Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:52:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238072.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_SRR6238072 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238072.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:52:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,090,489
Mapped reads	1,855,491 / 88.76%
Unmapped reads	234,998 / 11.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,058 / 0.96%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	106,294 / 5.08%
Duplication rate	4.34%
Clipped reads	802,217 / 38.37%

2.2. ACGT Content

Number/percentage of A's	33,592,122 / 27.11%
Number/percentage of C's	23,861,258 / 19.26%
Number/percentage of T's	38,327,046 / 30.93%
Number/percentage of G's	28,110,959 / 22.69%
Number/percentage of N's	7,143 / 0.01%
GC Percentage	41.95%

2.3. Coverage

Mean	0.04

Standard Deviation	0.4542

2.4. Mapping Quality

Mean Mapping Quality	43.39

2.5. Mismatches and indels

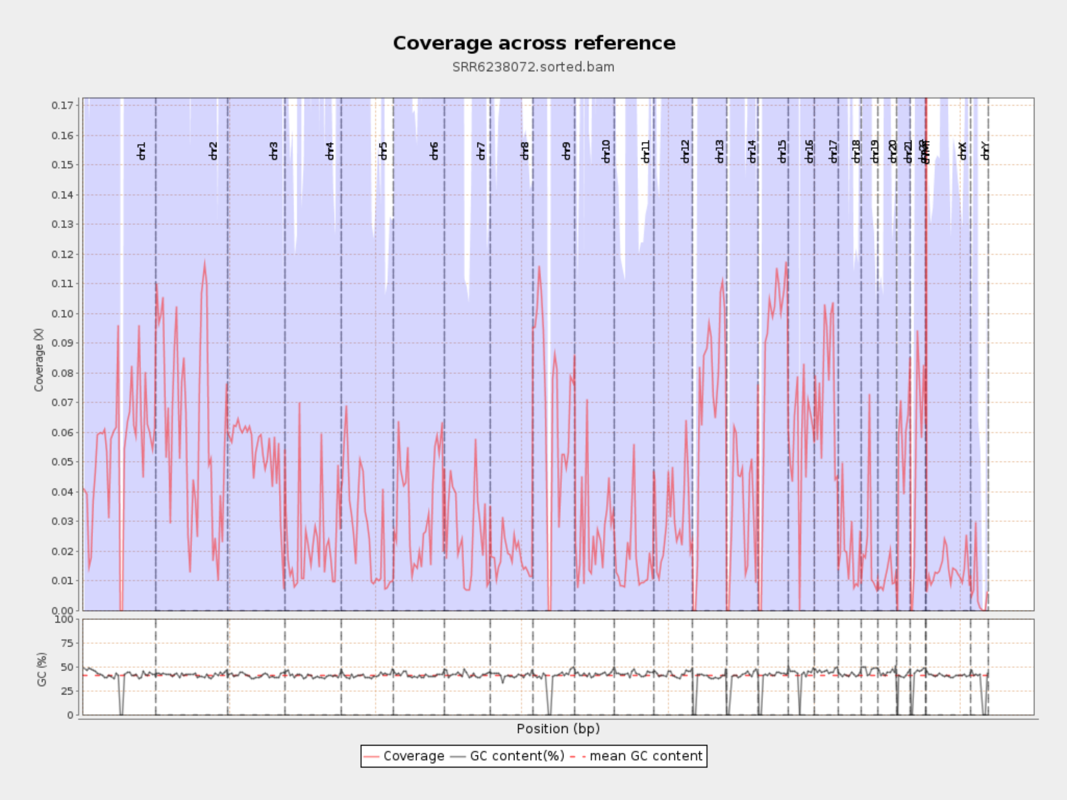
General error rate	0.76%
Mismatches	922,698
Insertions	9,532
Mapped reads with at least one insertion	0.51%
Deletions	29,131
Mapped reads with at least one deletion	1.55%
Homopolymer indels	45.9%

2.6. Chromosome stats

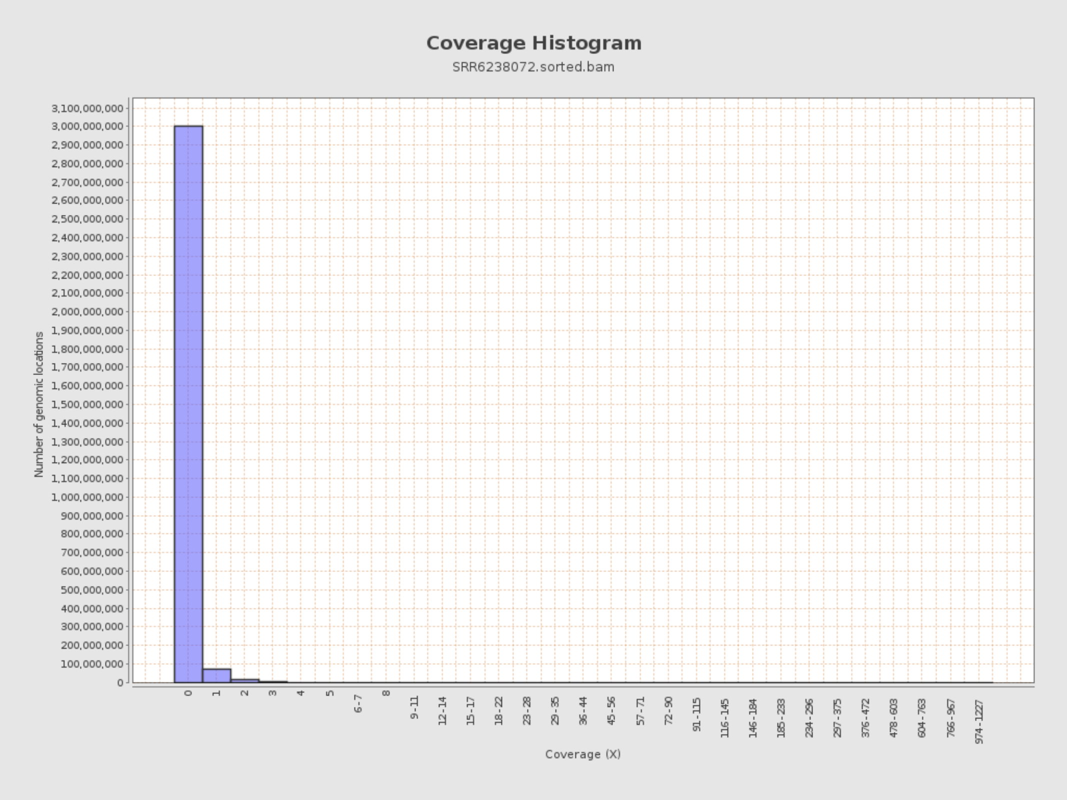
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13373802	0.0537	1.0602
chr2	243199373	15067709	0.062	0.4547
chr3	198022430	10533982	0.0532	0.2877
chr4	191154276	4339125	0.0227	0.244
chr5	180915260	4904226	0.0271	0.2142
chr6	171115067	5976722	0.0349	0.2479
chr7	159138663	4168705	0.0262	0.2271

chr8	146364022	2615194	0.0179	0.5022
chr9	141213431	9618995	0.0681	0.4491
chr10	135534747	3535824	0.0261	0.3595
chr11	135006516	2245181	0.0166	0.2107
chr12	133851895	4126722	0.0308	0.2355
chr13	115169878	8360420	0.0726	0.3378
chr14	107349540	3609543	0.0336	0.2796
chr15	102531392	8697763	0.0848	0.3693
chr16	90354753	5108601	0.0565	0.3618
chr17	81195210	6254991	0.077	0.3526
chr18	78077248	1524241	0.0195	0.8623
chr19	59128983	1294389	0.0219	0.5582
chr20	63025520	683231	0.0108	0.1728
chr21	48129895	2705858	0.0562	0.3533
chr22	51304566	2651152	0.0517	0.2876
chrMT	16571	64833	3.9124	3.0741
chrX	155270560	2104757	0.0136	0.1742
chrY	59373566	385686	0.0065	0.2718

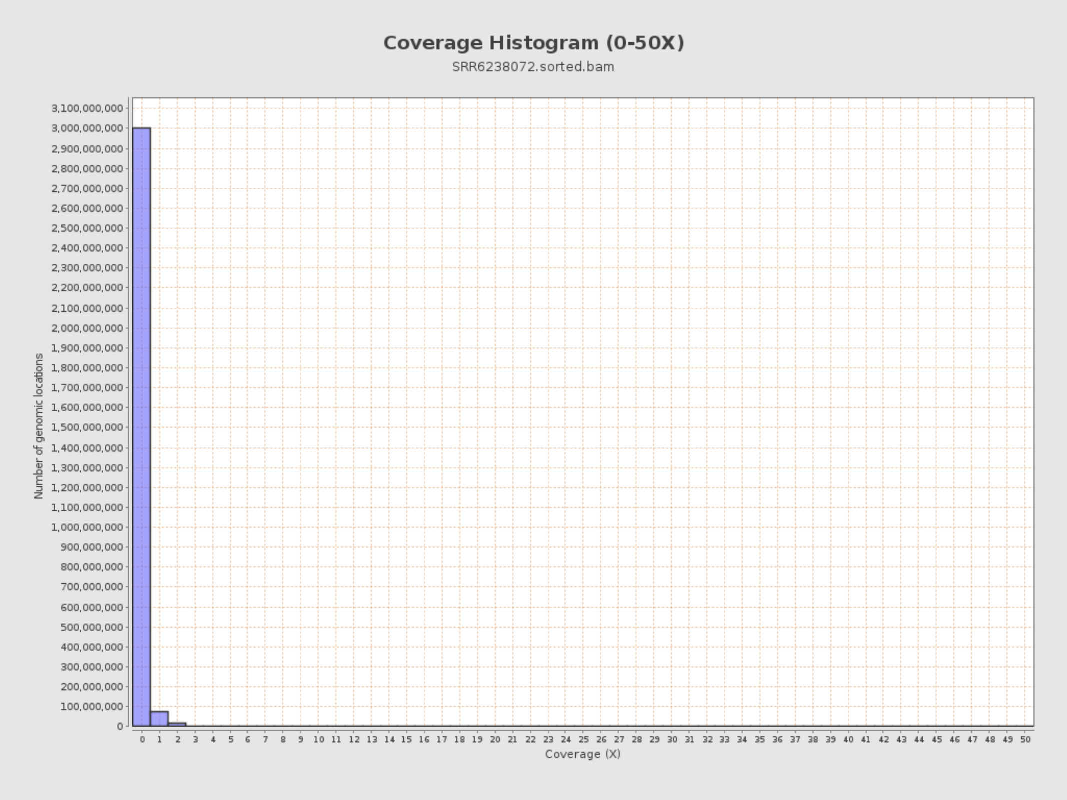
3. Results : Coverage across reference



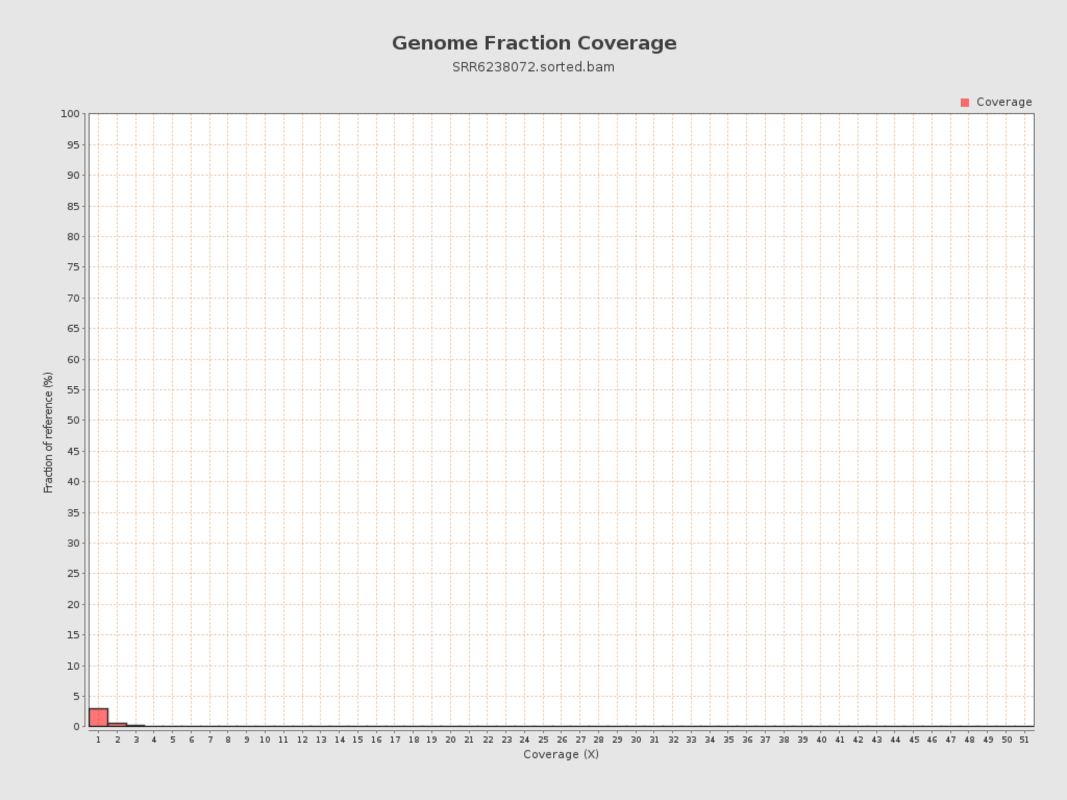
4. Results : Coverage Histogram



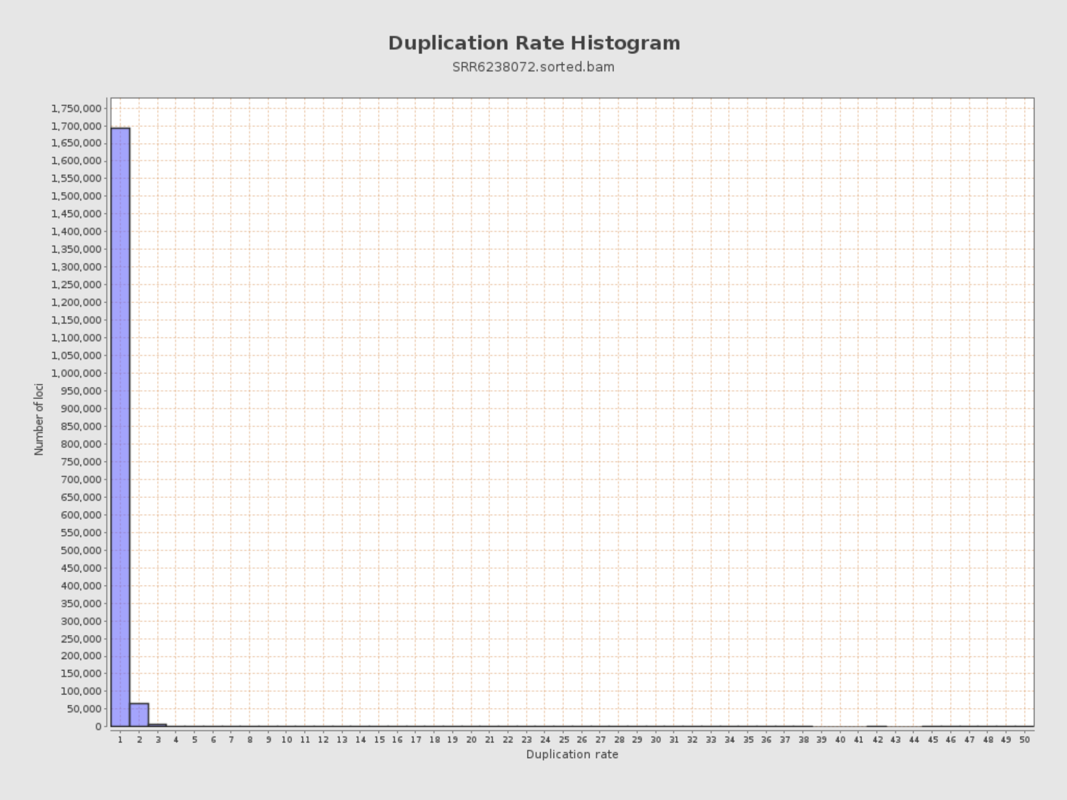
5. Results : Coverage Histogram (0-50X)



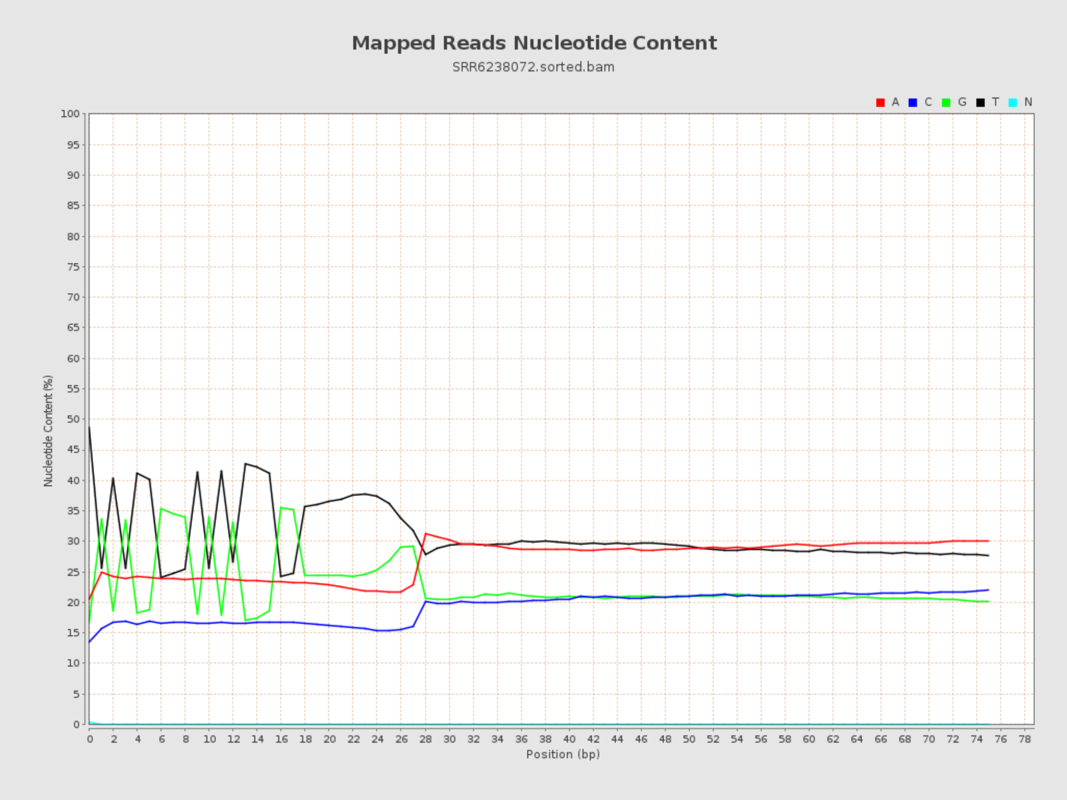
6. Results : Genome Fraction Coverage



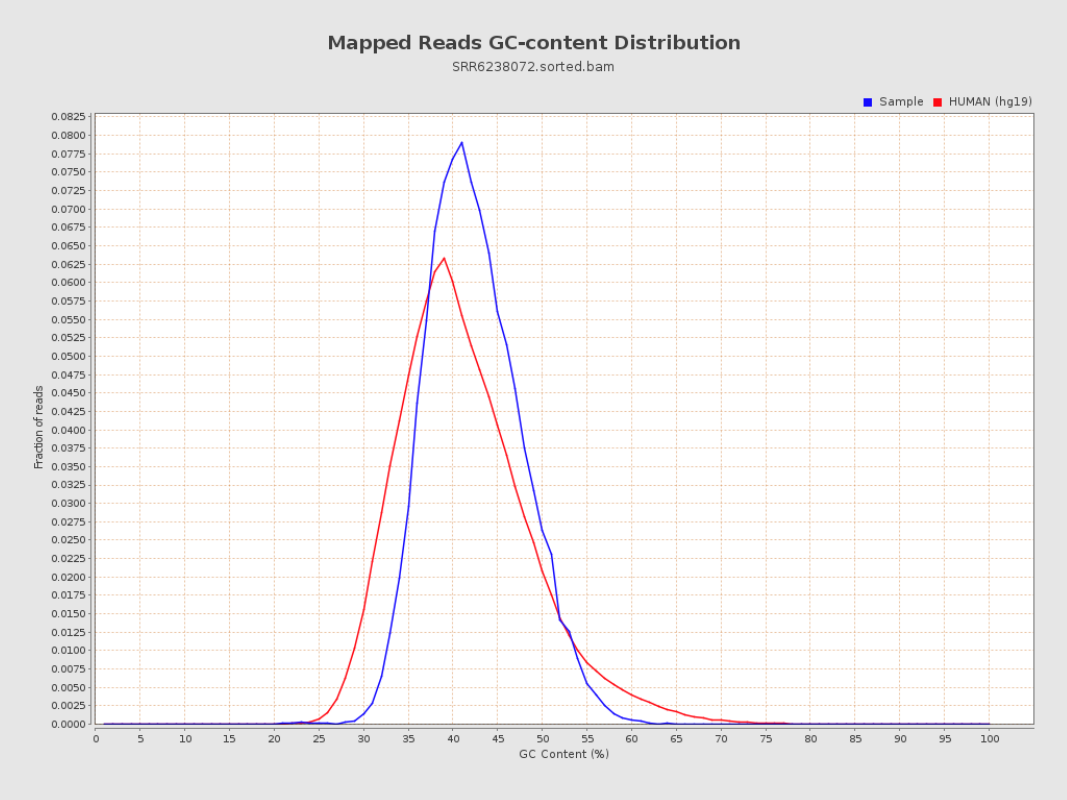
7. Results : Duplication Rate Histogram



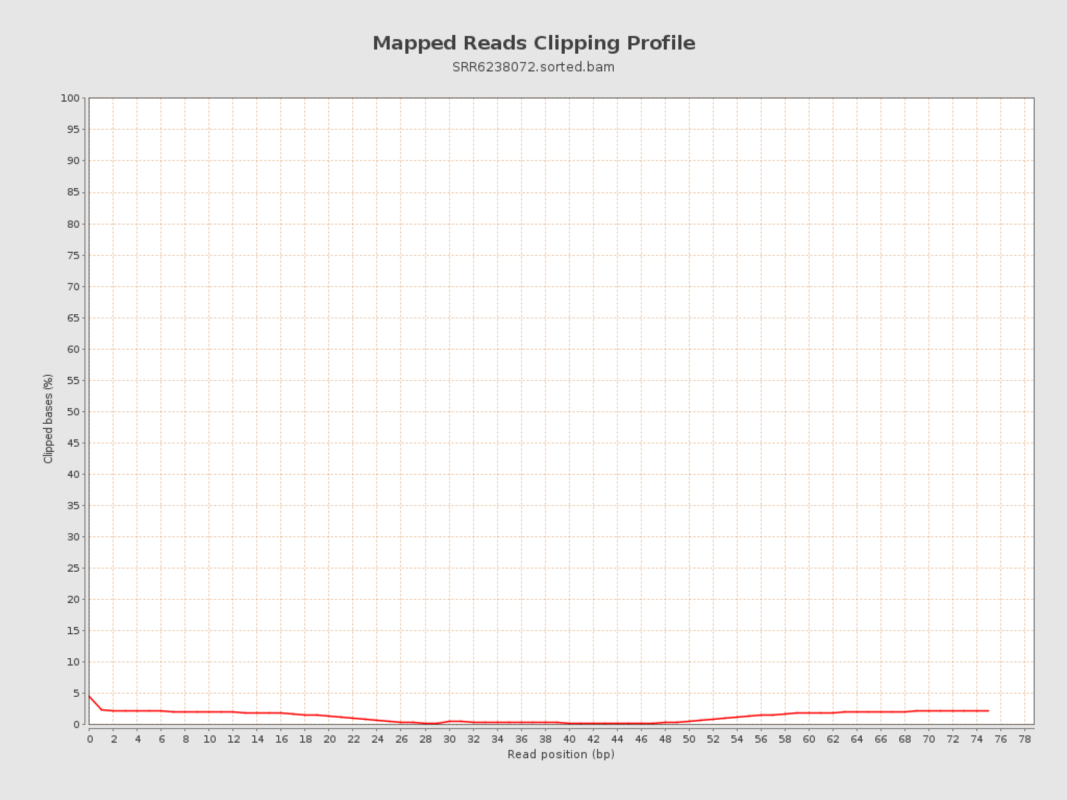
8. Results : Mapped Reads Nucleotide Content



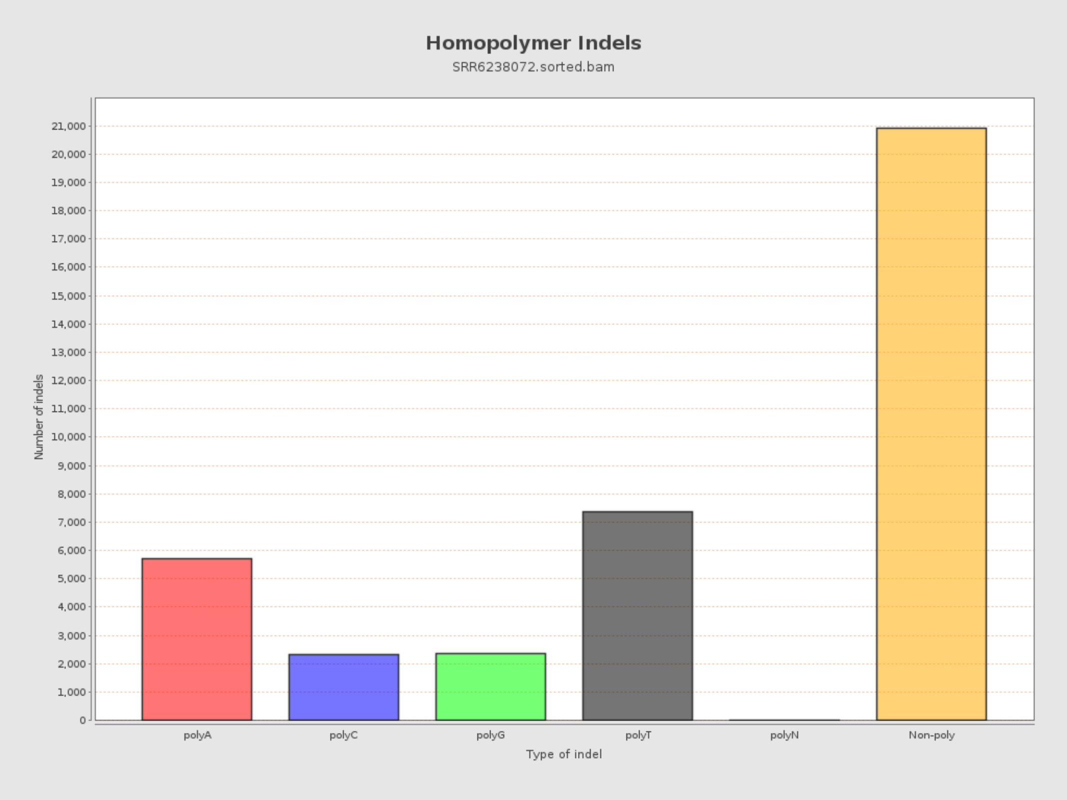
9. Results : Mapped Reads GC-content Distribution



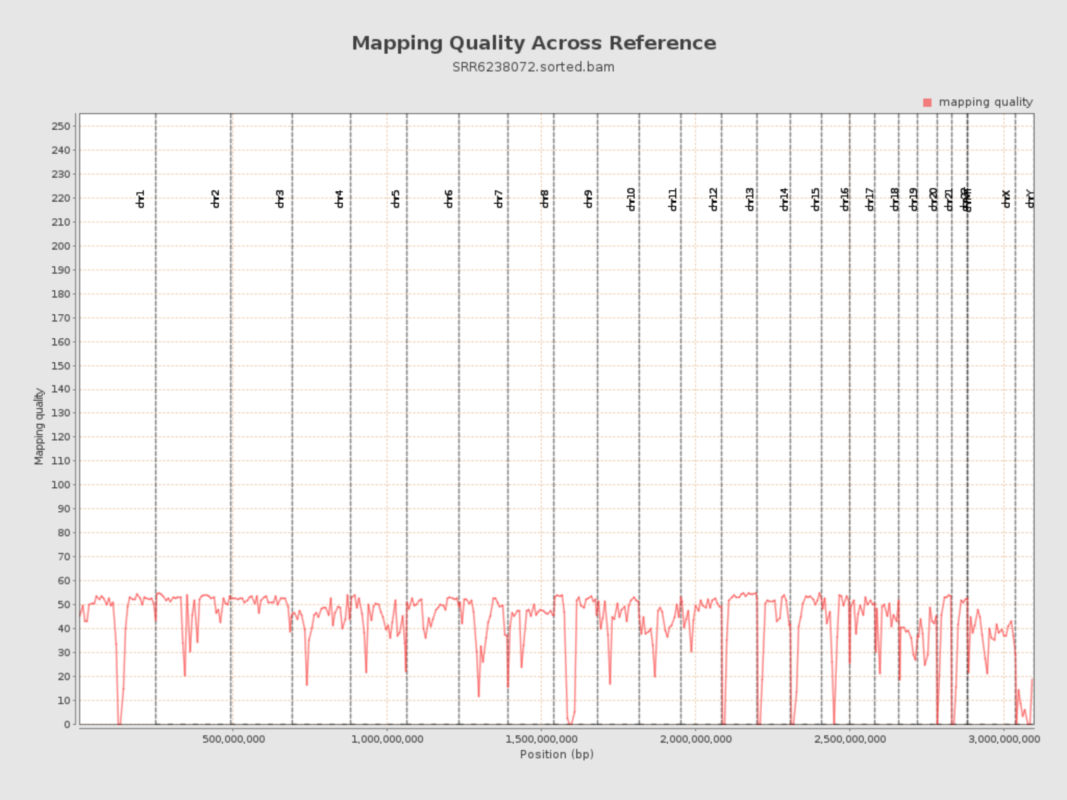
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram