Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:06:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004122.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_SRR6004122 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004122.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:06:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004122.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,118,739
Mapped reads	3,436,590 / 83.44%
Unmapped reads	682,149 / 16.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,146 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	259,784 / 6.31%
Duplication rate	6.03%
Clipped reads	1,606,552 / 39.01%

2.2. ACGT Content

Number/percentage of A's	63,006,896 / 27.76%
Number/percentage of C's	39,712,215 / 17.5%
Number/percentage of T's	75,404,314 / 33.23%
Number/percentage of G's	48,801,820 / 21.5%
Number/percentage of N's	23,030 / 0.01%
GC Percentage	39%

2.3. Coverage

Mean	0.0733

Standard Deviation	0.6722

2.4. Mapping Quality

Mean Mapping Quality	45.62

2.5. Mismatches and indels

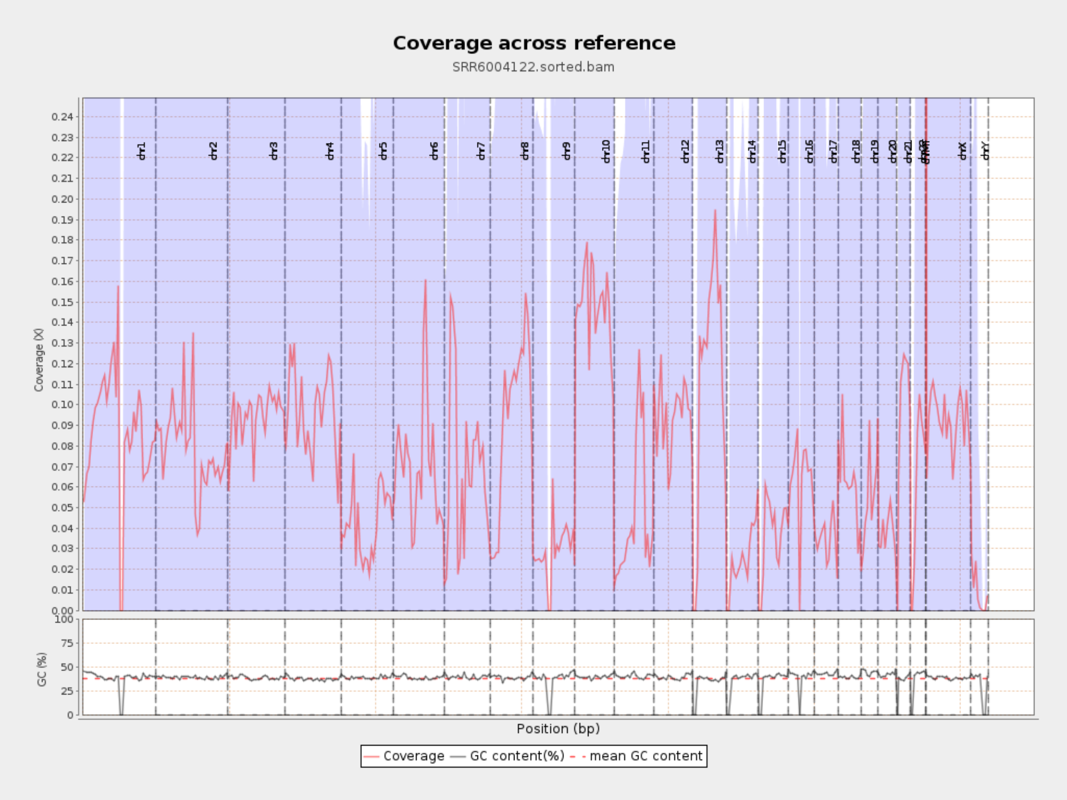
General error rate	0.98%
Mismatches	2,195,249
Insertions	19,467
Mapped reads with at least one insertion	0.56%
Deletions	66,449
Mapped reads with at least one deletion	1.91%
Homopolymer indels	47.9%

2.6. Chromosome stats

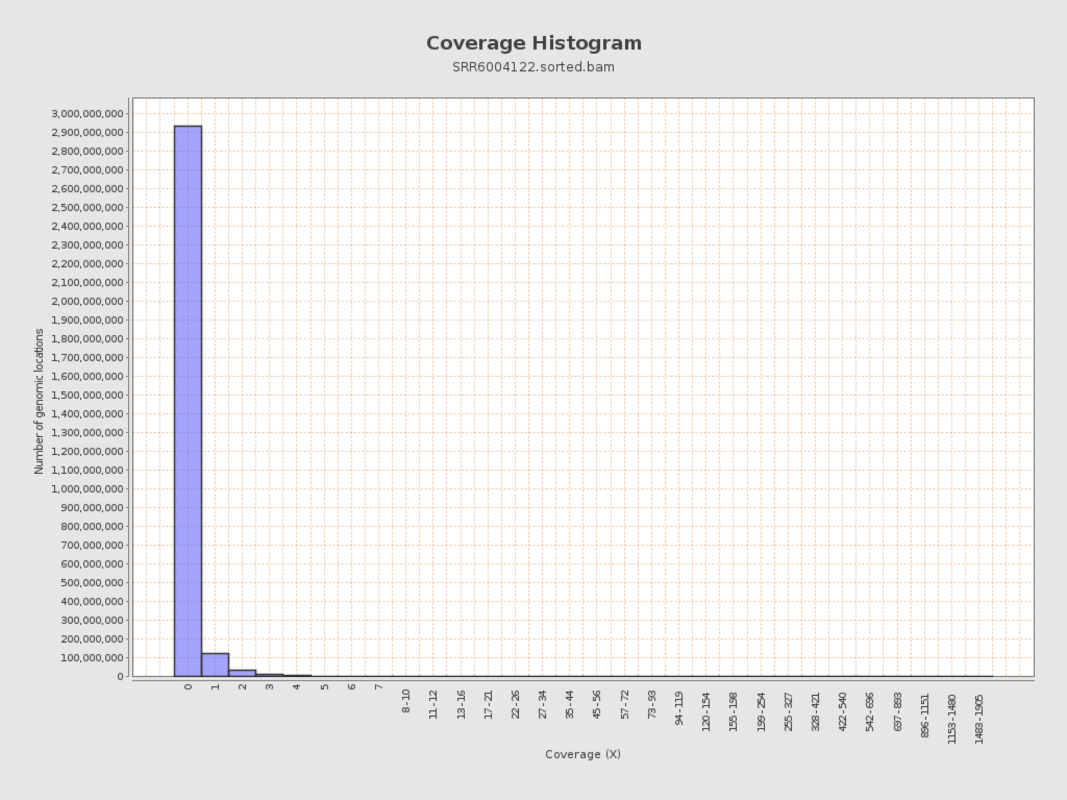
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21601845	0.0867	1.4025
chr2	243199373	19167570	0.0788	0.706
chr3	198022430	18664992	0.0943	0.4052
chr4	191154276	18630613	0.0975	0.4197
chr5	180915260	7646045	0.0423	0.2765
chr6	171115067	12199283	0.0713	0.4016
chr7	159138663	10747235	0.0675	0.5238

chr8	146364022	13802387	0.0943	1.1972
chr9	141213431	4115658	0.0291	0.4777
chr10	135534747	20130108	0.1485	0.736
chr11	135006516	6164385	0.0457	0.3798
chr12	133851895	12659319	0.0946	0.4042
chr13	115169878	13273763	0.1153	0.443
chr14	107349540	2603794	0.0243	0.28
chr15	102531392	3703191	0.0361	0.2513
chr16	90354753	5634364	0.0624	0.3951
chr17	81195210	2842184	0.035	0.2788
chr18	78077248	4891723	0.0627	1.2503
chr19	59128983	3210192	0.0543	0.833
chr20	63025520	2408361	0.0382	0.3165
chr21	48129895	4682211	0.0973	0.4279
chr22	51304566	3186423	0.0621	0.3202
chrMT	16571	139129	8.3959	6.4037
chrX	155270560	14433073	0.093	0.4523
chrY	59373566	520163	0.0088	0.1617

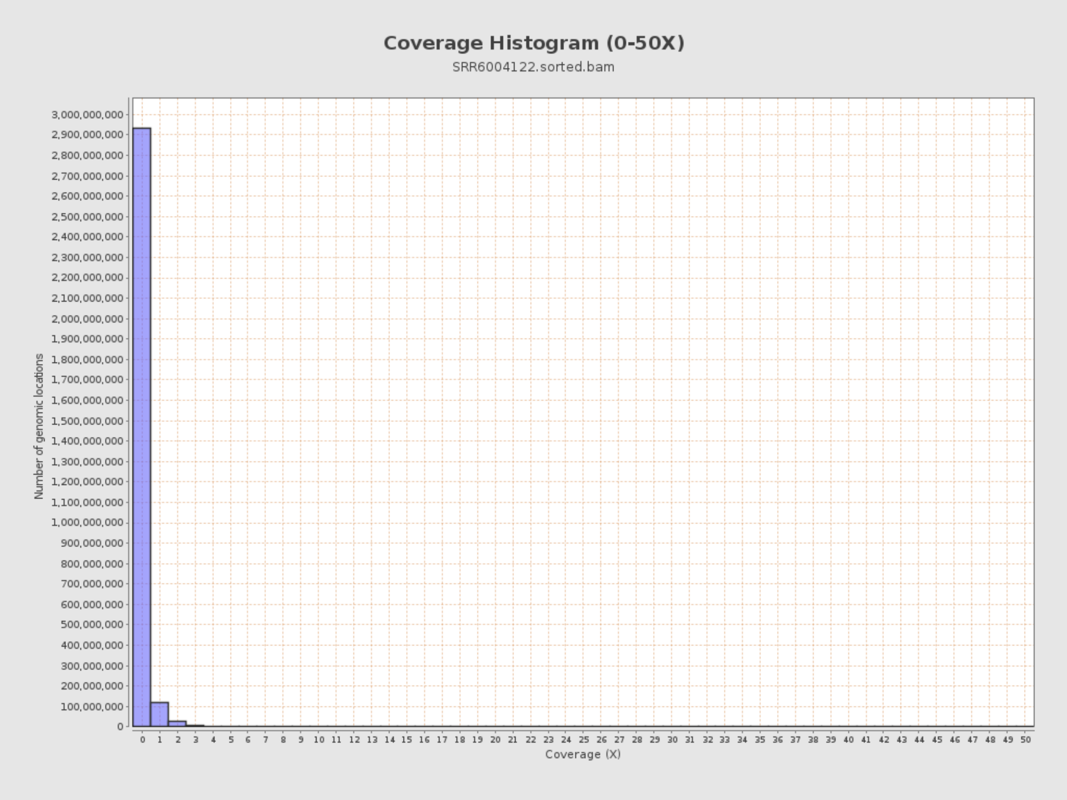
3. Results : Coverage across reference



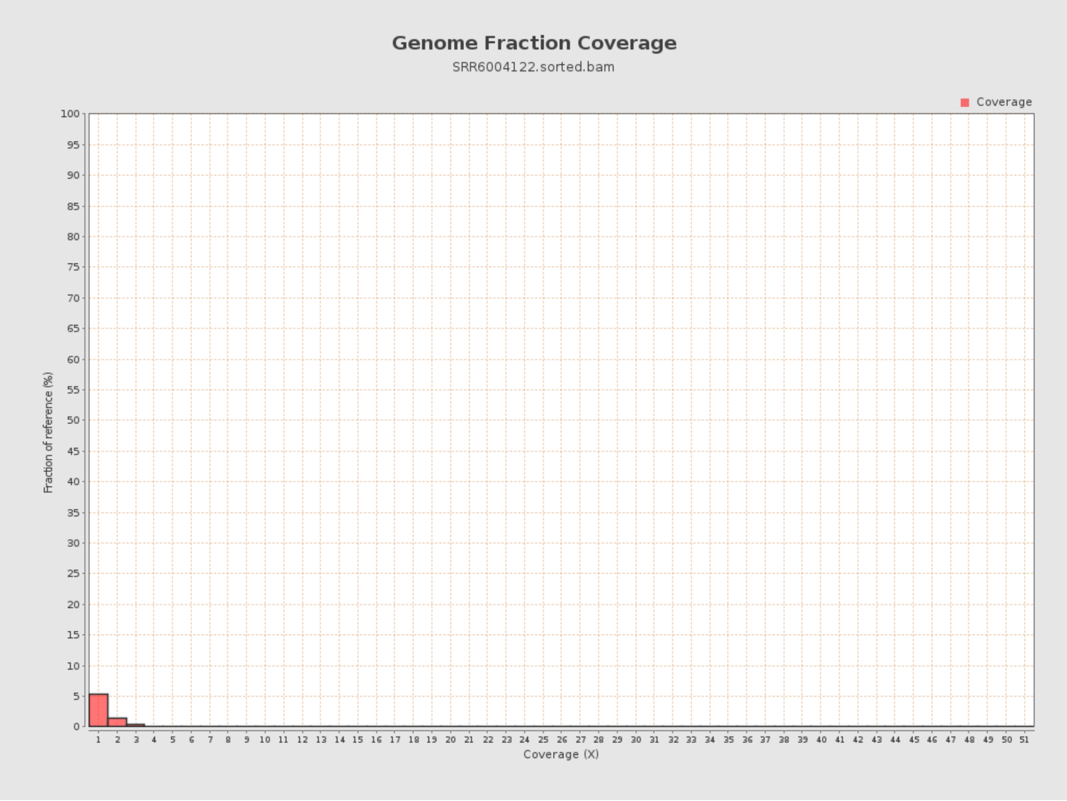
4. Results : Coverage Histogram



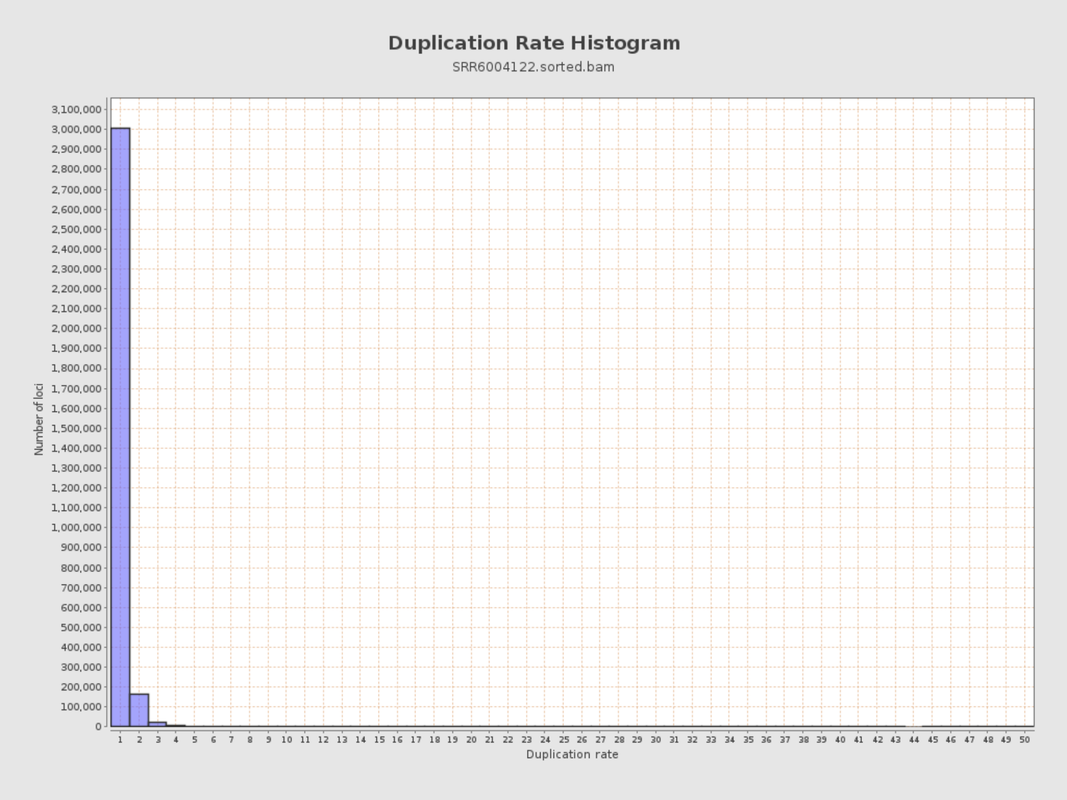
5. Results : Coverage Histogram (0-50X)



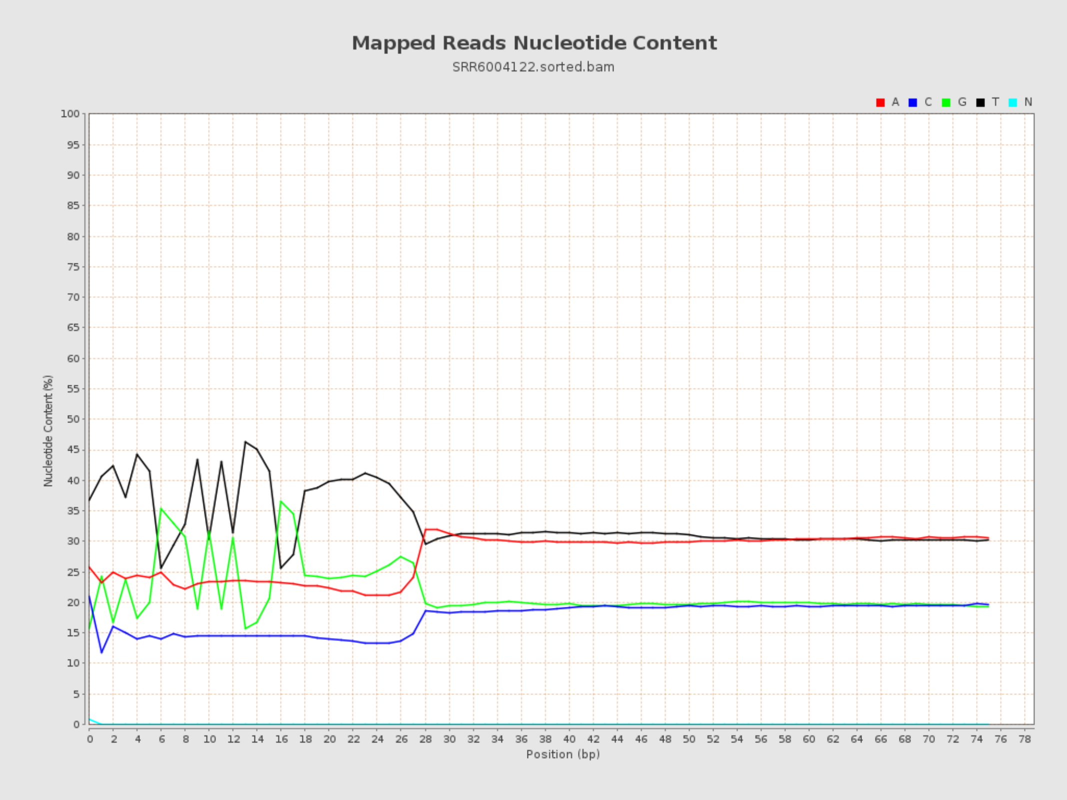
6. Results : Genome Fraction Coverage



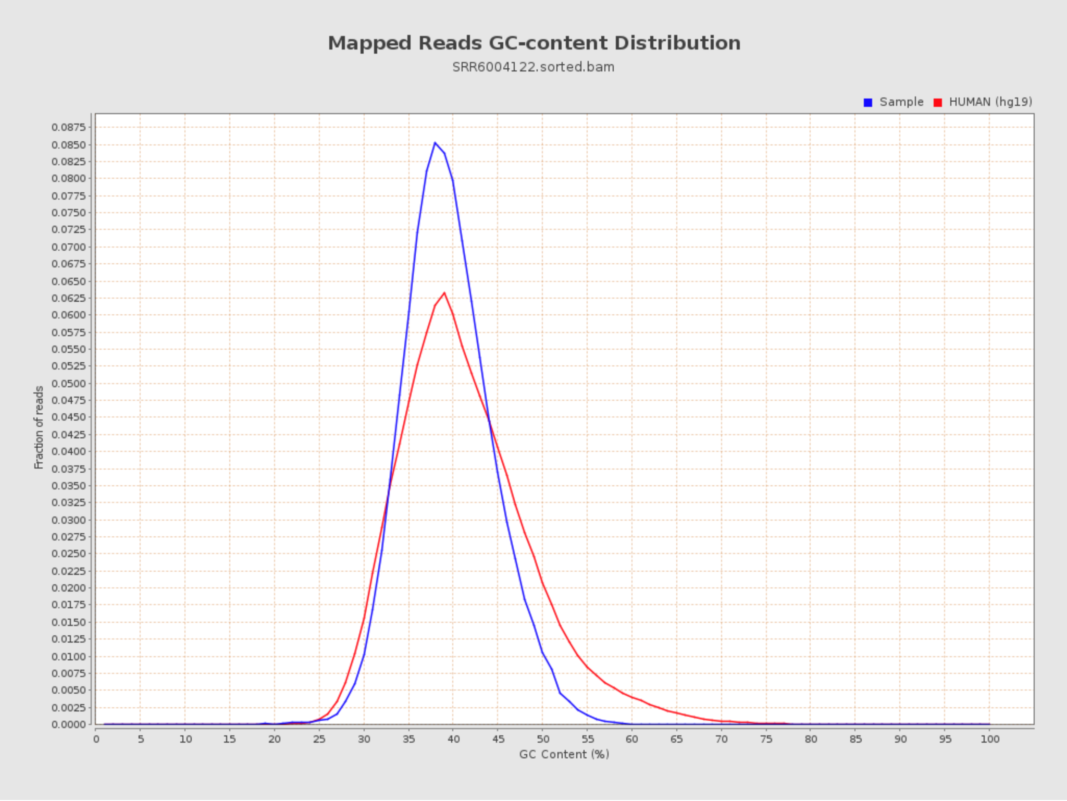
7. Results : Duplication Rate Histogram



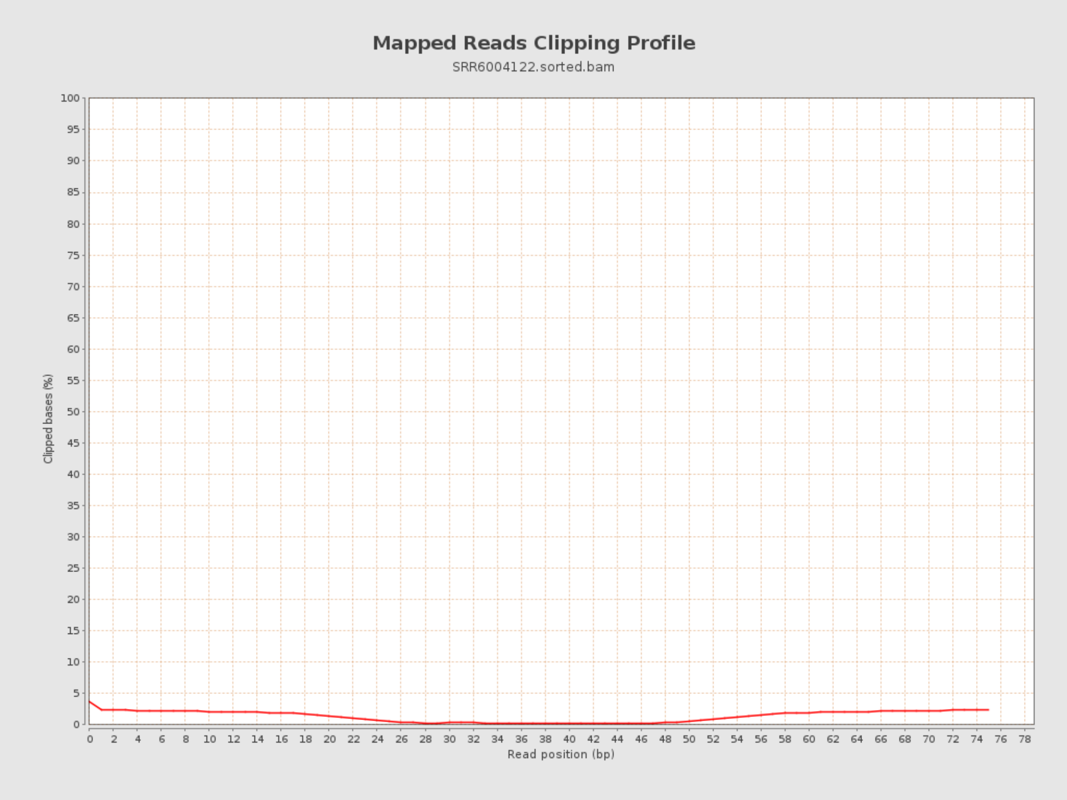
8. Results : Mapped Reads Nucleotide Content



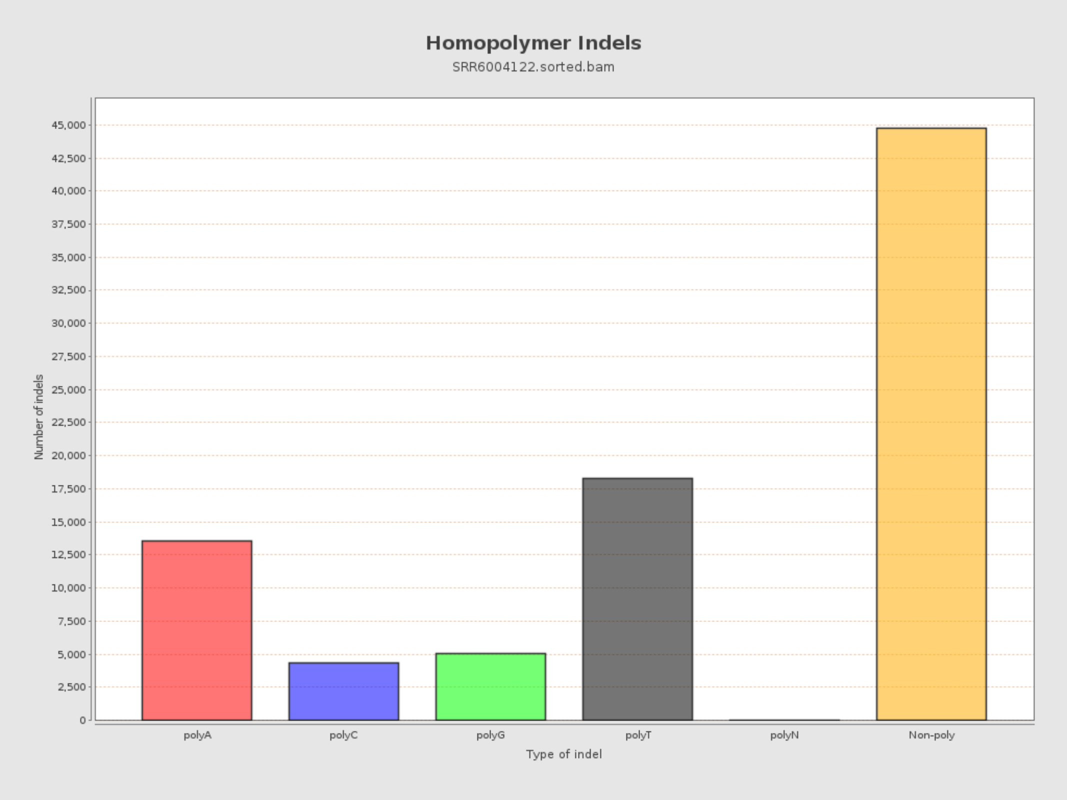
9. Results : Mapped Reads GC-content Distribution



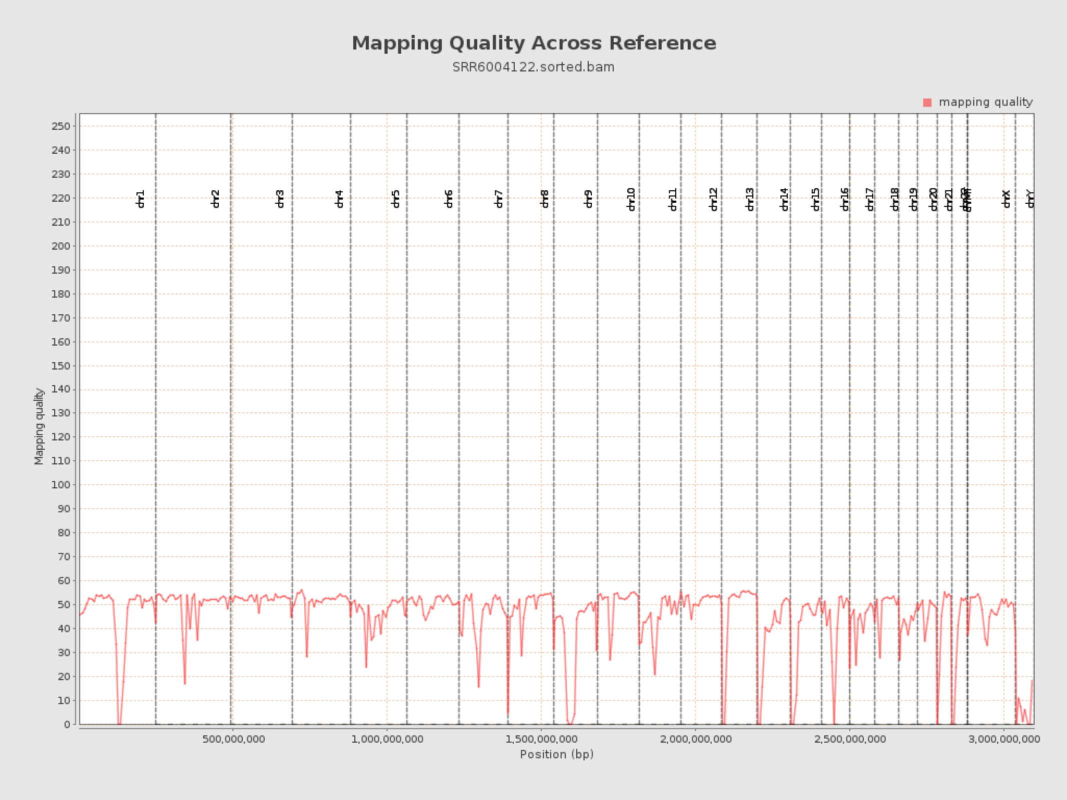
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram