Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:27:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238614.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_SRR6238614 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238614.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:27:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238614.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,305,521
Mapped reads	2,959,413 / 89.53%
Unmapped reads	346,108 / 10.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,211 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	627,848 / 18.99%
Duplication rate	16.56%
Clipped reads	1,764,759 / 53.39%

2.2. ACGT Content

Number/percentage of A's	46,180,673 / 24.94%
Number/percentage of C's	33,448,303 / 18.07%
Number/percentage of T's	61,036,403 / 32.97%
Number/percentage of G's	44,462,517 / 24.02%
Number/percentage of N's	9,762 / 0.01%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0598

Standard Deviation	0.7218

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

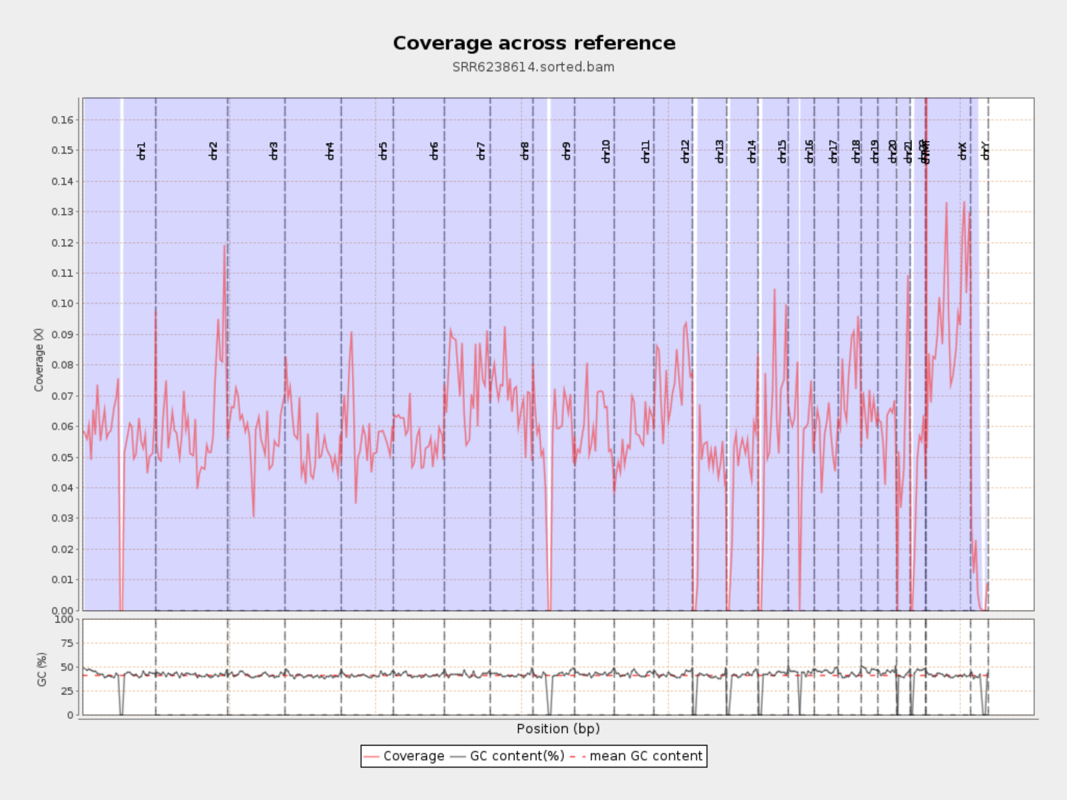
General error rate	0.55%
Mismatches	991,335
Insertions	12,404
Mapped reads with at least one insertion	0.42%
Deletions	46,296
Mapped reads with at least one deletion	1.55%
Homopolymer indels	43.08%

2.6. Chromosome stats

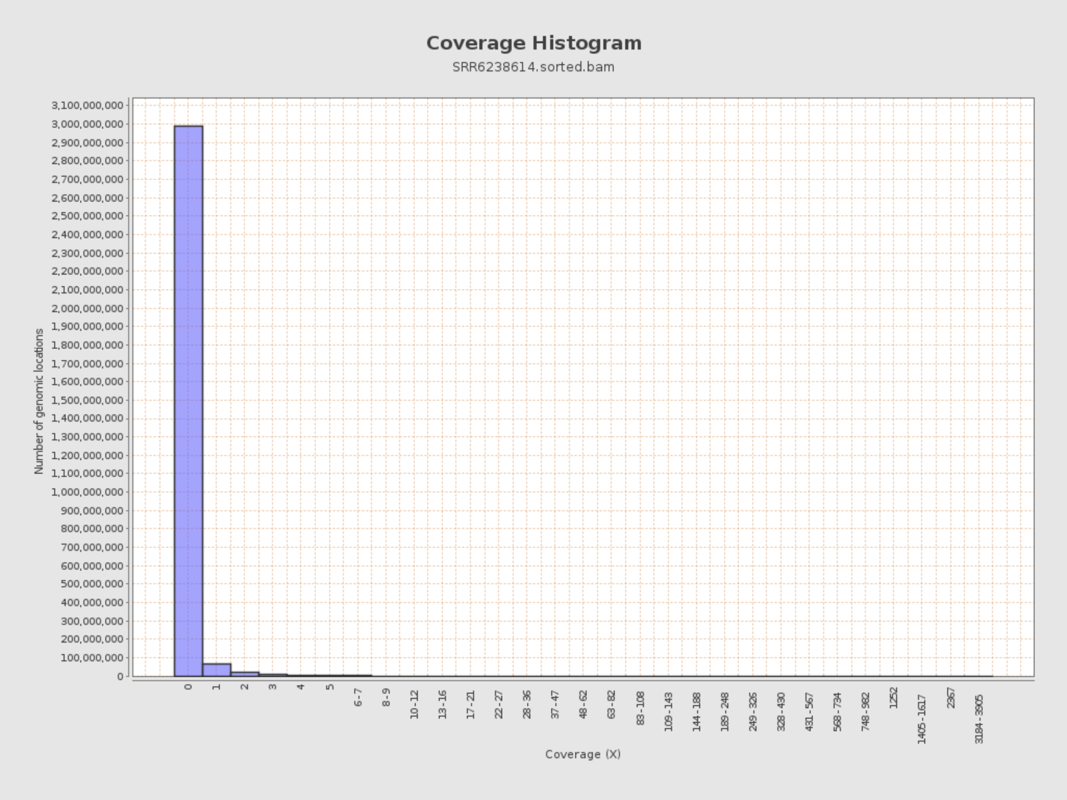
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13726652	0.0551	0.7603
chr2	243199373	14907312	0.0613	1.7344
chr3	198022430	11491563	0.058	0.401
chr4	191154276	10437260	0.0546	0.3874
chr5	180915260	10494615	0.058	0.3957
chr6	171115067	9589180	0.056	0.6565
chr7	159138663	11984758	0.0753	0.7075

chr8	146364022	10226474	0.0699	0.5641
chr9	141213431	7558008	0.0535	0.4619
chr10	135534747	8057299	0.0594	0.5077
chr11	135006516	7604895	0.0563	0.4591
chr12	133851895	10136441	0.0757	0.4589
chr13	115169878	4903591	0.0426	0.4651
chr14	107349540	4755474	0.0443	0.3517
chr15	102531392	5946388	0.058	0.5125
chr16	90354753	5085718	0.0563	0.4355
chr17	81195210	4581714	0.0564	0.399
chr18	78077248	6008718	0.077	1.3248
chr19	59128983	3786805	0.064	0.6195
chr20	63025520	3785793	0.0601	0.41
chr21	48129895	2720471	0.0565	0.4106
chr22	51304566	1956439	0.0381	0.3115
chrMT	16571	54078	3.2634	3.136
chrX	155270560	14886469	0.0959	0.5224
chrY	59373566	531328	0.0089	0.2859

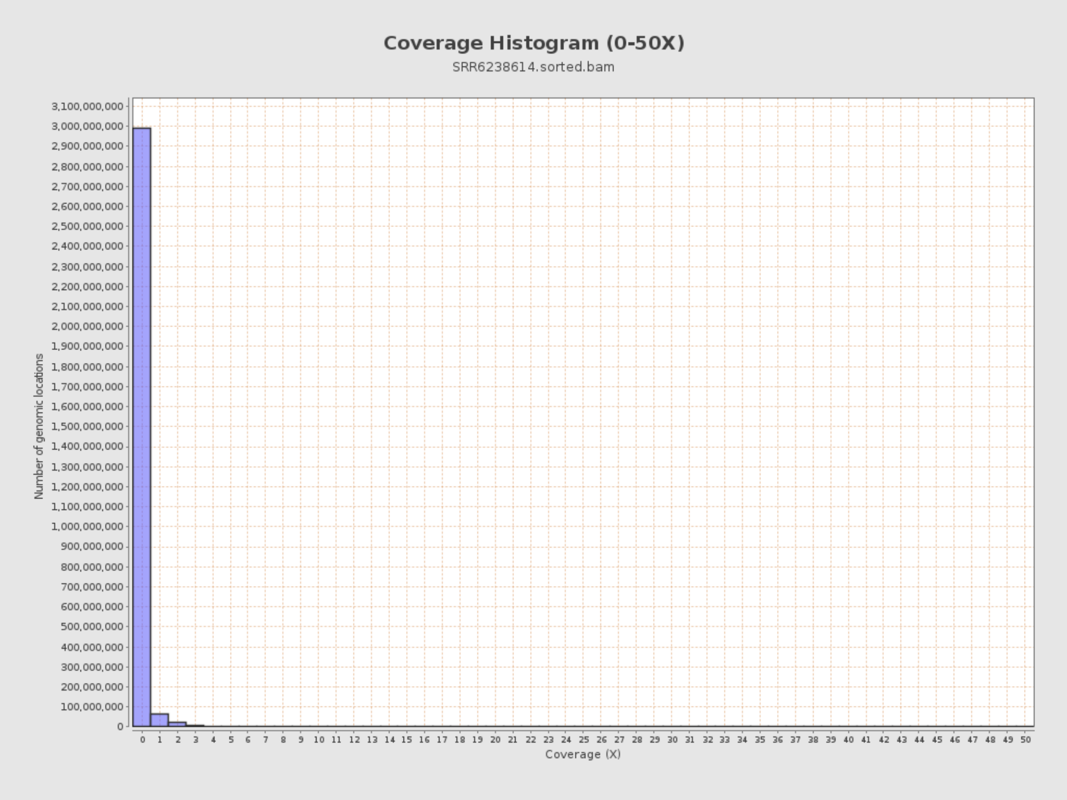
3. Results : Coverage across reference



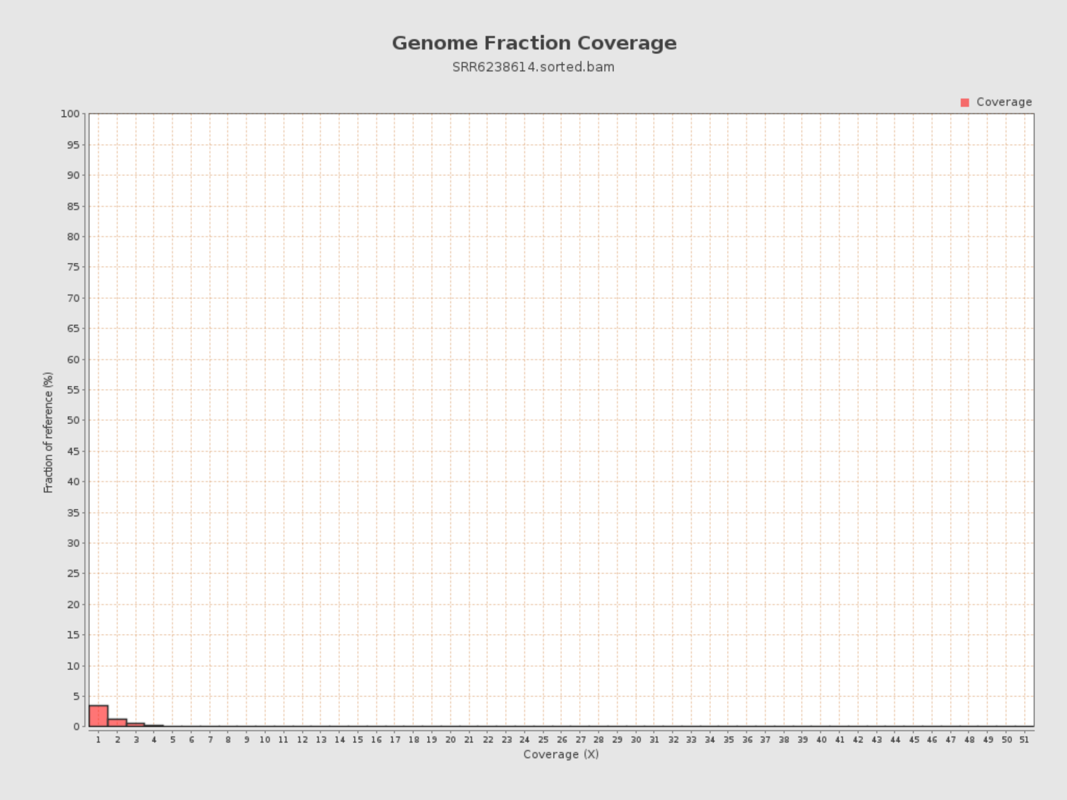
4. Results : Coverage Histogram



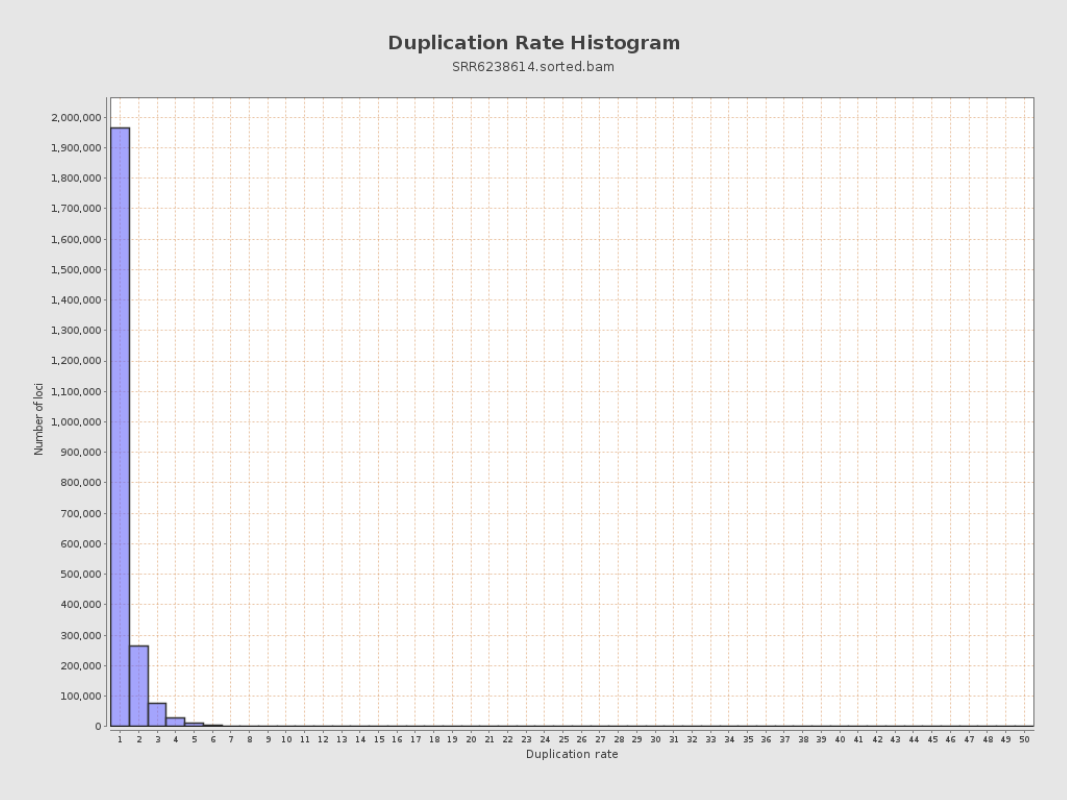
5. Results : Coverage Histogram (0-50X)



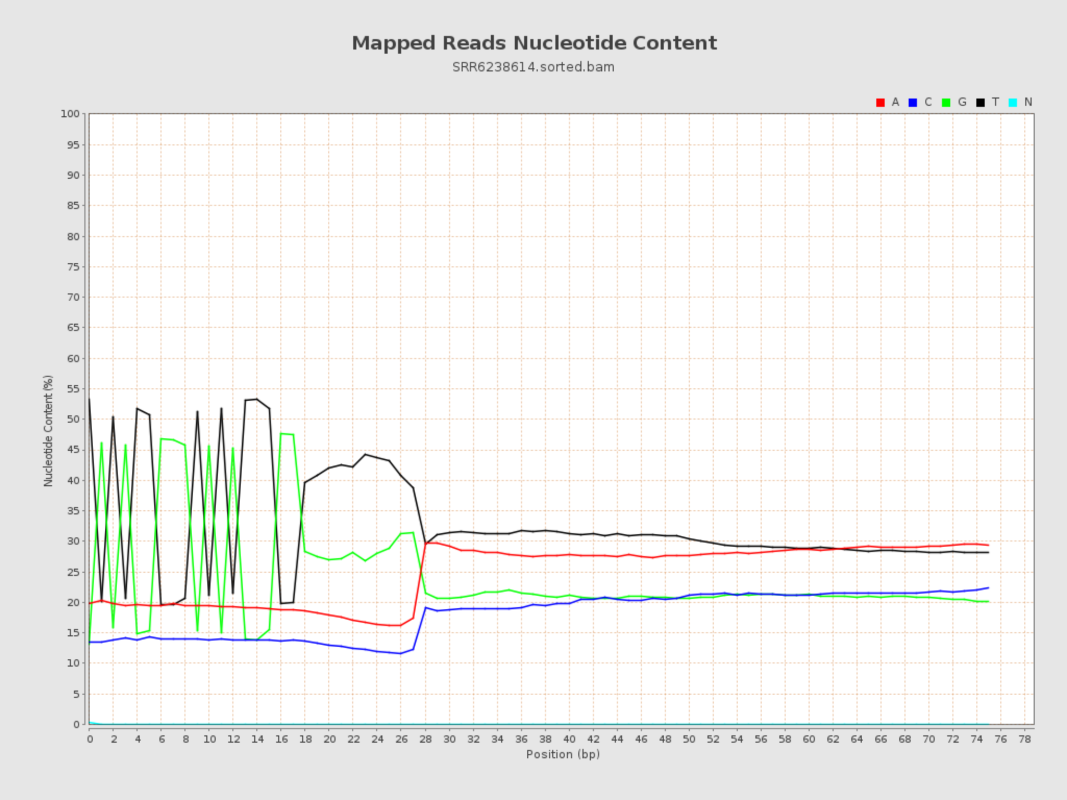
6. Results : Genome Fraction Coverage



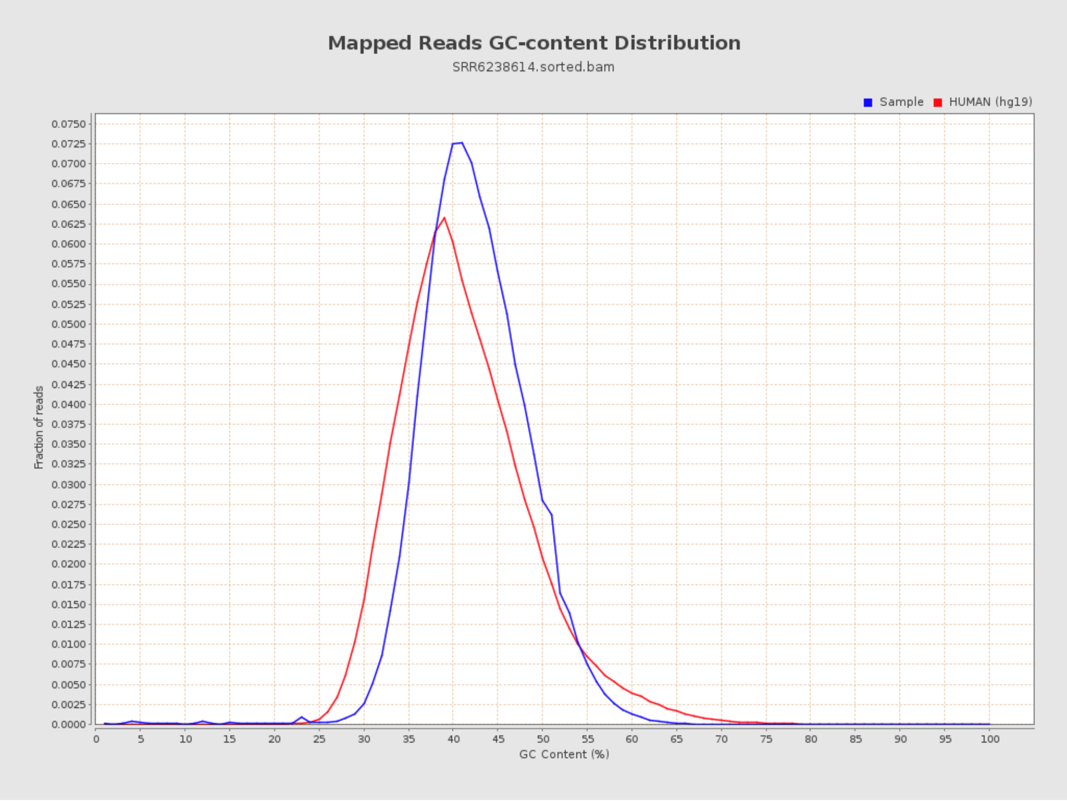
7. Results : Duplication Rate Histogram



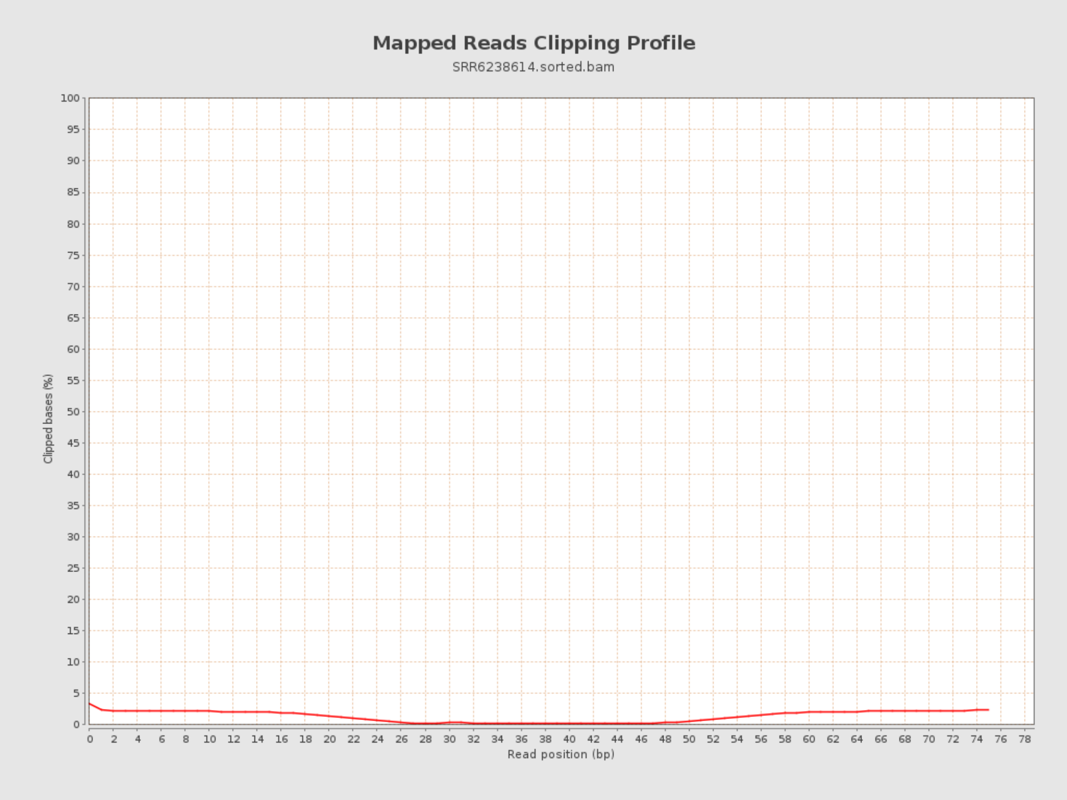
8. Results : Mapped Reads Nucleotide Content



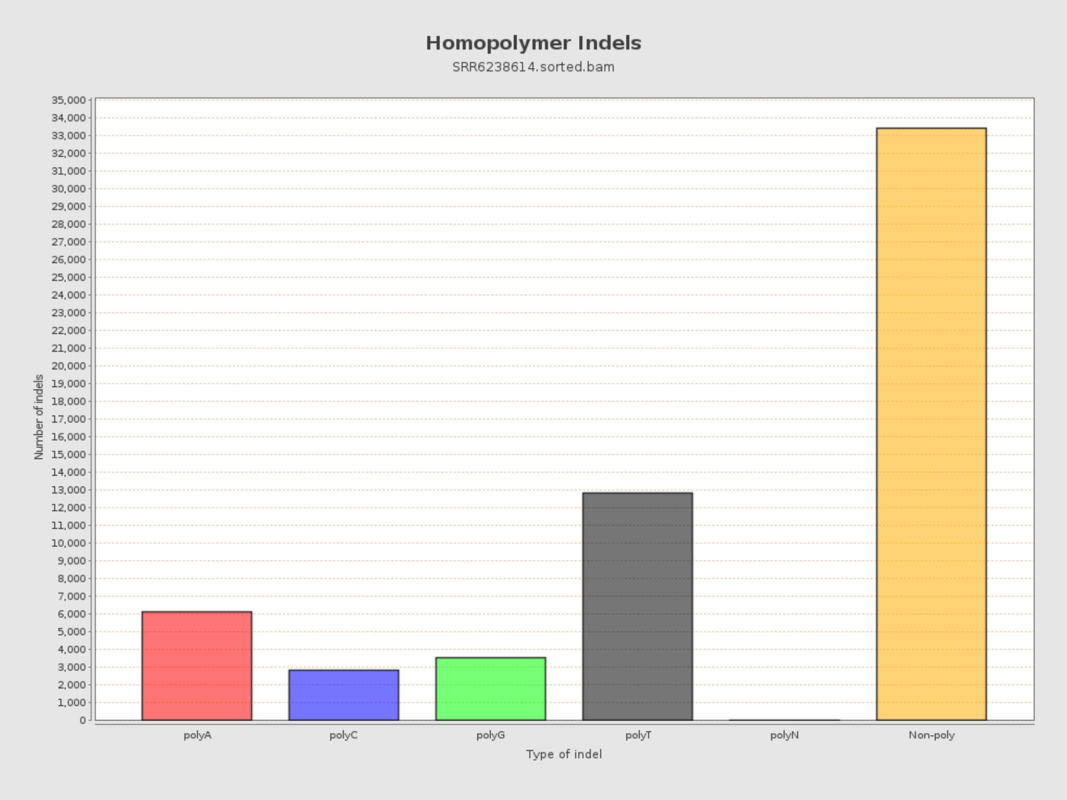
9. Results : Mapped Reads GC-content Distribution



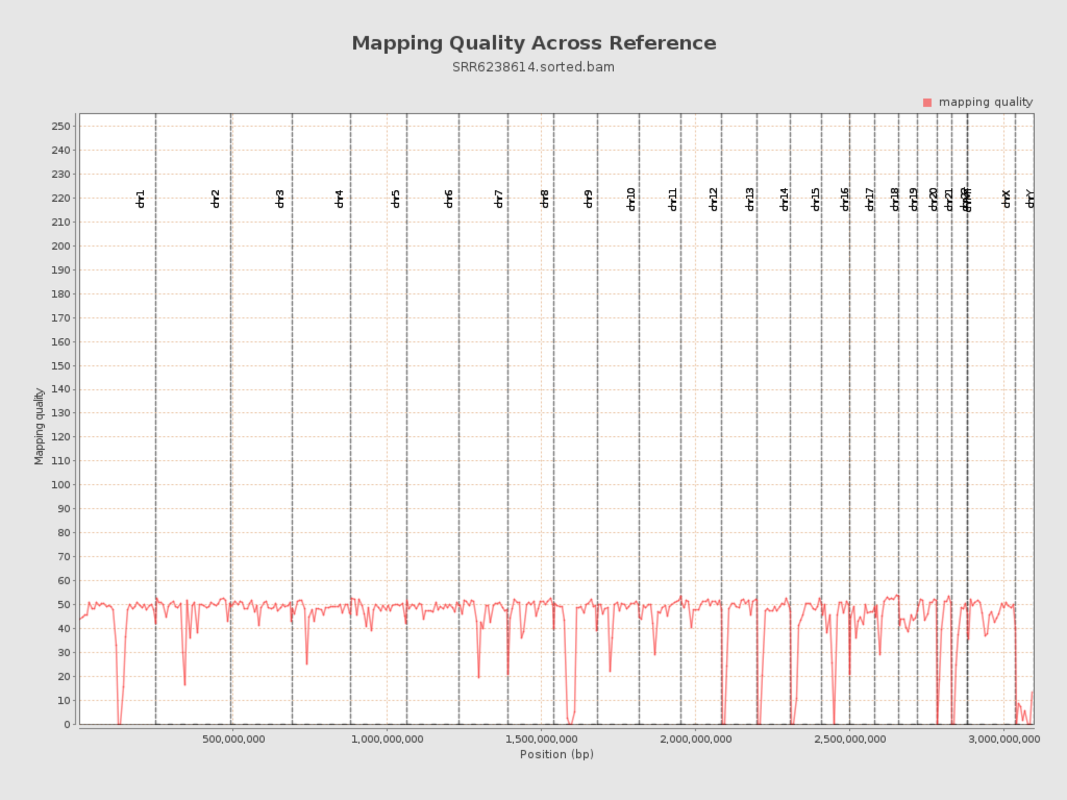
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram