Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:29:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238042.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_SRR6238042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238042.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:29:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,056,629
Mapped reads	1,548,328 / 75.28%
Unmapped reads	508,301 / 24.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,178 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	252,005 / 12.25%
Duplication rate	12.52%
Clipped reads	891,105 / 43.33%

2.2. ACGT Content

Number/percentage of A's	25,677,948 / 26.33%
Number/percentage of C's	17,505,339 / 17.95%
Number/percentage of T's	31,179,199 / 31.97%
Number/percentage of G's	22,970,880 / 23.56%
Number/percentage of N's	178,392 / 0.18%
GC Percentage	41.51%

2.3. Coverage

Mean	0.0315

Standard Deviation	0.3861

2.4. Mapping Quality

Mean Mapping Quality	46.51

2.5. Mismatches and indels

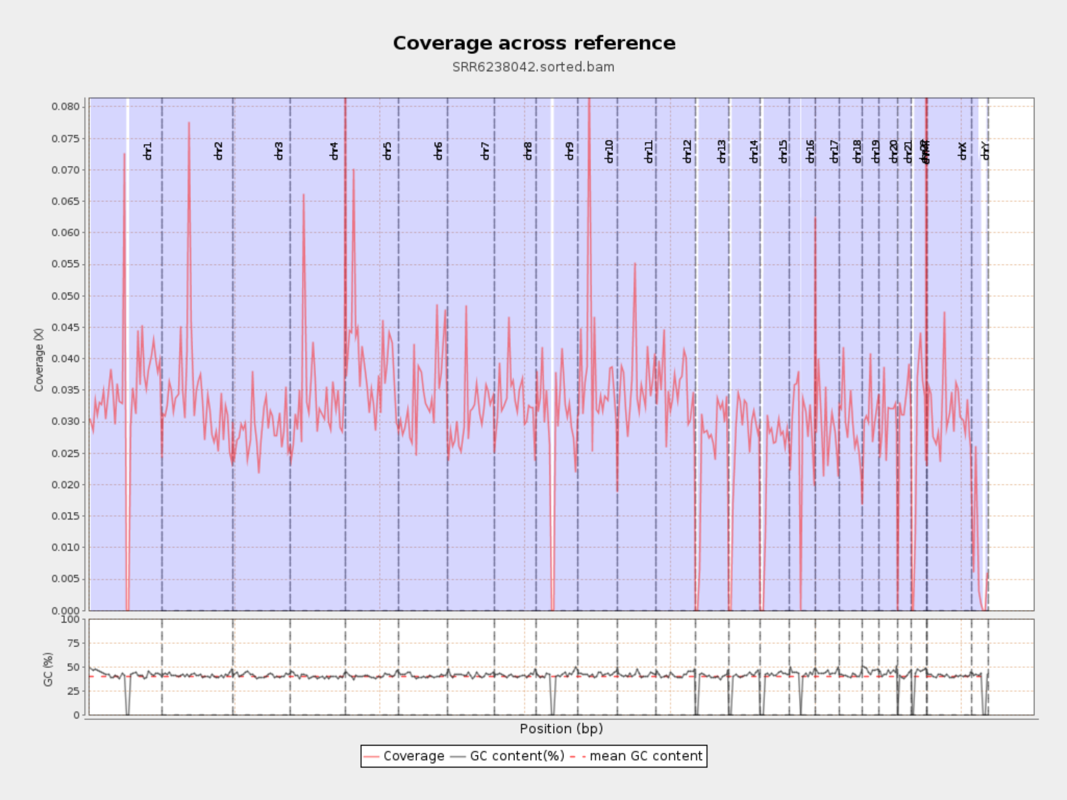
General error rate	0.88%
Mismatches	844,550
Insertions	7,777
Mapped reads with at least one insertion	0.5%
Deletions	29,016
Mapped reads with at least one deletion	1.85%
Homopolymer indels	46.2%

2.6. Chromosome stats

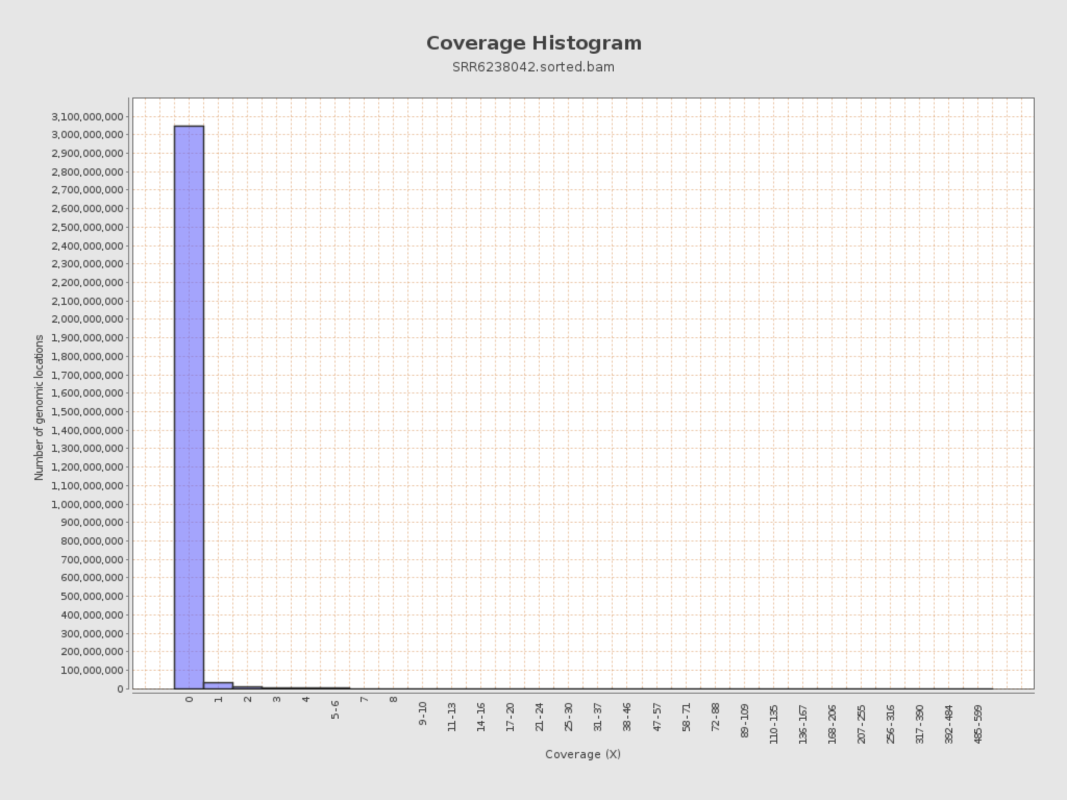
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8558522	0.0343	0.6
chr2	243199373	8313770	0.0342	0.4493
chr3	198022430	5705903	0.0288	0.2974
chr4	191154276	6367951	0.0333	0.3514
chr5	180915260	7141326	0.0395	0.3527
chr6	171115067	5840894	0.0341	0.3502
chr7	159138663	4983521	0.0313	0.3686

chr8	146364022	4867941	0.0333	0.395
chr9	141213431	4066309	0.0288	0.337
chr10	135534747	5136565	0.0379	0.5006
chr11	135006516	4812507	0.0356	0.404
chr12	133851895	4689890	0.035	0.3245
chr13	115169878	2852015	0.0248	0.2673
chr14	107349540	2777955	0.0259	0.2873
chr15	102531392	2359404	0.023	0.2596
chr16	90354753	2558902	0.0283	0.309
chr17	81195210	2317942	0.0285	0.3115
chr18	78077248	2347353	0.0301	0.5186
chr19	59128983	1836352	0.0311	0.4256
chr20	63025520	1931634	0.0306	0.3154
chr21	48129895	1462990	0.0304	0.3302
chr22	51304566	1315683	0.0256	0.267
chrMT	16571	65674	3.9632	3.773
chrX	155270560	4862930	0.0313	0.3244
chrY	59373566	385959	0.0065	0.229

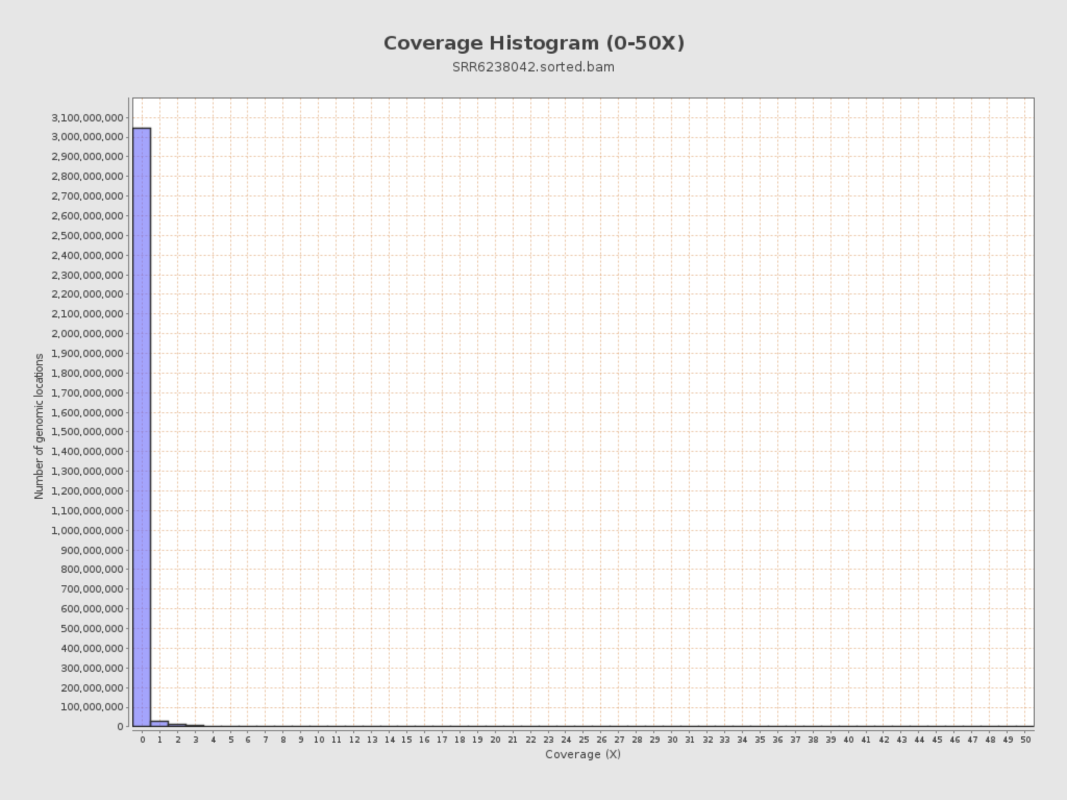
3. Results : Coverage across reference



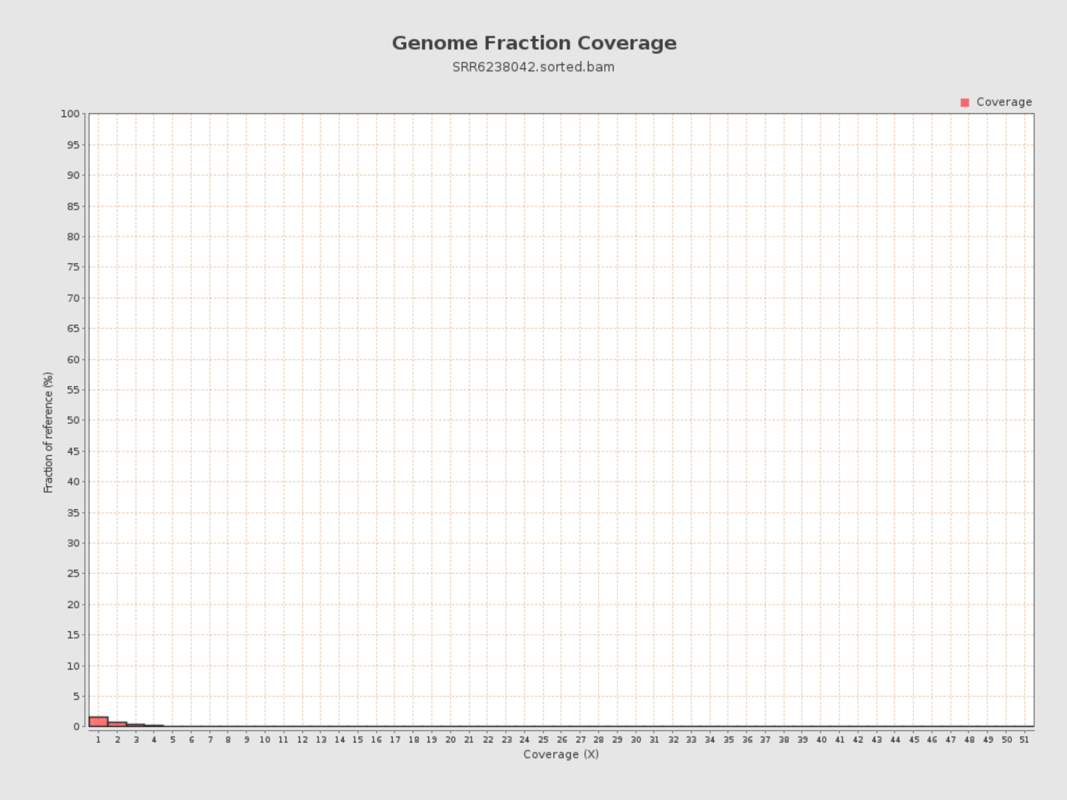
4. Results : Coverage Histogram



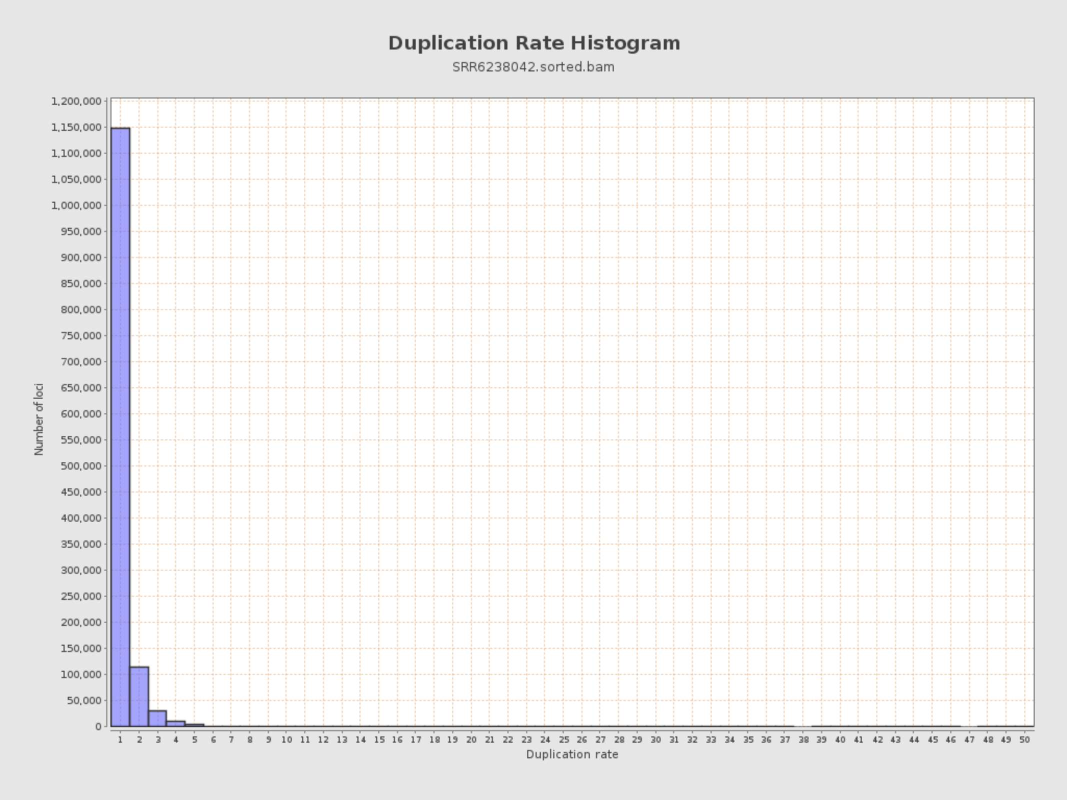
5. Results : Coverage Histogram (0-50X)



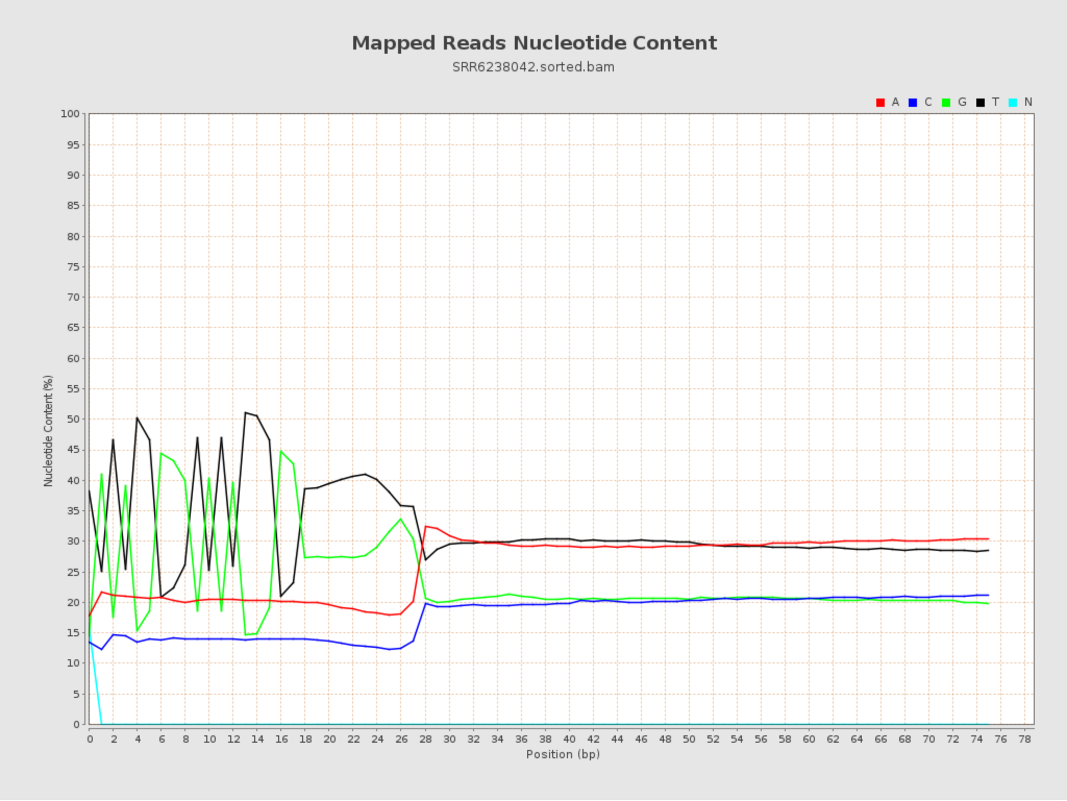
6. Results : Genome Fraction Coverage



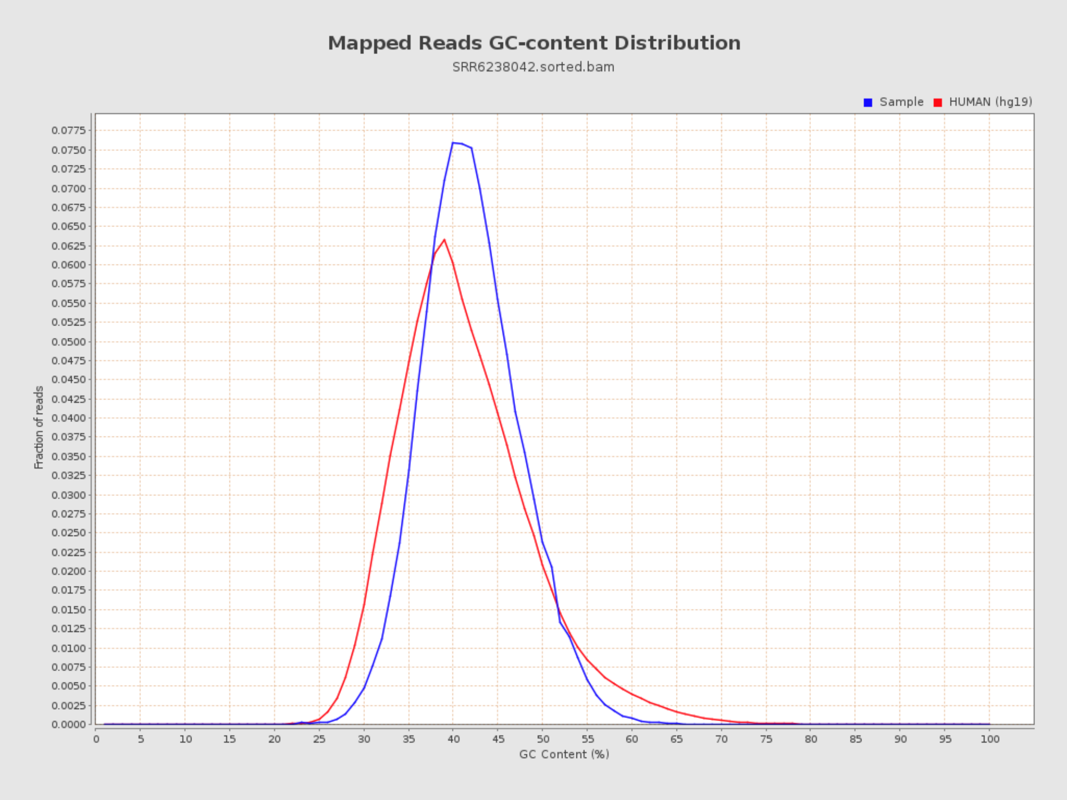
7. Results : Duplication Rate Histogram



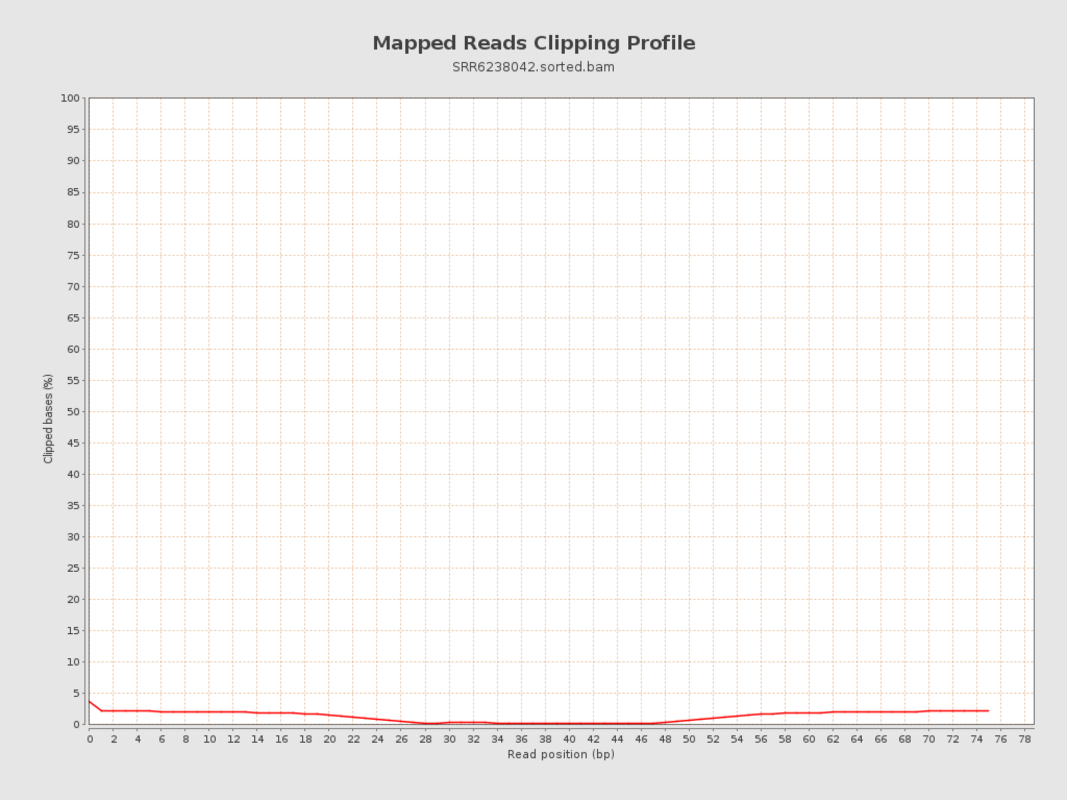
8. Results : Mapped Reads Nucleotide Content



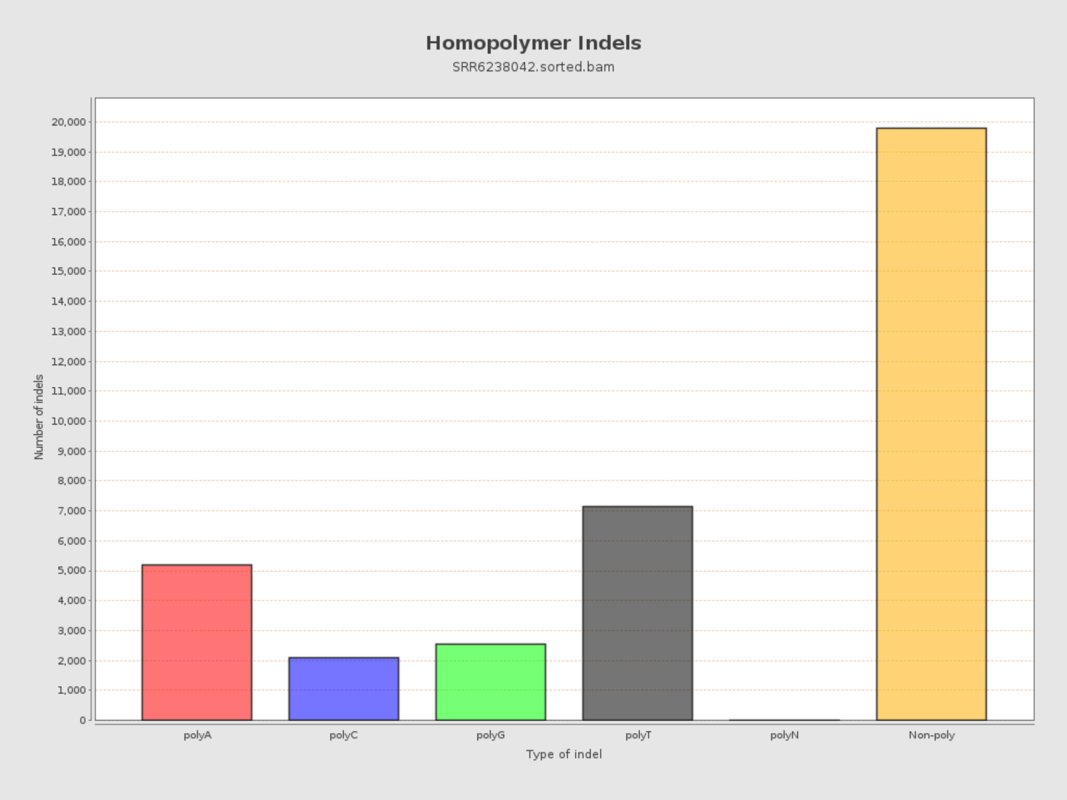
9. Results : Mapped Reads GC-content Distribution



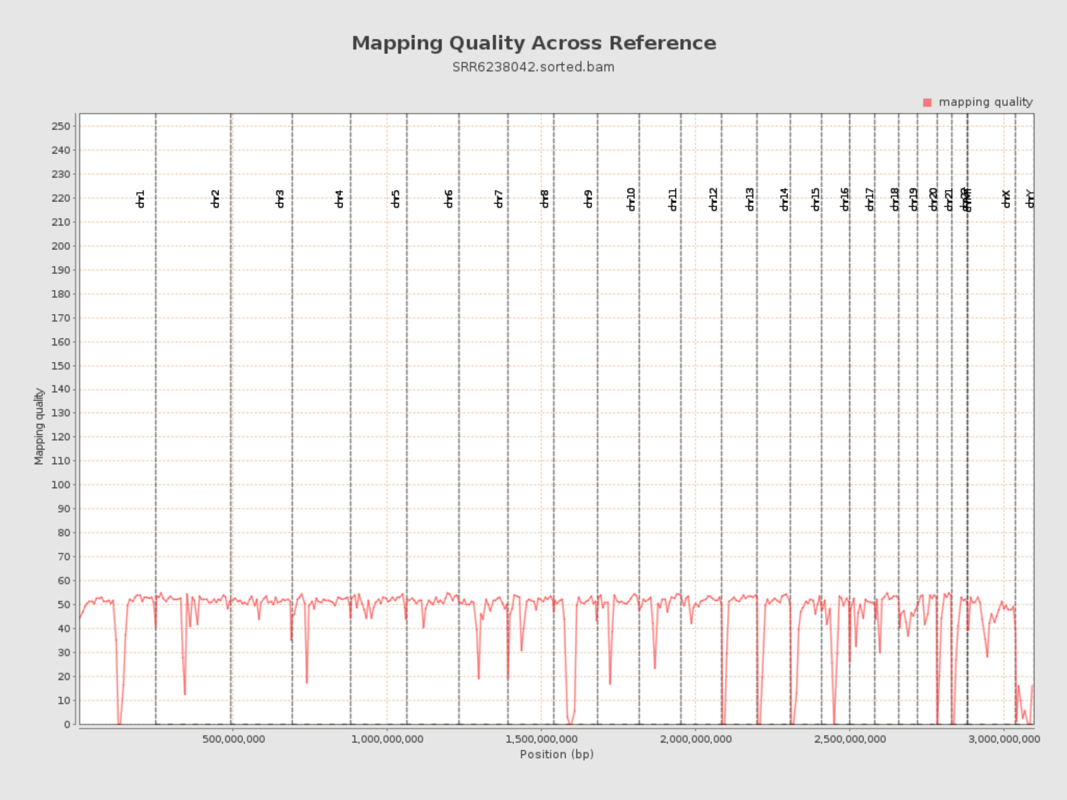
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram