Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:41:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004049.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_SRR6004049 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004049.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:41:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,685,949
Mapped reads	3,121,737 / 84.69%
Unmapped reads	564,212 / 15.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,502 / 1.02%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	338,261 / 9.18%
Duplication rate	8.57%
Clipped reads	1,604,446 / 43.53%

2.2. ACGT Content

Number/percentage of A's	56,780,426 / 27.98%
Number/percentage of C's	36,305,505 / 17.89%
Number/percentage of T's	65,501,041 / 32.28%
Number/percentage of G's	44,204,161 / 21.78%
Number/percentage of N's	152,255 / 0.08%
GC Percentage	39.67%

2.3. Coverage

Mean	0.0656

Standard Deviation	0.5509

2.4. Mapping Quality

Mean Mapping Quality	40.13

2.5. Mismatches and indels

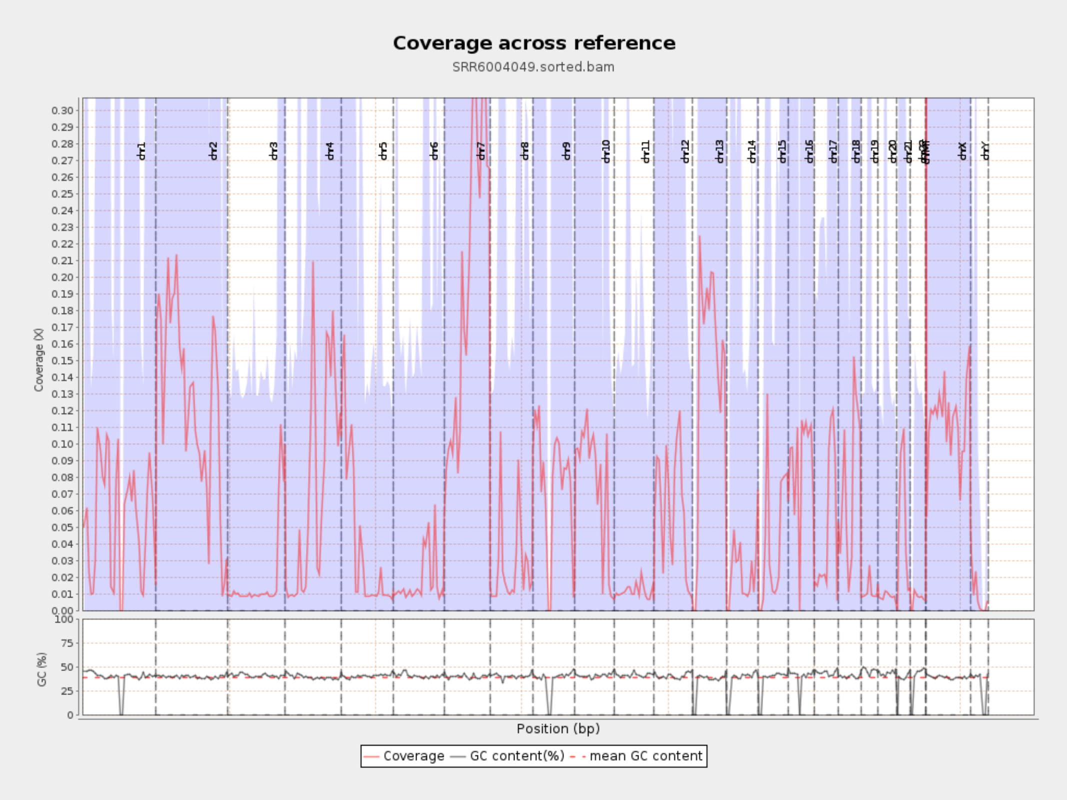
General error rate	0.9%
Mismatches	1,811,079
Insertions	14,190
Mapped reads with at least one insertion	0.45%
Deletions	68,944
Mapped reads with at least one deletion	2.18%
Homopolymer indels	44.64%

2.6. Chromosome stats

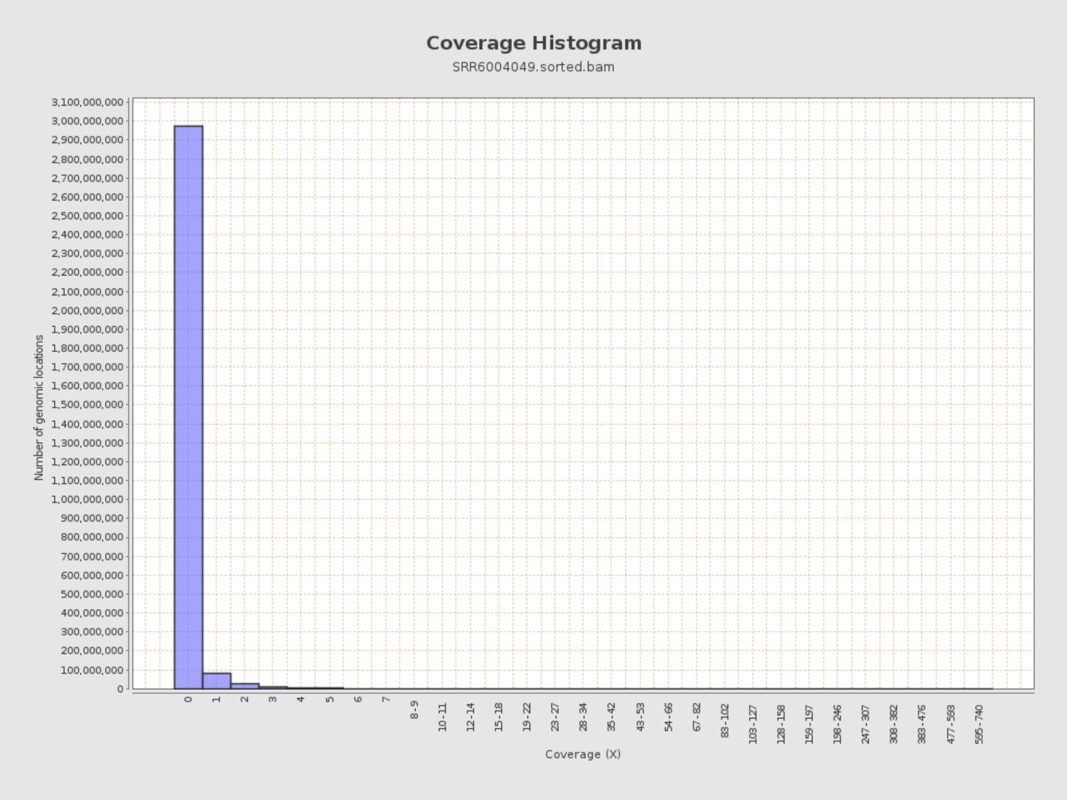
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13656697	0.0548	0.6919
chr2	243199373	30710649	0.1263	0.7115
chr3	198022430	3825264	0.0193	0.2127
chr4	191154276	14271560	0.0747	0.4341
chr5	180915260	7216706	0.0399	0.3034
chr6	171115067	3066404	0.0179	0.2201
chr7	159138663	31866501	0.2002	1.2034

chr8	146364022	4006465	0.0274	0.369
chr9	141213431	10843935	0.0768	0.5226
chr10	135534747	10424558	0.0769	0.592
chr11	135006516	1581517	0.0117	0.1741
chr12	133851895	8136077	0.0608	0.3804
chr13	115169878	16773033	0.1456	0.5764
chr14	107349540	2319901	0.0216	0.3006
chr15	102531392	4146485	0.0404	0.3433
chr16	90354753	7914917	0.0876	0.5547
chr17	81195210	4188803	0.0516	0.3381
chr18	78077248	6163452	0.0789	1.0691
chr19	59128983	699821	0.0118	0.4843
chr20	63025520	547398	0.0087	0.2237
chr21	48129895	2366423	0.0492	0.3558
chr22	51304566	356569	0.007	0.1105
chrMT	16571	20702	1.2493	1.5539
chrX	155270560	17446995	0.1124	0.5555
chrY	59373566	509068	0.0086	0.1697

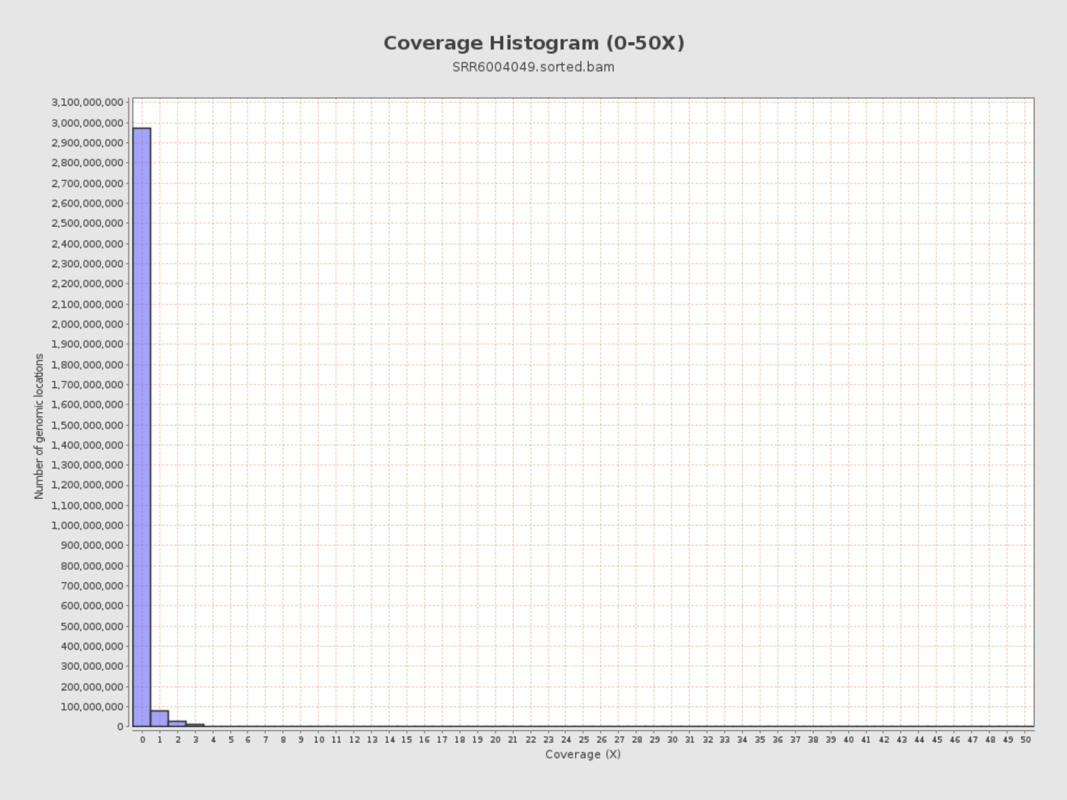
3. Results : Coverage across reference



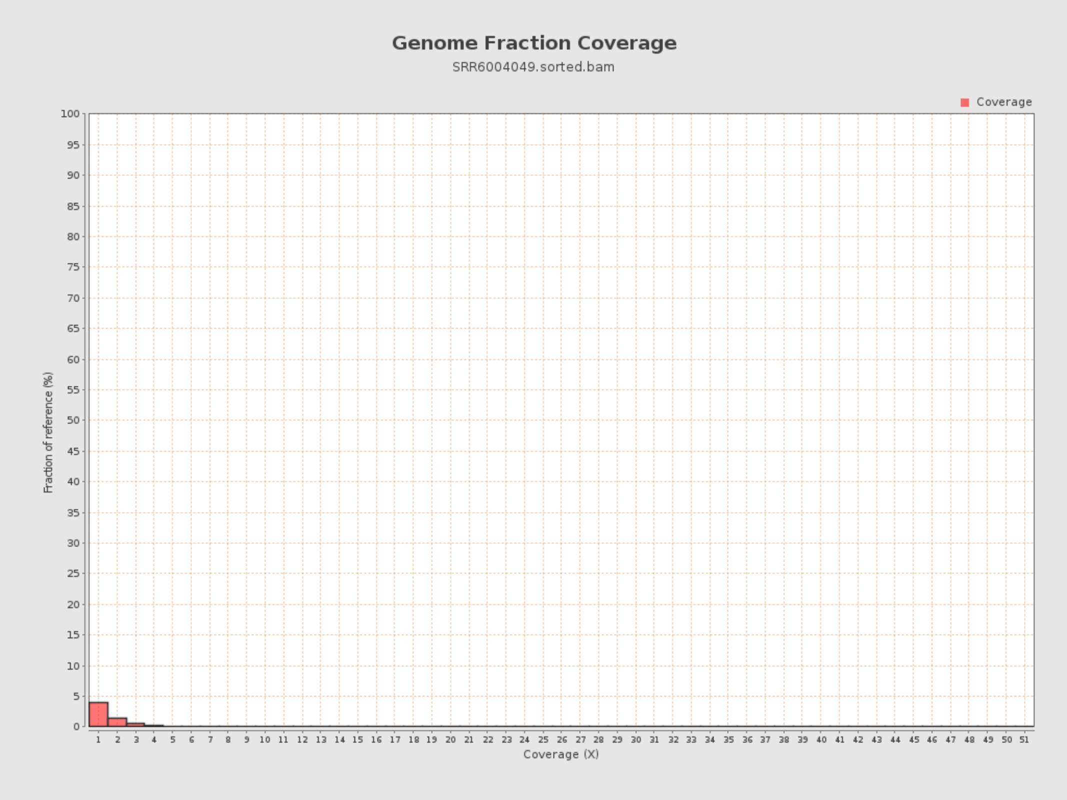
4. Results : Coverage Histogram



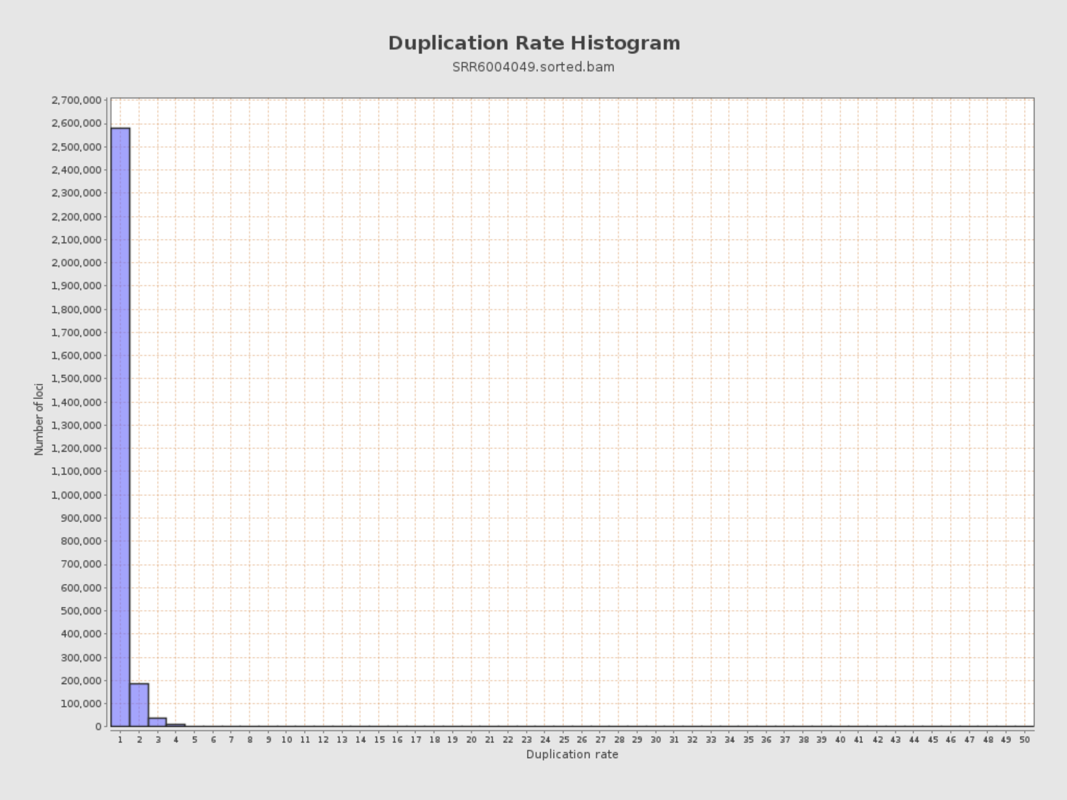
5. Results : Coverage Histogram (0-50X)



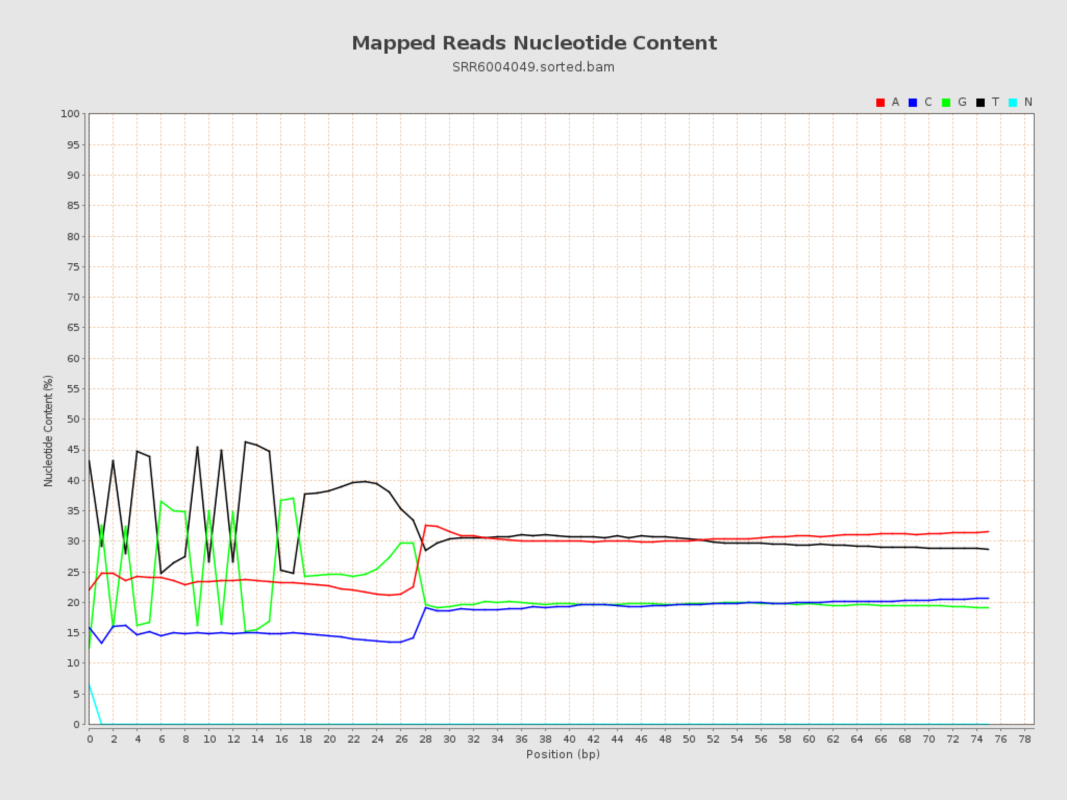
6. Results : Genome Fraction Coverage



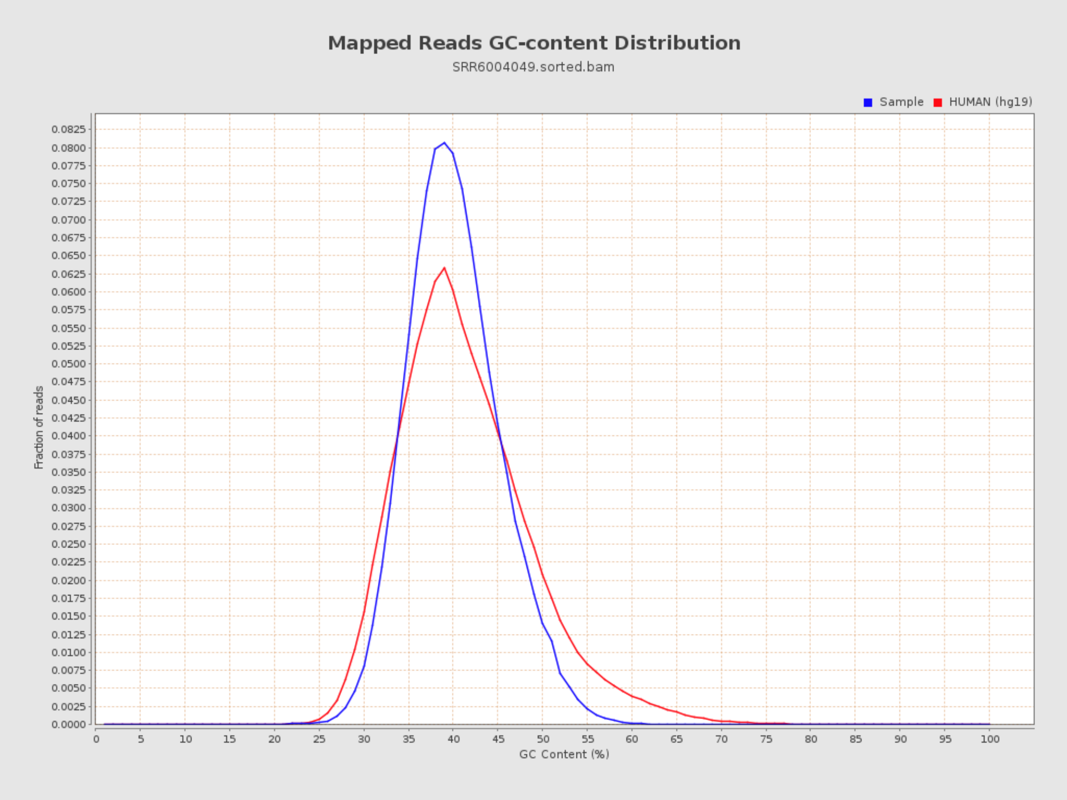
7. Results : Duplication Rate Histogram



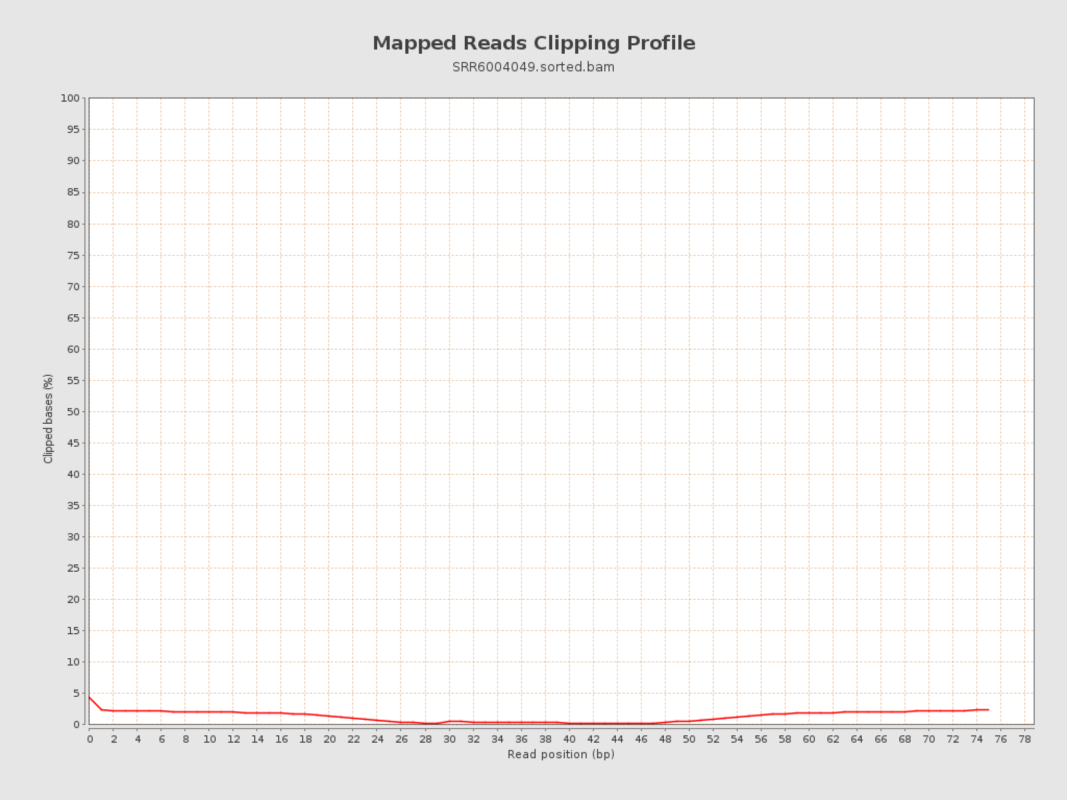
8. Results : Mapped Reads Nucleotide Content



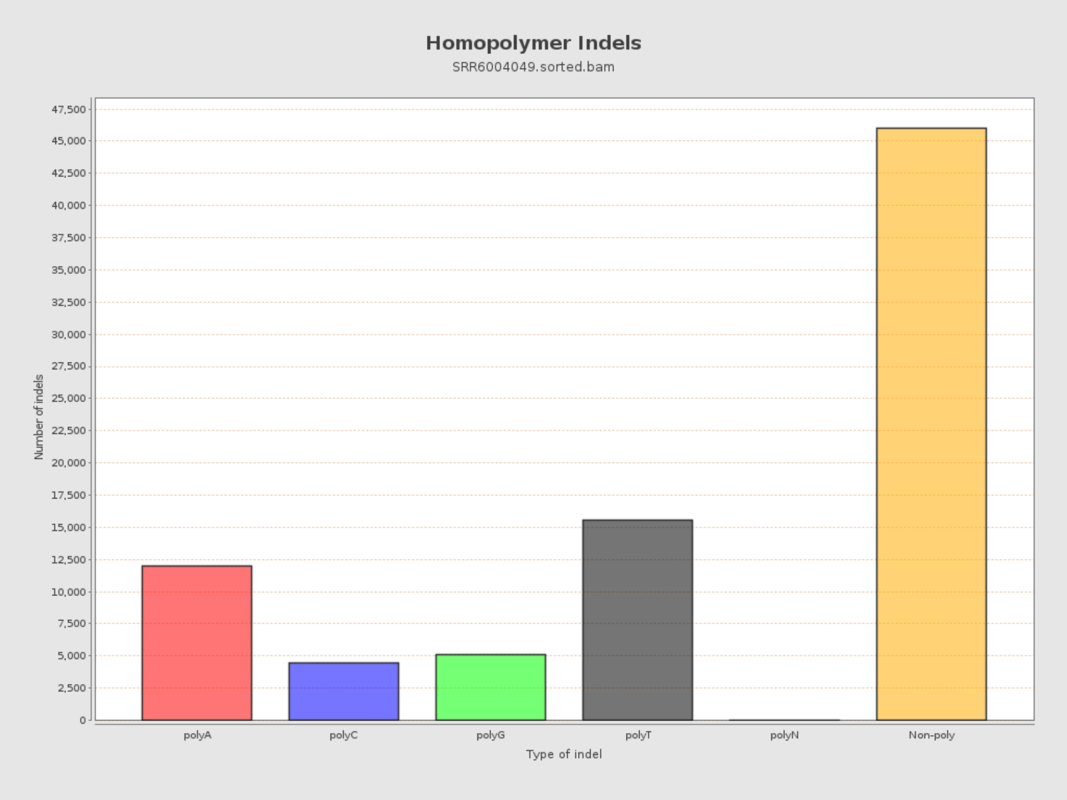
9. Results : Mapped Reads GC-content Distribution



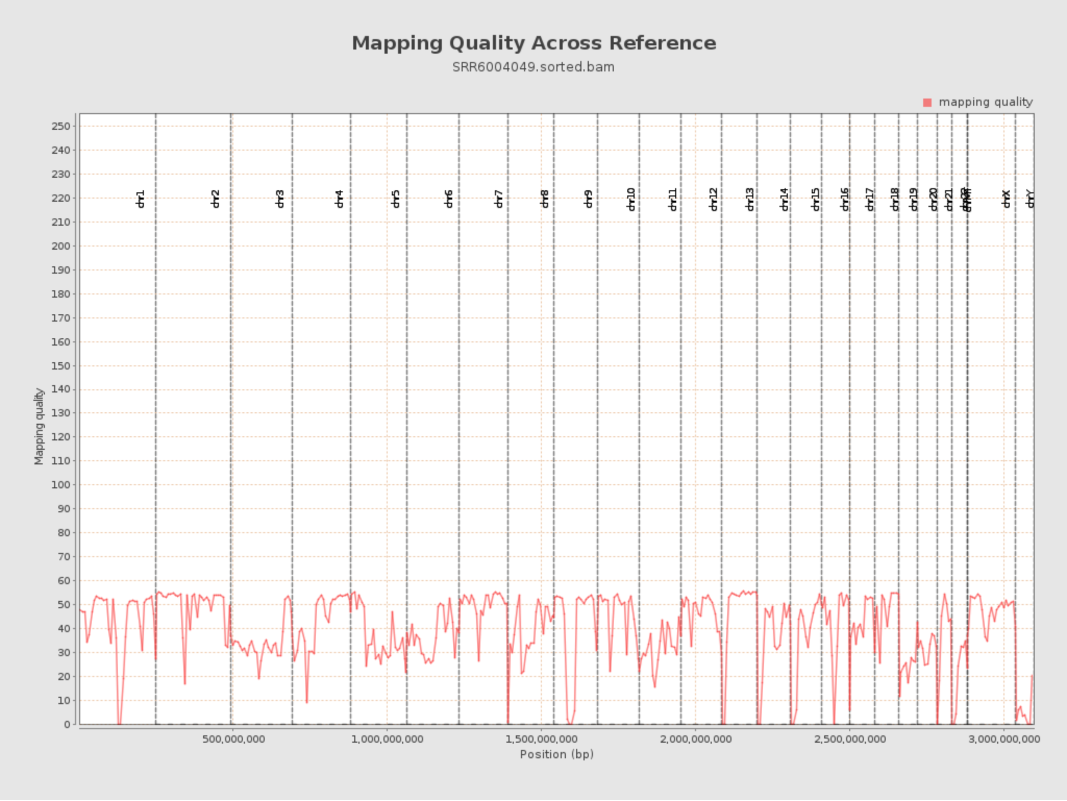
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram