Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:25:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230342.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_SRR6230342 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230342.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:25:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230342.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,926,997
Mapped reads	3,366,408 / 85.72%
Unmapped reads	560,589 / 14.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,391 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	158,274 / 4.03%
Duplication rate	3.46%
Clipped reads	1,513,927 / 38.55%

2.2. ACGT Content

Number/percentage of A's	61,897,184 / 27.61%
Number/percentage of C's	39,273,794 / 17.52%
Number/percentage of T's	73,696,775 / 32.88%
Number/percentage of G's	48,866,236 / 21.8%
Number/percentage of N's	431,746 / 0.19%
GC Percentage	39.32%

2.3. Coverage

Mean	0.0724

Standard Deviation	0.6326

2.4. Mapping Quality

Mean Mapping Quality	47.13

2.5. Mismatches and indels

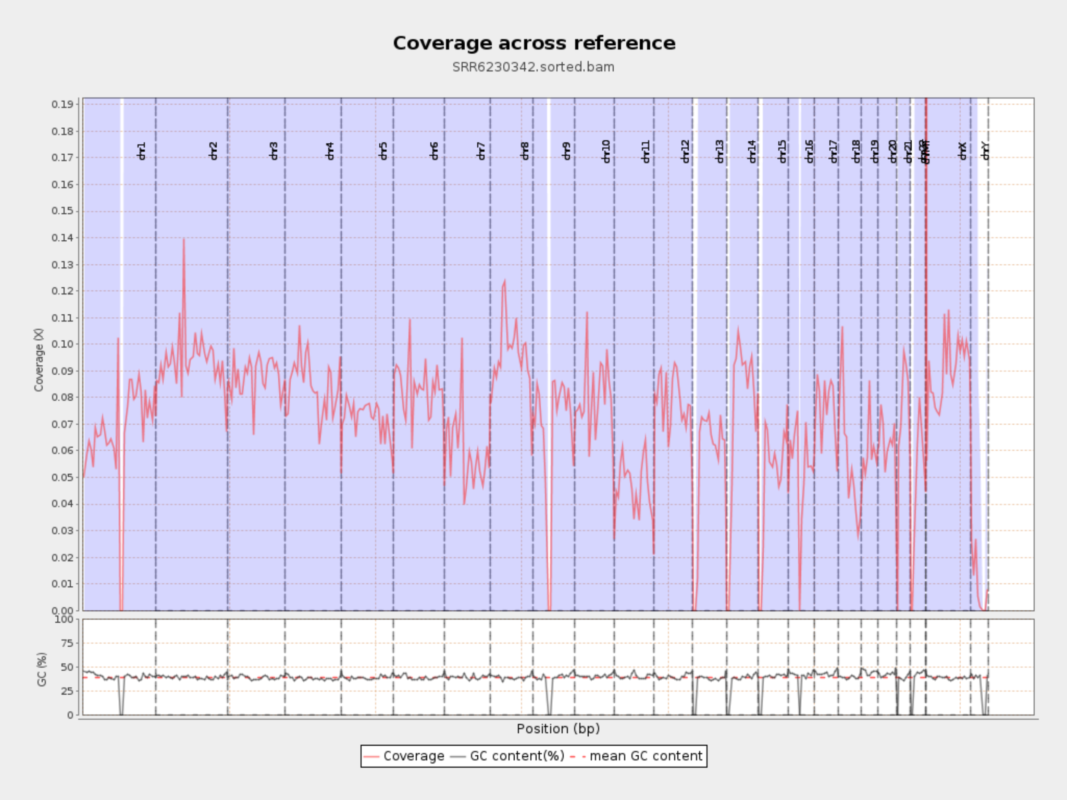
General error rate	0.98%
Mismatches	2,165,257
Insertions	20,376
Mapped reads with at least one insertion	0.6%
Deletions	59,346
Mapped reads with at least one deletion	1.75%
Homopolymer indels	48.45%

2.6. Chromosome stats

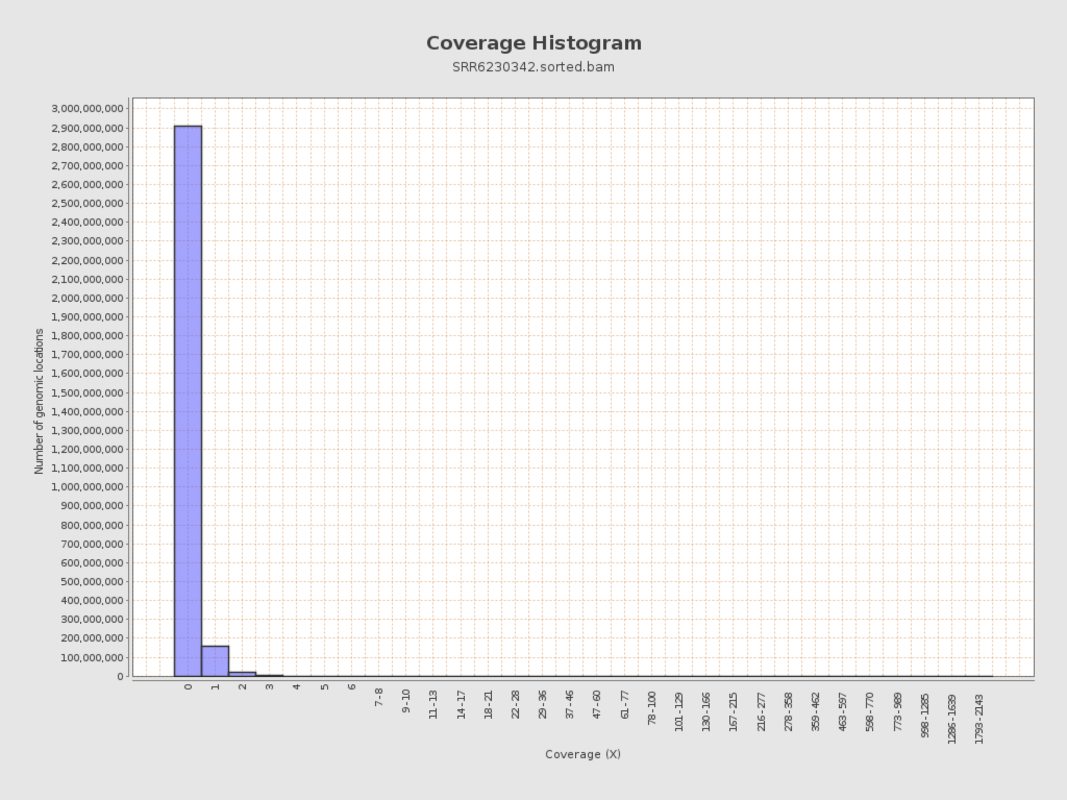
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16640273	0.0668	1.1065
chr2	243199373	22923389	0.0943	0.6475
chr3	198022430	17418503	0.088	0.3415
chr4	191154276	16141989	0.0844	0.3654
chr5	180915260	13032827	0.072	0.3162
chr6	171115067	14357887	0.0839	0.4738
chr7	159138663	9473224	0.0595	0.7261

chr8	146364022	14056172	0.096	1.3817
chr9	141213431	9485991	0.0672	0.6056
chr10	135534747	10838247	0.08	0.4977
chr11	135006516	6392756	0.0474	0.4539
chr12	133851895	10506934	0.0785	0.3366
chr13	115169878	6412733	0.0557	0.27
chr14	107349540	8165800	0.0761	0.3572
chr15	102531392	4966848	0.0484	0.252
chr16	90354753	4682971	0.0518	0.3286
chr17	81195210	6244246	0.0769	0.3566
chr18	78077248	4528383	0.058	1.2209
chr19	59128983	3543031	0.0599	0.6385
chr20	63025520	4030468	0.0639	0.3301
chr21	48129895	3429427	0.0713	0.3419
chr22	51304566	2370510	0.0462	0.2445
chrMT	16571	122386	7.3856	4.3837
chrX	155270560	13940129	0.0898	0.4096
chrY	59373566	558069	0.0094	0.1822

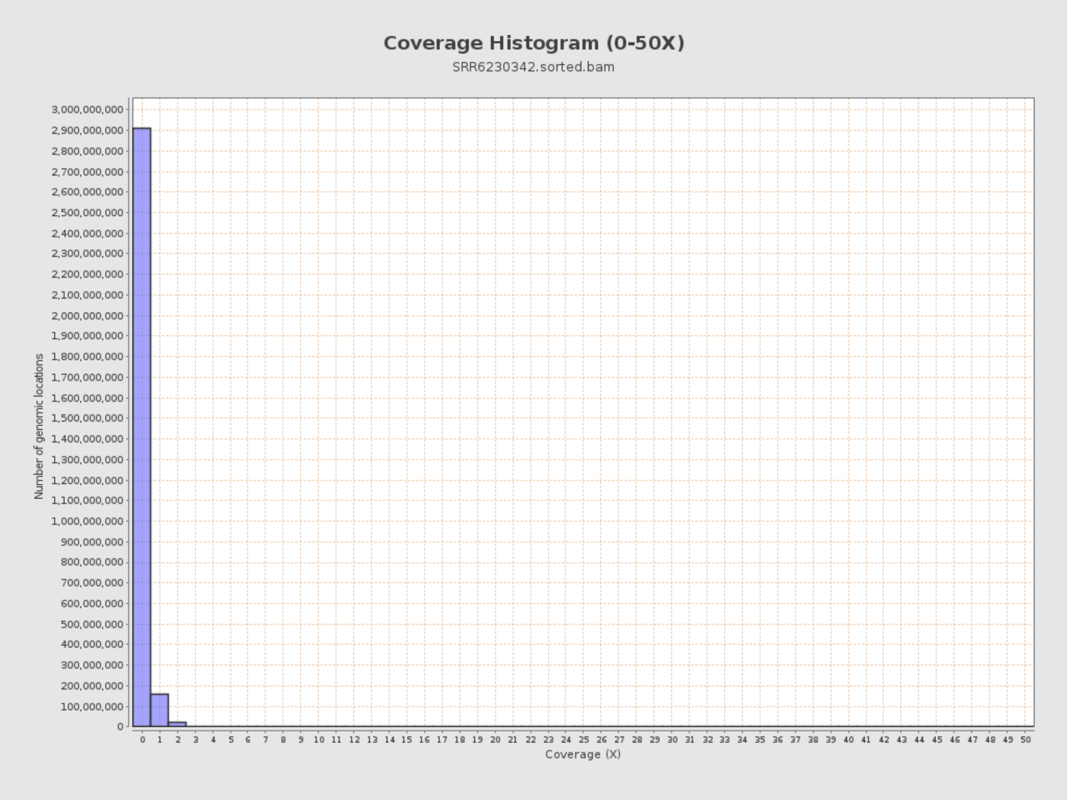
3. Results : Coverage across reference



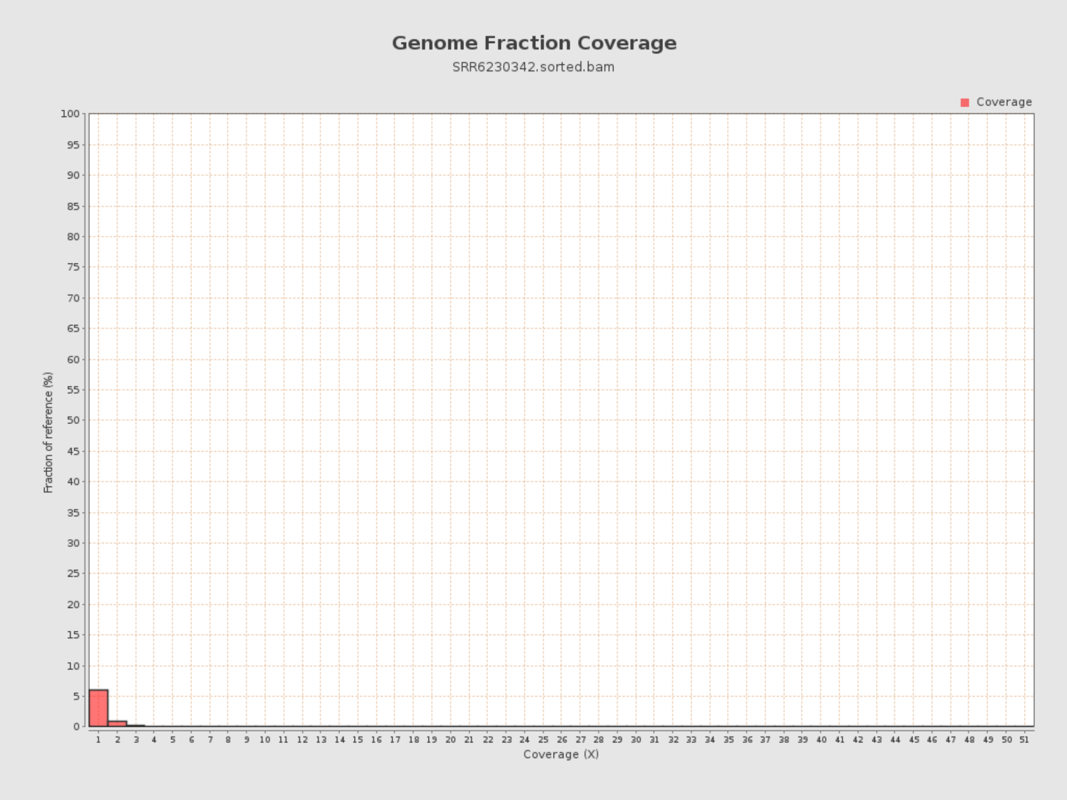
4. Results : Coverage Histogram



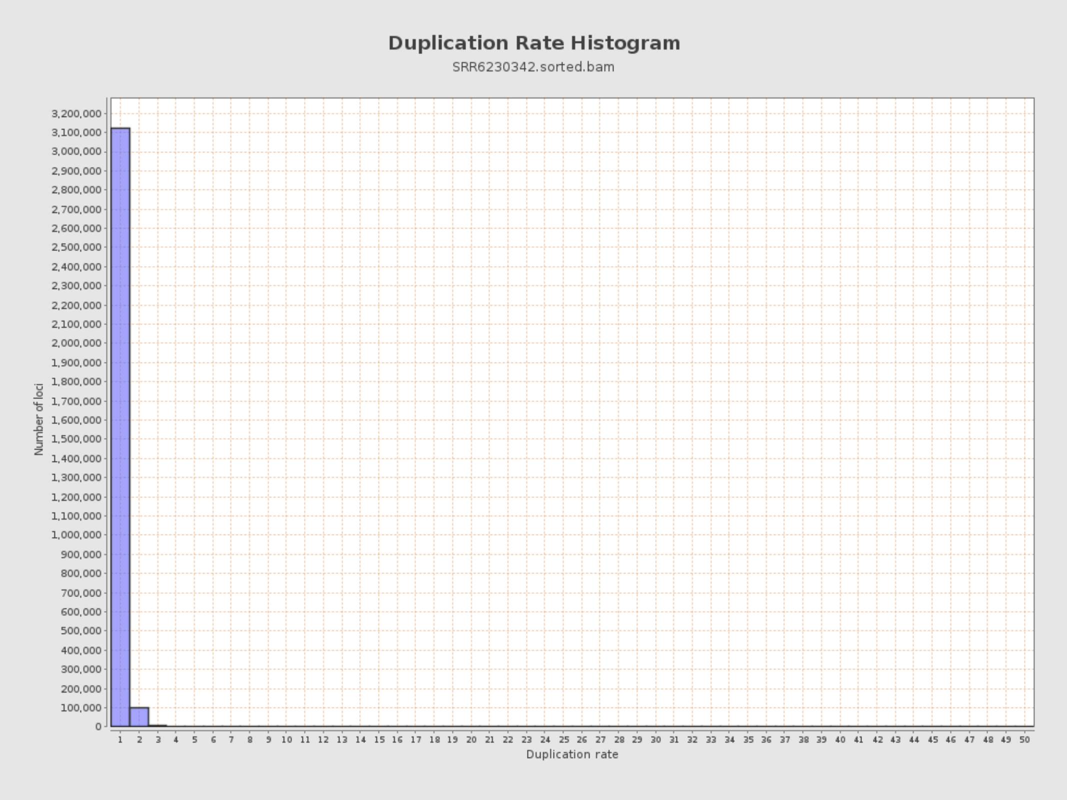
5. Results : Coverage Histogram (0-50X)



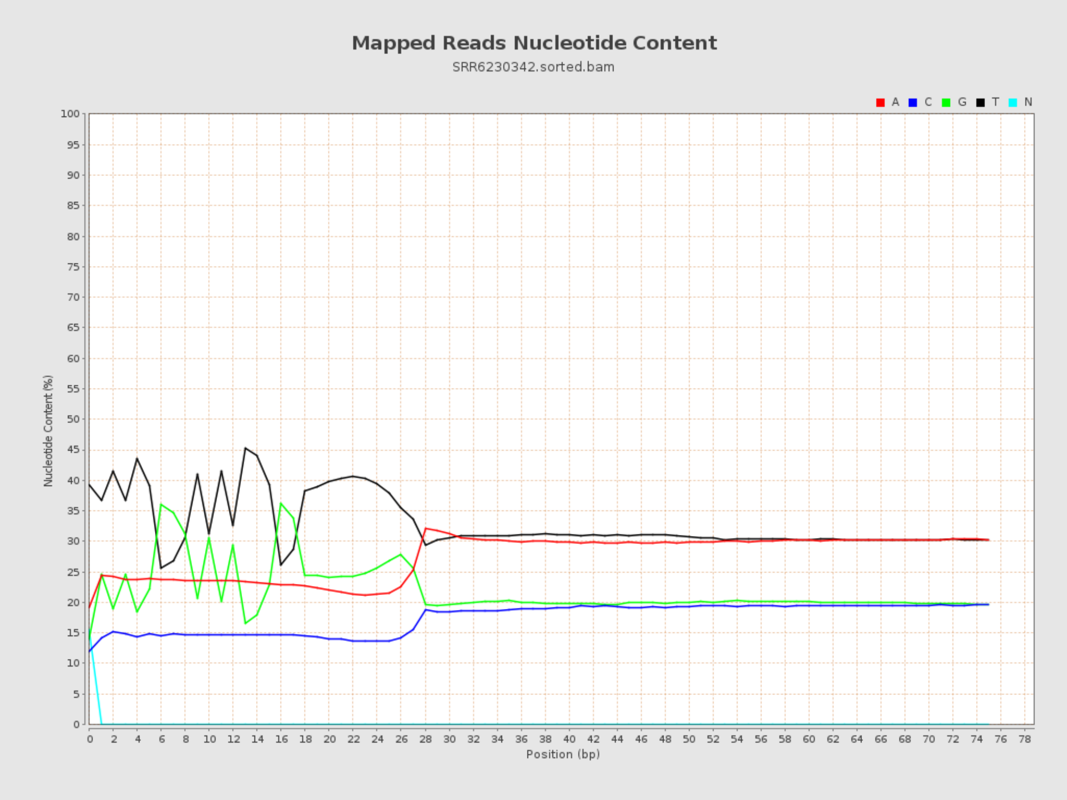
6. Results : Genome Fraction Coverage



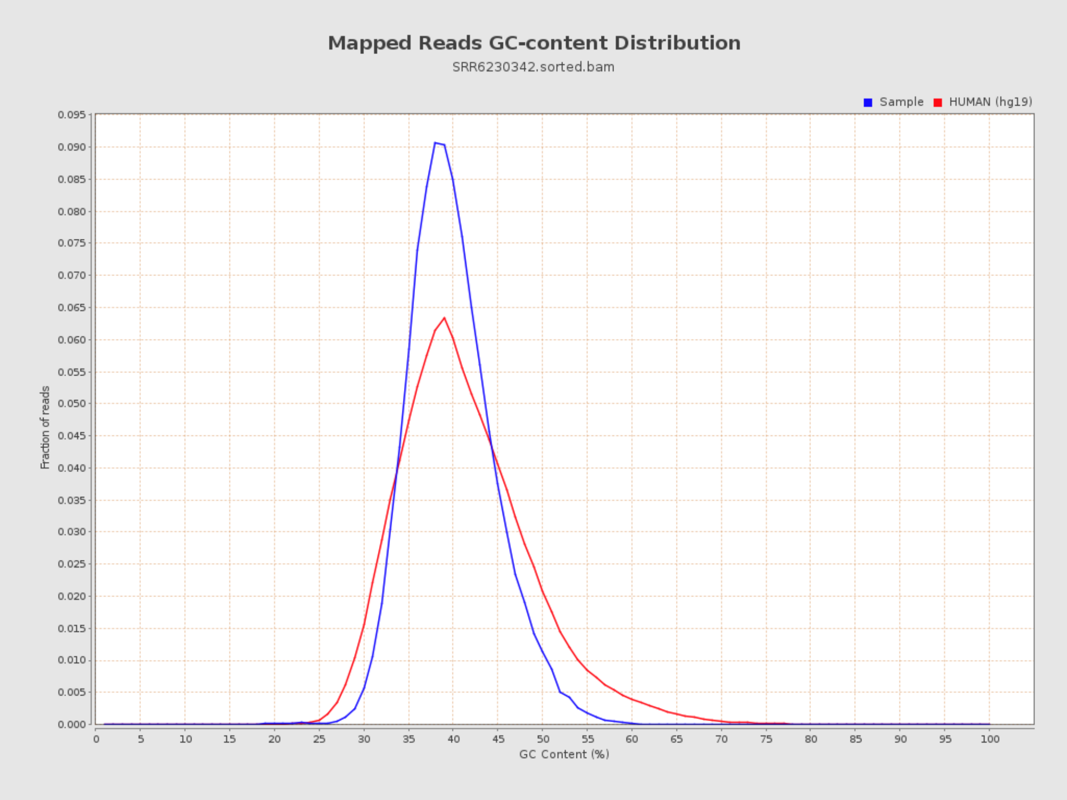
7. Results : Duplication Rate Histogram



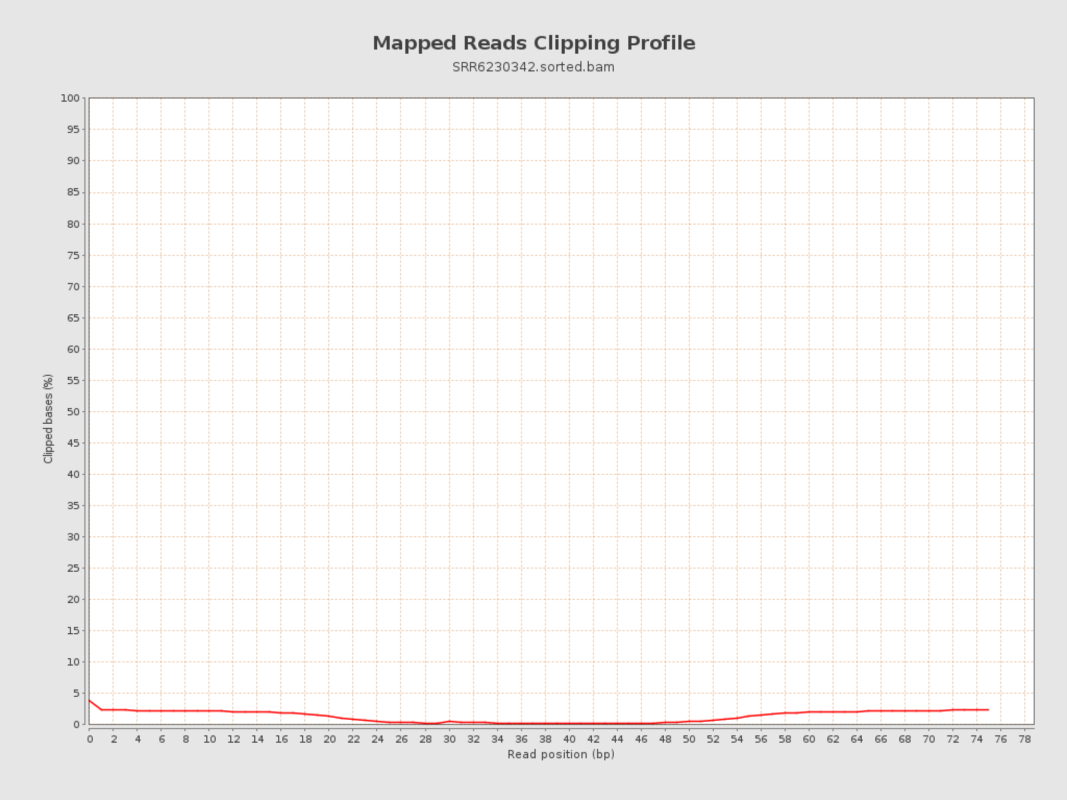
8. Results : Mapped Reads Nucleotide Content



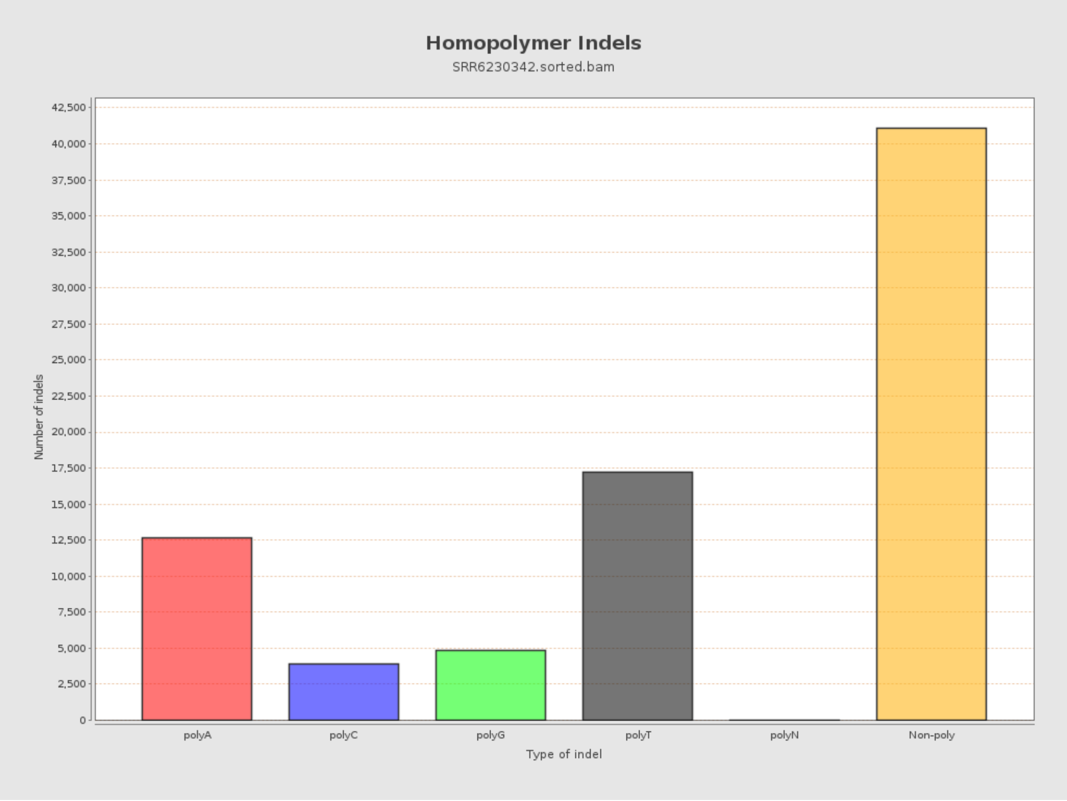
9. Results : Mapped Reads GC-content Distribution



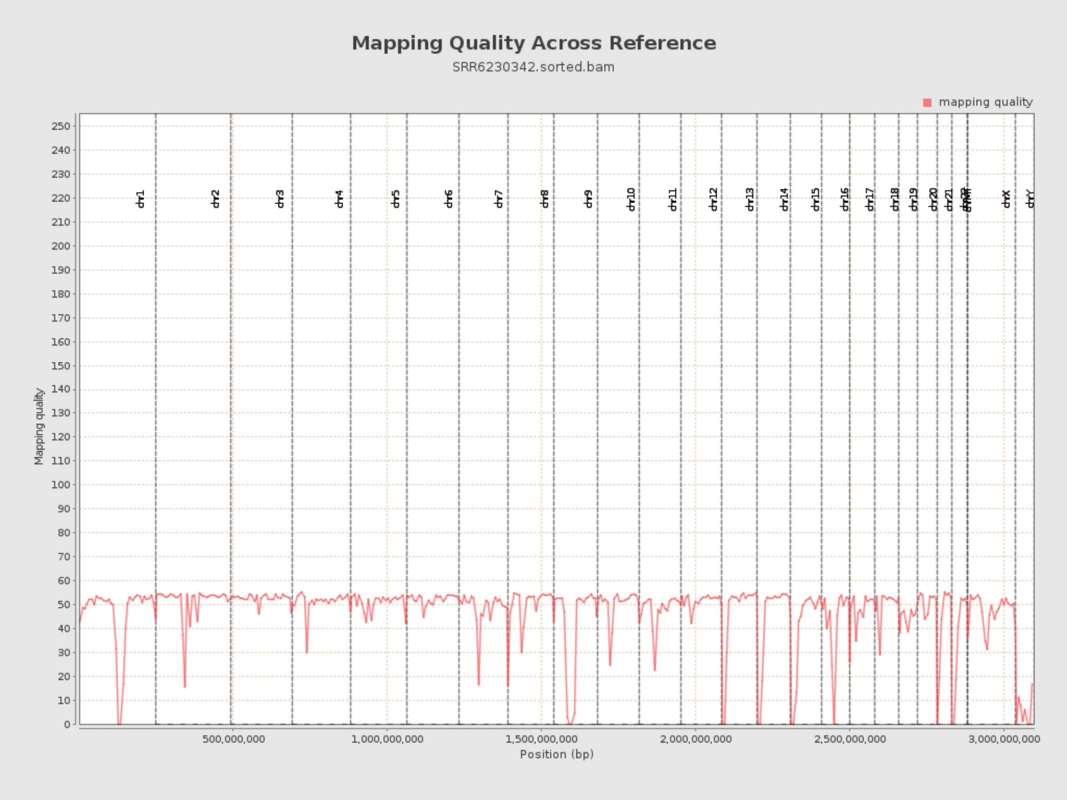
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram