Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:58:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230335.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_SRR6230335 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230335.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:58:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230335.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,794,752
Mapped reads	2,162,415 / 77.37%
Unmapped reads	632,337 / 22.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,149 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	155,758 / 5.57%
Duplication rate	5.91%
Clipped reads	1,076,619 / 38.52%

2.2. ACGT Content

Number/percentage of A's	38,863,256 / 27.51%
Number/percentage of C's	24,104,455 / 17.06%
Number/percentage of T's	48,076,593 / 34.03%
Number/percentage of G's	29,971,886 / 21.21%
Number/percentage of N's	264,262 / 0.19%
GC Percentage	38.28%

2.3. Coverage

Mean	0.0457

Standard Deviation	0.409

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

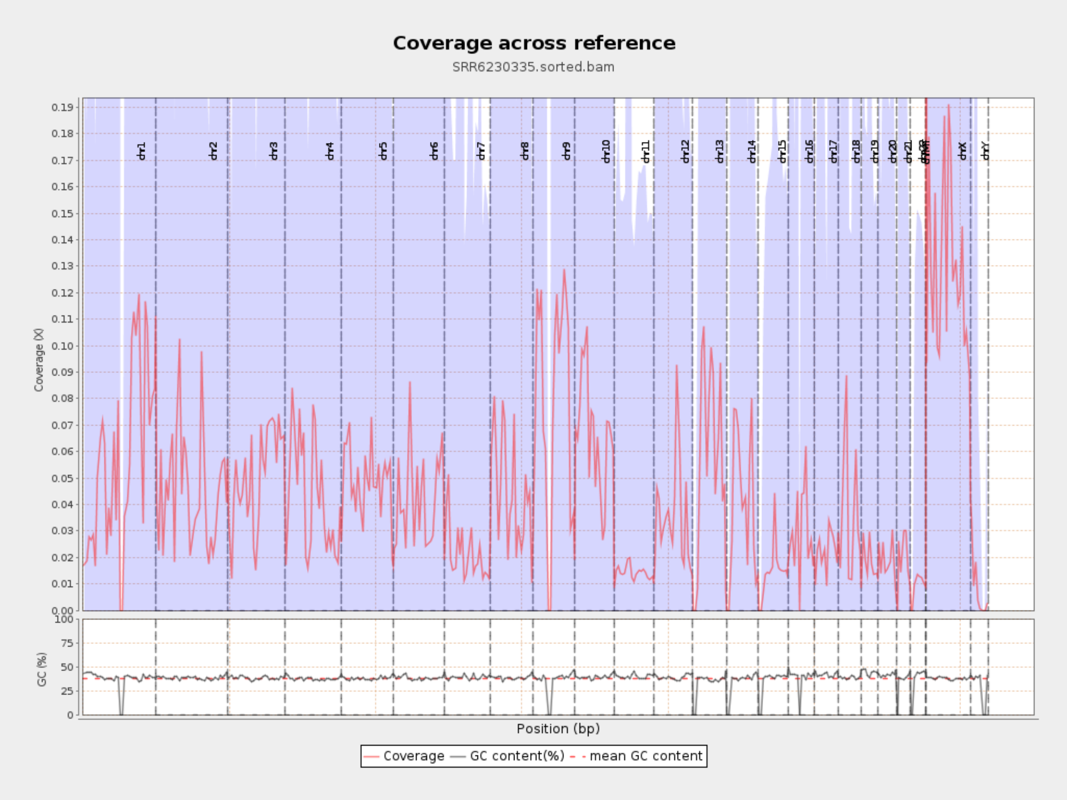
General error rate	1.14%
Mismatches	1,588,360
Insertions	12,638
Mapped reads with at least one insertion	0.58%
Deletions	37,047
Mapped reads with at least one deletion	1.69%
Homopolymer indels	48.67%

2.6. Chromosome stats

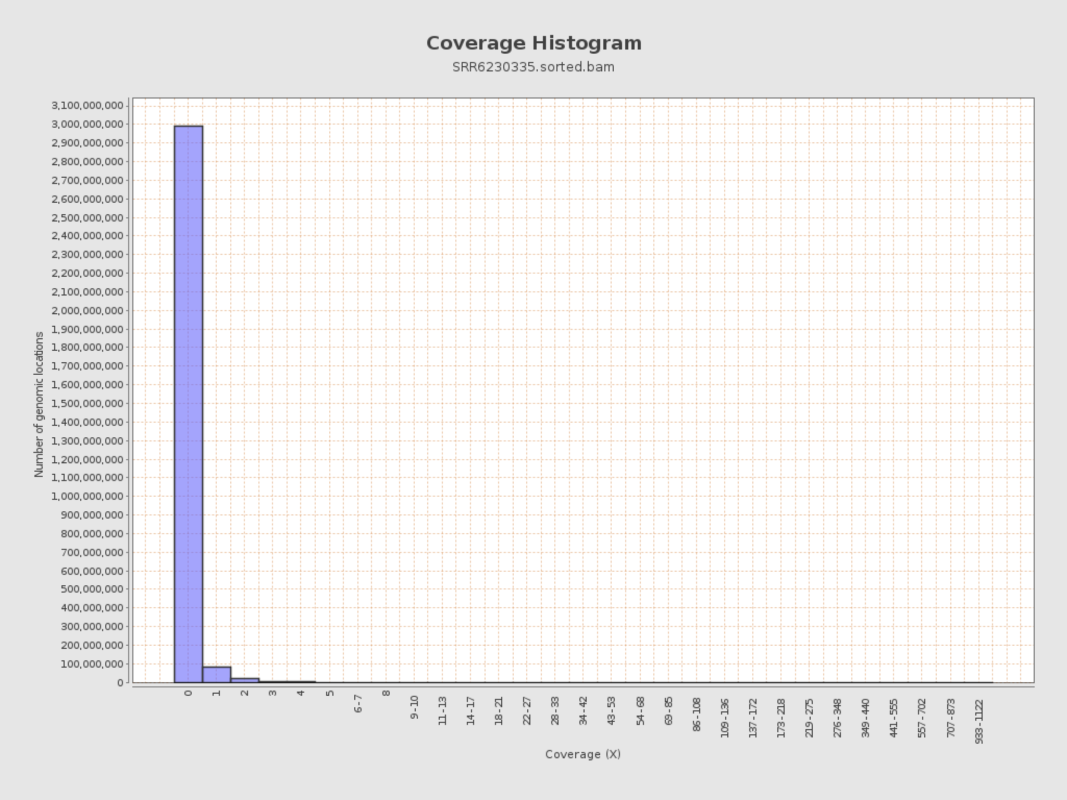
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14019234	0.0562	0.6636
chr2	243199373	10986178	0.0452	0.3918
chr3	198022430	10106729	0.051	0.2864
chr4	191154276	8344288	0.0437	0.2945
chr5	180915260	8782133	0.0485	0.2795
chr6	171115067	7327499	0.0428	0.3837
chr7	159138663	3423822	0.0215	0.2325

chr8	146364022	6535874	0.0447	0.7478
chr9	141213431	11416804	0.0808	0.483
chr10	135534747	9013202	0.0665	0.4429
chr11	135006516	1942713	0.0144	0.1919
chr12	133851895	4762018	0.0356	0.2512
chr13	115169878	6813041	0.0592	0.3119
chr14	107349540	4414873	0.0411	0.2896
chr15	102531392	1508737	0.0147	0.1509
chr16	90354753	2650856	0.0293	0.242
chr17	81195210	1832775	0.0226	0.2104
chr18	78077248	3057194	0.0392	0.6333
chr19	59128983	1106916	0.0187	0.4498
chr20	63025520	1209218	0.0192	0.1905
chr21	48129895	944990	0.0196	0.2319
chr22	51304566	474616	0.0093	0.1154
chrMT	16571	156310	9.4327	5.7741
chrX	155270560	20059562	0.1292	0.5635
chrY	59373566	451345	0.0076	0.1659

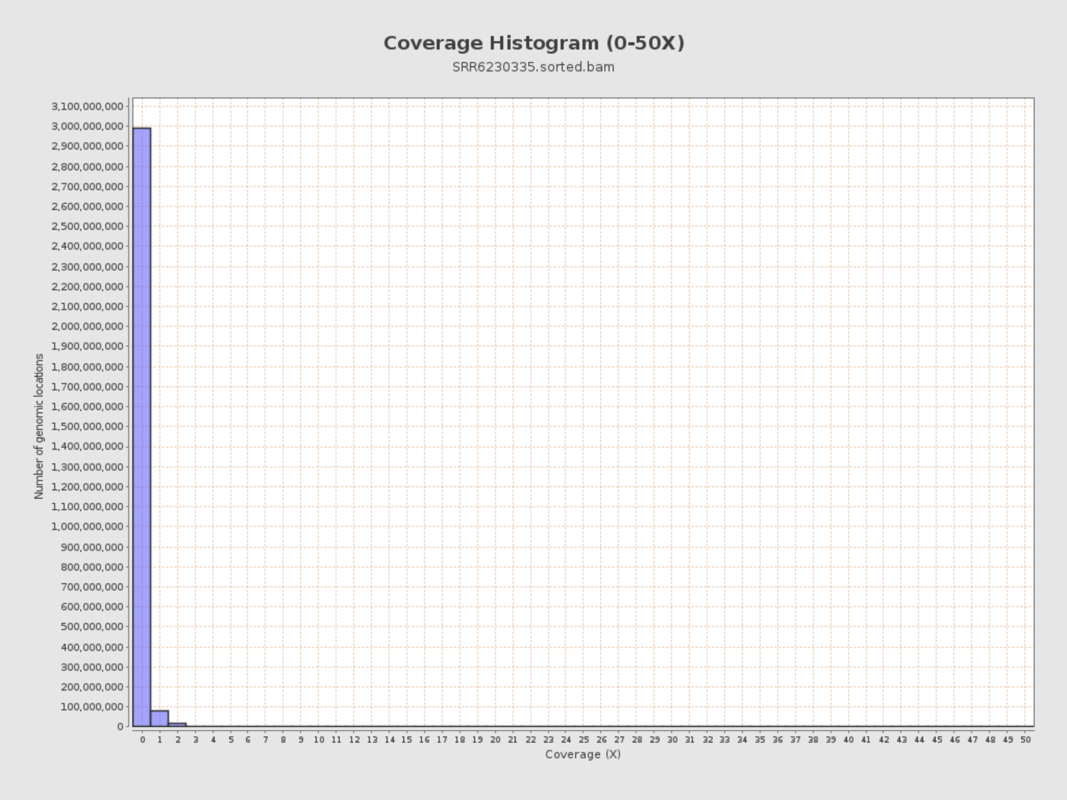
3. Results : Coverage across reference



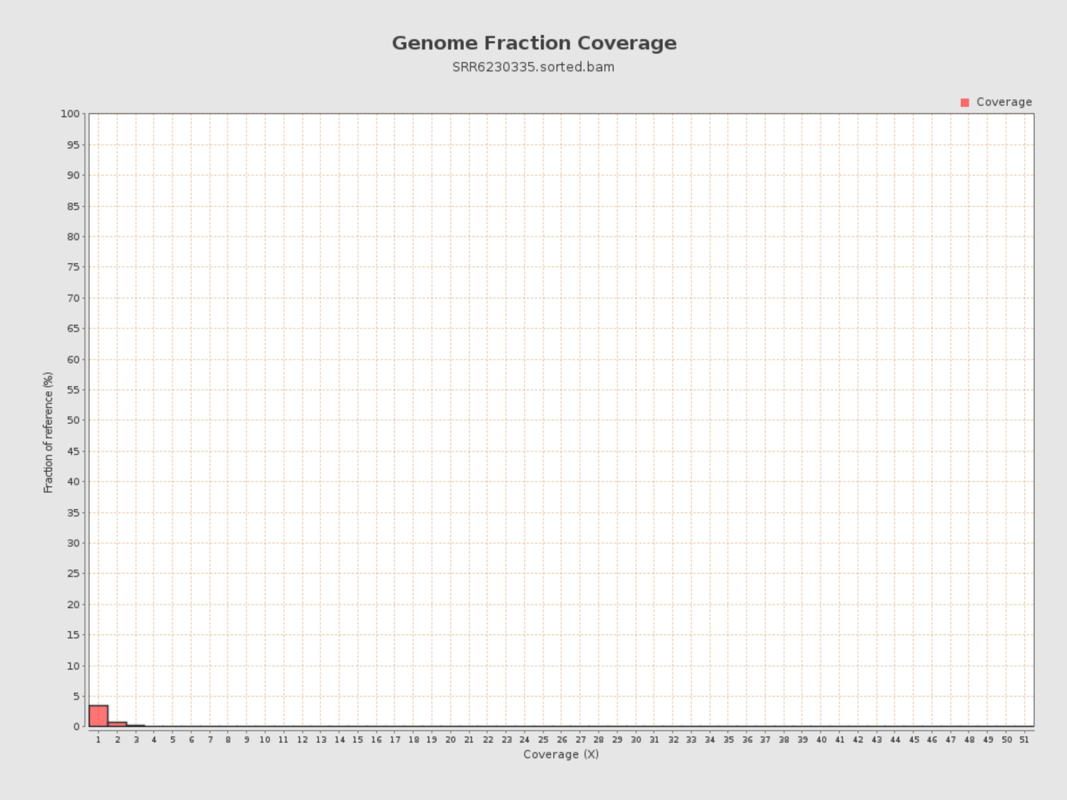
4. Results : Coverage Histogram



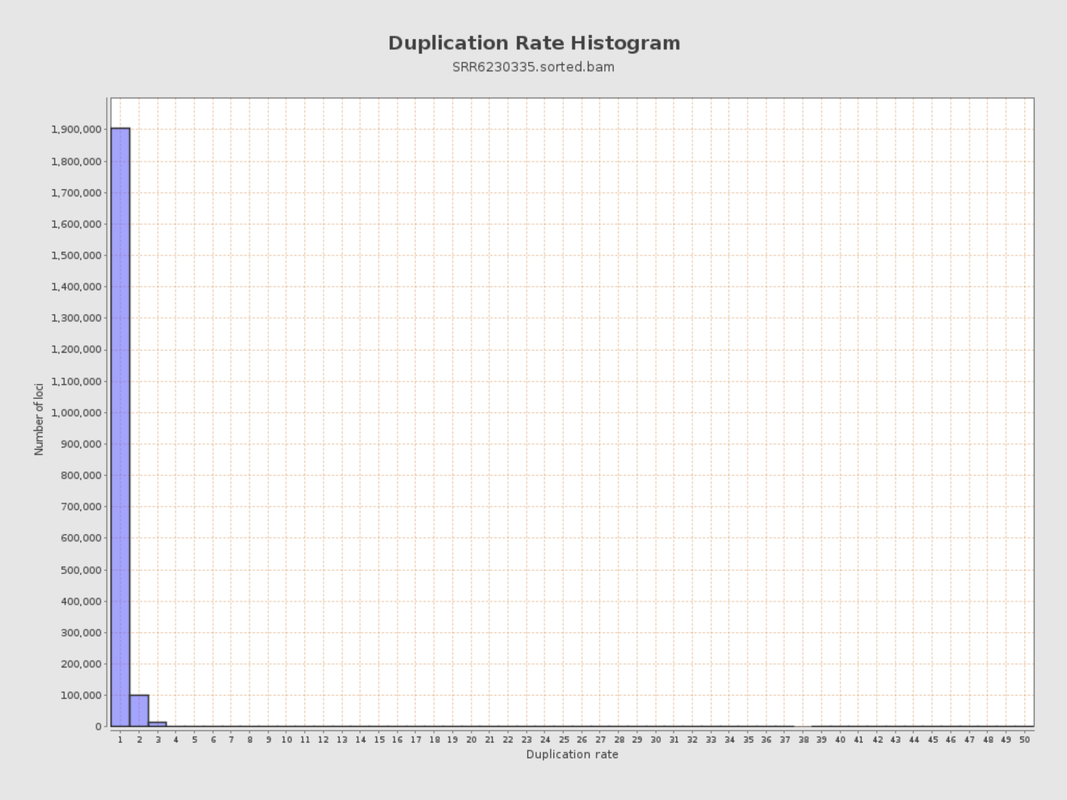
5. Results : Coverage Histogram (0-50X)



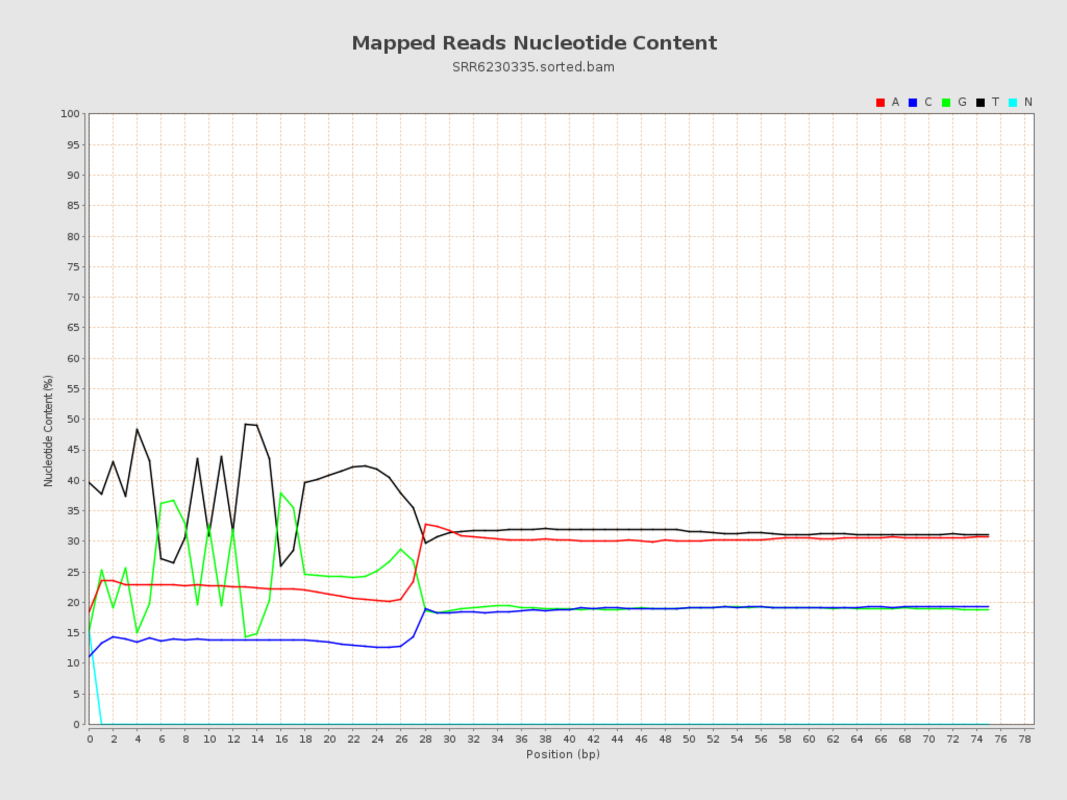
6. Results : Genome Fraction Coverage



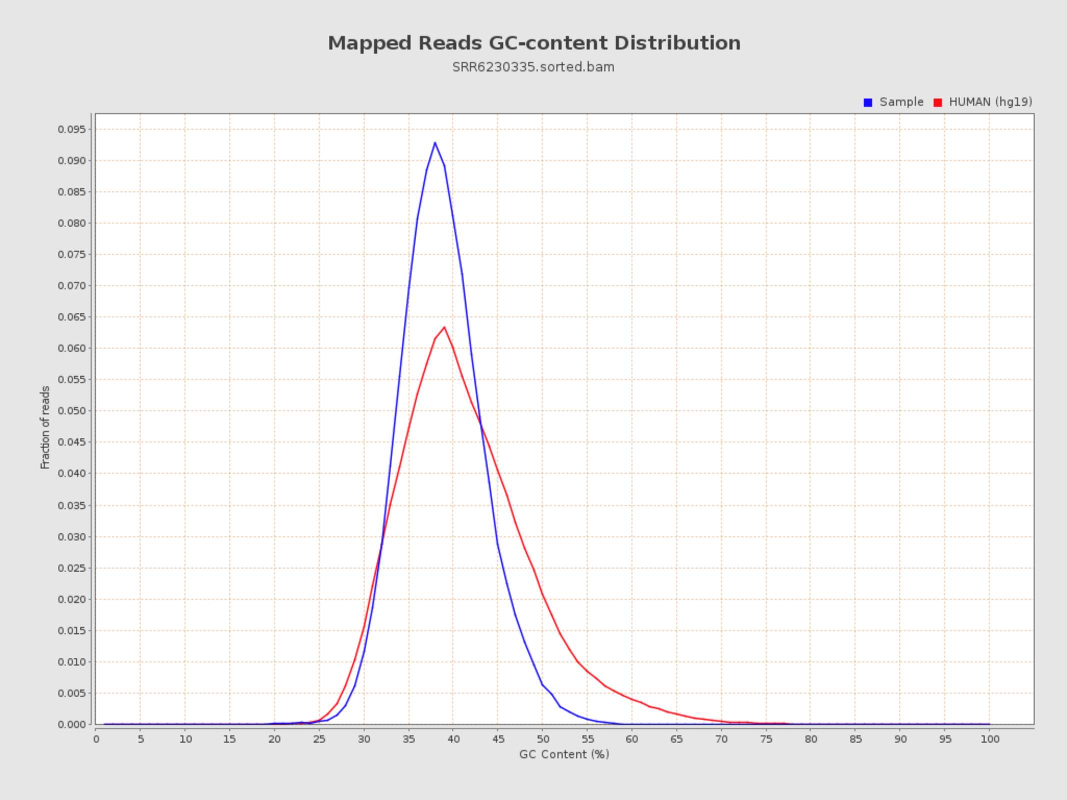
7. Results : Duplication Rate Histogram



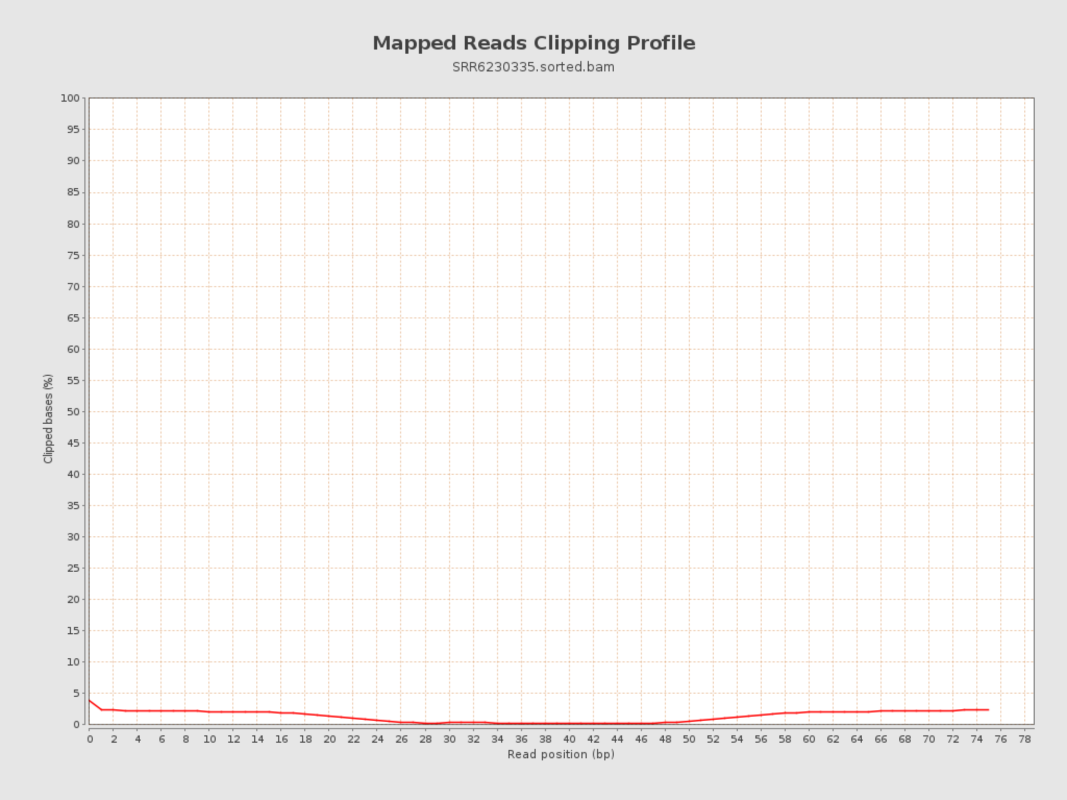
8. Results : Mapped Reads Nucleotide Content



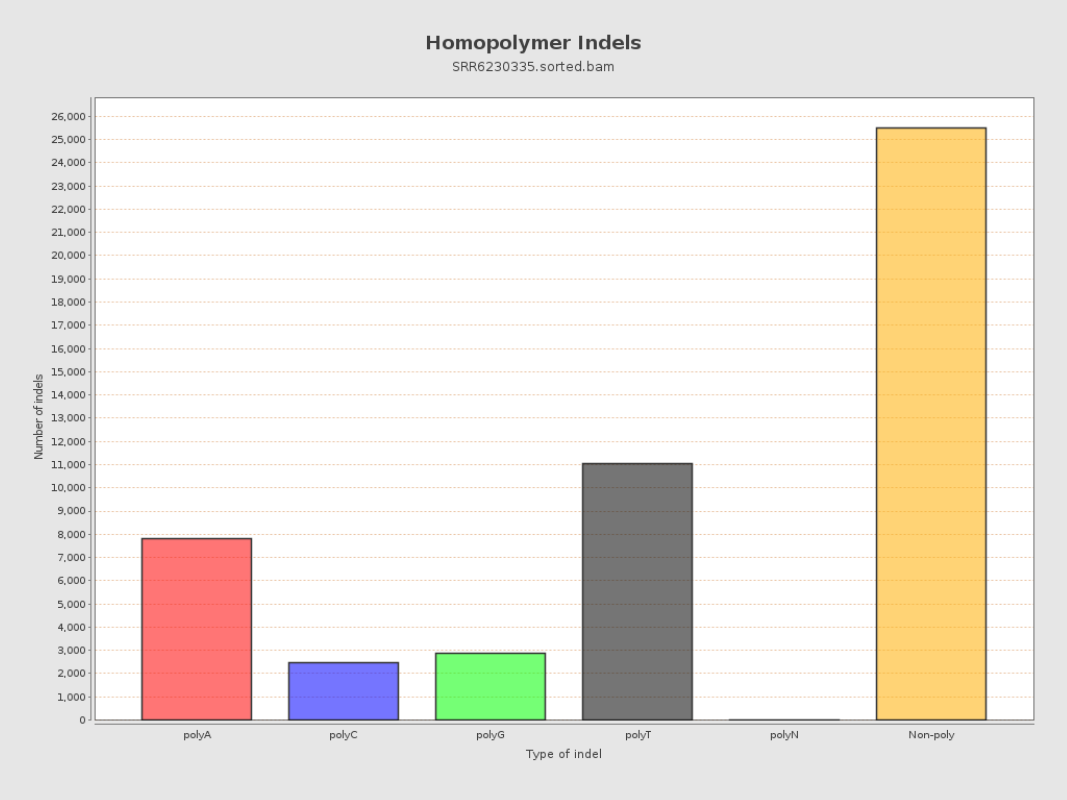
9. Results : Mapped Reads GC-content Distribution



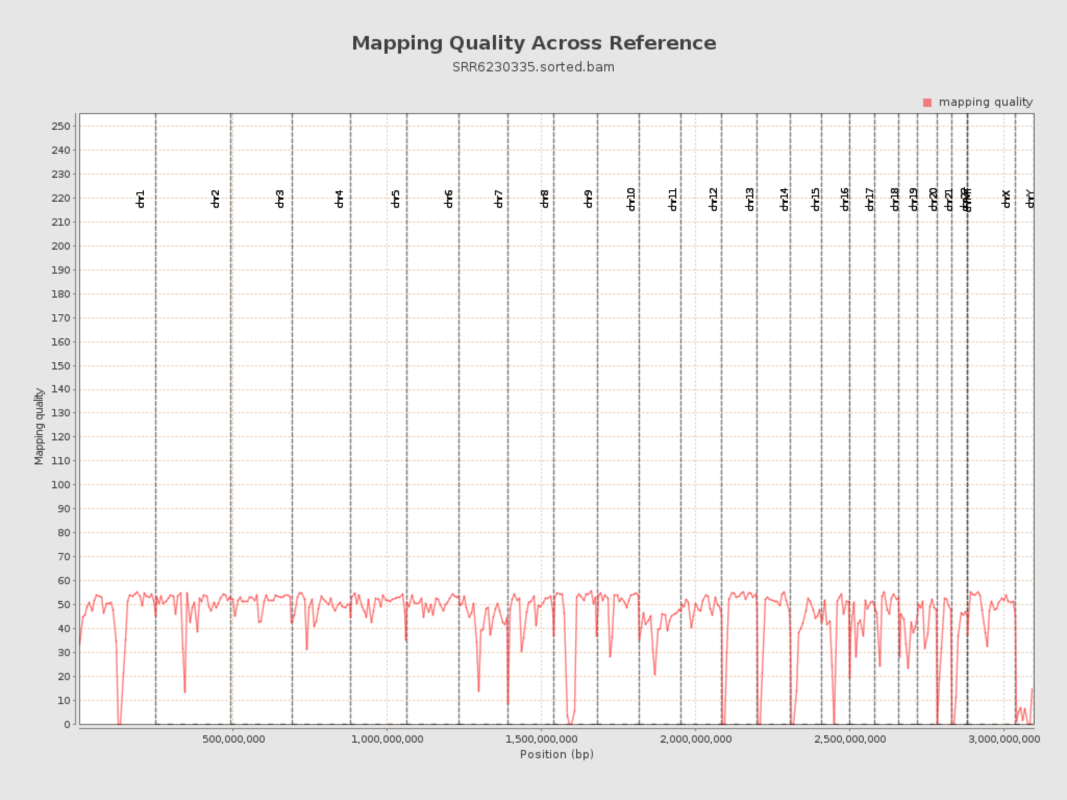
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram