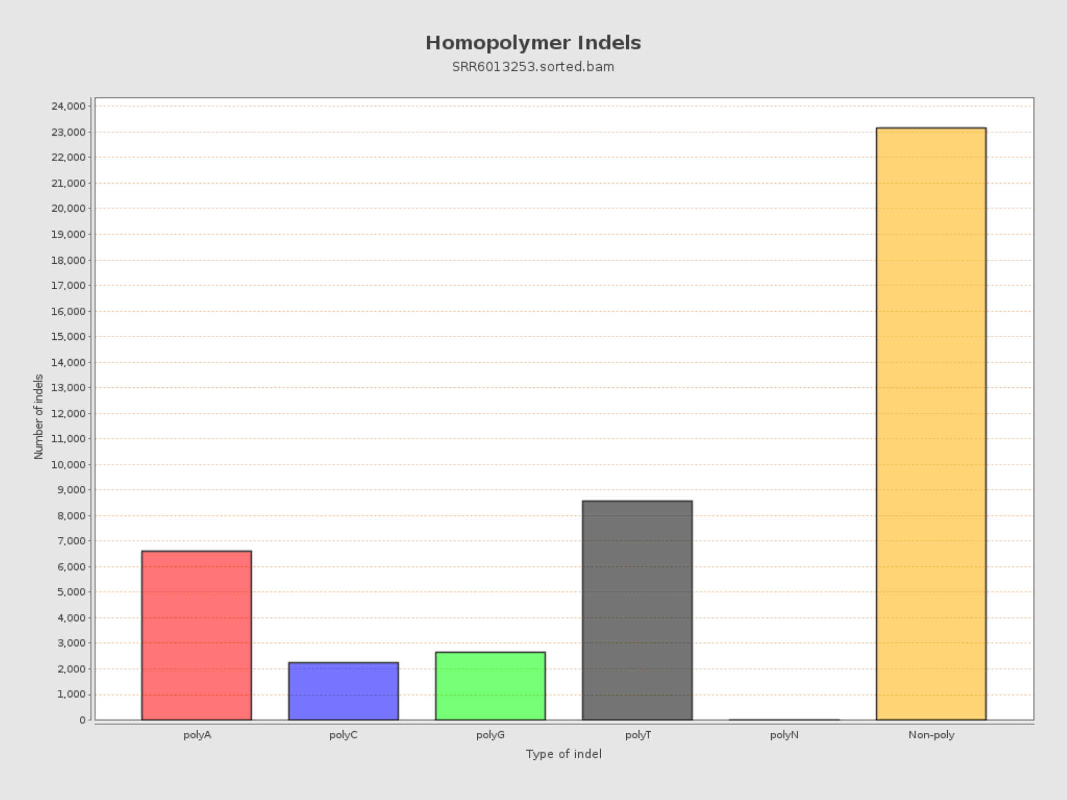
9. Results : Mapped Reads GC-content Distribution



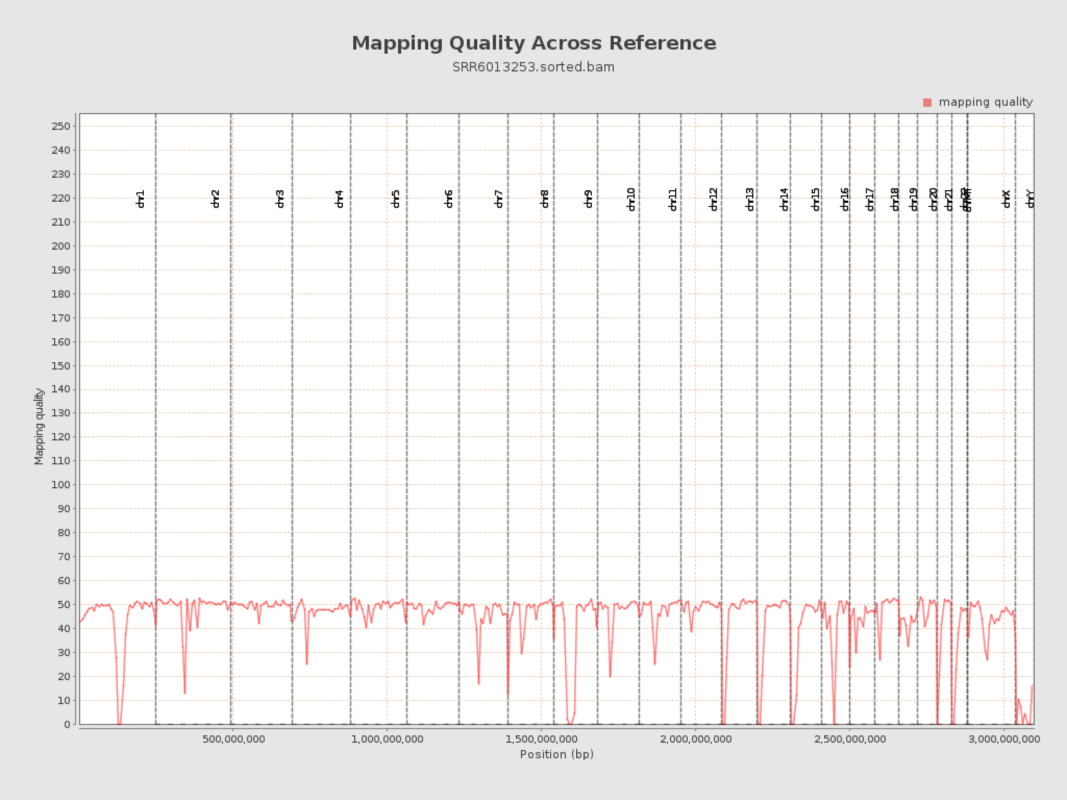
10. Results : Mapped Reads Clipping Profile



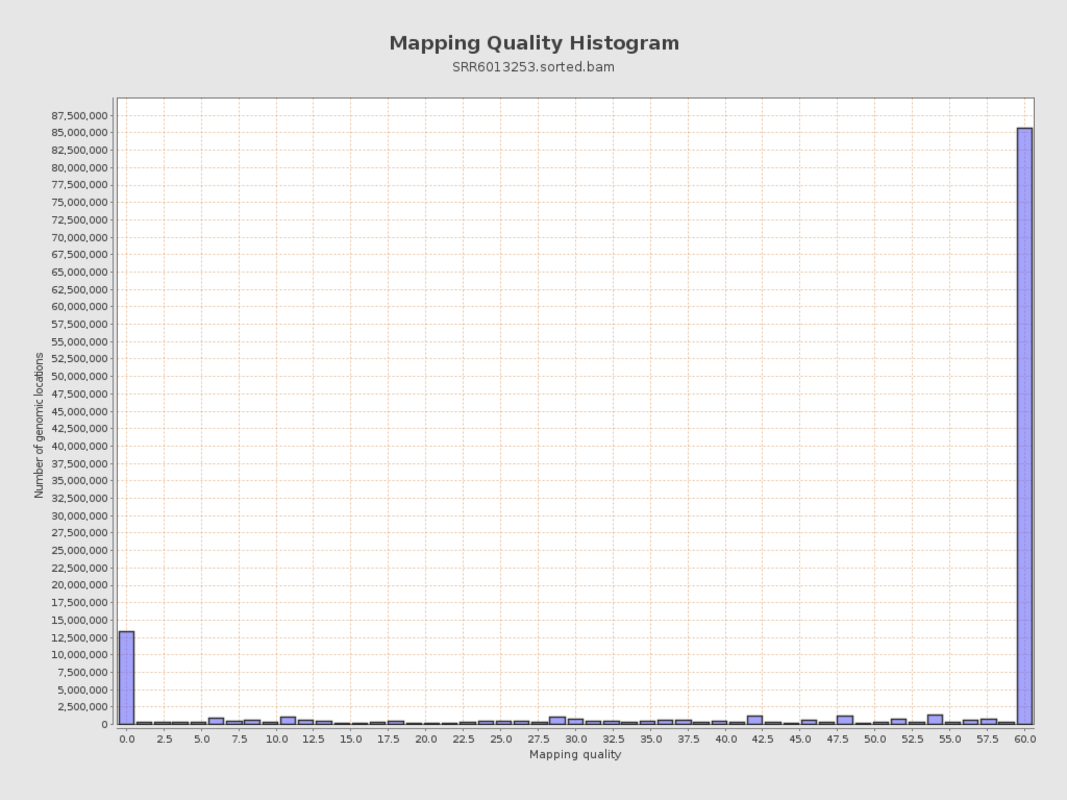
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



`