Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:10:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238276.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_SRR6238276 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238276.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:10:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238276.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,155,276
Mapped reads	2,837,094 / 89.92%
Unmapped reads	318,182 / 10.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,328 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	130,672 / 4.14%
Duplication rate	3.39%
Clipped reads	1,473,821 / 46.71%

2.2. ACGT Content

Number/percentage of A's	51,122,510 / 27.61%
Number/percentage of C's	35,205,432 / 19.02%
Number/percentage of T's	56,677,332 / 30.61%
Number/percentage of G's	42,086,225 / 22.73%
Number/percentage of N's	45,342 / 0.02%
GC Percentage	41.75%

2.3. Coverage

Mean	0.0598

Standard Deviation	0.5121

2.4. Mapping Quality

Mean Mapping Quality	44.14

2.5. Mismatches and indels

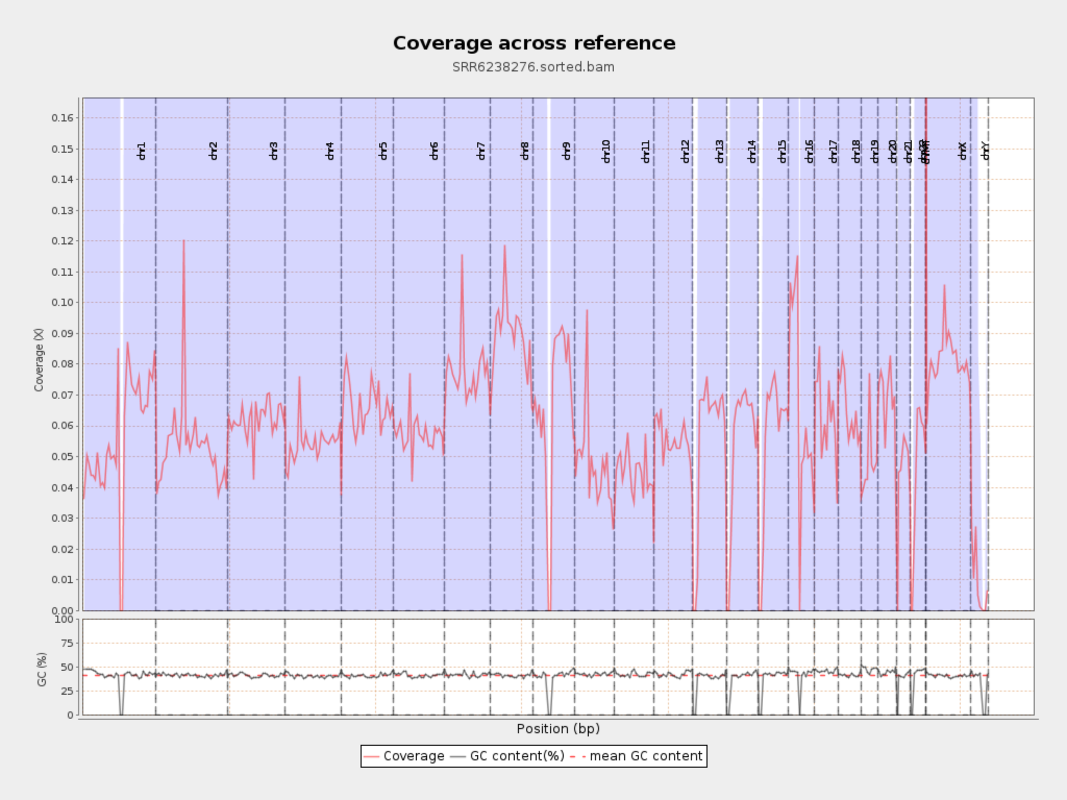
General error rate	0.9%
Mismatches	1,633,660
Insertions	15,228
Mapped reads with at least one insertion	0.53%
Deletions	57,808
Mapped reads with at least one deletion	2.01%
Homopolymer indels	45.24%

2.6. Chromosome stats

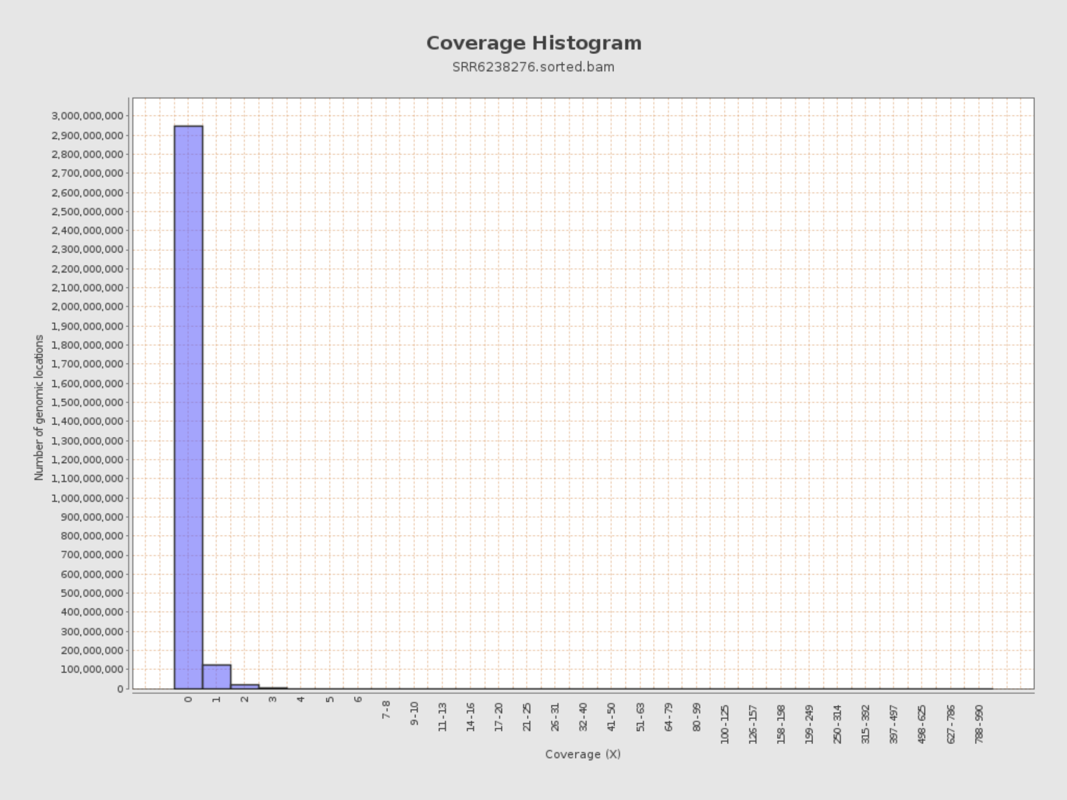
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14029965	0.0563	0.8498
chr2	243199373	13076613	0.0538	0.6782
chr3	198022430	12267363	0.0619	0.2964
chr4	191154276	10404992	0.0544	0.3141
chr5	180915260	11977014	0.0662	0.3055
chr6	171115067	9792186	0.0572	0.3717
chr7	159138663	12338469	0.0775	0.7829

chr8	146364022	13079165	0.0894	0.6855
chr9	141213431	9417540	0.0667	0.5007
chr10	135534747	6423828	0.0474	0.4853
chr11	135006516	6057135	0.0449	0.3875
chr12	133851895	7453667	0.0557	0.2863
chr13	115169878	6445848	0.056	0.2784
chr14	107349540	5885937	0.0548	0.3153
chr15	102531392	5549425	0.0541	0.2821
chr16	90354753	5891042	0.0652	0.3509
chr17	81195210	5214033	0.0642	0.3781
chr18	78077248	5132081	0.0657	0.8887
chr19	59128983	2896522	0.049	0.6512
chr20	63025520	4363595	0.0692	0.3212
chr21	48129895	2148378	0.0446	0.2915
chr22	51304566	2244815	0.0438	0.2468
chrMT	16571	7119	0.4296	0.8125
chrX	155270560	12604784	0.0812	0.3927
chrY	59373566	531180	0.0089	0.2195

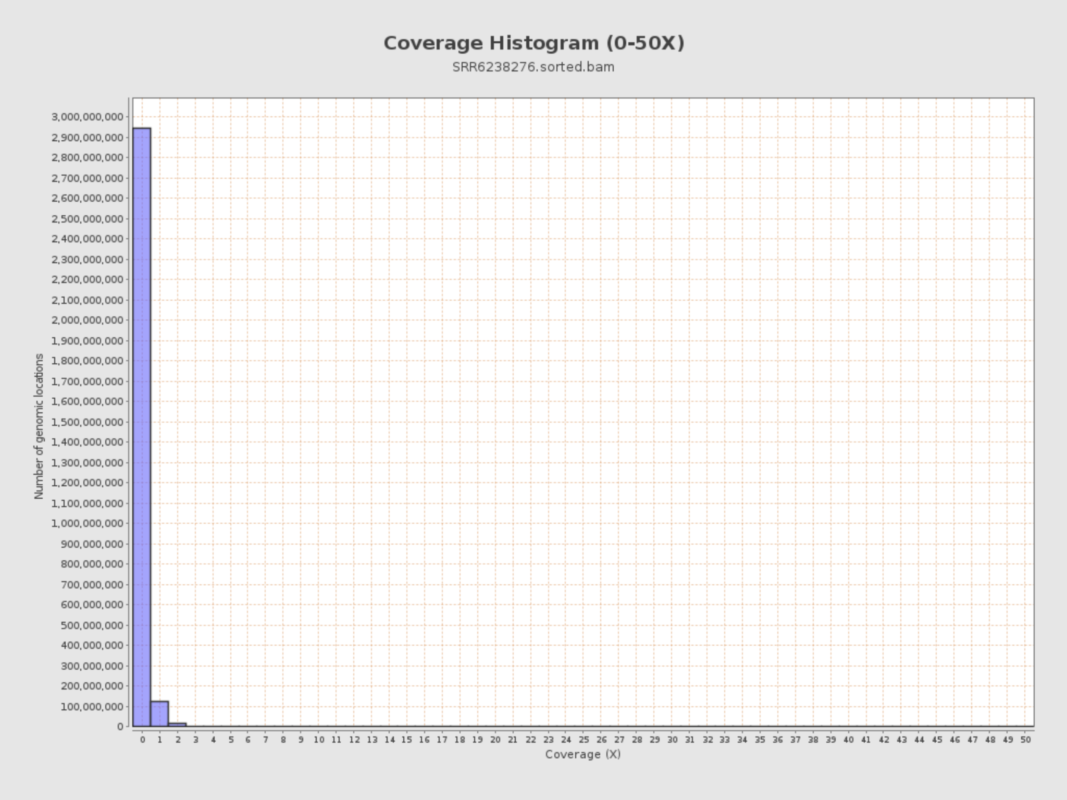
3. Results : Coverage across reference



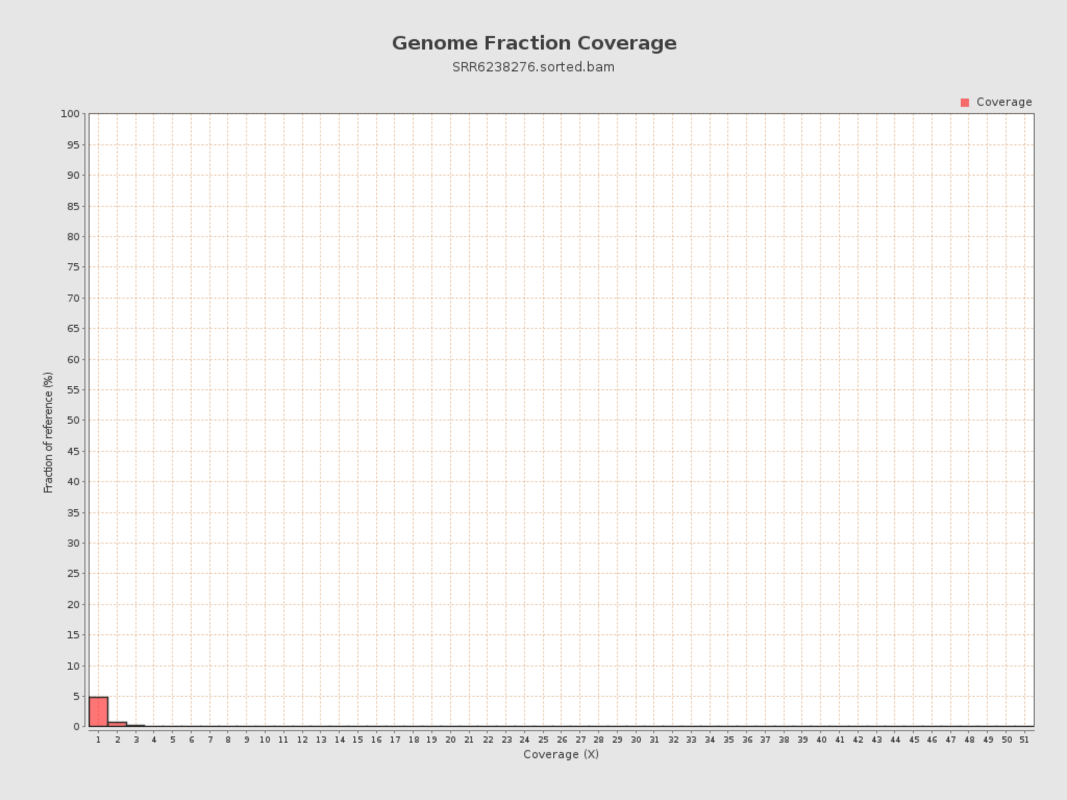
4. Results : Coverage Histogram



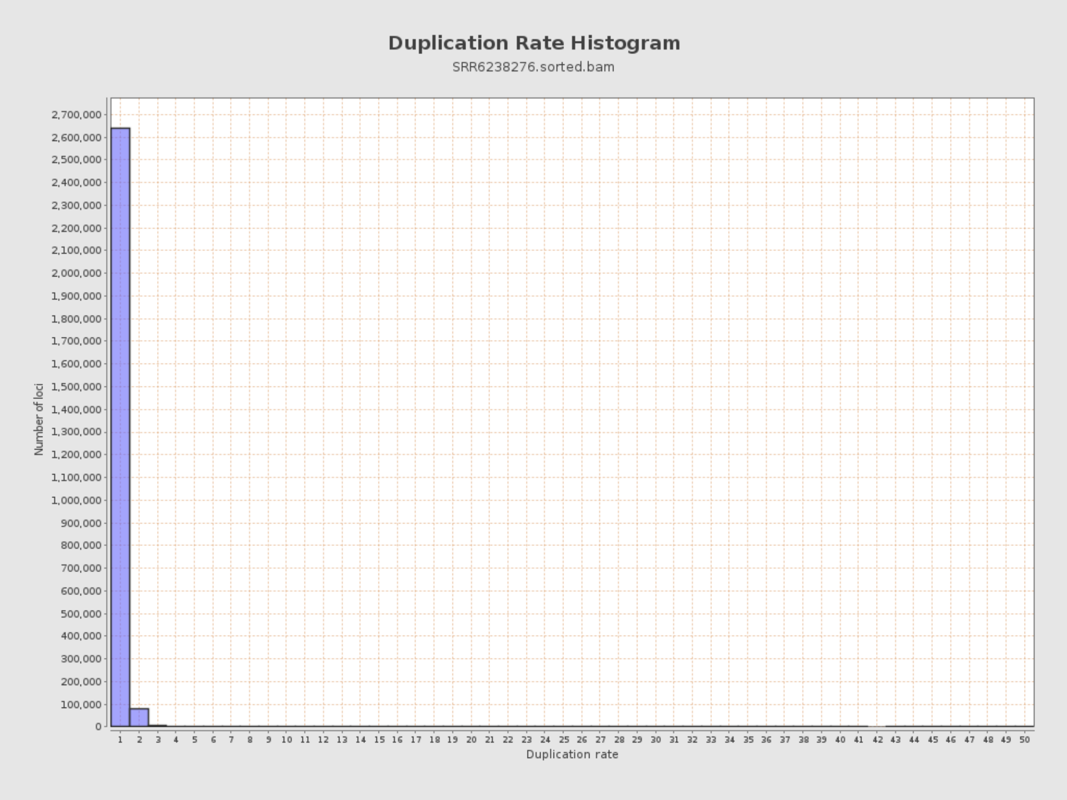
5. Results : Coverage Histogram (0-50X)



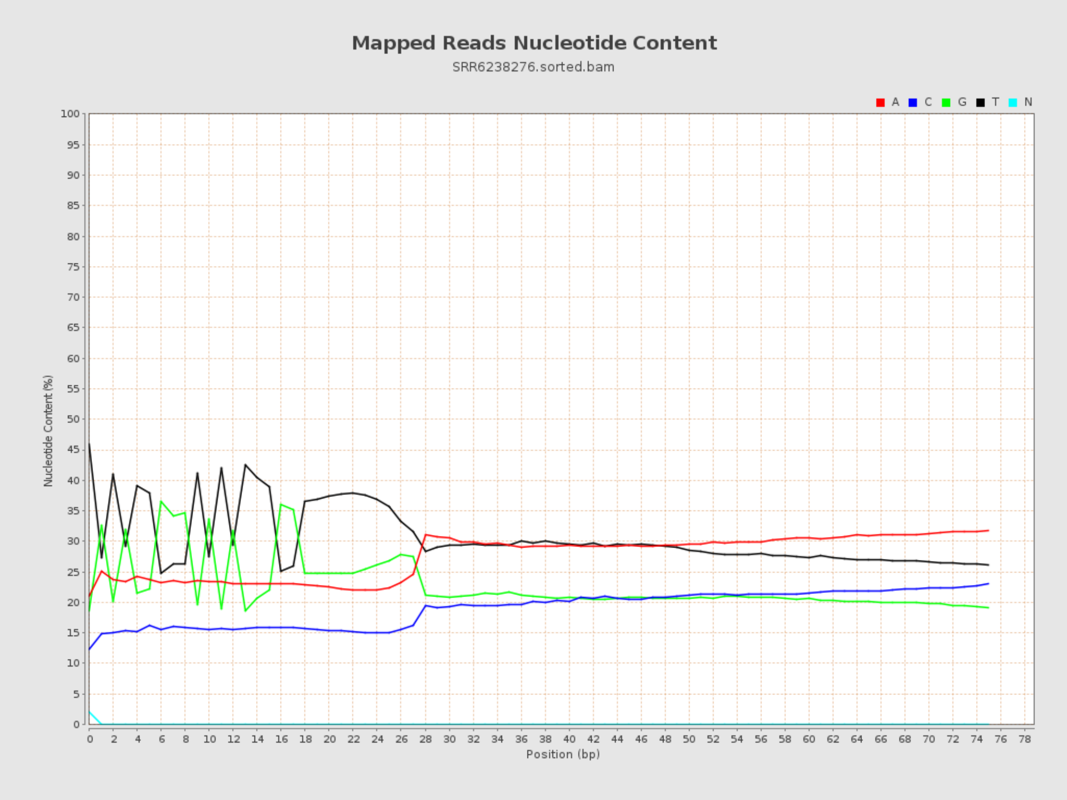
6. Results : Genome Fraction Coverage



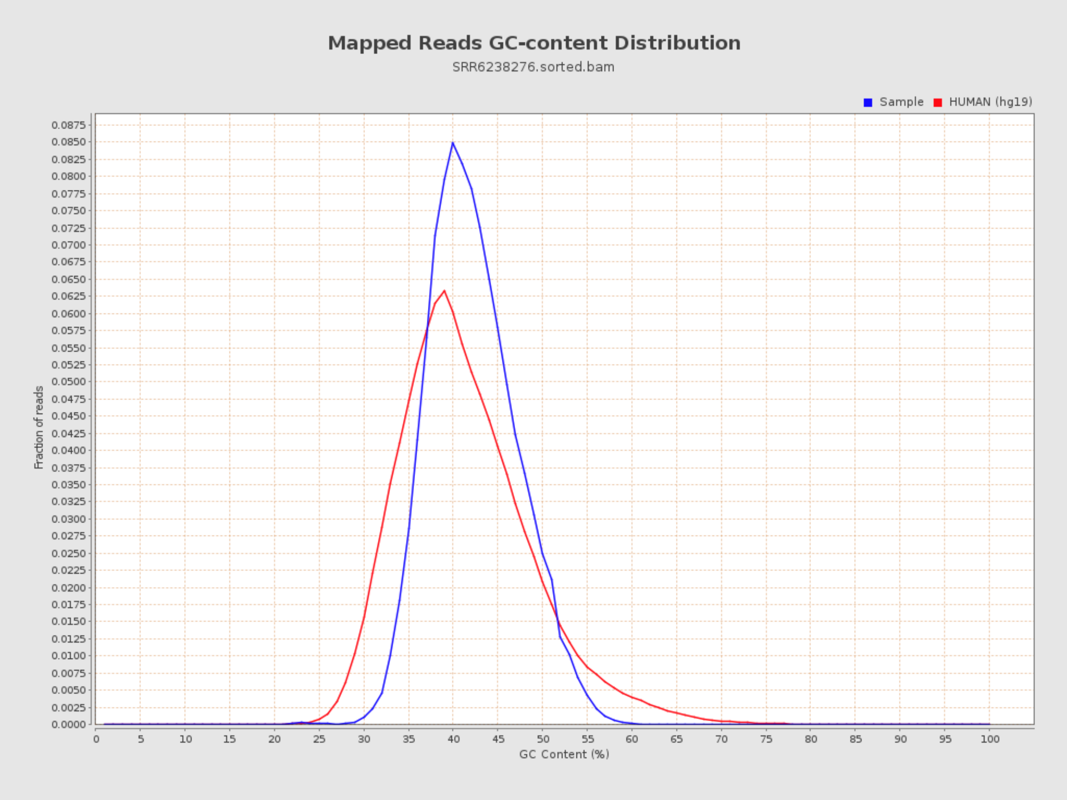
7. Results : Duplication Rate Histogram



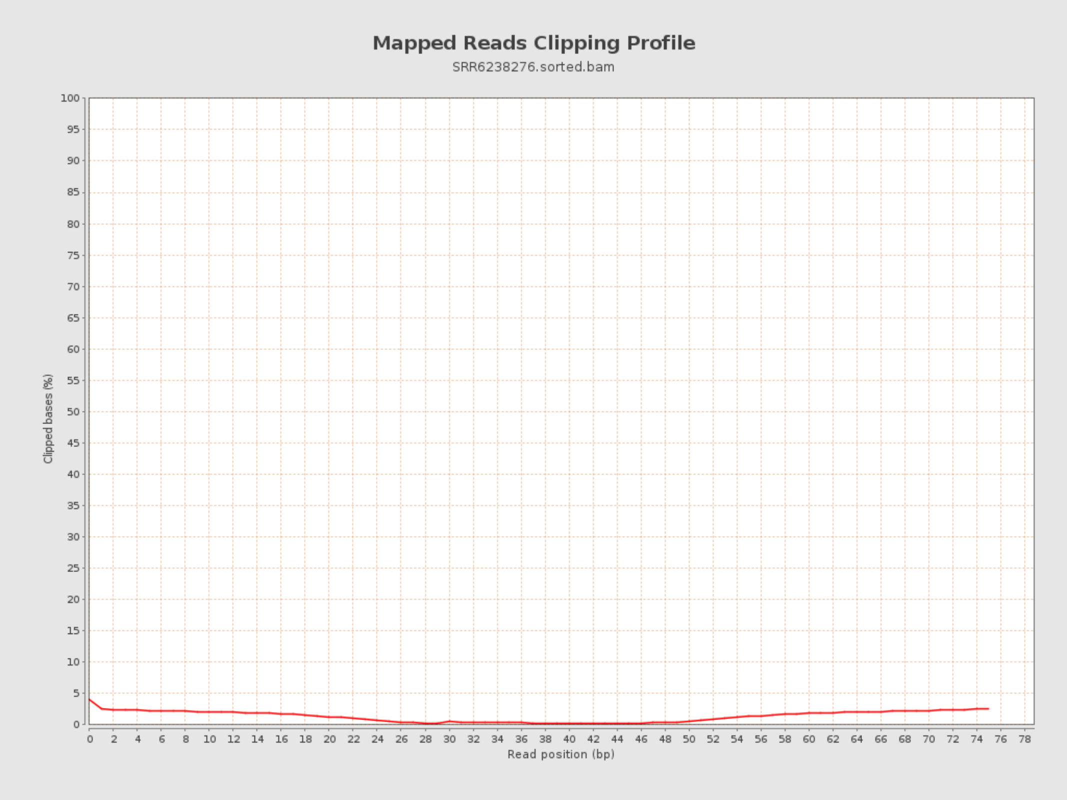
8. Results : Mapped Reads Nucleotide Content



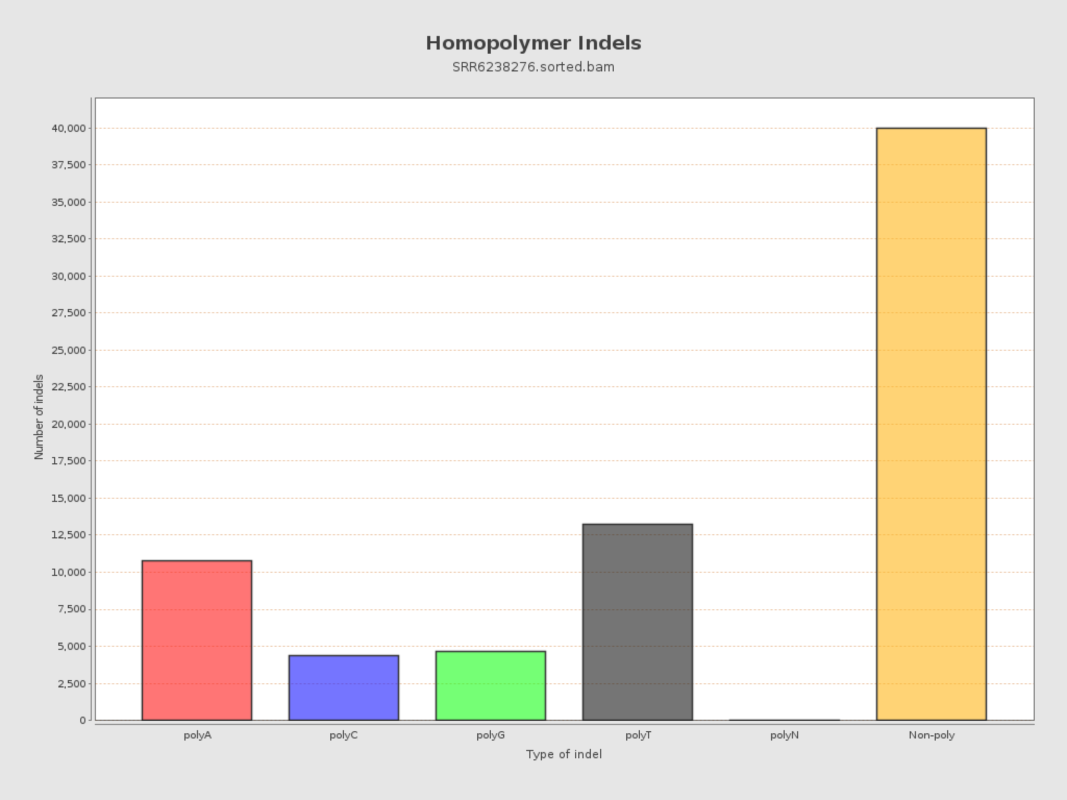
9. Results : Mapped Reads GC-content Distribution



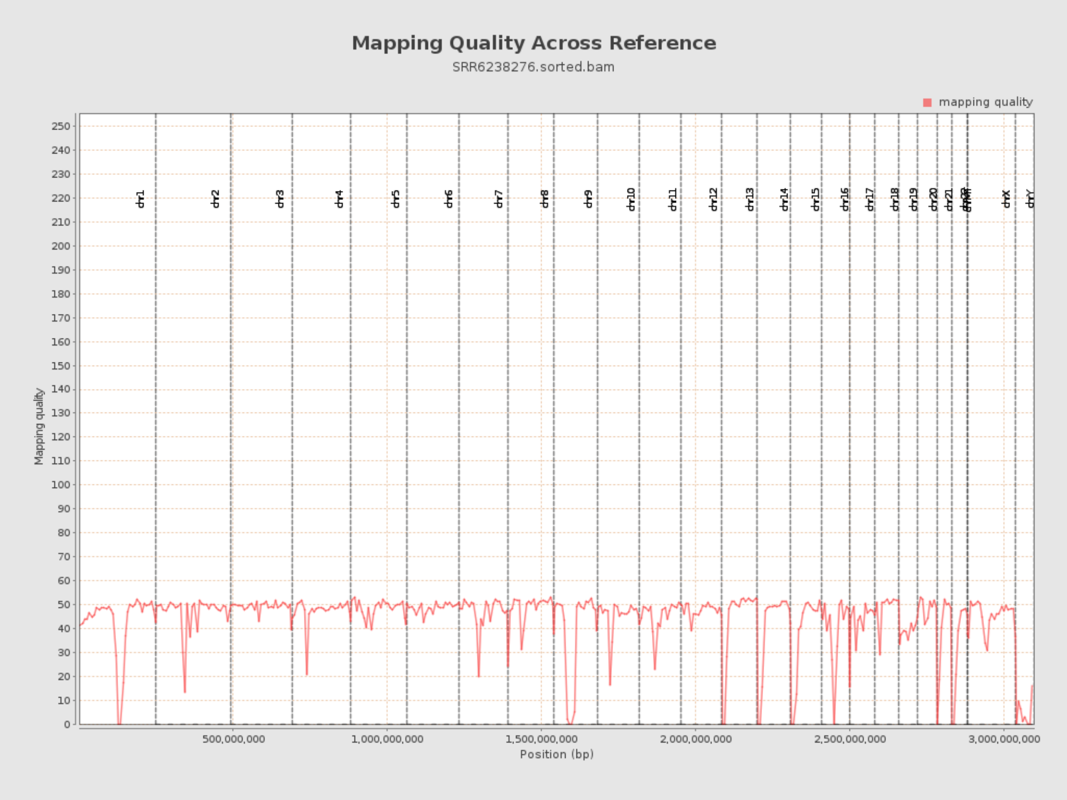
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram