Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:38:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004030.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_SRR6004030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004030.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:38:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,186,882
Mapped reads	1,035,984 / 87.29%
Unmapped reads	150,898 / 12.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,921 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	24,753 / 2.09%
Duplication rate	1.59%
Clipped reads	480,205 / 40.46%

2.2. ACGT Content

Number/percentage of A's	19,851,542 / 28.7%
Number/percentage of C's	12,579,635 / 18.19%
Number/percentage of T's	21,295,619 / 30.79%
Number/percentage of G's	15,421,161 / 22.3%
Number/percentage of N's	14,208 / 0.02%
GC Percentage	40.49%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.2637

2.4. Mapping Quality

Mean Mapping Quality	44.2

2.5. Mismatches and indels

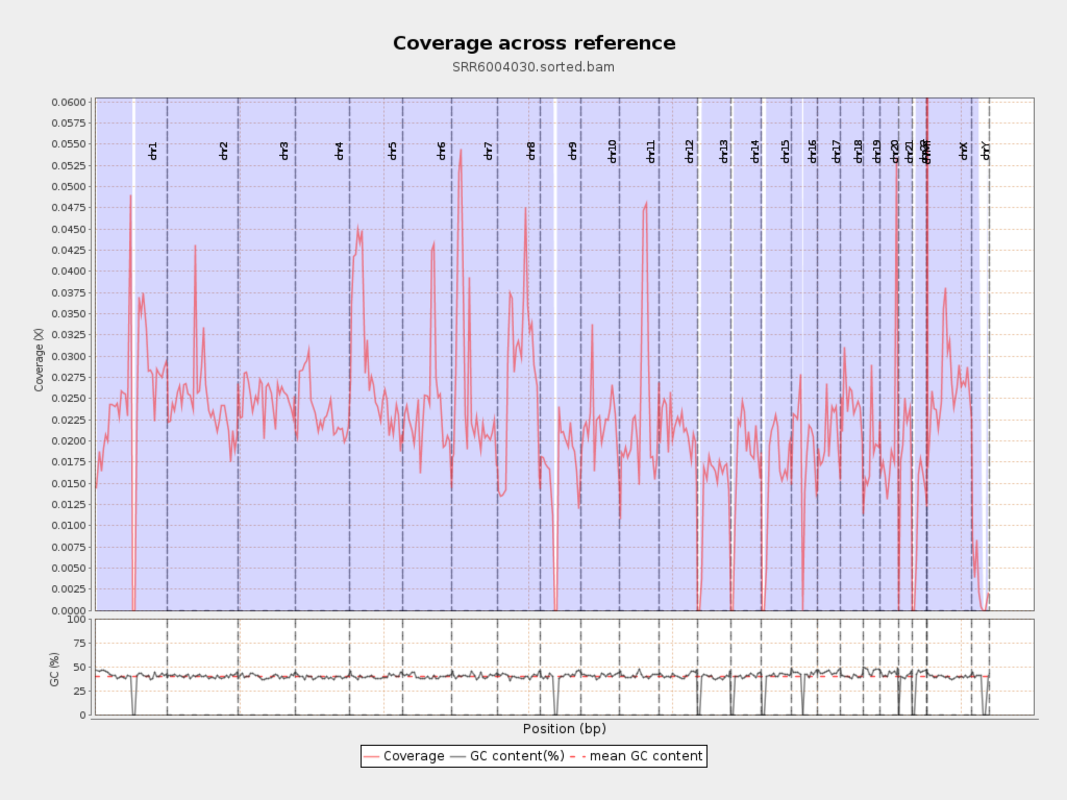
General error rate	0.89%
Mismatches	608,061
Insertions	6,322
Mapped reads with at least one insertion	0.61%
Deletions	17,412
Mapped reads with at least one deletion	1.66%
Homopolymer indels	46.47%

2.6. Chromosome stats

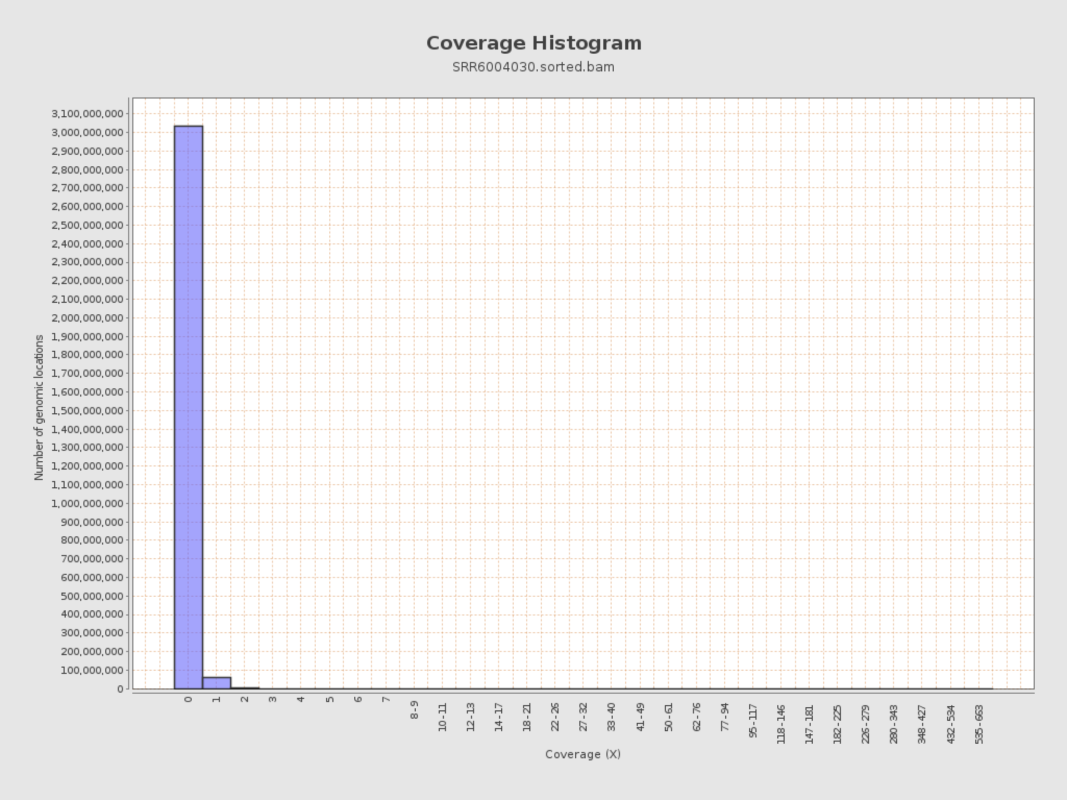
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6179442	0.0248	0.5331
chr2	243199373	5994115	0.0246	0.2578
chr3	198022430	4965350	0.0251	0.1661
chr4	191154276	4495598	0.0235	0.1658
chr5	180915260	5250164	0.029	0.1806
chr6	171115067	4131472	0.0241	0.1772
chr7	159138663	4121312	0.0259	0.3006

chr8	146364022	4162773	0.0284	0.4316
chr9	141213431	2296768	0.0163	0.2086
chr10	135534747	3000150	0.0221	0.2086
chr11	135006516	3127819	0.0232	0.2379
chr12	133851895	2885056	0.0216	0.158
chr13	115169878	1583893	0.0138	0.1225
chr14	107349540	1838436	0.0171	0.1443
chr15	102531392	1574378	0.0154	0.1315
chr16	90354753	1677675	0.0186	0.1598
chr17	81195210	1669293	0.0206	0.1642
chr18	78077248	1915414	0.0245	0.4279
chr19	59128983	1106221	0.0187	0.3567
chr20	63025520	1375519	0.0218	0.1649
chr21	48129895	923369	0.0192	0.1547
chr22	51304566	568102	0.0111	0.1092
chrMT	16571	26544	1.6018	1.9076
chrX	155270560	4148621	0.0267	0.1891
chrY	59373566	173069	0.0029	0.07

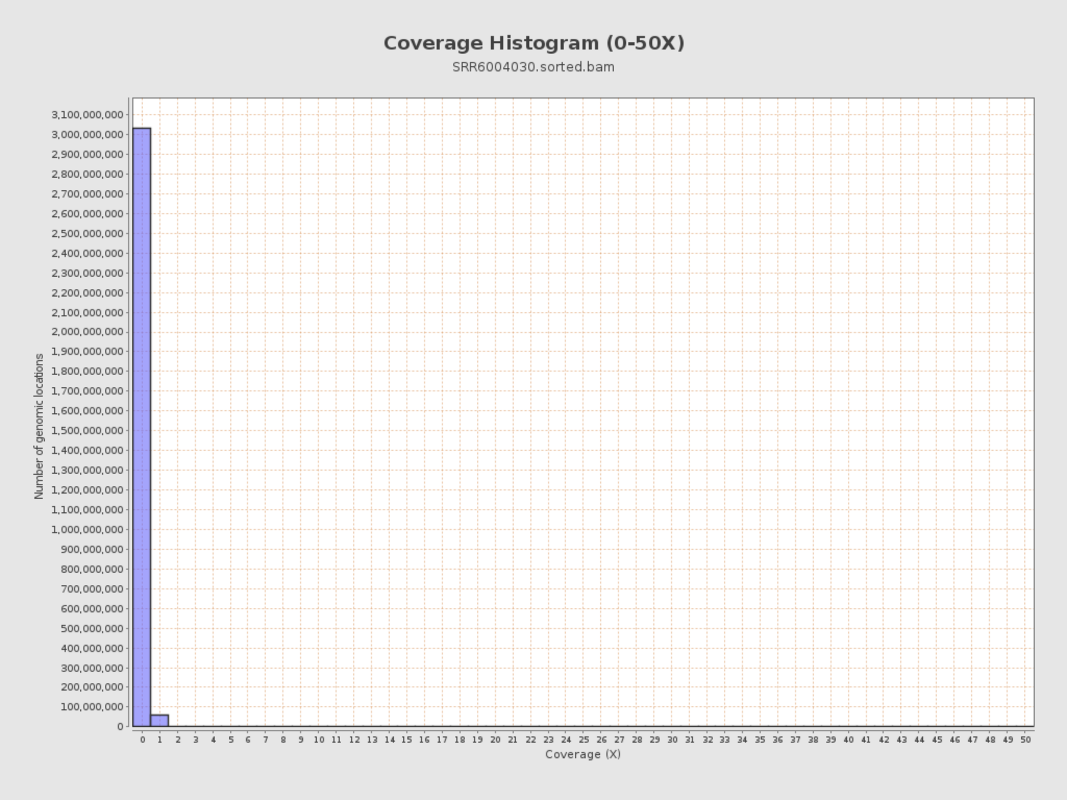
3. Results : Coverage across reference



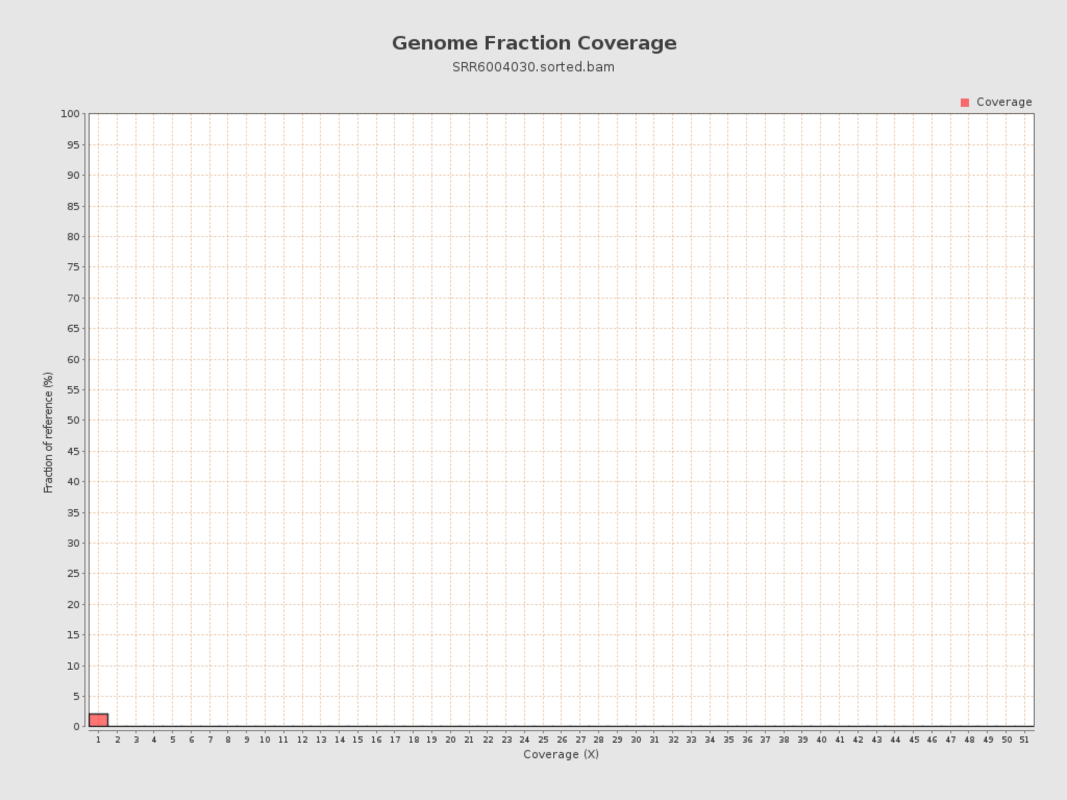
4. Results : Coverage Histogram



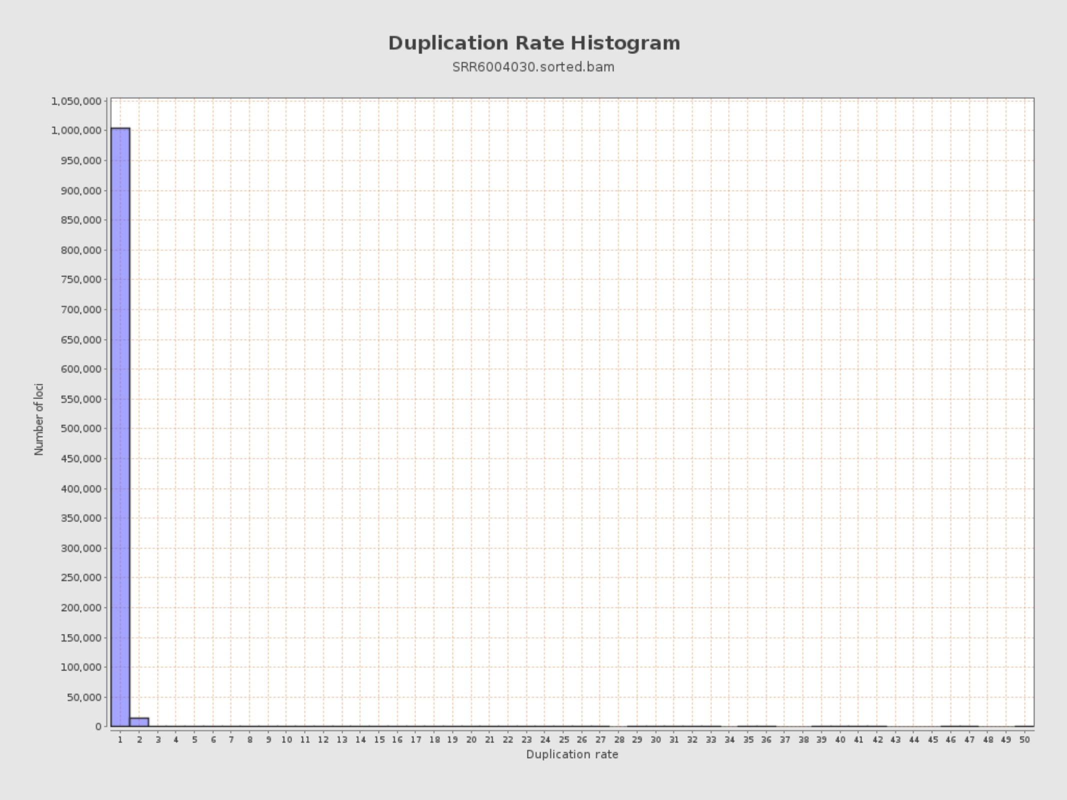
5. Results : Coverage Histogram (0-50X)



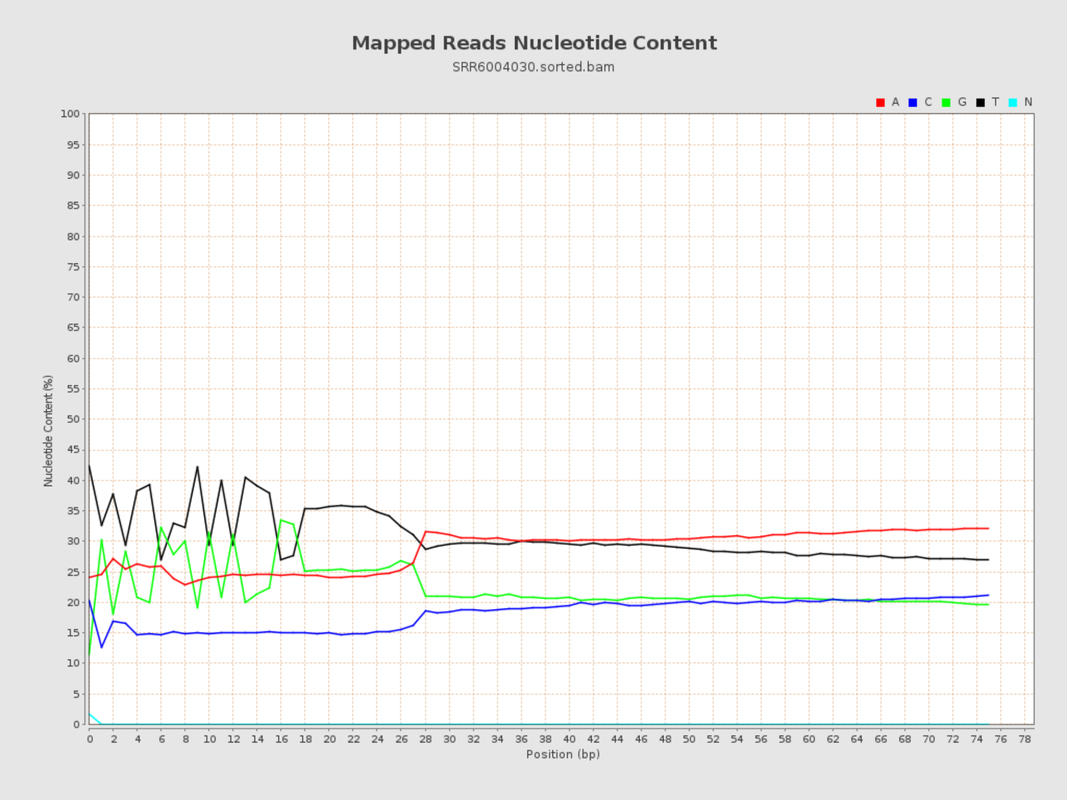
6. Results : Genome Fraction Coverage



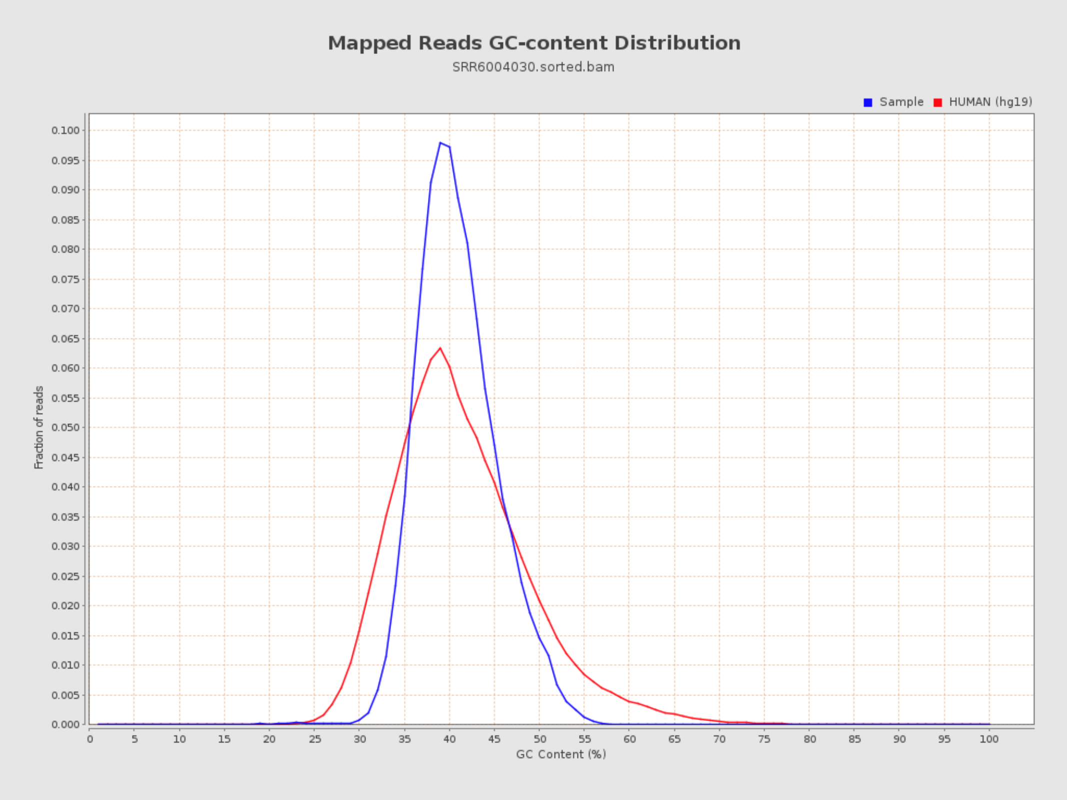
7. Results : Duplication Rate Histogram



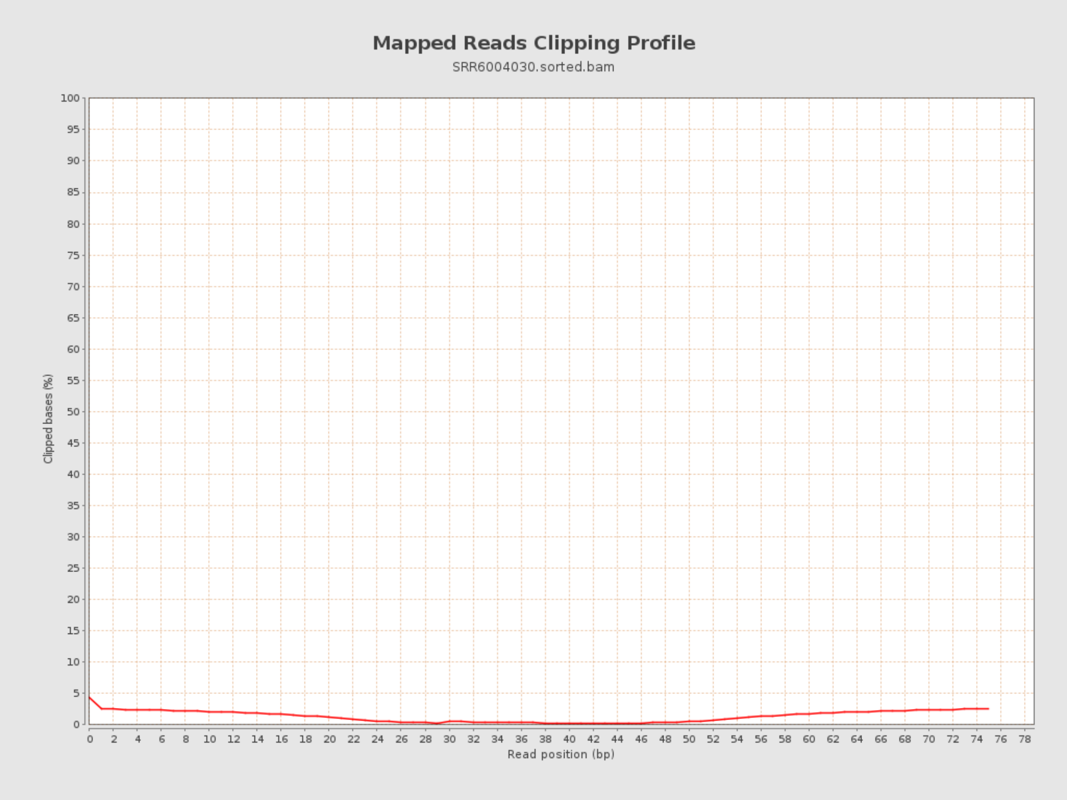
8. Results : Mapped Reads Nucleotide Content



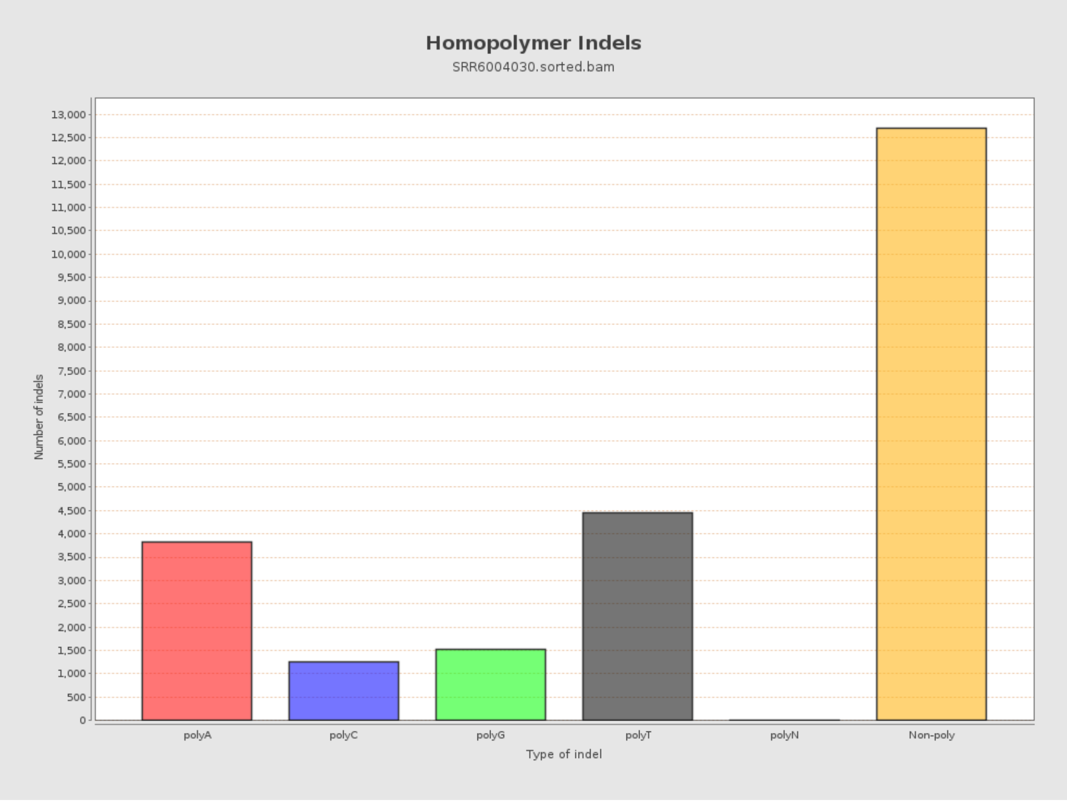
9. Results : Mapped Reads GC-content Distribution



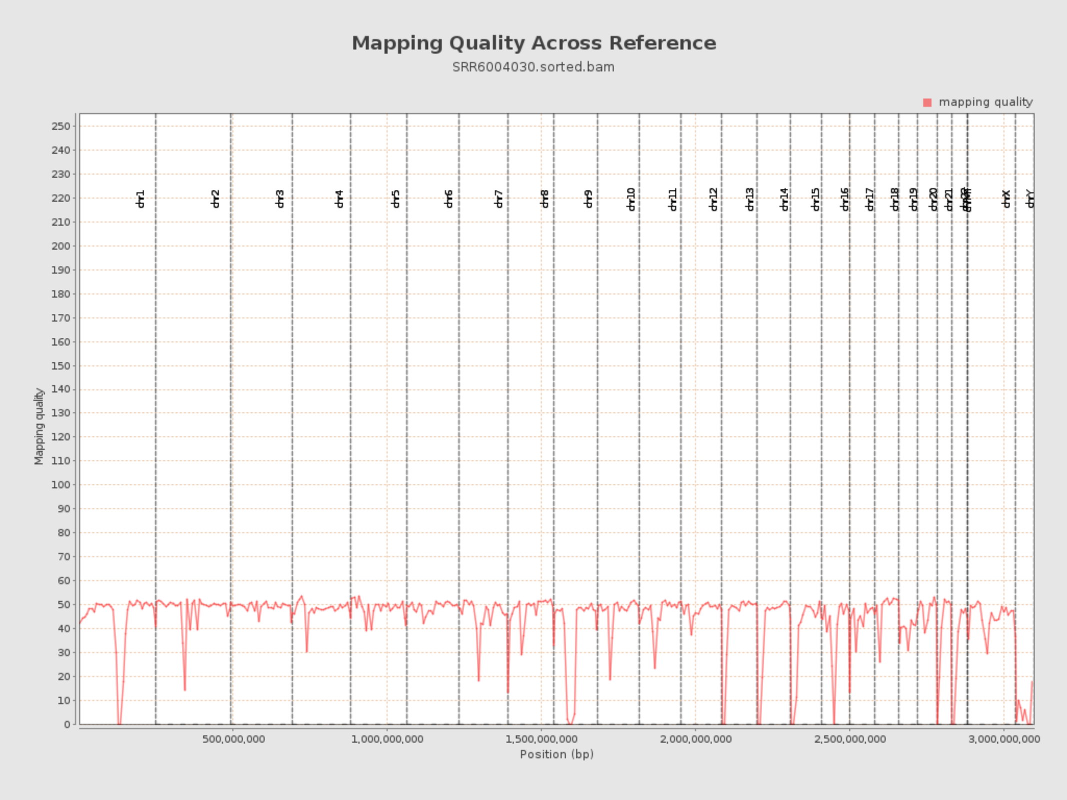
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram