Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:48:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013204.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_SRR6013204 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013204.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:48:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013204.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,959,692
Mapped reads	1,727,015 / 88.13%
Unmapped reads	232,677 / 11.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,105 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	84,900 / 4.33%
Duplication rate	3.94%
Clipped reads	769,696 / 39.28%

2.2. ACGT Content

Number/percentage of A's	32,091,148 / 27.8%
Number/percentage of C's	21,092,256 / 18.27%
Number/percentage of T's	36,950,698 / 32.01%
Number/percentage of G's	25,275,953 / 21.9%
Number/percentage of N's	24,703 / 0.02%
GC Percentage	40.17%

2.3. Coverage

Mean	0.0373

Standard Deviation	0.3663

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

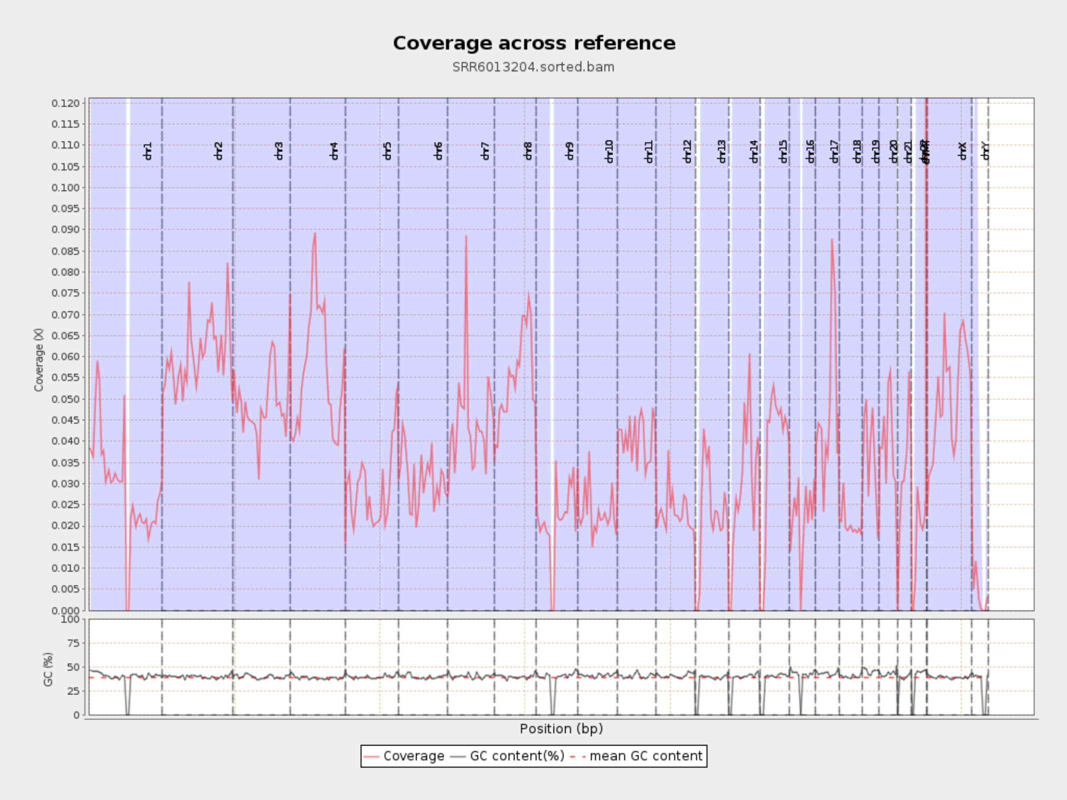
General error rate	0.79%
Mismatches	893,066
Insertions	8,111
Mapped reads with at least one insertion	0.47%
Deletions	25,166
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.44%

2.6. Chromosome stats

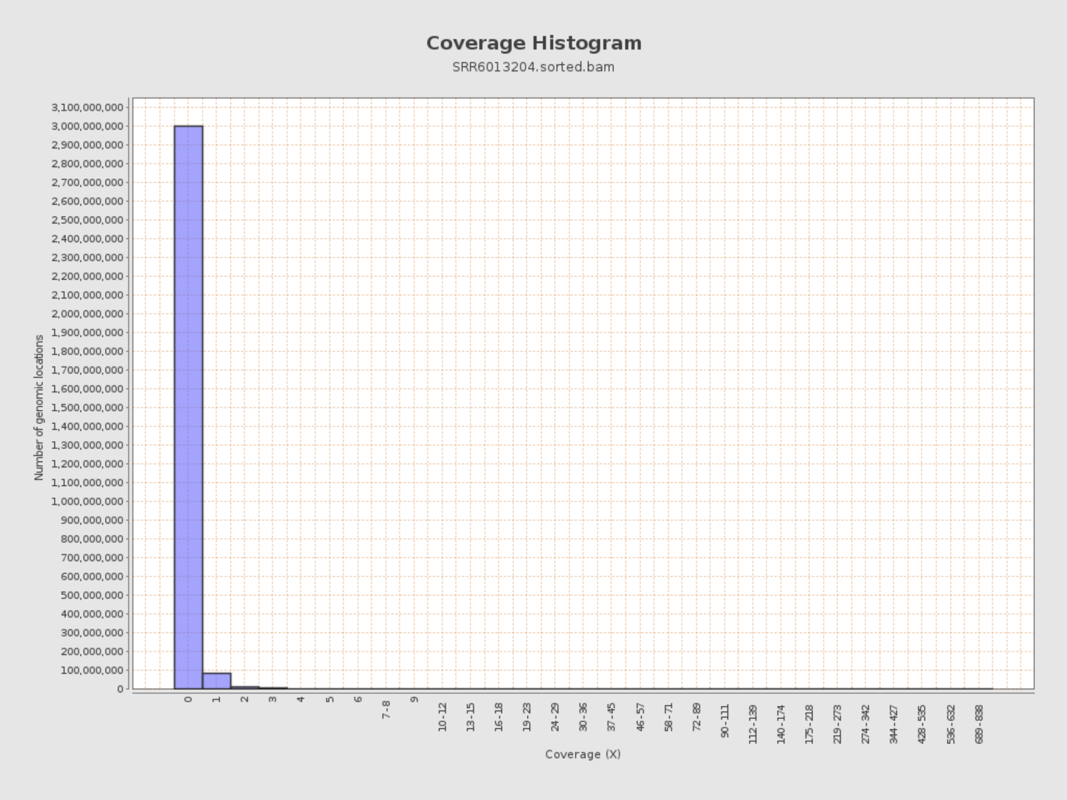
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7167821	0.0288	0.5209
chr2	243199373	14767590	0.0607	0.4418
chr3	198022430	9645715	0.0487	0.2549
chr4	191154276	10866240	0.0568	0.2851
chr5	180915260	5180443	0.0286	0.1971
chr6	171115067	5280934	0.0309	0.2382
chr7	159138663	7118954	0.0447	0.7136

chr8	146364022	8127569	0.0555	0.5577
chr9	141213431	2981560	0.0211	0.2718
chr10	135534747	3120566	0.023	0.2332
chr11	135006516	5472273	0.0405	0.2651
chr12	133851895	3118098	0.0233	0.184
chr13	115169878	2568934	0.0223	0.1737
chr14	107349540	3143564	0.0293	0.2131
chr15	102531392	3824438	0.0373	0.2264
chr16	90354753	1986940	0.022	0.1855
chr17	81195210	3847964	0.0474	0.2639
chr18	78077248	1602865	0.0205	0.4442
chr19	59128983	2156600	0.0365	0.3761
chr20	63025520	2500470	0.0397	0.2358
chr21	48129895	1553118	0.0323	0.2144
chr22	51304566	813258	0.0159	0.1423
chrMT	16571	626807	37.8255	19.6292
chrX	155270560	7758791	0.05	0.2846
chrY	59373566	246931	0.0042	0.0932

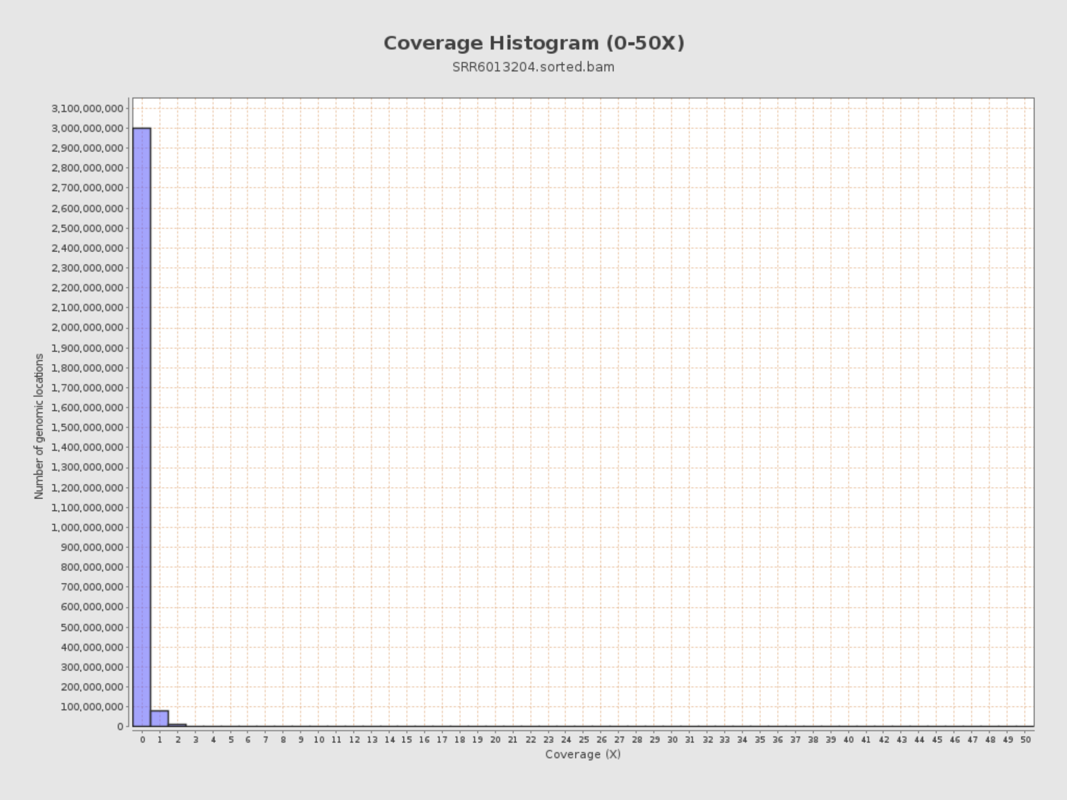
3. Results : Coverage across reference



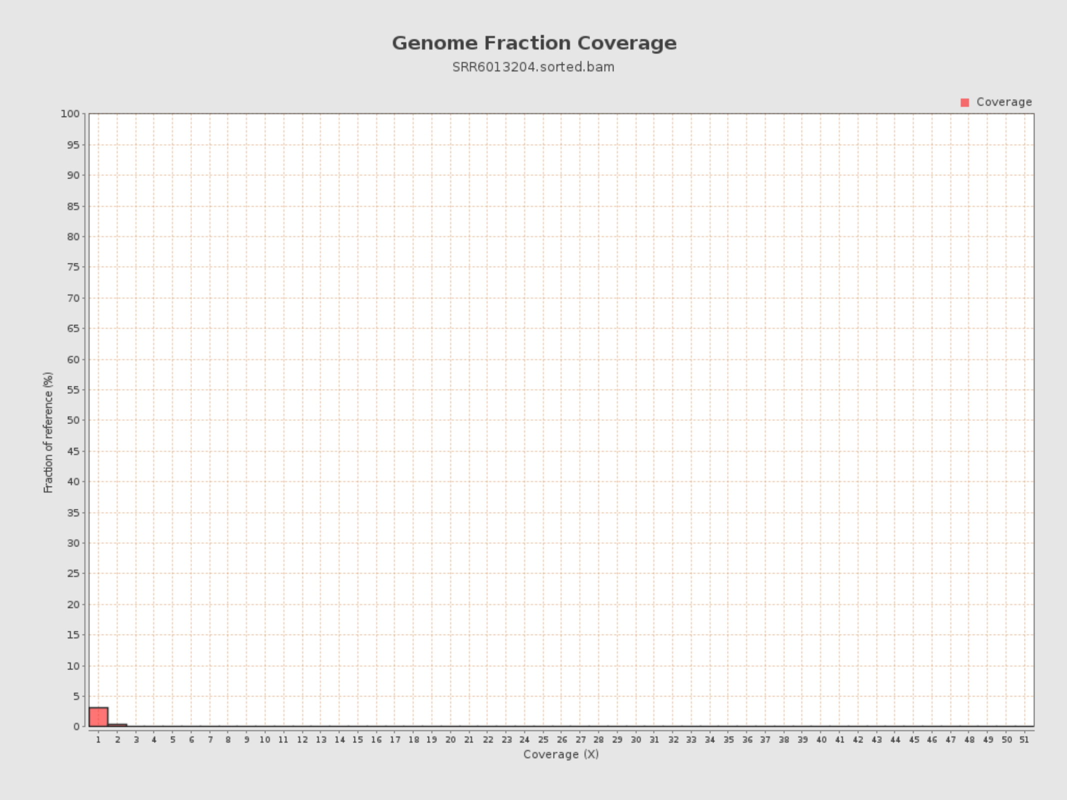
4. Results : Coverage Histogram



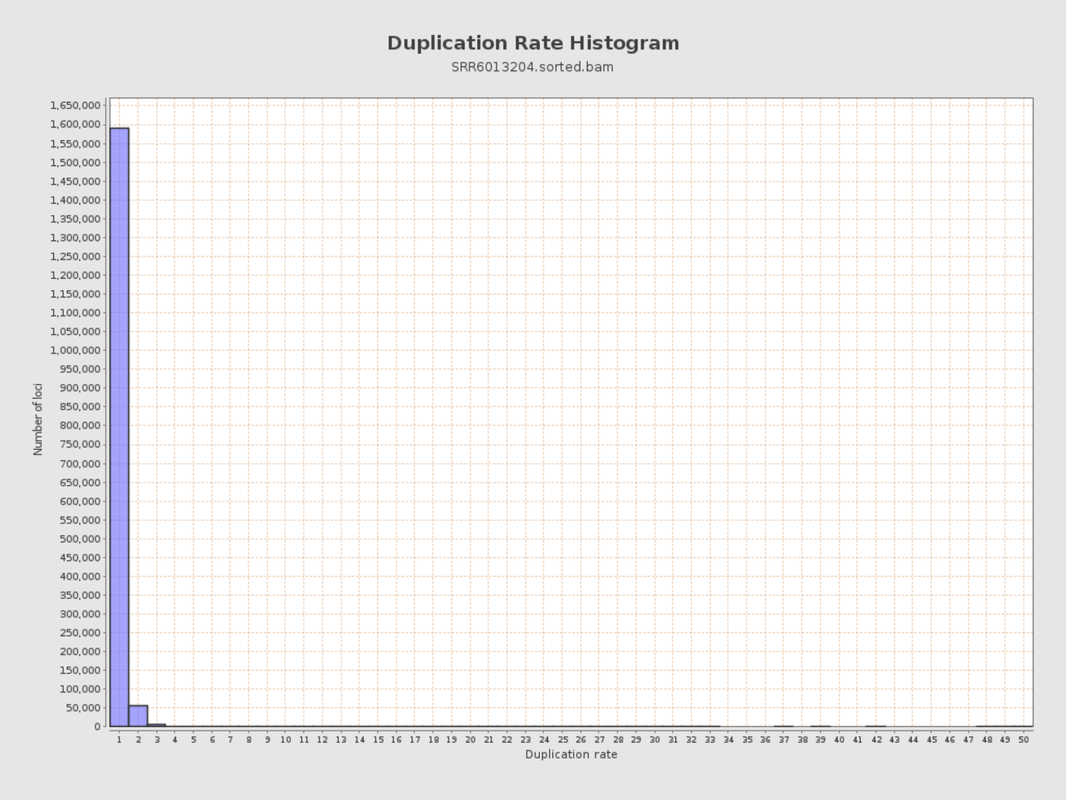
5. Results : Coverage Histogram (0-50X)



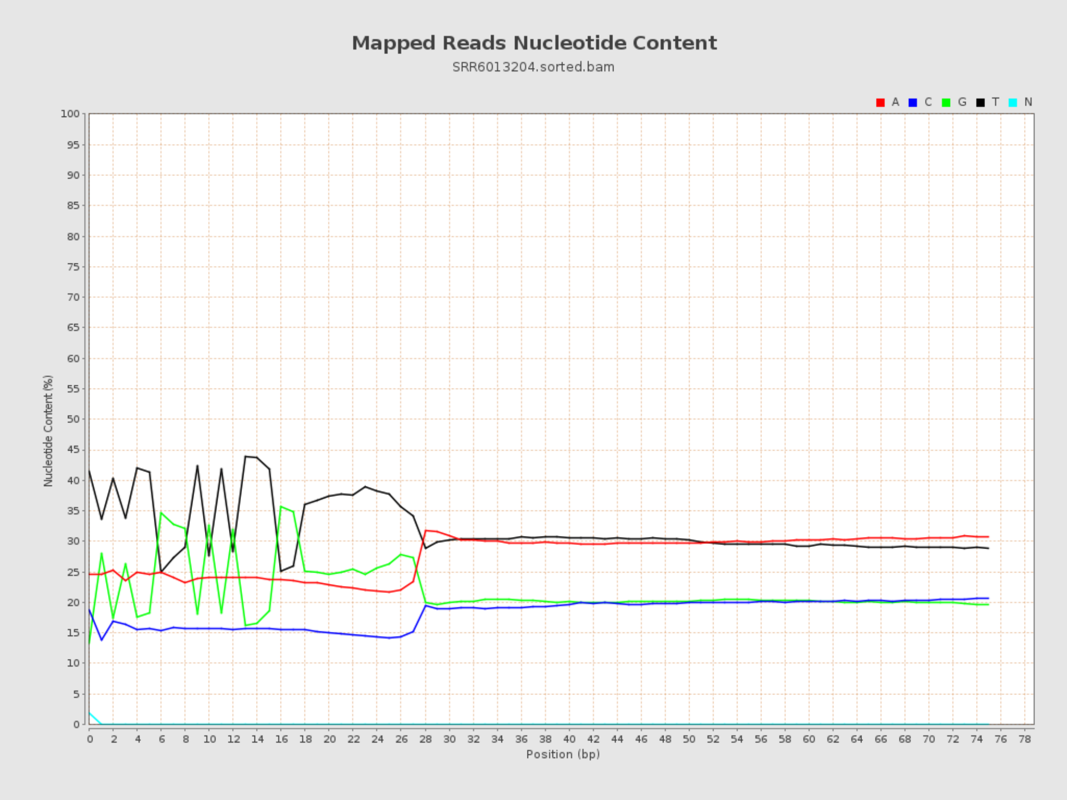
6. Results : Genome Fraction Coverage



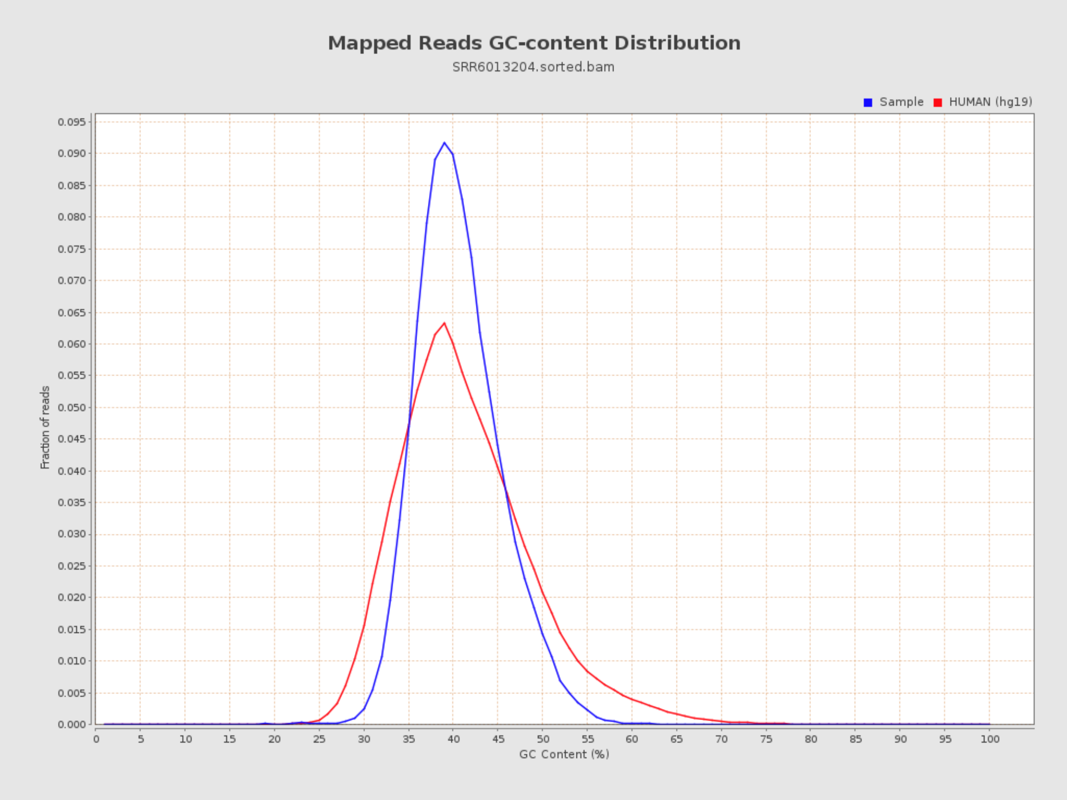
7. Results : Duplication Rate Histogram



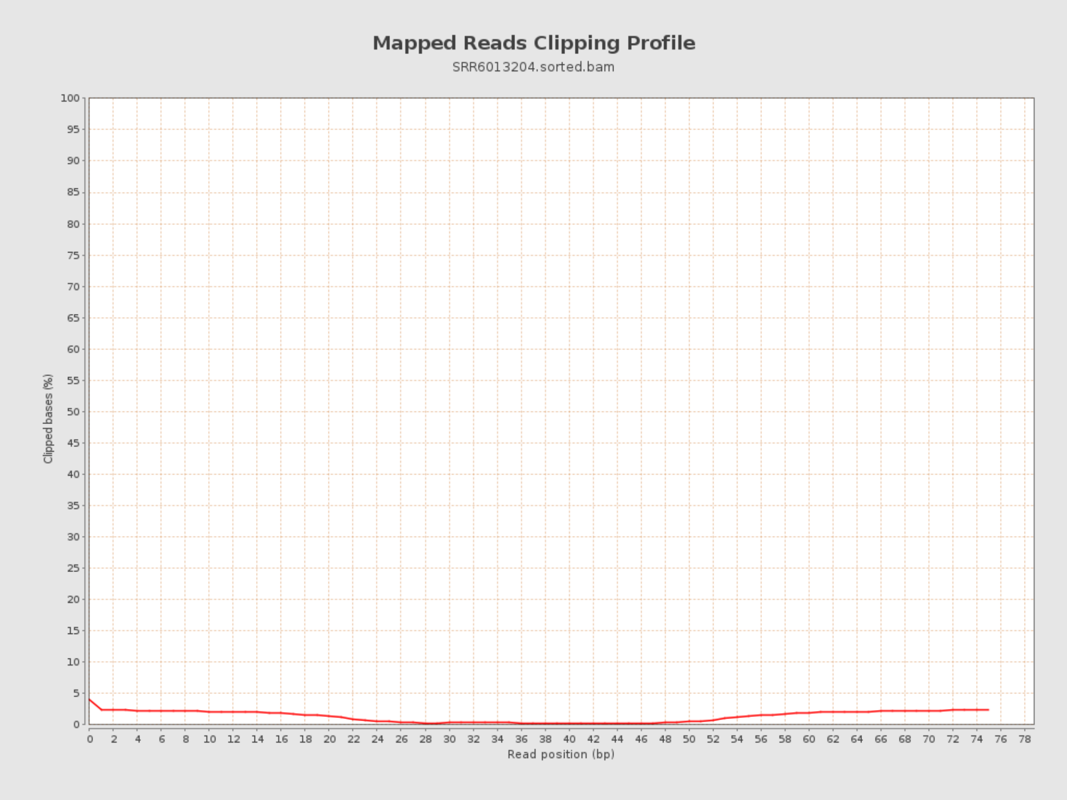
8. Results : Mapped Reads Nucleotide Content



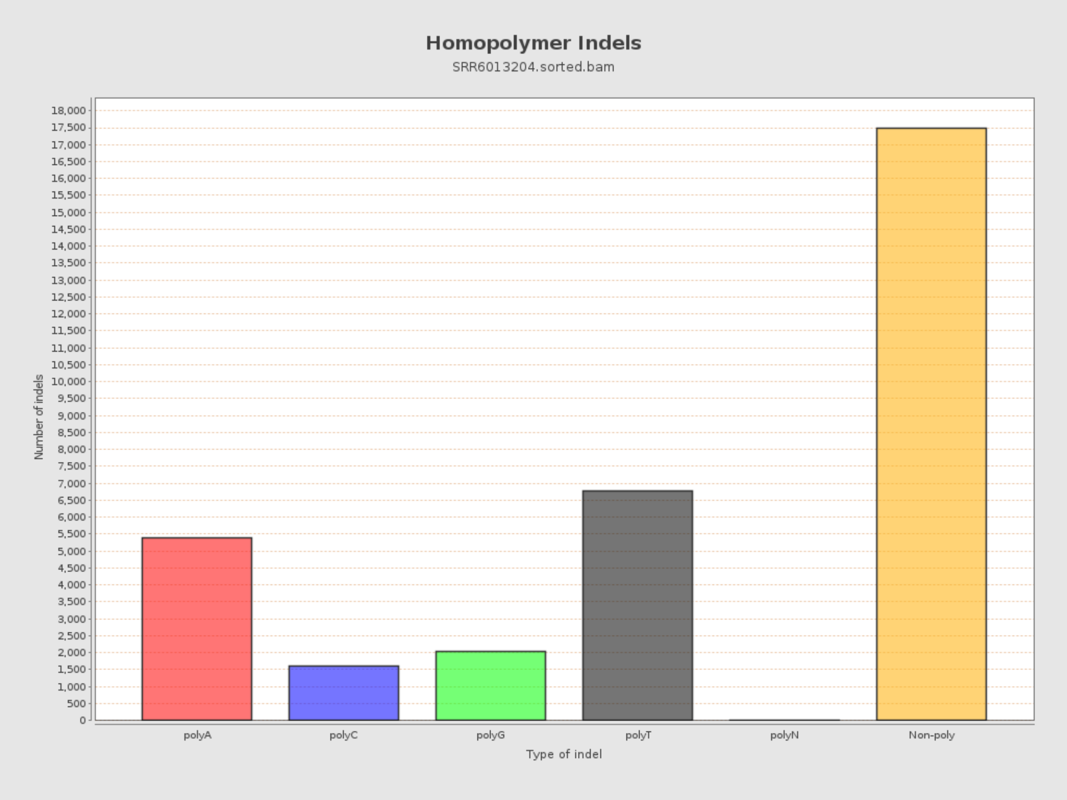
9. Results : Mapped Reads GC-content Distribution



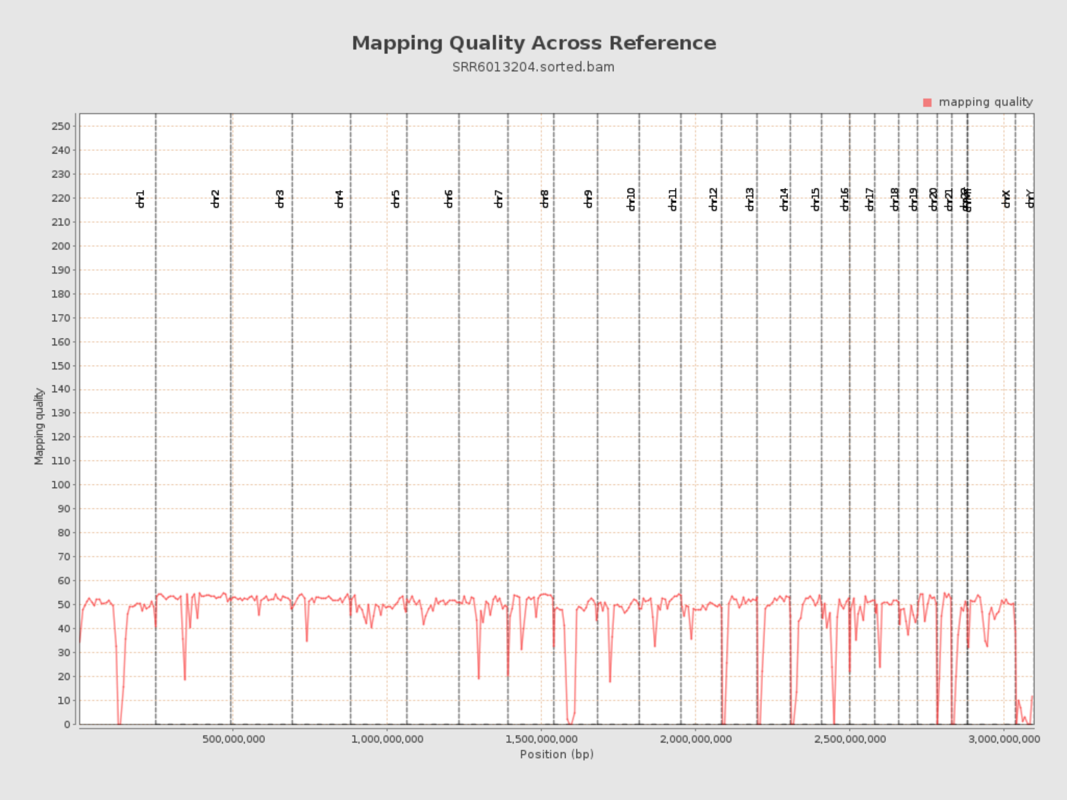
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram