Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:19:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238082.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_SRR6238082 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238082.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:19:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238082.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,880,733
Mapped reads	3,356,609 / 86.49%
Unmapped reads	524,124 / 13.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,850 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	267,649 / 6.9%
Duplication rate	6.18%
Clipped reads	963,044 / 24.82%

2.2. ACGT Content

Number/percentage of A's	69,225,077 / 29.24%
Number/percentage of C's	46,364,270 / 19.58%
Number/percentage of T's	72,240,526 / 30.51%
Number/percentage of G's	48,940,614 / 20.67%
Number/percentage of N's	15,298 / 0.01%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0765

Standard Deviation	0.8366

2.4. Mapping Quality

Mean Mapping Quality	47.86

2.5. Mismatches and indels

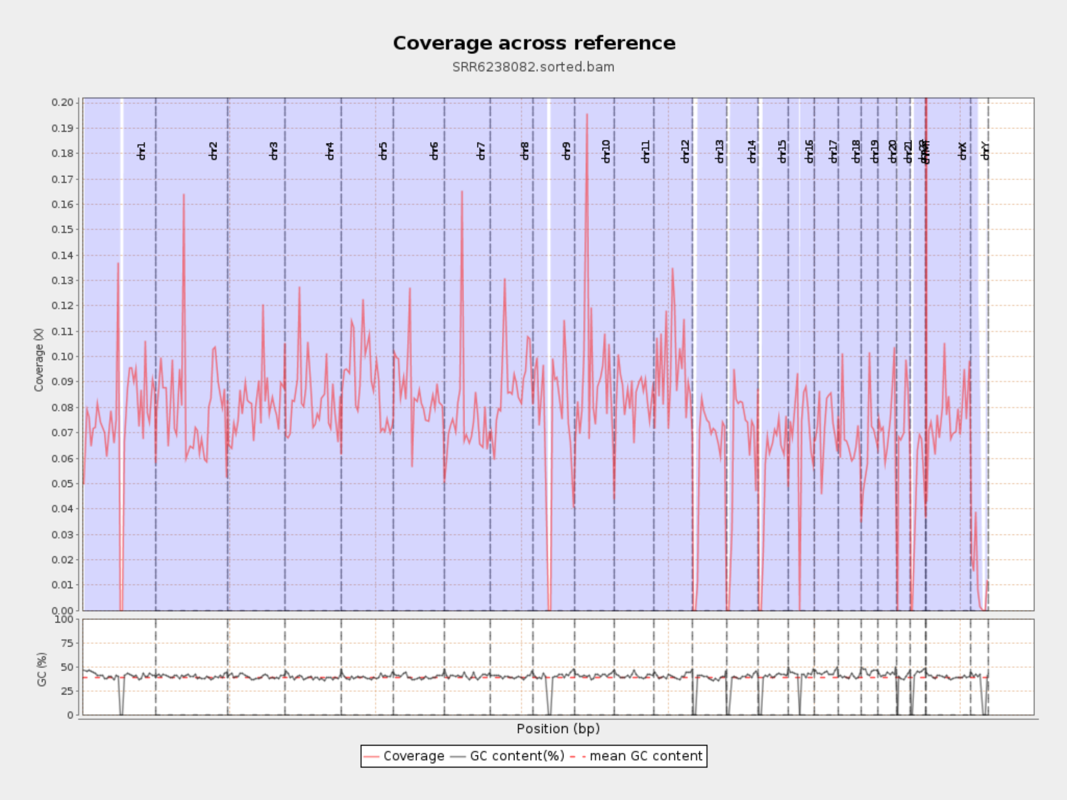
General error rate	0.78%
Mismatches	1,804,587
Insertions	21,079
Mapped reads with at least one insertion	0.62%
Deletions	77,960
Mapped reads with at least one deletion	2.29%
Homopolymer indels	47.34%

2.6. Chromosome stats

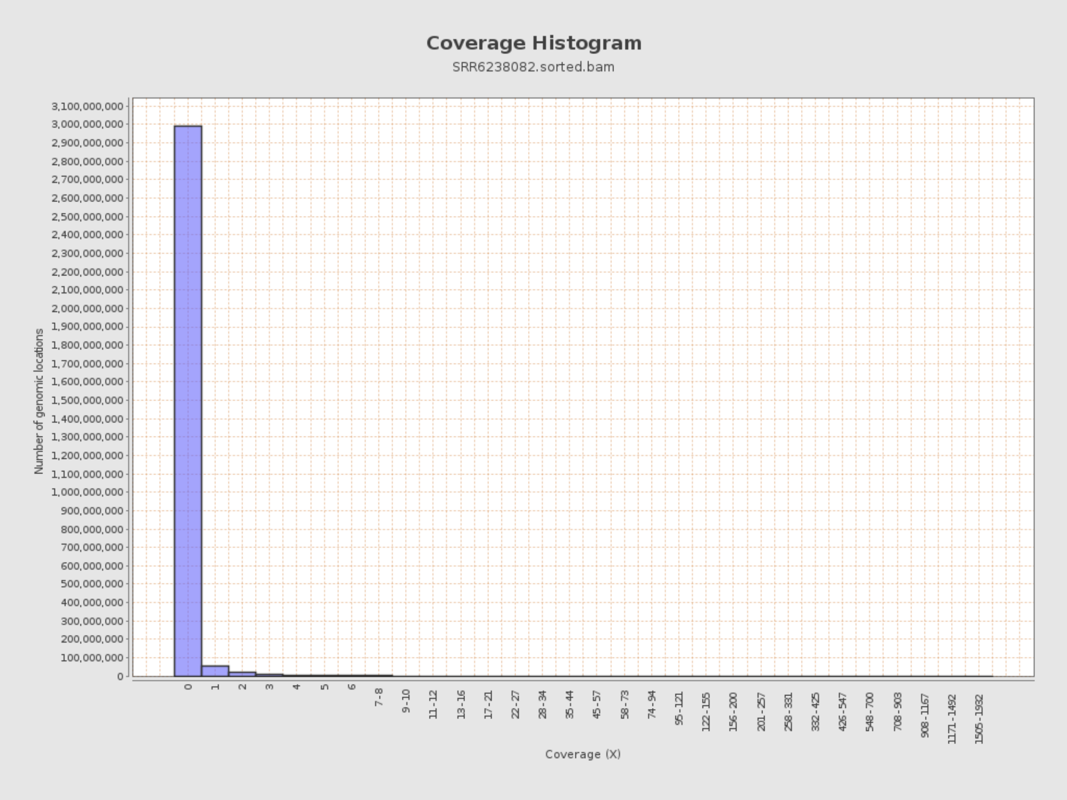
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18616022	0.0747	1.5621
chr2	243199373	19633393	0.0807	0.8524
chr3	198022430	16053907	0.0811	0.569
chr4	191154276	15805456	0.0827	0.6035
chr5	180915260	16289788	0.09	0.5966
chr6	171115067	14737561	0.0861	0.7039
chr7	159138663	12075733	0.0759	1.1719

chr8	146364022	13025030	0.089	0.8265
chr9	141213431	10500488	0.0744	0.7621
chr10	135534747	12538210	0.0925	1.0352
chr11	135006516	11427334	0.0846	0.7142
chr12	133851895	12843584	0.096	0.6282
chr13	115169878	6855540	0.0595	0.477
chr14	107349540	6739792	0.0628	0.5122
chr15	102531392	5577611	0.0544	0.4549
chr16	90354753	6171175	0.0683	0.5751
chr17	81195210	5970109	0.0735	0.5982
chr18	78077248	5332338	0.0683	1.3159
chr19	59128983	3866615	0.0654	1.0137
chr20	63025520	4721593	0.0749	0.5543
chr21	48129895	3317025	0.0689	0.5579
chr22	51304566	2220882	0.0433	0.3966
chrMT	16571	85333	5.1495	5.1206
chrX	155270560	11820532	0.0761	0.5724
chrY	59373566	691751	0.0117	0.3218

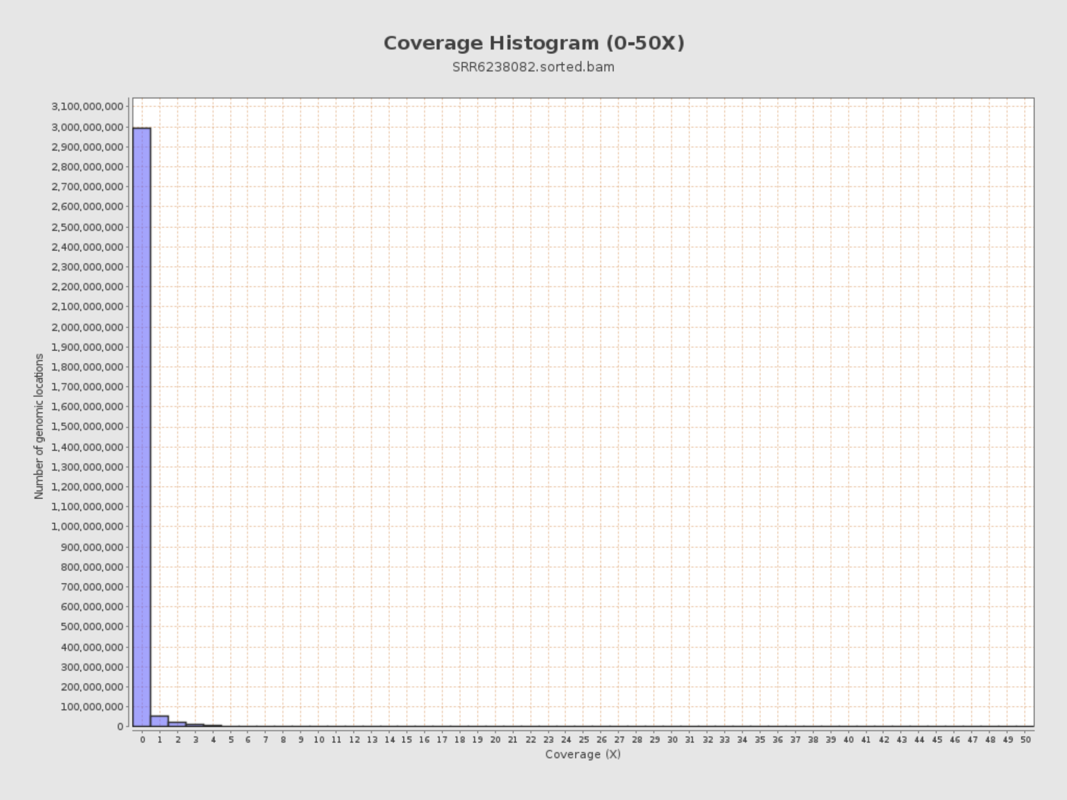
3. Results : Coverage across reference



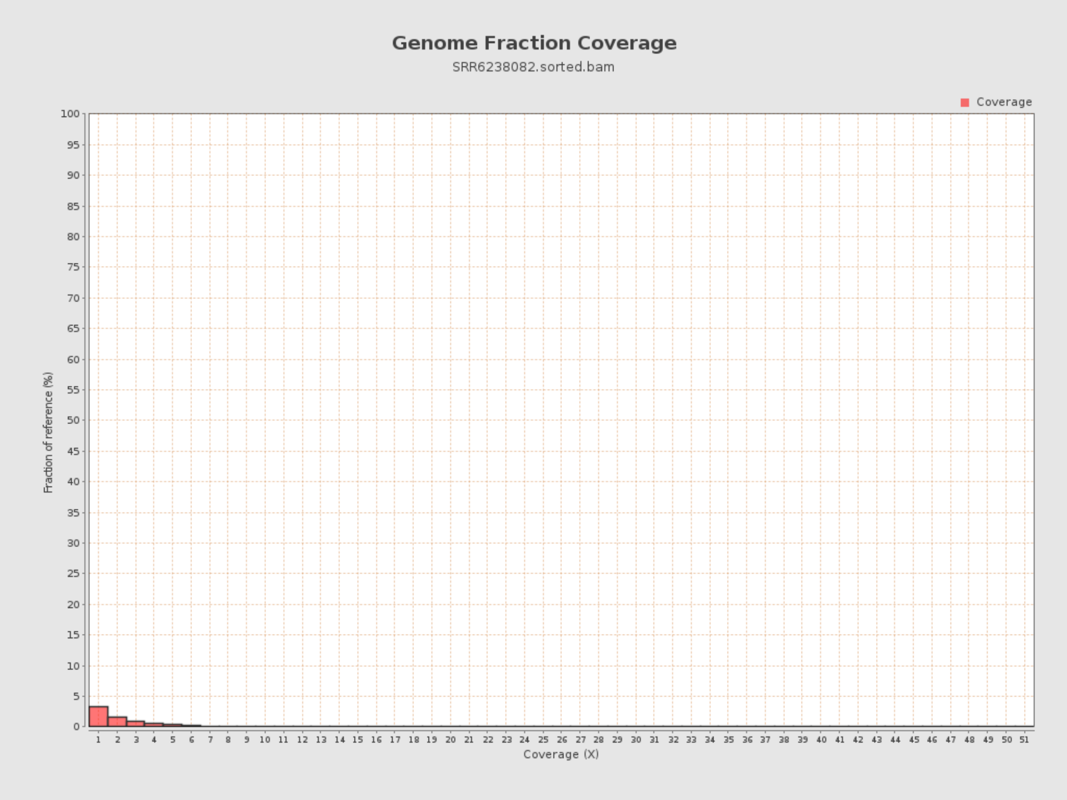
4. Results : Coverage Histogram



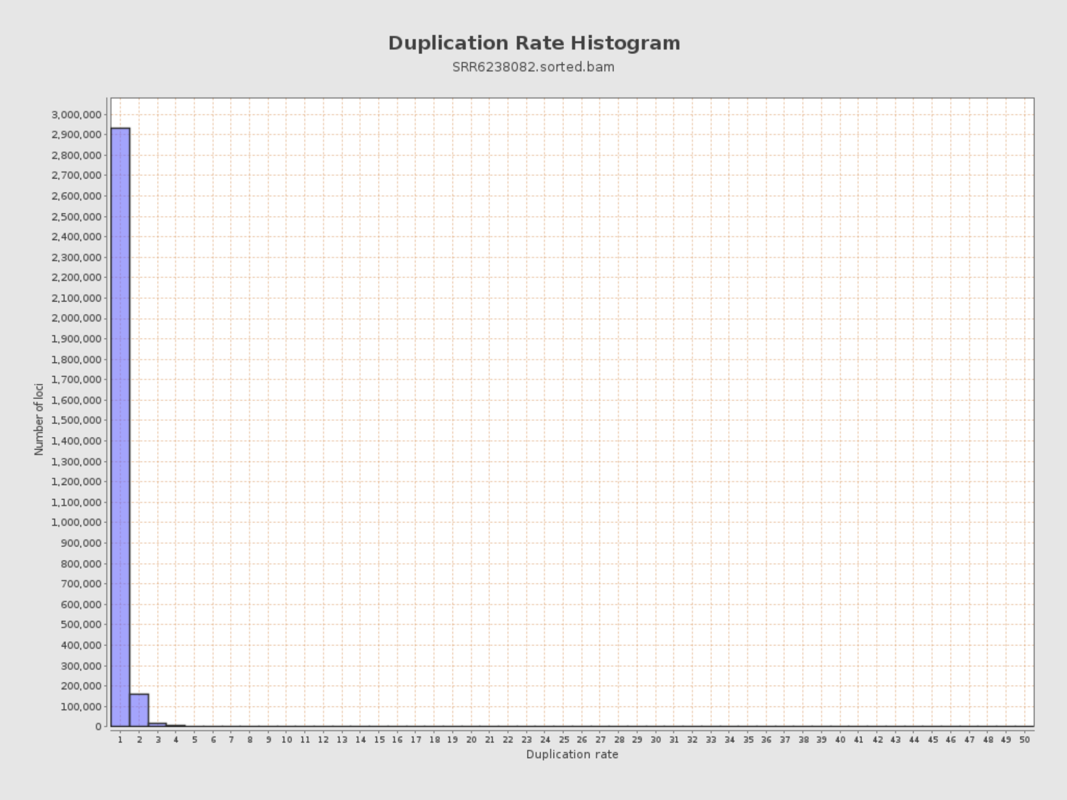
5. Results : Coverage Histogram (0-50X)



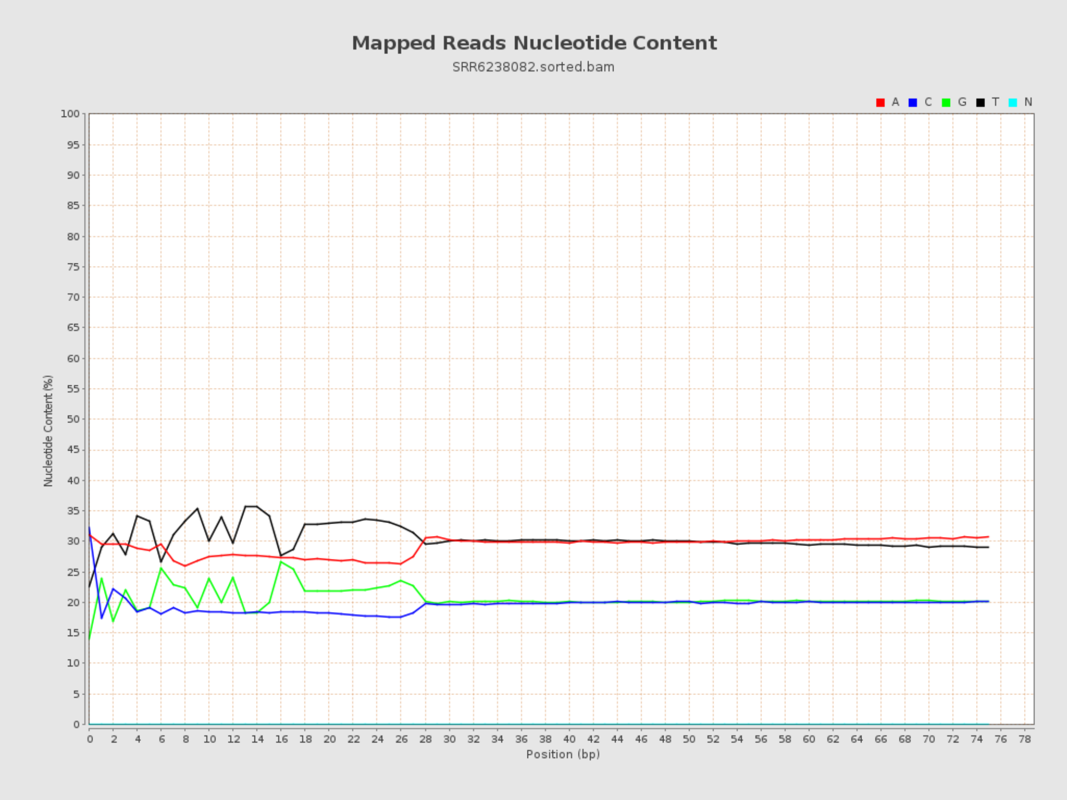
6. Results : Genome Fraction Coverage



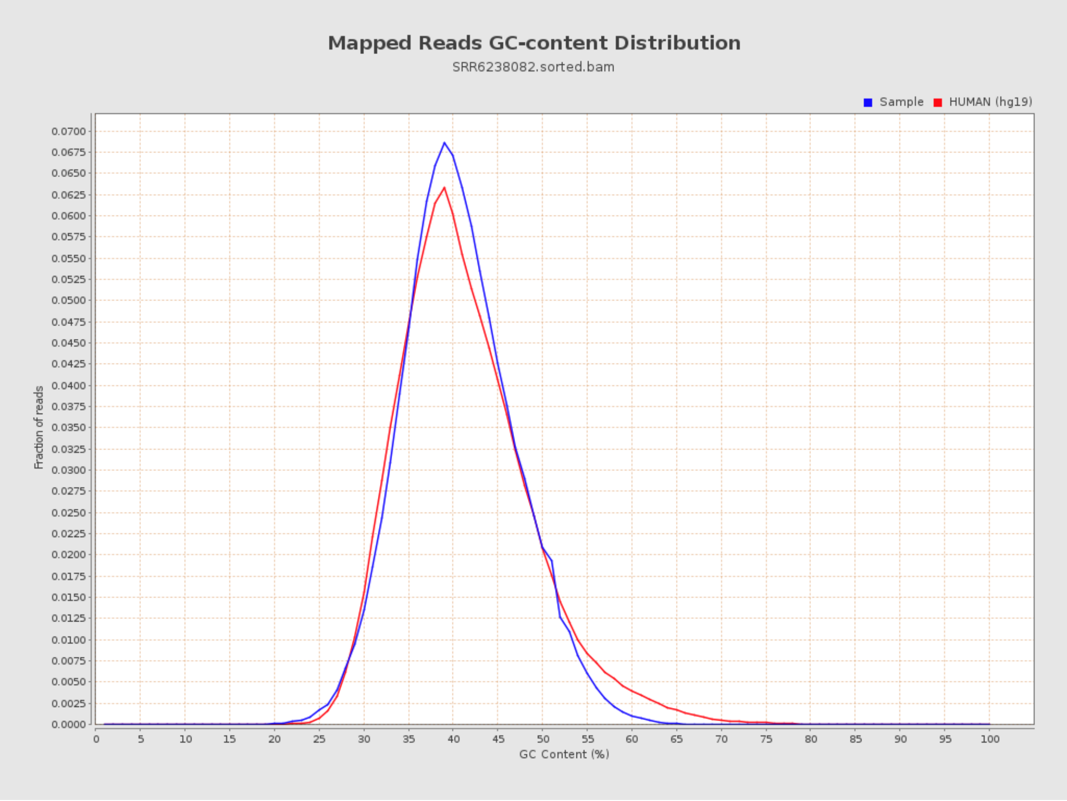
7. Results : Duplication Rate Histogram



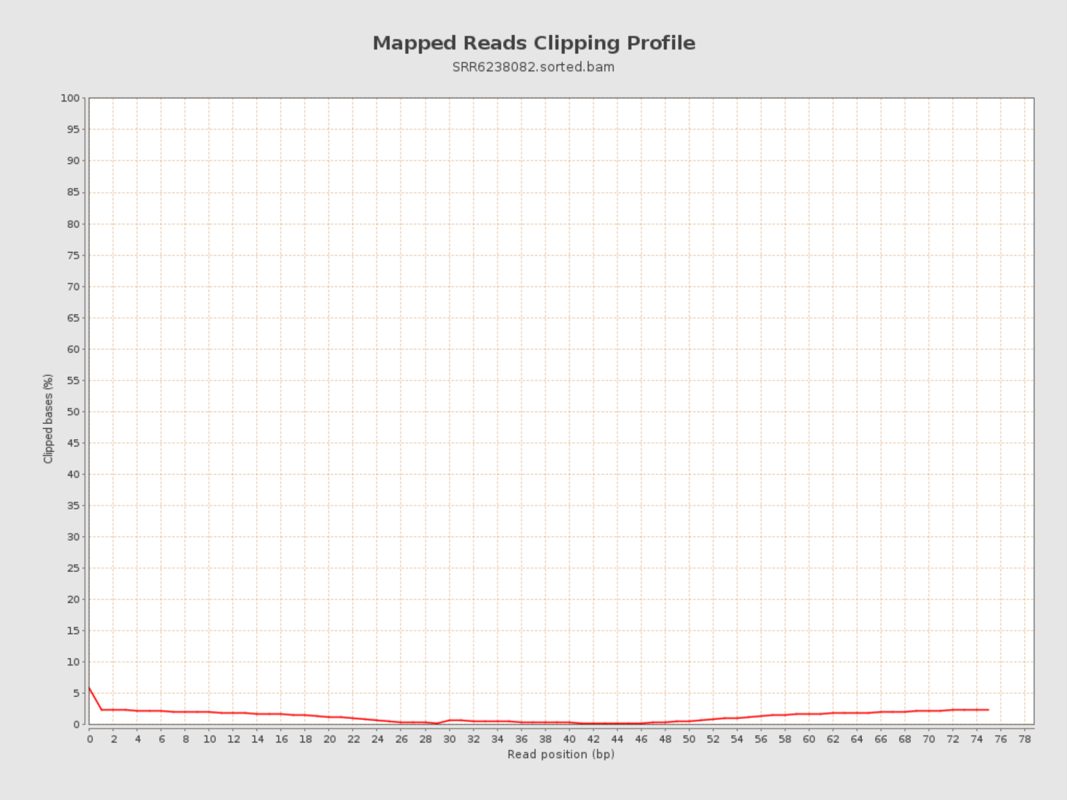
8. Results : Mapped Reads Nucleotide Content



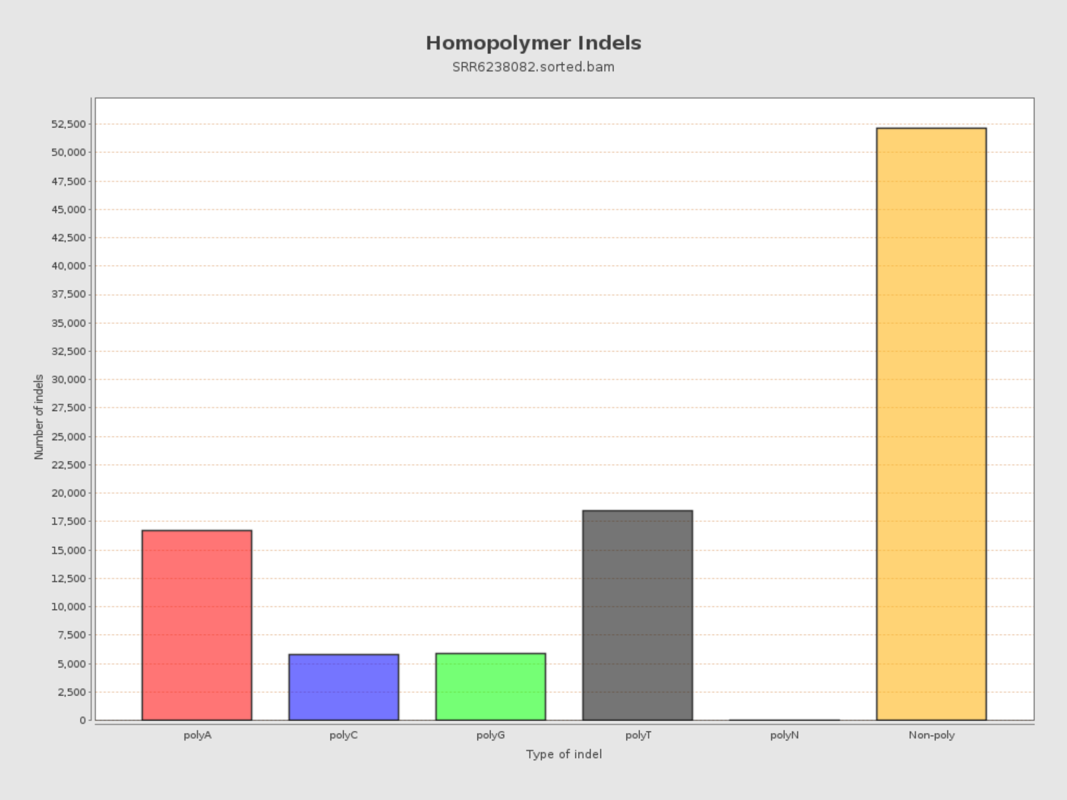
9. Results : Mapped Reads GC-content Distribution



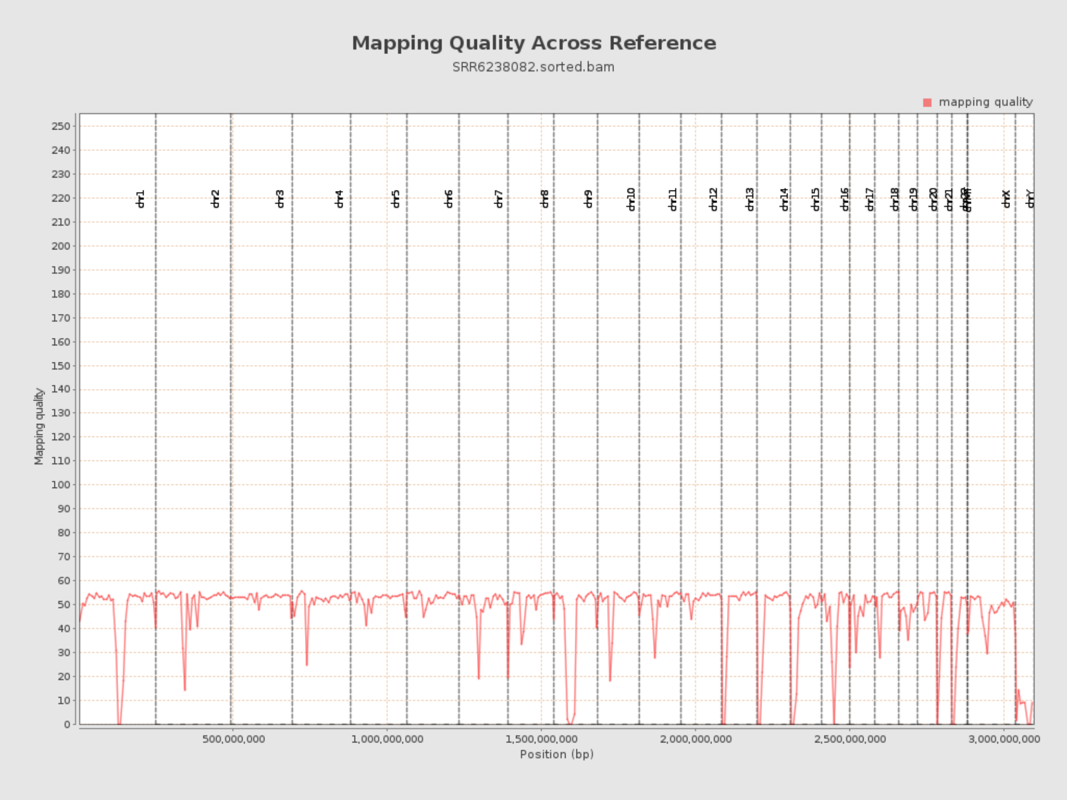
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram