Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:32:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004114.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_SRR6004114 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004114.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:32:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,645,475
Mapped reads	1,505,502 / 91.49%
Unmapped reads	139,973 / 8.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,345 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	39,489 / 2.4%
Duplication rate	1.89%
Clipped reads	644,745 / 39.18%

2.2. ACGT Content

Number/percentage of A's	28,420,443 / 28.14%
Number/percentage of C's	19,176,417 / 18.98%
Number/percentage of T's	30,667,917 / 30.36%
Number/percentage of G's	22,724,423 / 22.5%
Number/percentage of N's	22,165 / 0.02%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0326

Standard Deviation	0.2837

2.4. Mapping Quality

Mean Mapping Quality	44.09

2.5. Mismatches and indels

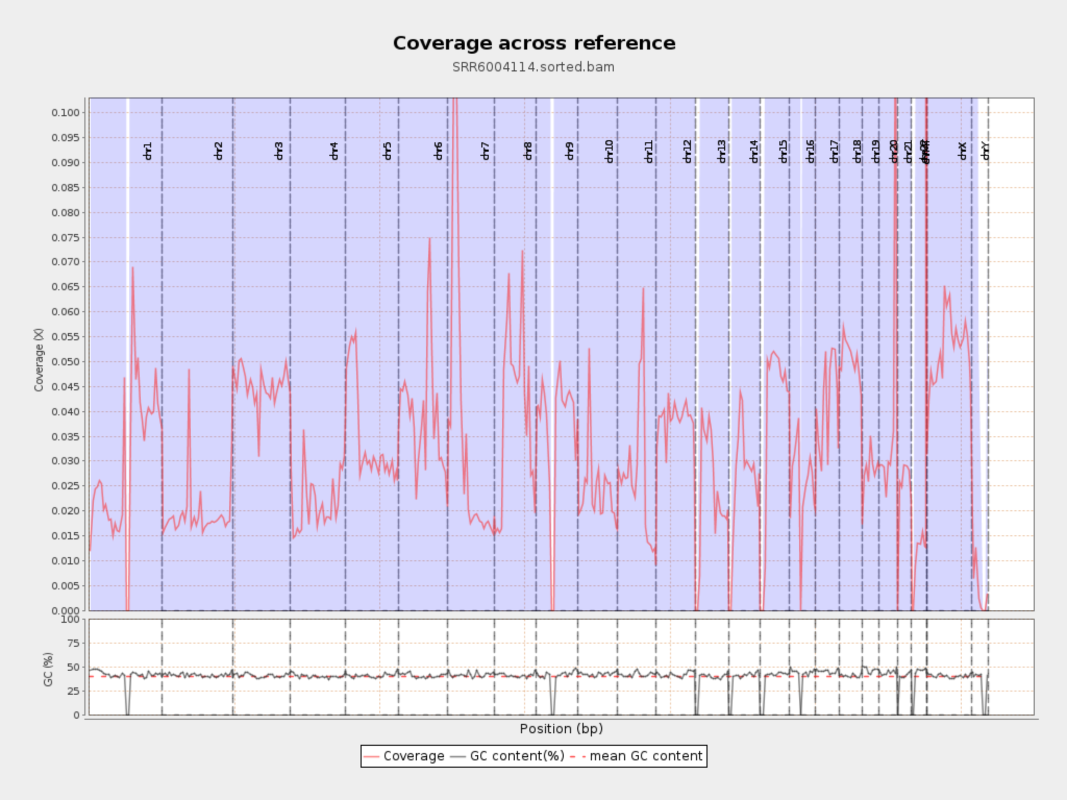
General error rate	0.86%
Mismatches	856,810
Insertions	8,942
Mapped reads with at least one insertion	0.59%
Deletions	27,416
Mapped reads with at least one deletion	1.8%
Homopolymer indels	46.78%

2.6. Chromosome stats

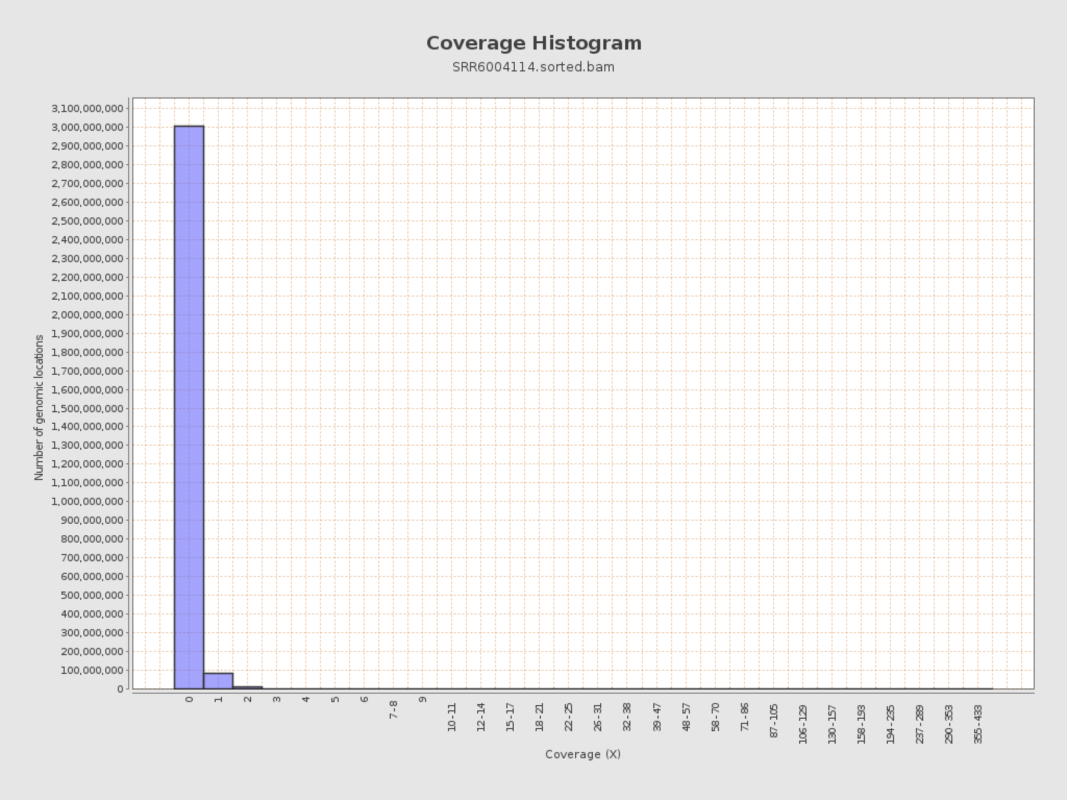
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7415822	0.0298	0.4064
chr2	243199373	4711939	0.0194	0.3558
chr3	198022430	8967814	0.0453	0.2315
chr4	191154276	4135162	0.0216	0.1743
chr5	180915260	6320569	0.0349	0.2055
chr6	171115067	6790713	0.0397	0.2338
chr7	159138663	5872551	0.0369	0.2933

chr8	146364022	5811664	0.0397	0.3485
chr9	141213431	5183503	0.0367	0.3299
chr10	135534747	3299220	0.0243	0.2821
chr11	135006516	3754969	0.0278	0.2335
chr12	133851895	5149227	0.0385	0.2187
chr13	115169878	2665180	0.0231	0.1647
chr14	107349540	2774566	0.0258	0.2034
chr15	102531392	3989958	0.0389	0.2154
chr16	90354753	2320795	0.0257	0.2174
chr17	81195210	3421756	0.0421	0.2363
chr18	78077248	3965698	0.0508	0.5858
chr19	59128983	1686785	0.0285	0.3161
chr20	63025520	2699645	0.0428	0.2366
chr21	48129895	1171405	0.0243	0.1988
chr22	51304566	525372	0.0102	0.1081
chrMT	16571	31797	1.9188	2.0083
chrX	155270560	8103714	0.0522	0.2698
chrY	59373566	287515	0.0048	0.1135

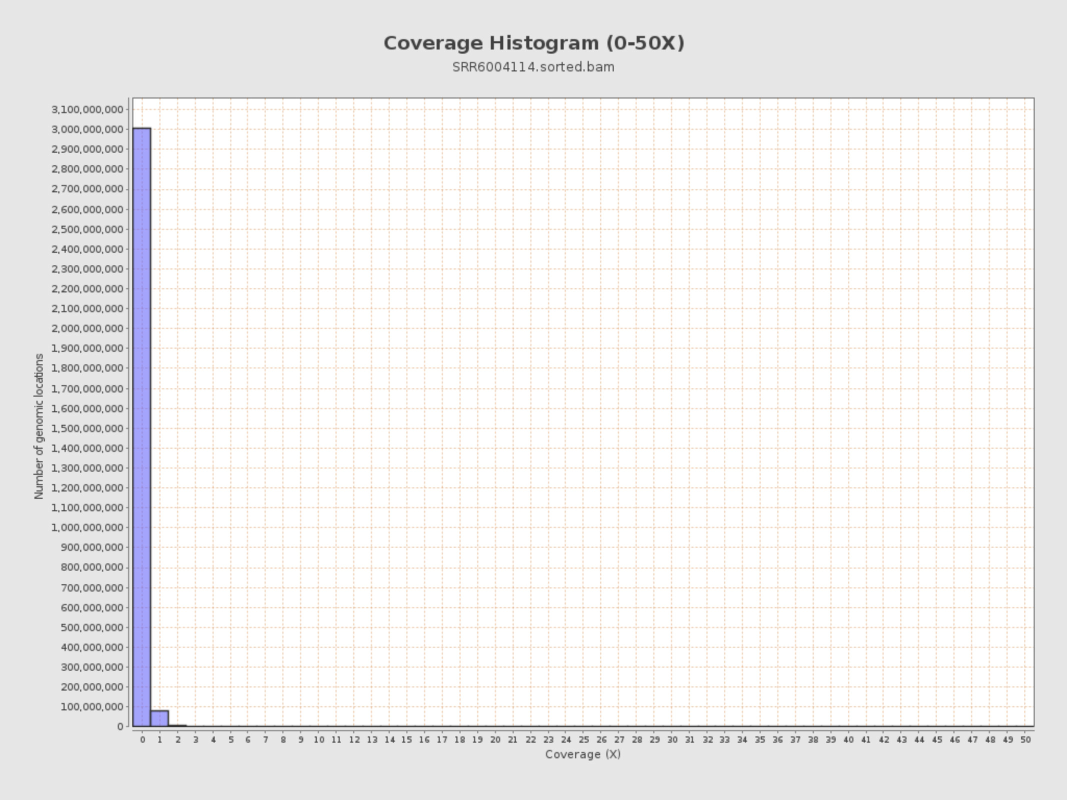
3. Results : Coverage across reference



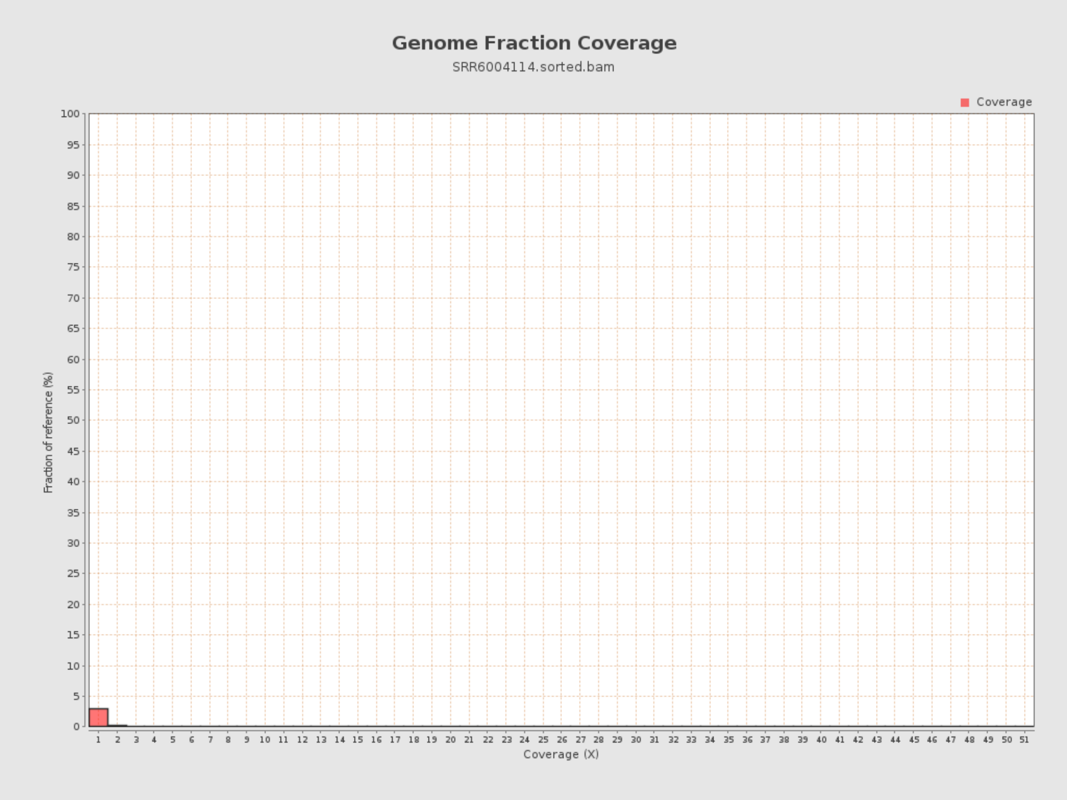
4. Results : Coverage Histogram



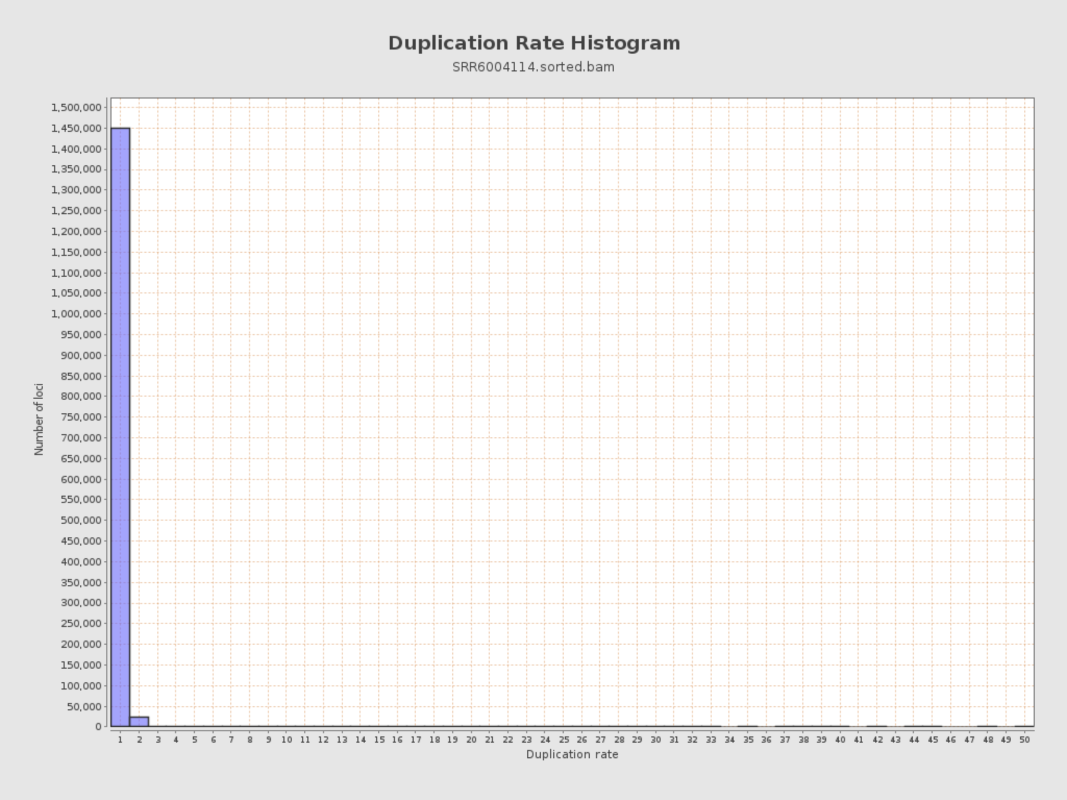
5. Results : Coverage Histogram (0-50X)



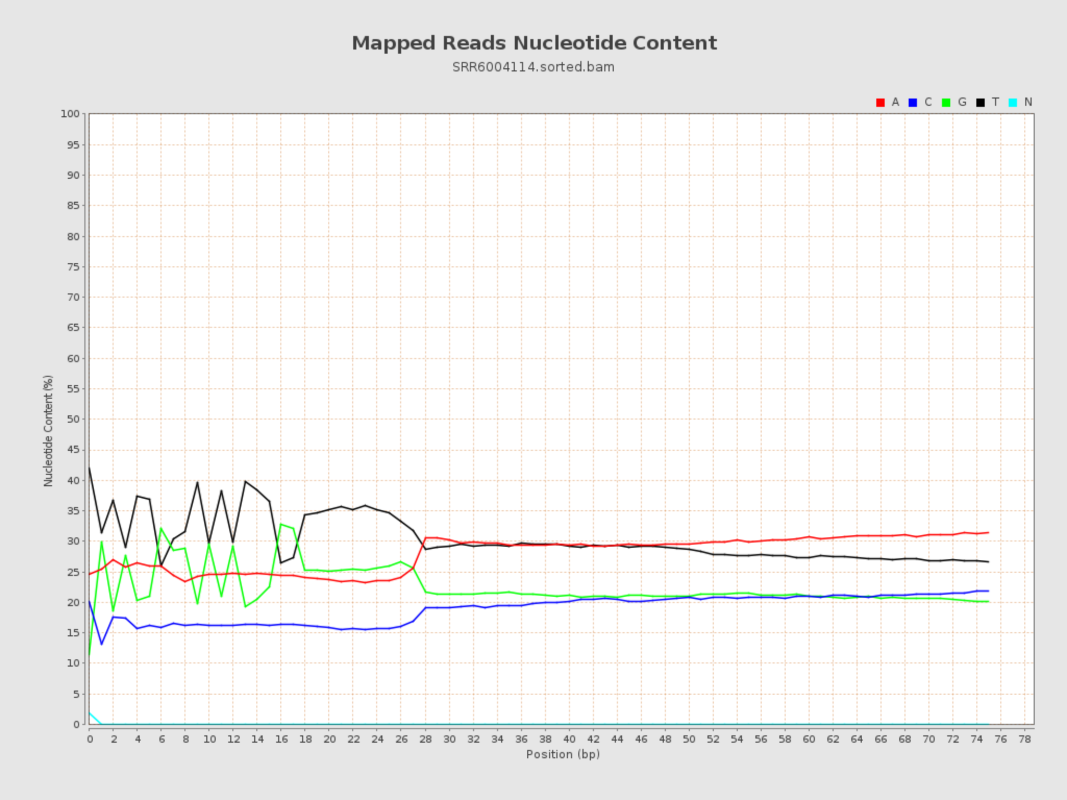
6. Results : Genome Fraction Coverage



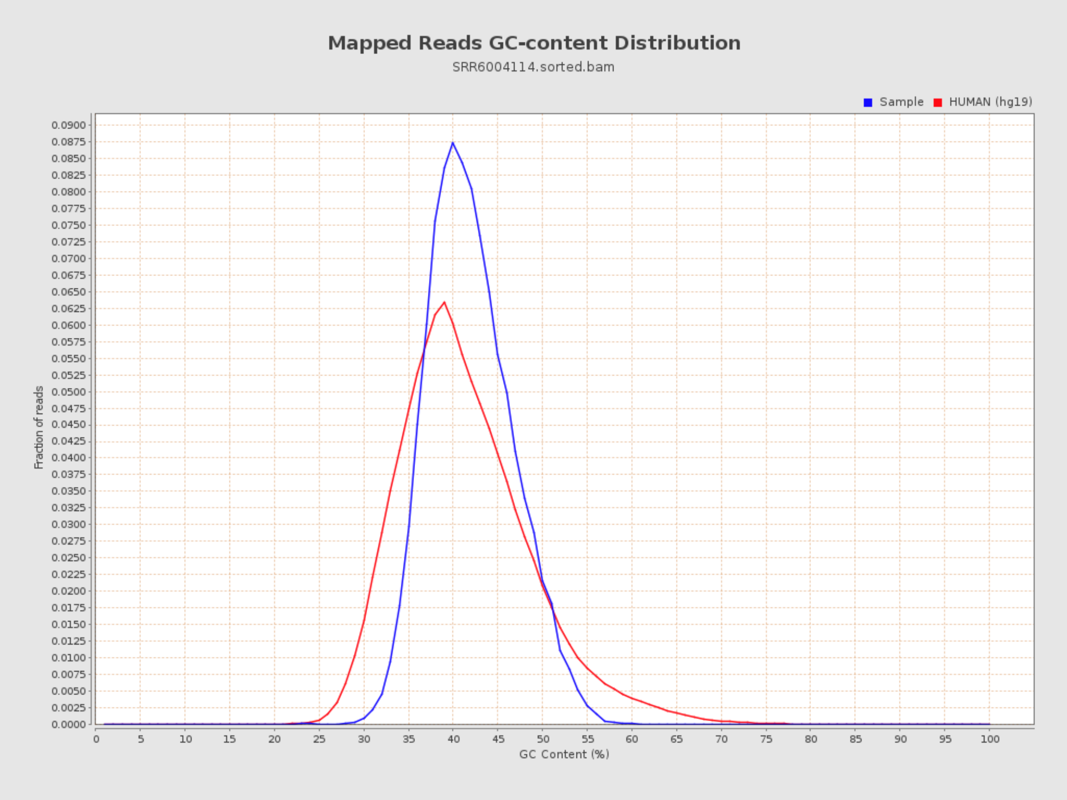
7. Results : Duplication Rate Histogram



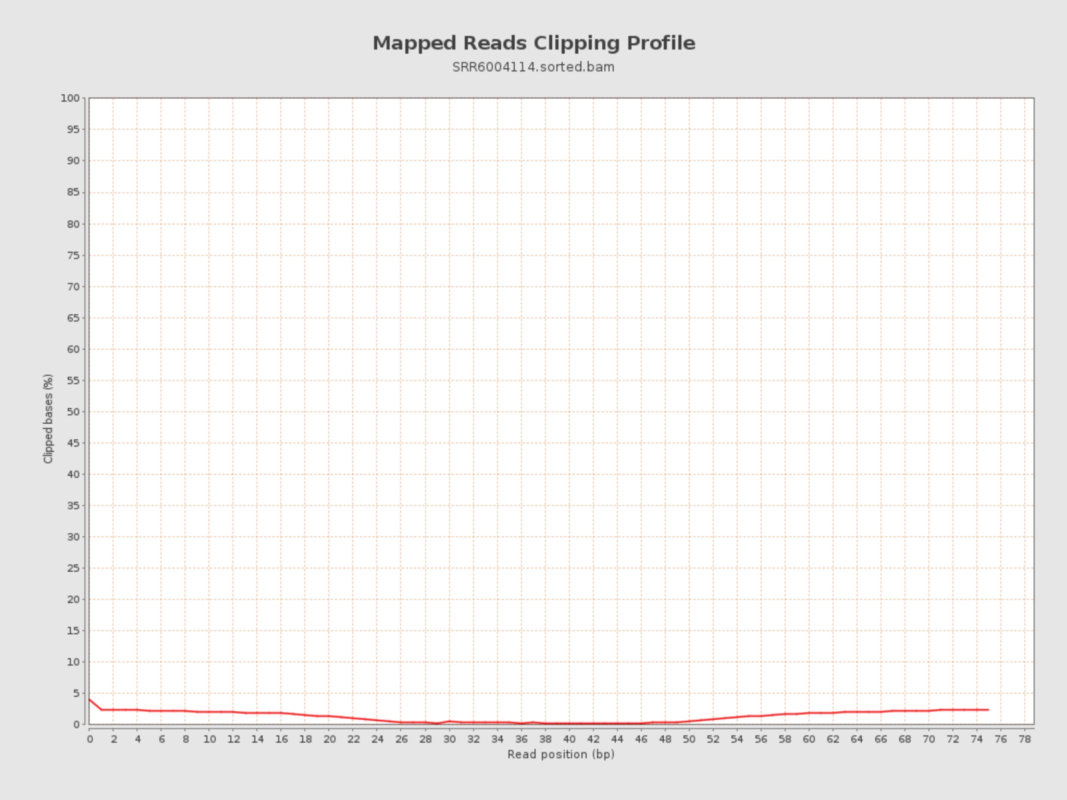
8. Results : Mapped Reads Nucleotide Content



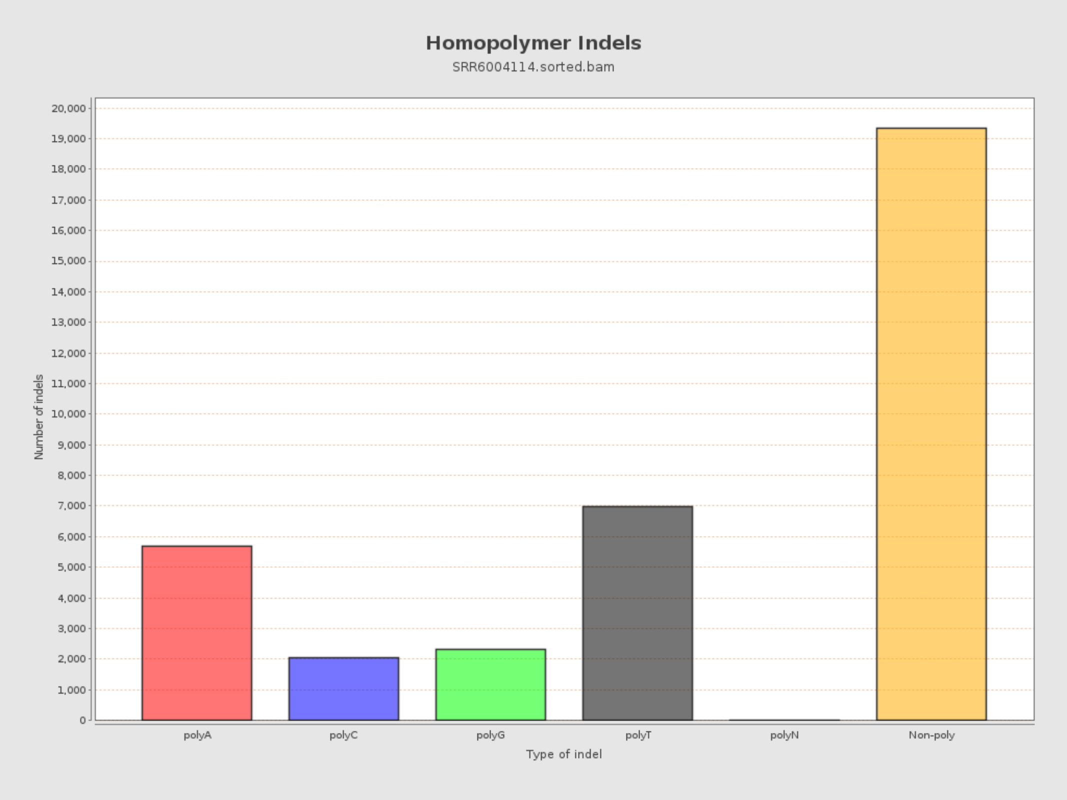
9. Results : Mapped Reads GC-content Distribution



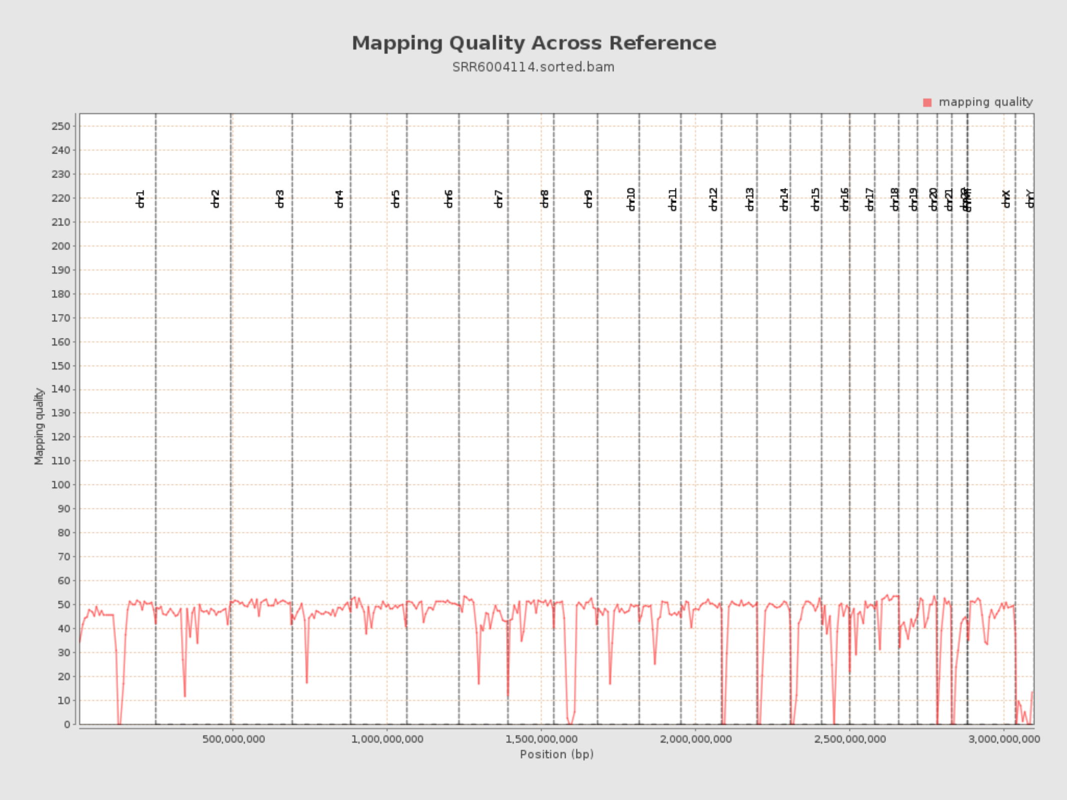
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram