Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:22:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004006.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_SRR6004006 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004006.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:22:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,819,137
Mapped reads	4,175,653 / 86.65%
Unmapped reads	643,484 / 13.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,160 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	215,893 / 4.48%
Duplication rate	3.35%
Clipped reads	1,762,134 / 36.57%

2.2. ACGT Content

Number/percentage of A's	76,981,545 / 27.23%
Number/percentage of C's	54,396,200 / 19.24%
Number/percentage of T's	88,398,031 / 31.27%
Number/percentage of G's	62,845,481 / 22.23%
Number/percentage of N's	37,898 / 0.01%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0913

Standard Deviation	0.9815

2.4. Mapping Quality

Mean Mapping Quality	44.49

2.5. Mismatches and indels

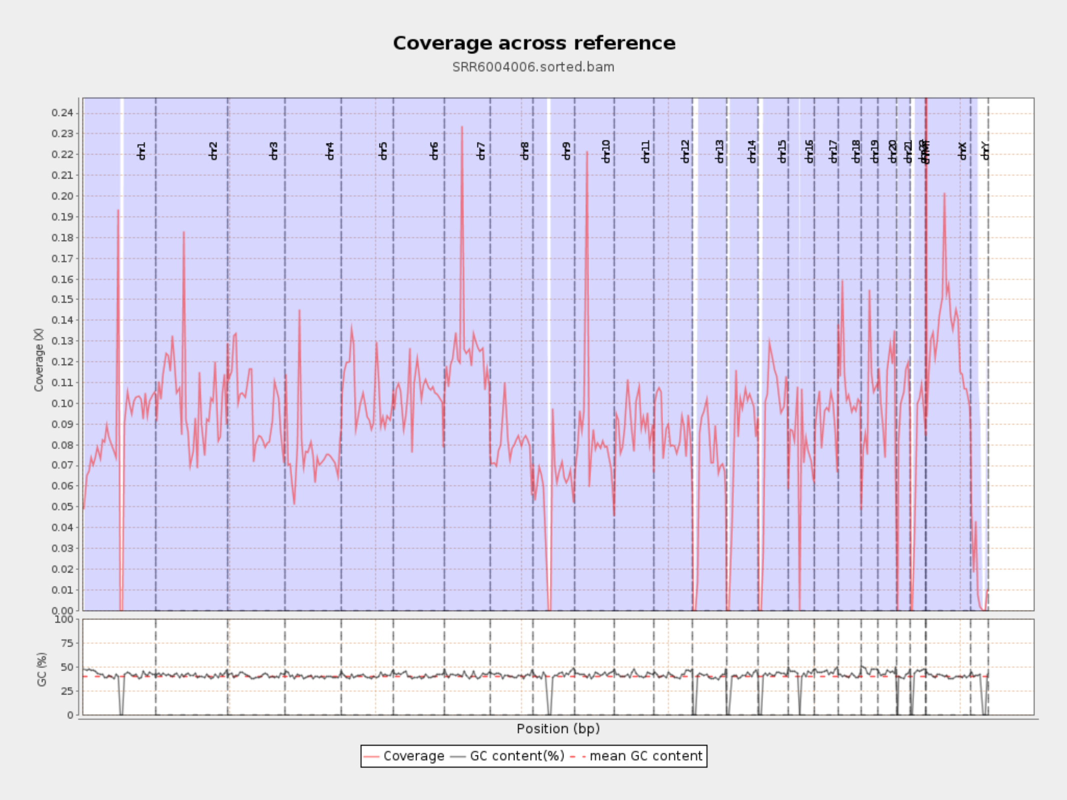
General error rate	0.99%
Mismatches	2,763,013
Insertions	24,723
Mapped reads with at least one insertion	0.59%
Deletions	70,311
Mapped reads with at least one deletion	1.67%
Homopolymer indels	45.33%

2.6. Chromosome stats

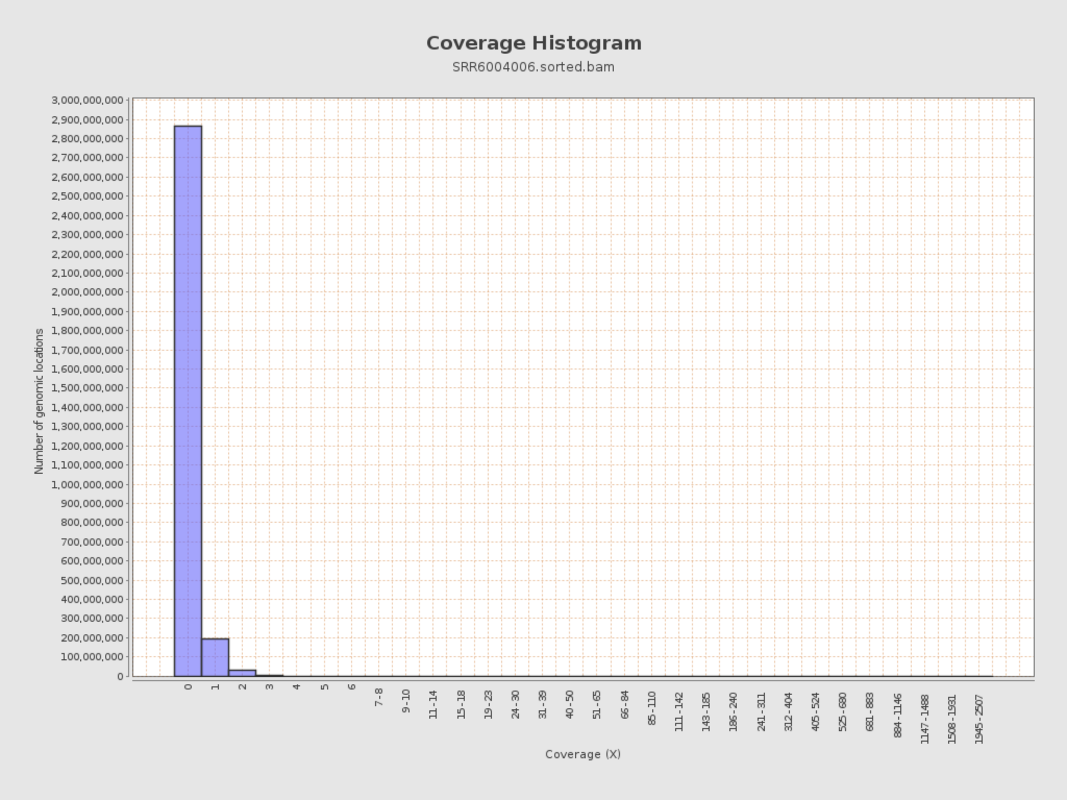
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21172918	0.0849	2.1989
chr2	243199373	24838127	0.1021	1.0347
chr3	198022430	19555685	0.0988	0.4197
chr4	191154276	14607440	0.0764	0.4235
chr5	180915260	18618532	0.1029	0.3967
chr6	171115067	17906559	0.1046	0.4878
chr7	159138663	20124241	0.1265	1.6115

chr8	146364022	11699580	0.0799	0.7782
chr9	141213431	8029907	0.0569	0.7526
chr10	135534747	11742954	0.0866	1.1612
chr11	135006516	12127075	0.0898	0.6246
chr12	133851895	11724174	0.0876	0.363
chr13	115169878	7724086	0.0671	0.2993
chr14	107349540	8720510	0.0812	0.4147
chr15	102531392	9005478	0.0878	0.349
chr16	90354753	6797992	0.0752	0.5824
chr17	81195210	7643142	0.0941	0.469
chr18	78077248	8600380	0.1102	1.8027
chr19	59128983	5952531	0.1007	1.414
chr20	63025520	6762247	0.1073	0.4201
chr21	48129895	4514245	0.0938	0.4321
chr22	51304566	3581246	0.0698	0.3079
chrMT	16571	26035	1.5711	1.5654
chrX	155270560	20431911	0.1316	0.5683
chrY	59373566	870380	0.0147	0.2896

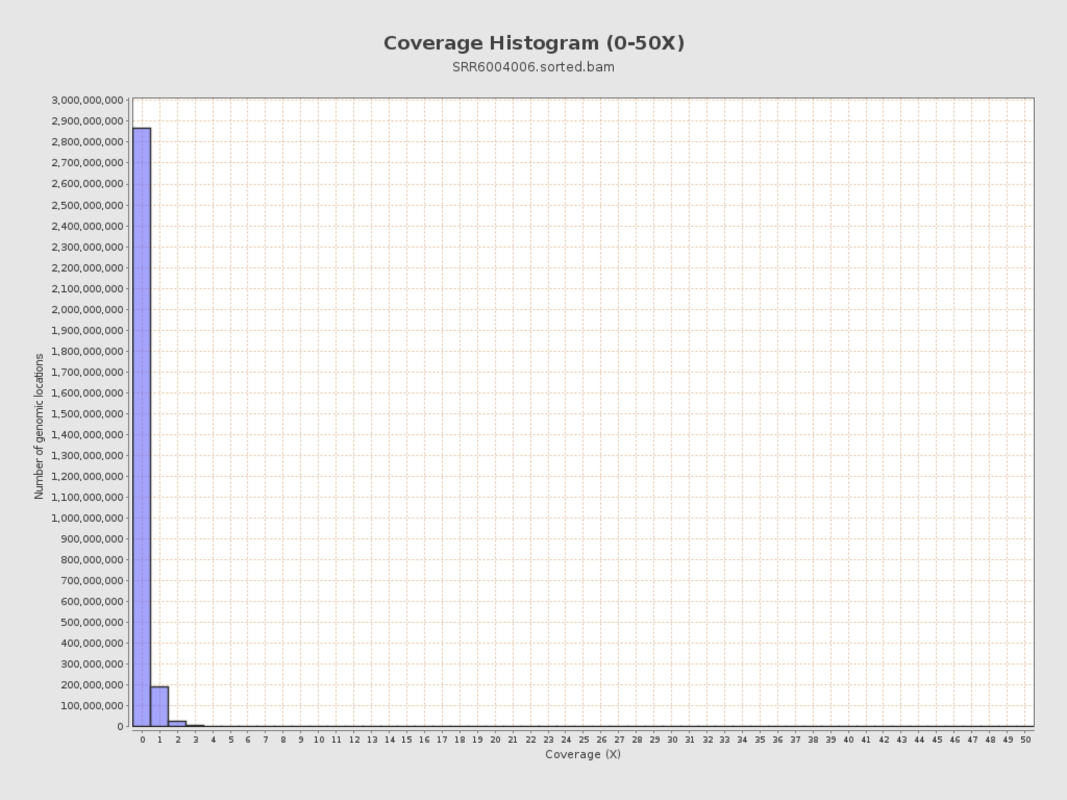
3. Results : Coverage across reference



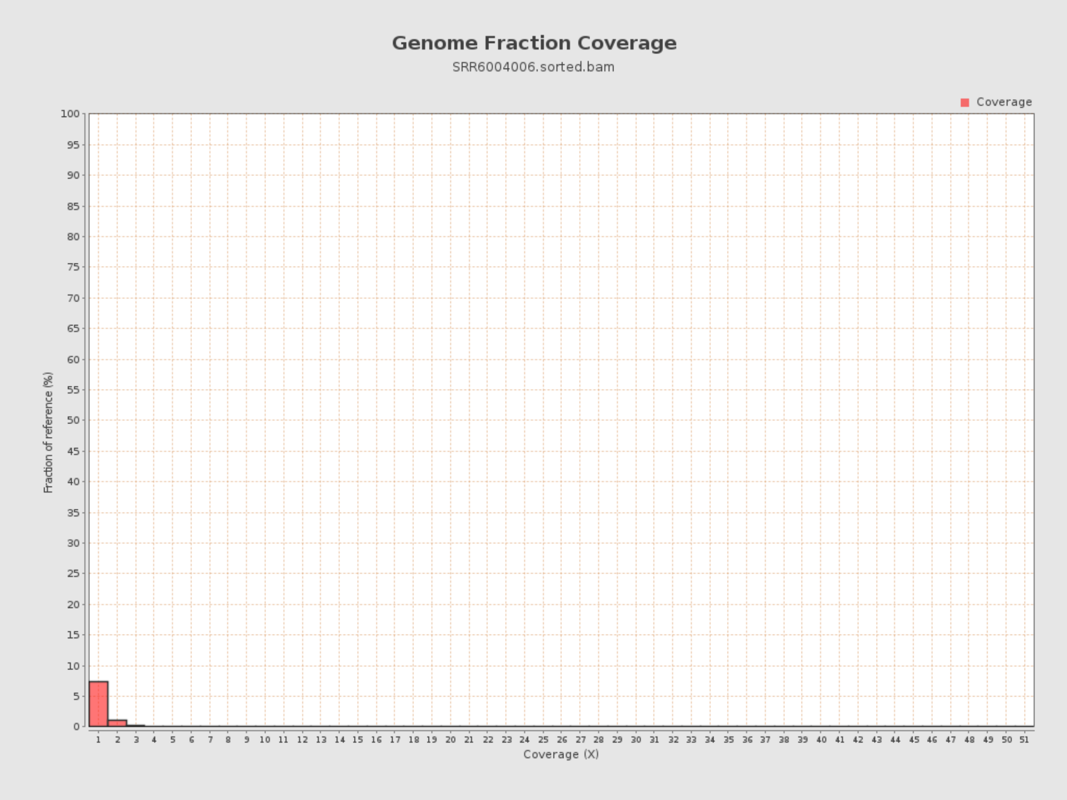
4. Results : Coverage Histogram



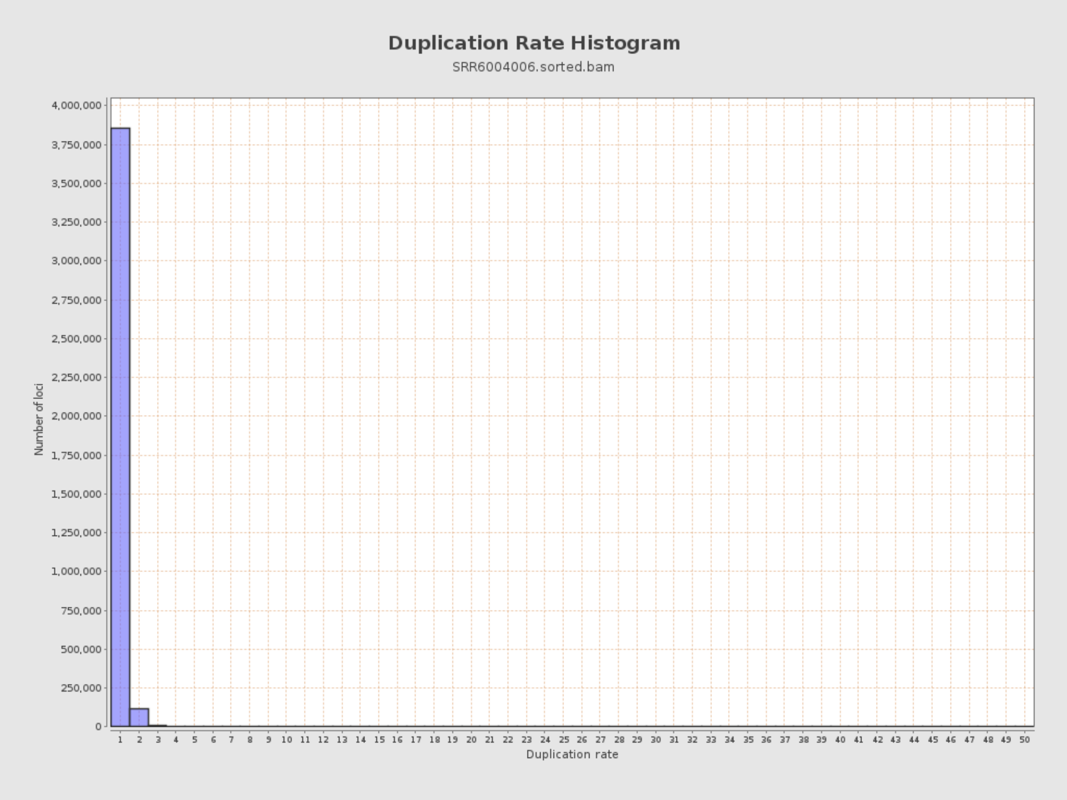
5. Results : Coverage Histogram (0-50X)



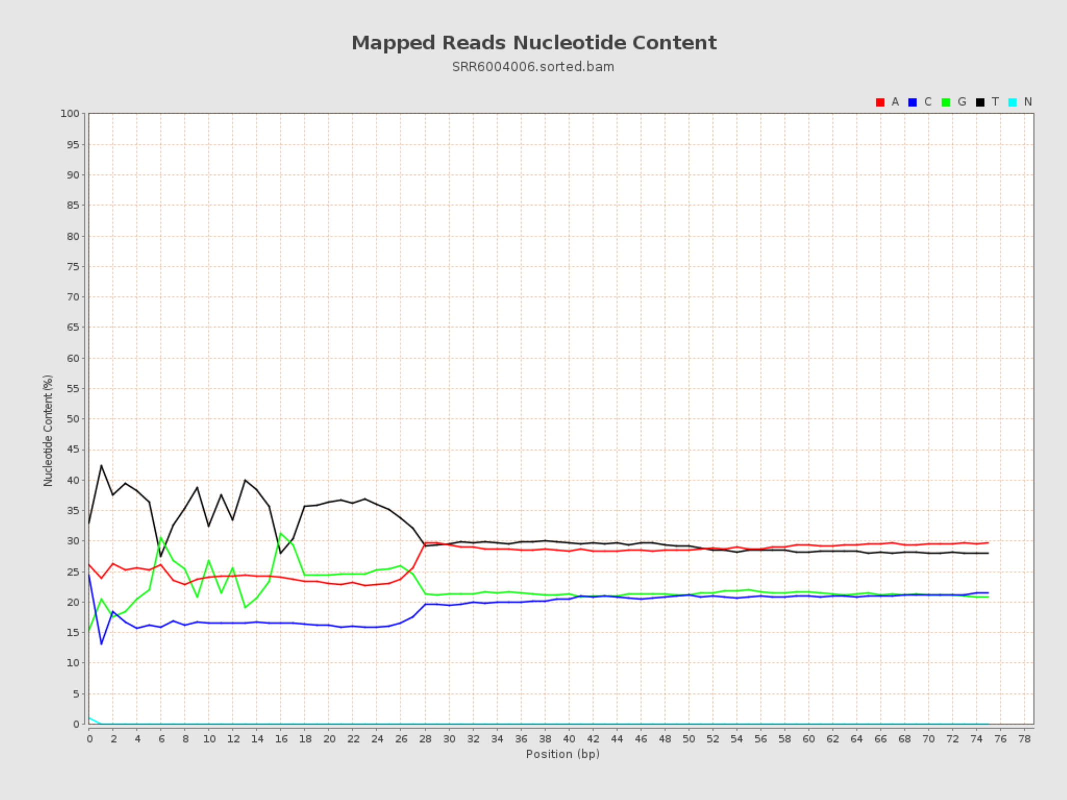
6. Results : Genome Fraction Coverage



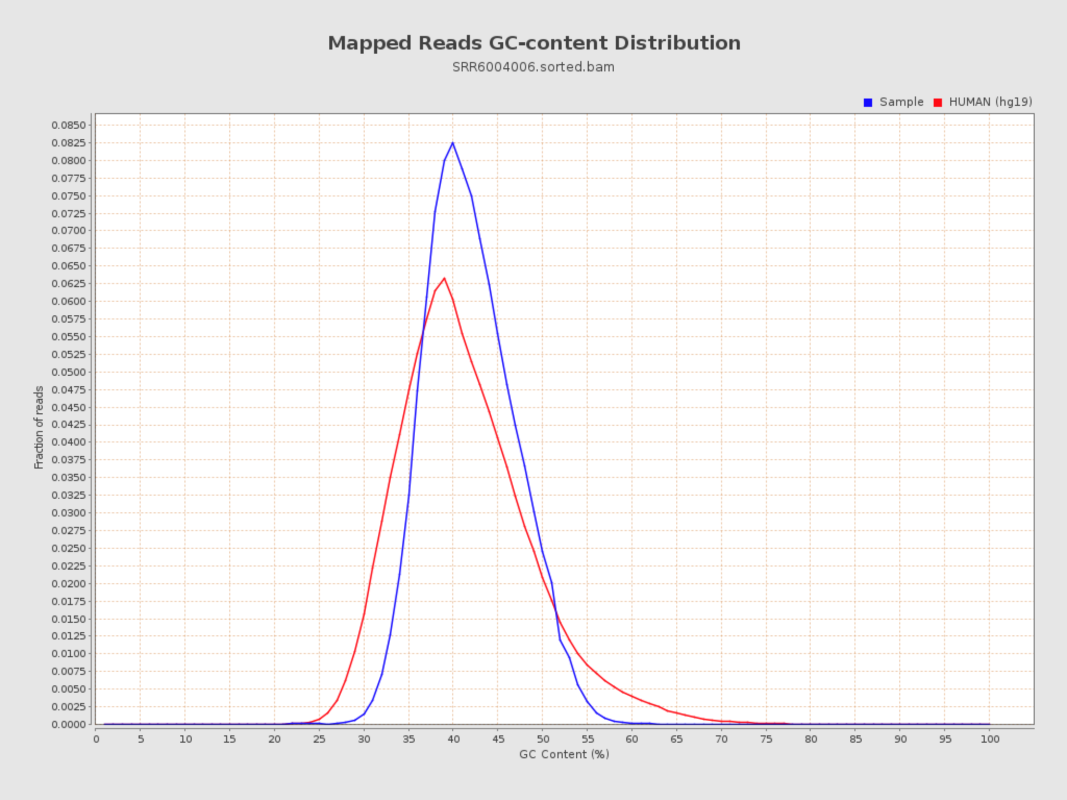
7. Results : Duplication Rate Histogram



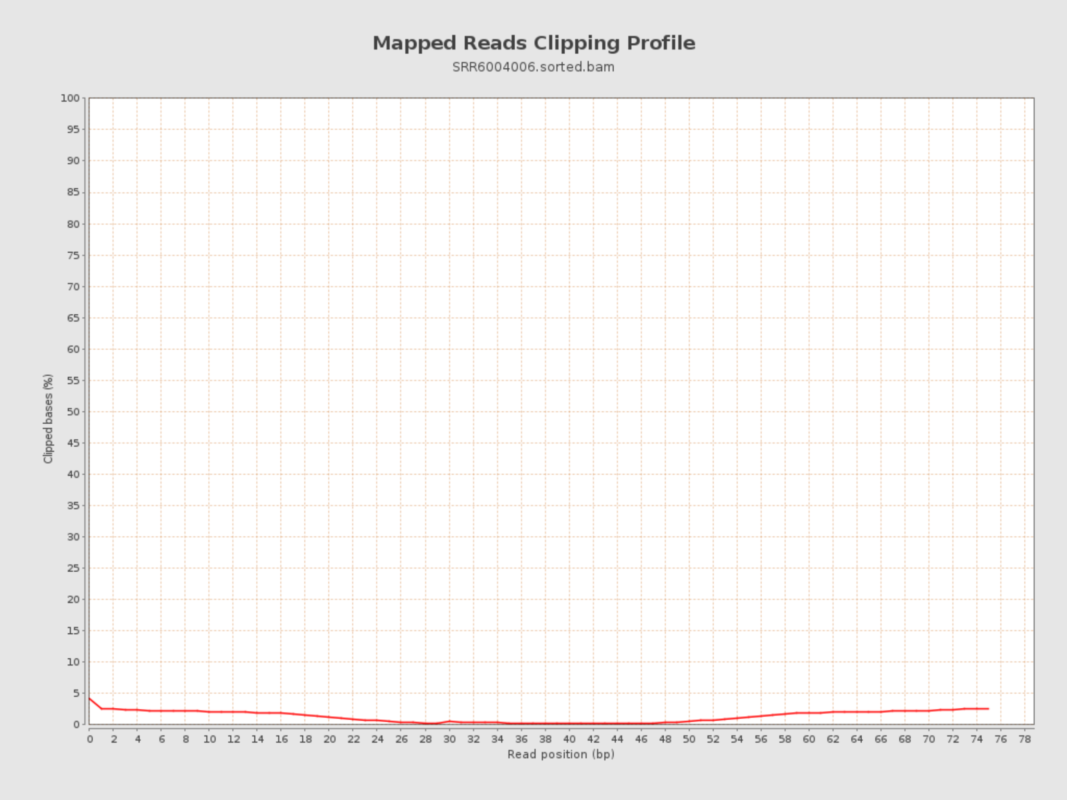
8. Results : Mapped Reads Nucleotide Content



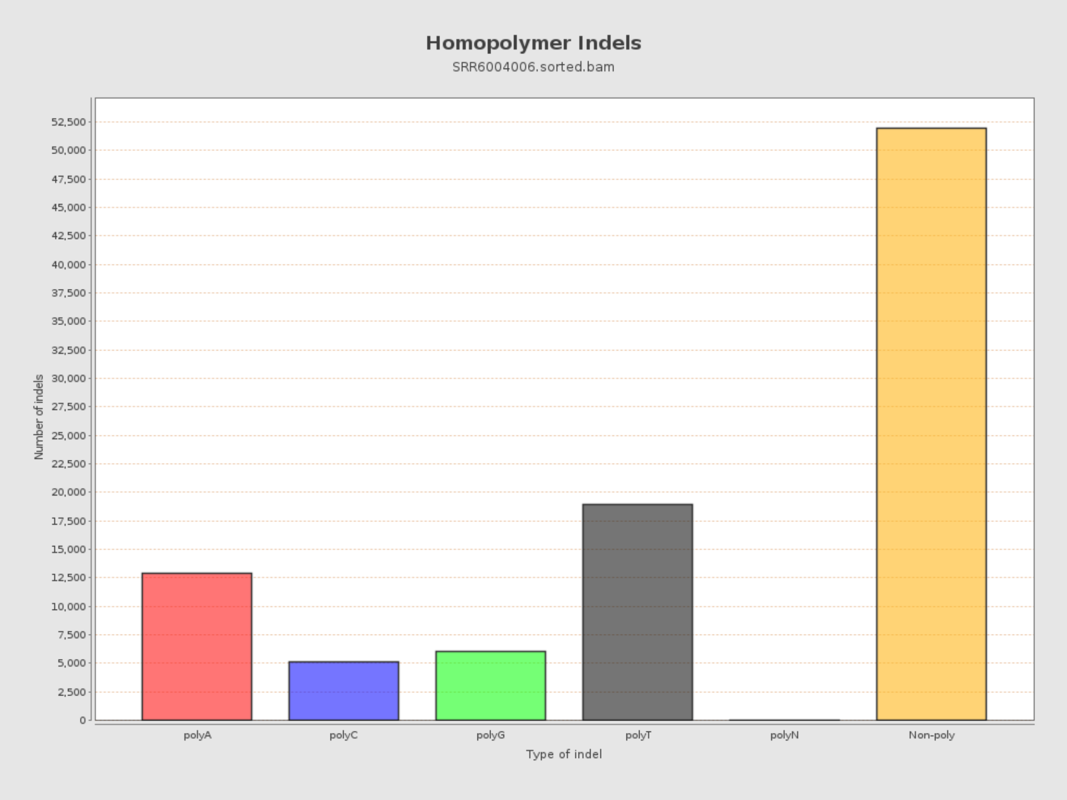
9. Results : Mapped Reads GC-content Distribution



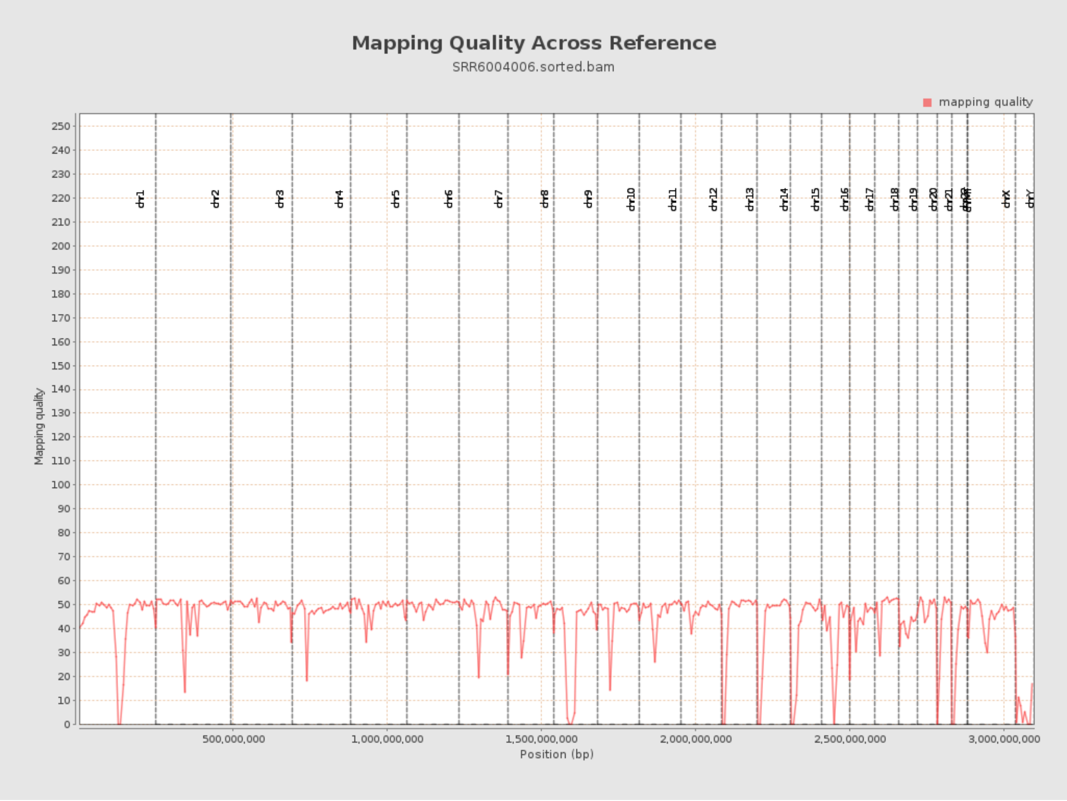
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram