Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:43:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238522.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_SRR6238522 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238522.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:43:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238522.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,723,832
Mapped reads	3,421,983 / 91.89%
Unmapped reads	301,849 / 8.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,270 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	702,163 / 18.86%
Duplication rate	16.57%
Clipped reads	2,206,586 / 59.26%

2.2. ACGT Content

Number/percentage of A's	51,613,784 / 24.55%
Number/percentage of C's	36,636,190 / 17.43%
Number/percentage of T's	70,823,331 / 33.69%
Number/percentage of G's	51,142,557 / 24.33%
Number/percentage of N's	14,202 / 0.01%
GC Percentage	41.75%

2.3. Coverage

Mean	0.0679

Standard Deviation	0.7992

2.4. Mapping Quality

Mean Mapping Quality	40.85

2.5. Mismatches and indels

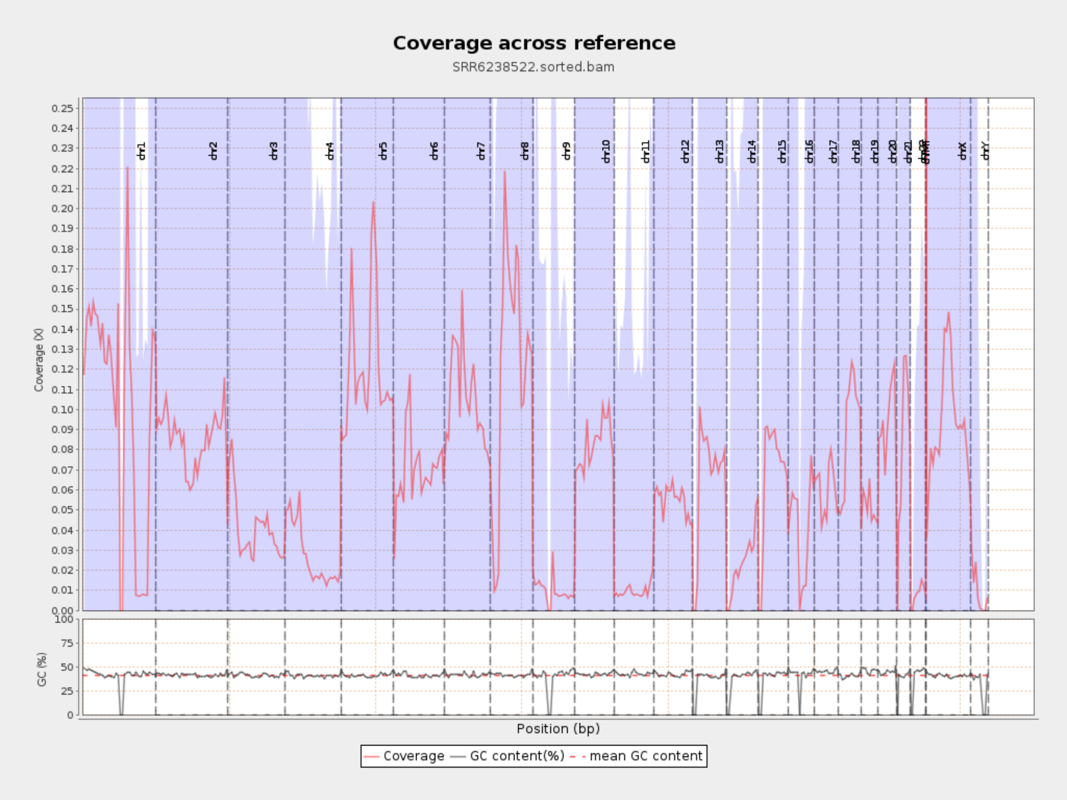
General error rate	0.57%
Mismatches	1,170,335
Insertions	12,504
Mapped reads with at least one insertion	0.36%
Deletions	58,100
Mapped reads with at least one deletion	1.68%
Homopolymer indels	42.62%

2.6. Chromosome stats

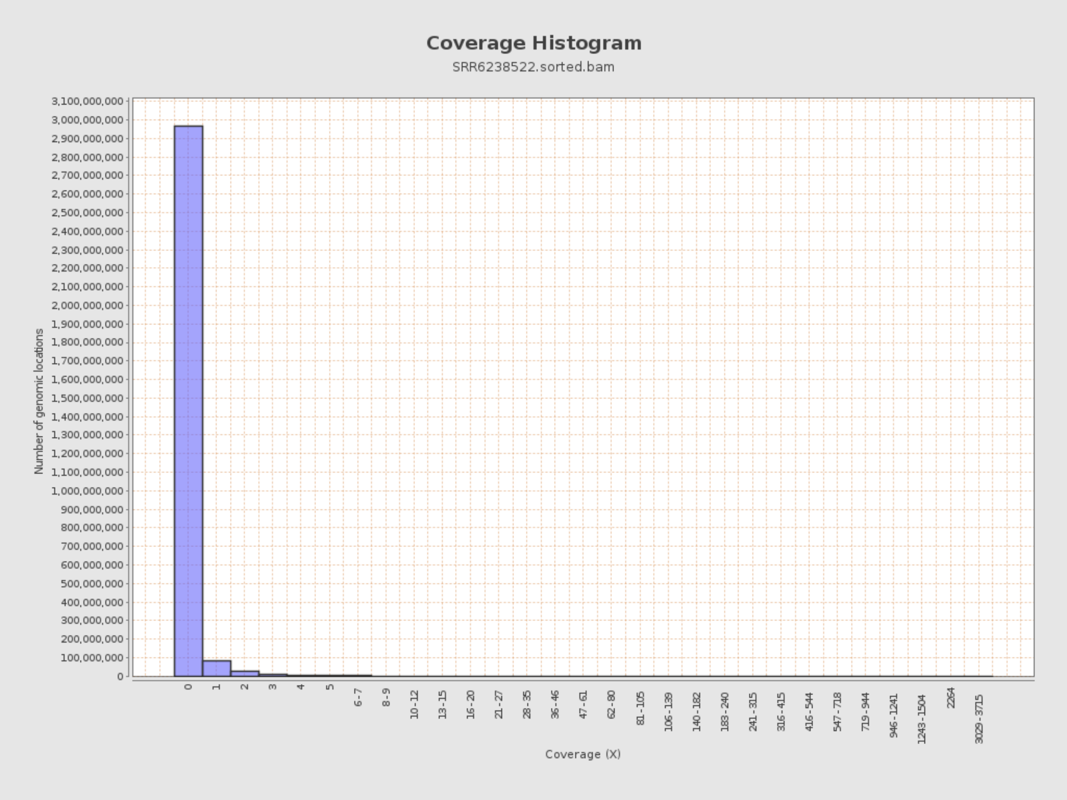
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24948792	0.1001	1.3374
chr2	243199373	20820209	0.0856	1.6739
chr3	198022430	8079253	0.0408	0.3163
chr4	191154276	5247041	0.0274	0.2617
chr5	180915260	21958017	0.1214	0.5382
chr6	171115067	12094284	0.0707	0.7425
chr7	159138663	16801950	0.1056	1.1202

chr8	146364022	17812007	0.1217	0.7979
chr9	141213431	1370950	0.0097	0.2407
chr10	135534747	11291064	0.0833	0.5453
chr11	135006516	1318710	0.0098	0.1602
chr12	133851895	7416975	0.0554	0.3642
chr13	115169878	7606545	0.066	0.5131
chr14	107349540	2471965	0.023	0.234
chr15	102531392	6824225	0.0666	0.5306
chr16	90354753	3550277	0.0393	0.3492
chr17	81195210	4990071	0.0615	0.3827
chr18	78077248	7022645	0.0899	1.1458
chr19	59128983	3044610	0.0515	0.8792
chr20	63025520	6106111	0.0969	0.4843
chr21	48129895	3953666	0.0821	0.4582
chr22	51304566	422693	0.0082	0.127
chrMT	16571	26069	1.5732	2.034
chrX	155270560	14585332	0.0939	0.4853
chrY	59373566	565905	0.0095	0.3016

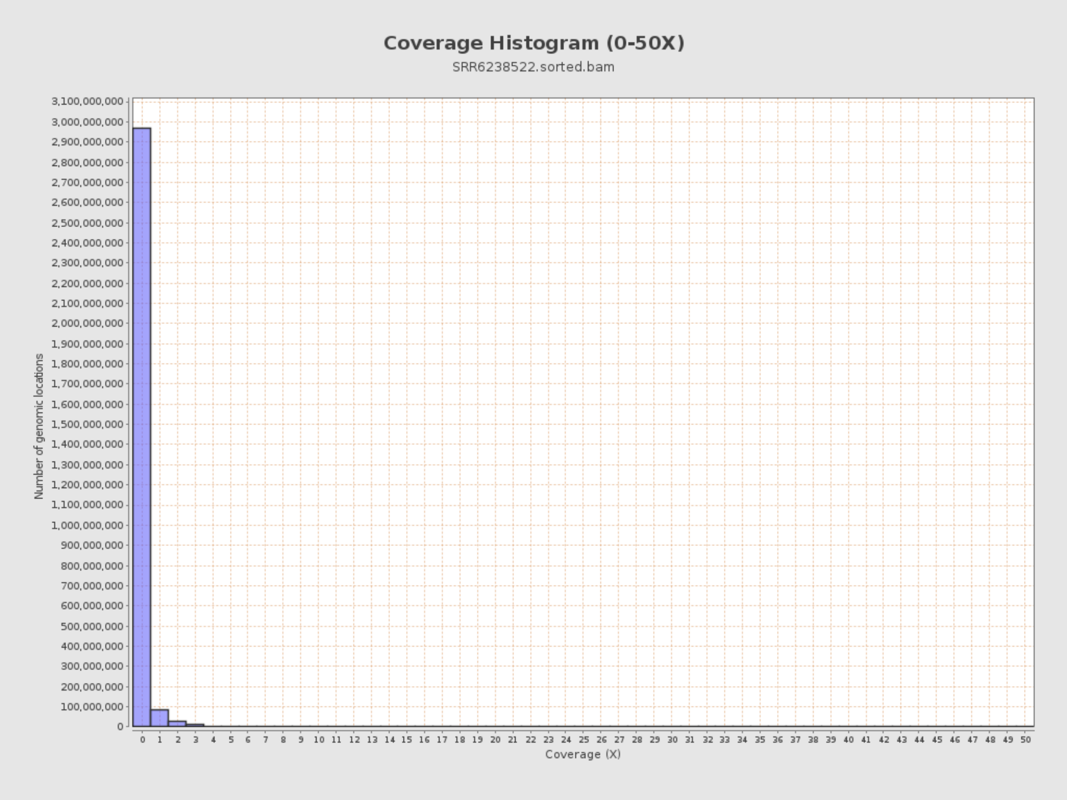
3. Results : Coverage across reference



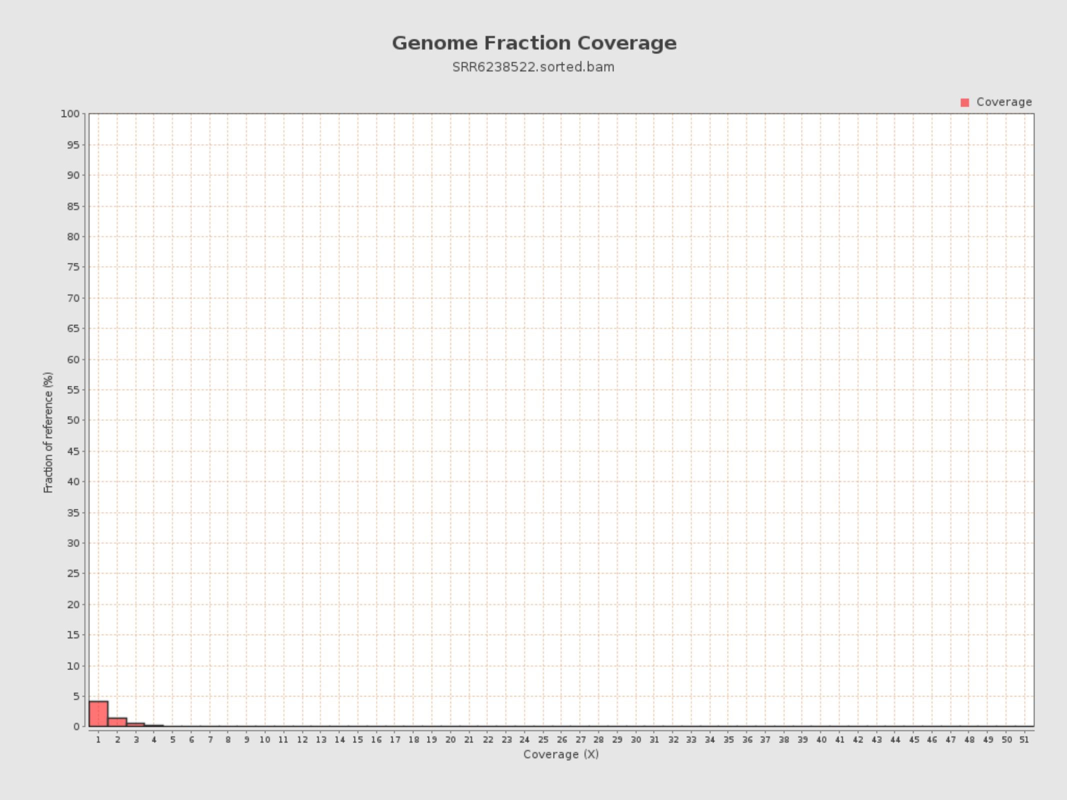
4. Results : Coverage Histogram



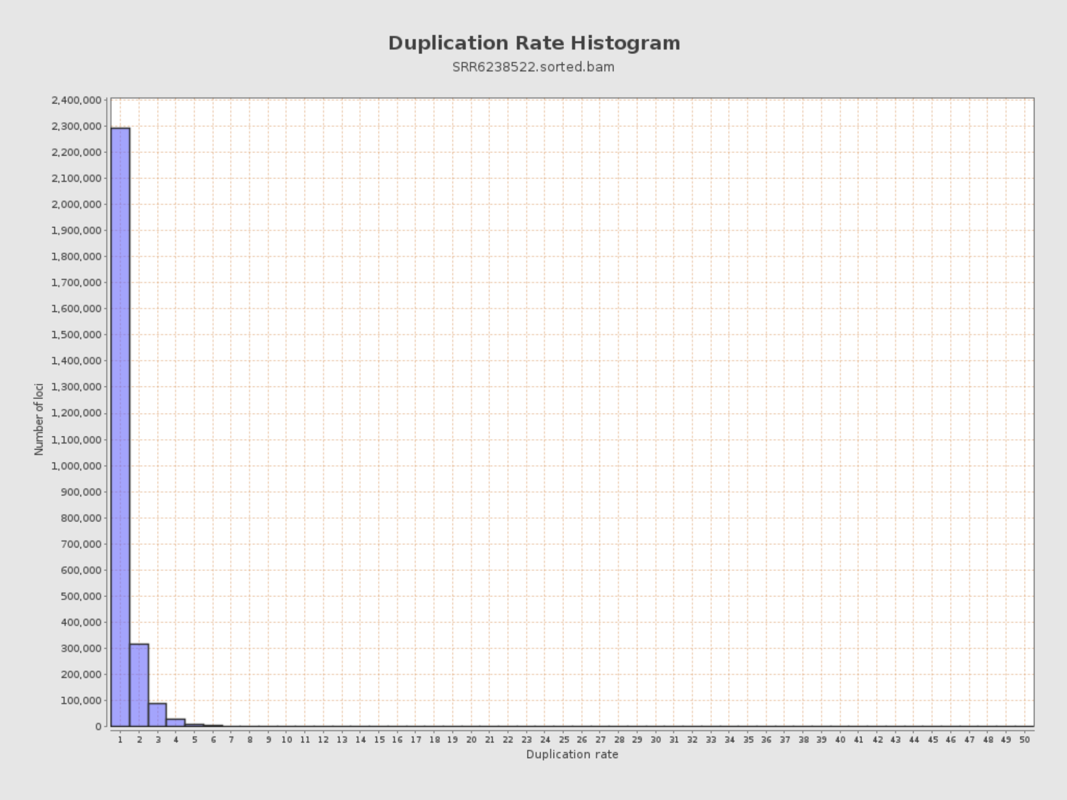
5. Results : Coverage Histogram (0-50X)



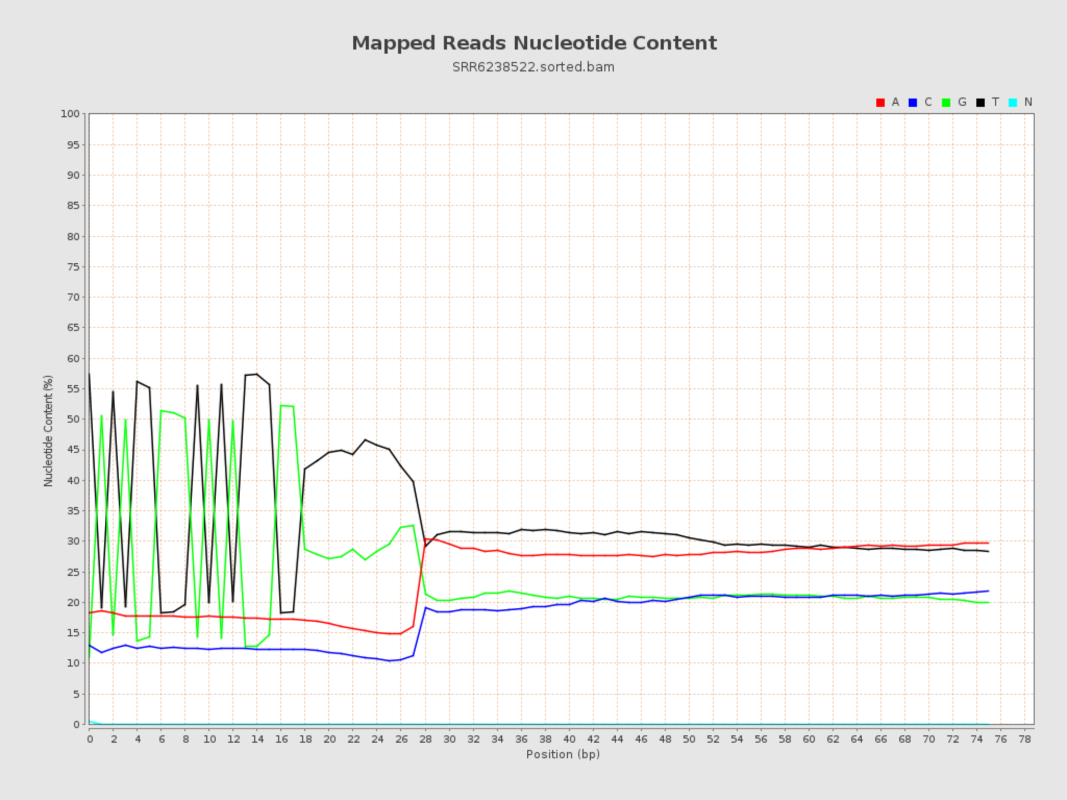
6. Results : Genome Fraction Coverage



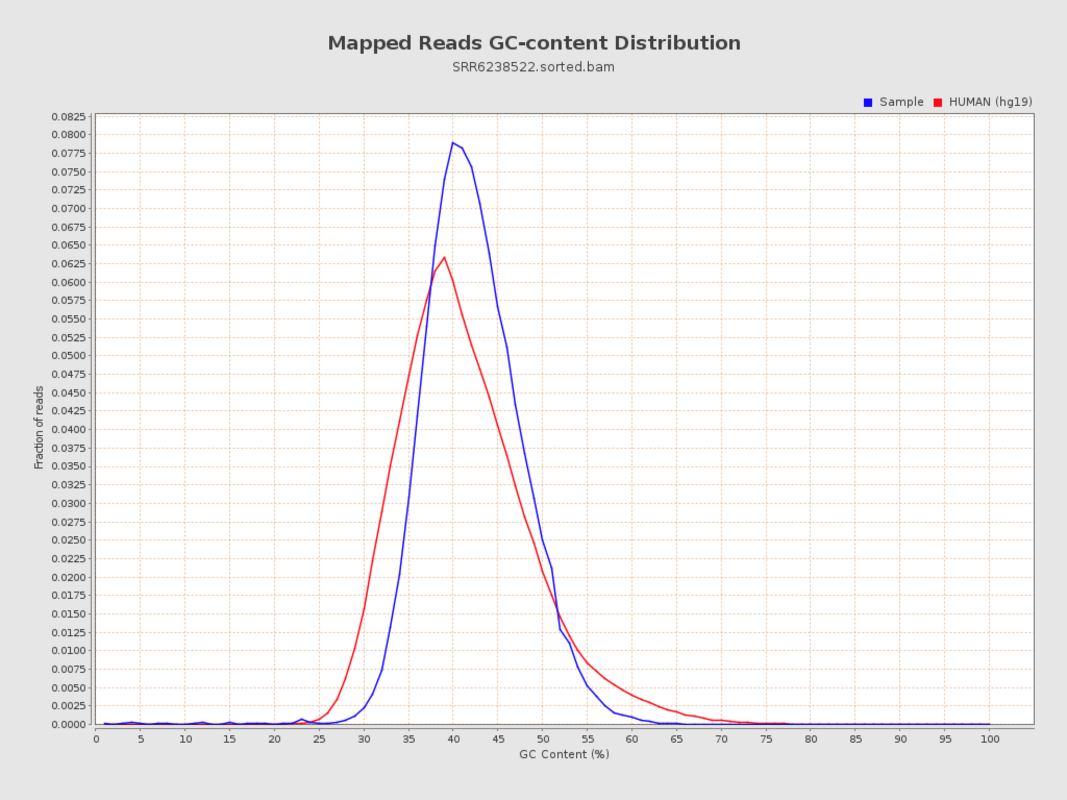
7. Results : Duplication Rate Histogram



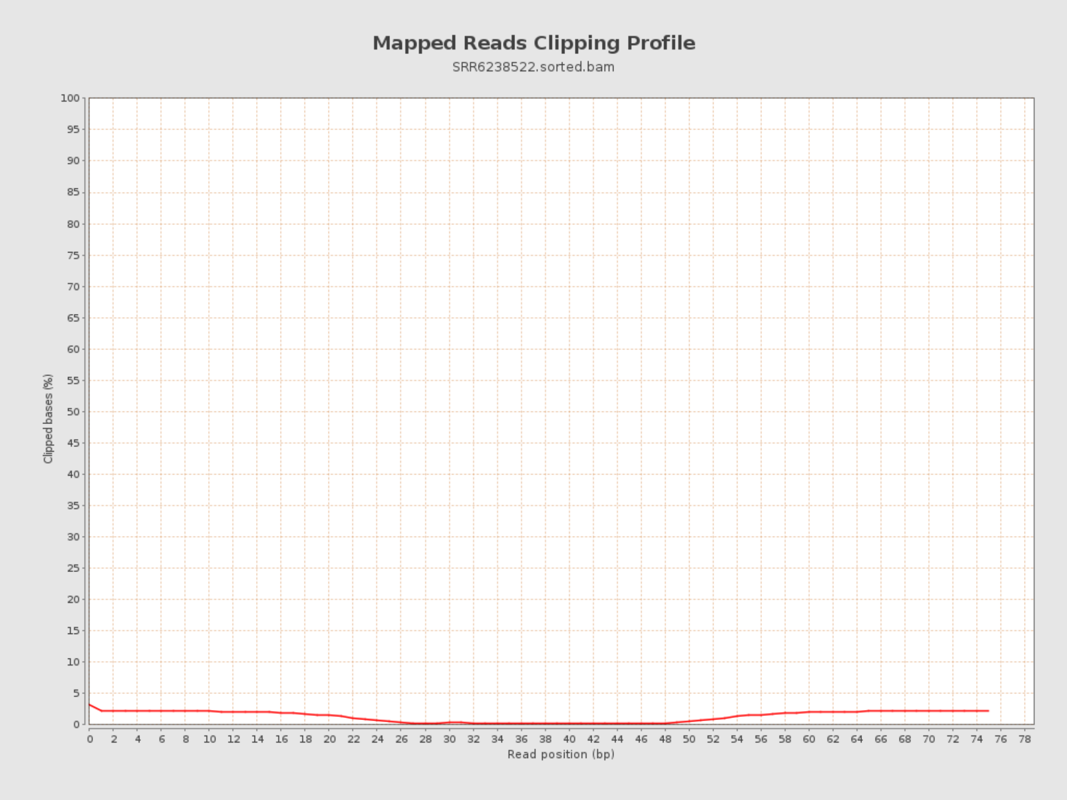
8. Results : Mapped Reads Nucleotide Content



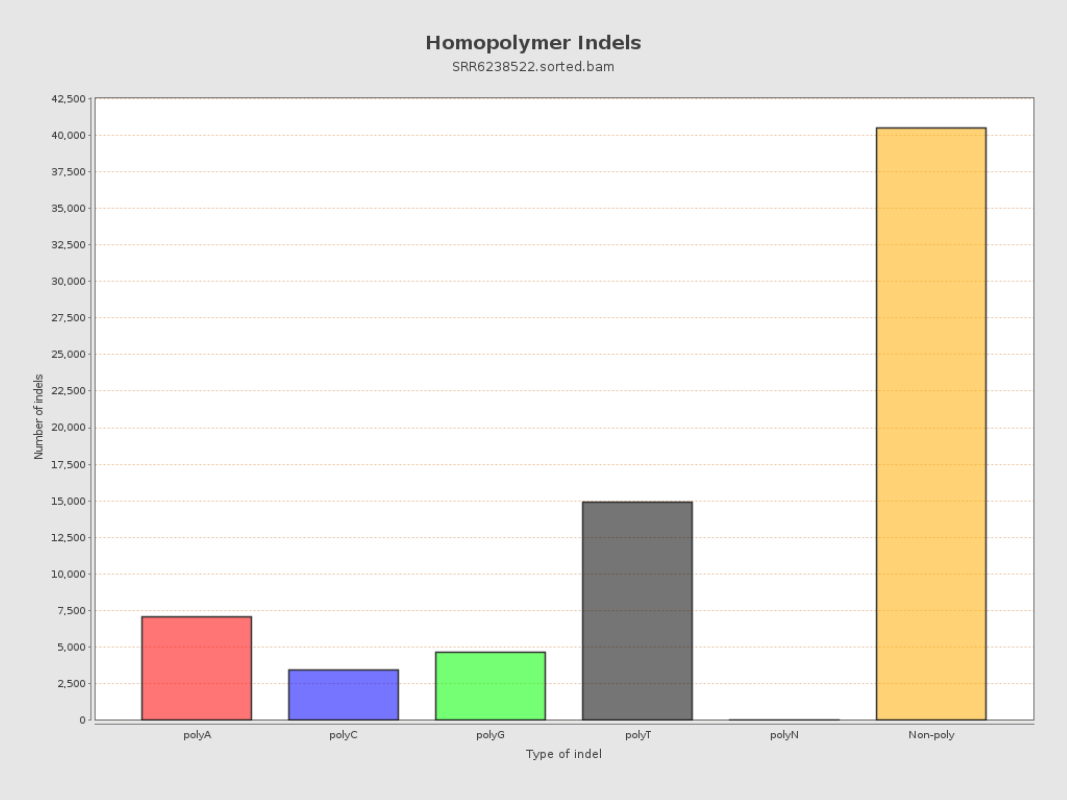
9. Results : Mapped Reads GC-content Distribution



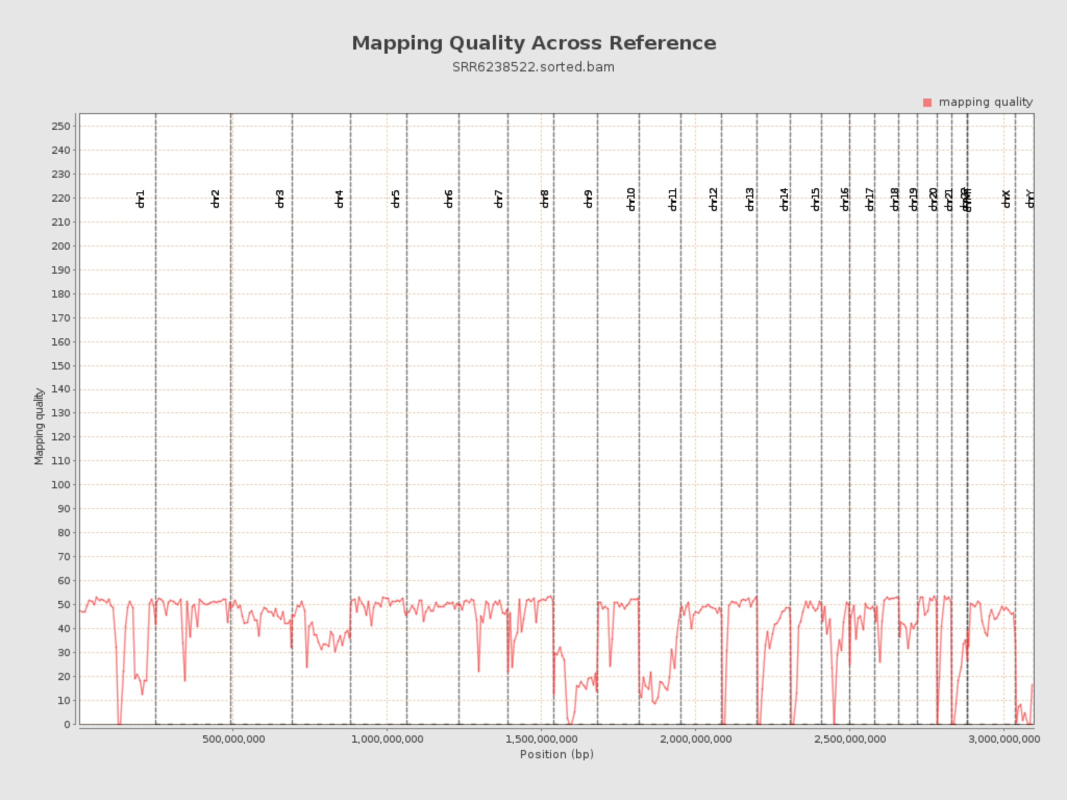
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram