Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:52:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238539.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_SRR6238539 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238539.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:52:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238539.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,808,739
Mapped reads	1,575,280 / 87.09%
Unmapped reads	233,459 / 12.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,564 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	400,870 / 22.16%
Duplication rate	19.14%
Clipped reads	1,101,662 / 60.91%

2.2. ACGT Content

Number/percentage of A's	23,115,924 / 24.43%
Number/percentage of C's	16,602,445 / 17.55%
Number/percentage of T's	31,966,697 / 33.79%
Number/percentage of G's	22,913,895 / 24.22%
Number/percentage of N's	5,970 / 0.01%
GC Percentage	41.77%

2.3. Coverage

Mean	0.0306

Standard Deviation	0.5232

2.4. Mapping Quality

Mean Mapping Quality	43.06

2.5. Mismatches and indels

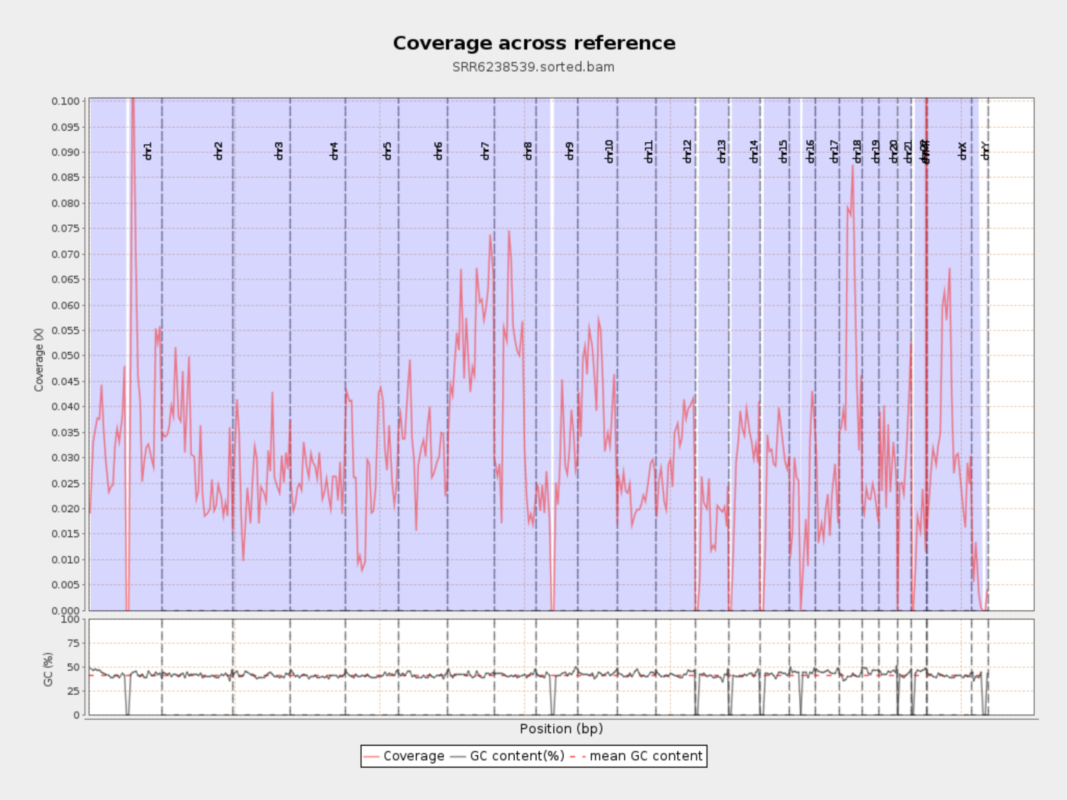
General error rate	0.7%
Mismatches	647,335
Insertions	6,175
Mapped reads with at least one insertion	0.39%
Deletions	38,938
Mapped reads with at least one deletion	2.44%
Homopolymer indels	40.33%

2.6. Chromosome stats

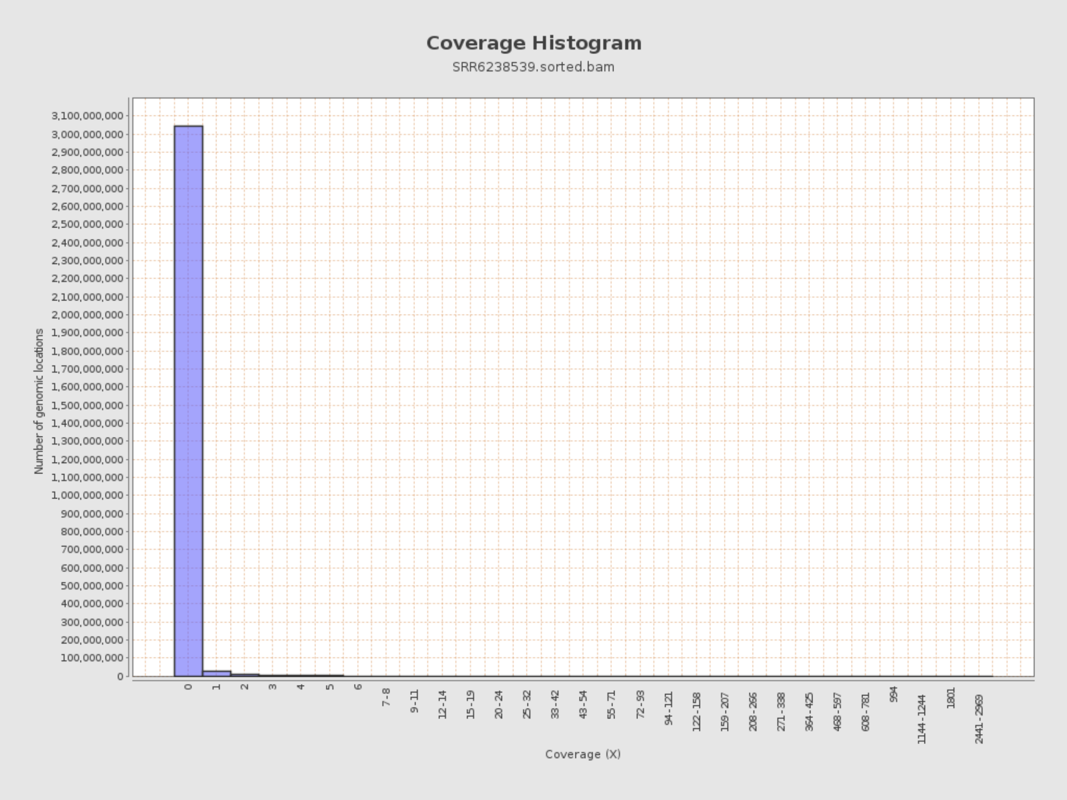
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9297435	0.0373	0.4117
chr2	243199373	7362603	0.0303	1.3196
chr3	198022430	5169450	0.0261	0.2801
chr4	191154276	4862418	0.0254	0.2709
chr5	180915260	4964115	0.0274	0.2844
chr6	171115067	5565543	0.0325	0.5026
chr7	159138663	8714459	0.0548	0.5243

chr8	146364022	5783356	0.0395	0.4342
chr9	141213431	3471027	0.0246	0.297
chr10	135534747	5972058	0.0441	0.3996
chr11	135006516	3149548	0.0233	0.2651
chr12	133851895	4214415	0.0315	0.3079
chr13	115169878	1846731	0.016	0.3531
chr14	107349540	2984861	0.0278	0.2932
chr15	102531392	2665288	0.026	0.3528
chr16	90354753	1961071	0.0217	0.271
chr17	81195210	1650788	0.0203	0.2426
chr18	78077248	4181529	0.0536	1.0281
chr19	59128983	1281257	0.0217	0.3079
chr20	63025520	1884749	0.0299	0.2993
chr21	48129895	1410595	0.0293	0.3033
chr22	51304566	654193	0.0128	0.188
chrMT	16571	15740	0.9499	1.7551
chrX	155270560	5342535	0.0344	0.3237
chrY	59373566	265306	0.0045	0.1985

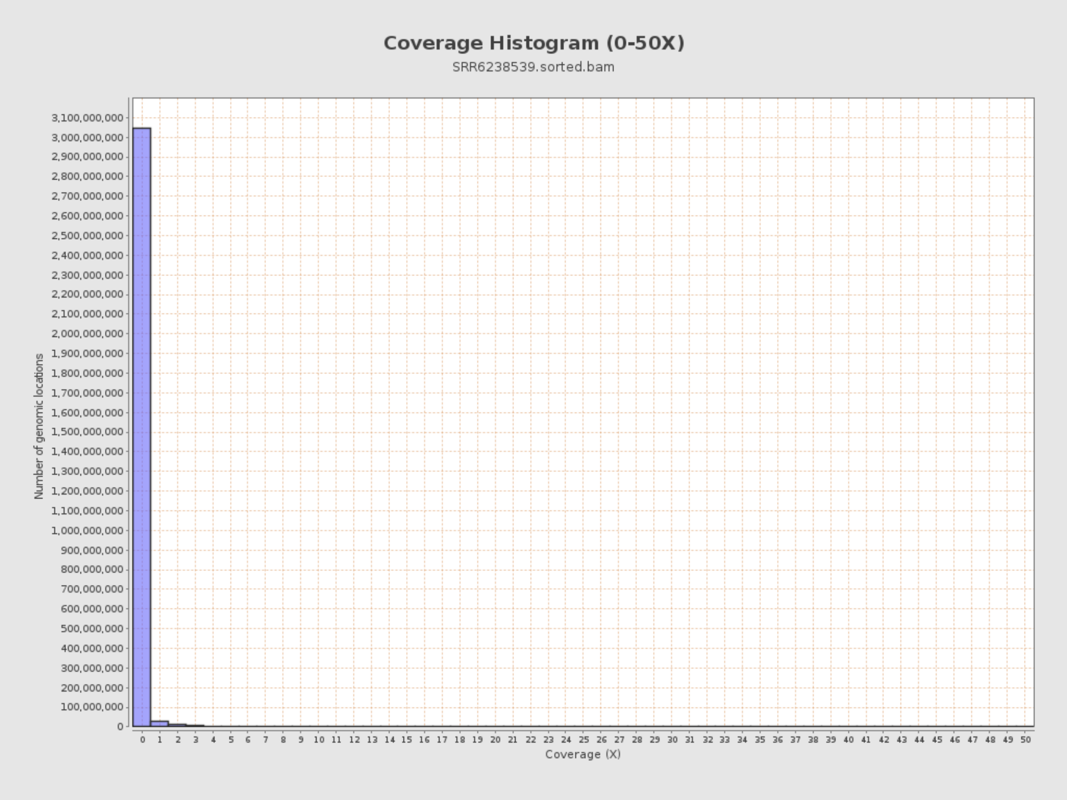
3. Results : Coverage across reference



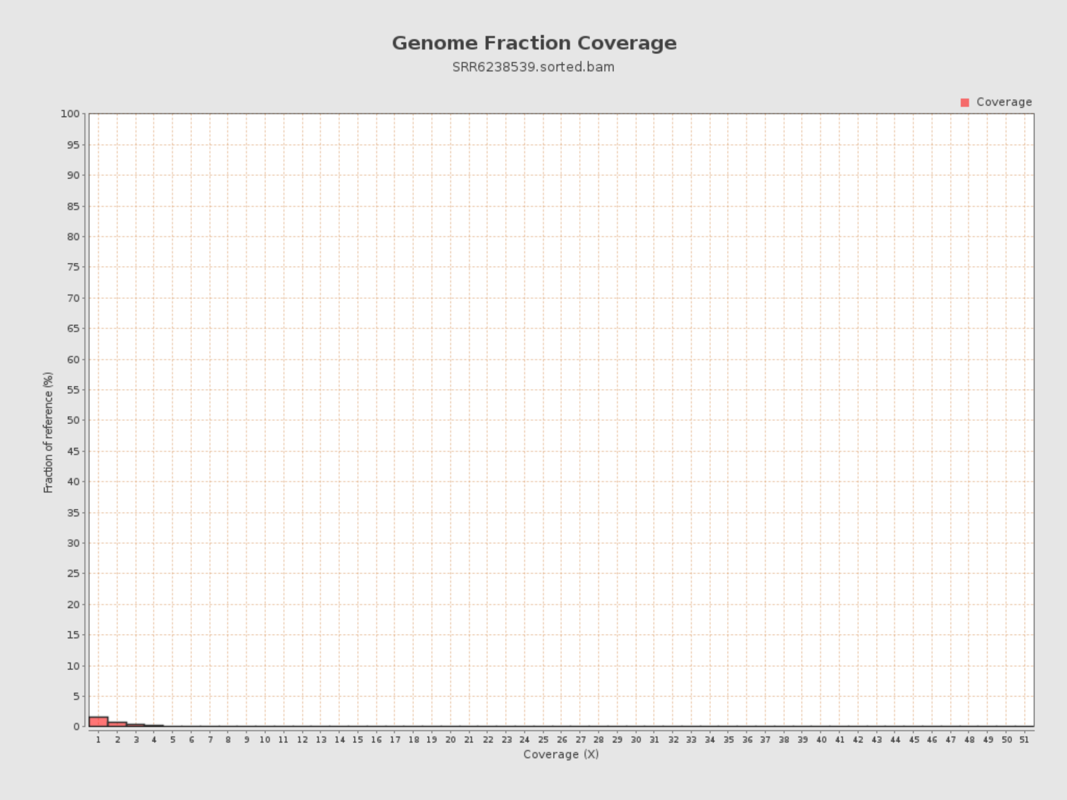
4. Results : Coverage Histogram



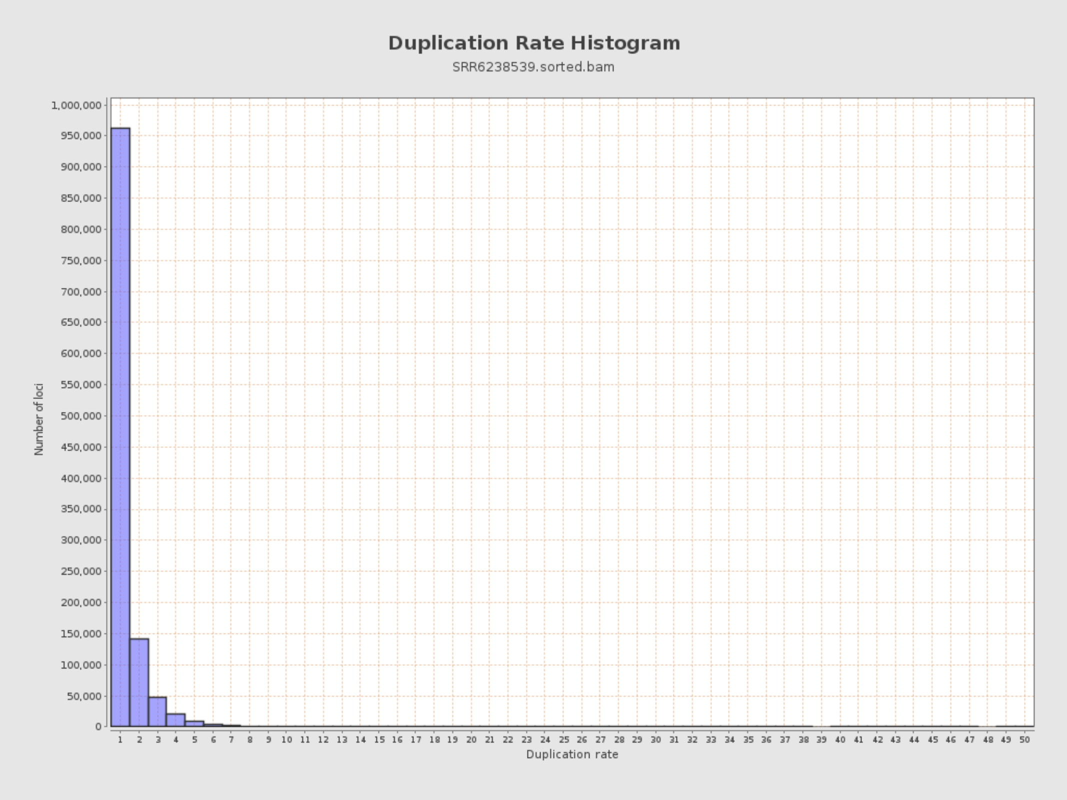
5. Results : Coverage Histogram (0-50X)



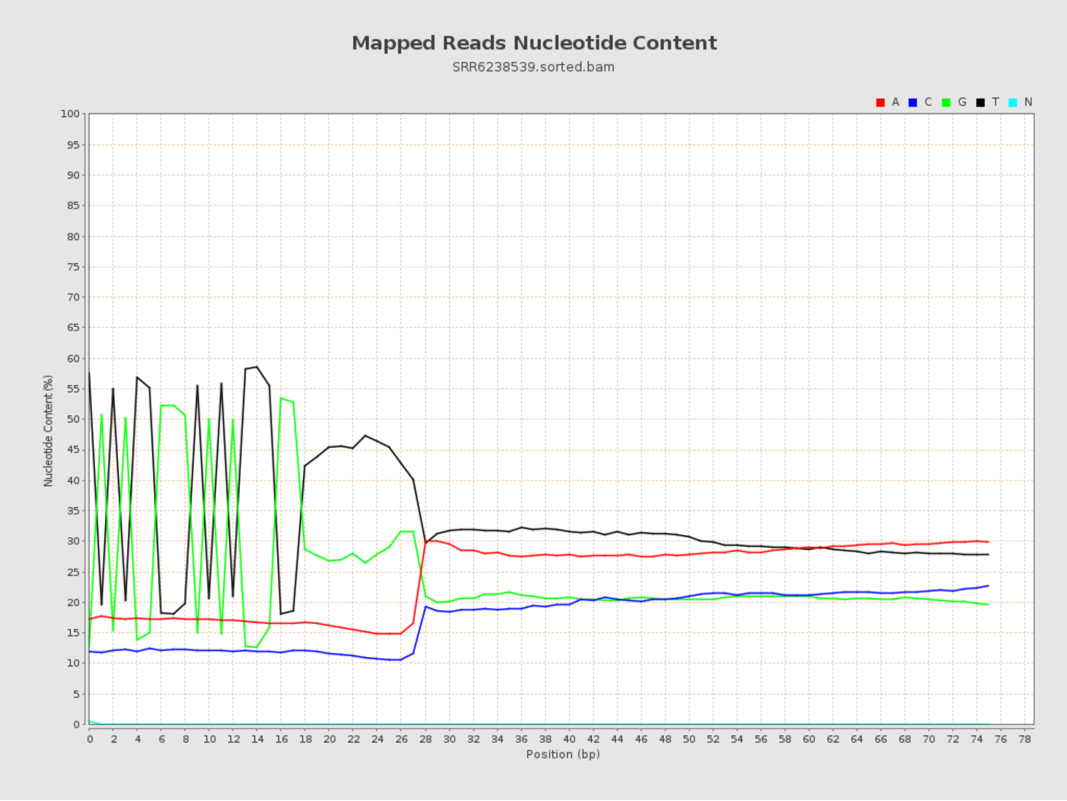
6. Results : Genome Fraction Coverage



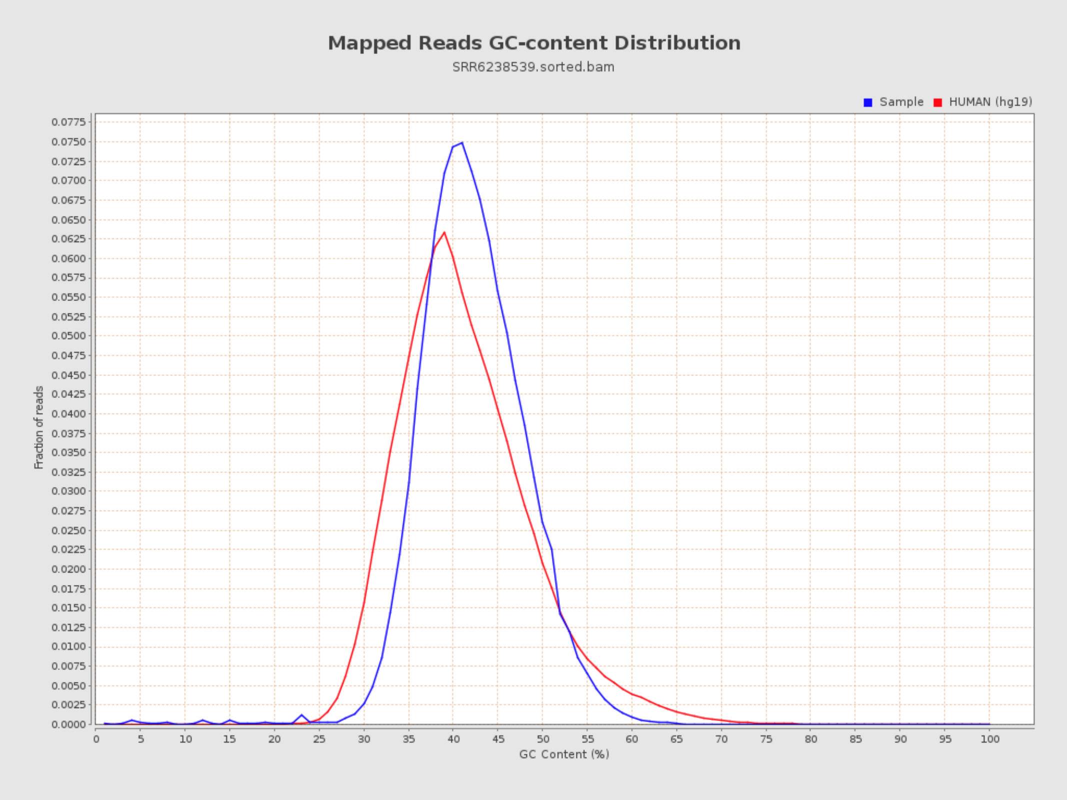
7. Results : Duplication Rate Histogram



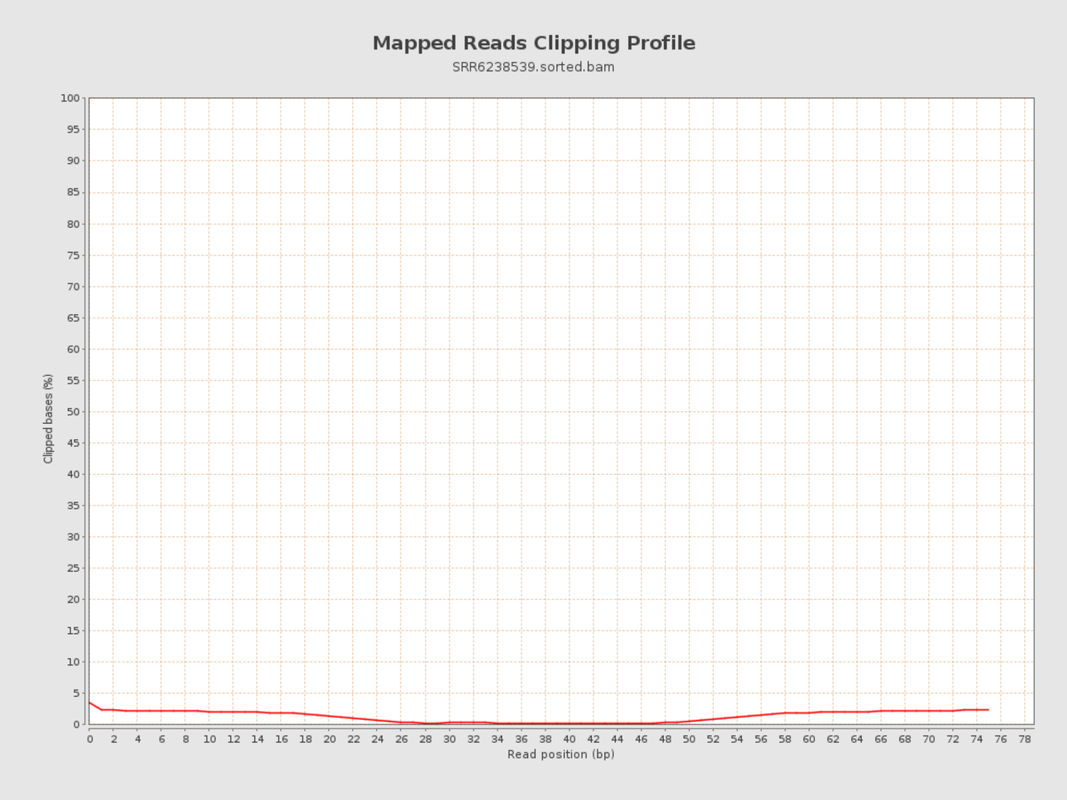
8. Results : Mapped Reads Nucleotide Content



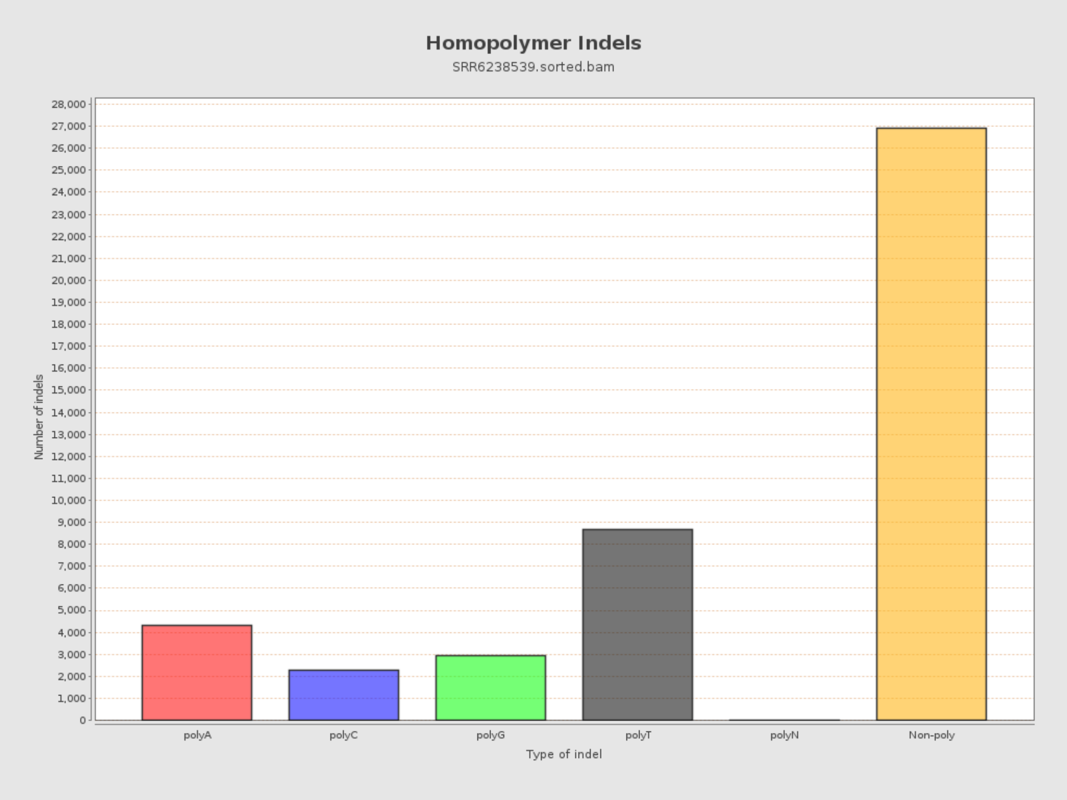
9. Results : Mapped Reads GC-content Distribution



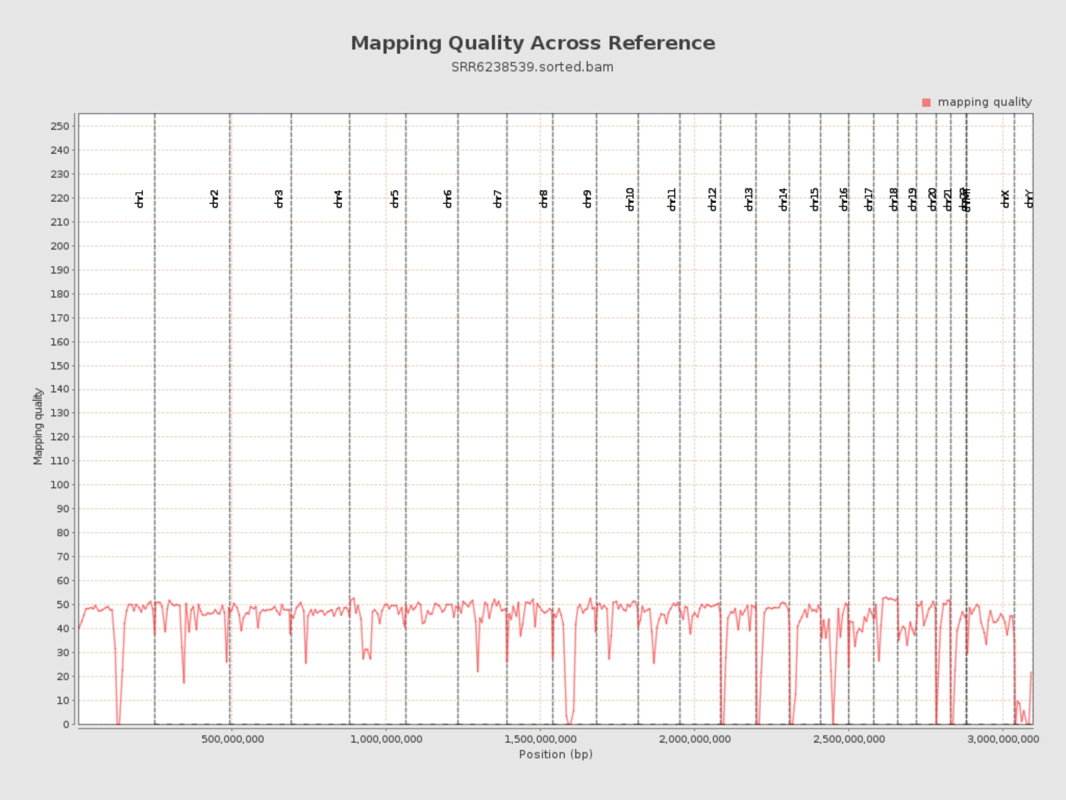
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram