Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:41:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238491.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_SRR6238491 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238491.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:41:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238491.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,623,196
Mapped reads	3,165,754 / 87.37%
Unmapped reads	457,442 / 12.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,920 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	1,488,276 / 41.08%
Duplication rate	20.84%
Clipped reads	2,023,781 / 55.86%

2.2. ACGT Content

Number/percentage of A's	48,531,330 / 24.89%
Number/percentage of C's	33,543,165 / 17.2%
Number/percentage of T's	66,795,124 / 34.25%
Number/percentage of G's	46,120,228 / 23.65%
Number/percentage of N's	4,564 / 0%
GC Percentage	40.85%

2.3. Coverage

Mean	0.063

Standard Deviation	1.3227

2.4. Mapping Quality

Mean Mapping Quality	40.34

2.5. Mismatches and indels

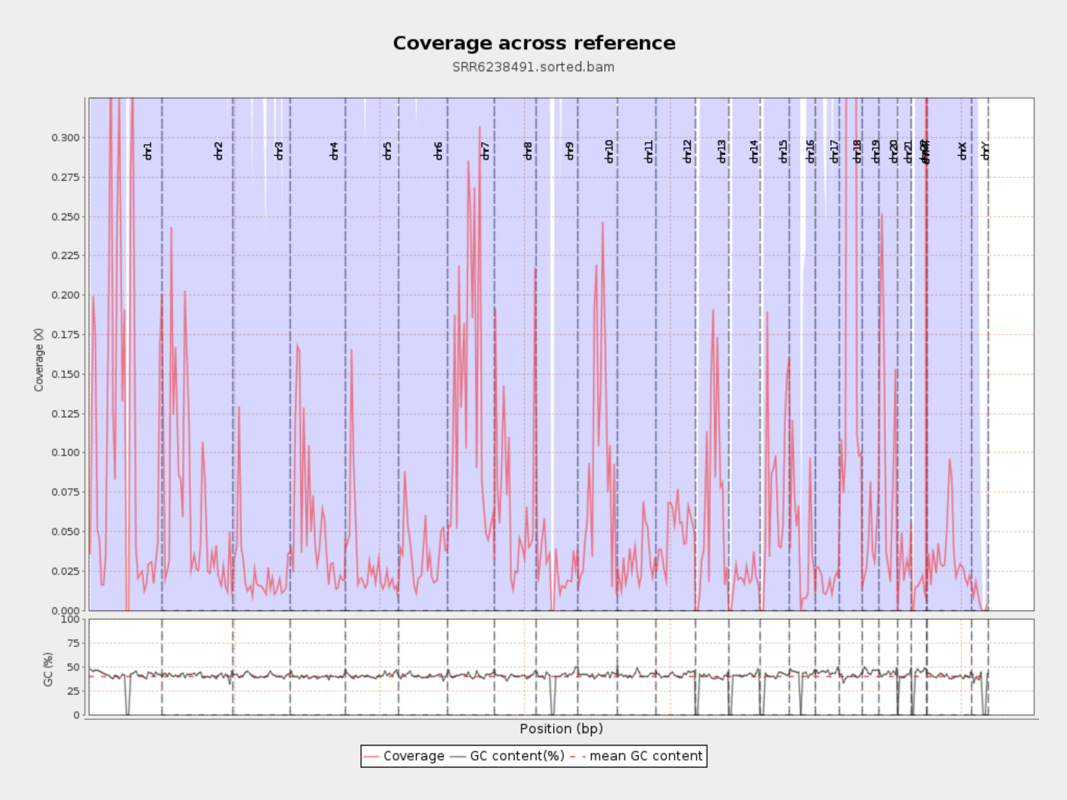
General error rate	0.57%
Mismatches	1,080,516
Insertions	13,415
Mapped reads with at least one insertion	0.42%
Deletions	48,708
Mapped reads with at least one deletion	1.52%
Homopolymer indels	41.67%

2.6. Chromosome stats

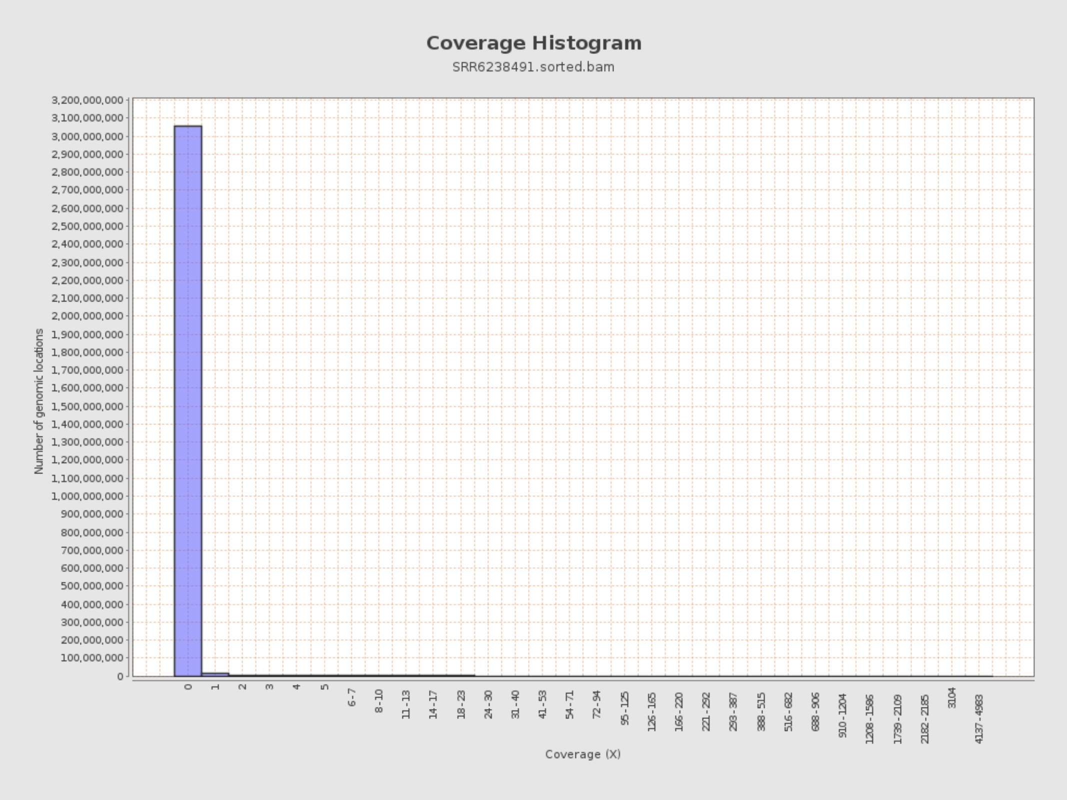
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26194263	0.1051	1.83
chr2	243199373	16112590	0.0663	2.3831
chr3	198022430	4797523	0.0242	0.5601
chr4	191154276	10638382	0.0557	0.8683
chr5	180915260	5960709	0.0329	0.6658
chr6	171115067	6097319	0.0356	1.0945
chr7	159138663	21636705	0.136	1.5844

chr8	146364022	10261966	0.0701	1.3703
chr9	141213431	3533382	0.025	0.5663
chr10	135534747	12914702	0.0953	1.2525
chr11	135006516	4220995	0.0313	0.6168
chr12	133851895	6772883	0.0506	0.8216
chr13	115169878	7880164	0.0684	1.1738
chr14	107349540	2034078	0.0189	0.5007
chr15	102531392	7795946	0.076	1.1627
chr16	90354753	4051958	0.0448	0.8164
chr17	81195210	1536064	0.0189	0.4403
chr18	78077248	24890507	0.3188	3.4147
chr19	59128983	2591013	0.0438	1.1357
chr20	63025520	6938173	0.1101	1.3203
chr21	48129895	1450687	0.0301	0.6219
chr22	51304566	653878	0.0127	0.3865
chrMT	16571	428207	25.8407	27.6341
chrX	155270560	5322651	0.0343	0.6734
chrY	59373566	361746	0.0061	0.3849

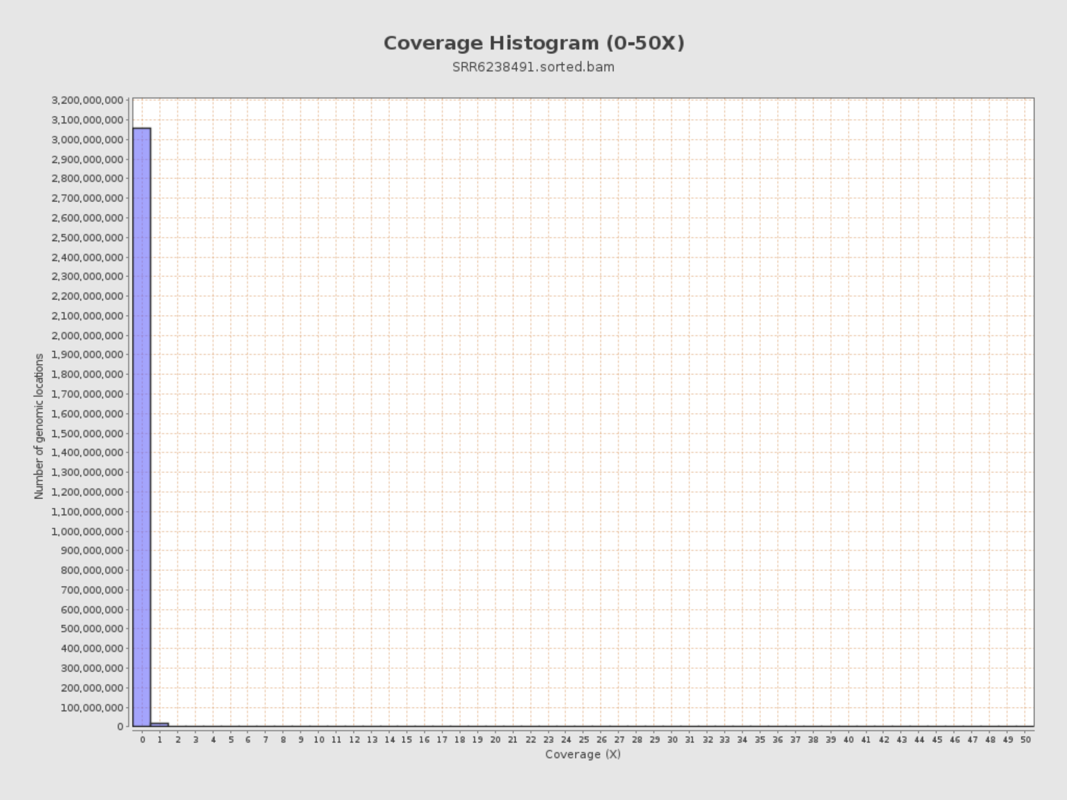
3. Results : Coverage across reference



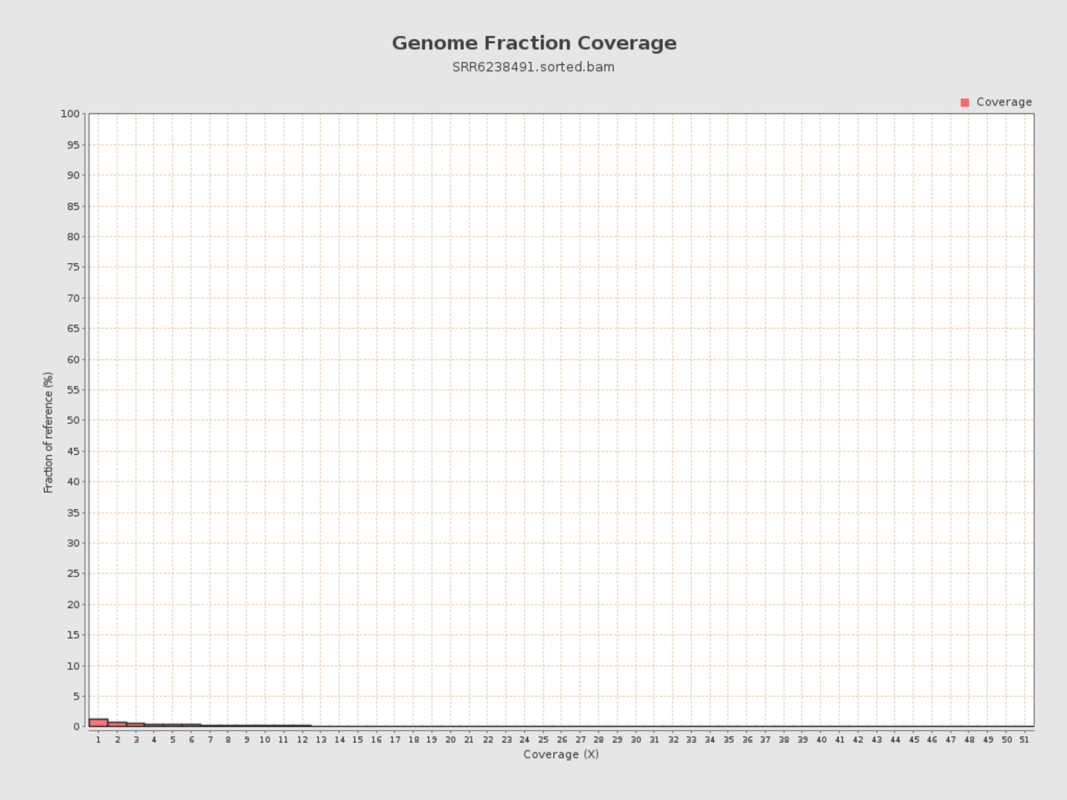
4. Results : Coverage Histogram



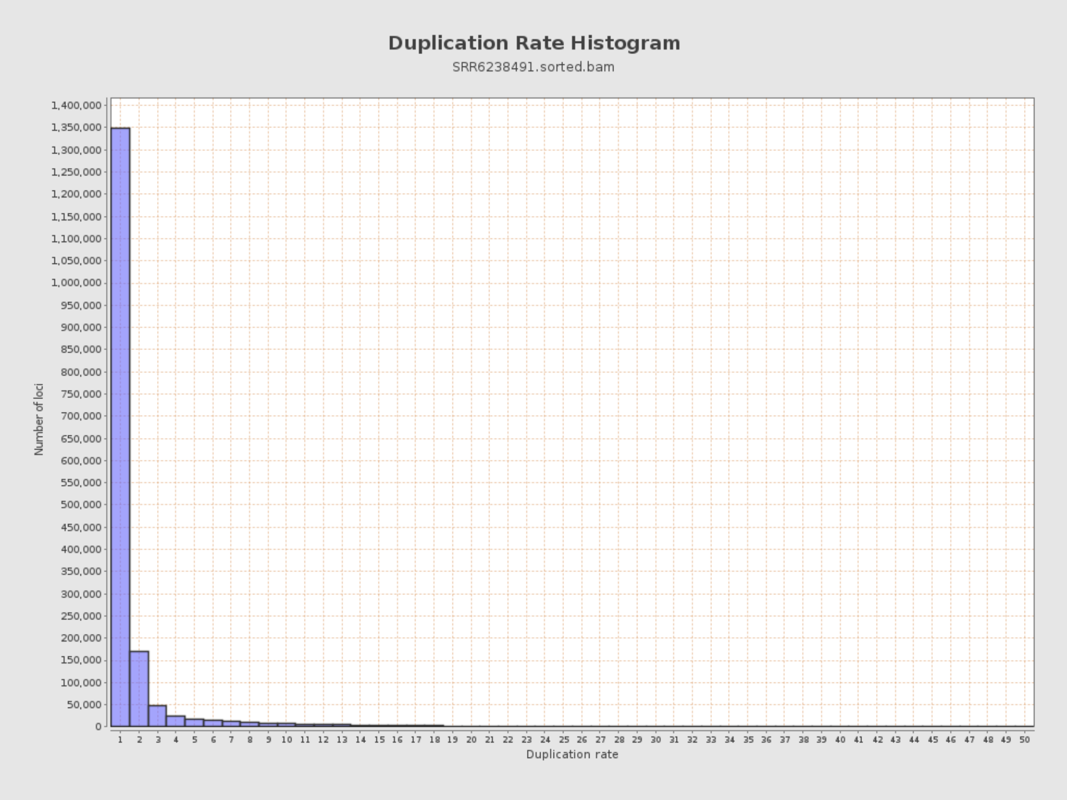
5. Results : Coverage Histogram (0-50X)



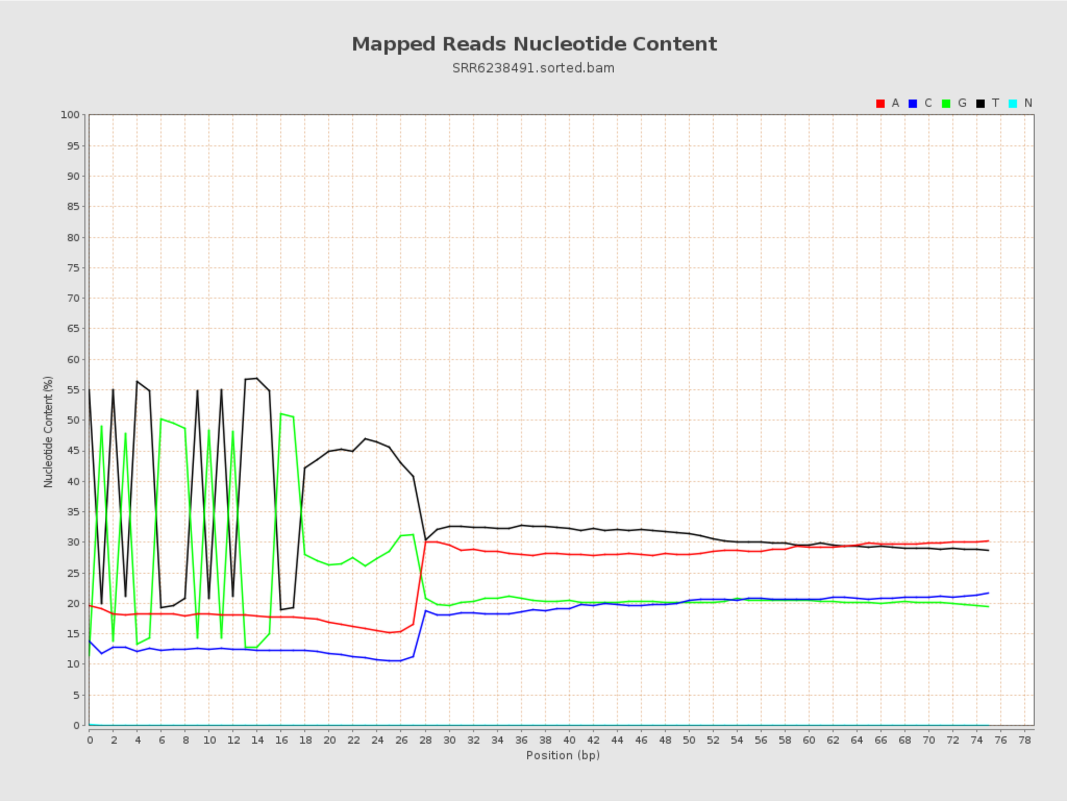
6. Results : Genome Fraction Coverage



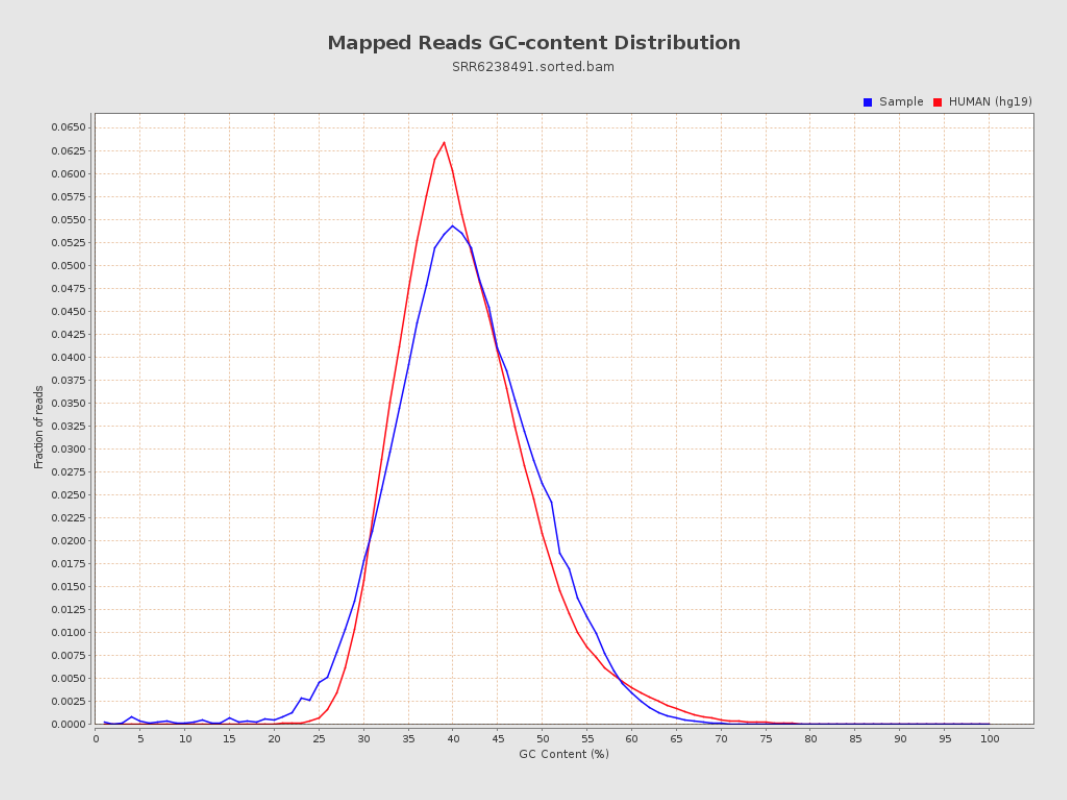
7. Results : Duplication Rate Histogram



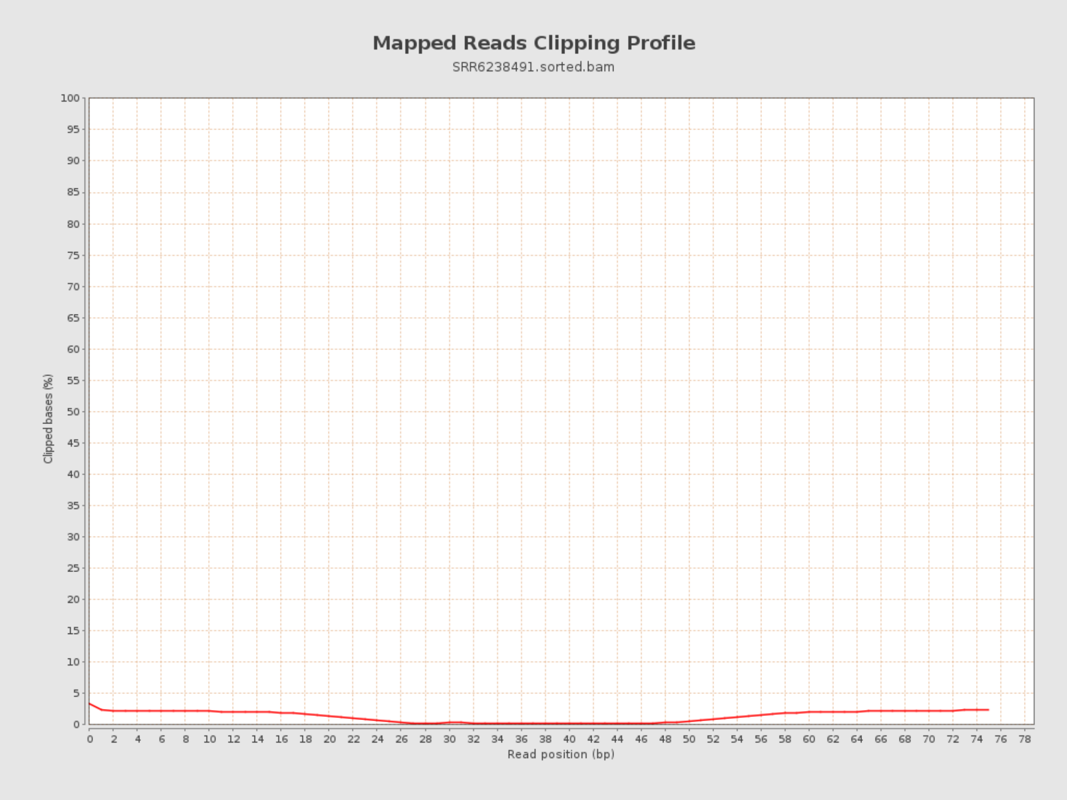
8. Results : Mapped Reads Nucleotide Content



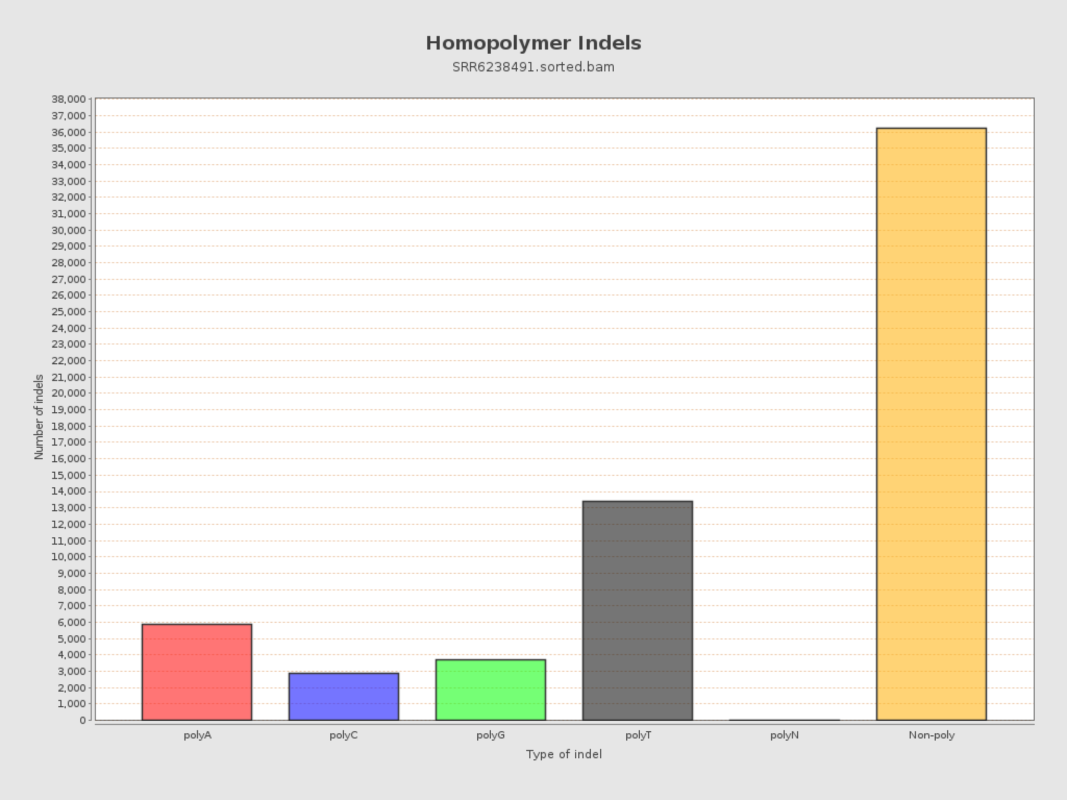
9. Results : Mapped Reads GC-content Distribution



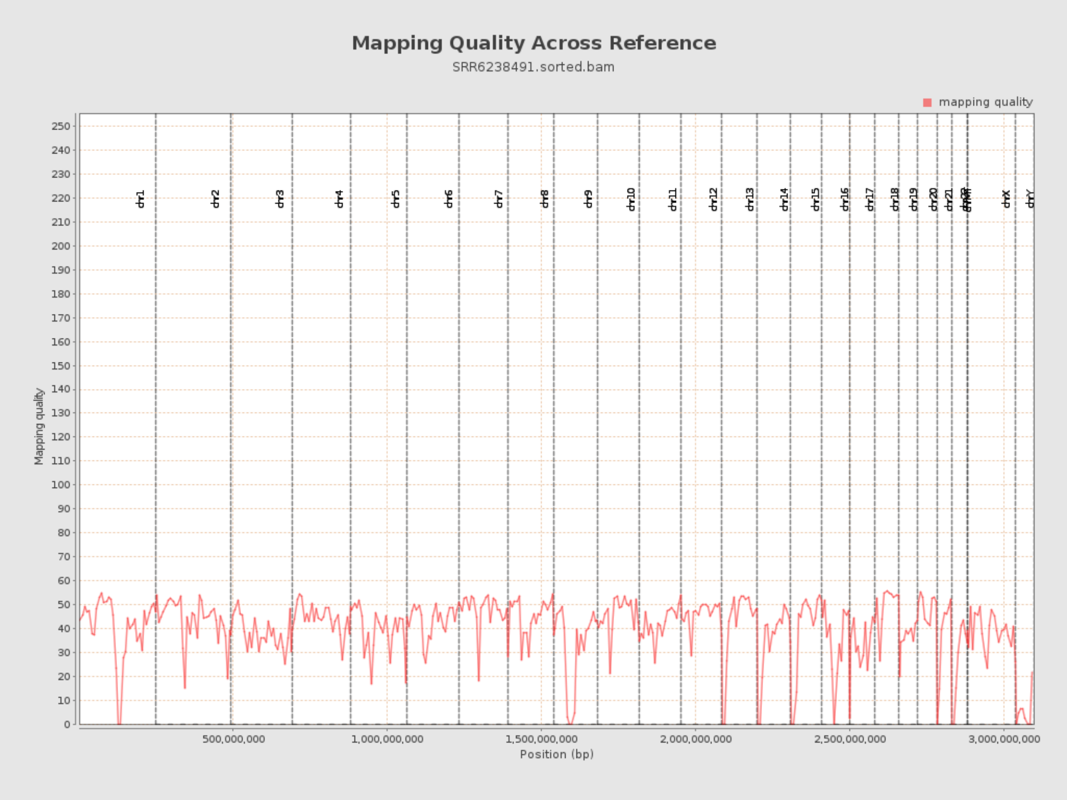
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram