Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:25:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004112.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_SRR6004112 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004112.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:25:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,924,606
Mapped reads	2,281,146 / 78%
Unmapped reads	643,460 / 22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,341 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	193,073 / 6.6%
Duplication rate	7.01%
Clipped reads	1,340,944 / 45.85%

2.2. ACGT Content

Number/percentage of A's	37,870,187 / 26.12%
Number/percentage of C's	25,486,516 / 17.58%
Number/percentage of T's	48,297,381 / 33.31%
Number/percentage of G's	33,326,230 / 22.98%
Number/percentage of N's	18,137 / 0.01%
GC Percentage	40.56%

2.3. Coverage

Mean	0.0469

Standard Deviation	0.4194

2.4. Mapping Quality

Mean Mapping Quality	45.93

2.5. Mismatches and indels

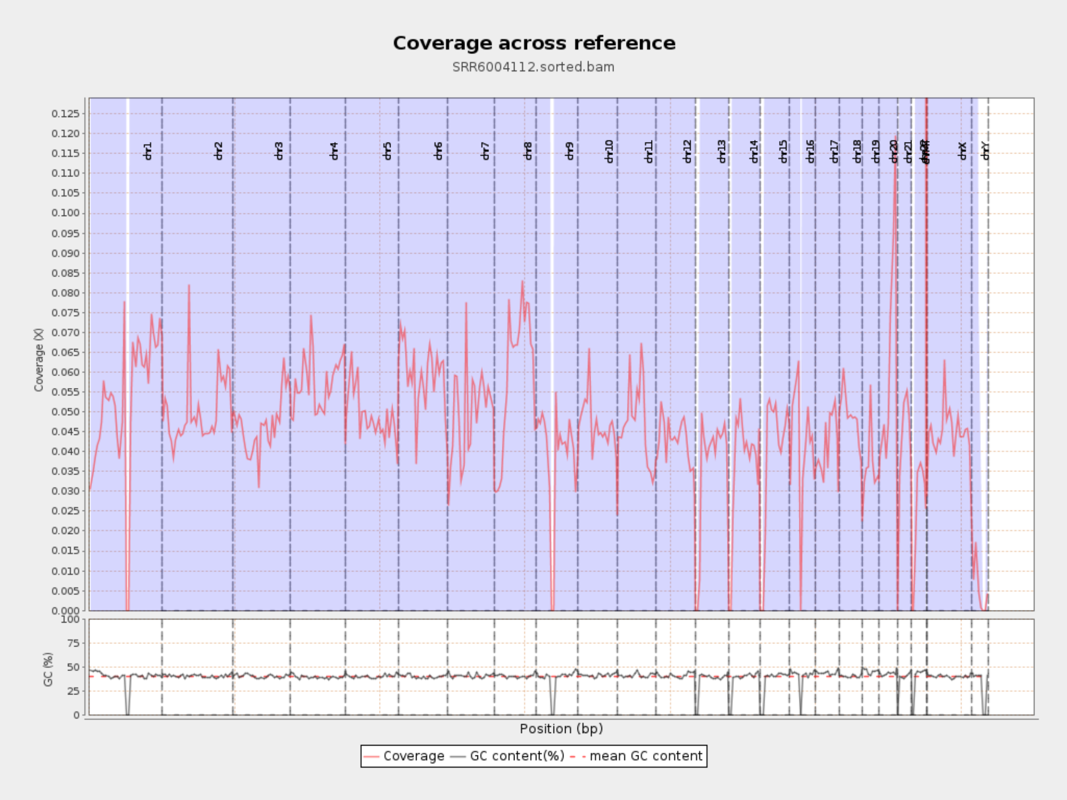
General error rate	1.04%
Mismatches	1,486,692
Insertions	11,555
Mapped reads with at least one insertion	0.5%
Deletions	46,311
Mapped reads with at least one deletion	2.01%
Homopolymer indels	48.45%

2.6. Chromosome stats

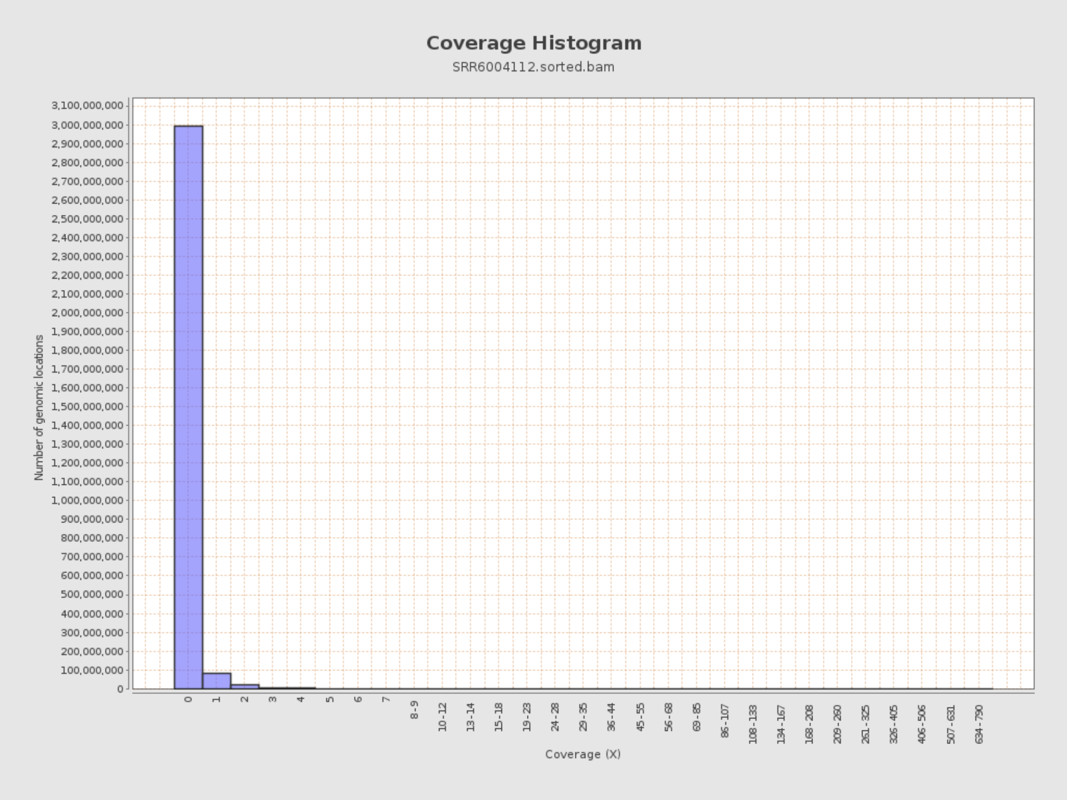
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13088302	0.0525	0.6916
chr2	243199373	12155689	0.05	0.5114
chr3	198022430	9246360	0.0467	0.2818
chr4	191154276	10999122	0.0575	0.3225
chr5	180915260	8903554	0.0492	0.2906
chr6	171115067	10166723	0.0594	0.3722
chr7	159138663	8003253	0.0503	0.6024

chr8	146364022	8709774	0.0595	0.5106
chr9	141213431	5449873	0.0386	0.3766
chr10	135534747	6393669	0.0472	0.3609
chr11	135006516	6322796	0.0468	0.4129
chr12	133851895	5749746	0.043	0.276
chr13	115169878	4140679	0.036	0.2472
chr14	107349540	3878295	0.0361	0.267
chr15	102531392	3995469	0.039	0.2611
chr16	90354753	3839283	0.0425	0.2885
chr17	81195210	3365629	0.0415	0.2887
chr18	78077248	3869668	0.0496	0.7093
chr19	59128983	2184254	0.0369	0.4689
chr20	63025520	3944387	0.0626	0.3403
chr21	48129895	1986485	0.0413	0.2799
chr22	51304566	1245597	0.0243	0.2006
chrMT	16571	150943	9.1089	6.2444
chrX	155270560	6944828	0.0447	0.3177
chrY	59373566	339622	0.0057	0.1256

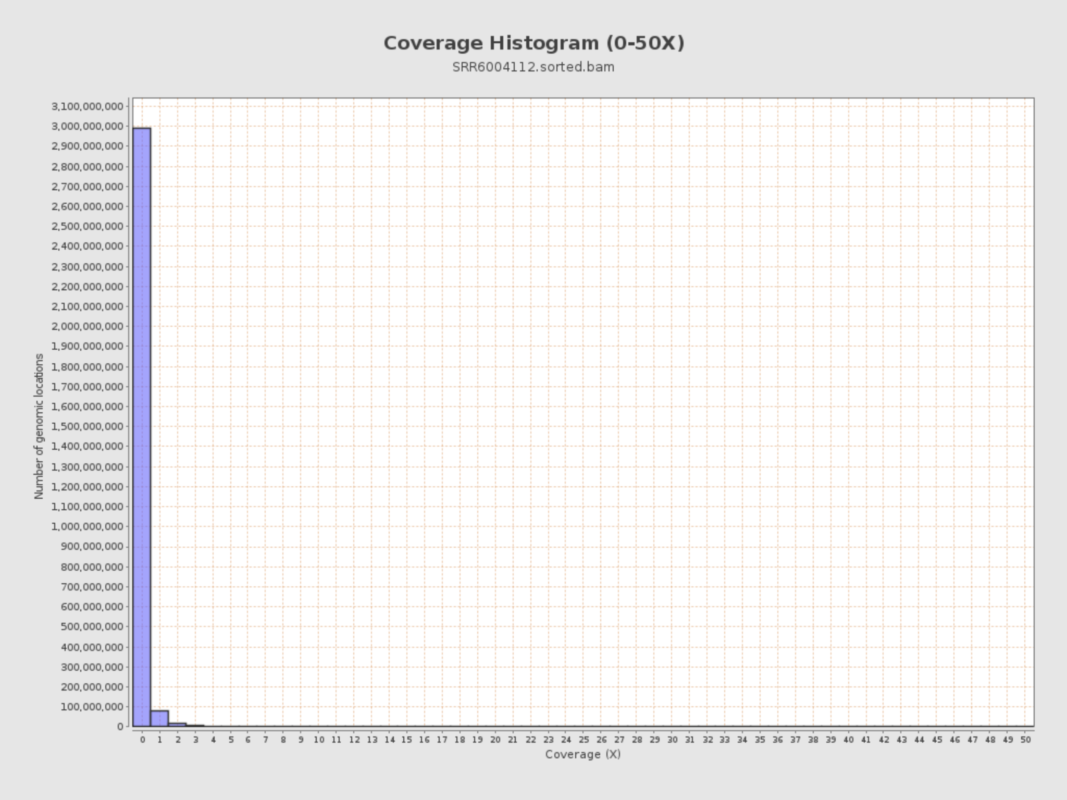
3. Results : Coverage across reference



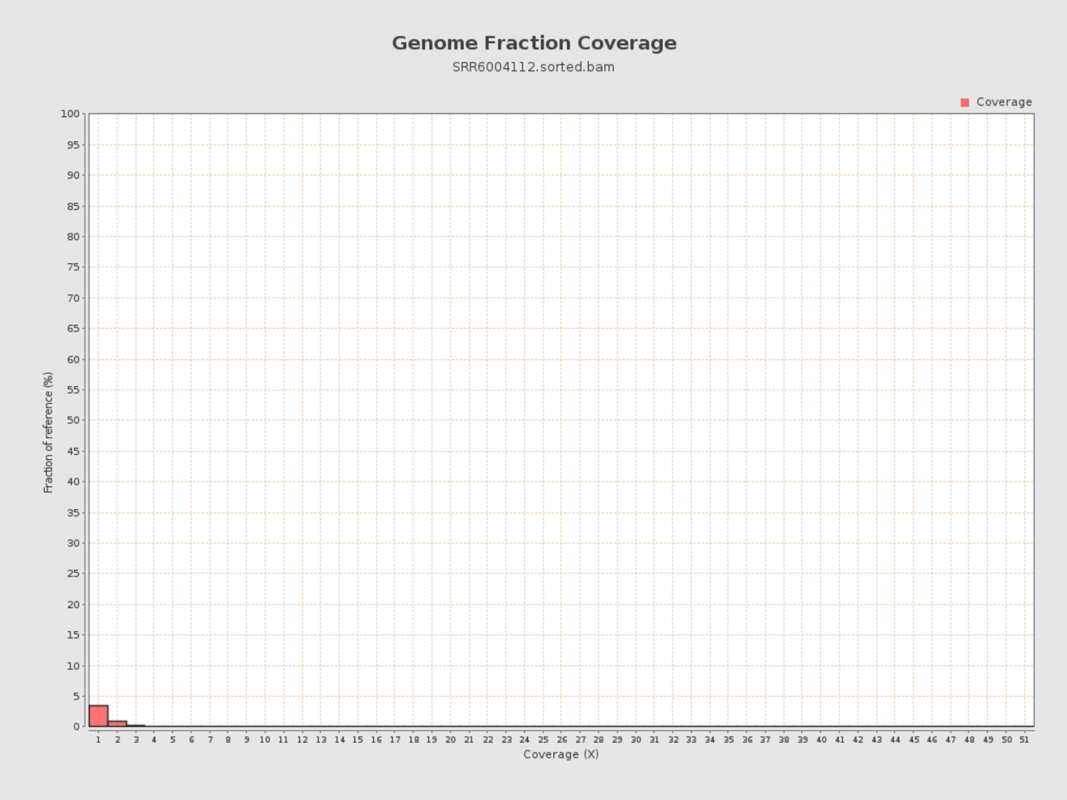
4. Results : Coverage Histogram



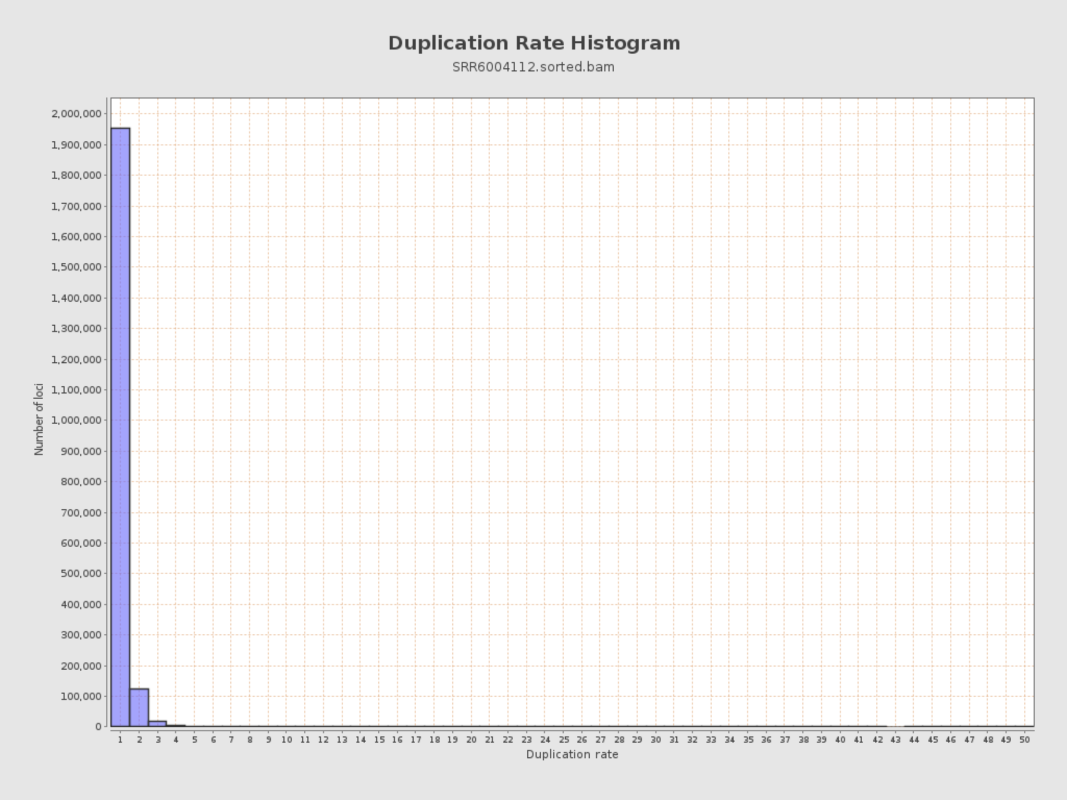
5. Results : Coverage Histogram (0-50X)



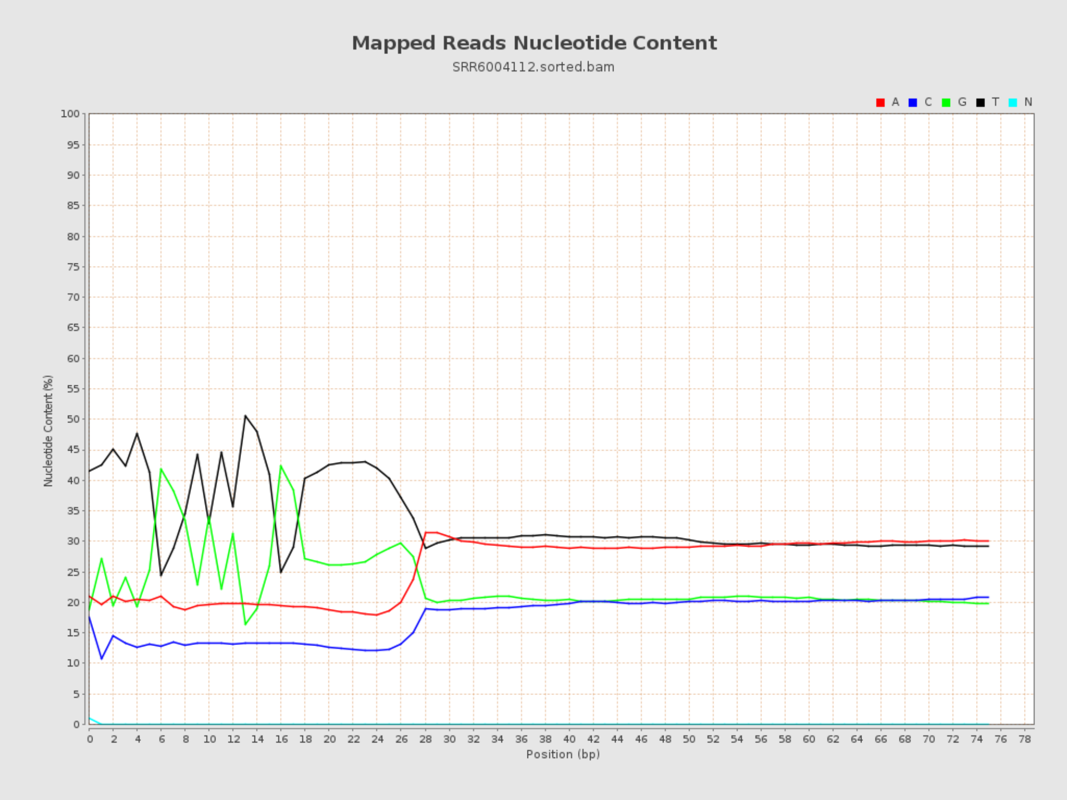
6. Results : Genome Fraction Coverage



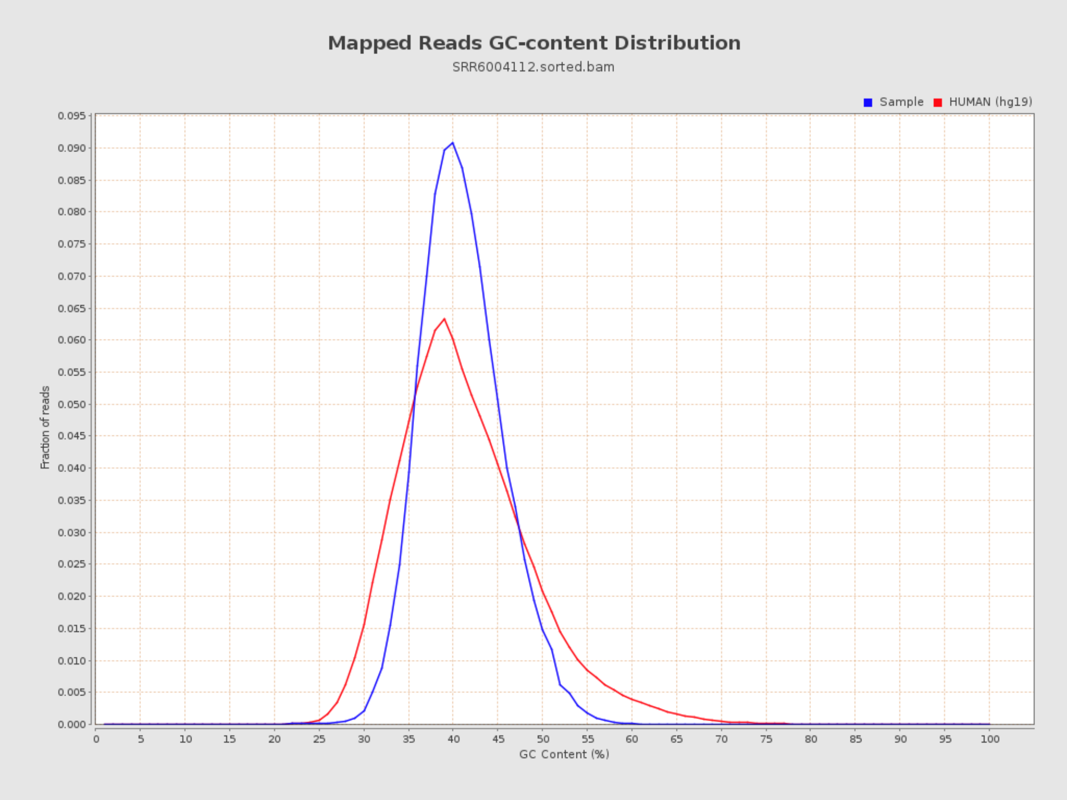
7. Results : Duplication Rate Histogram



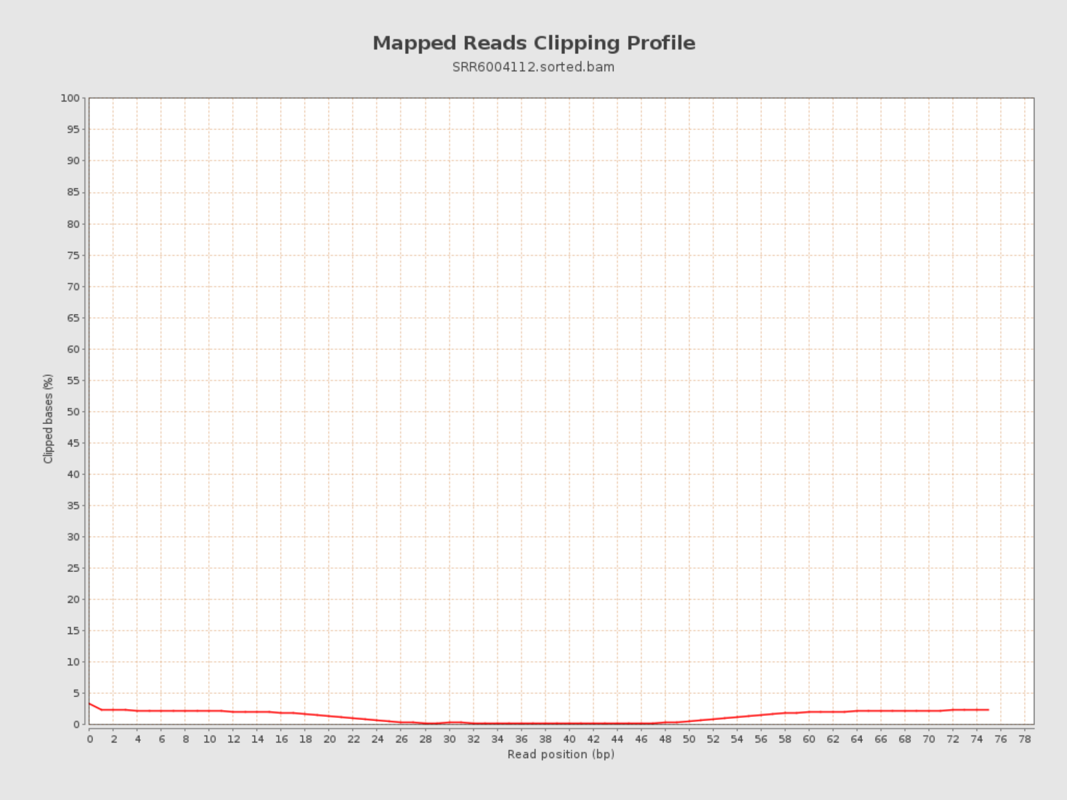
8. Results : Mapped Reads Nucleotide Content



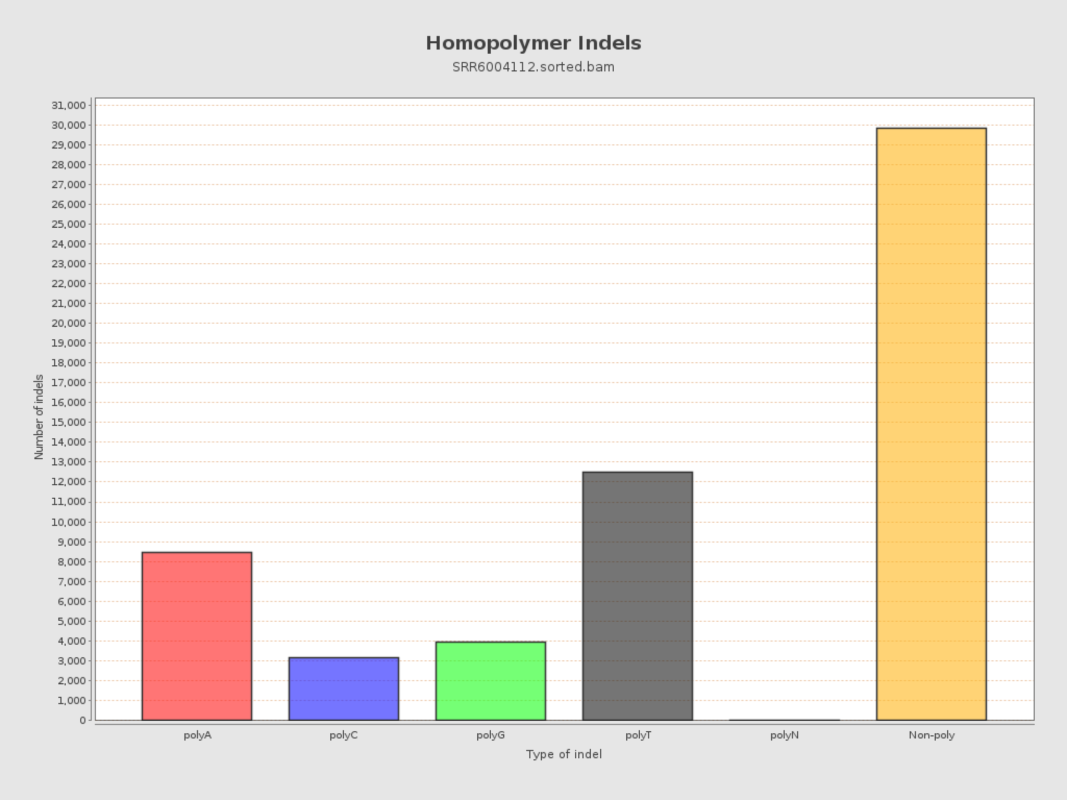
9. Results : Mapped Reads GC-content Distribution



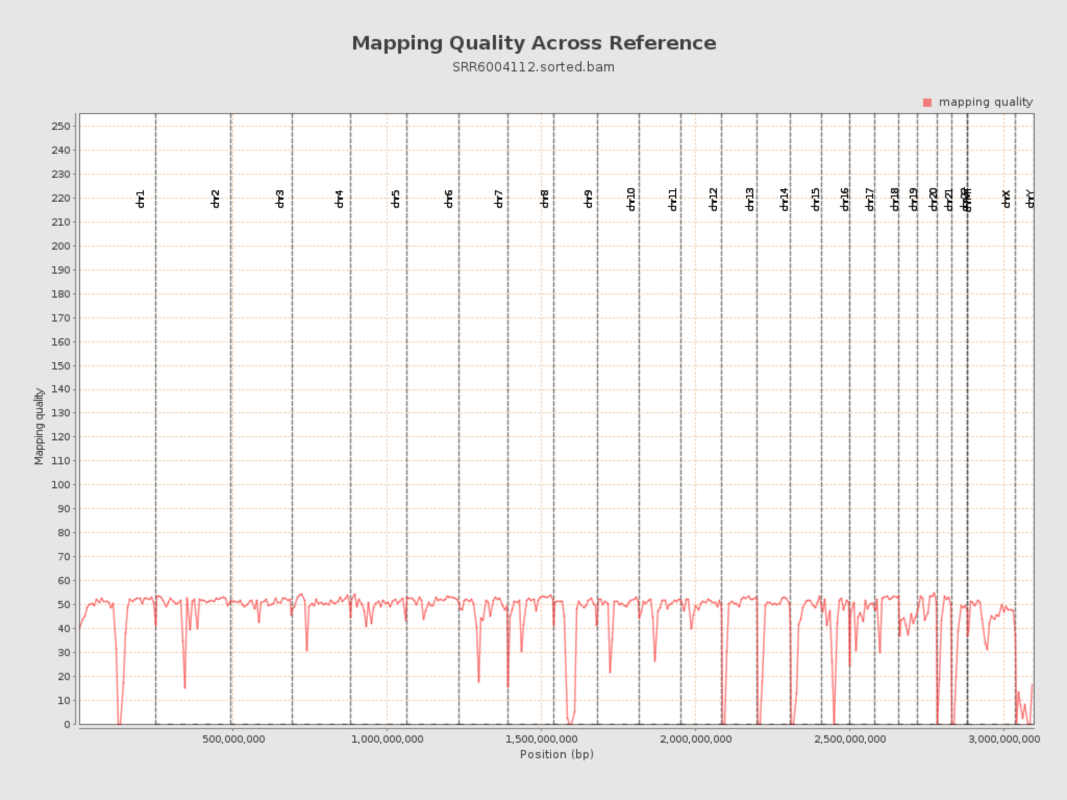
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram