Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:08:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238543.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_SRR6238543 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238543.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:08:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238543.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,876,297
Mapped reads	2,549,597 / 88.64%
Unmapped reads	326,700 / 11.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,300 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	643,936 / 22.39%
Duplication rate	18.69%
Clipped reads	1,651,188 / 57.41%

2.2. ACGT Content

Number/percentage of A's	39,654,641 / 25.35%
Number/percentage of C's	27,668,977 / 17.68%
Number/percentage of T's	51,986,554 / 33.23%
Number/percentage of G's	37,136,464 / 23.74%
Number/percentage of N's	10,693 / 0.01%
GC Percentage	41.42%

2.3. Coverage

Mean	0.0506

Standard Deviation	0.6689

2.4. Mapping Quality

Mean Mapping Quality	38.32

2.5. Mismatches and indels

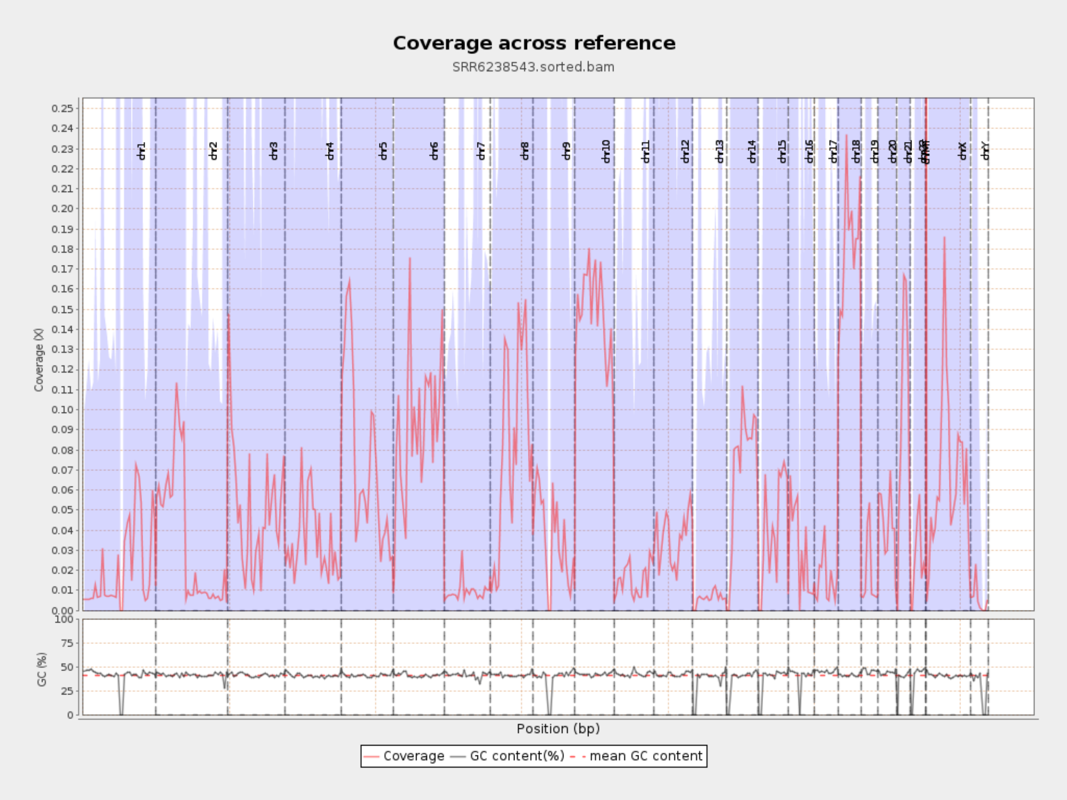
General error rate	0.66%
Mismatches	1,017,176
Insertions	10,025
Mapped reads with at least one insertion	0.39%
Deletions	55,635
Mapped reads with at least one deletion	2.16%
Homopolymer indels	40.94%

2.6. Chromosome stats

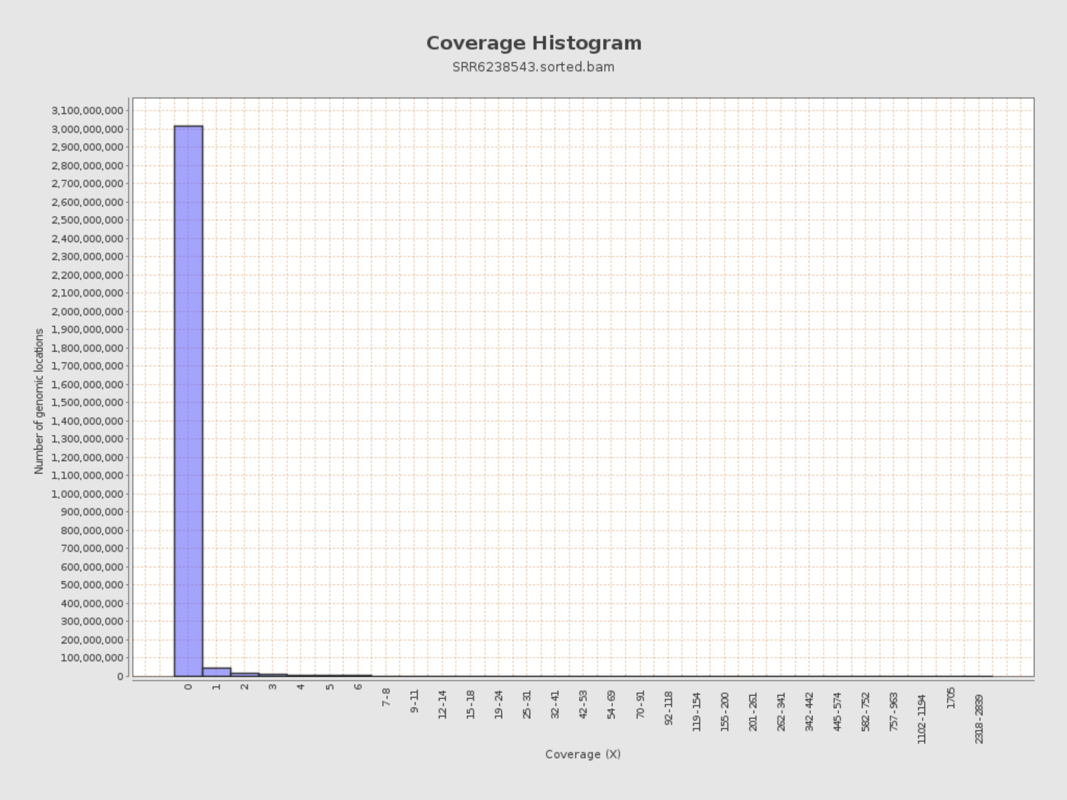
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5208801	0.0209	0.4473
chr2	243199373	8466654	0.0348	1.3794
chr3	198022430	10120953	0.0511	0.4005
chr4	191154276	6598850	0.0345	0.3241
chr5	180915260	13146507	0.0727	0.4777
chr6	171115067	16044691	0.0938	0.9647
chr7	159138663	1510734	0.0095	0.3319

chr8	146364022	11986342	0.0819	0.7874
chr9	141213431	5123585	0.0363	0.544
chr10	135534747	20128350	0.1485	0.7902
chr11	135006516	2038779	0.0151	0.3118
chr12	133851895	4850752	0.0362	0.3458
chr13	115169878	719887	0.0063	0.289
chr14	107349540	7740477	0.0721	0.5017
chr15	102531392	4241679	0.0414	0.4294
chr16	90354753	2585526	0.0286	0.3487
chr17	81195210	1214333	0.015	0.2258
chr18	78077248	14246659	0.1825	1.54
chr19	59128983	1091756	0.0185	0.5366
chr20	63025520	2804516	0.0445	0.3949
chr21	48129895	4633829	0.0963	0.5605
chr22	51304566	1314703	0.0256	0.2789
chrMT	16571	20845	1.2579	1.7739
chrX	155270560	10357010	0.0667	0.5449
chrY	59373566	356211	0.006	0.2447

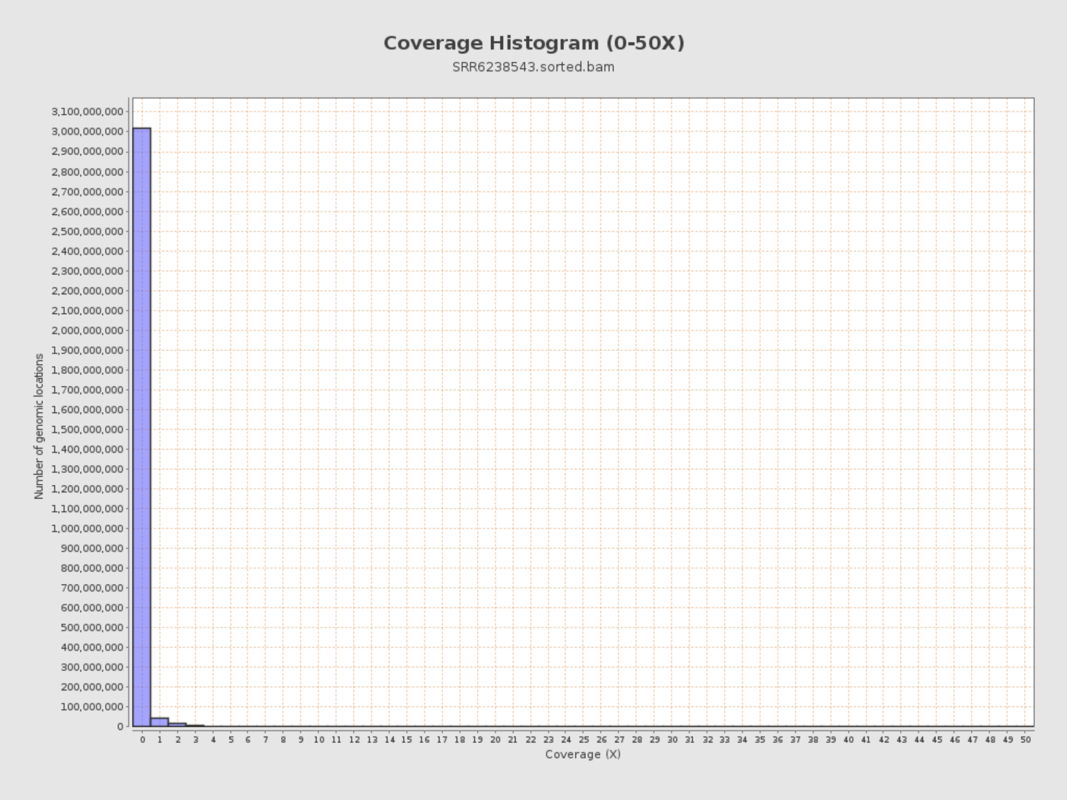
3. Results : Coverage across reference



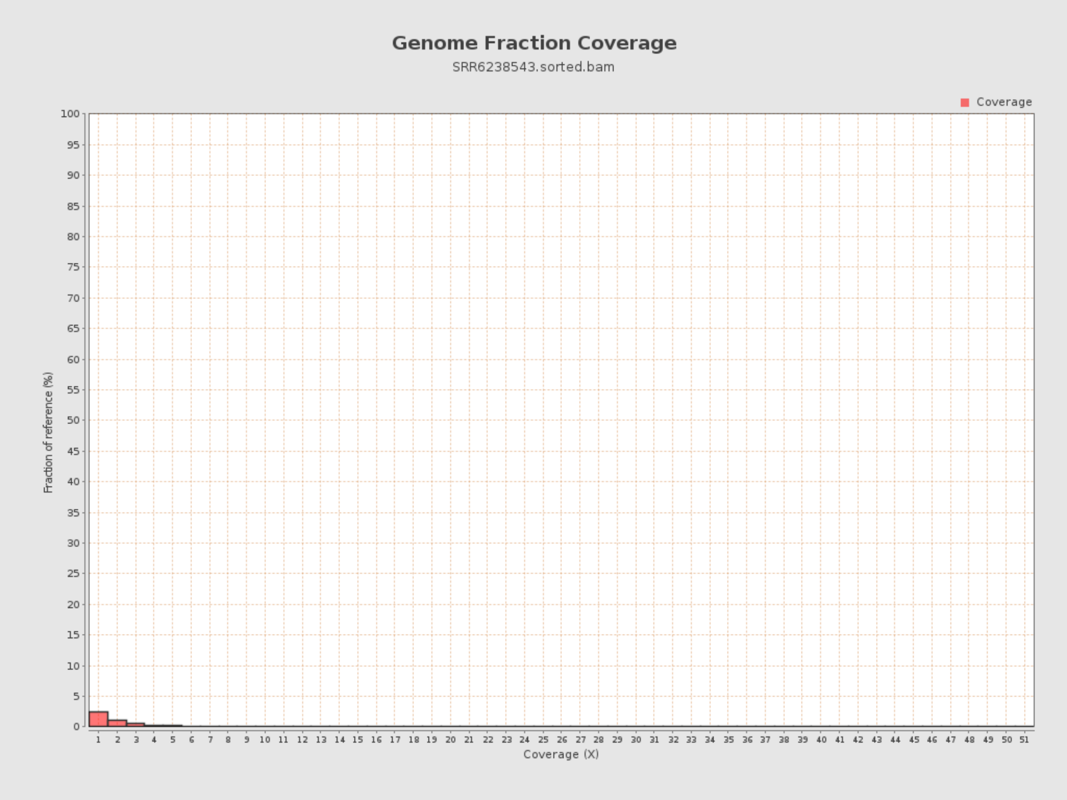
4. Results : Coverage Histogram



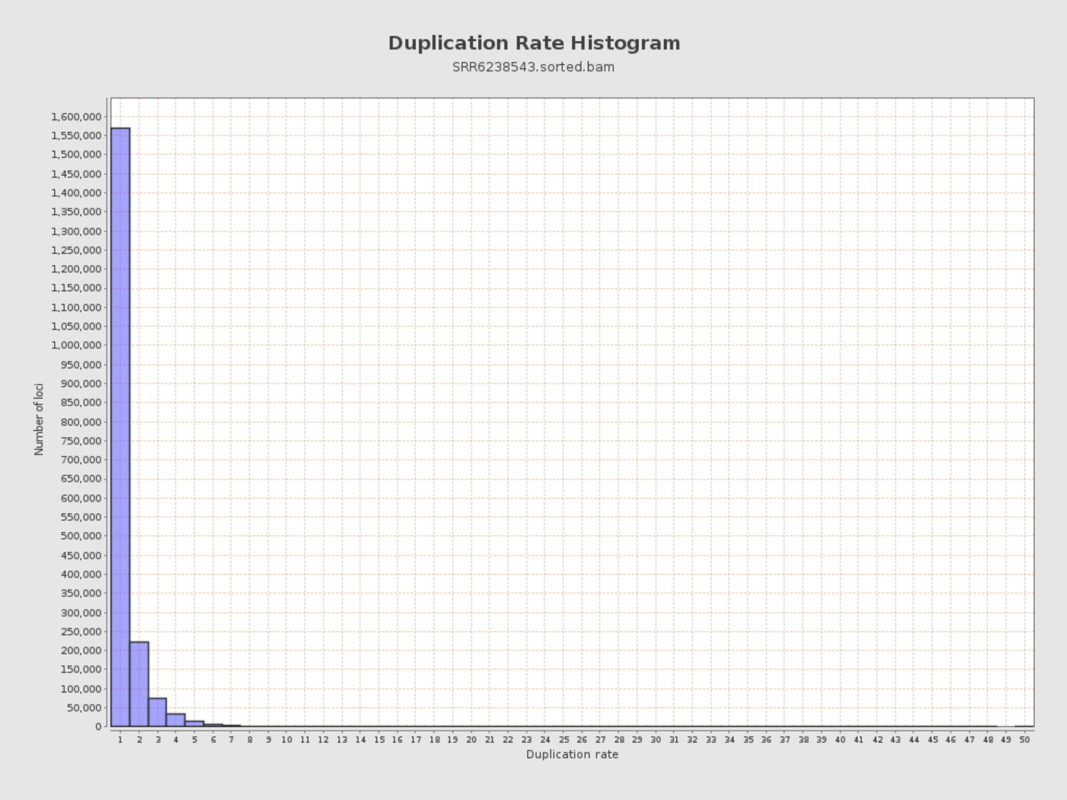
5. Results : Coverage Histogram (0-50X)



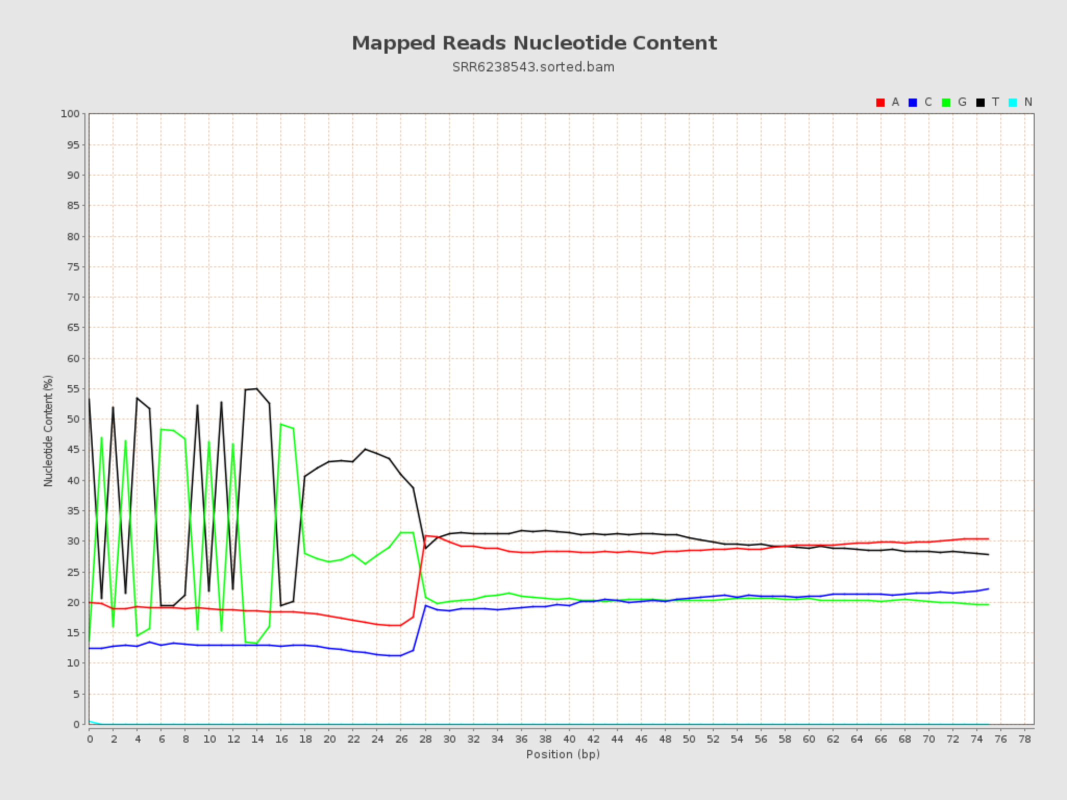
6. Results : Genome Fraction Coverage



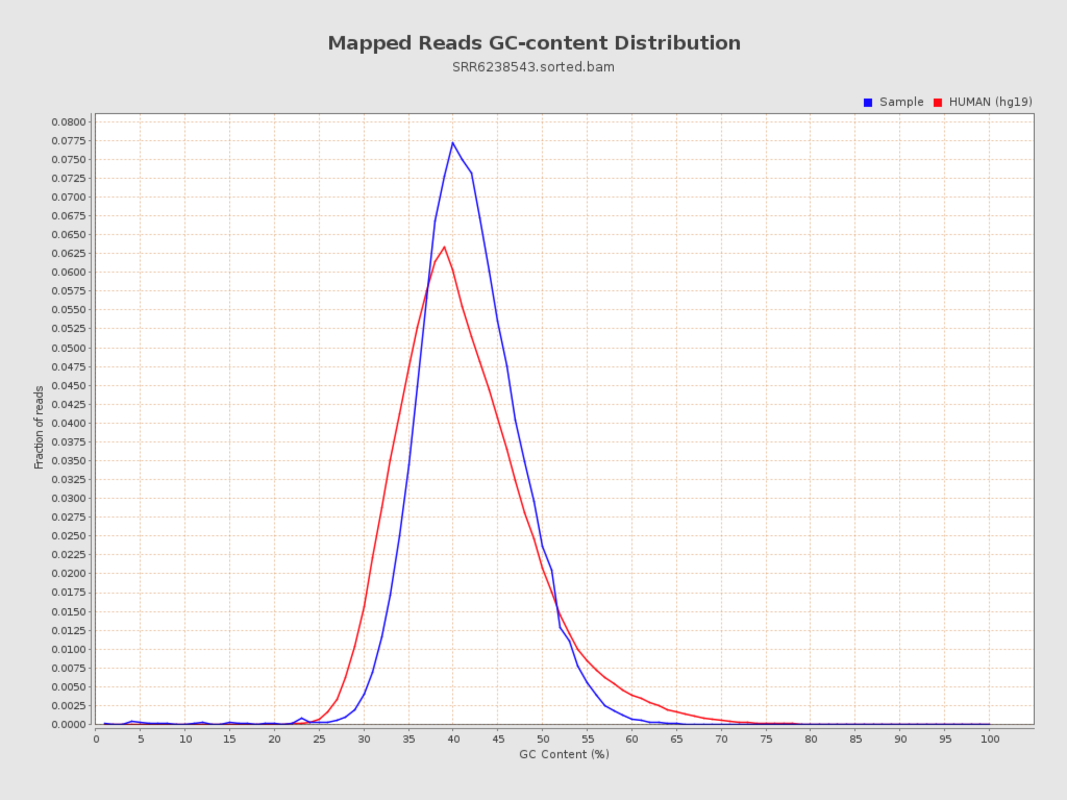
7. Results : Duplication Rate Histogram



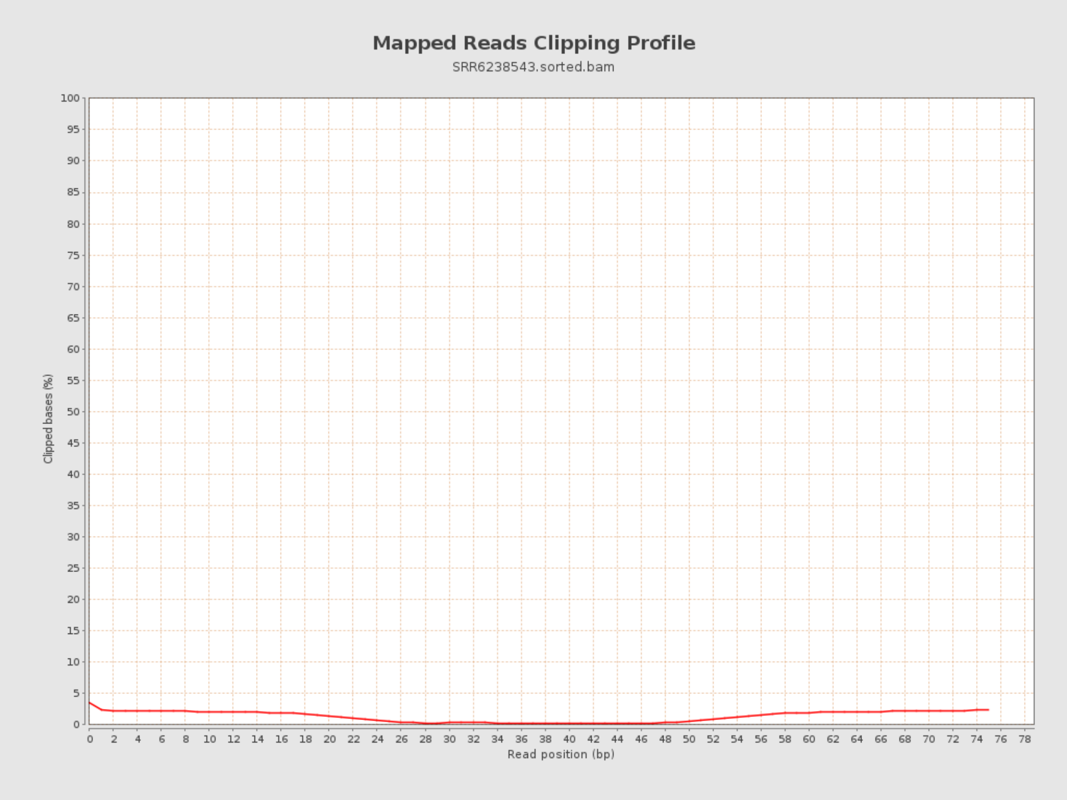
8. Results : Mapped Reads Nucleotide Content



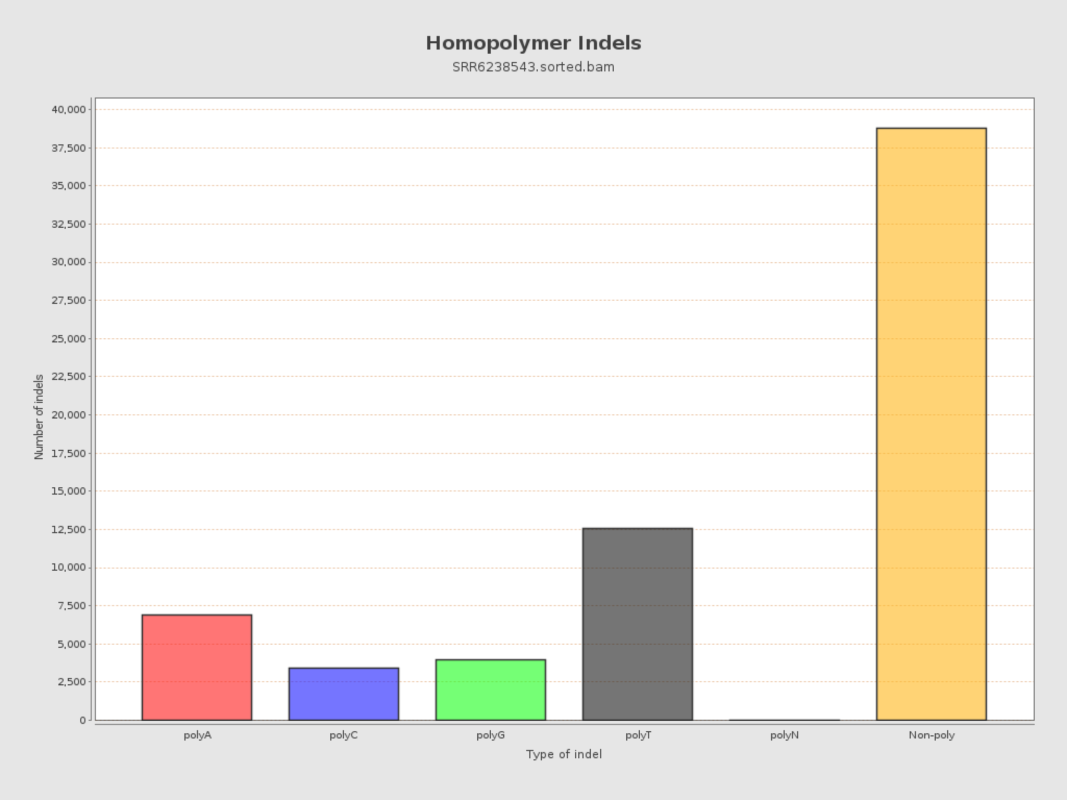
9. Results : Mapped Reads GC-content Distribution



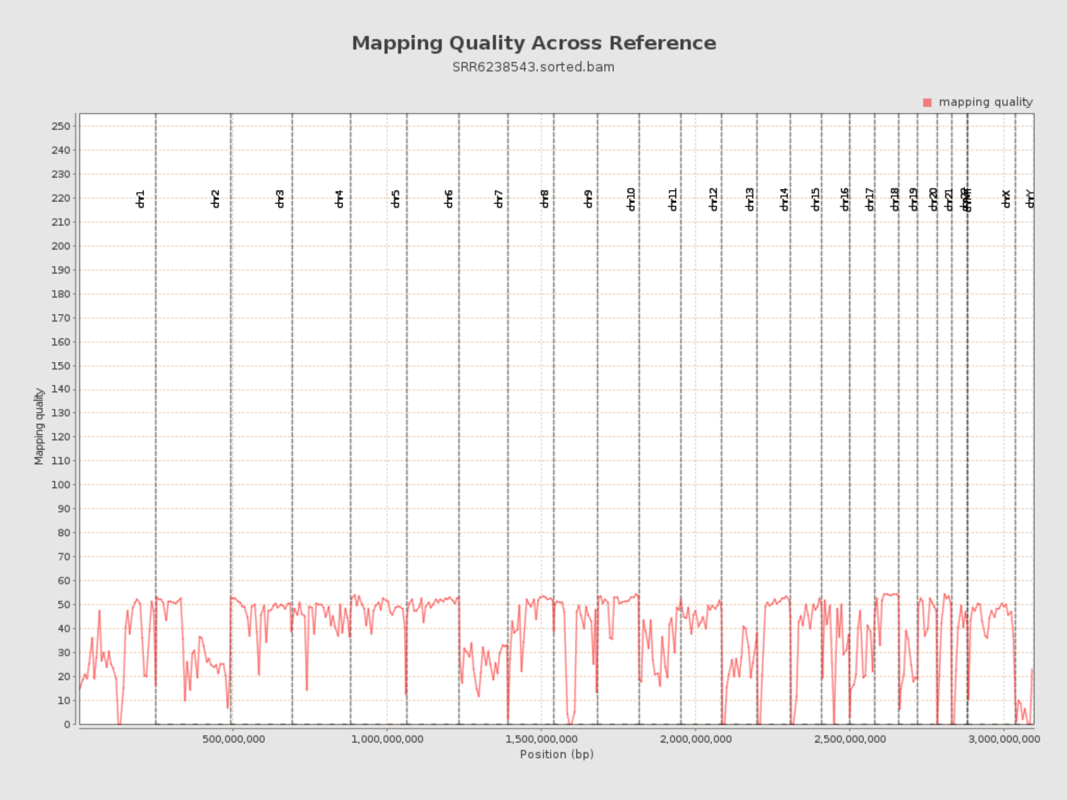
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram