Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:26:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230378.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_SRR6230378 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230378.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:26:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230378.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,235,788
Mapped reads	2,844,317 / 87.9%
Unmapped reads	391,471 / 12.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,509 / 1.31%
Read min/max/mean length	30 / 76 / 76.46
Duplicated reads (estimated)	318,060 / 9.83%
Duplication rate	8.72%
Clipped reads	1,430,968 / 44.22%

2.2. ACGT Content

Number/percentage of A's	50,711,602 / 27.06%
Number/percentage of C's	35,582,947 / 18.98%
Number/percentage of T's	58,161,699 / 31.03%
Number/percentage of G's	42,942,342 / 22.91%
Number/percentage of N's	38,599 / 0.02%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0606

Standard Deviation	0.494

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

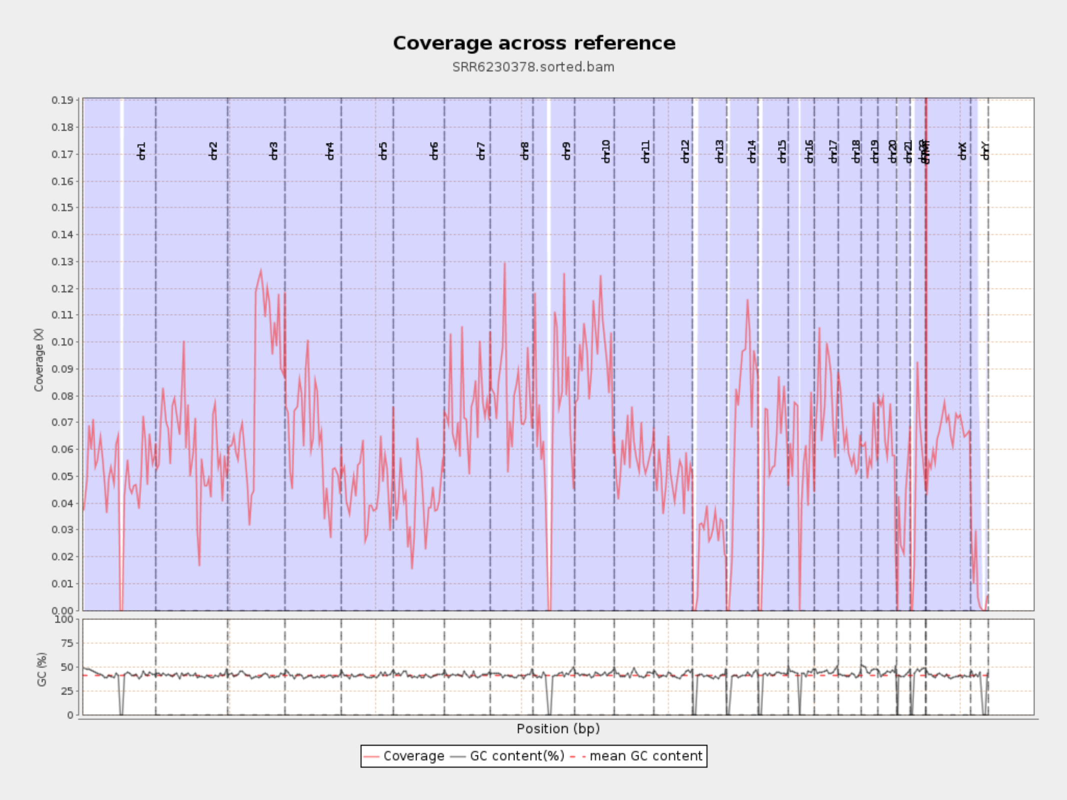
General error rate	0.86%
Mismatches	1,580,572
Insertions	15,820
Mapped reads with at least one insertion	0.55%
Deletions	46,487
Mapped reads with at least one deletion	1.62%
Homopolymer indels	46.39%

2.6. Chromosome stats

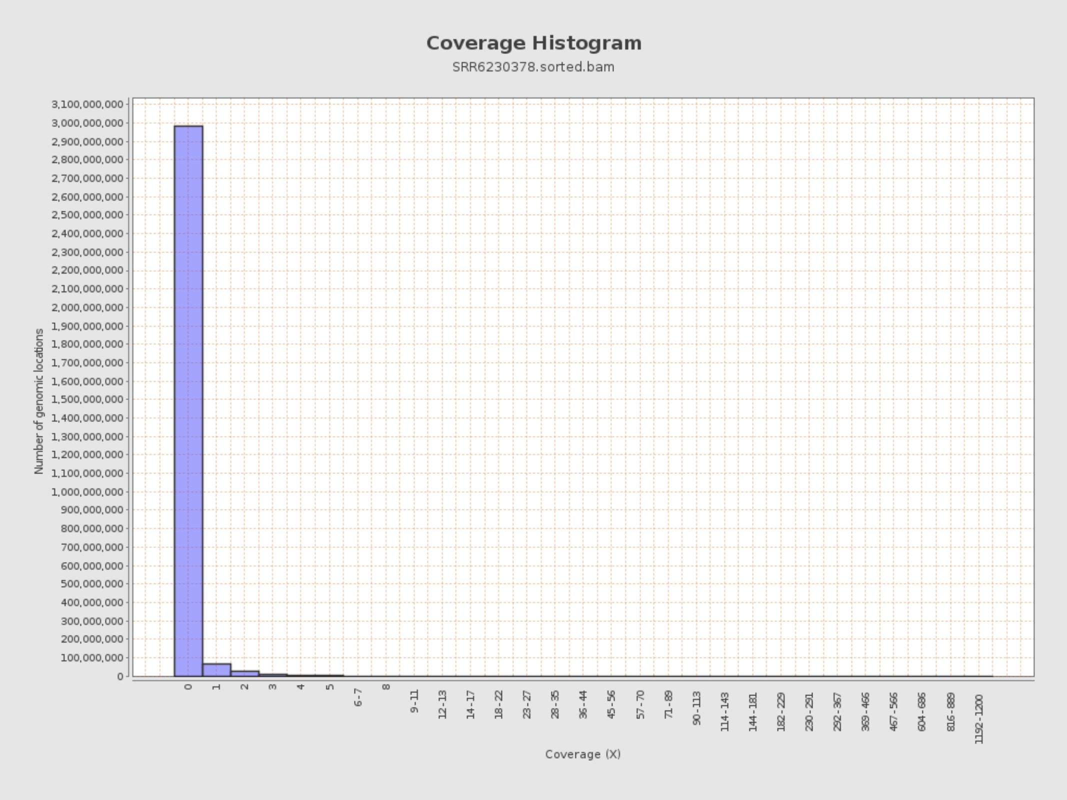
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12552057	0.0504	0.5733
chr2	243199373	14818546	0.0609	0.6718
chr3	198022430	16533942	0.0835	0.4408
chr4	191154276	12071615	0.0632	0.4261
chr5	180915260	8305414	0.0459	0.325
chr6	171115067	6929219	0.0405	0.3318
chr7	159138663	11953361	0.0751	0.7308

chr8	146364022	11830011	0.0808	0.6564
chr9	141213431	9961779	0.0705	0.5049
chr10	135534747	12922915	0.0953	0.5559
chr11	135006516	7840986	0.0581	0.5181
chr12	133851895	6668783	0.0498	0.346
chr13	115169878	2939149	0.0255	0.2405
chr14	107349540	7744804	0.0721	0.4347
chr15	102531392	5619122	0.0548	0.3589
chr16	90354753	4866588	0.0539	0.3788
chr17	81195210	6484735	0.0799	0.4916
chr18	78077248	4941130	0.0633	0.6942
chr19	59128983	3530474	0.0597	0.4676
chr20	63025520	4137068	0.0656	0.4008
chr21	48129895	1807389	0.0376	0.3299
chr22	51304566	2380698	0.0464	0.3236
chrMT	16571	44773	2.7019	3.1117
chrX	155270560	10092728	0.065	0.4056
chrY	59373566	535765	0.009	0.2431

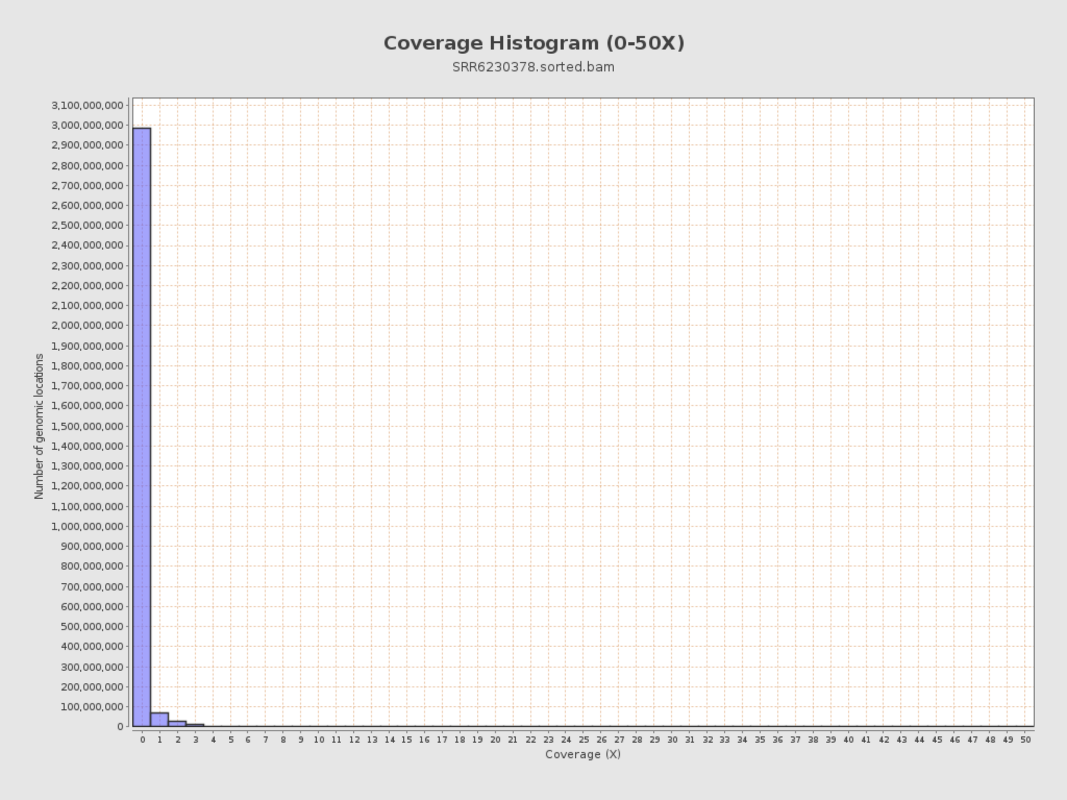
3. Results : Coverage across reference



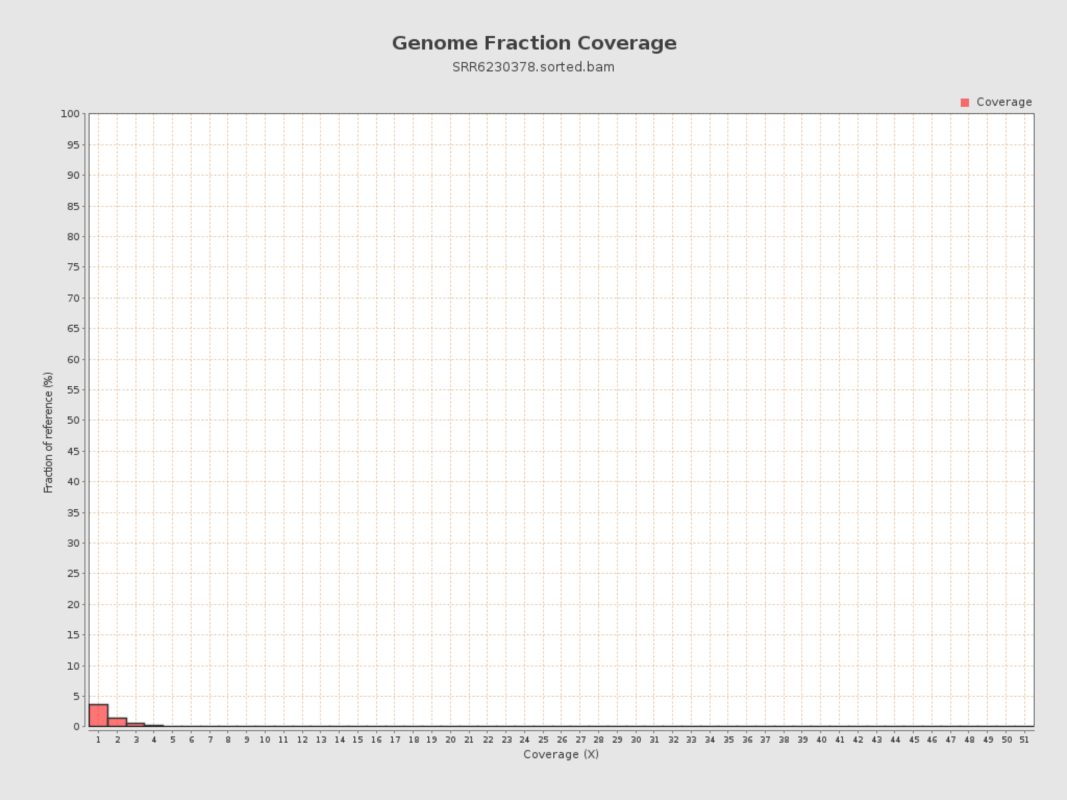
4. Results : Coverage Histogram



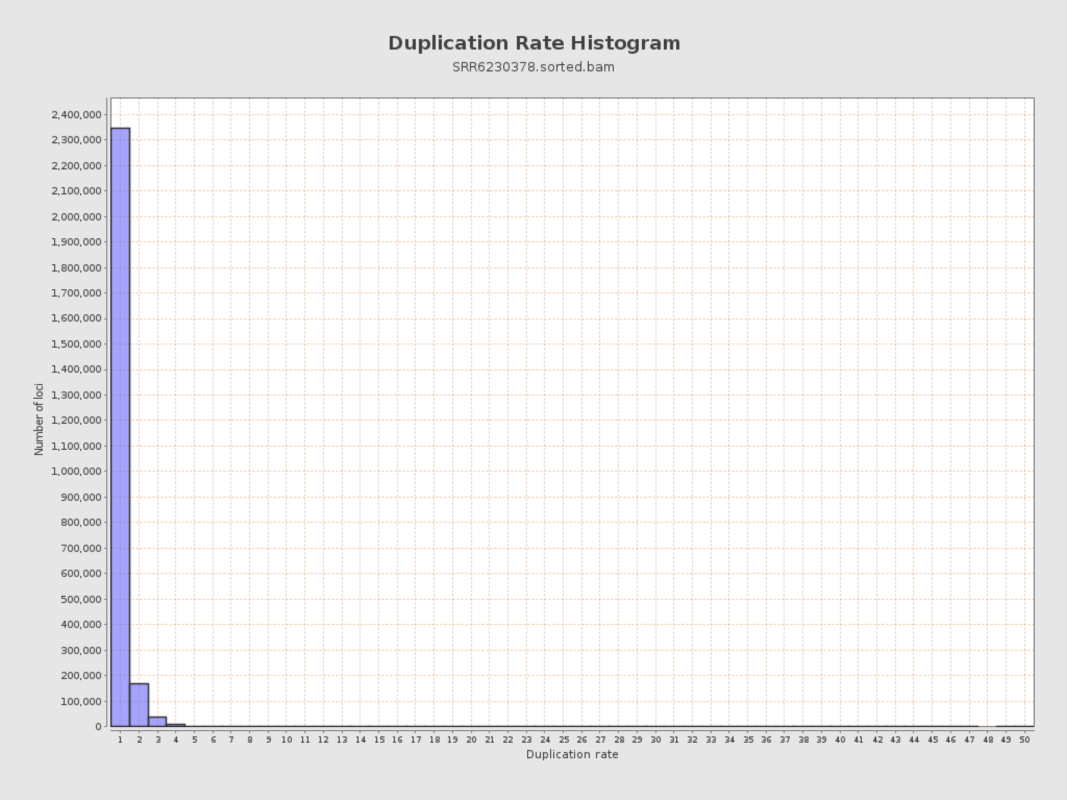
5. Results : Coverage Histogram (0-50X)



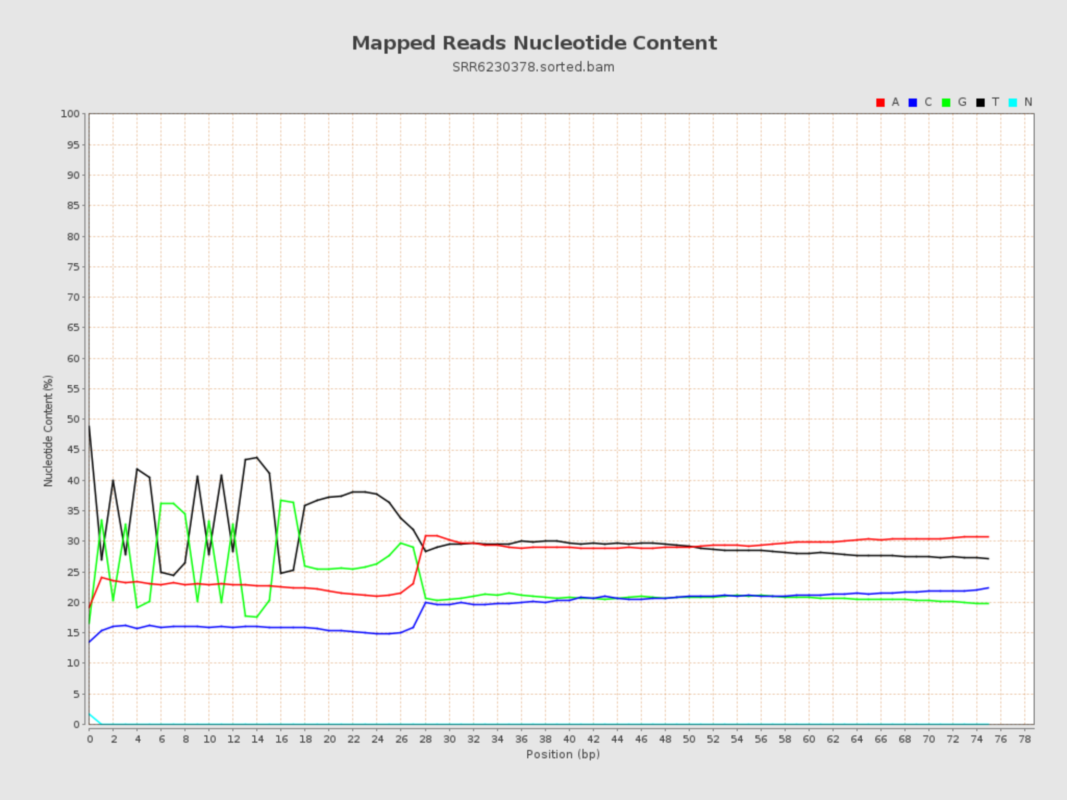
6. Results : Genome Fraction Coverage



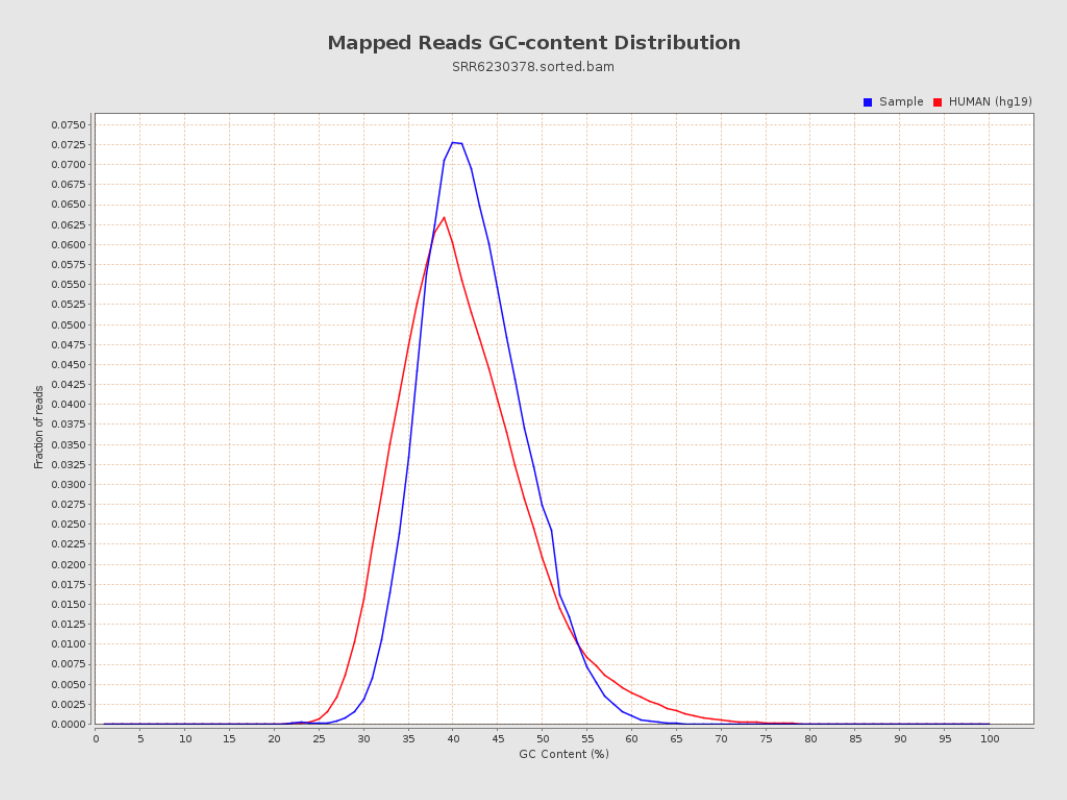
7. Results : Duplication Rate Histogram



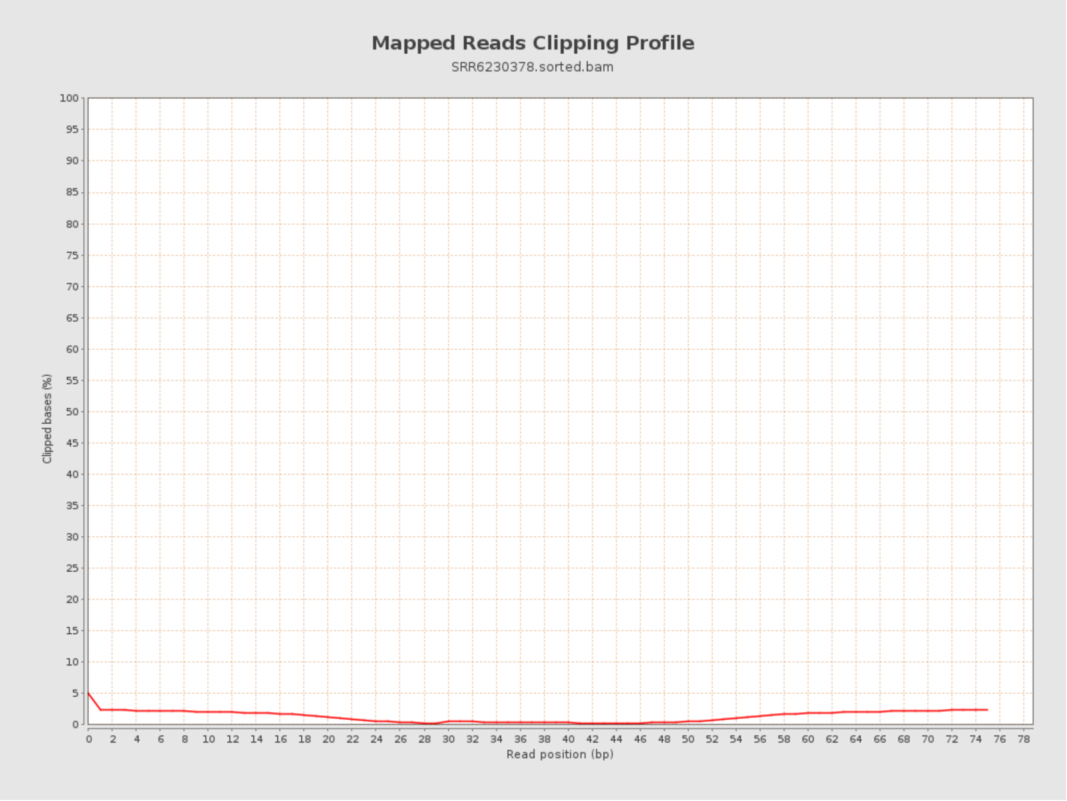
8. Results : Mapped Reads Nucleotide Content



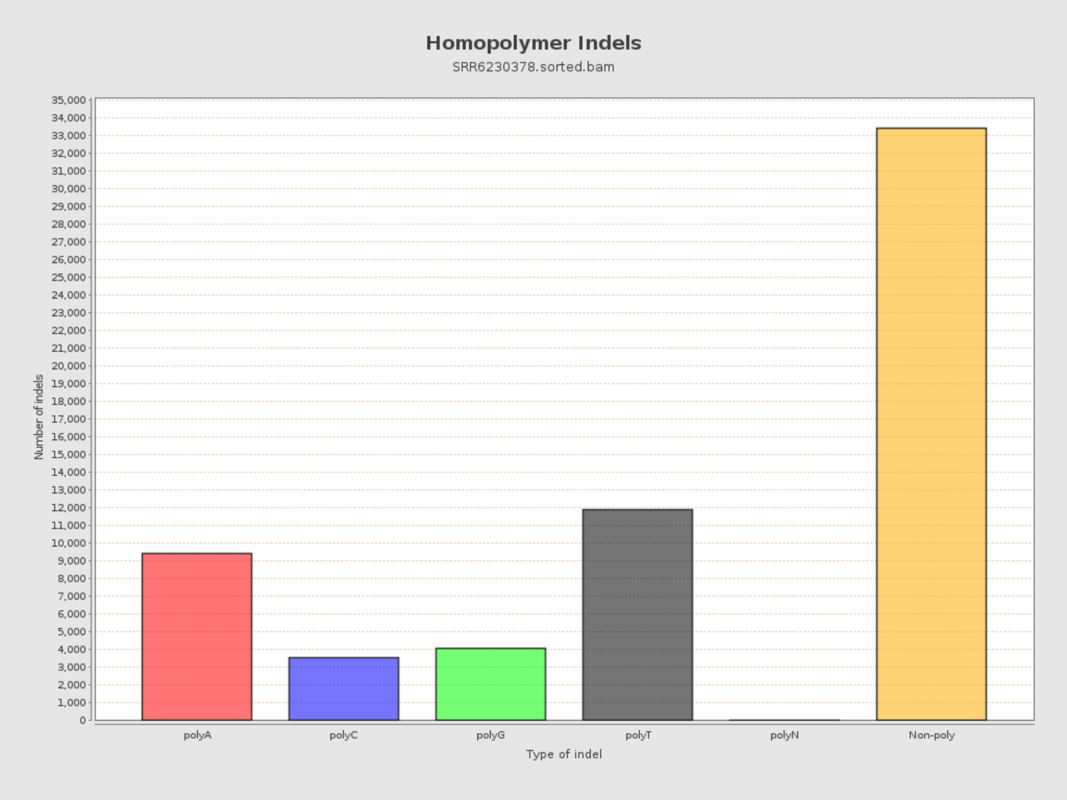
9. Results : Mapped Reads GC-content Distribution



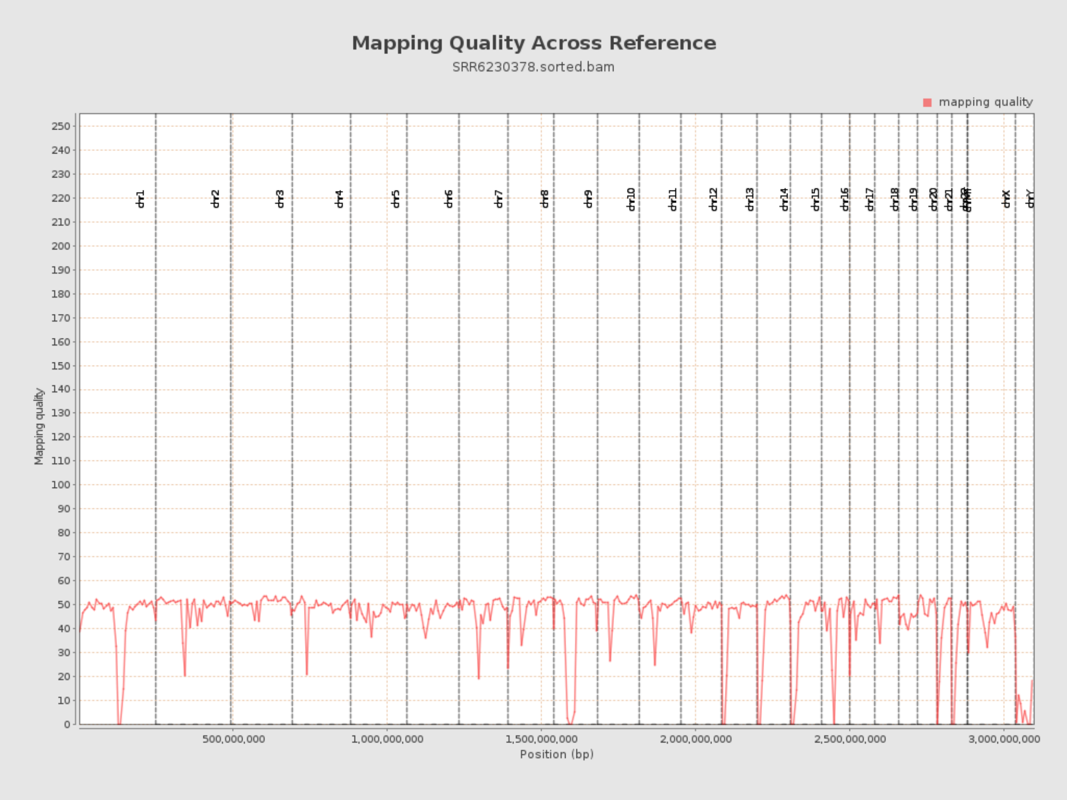
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram