Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:57:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230352.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_SRR6230352 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230352.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:57:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230352.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,242,934
Mapped reads	1,836,907 / 81.9%
Unmapped reads	406,027 / 18.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,981 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	81,353 / 3.63%
Duplication rate	3.5%
Clipped reads	897,981 / 40.04%

2.2. ACGT Content

Number/percentage of A's	32,500,615 / 27.06%
Number/percentage of C's	20,600,741 / 17.15%
Number/percentage of T's	40,146,891 / 33.43%
Number/percentage of G's	26,634,758 / 22.18%
Number/percentage of N's	225,049 / 0.19%
GC Percentage	39.33%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.3519

2.4. Mapping Quality

Mean Mapping Quality	47.17

2.5. Mismatches and indels

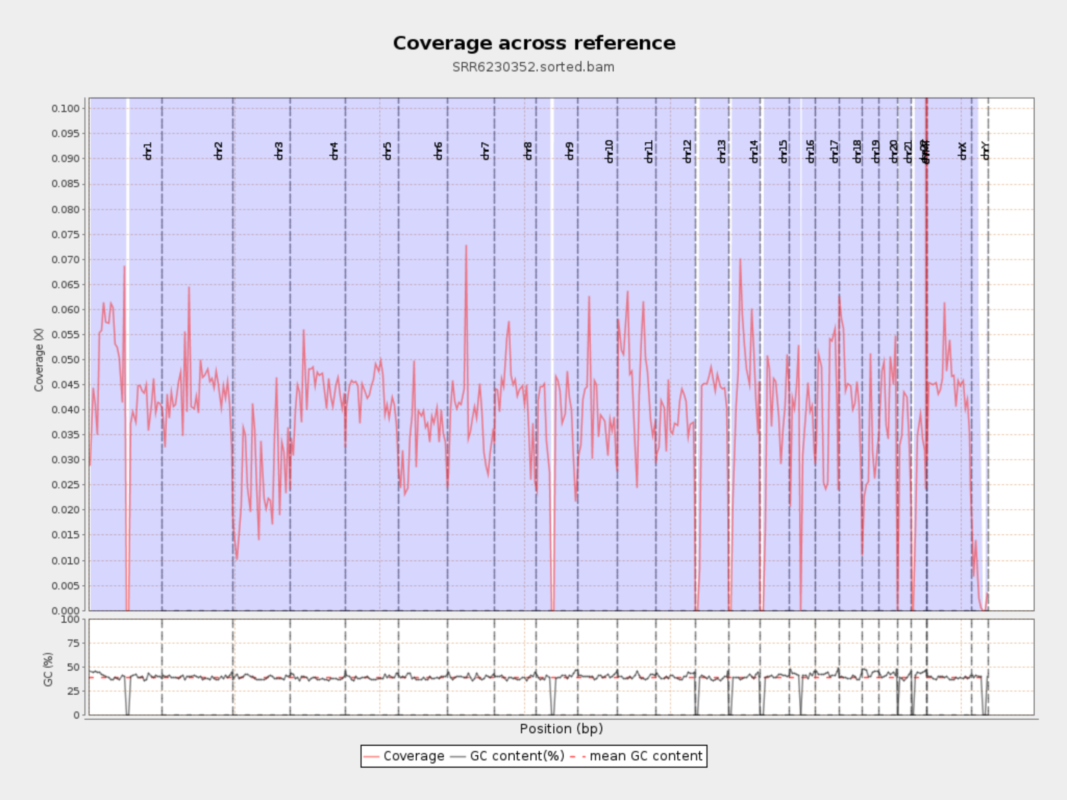
General error rate	0.95%
Mismatches	1,117,585
Insertions	10,453
Mapped reads with at least one insertion	0.56%
Deletions	32,275
Mapped reads with at least one deletion	1.74%
Homopolymer indels	48.08%

2.6. Chromosome stats

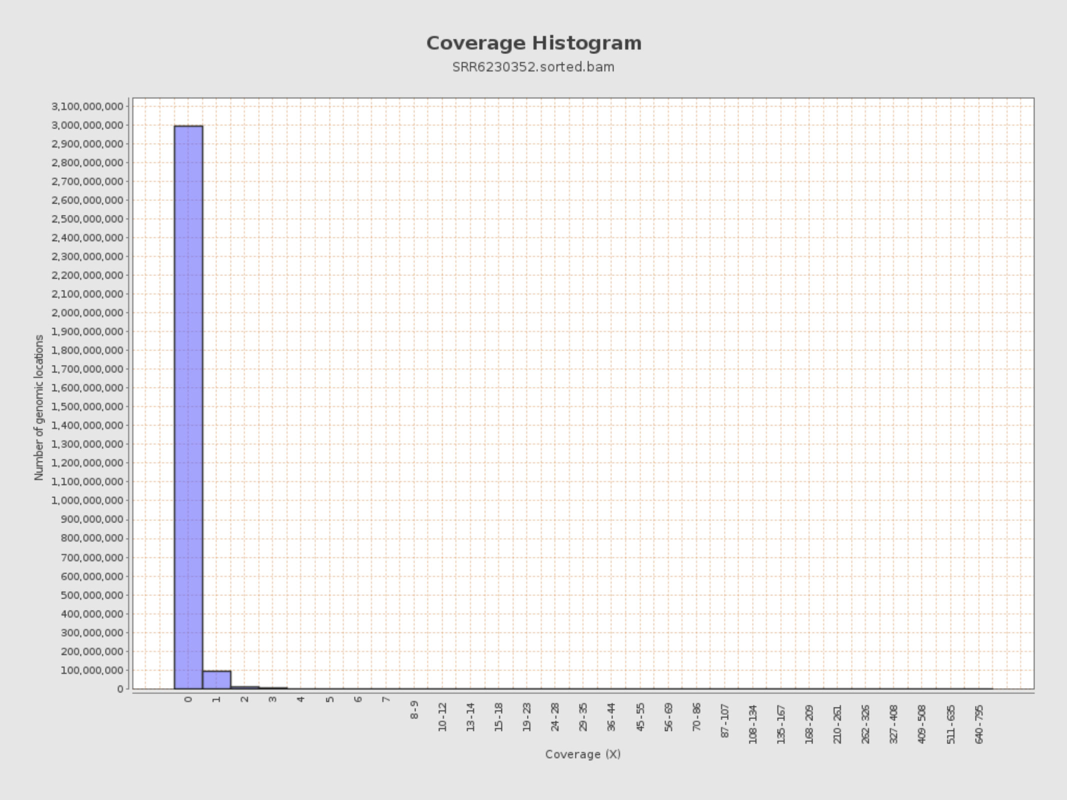
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10948110	0.0439	0.6109
chr2	243199373	10645268	0.0438	0.3582
chr3	198022430	5173431	0.0261	0.1821
chr4	191154276	8348210	0.0437	0.247
chr5	180915260	7851455	0.0434	0.235
chr6	171115067	5964184	0.0349	0.2746
chr7	159138663	6271170	0.0394	0.4896

chr8	146364022	6264376	0.0428	0.5425
chr9	141213431	4943624	0.035	0.3556
chr10	135534747	5315874	0.0392	0.3122
chr11	135006516	6292405	0.0466	0.3444
chr12	133851895	5085435	0.038	0.2244
chr13	115169878	4303702	0.0374	0.2175
chr14	107349540	4498173	0.0419	0.2447
chr15	102531392	3527397	0.0344	0.2093
chr16	90354753	3270679	0.0362	0.2439
chr17	81195210	3273976	0.0403	0.252
chr18	78077248	3572790	0.0458	0.5863
chr19	59128983	1777455	0.0301	0.4007
chr20	63025520	2762695	0.0438	0.245
chr21	48129895	1558996	0.0324	0.2214
chr22	51304566	1252623	0.0244	0.1744
chrMT	16571	42744	2.5794	2.1375
chrX	155270560	6933516	0.0447	0.2667
chrY	59373566	282306	0.0048	0.112

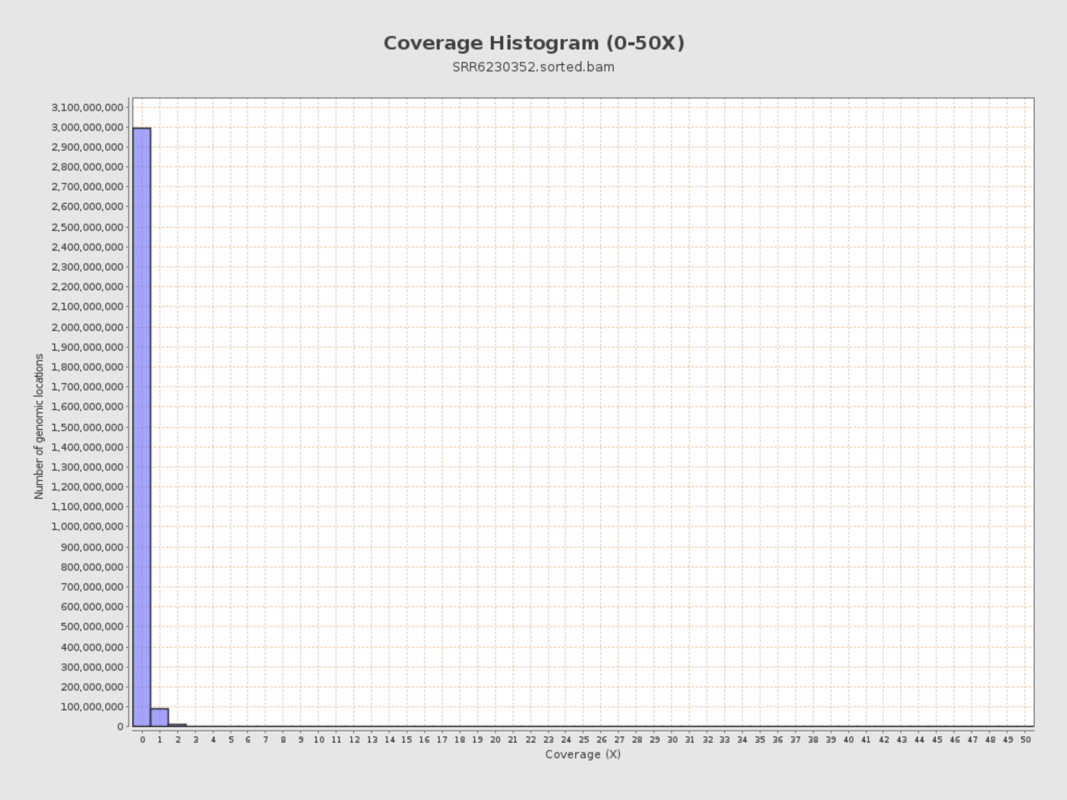
3. Results : Coverage across reference



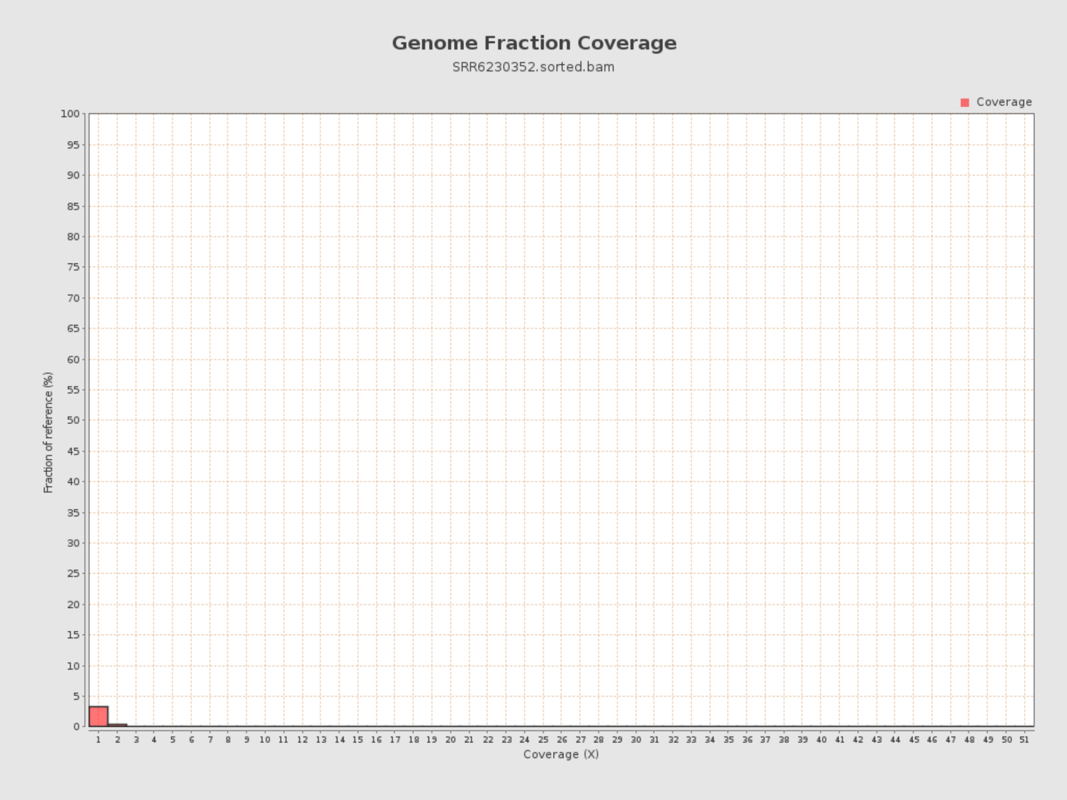
4. Results : Coverage Histogram



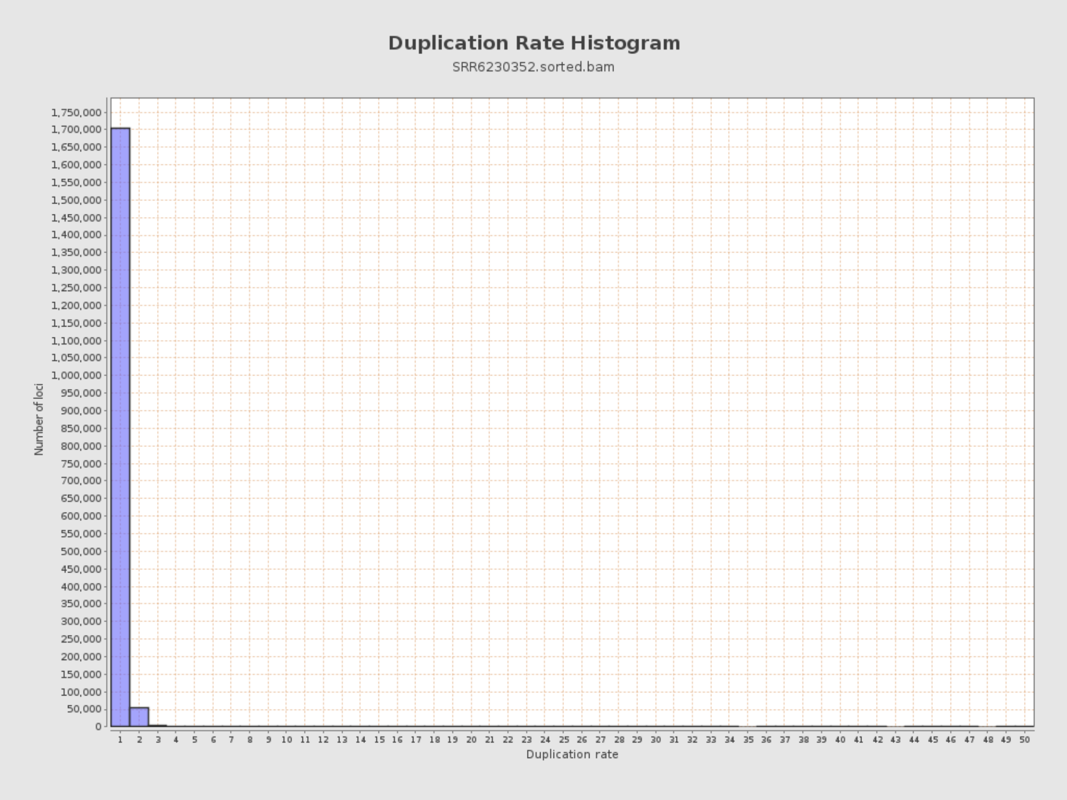
5. Results : Coverage Histogram (0-50X)



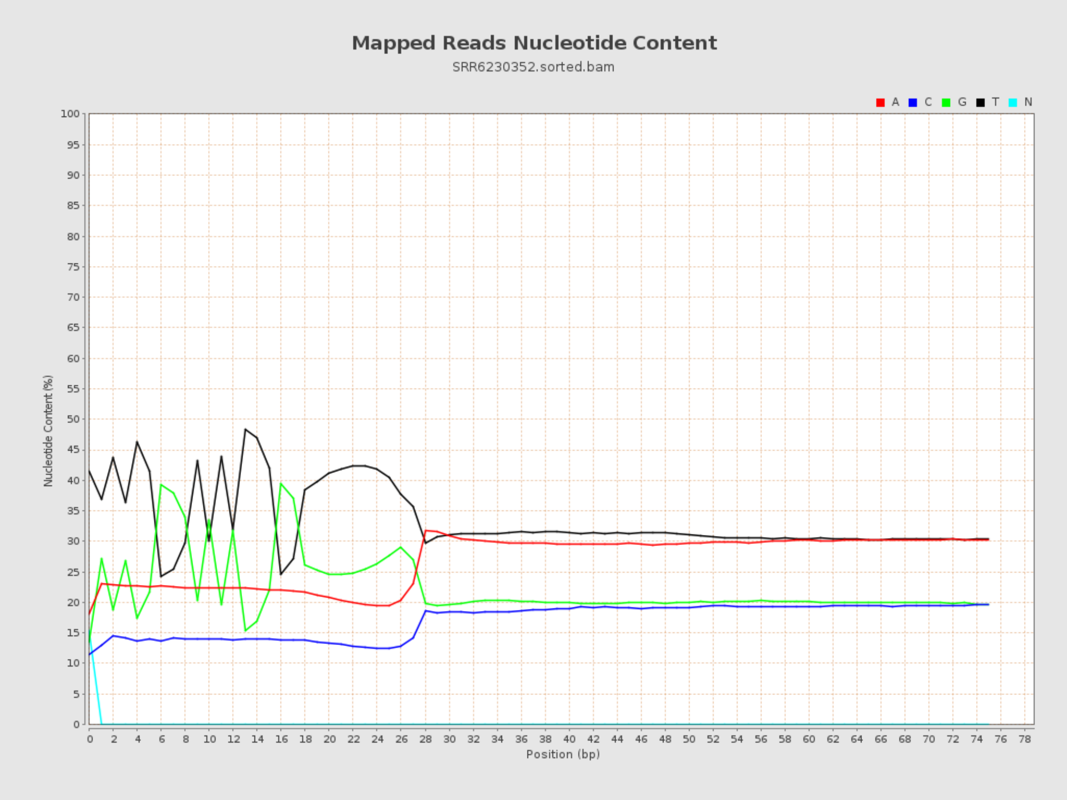
6. Results : Genome Fraction Coverage



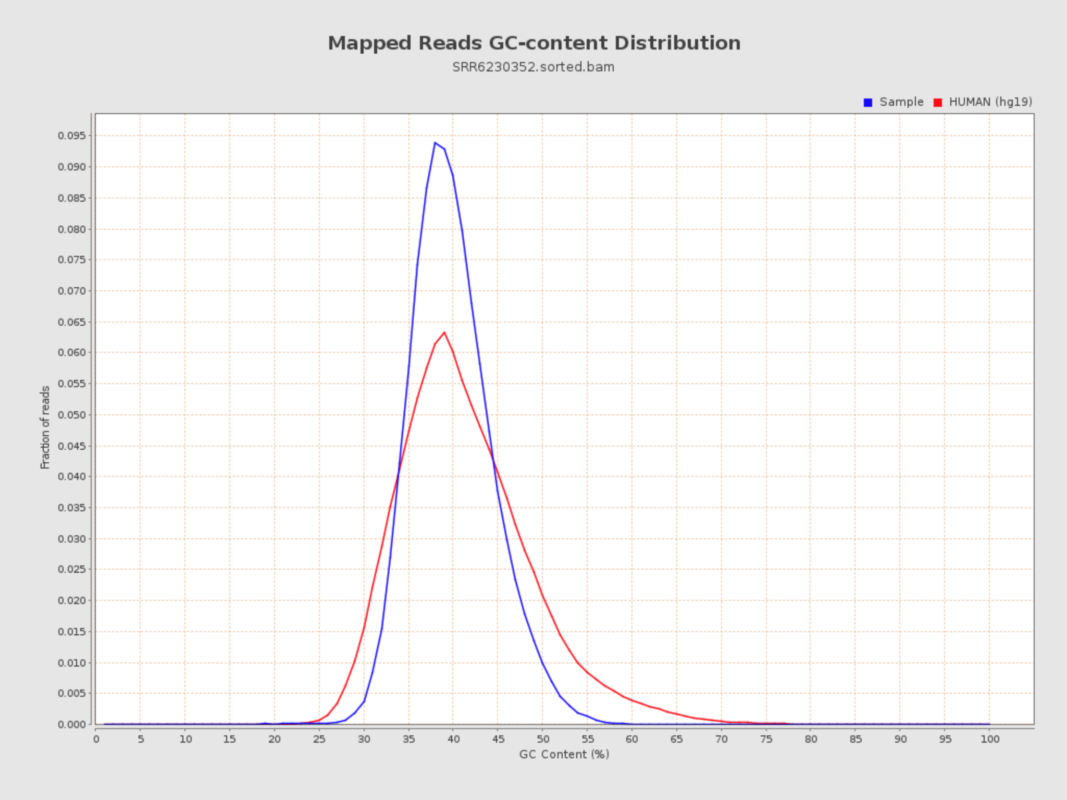
7. Results : Duplication Rate Histogram



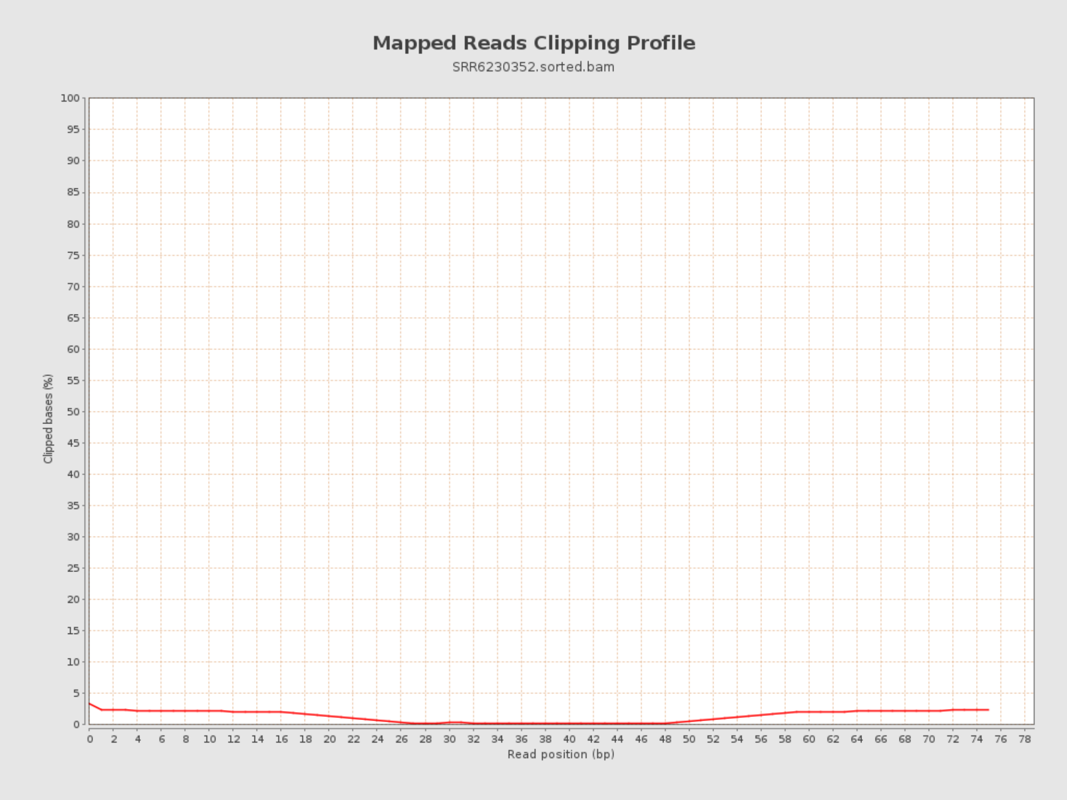
8. Results : Mapped Reads Nucleotide Content



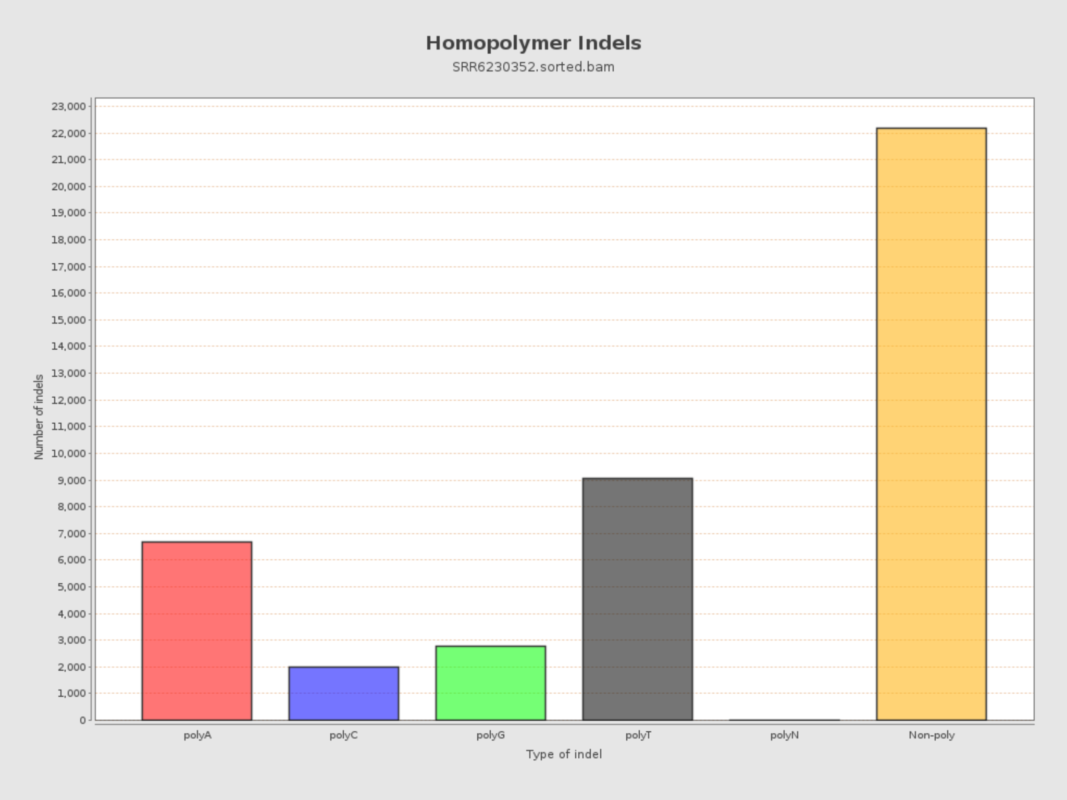
9. Results : Mapped Reads GC-content Distribution



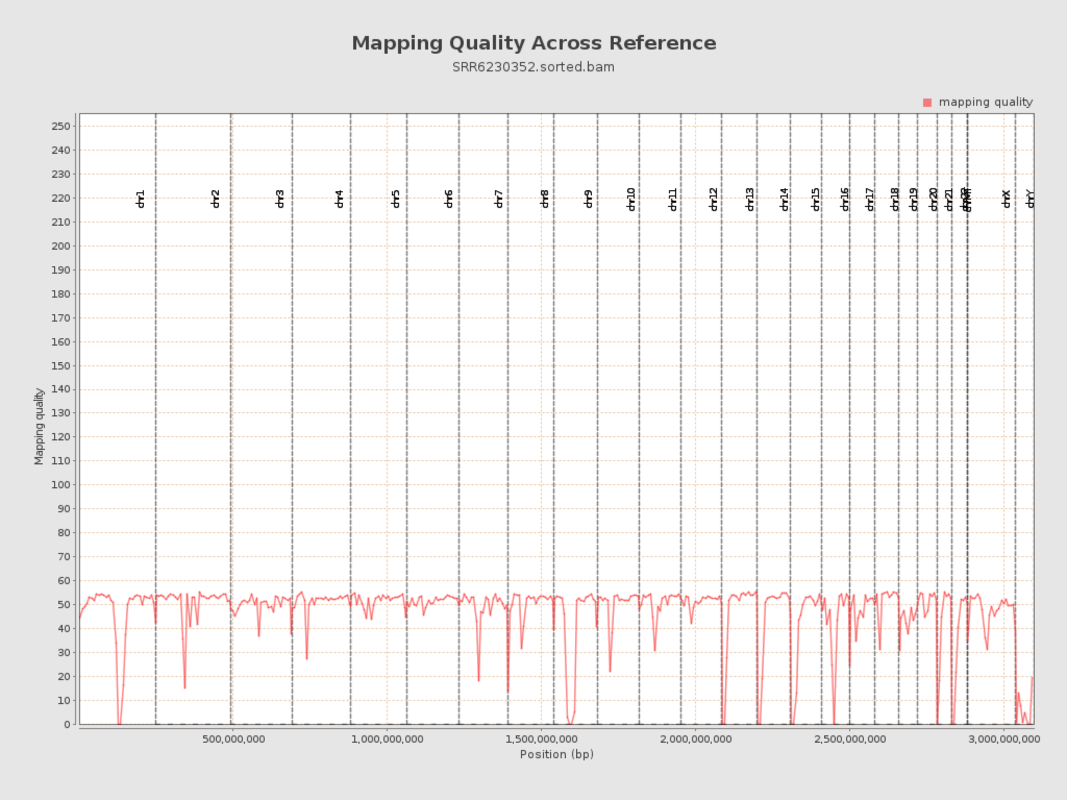
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram