Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:47:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004014.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_SRR6004014 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004014.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:47:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,182,789
Mapped reads	1,966,275 / 90.08%
Unmapped reads	216,514 / 9.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,625 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	115,603 / 5.3%
Duplication rate	4.75%
Clipped reads	873,704 / 40.03%

2.2. ACGT Content

Number/percentage of A's	37,390,251 / 28.37%
Number/percentage of C's	24,659,954 / 18.71%
Number/percentage of T's	41,475,828 / 31.48%
Number/percentage of G's	28,221,520 / 21.42%
Number/percentage of N's	24,312 / 0.02%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.387

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

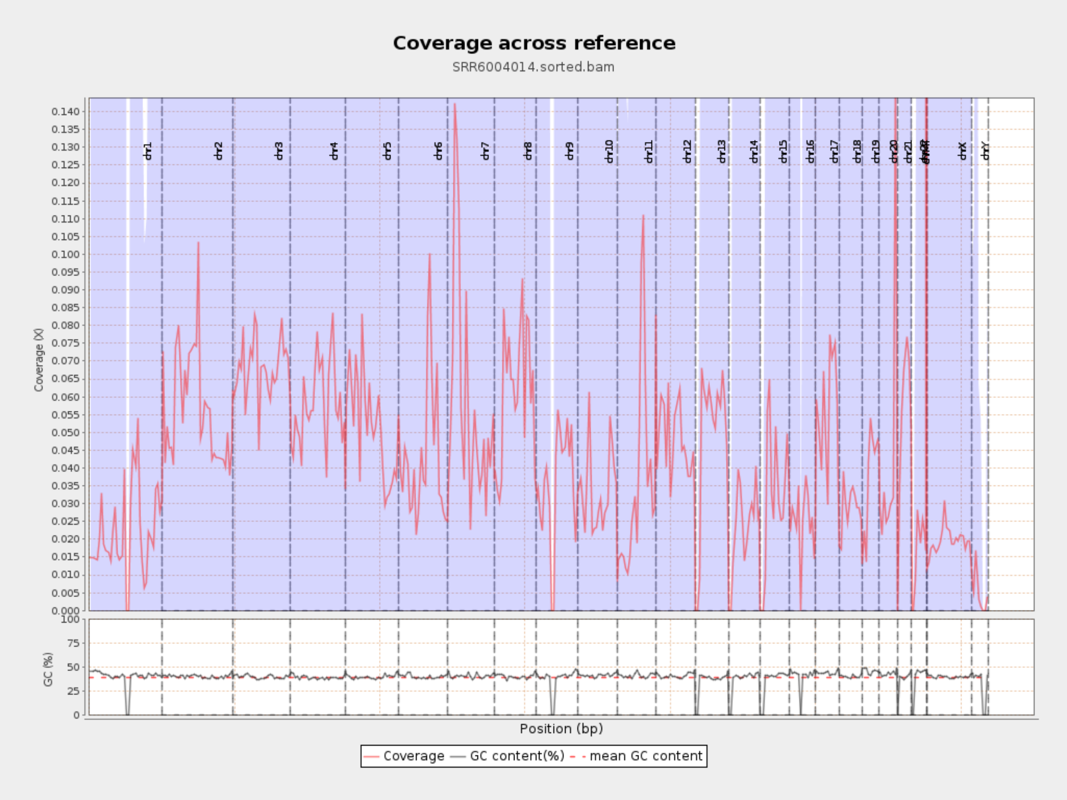
General error rate	0.87%
Mismatches	1,122,028
Insertions	9,775
Mapped reads with at least one insertion	0.49%
Deletions	30,911
Mapped reads with at least one deletion	1.55%
Homopolymer indels	46.81%

2.6. Chromosome stats

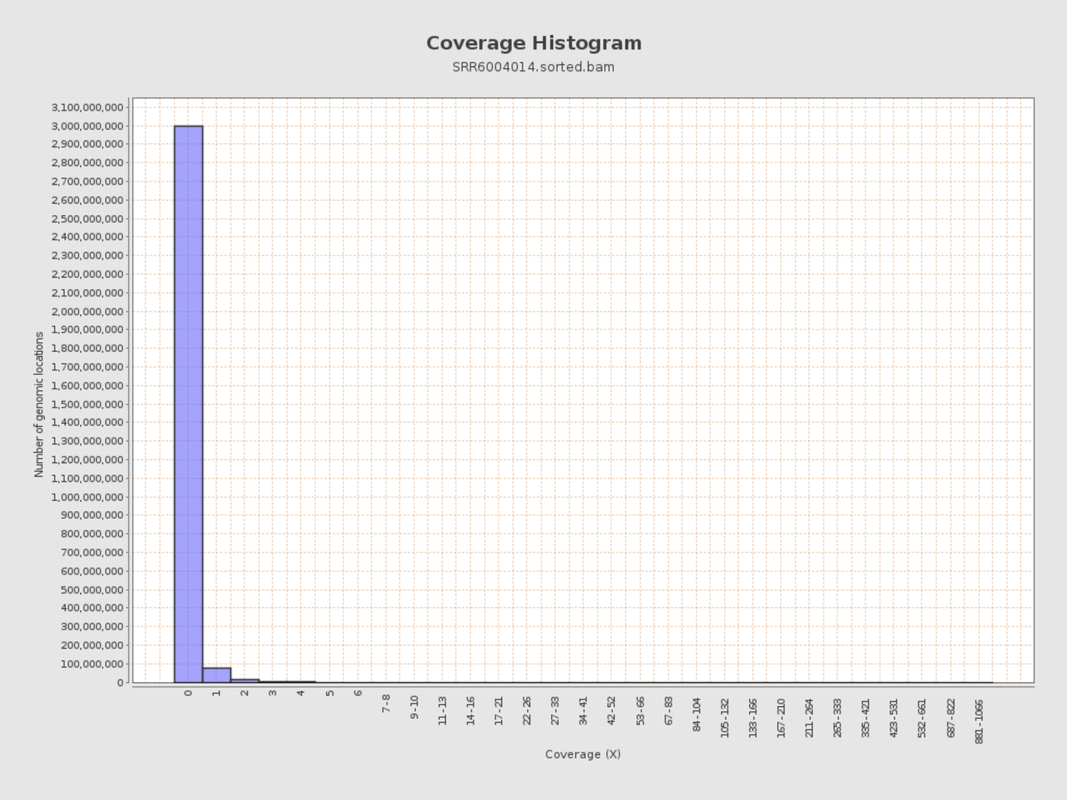
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5418135	0.0217	0.5041
chr2	243199373	13681052	0.0563	0.4141
chr3	198022430	13490346	0.0681	0.3335
chr4	191154276	11047511	0.0578	0.3282
chr5	180915260	9286828	0.0513	0.2917
chr6	171115067	7377663	0.0431	0.2823
chr7	159138663	9472303	0.0595	0.6668

chr8	146364022	8913847	0.0609	0.7071
chr9	141213431	4951673	0.0351	0.323
chr10	135534747	4568106	0.0337	0.3465
chr11	135006516	4814803	0.0357	0.2888
chr12	133851895	6382597	0.0477	0.2844
chr13	115169878	5581803	0.0485	0.2847
chr14	107349540	2533321	0.0236	0.2202
chr15	102531392	3254804	0.0317	0.2258
chr16	90354753	2215505	0.0245	0.2303
chr17	81195210	4595947	0.0566	0.3212
chr18	78077248	2279538	0.0292	0.6061
chr19	59128983	2240290	0.0379	0.3825
chr20	63025520	2917943	0.0463	0.2981
chr21	48129895	2622786	0.0545	0.3199
chr22	51304566	831767	0.0162	0.1562
chrMT	16571	53245	3.2131	3.0907
chrX	155270560	3026870	0.0195	0.1927
chrY	59373566	267434	0.0045	0.1353

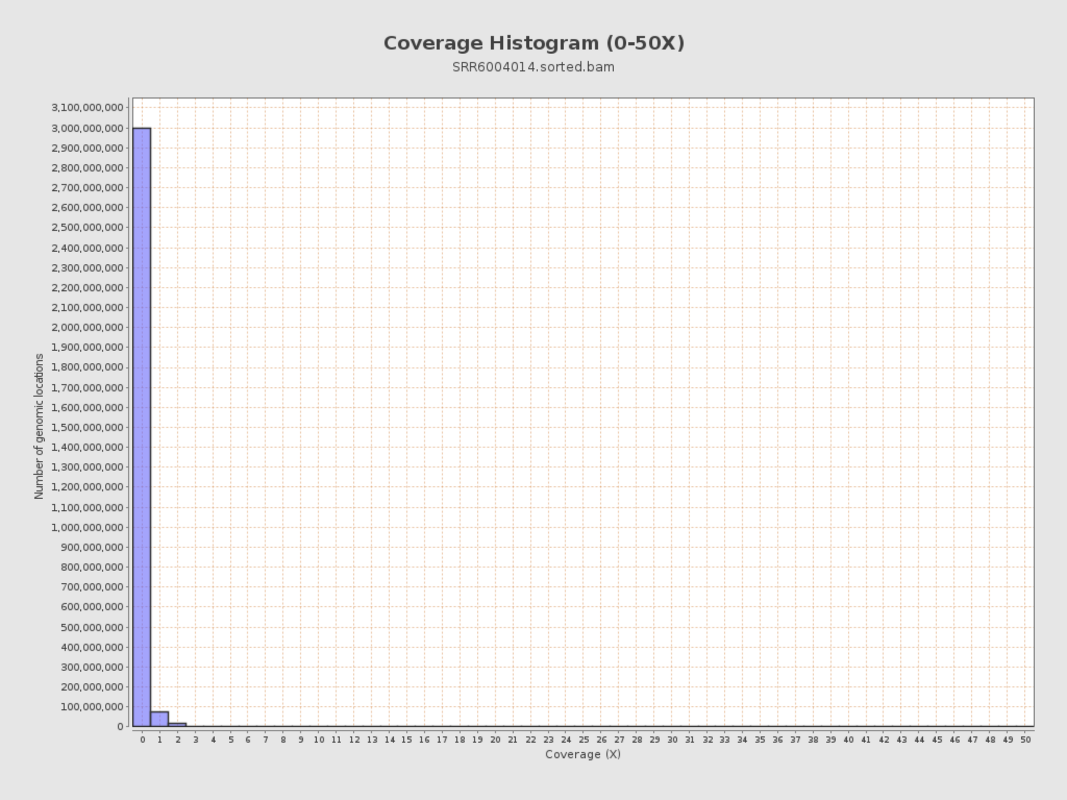
3. Results : Coverage across reference



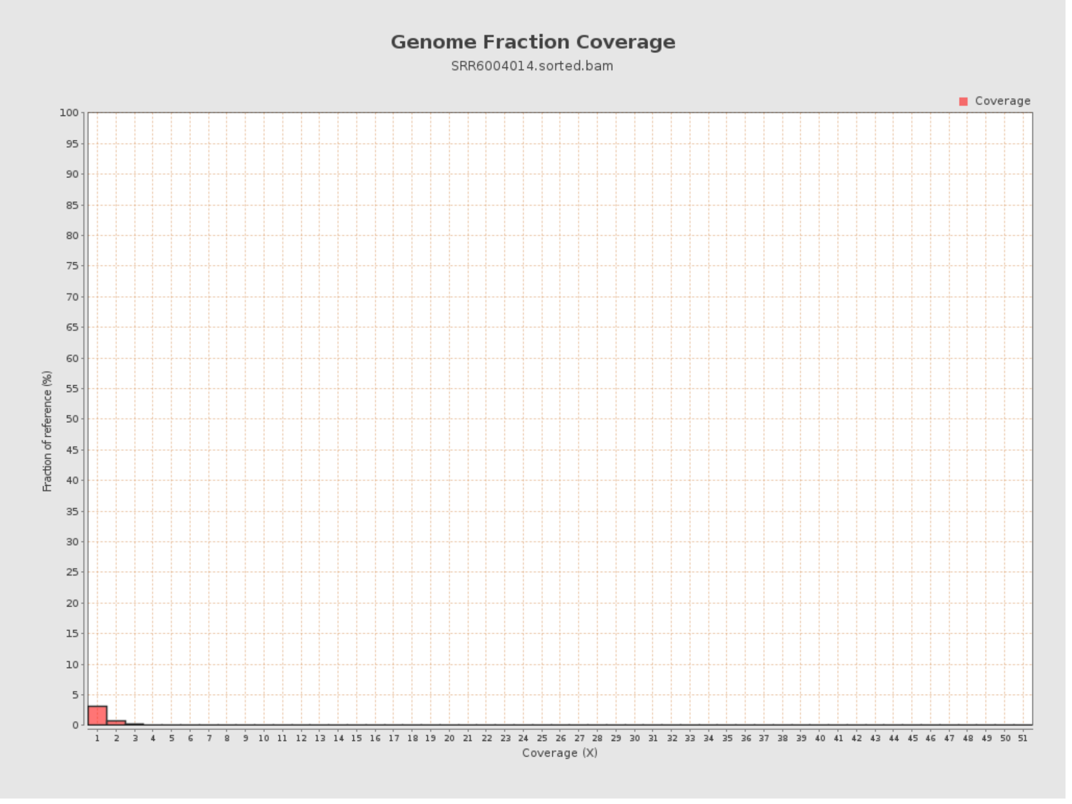
4. Results : Coverage Histogram



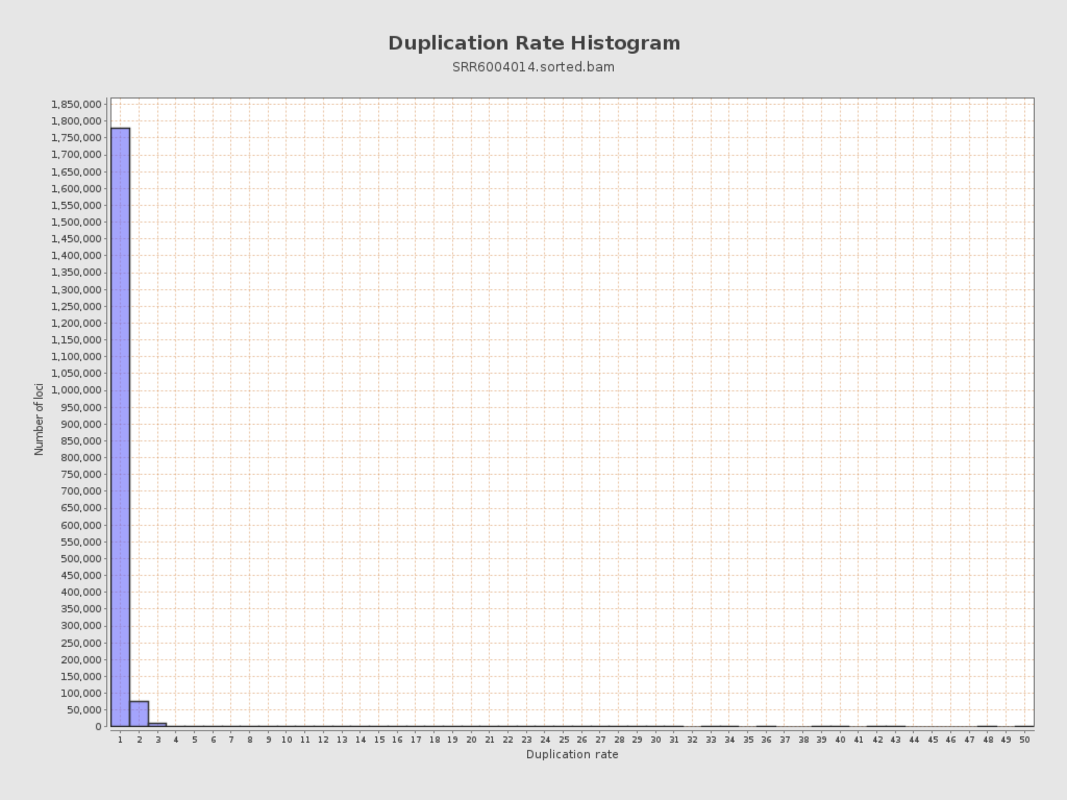
5. Results : Coverage Histogram (0-50X)



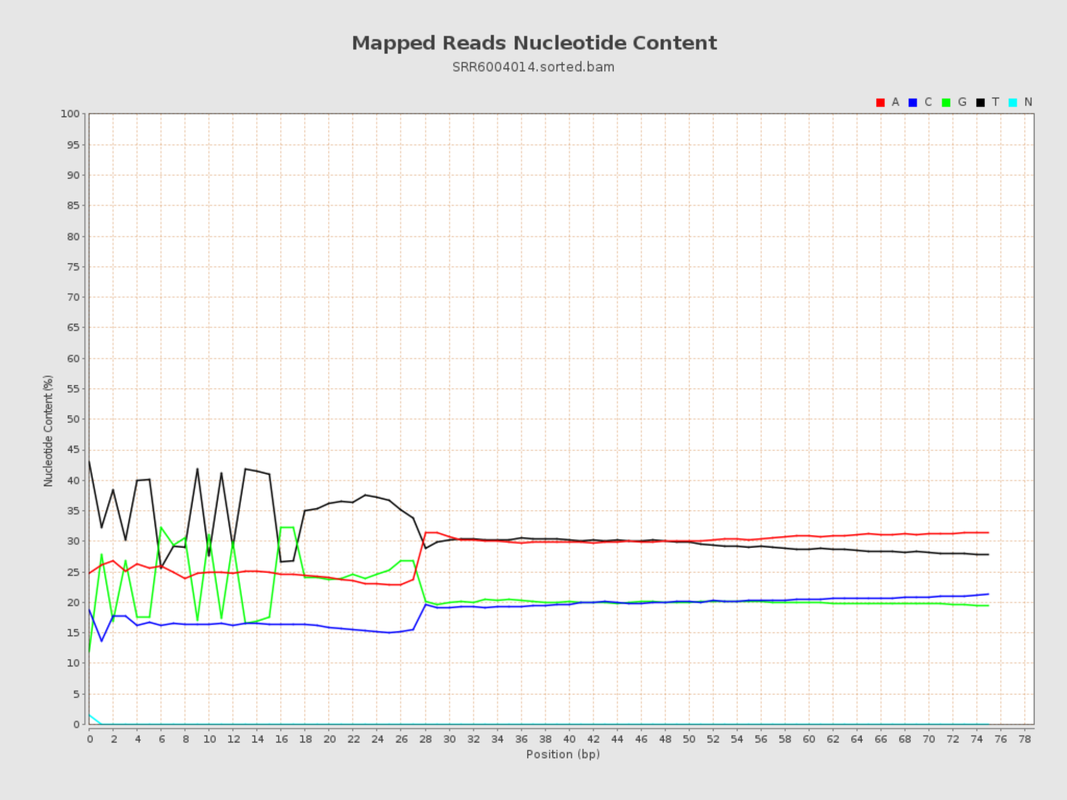
6. Results : Genome Fraction Coverage



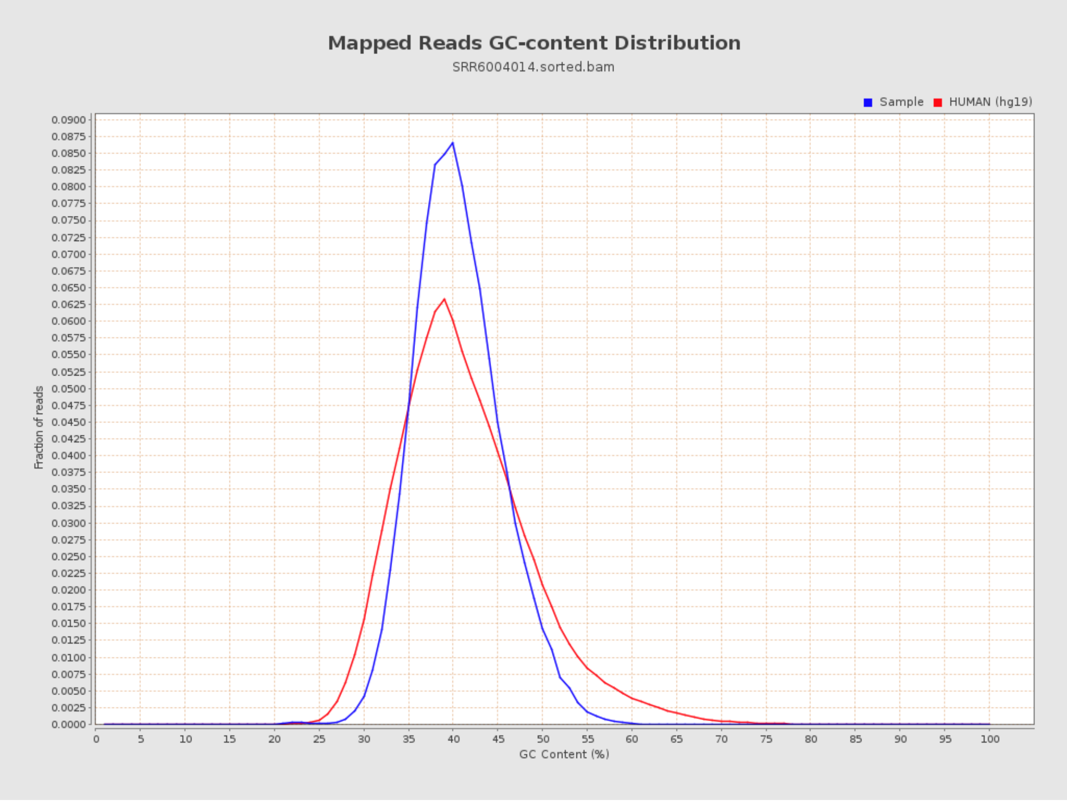
7. Results : Duplication Rate Histogram



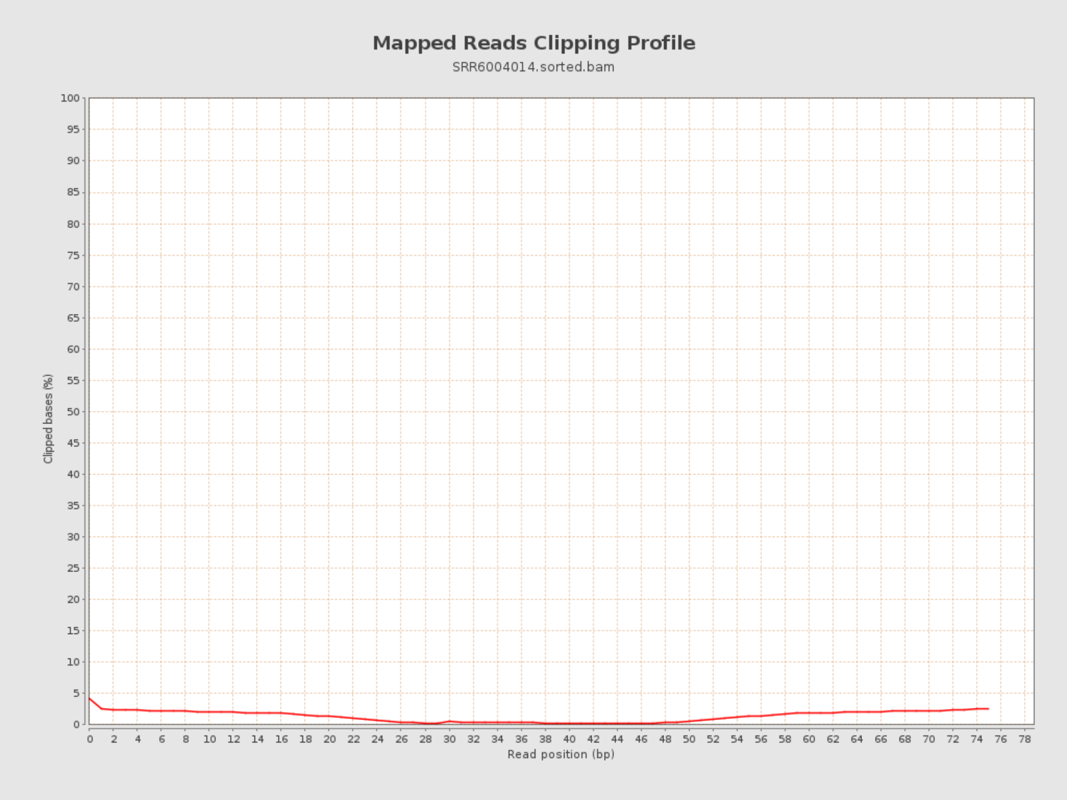
8. Results : Mapped Reads Nucleotide Content



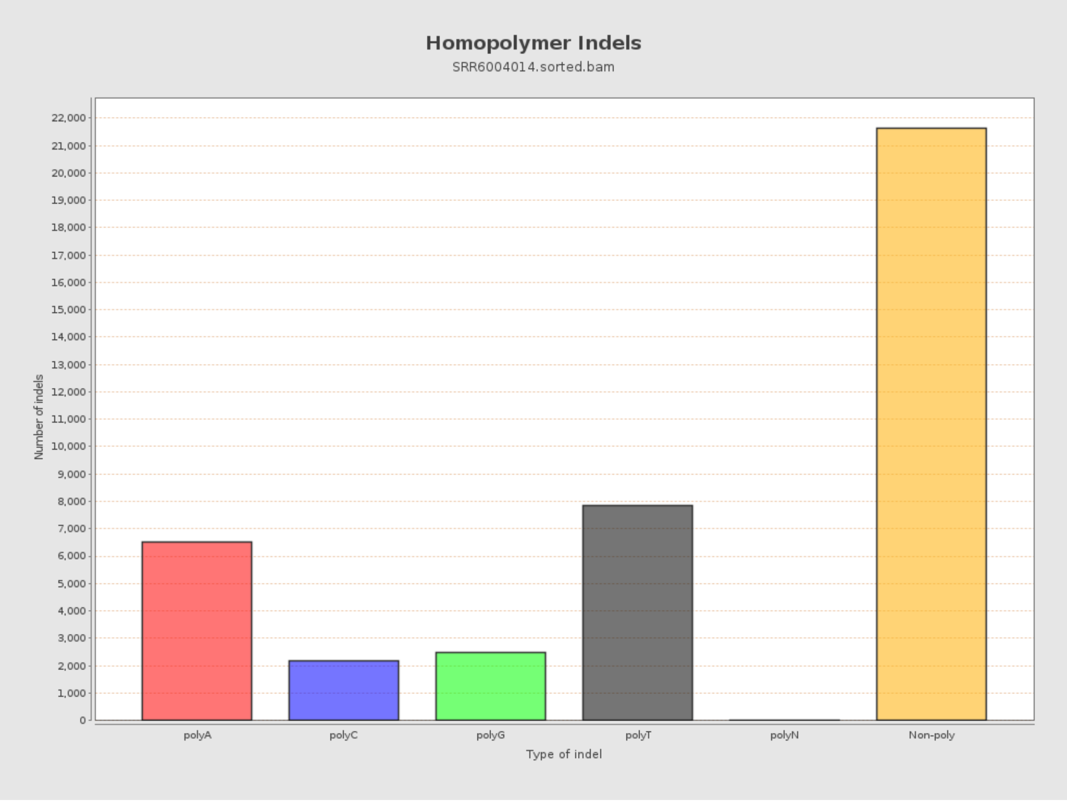
9. Results : Mapped Reads GC-content Distribution



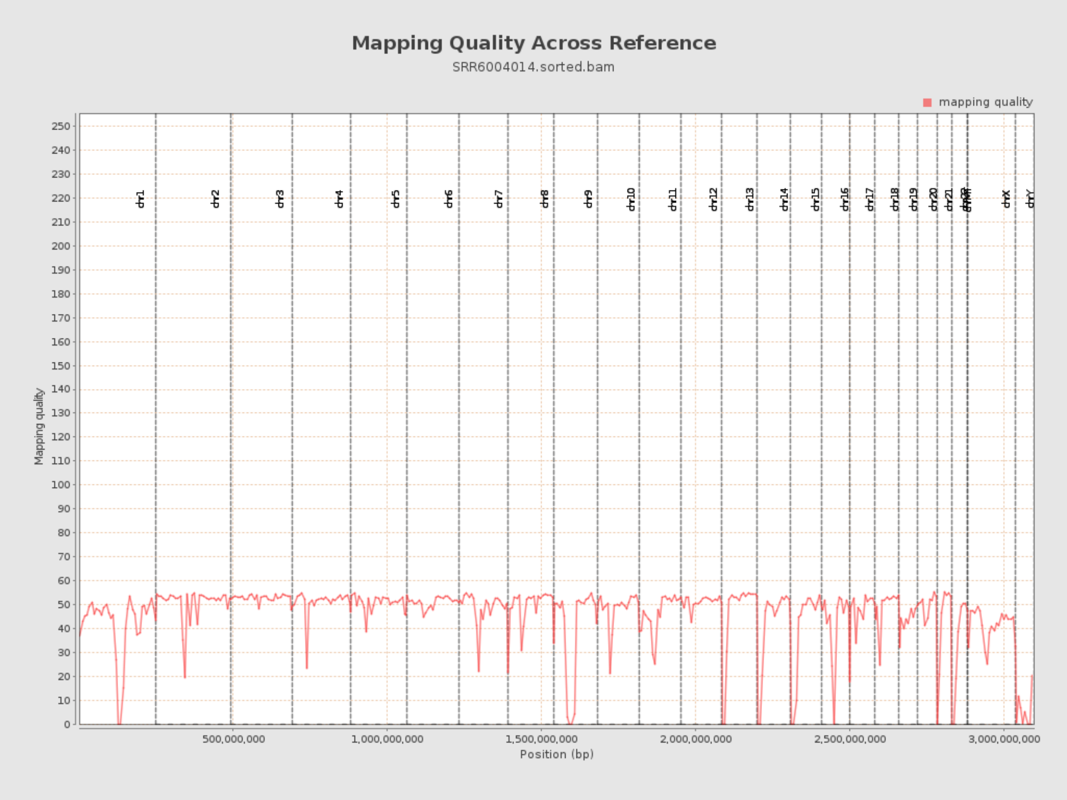
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram