Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:49:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230384.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_SRR6230384 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230384.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:49:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230384.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,484,811
Mapped reads	2,124,706 / 85.51%
Unmapped reads	360,105 / 14.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,386 / 1.34%
Read min/max/mean length	30 / 76 / 76.47
Duplicated reads (estimated)	292,905 / 11.79%
Duplication rate	10.29%
Clipped reads	1,138,509 / 45.82%

2.2. ACGT Content

Number/percentage of A's	38,420,893 / 27.68%
Number/percentage of C's	25,646,816 / 18.48%
Number/percentage of T's	43,754,970 / 31.52%
Number/percentage of G's	30,966,428 / 22.31%
Number/percentage of N's	26,511 / 0.02%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0449

Standard Deviation	0.4921

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

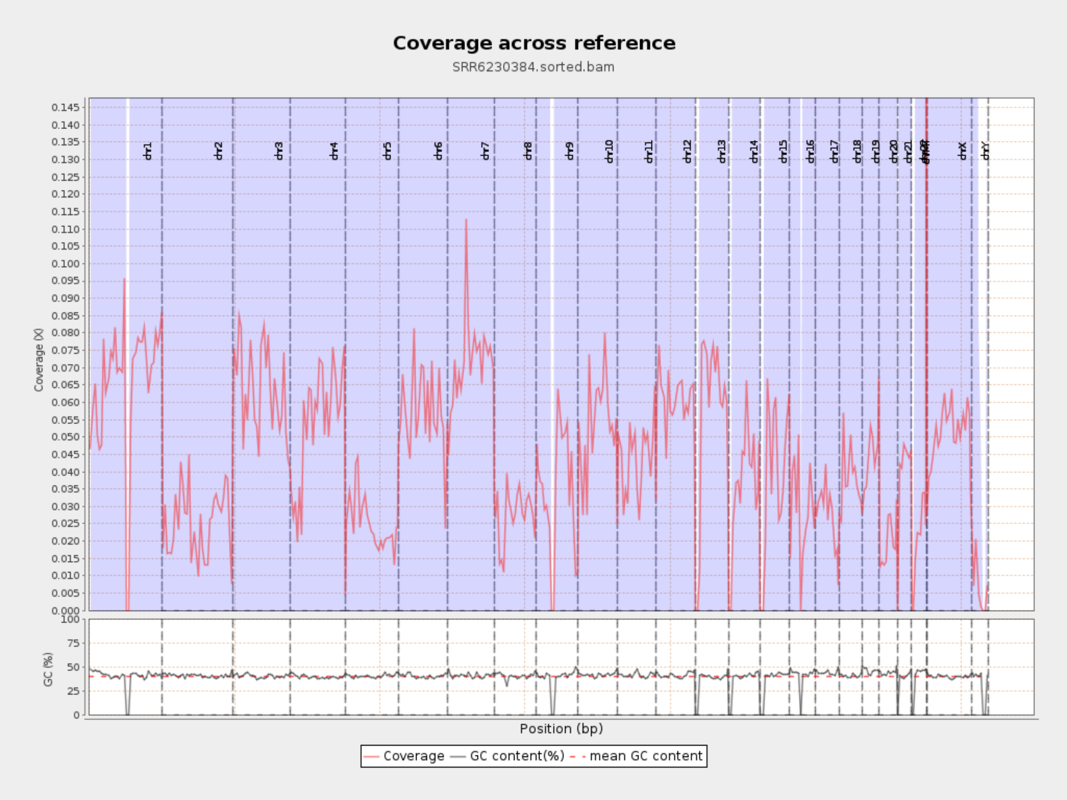
General error rate	0.89%
Mismatches	1,208,710
Insertions	12,078
Mapped reads with at least one insertion	0.56%
Deletions	35,363
Mapped reads with at least one deletion	1.65%
Homopolymer indels	46.74%

2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16301881	0.0654	0.8074
chr2	243199373	6194540	0.0255	0.4585
chr3	198022430	12623936	0.0638	0.4117
chr4	191154276	10301886	0.0539	0.3963
chr5	180915260	4534529	0.0251	0.2557
chr6	171115067	9798536	0.0573	0.4409
chr7	159138663	11511421	0.0723	0.7188

chr8	146364022	4024278	0.0275	0.8471
chr9	141213431	4906216	0.0347	0.3621
chr10	135534747	7318183	0.054	0.465
chr11	135006516	5862556	0.0434	0.3983
chr12	133851895	8186067	0.0612	0.4031
chr13	115169878	6545858	0.0568	0.3881
chr14	107349540	3797493	0.0354	0.3218
chr15	102531392	3939215	0.0384	0.3178
chr16	90354753	2638211	0.0292	0.3081
chr17	81195210	2250521	0.0277	0.2822
chr18	78077248	3000182	0.0384	0.7286
chr19	59128983	2600001	0.044	0.5062
chr20	63025520	1198061	0.019	0.2693
chr21	48129895	1934565	0.0402	0.34
chr22	51304566	1034970	0.0202	0.2237
chrMT	16571	9825	0.5929	1.1114
chrX	155270560	7961739	0.0513	0.3896
chrY	59373566	399351	0.0067	0.1627

3. Results : Coverage across reference



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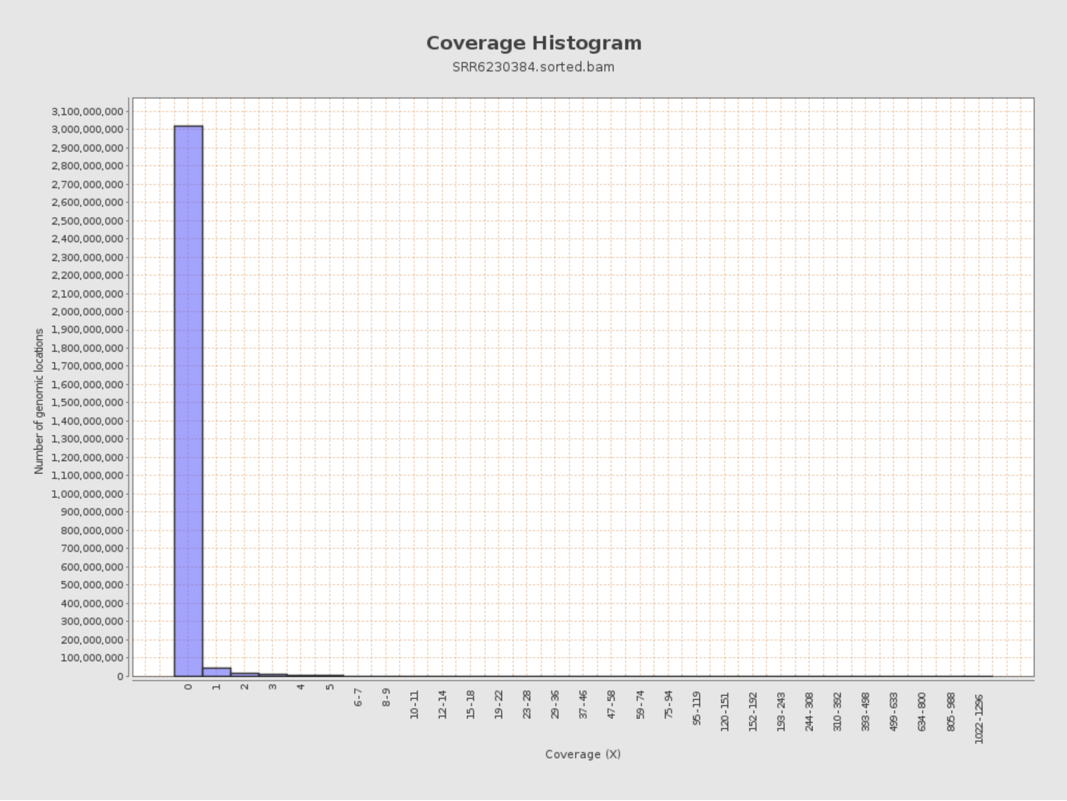
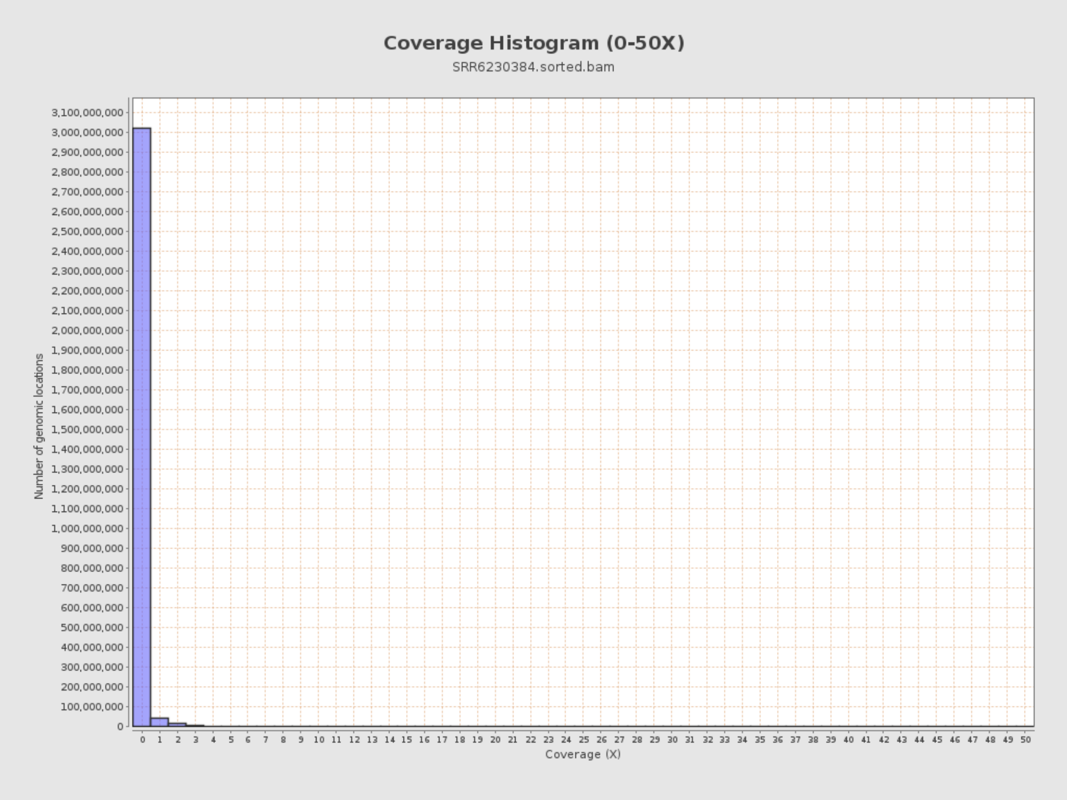
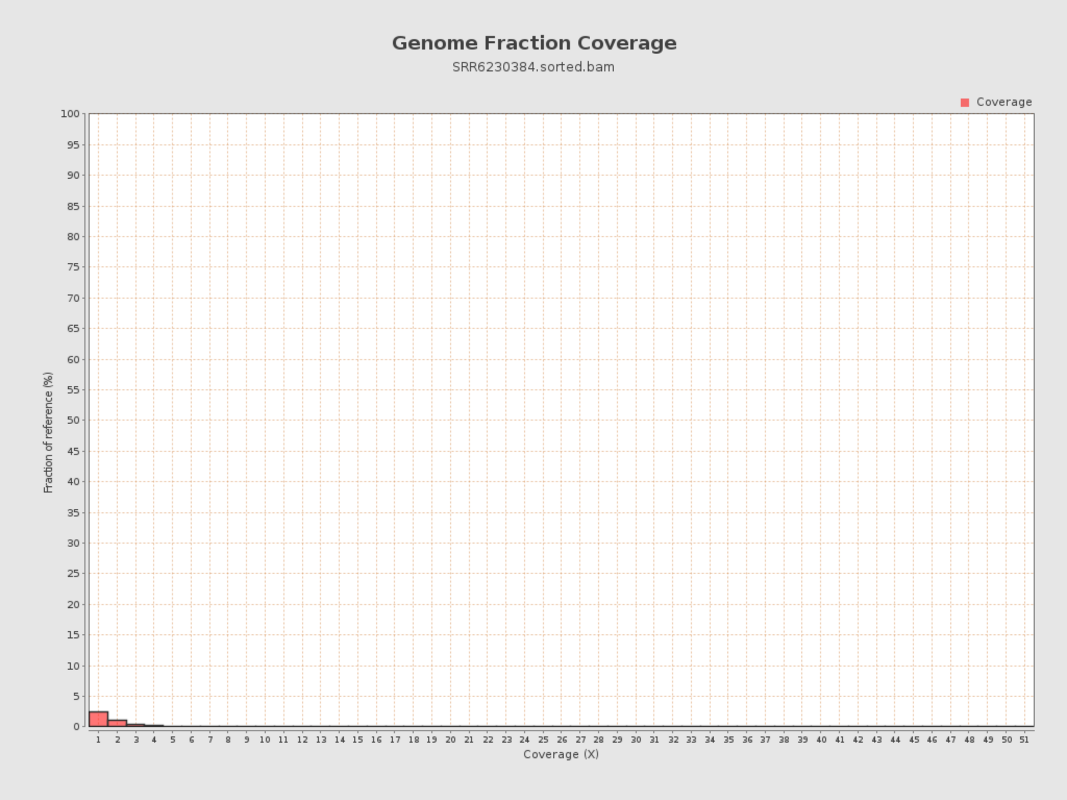
4. Results : Coverage Histogram



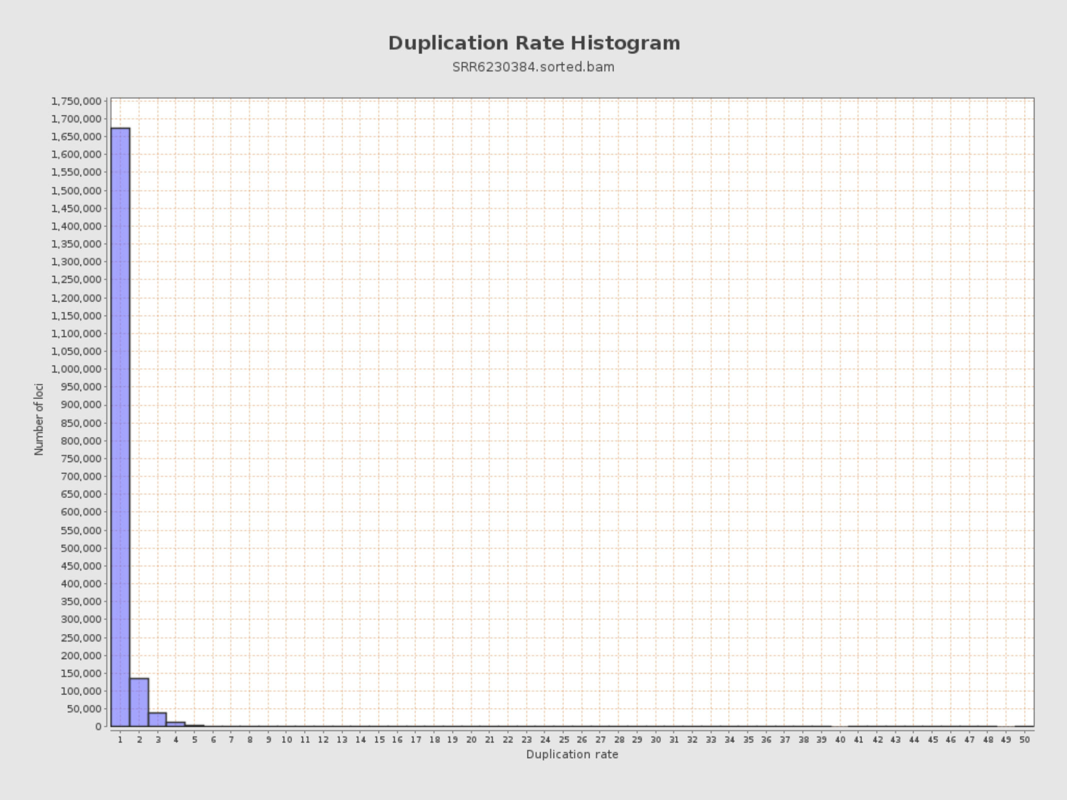
5. Results : Coverage Histogram (0-50X)



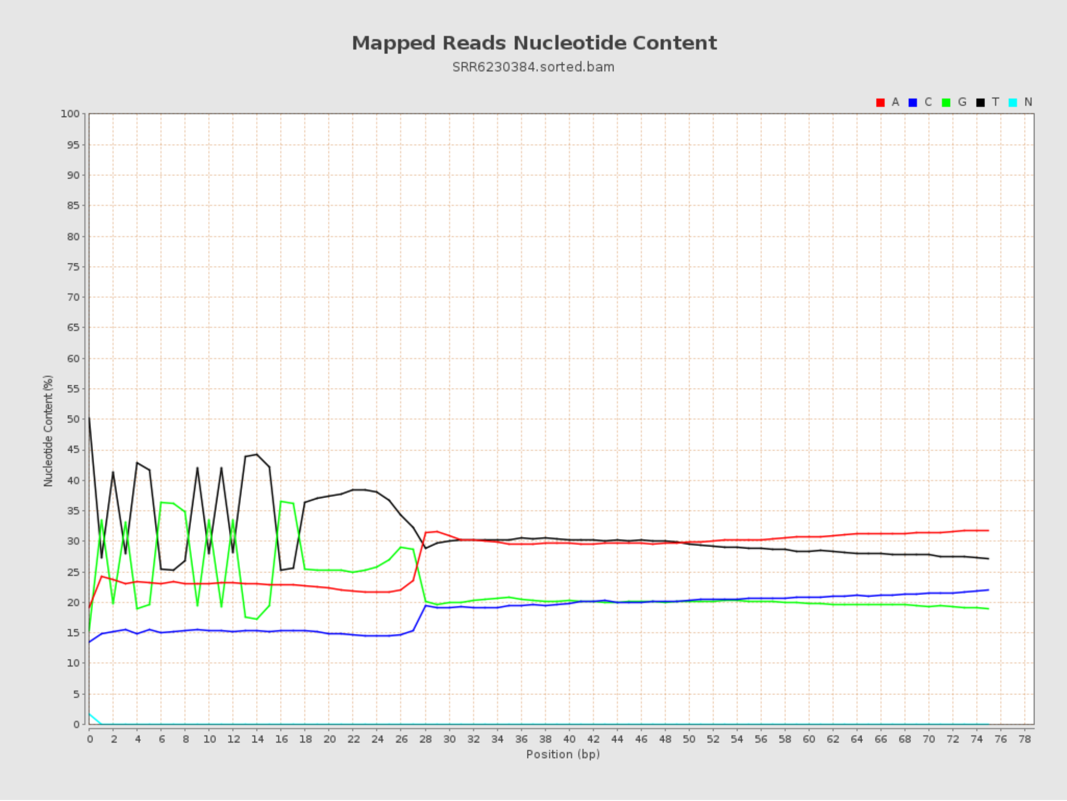
6. Results : Genome Fraction Coverage



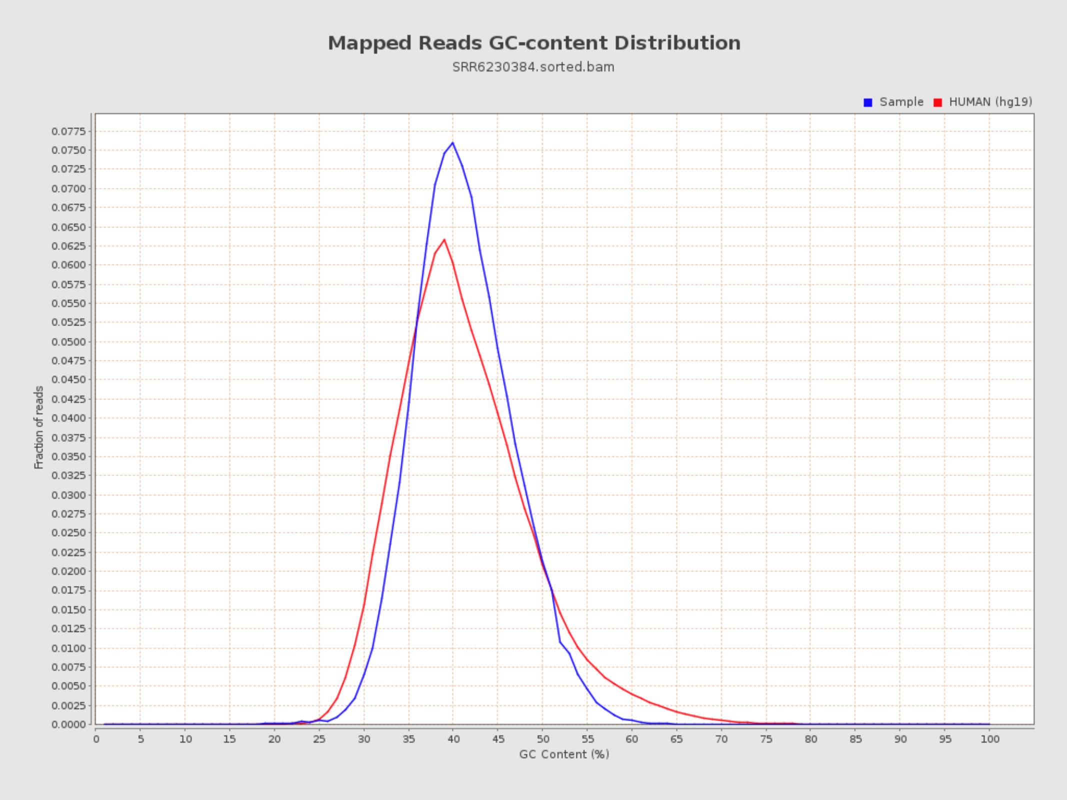
7. Results : Duplication Rate Histogram



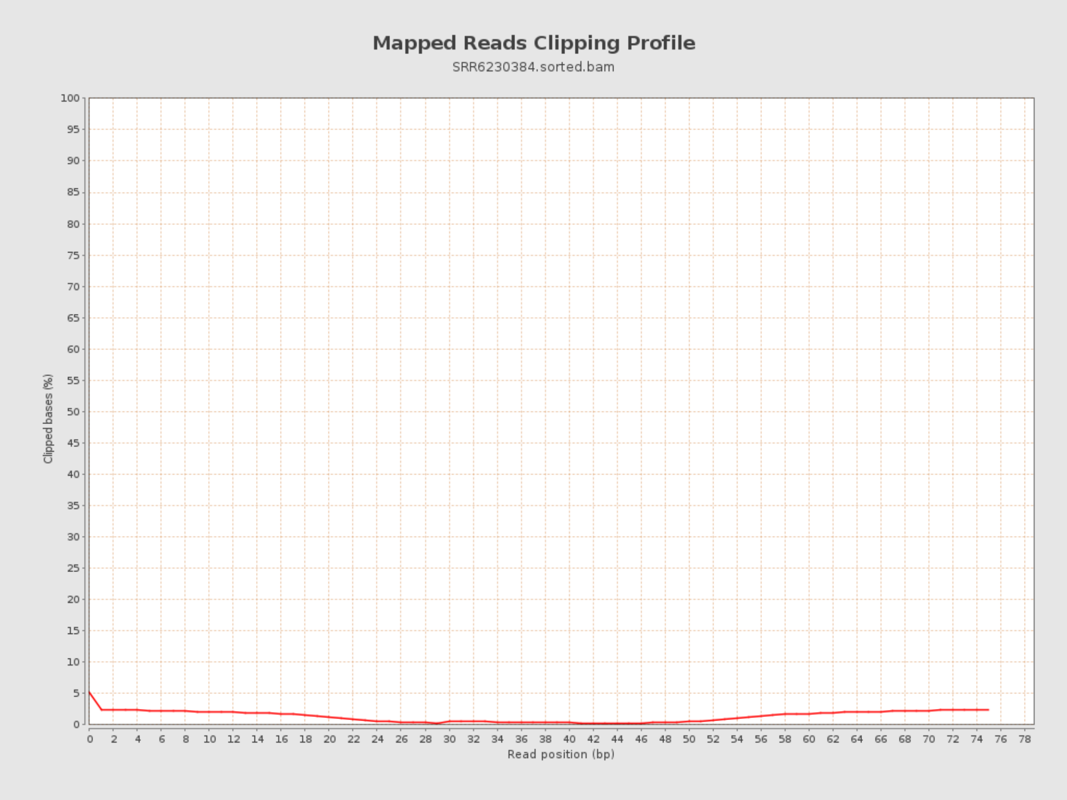
8. Results : Mapped Reads Nucleotide Content



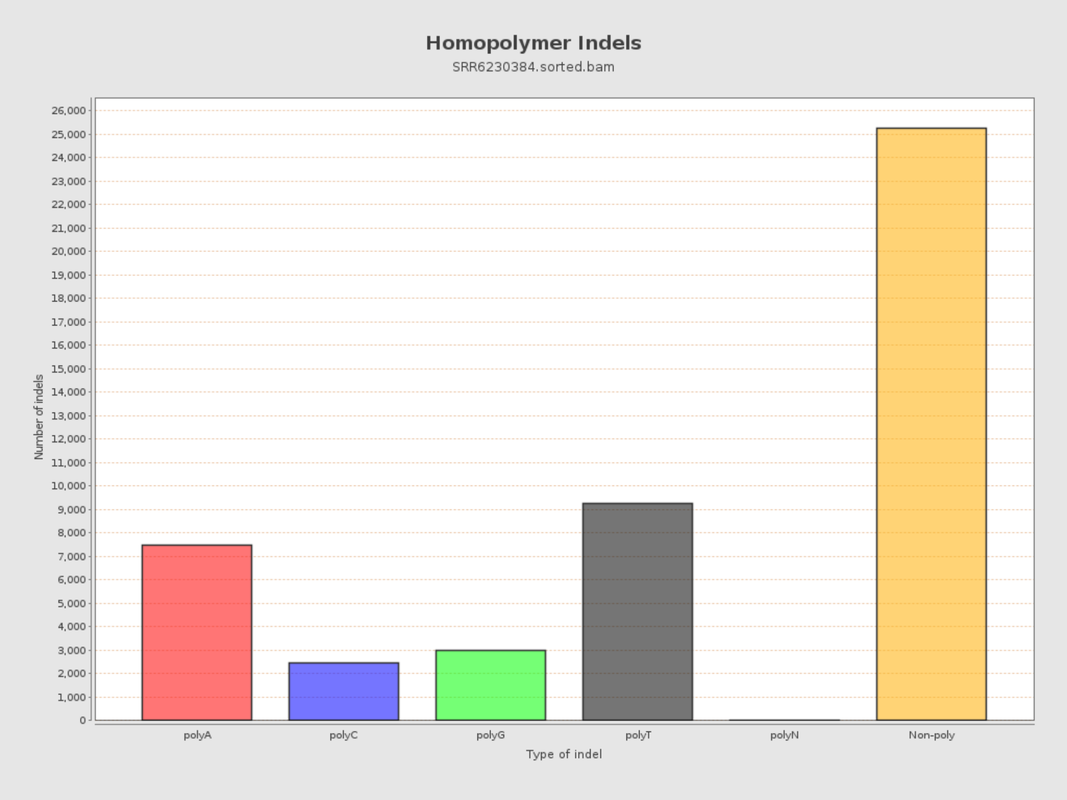
9. Results : Mapped Reads GC-content Distribution



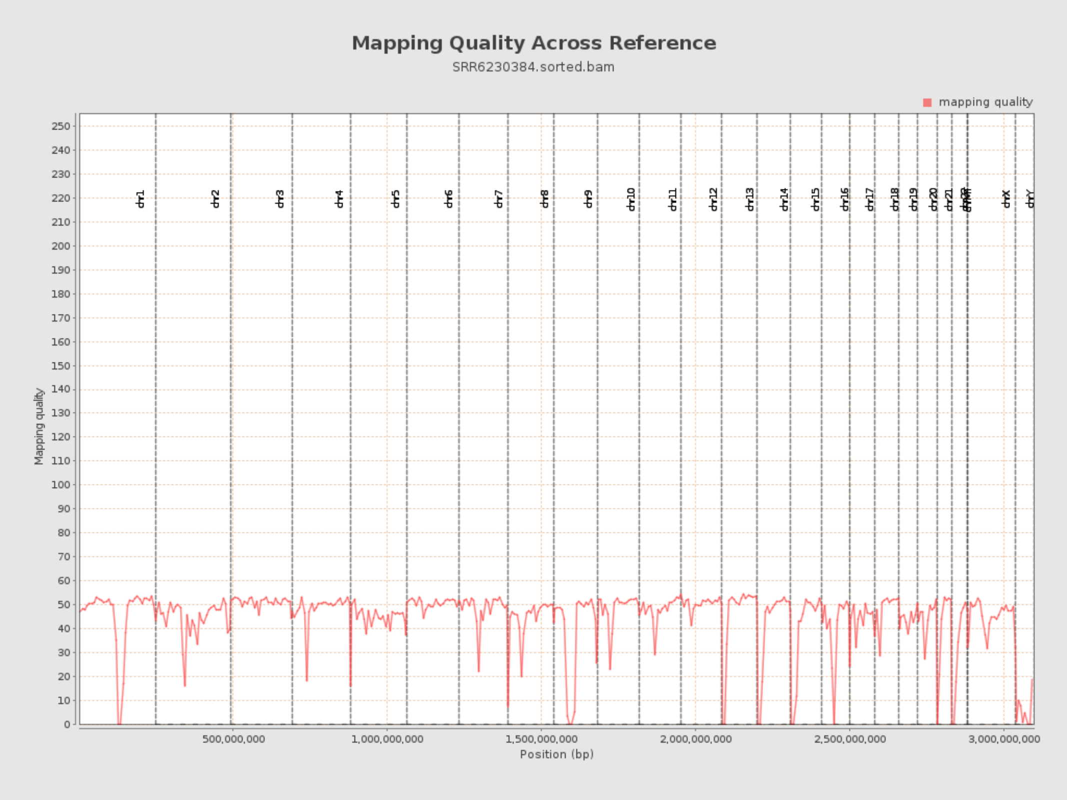
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram