Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:01:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238624.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_SRR6238624 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238624.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:01:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238624.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,178,599
Mapped reads	2,768,418 / 87.1%
Unmapped reads	410,181 / 12.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,452 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	805,852 / 25.35%
Duplication rate	19.33%
Clipped reads	1,793,875 / 56.44%

2.2. ACGT Content

Number/percentage of A's	42,699,706 / 25.09%
Number/percentage of C's	30,193,653 / 17.74%
Number/percentage of T's	56,702,710 / 33.32%
Number/percentage of G's	40,556,436 / 23.83%
Number/percentage of N's	8,458 / 0%
GC Percentage	41.58%

2.3. Coverage

Mean	0.055

Standard Deviation	0.8369

2.4. Mapping Quality

Mean Mapping Quality	40.5

2.5. Mismatches and indels

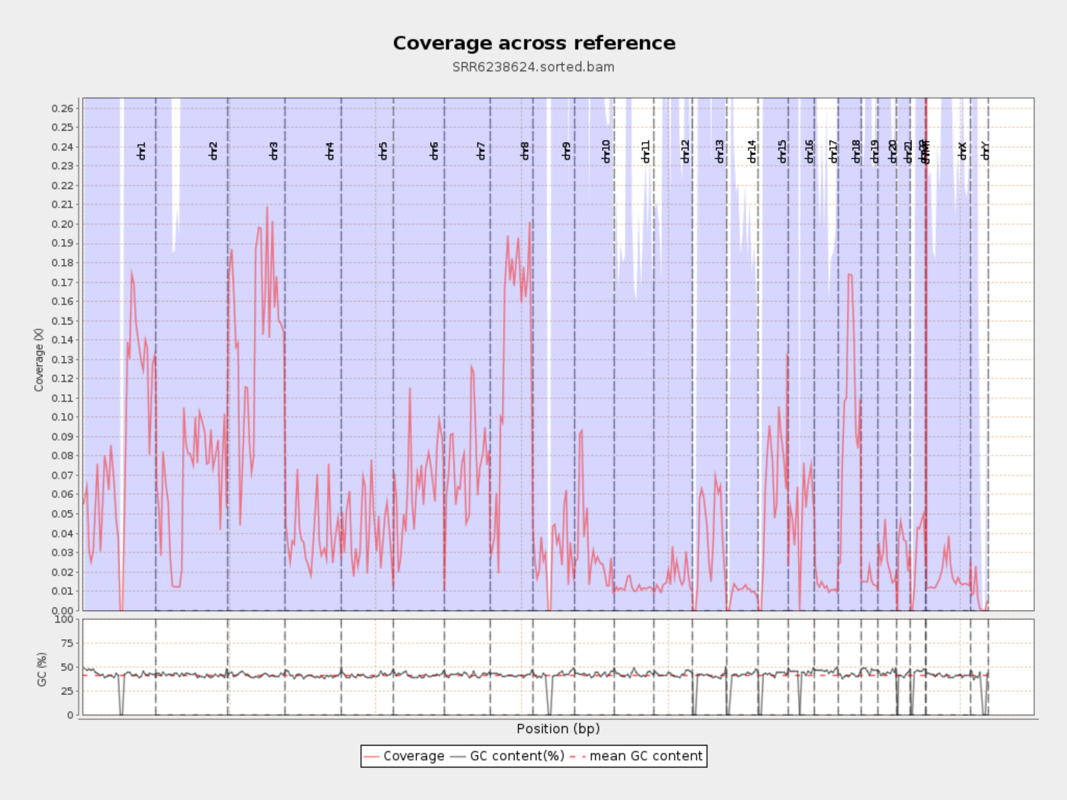
General error rate	0.63%
Mismatches	1,060,679
Insertions	10,763
Mapped reads with at least one insertion	0.39%
Deletions	56,127
Mapped reads with at least one deletion	2.01%
Homopolymer indels	40.42%

2.6. Chromosome stats

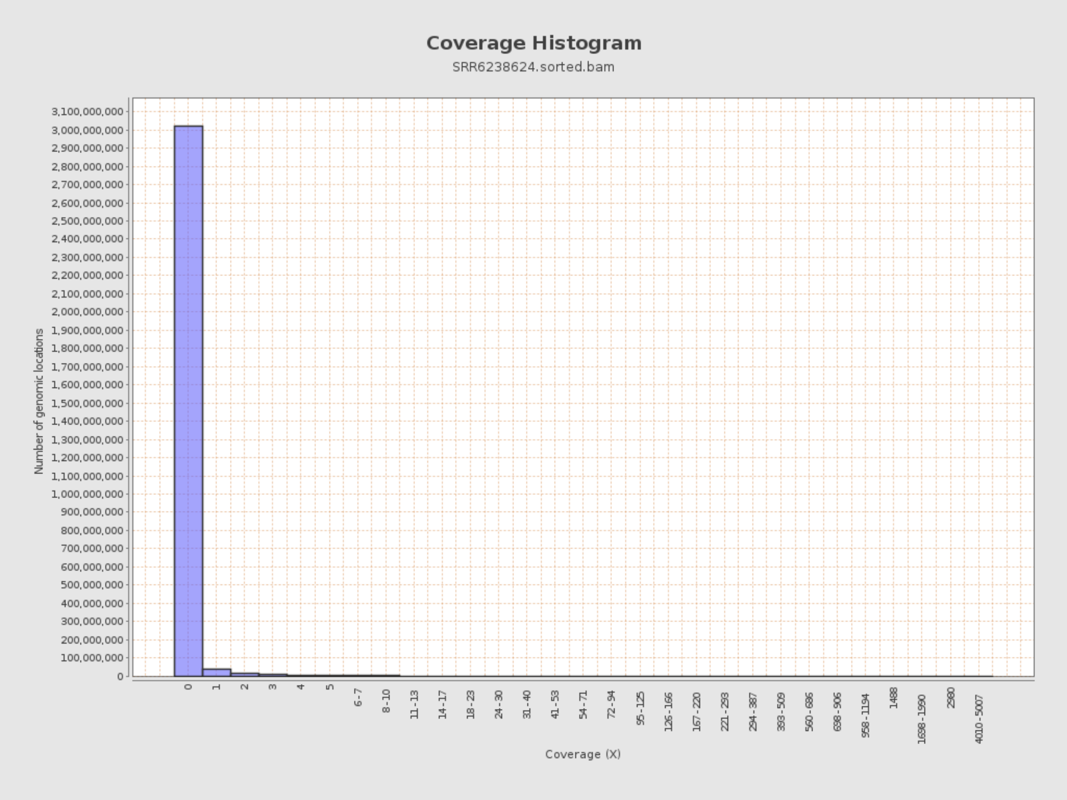
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21035538	0.0844	0.6735
chr2	243199373	16062553	0.066	2.2046
chr3	198022430	28319213	0.143	0.7818
chr4	191154276	7402352	0.0387	0.389
chr5	180915260	7385637	0.0408	0.4065
chr6	171115067	11225365	0.0656	0.8565
chr7	159138663	12079637	0.0759	0.7466

chr8	146364022	19873831	0.1358	0.8954
chr9	141213431	4116404	0.0292	0.4186
chr10	135534747	4427756	0.0327	0.4459
chr11	135006516	1623524	0.012	0.2358
chr12	133851895	2276051	0.017	0.2587
chr13	115169878	4387735	0.0381	0.5192
chr14	107349540	1025636	0.0096	0.1895
chr15	102531392	6429488	0.0627	0.5936
chr16	90354753	4531320	0.0502	0.4867
chr17	81195210	1034220	0.0127	0.214
chr18	78077248	8276114	0.106	1.3742
chr19	59128983	917047	0.0155	0.3923
chr20	63025520	1623287	0.0258	0.3421
chr21	48129895	1516722	0.0315	0.3651
chr22	51304566	1539724	0.03	0.3425
chrMT	16571	57965	3.498	4.4145
chrX	155270560	2709428	0.0174	0.2705
chrY	59373566	378830	0.0064	0.2748

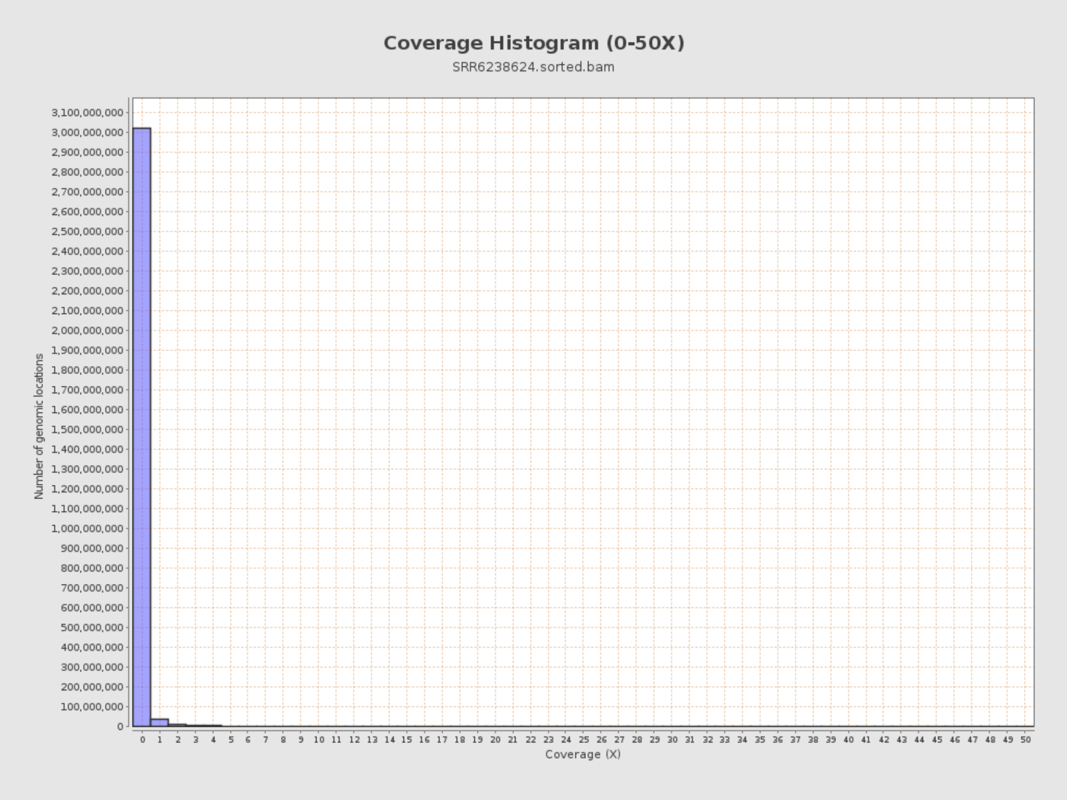
3. Results : Coverage across reference



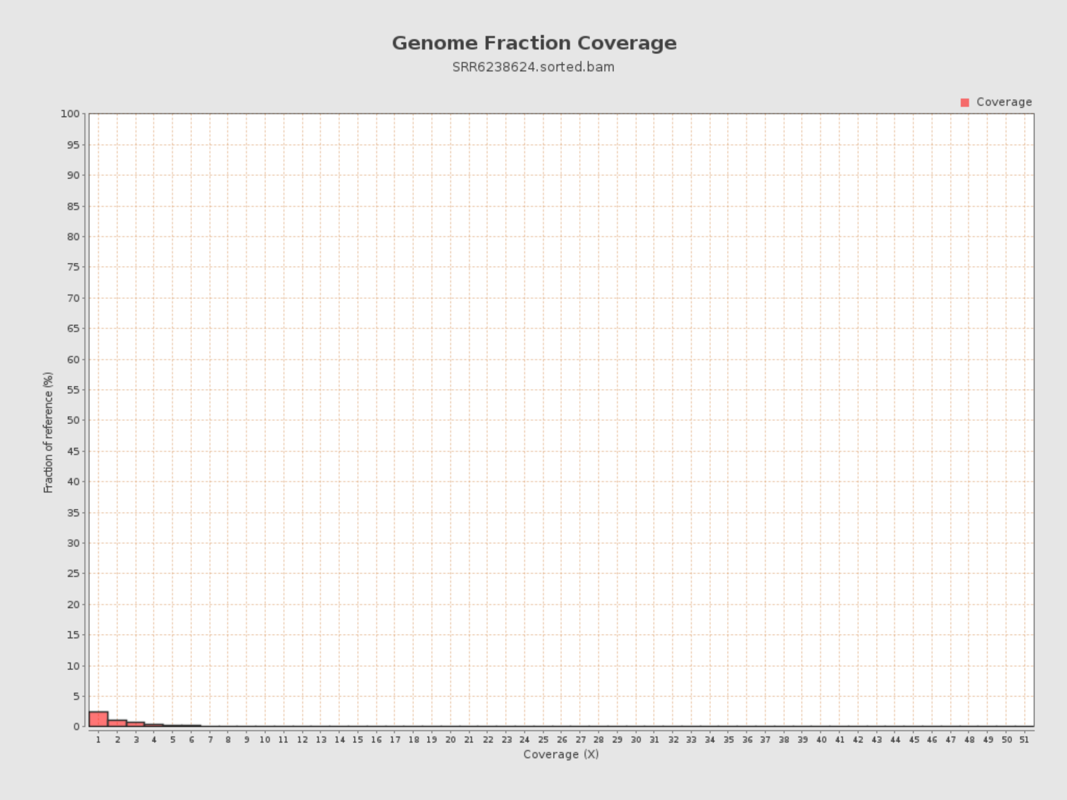
4. Results : Coverage Histogram



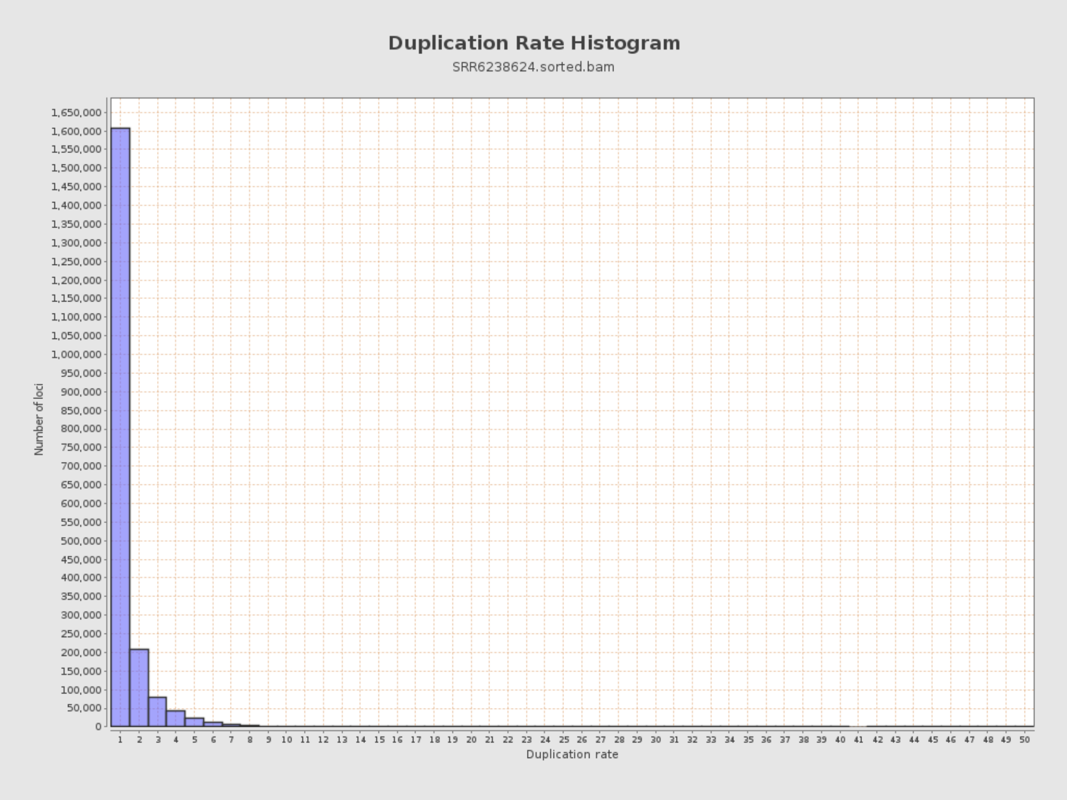
5. Results : Coverage Histogram (0-50X)



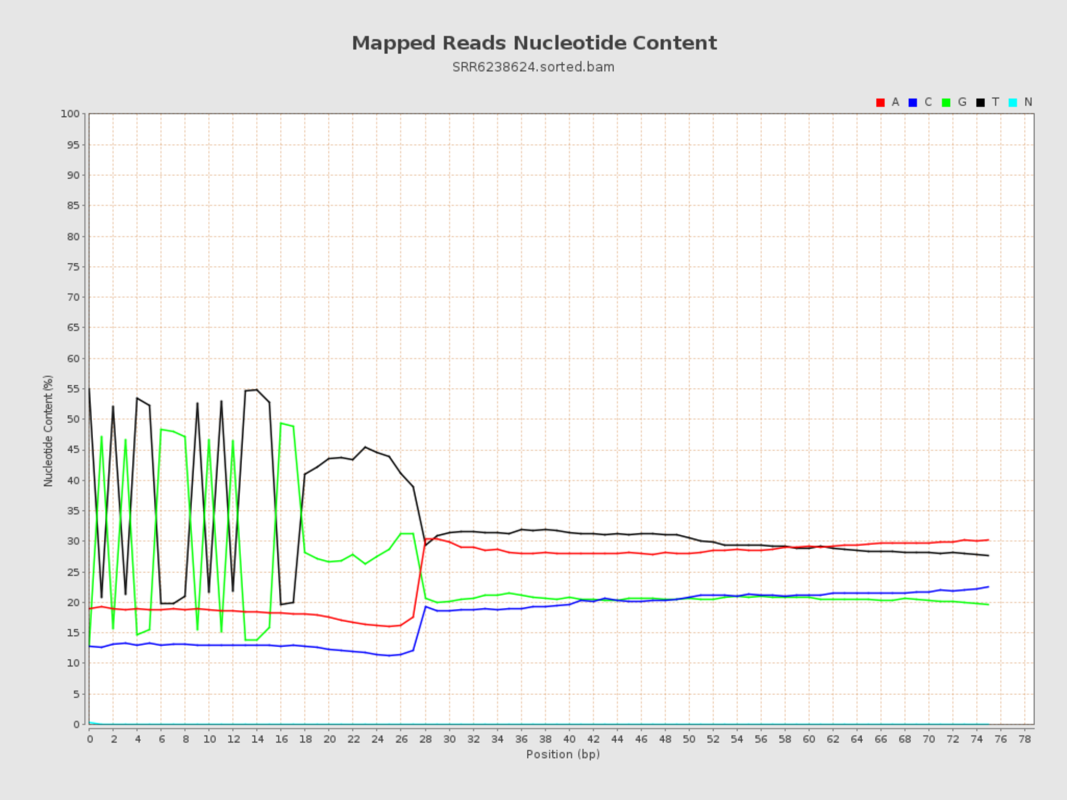
6. Results : Genome Fraction Coverage



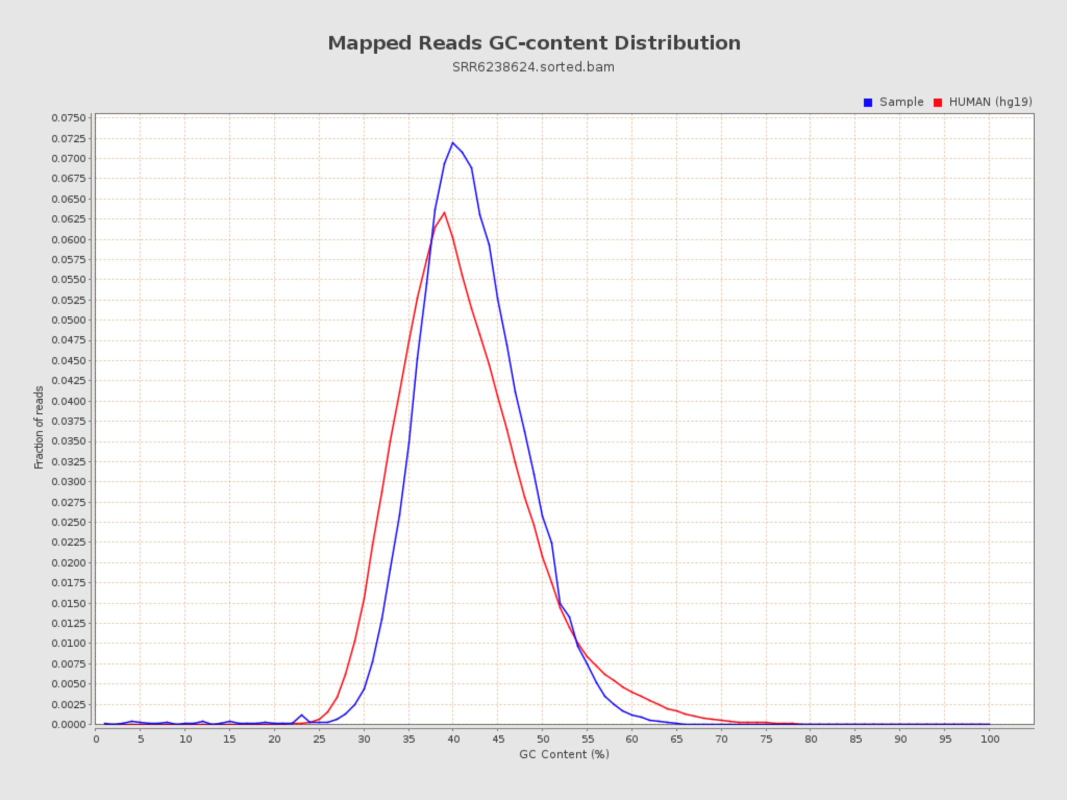
7. Results : Duplication Rate Histogram



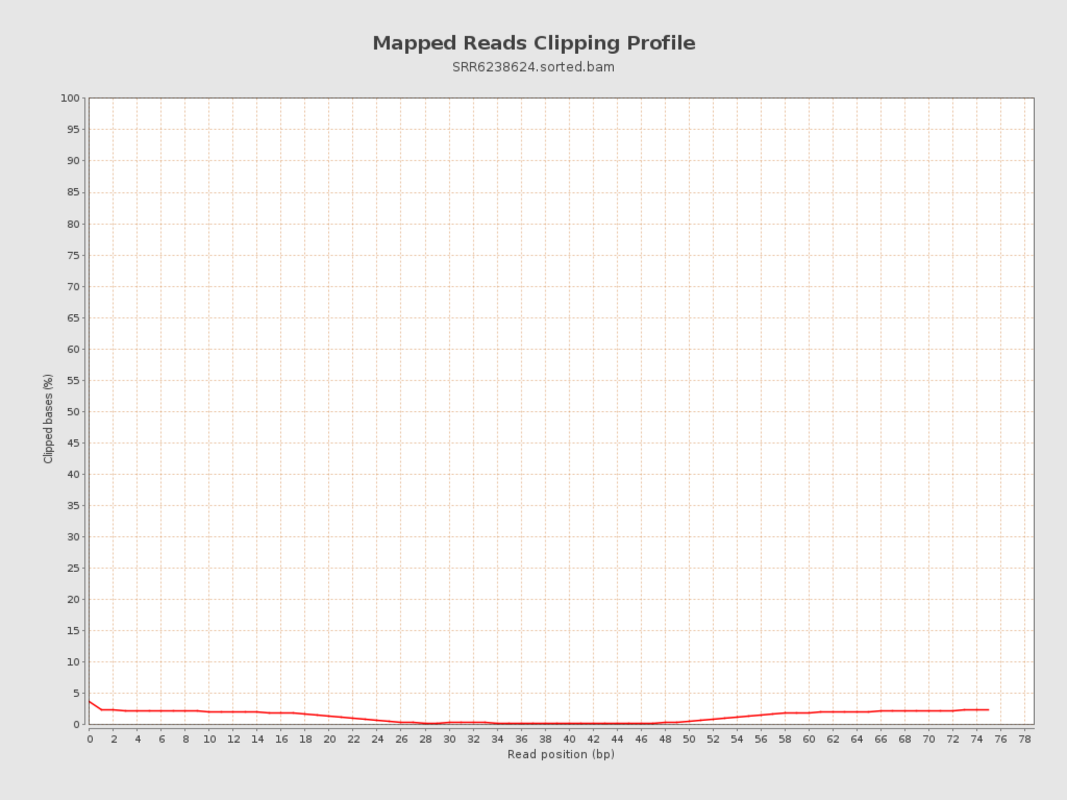
8. Results : Mapped Reads Nucleotide Content



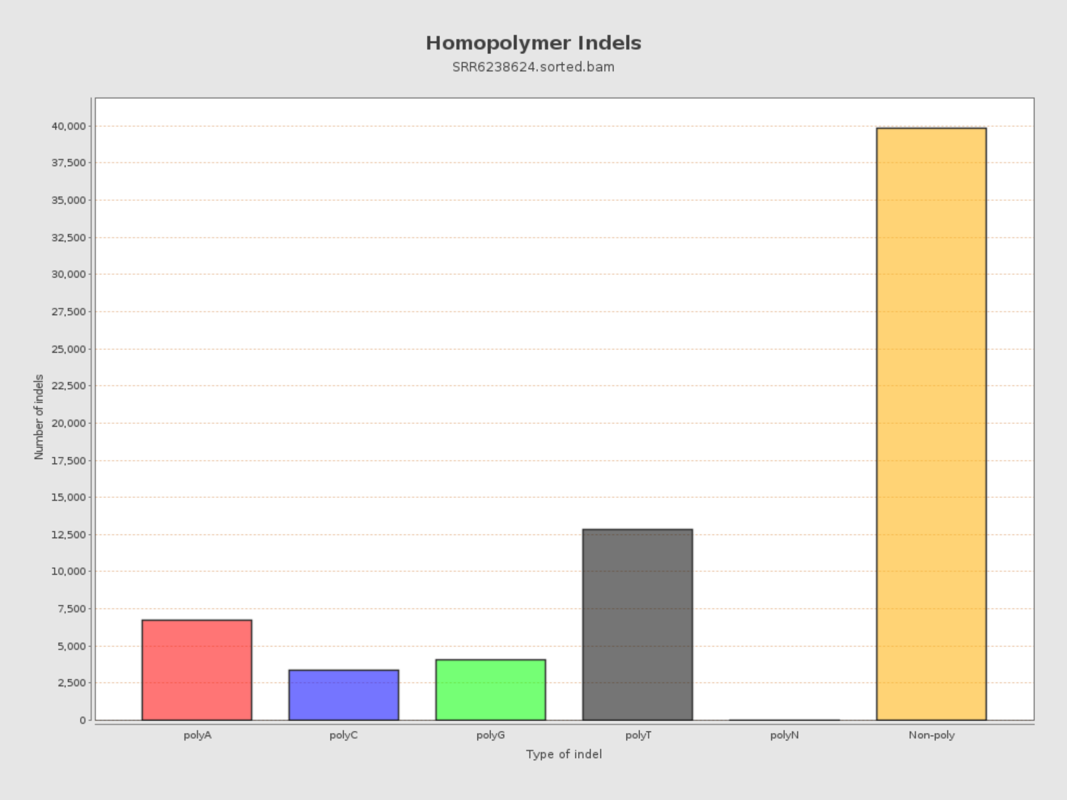
9. Results : Mapped Reads GC-content Distribution



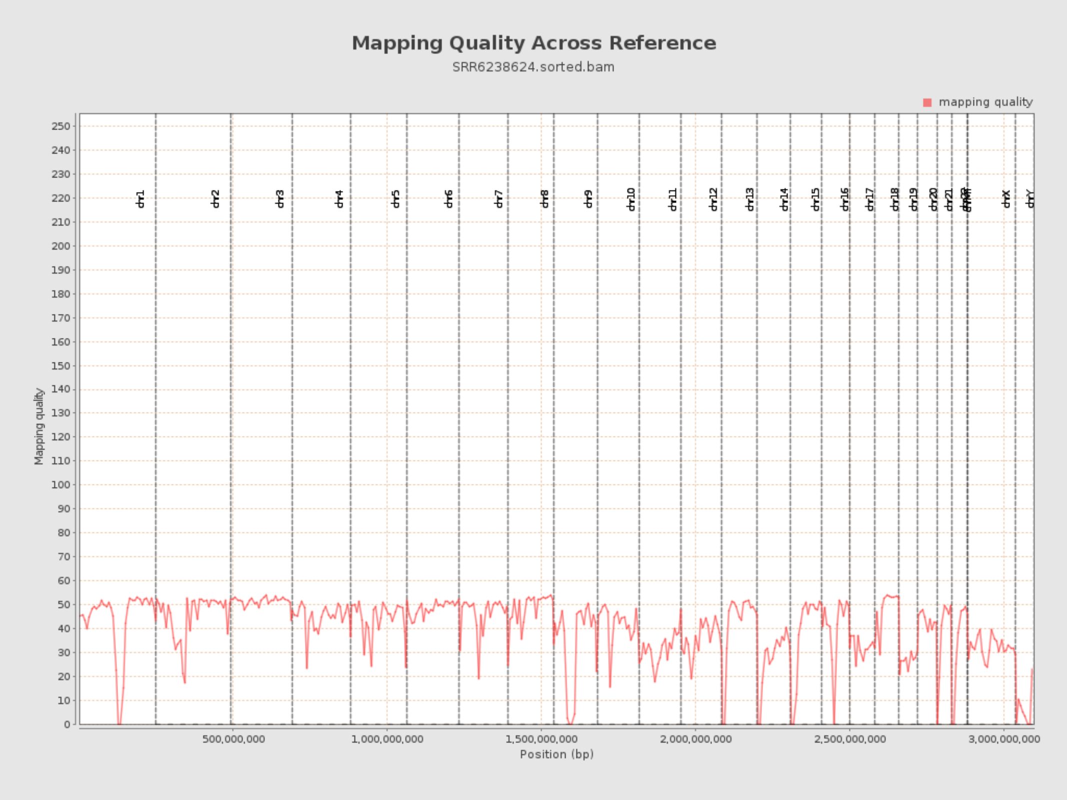
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram