Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:41:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004031.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_SRR6004031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004031.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:41:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,913,848
Mapped reads	1,706,635 / 89.17%
Unmapped reads	207,213 / 10.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,573 / 1.07%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	70,740 / 3.7%
Duplication rate	3.05%
Clipped reads	760,264 / 39.72%

2.2. ACGT Content

Number/percentage of A's	33,110,429 / 28.89%
Number/percentage of C's	21,258,330 / 18.55%
Number/percentage of T's	36,344,941 / 31.71%
Number/percentage of G's	23,888,651 / 20.84%
Number/percentage of N's	8,653 / 0.01%
GC Percentage	39.39%

2.3. Coverage

Mean	0.037

Standard Deviation	0.4028

2.4. Mapping Quality

Mean Mapping Quality	46.59

2.5. Mismatches and indels

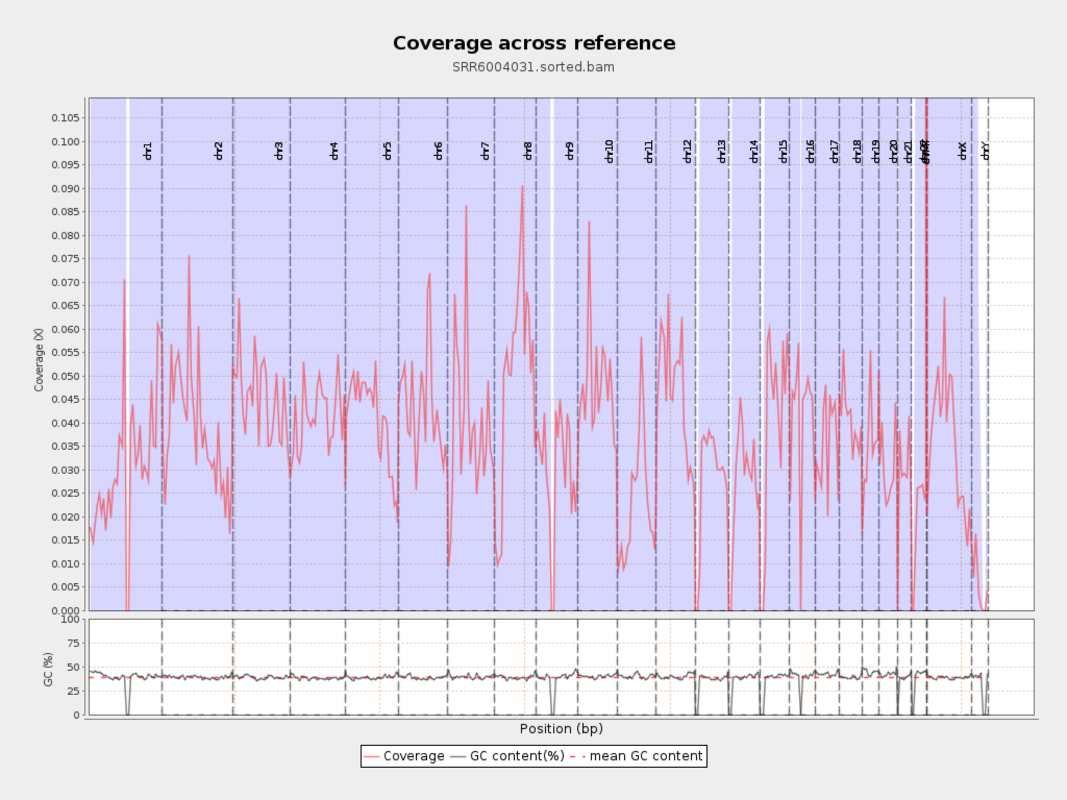
General error rate	0.94%
Mismatches	1,061,728
Insertions	9,158
Mapped reads with at least one insertion	0.53%
Deletions	30,765
Mapped reads with at least one deletion	1.78%
Homopolymer indels	45.71%

2.6. Chromosome stats

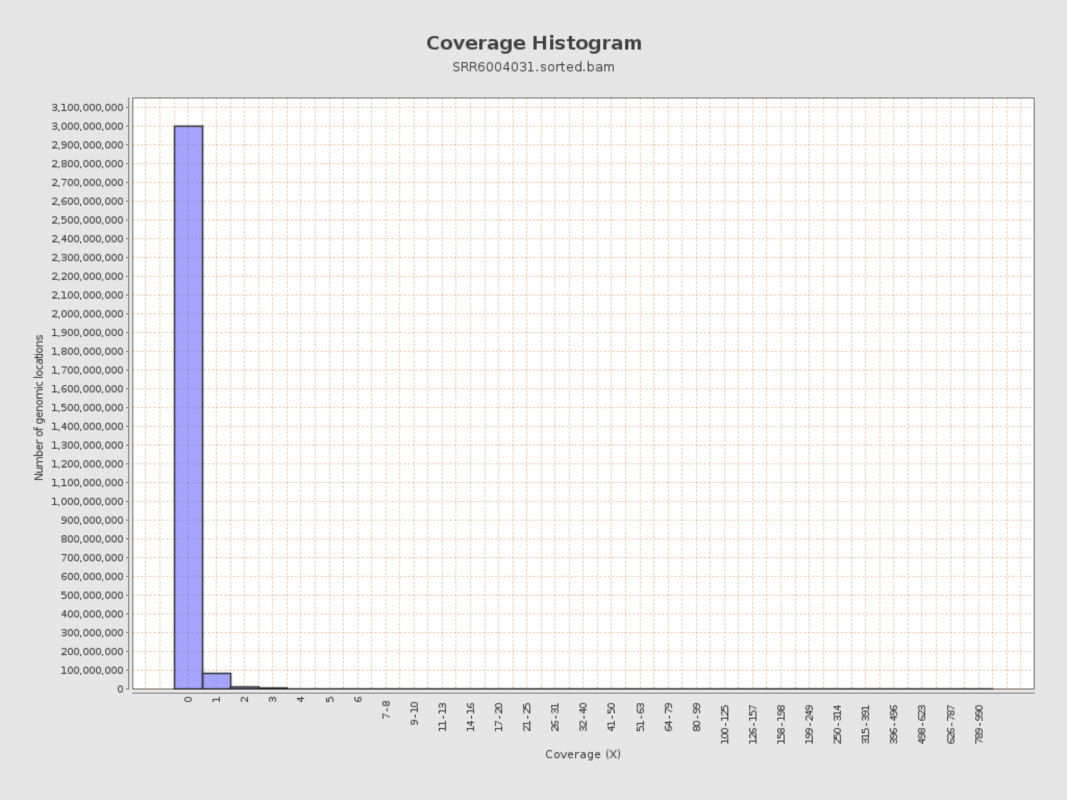
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7626425	0.0306	0.8143
chr2	243199373	9353921	0.0385	0.3748
chr3	198022430	8982189	0.0454	0.2441
chr4	191154276	7923483	0.0415	0.2436
chr5	180915260	7439539	0.0411	0.2368
chr6	171115067	7457928	0.0436	0.2564
chr7	159138663	6304636	0.0396	0.6114

chr8	146364022	7194104	0.0492	0.6
chr9	141213431	4219110	0.0299	0.3217
chr10	135534747	6486266	0.0479	0.3887
chr11	135006516	3136589	0.0232	0.2331
chr12	133851895	6212076	0.0464	0.254
chr13	115169878	3198400	0.0278	0.1909
chr14	107349540	2896962	0.027	0.2037
chr15	102531392	4082977	0.0398	0.2279
chr16	90354753	3701728	0.041	0.2698
chr17	81195210	2907863	0.0358	0.2336
chr18	78077248	3190831	0.0409	0.6666
chr19	59128983	2128165	0.036	0.5526
chr20	63025520	1933877	0.0307	0.2125
chr21	48129895	1397656	0.029	0.2112
chr22	51304566	941411	0.0183	0.1515
chrMT	16571	67487	4.0726	3.447
chrX	155270560	5577003	0.0359	0.2487
chrY	59373566	301032	0.0051	0.1196

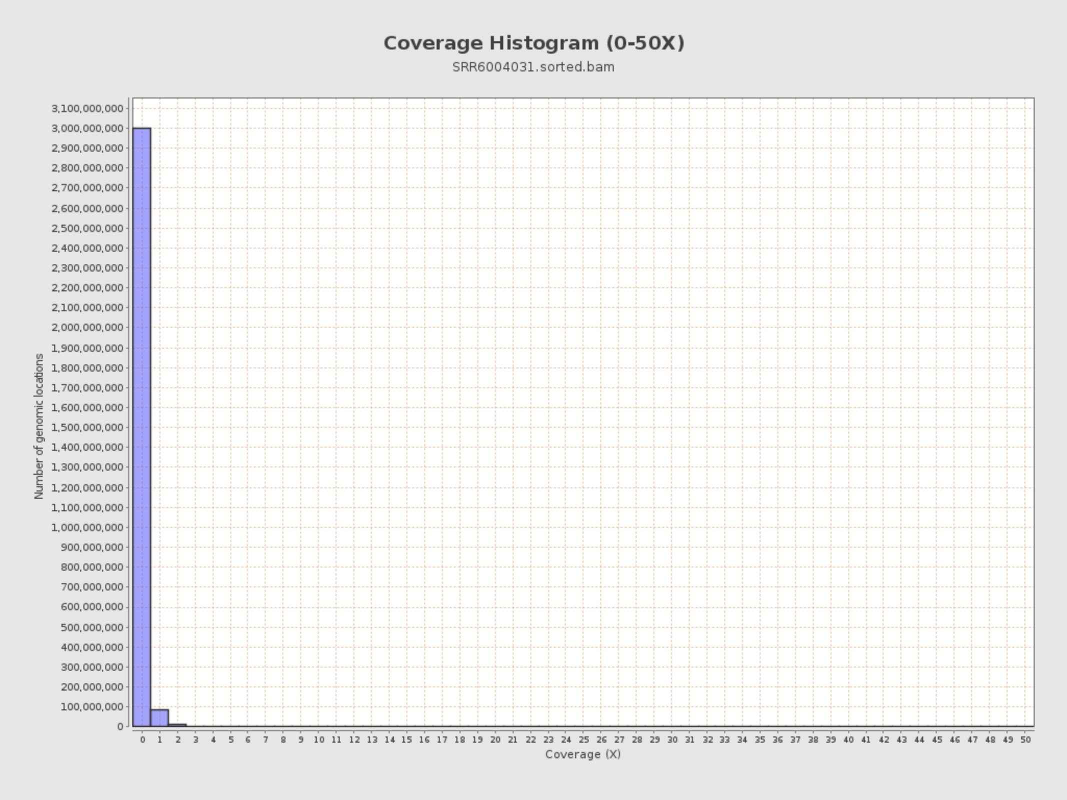
3. Results : Coverage across reference



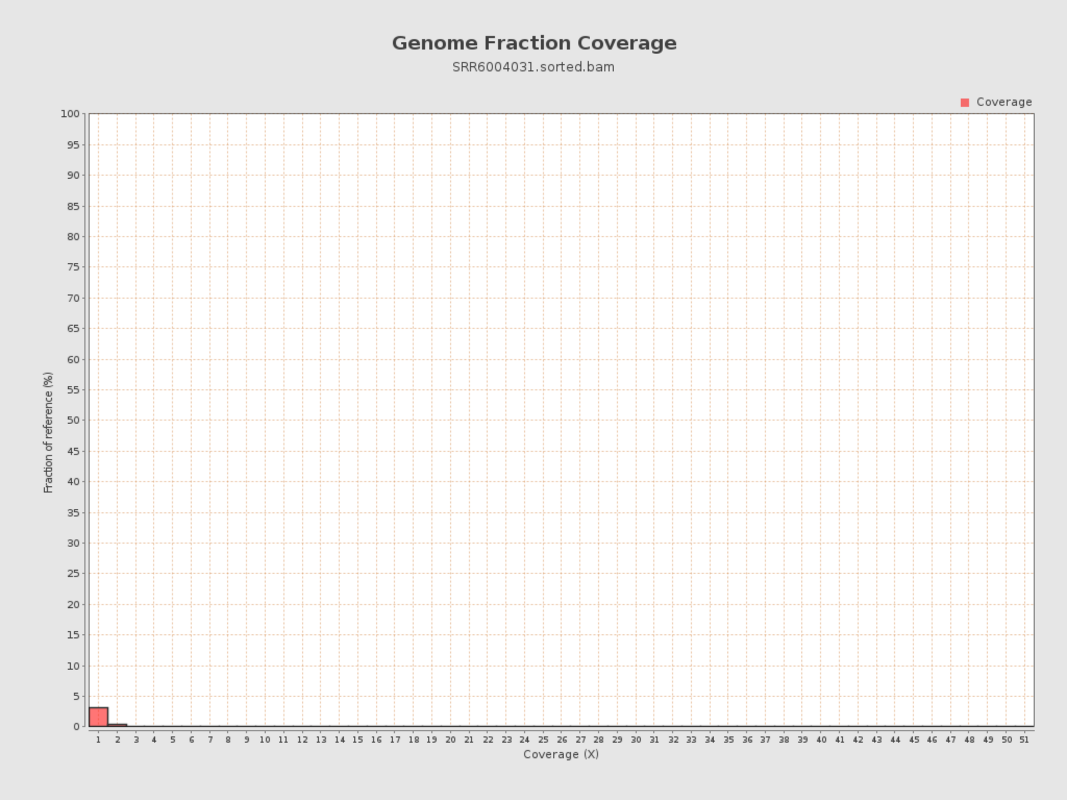
4. Results : Coverage Histogram



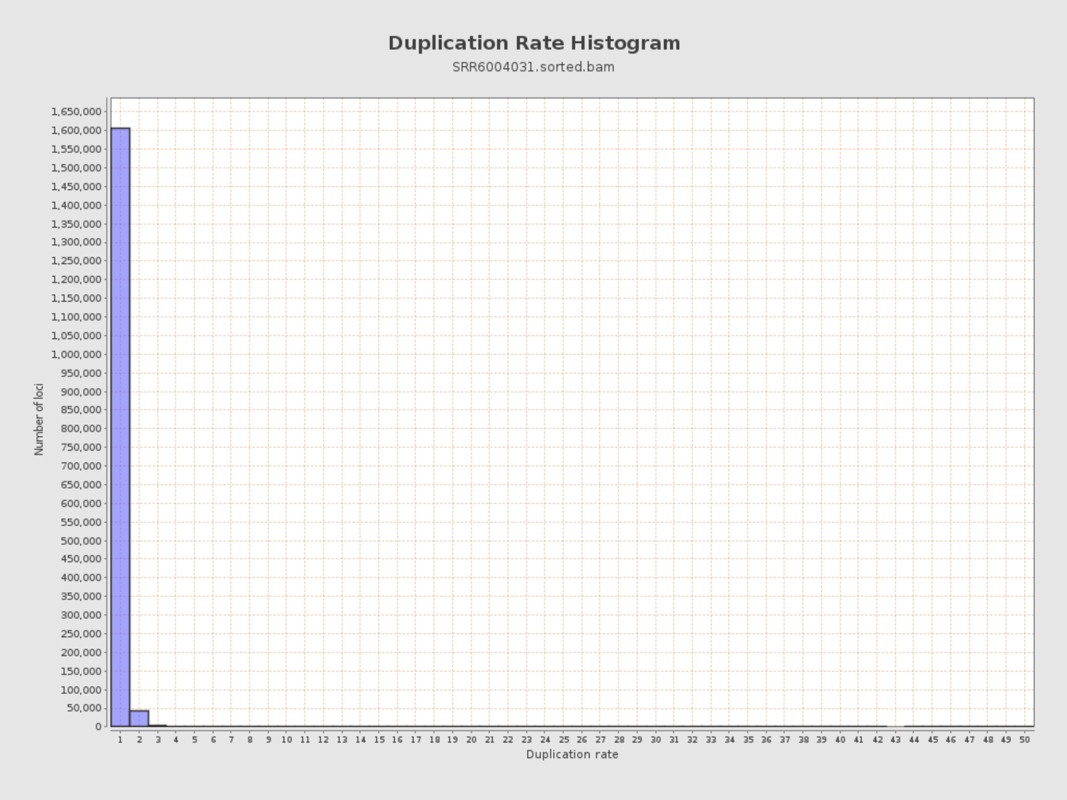
5. Results : Coverage Histogram (0-50X)



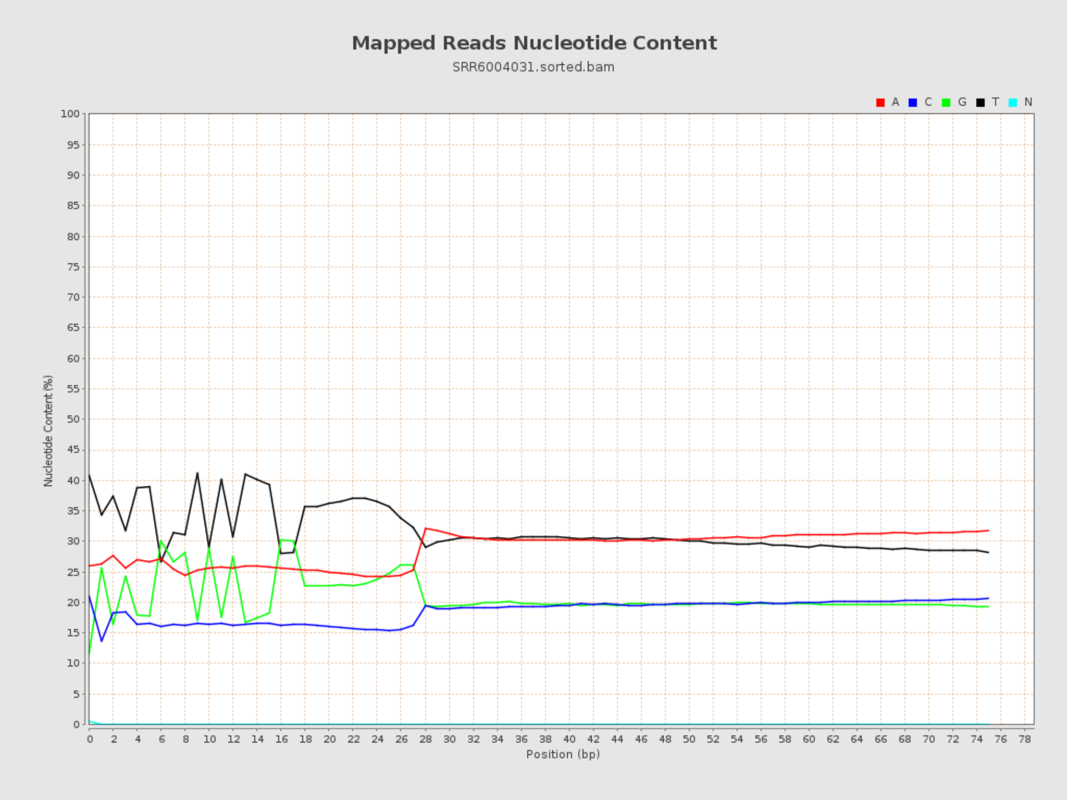
6. Results : Genome Fraction Coverage



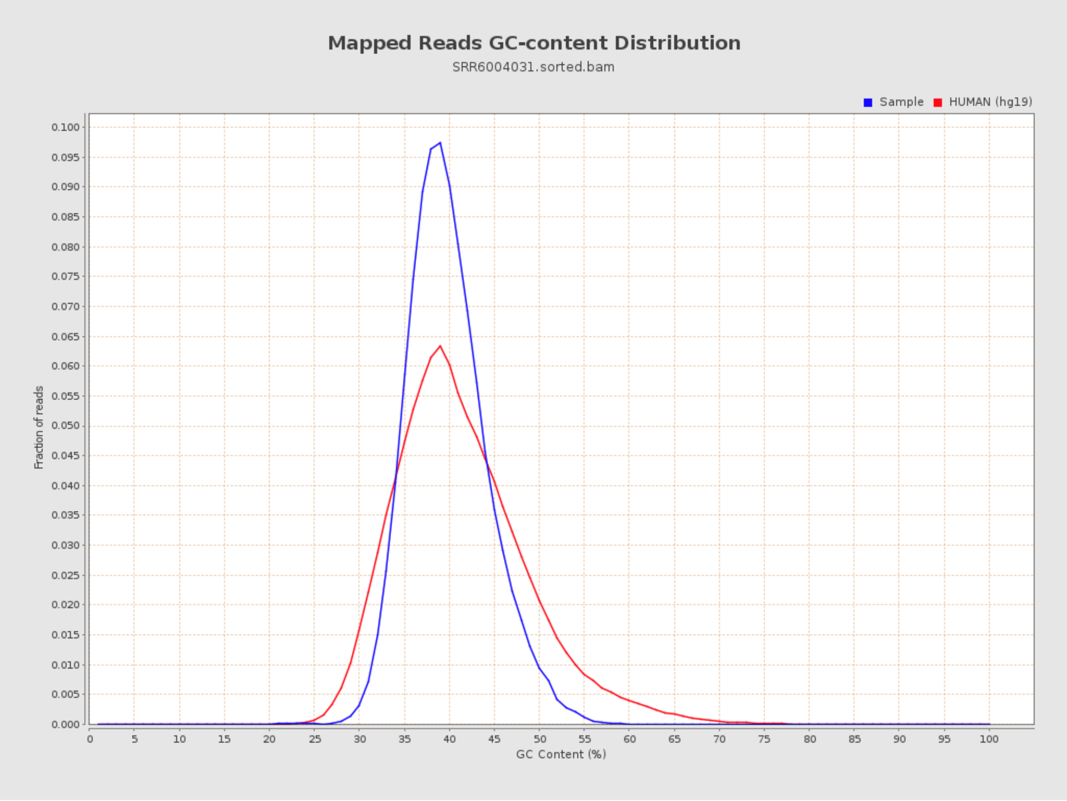
7. Results : Duplication Rate Histogram



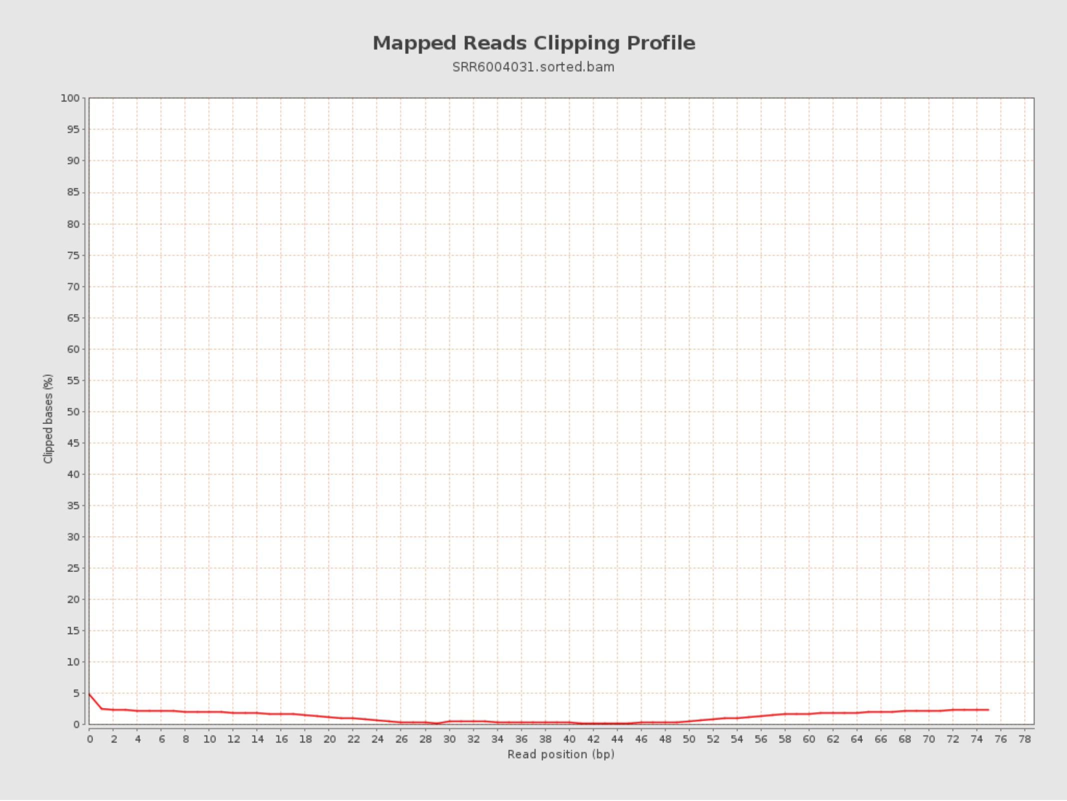
8. Results : Mapped Reads Nucleotide Content



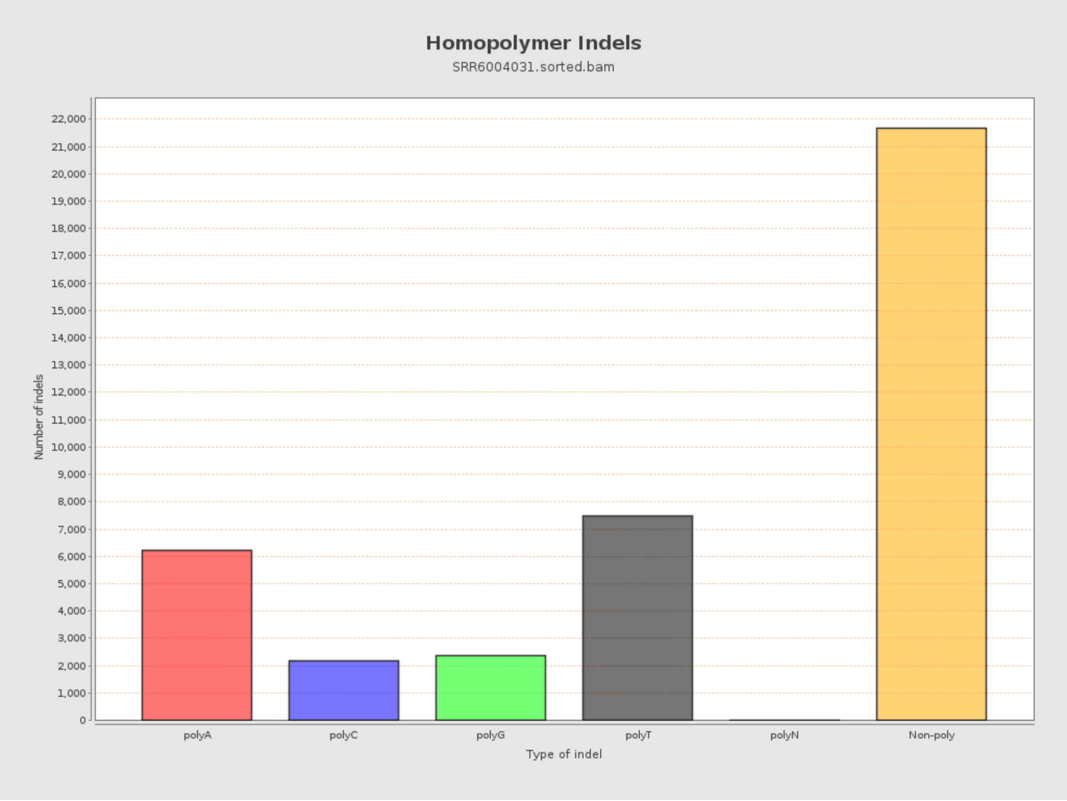
9. Results : Mapped Reads GC-content Distribution



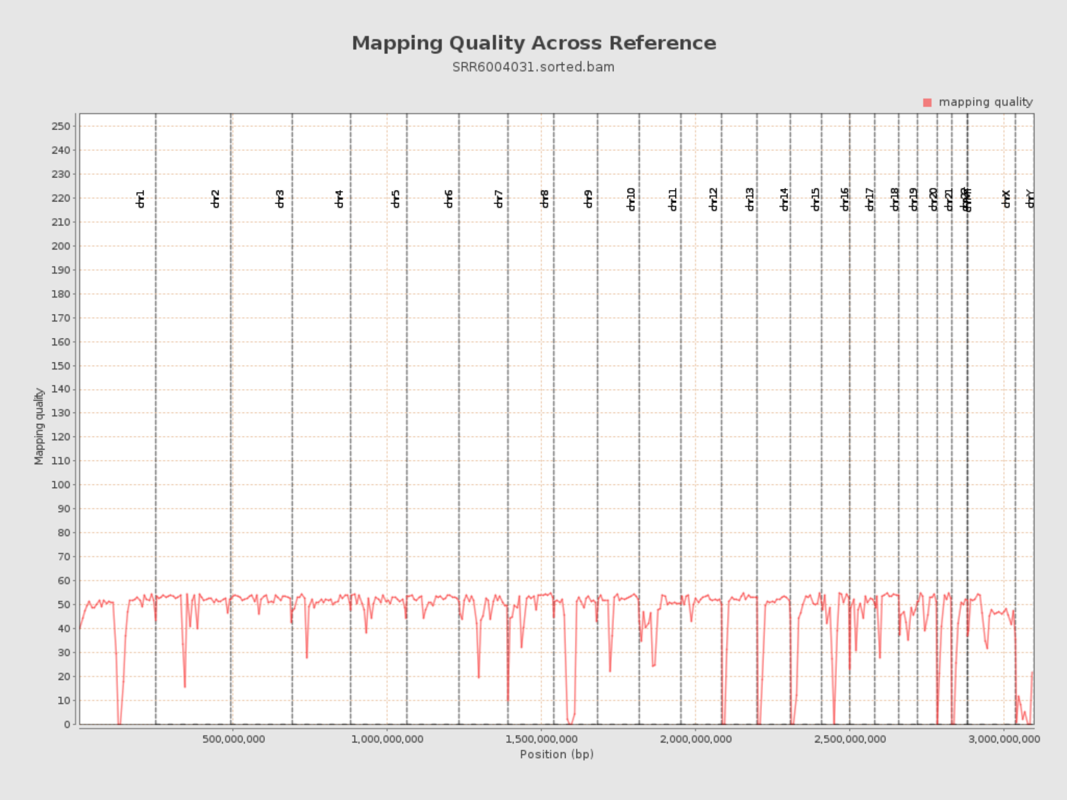
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram