Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:11:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238513.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_SRR6238513 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238513.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:11:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238513.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,706,112
Mapped reads	1,299,448 / 76.16%
Unmapped reads	406,664 / 23.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,512 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	494,514 / 28.98%
Duplication rate	22.3%
Clipped reads	859,674 / 50.39%

2.2. ACGT Content

Number/percentage of A's	19,018,550 / 24.02%
Number/percentage of C's	13,480,223 / 17.02%
Number/percentage of T's	27,430,795 / 34.64%
Number/percentage of G's	19,253,955 / 24.31%
Number/percentage of N's	4,937 / 0.01%
GC Percentage	41.34%

2.3. Coverage

Mean	0.0256

Standard Deviation	0.5936

2.4. Mapping Quality

Mean Mapping Quality	44

2.5. Mismatches and indels

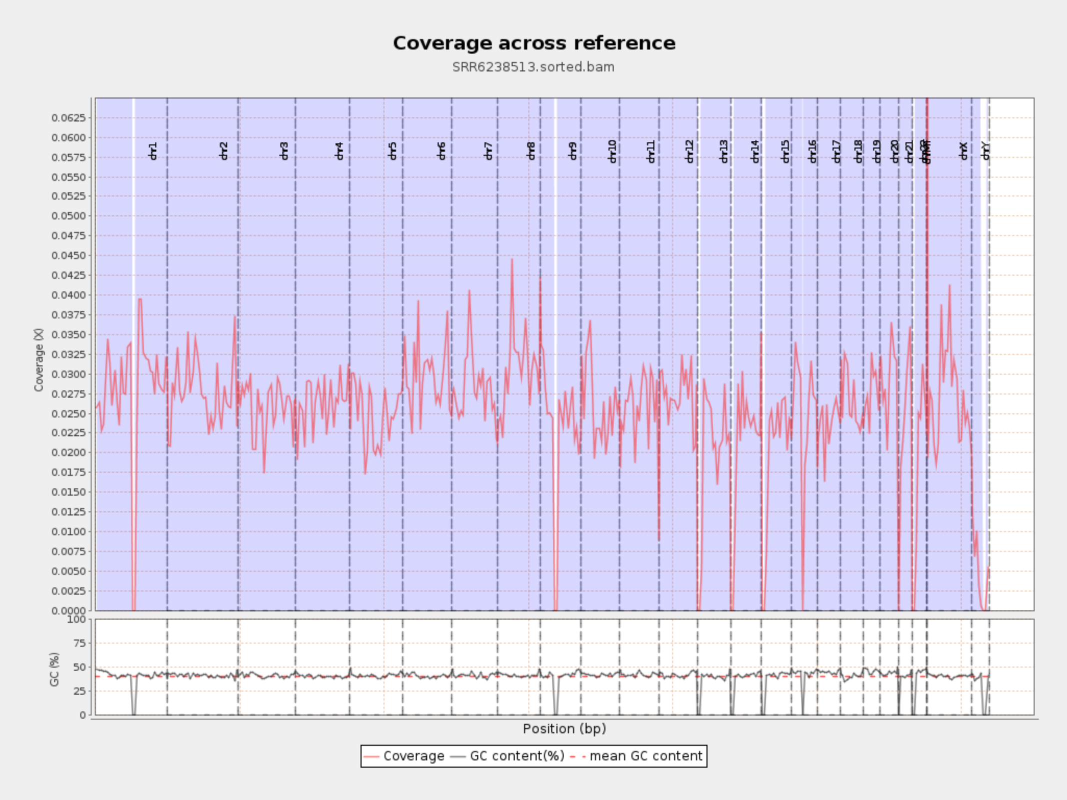
General error rate	0.65%
Mismatches	507,288
Insertions	5,679
Mapped reads with at least one insertion	0.43%
Deletions	24,225
Mapped reads with at least one deletion	1.84%
Homopolymer indels	42.21%

2.6. Chromosome stats

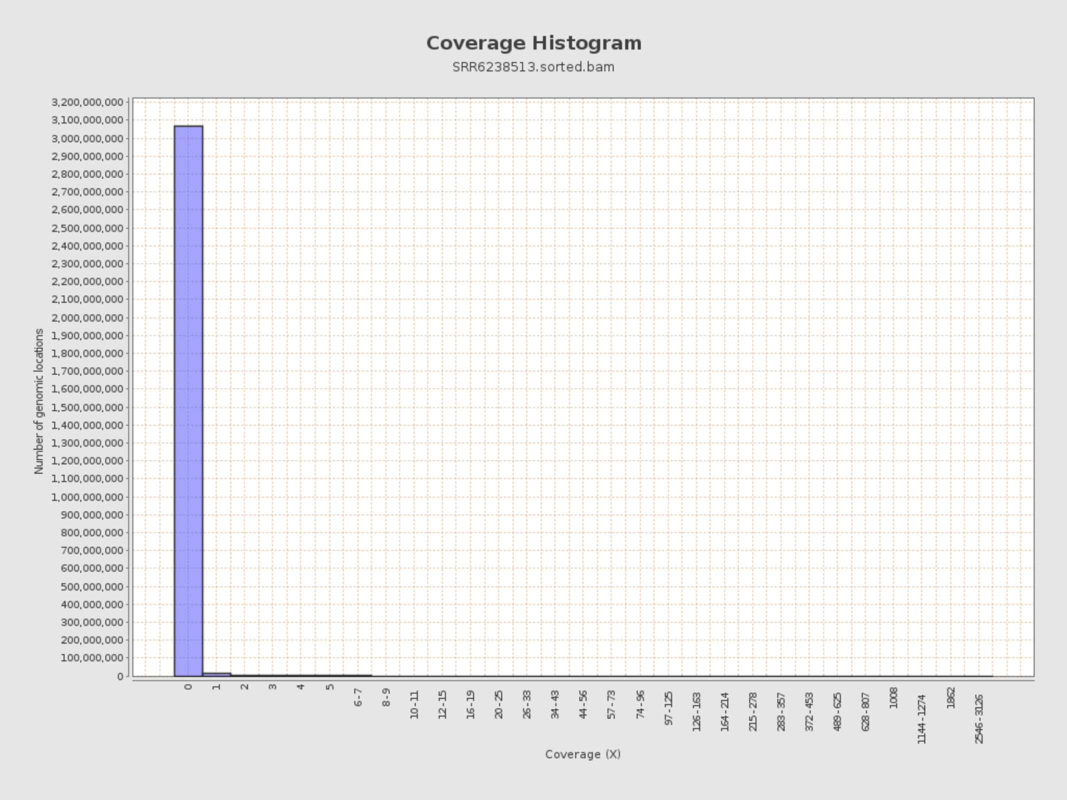
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6945681	0.0279	0.468
chr2	243199373	6768362	0.0278	1.4032
chr3	198022430	5113098	0.0258	0.4209
chr4	191154276	5037708	0.0264	0.404
chr5	180915260	4507373	0.0249	0.3957
chr6	171115067	5117785	0.0299	0.6089
chr7	159138663	4521970	0.0284	0.4996

chr8	146364022	4496652	0.0307	0.49
chr9	141213431	3265969	0.0231	0.4023
chr10	135534747	3566735	0.0263	0.4127
chr11	135006516	3518507	0.0261	0.4251
chr12	133851895	3647445	0.0272	0.433
chr13	115169878	2257744	0.0196	0.4523
chr14	107349540	2211479	0.0206	0.3639
chr15	102531392	1987965	0.0194	0.4104
chr16	90354753	2238898	0.0248	0.4143
chr17	81195210	1934544	0.0238	0.3906
chr18	78077248	2067943	0.0265	1.0054
chr19	59128983	1631085	0.0276	0.4481
chr20	63025520	1817798	0.0288	0.4189
chr21	48129895	1152914	0.024	0.4047
chr22	51304566	933394	0.0182	0.3517
chrMT	16571	13747	0.8296	1.8652
chrX	155270560	4208148	0.0271	0.4163
chrY	59373566	265630	0.0045	0.2198

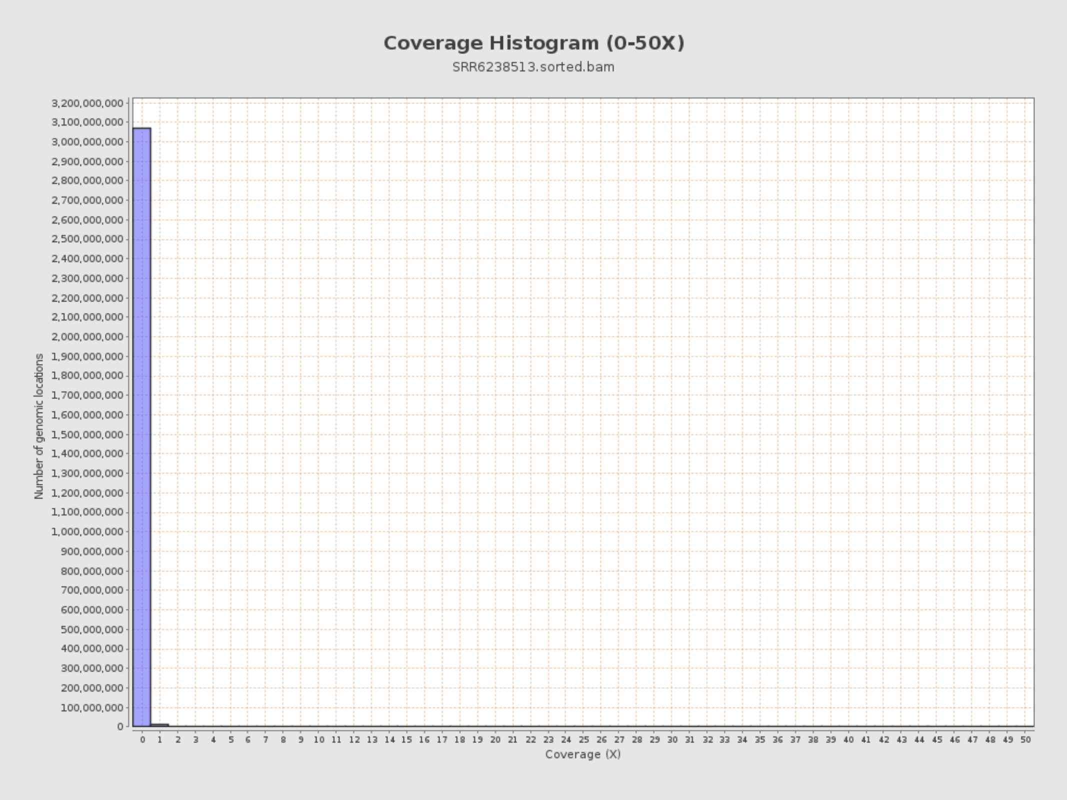
3. Results : Coverage across reference



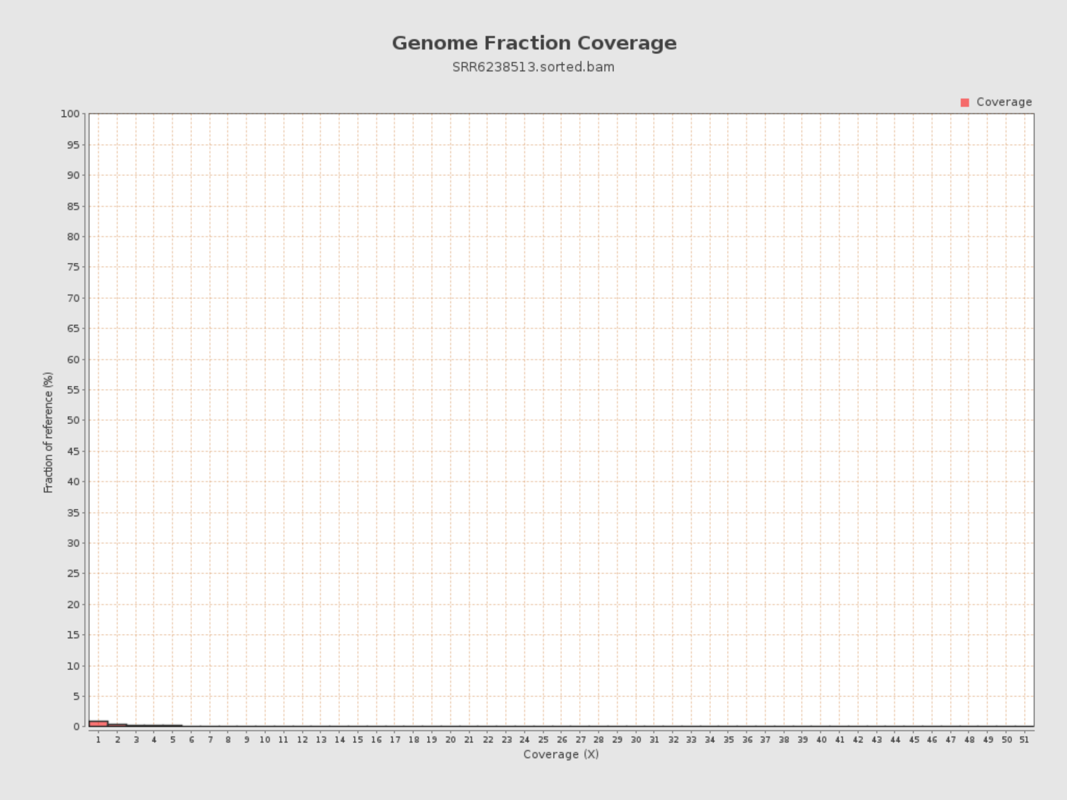
4. Results : Coverage Histogram



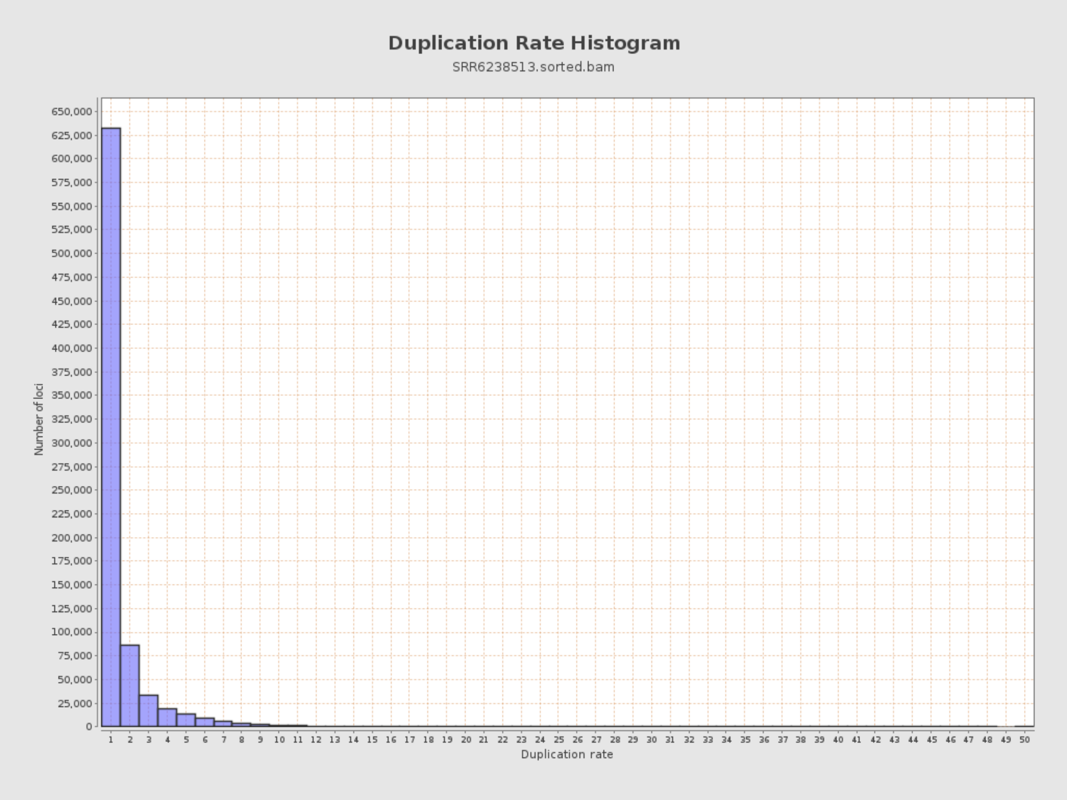
5. Results : Coverage Histogram (0-50X)



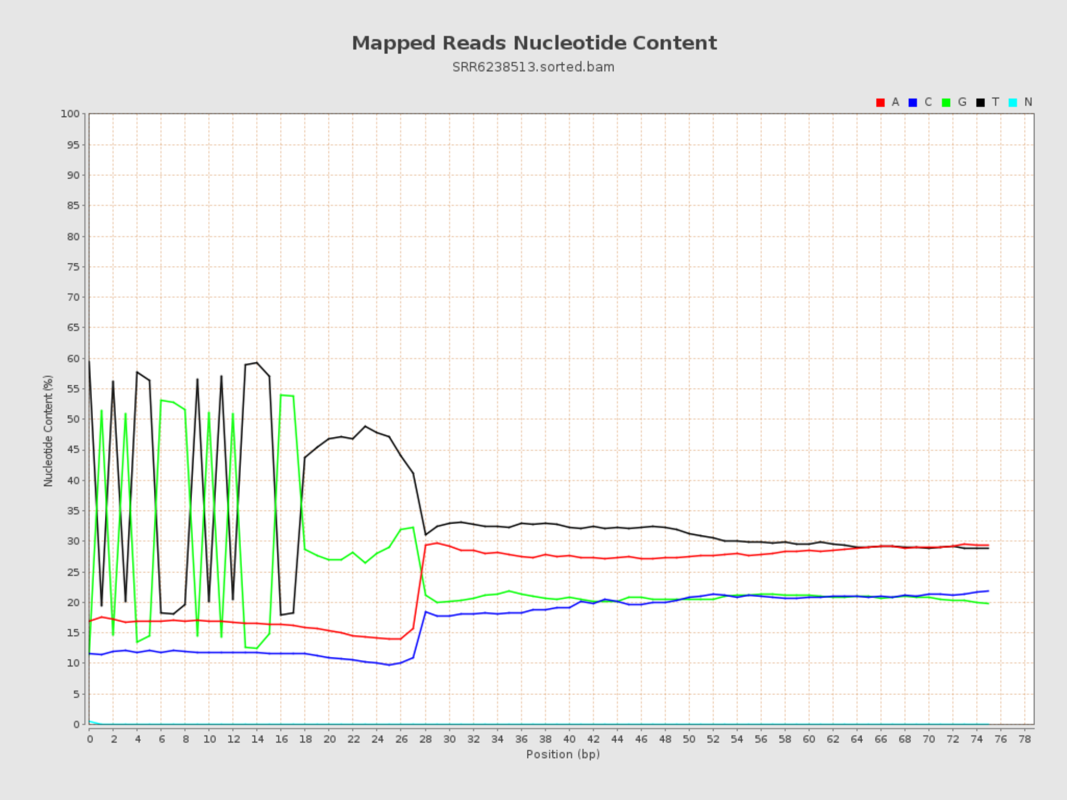
6. Results : Genome Fraction Coverage



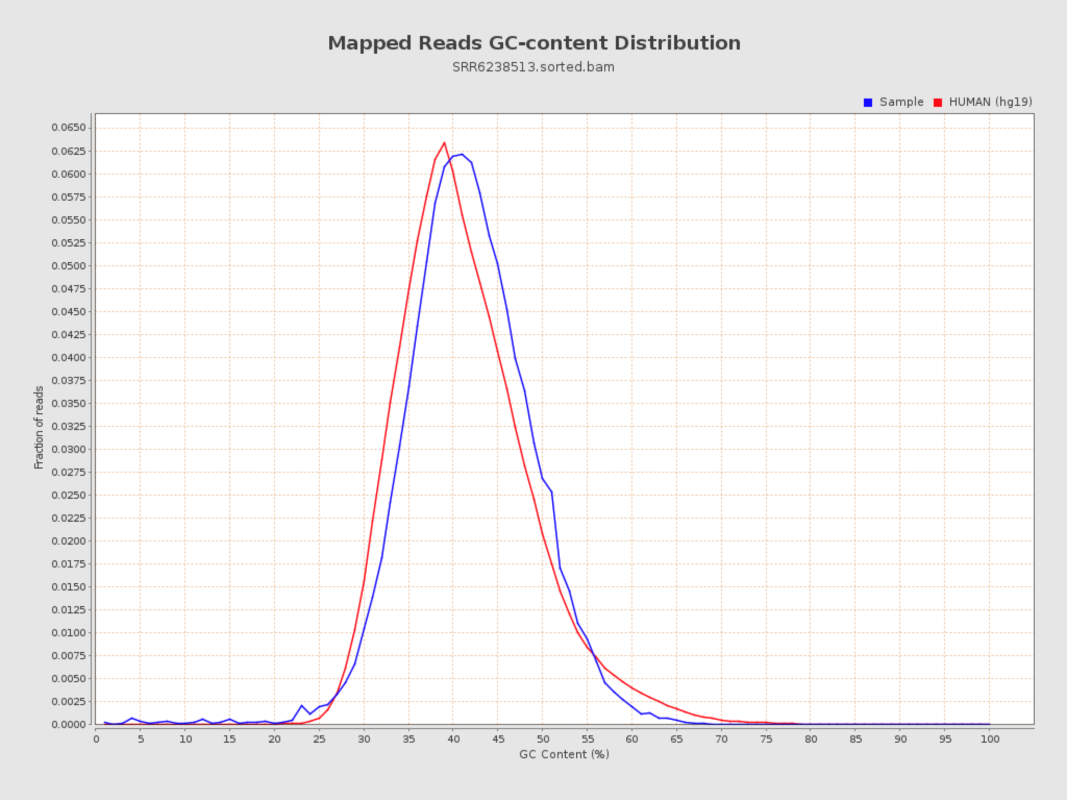
7. Results : Duplication Rate Histogram



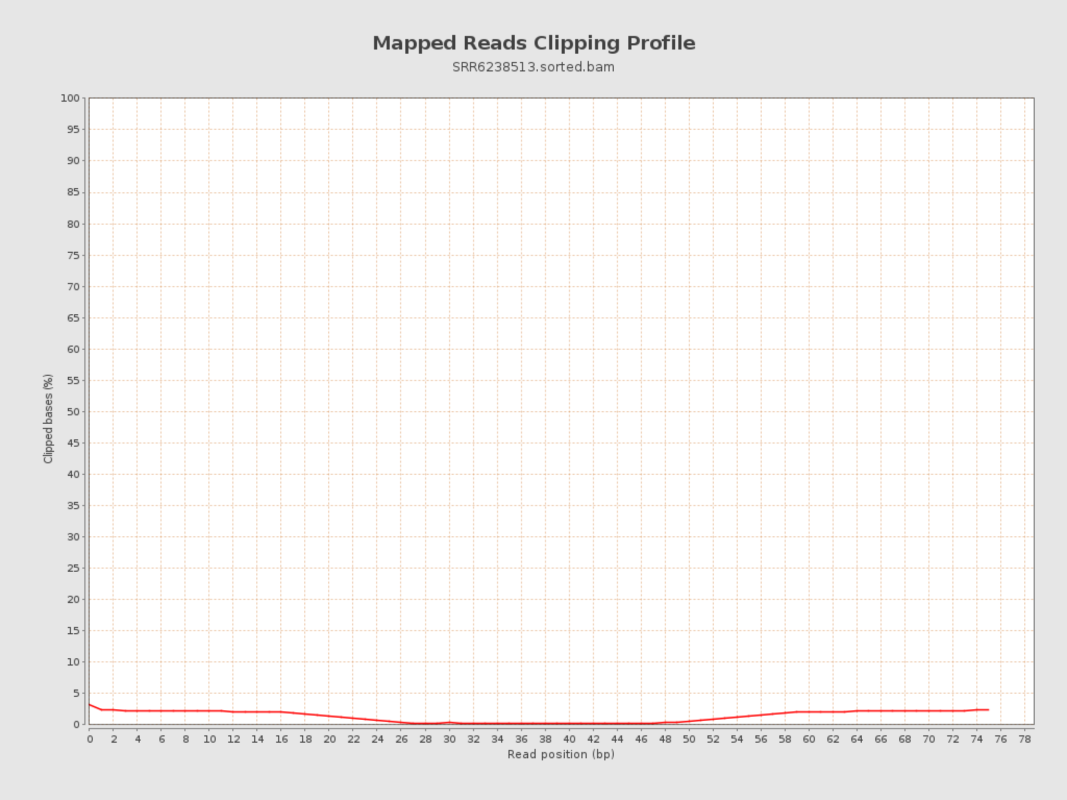
8. Results : Mapped Reads Nucleotide Content



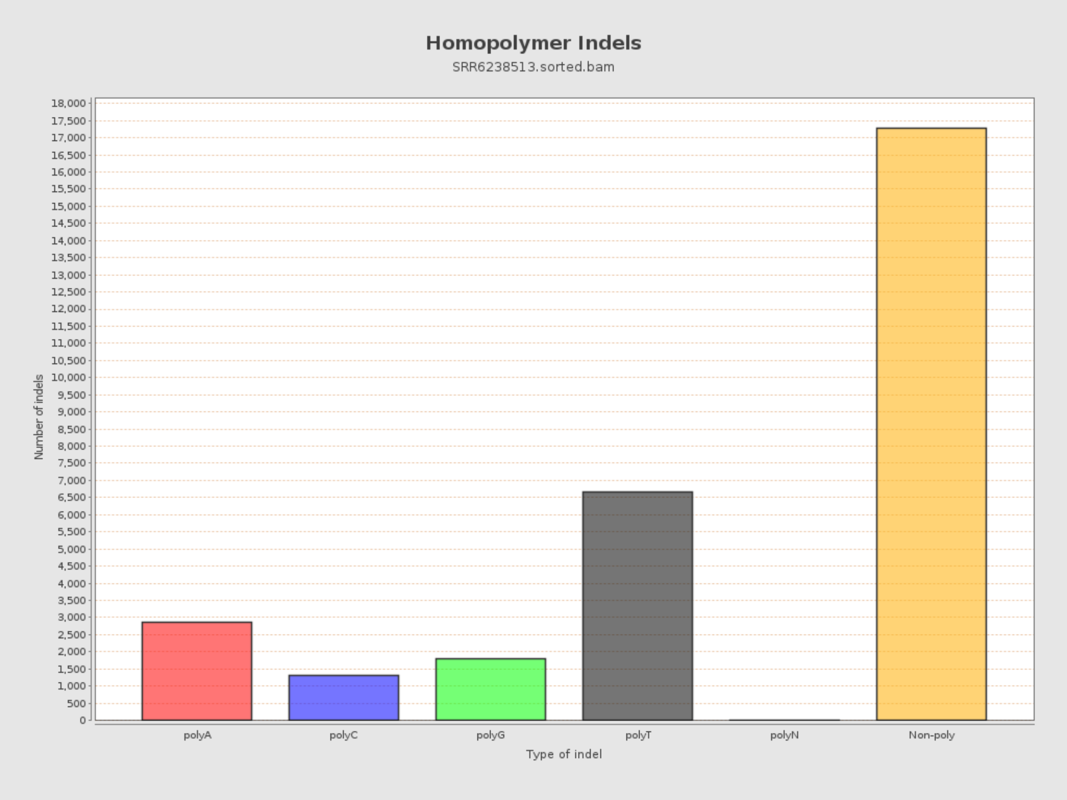
9. Results : Mapped Reads GC-content Distribution



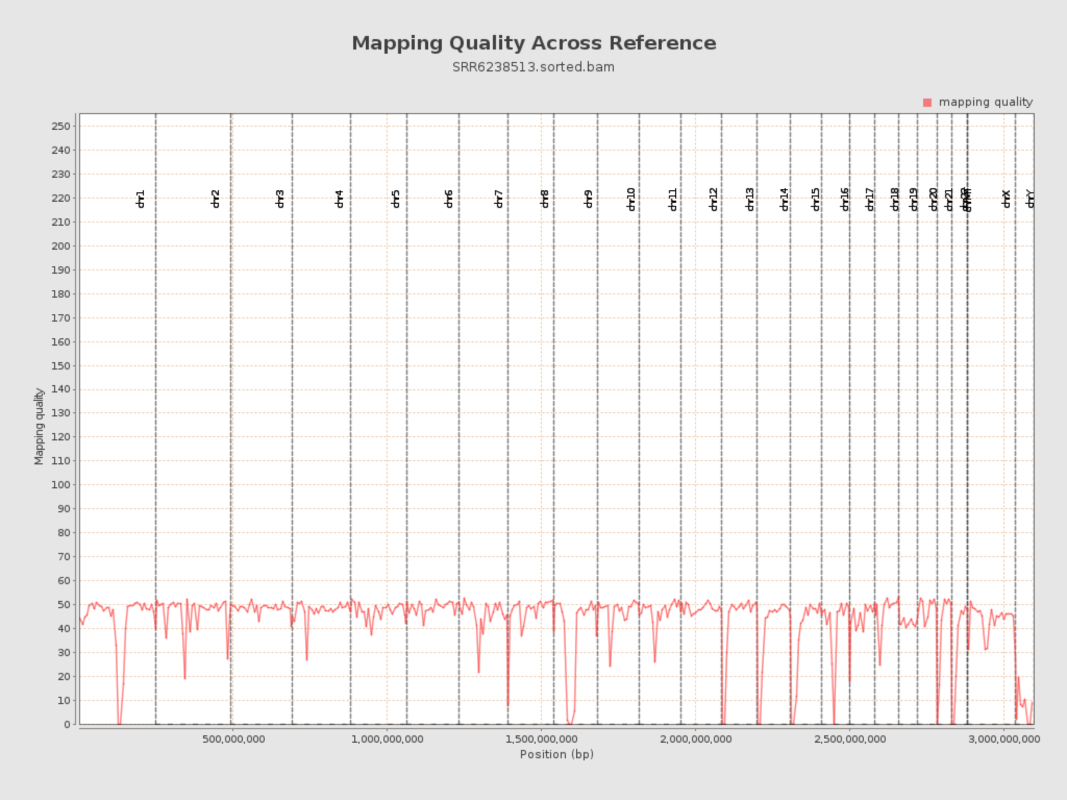
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram