Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:14:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004124.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_SRR6004124 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004124.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:14:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004124.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,169,090
Mapped reads	2,467,861 / 77.87%
Unmapped reads	701,229 / 22.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,783 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	115,379 / 3.64%
Duplication rate	3.15%
Clipped reads	1,155,656 / 36.47%

2.2. ACGT Content

Number/percentage of A's	45,722,109 / 27.9%
Number/percentage of C's	29,045,573 / 17.72%
Number/percentage of T's	52,958,831 / 32.32%
Number/percentage of G's	36,128,369 / 22.05%
Number/percentage of N's	17,253 / 0.01%
GC Percentage	39.77%

2.3. Coverage

Mean	0.053

Standard Deviation	0.6072

2.4. Mapping Quality

Mean Mapping Quality	43.59

2.5. Mismatches and indels

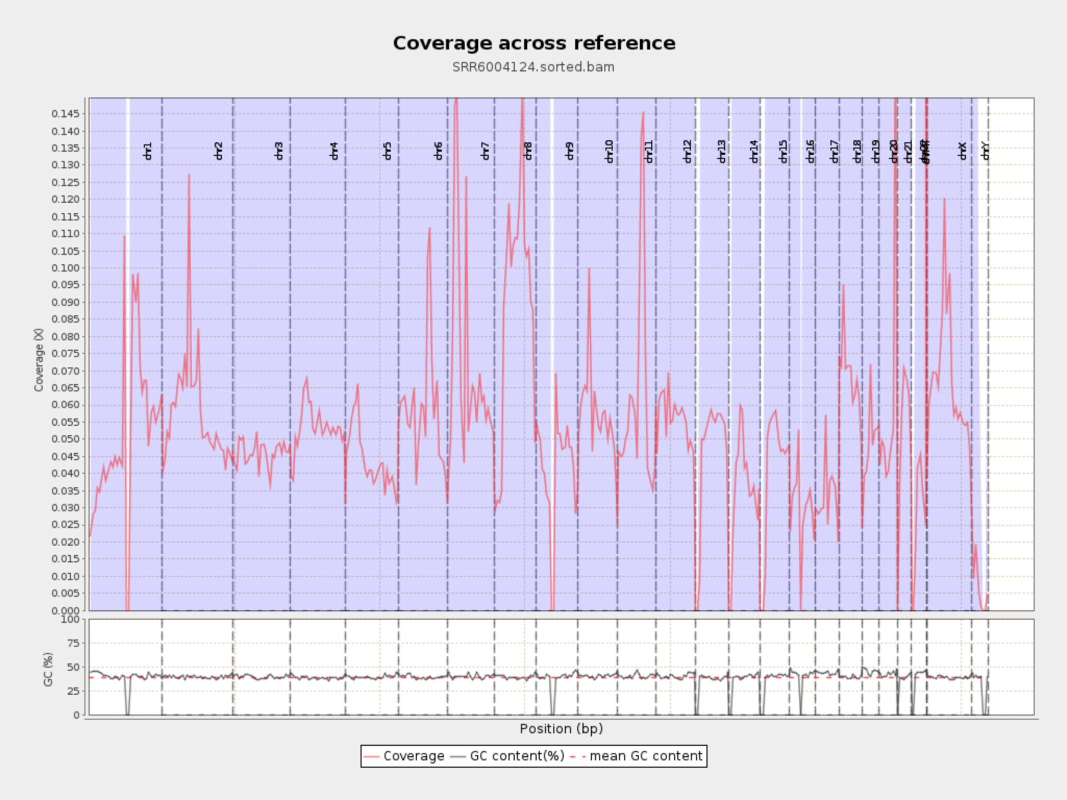
General error rate	1.04%
Mismatches	1,673,267
Insertions	15,566
Mapped reads with at least one insertion	0.62%
Deletions	45,415
Mapped reads with at least one deletion	1.82%
Homopolymer indels	46.94%

2.6. Chromosome stats

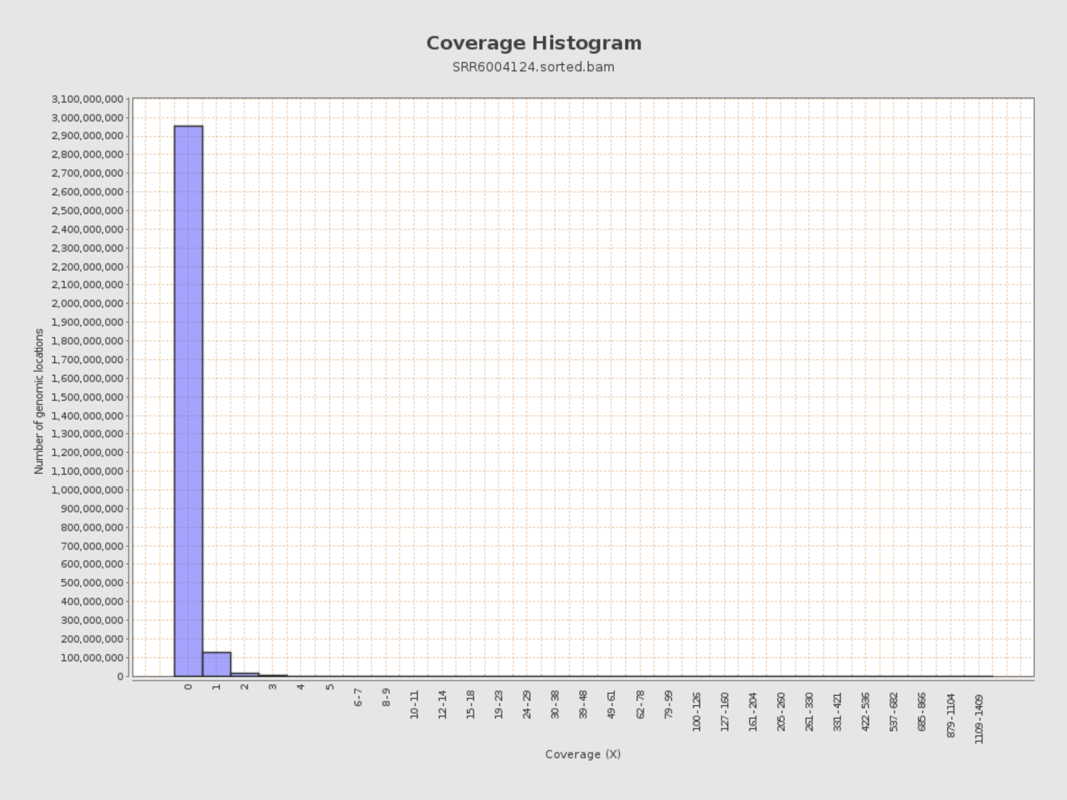
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12673227	0.0508	1.2308
chr2	243199373	14097035	0.058	0.6821
chr3	198022430	9089361	0.0459	0.2459
chr4	191154276	10217368	0.0535	0.2705
chr5	180915260	7984051	0.0441	0.2453
chr6	171115067	10124408	0.0592	0.3299
chr7	159138663	11597498	0.0729	1.0314

chr8	146364022	12960639	0.0886	0.9099
chr9	141213431	5780181	0.0409	0.5419
chr10	135534747	7894781	0.0582	0.4941
chr11	135006516	8410569	0.0623	0.4501
chr12	133851895	7455844	0.0557	0.2784
chr13	115169878	5169879	0.0449	0.2338
chr14	107349540	3715027	0.0346	0.2829
chr15	102531392	4188519	0.0409	0.2365
chr16	90354753	2695475	0.0298	0.2805
chr17	81195210	2714887	0.0334	0.2444
chr18	78077248	5399339	0.0692	1.0637
chr19	59128983	2907464	0.0492	0.7496
chr20	63025520	4063495	0.0645	0.3164
chr21	48129895	2501152	0.052	0.2832
chr22	51304566	1336860	0.0261	0.1764
chrMT	16571	124627	7.5208	4.8809
chrX	155270560	10438161	0.0672	0.3893
chrY	59373566	407663	0.0069	0.1376

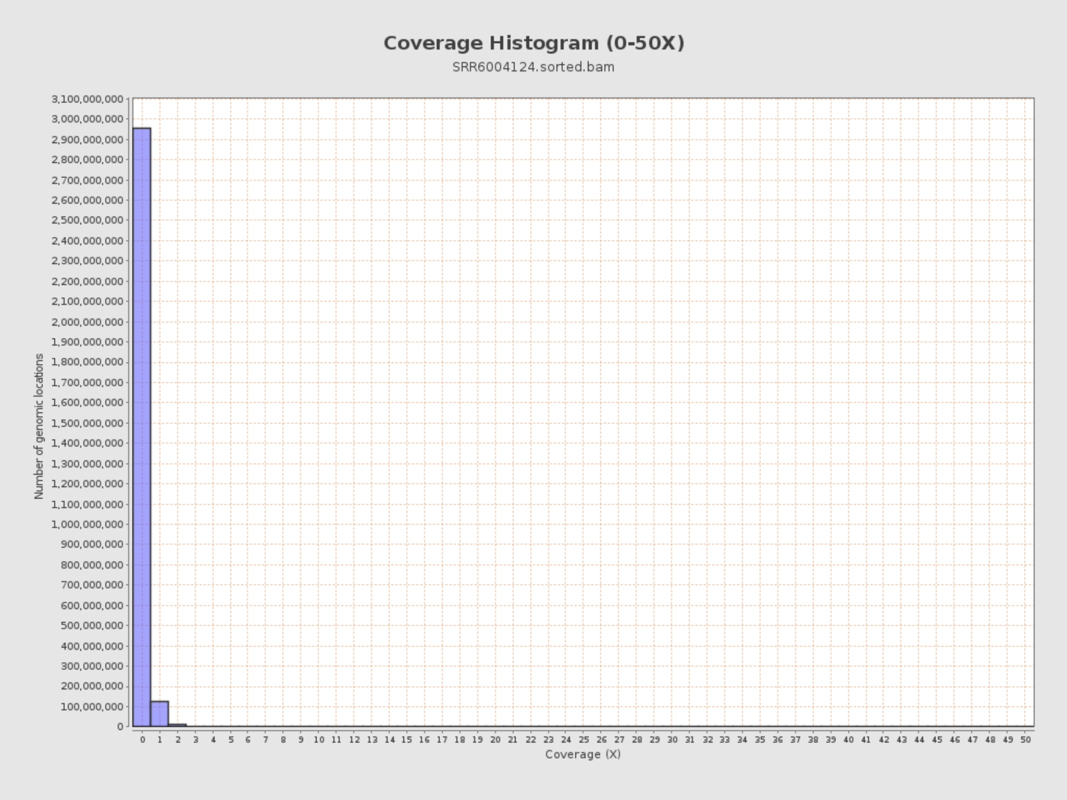
3. Results : Coverage across reference



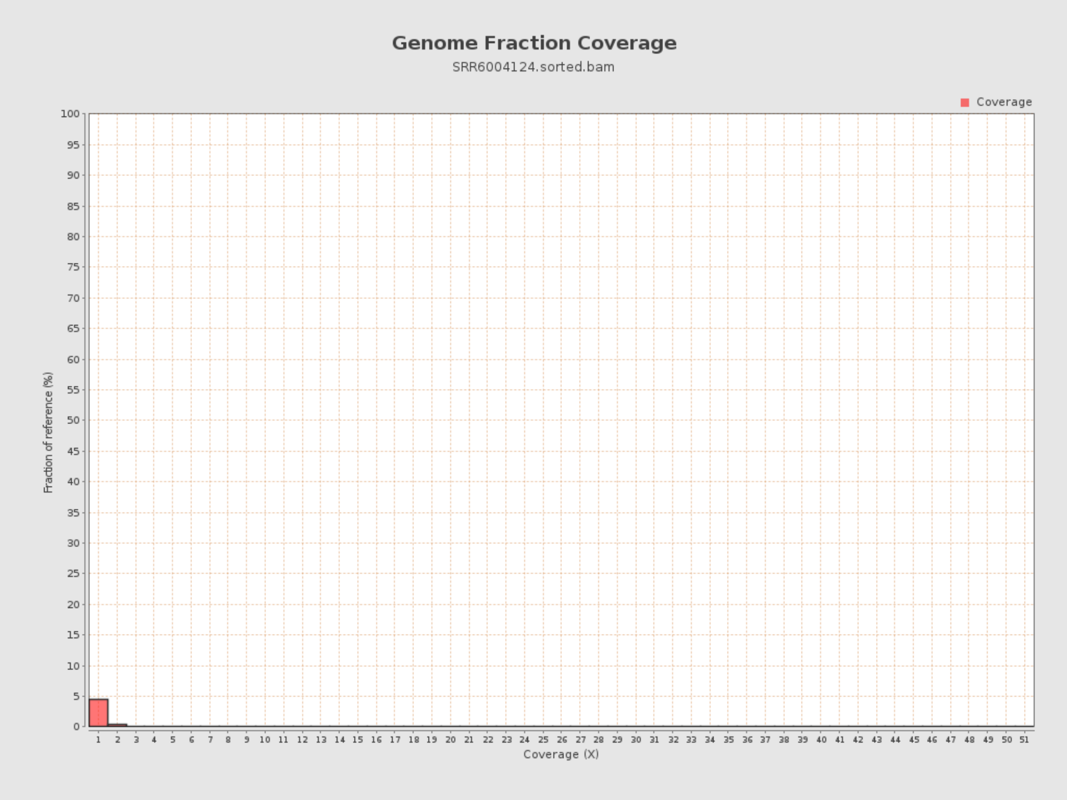
4. Results : Coverage Histogram



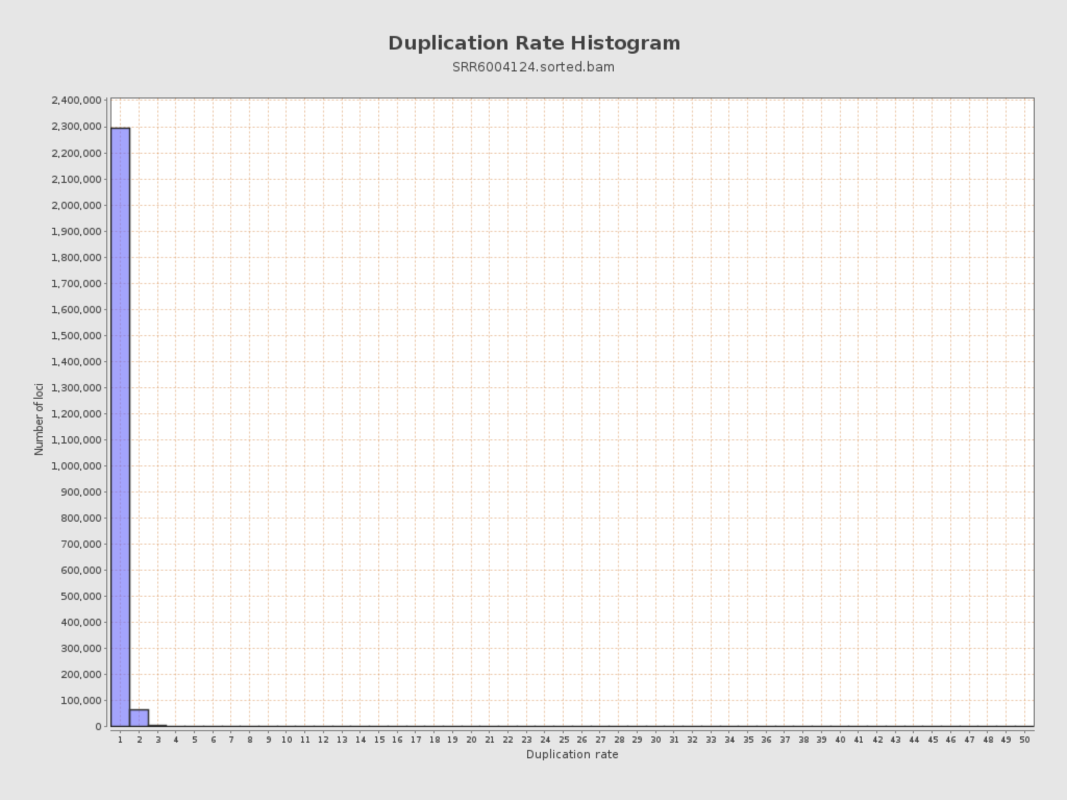
5. Results : Coverage Histogram (0-50X)



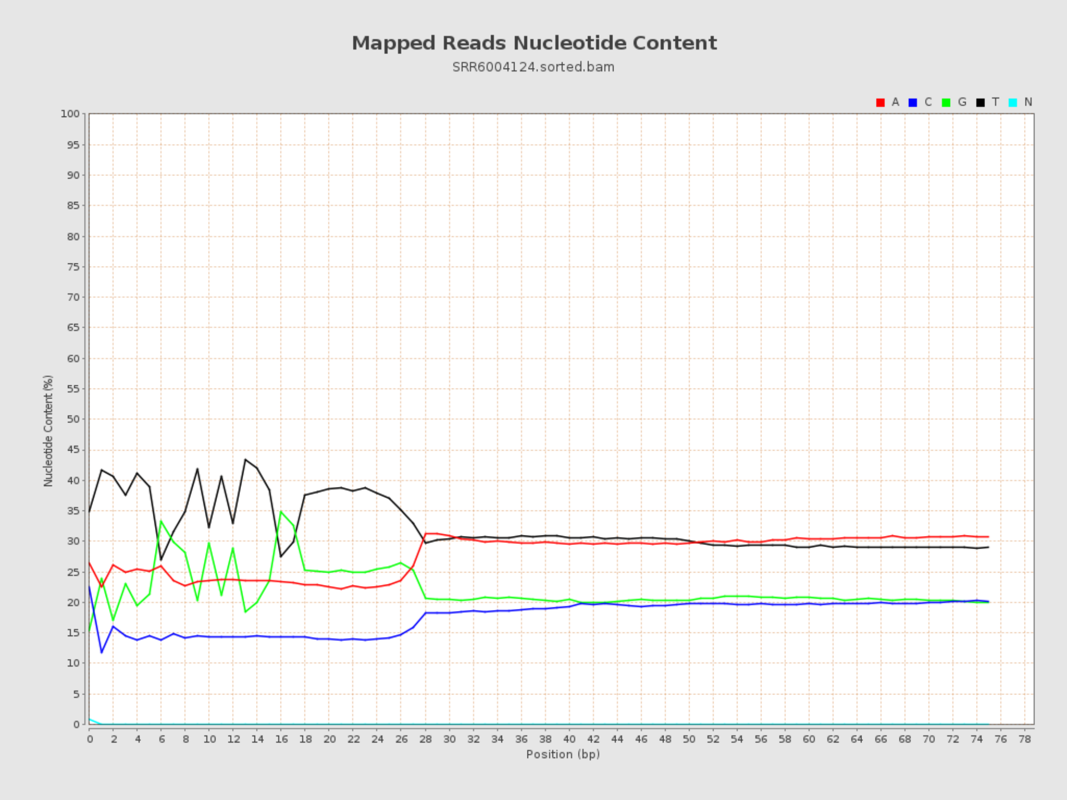
6. Results : Genome Fraction Coverage



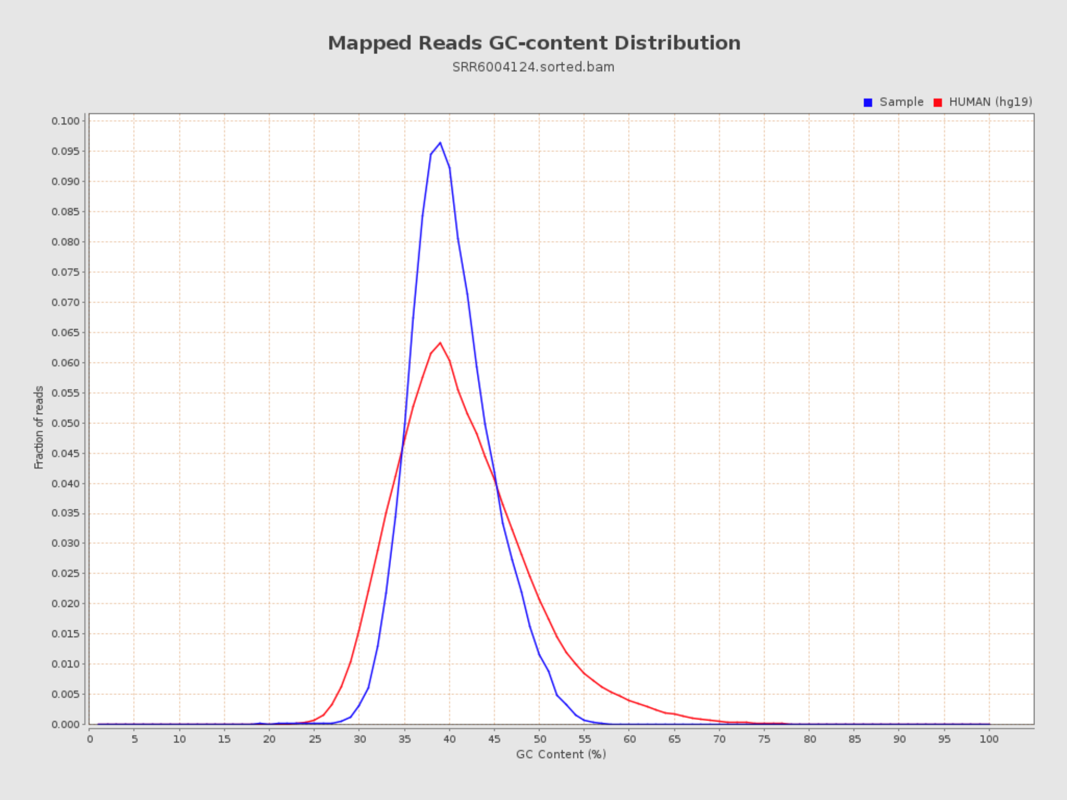
7. Results : Duplication Rate Histogram



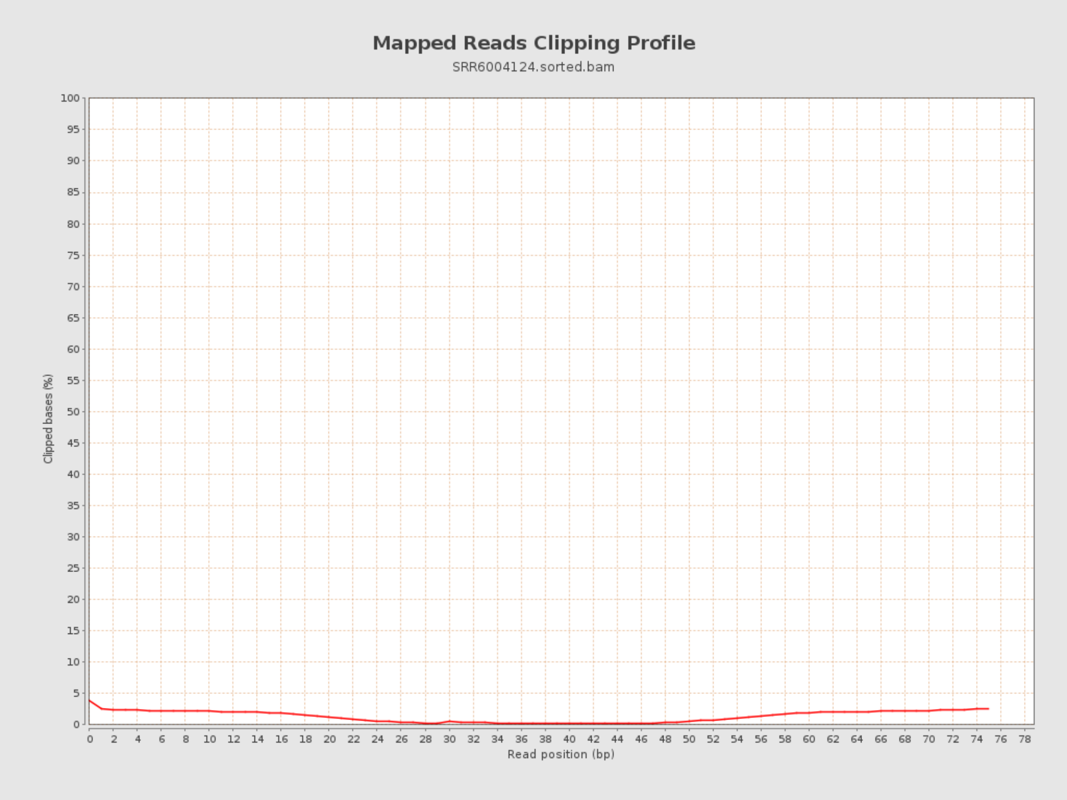
8. Results : Mapped Reads Nucleotide Content



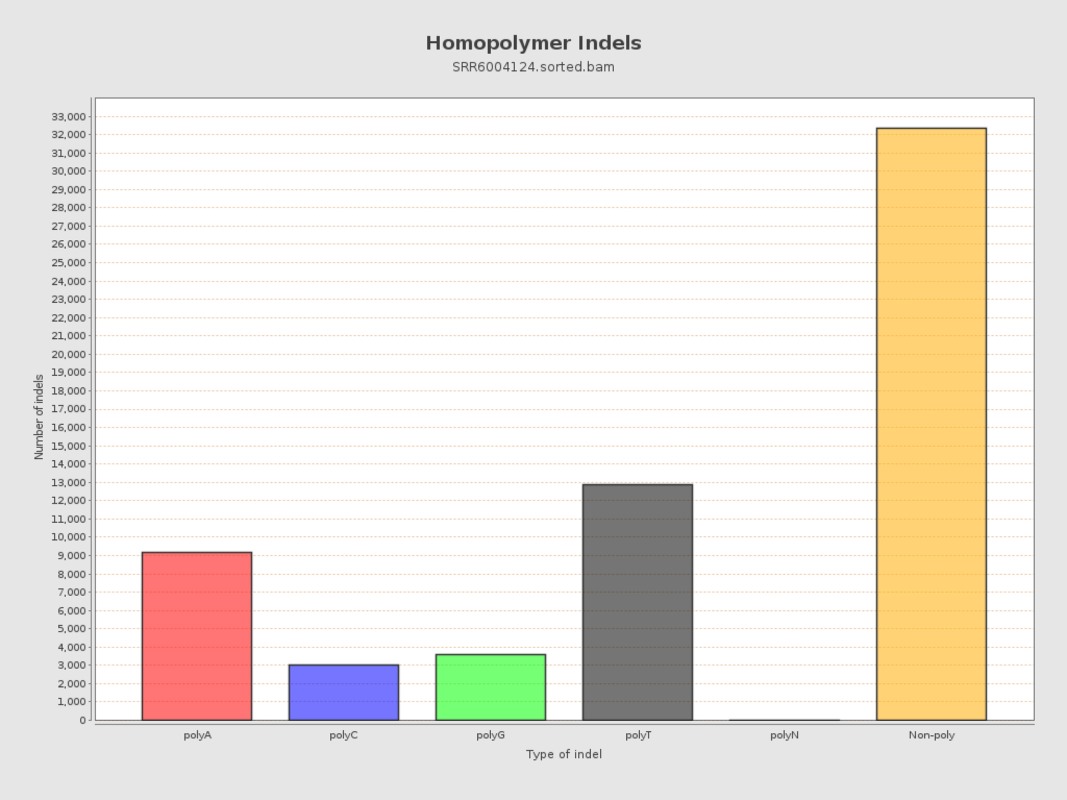
9. Results : Mapped Reads GC-content Distribution



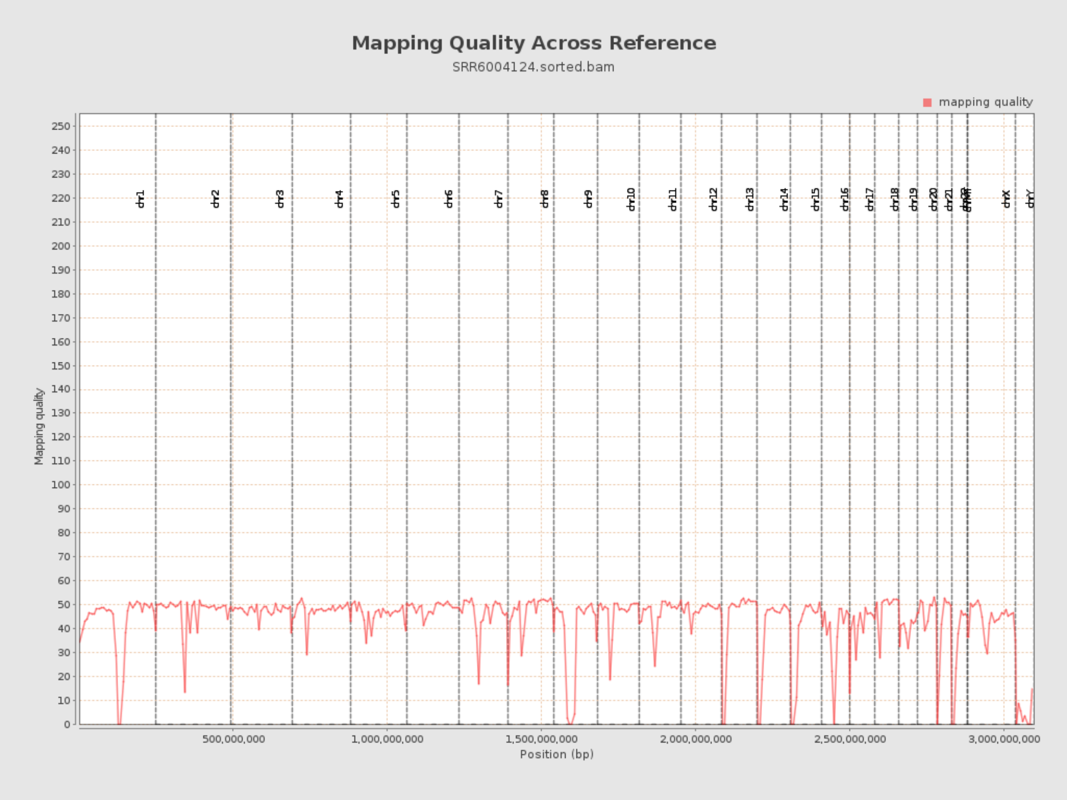
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram