Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:30:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238633.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_SRR6238633 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238633.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:30:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238633.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,623,610
Mapped reads	1,466,808 / 90.34%
Unmapped reads	156,802 / 9.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,989 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	268,909 / 16.56%
Duplication rate	15.48%
Clipped reads	980,247 / 60.37%

2.2. ACGT Content

Number/percentage of A's	21,656,301 / 24.17%
Number/percentage of C's	15,455,432 / 17.25%
Number/percentage of T's	30,552,160 / 34.1%
Number/percentage of G's	21,928,811 / 24.47%
Number/percentage of N's	4,366 / 0%
GC Percentage	41.72%

2.3. Coverage

Mean	0.029

Standard Deviation	0.3973

2.4. Mapping Quality

Mean Mapping Quality	43.42

2.5. Mismatches and indels

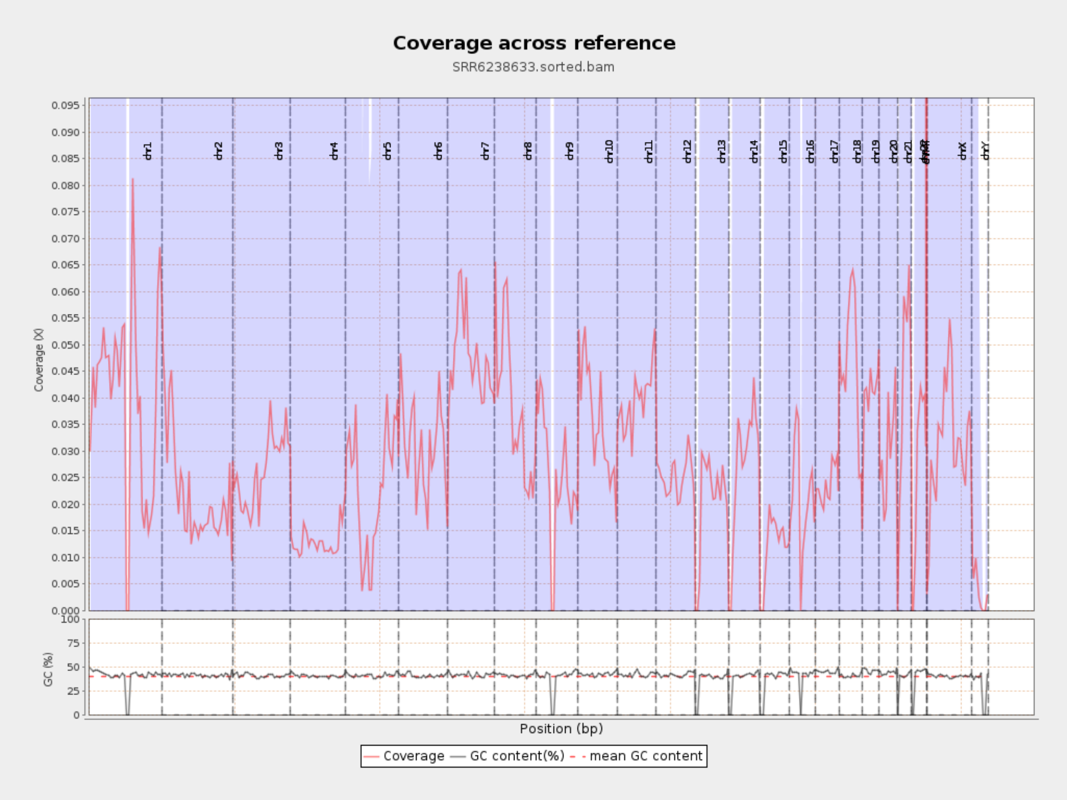
General error rate	0.61%
Mismatches	532,758
Insertions	5,711
Mapped reads with at least one insertion	0.39%
Deletions	26,139
Mapped reads with at least one deletion	1.77%
Homopolymer indels	42.14%

2.6. Chromosome stats

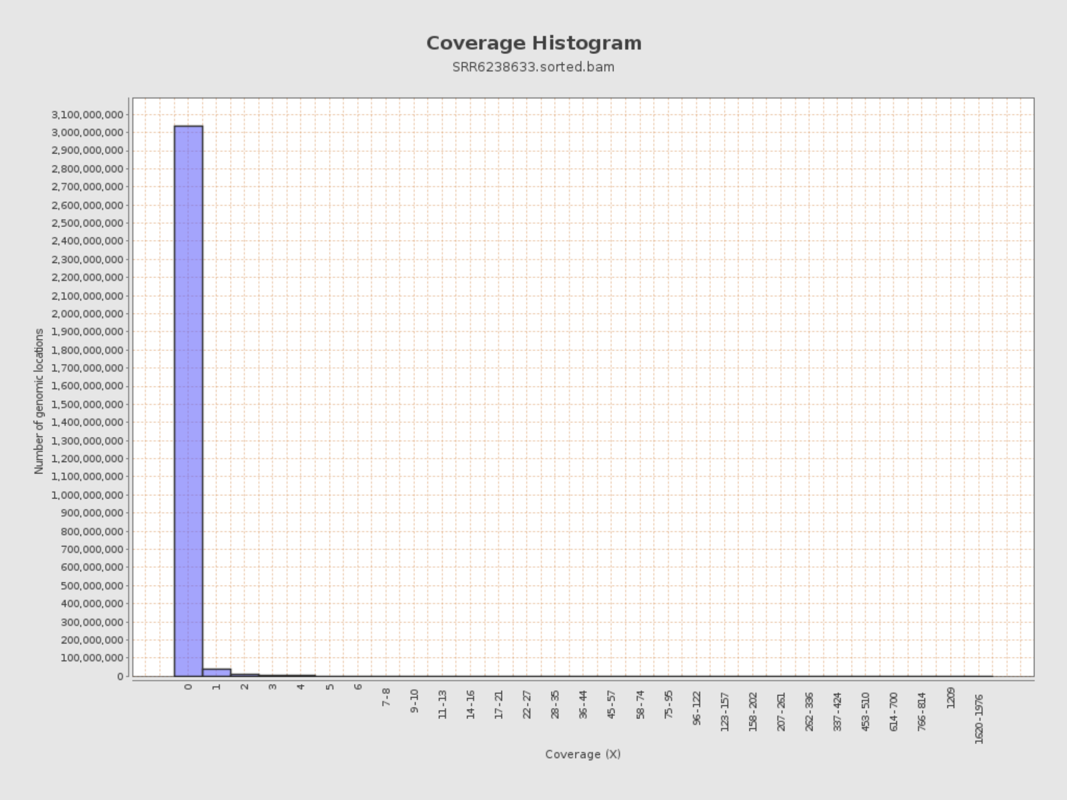
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9907607	0.0397	0.4894
chr2	243199373	5354604	0.022	0.8741
chr3	198022430	5222303	0.0264	0.2344
chr4	191154276	2480628	0.013	0.1637
chr5	180915260	4185794	0.0231	0.2202
chr6	171115067	5298184	0.031	0.3835
chr7	159138663	7621801	0.0479	0.4779

chr8	146364022	5531427	0.0378	0.3441
chr9	141213431	3504327	0.0248	0.2615
chr10	135534747	4884088	0.036	0.2902
chr11	135006516	5367854	0.0398	0.3156
chr12	133851895	3366728	0.0252	0.2305
chr13	115169878	2374554	0.0206	0.269
chr14	107349540	2930509	0.0273	0.2425
chr15	102531392	1259131	0.0123	0.2447
chr16	90354753	1970399	0.0218	0.2249
chr17	81195210	1923486	0.0237	0.2246
chr18	78077248	3703596	0.0474	0.6751
chr19	59128983	2410340	0.0408	0.4043
chr20	63025520	1893753	0.03	0.2535
chr21	48129895	1997284	0.0415	0.3004
chr22	51304566	1355854	0.0264	0.2351
chrMT	16571	16184	0.9766	1.4608
chrX	155270560	4868688	0.0314	0.2558
chrY	59373566	212239	0.0036	0.1539

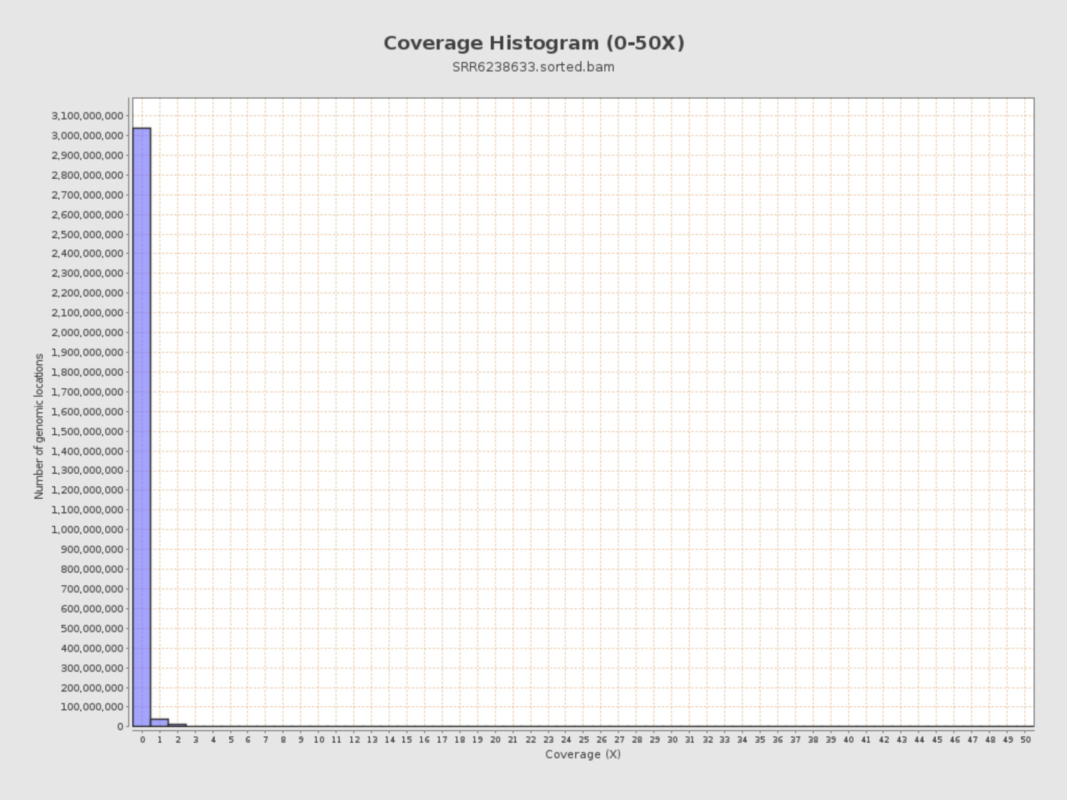
3. Results : Coverage across reference



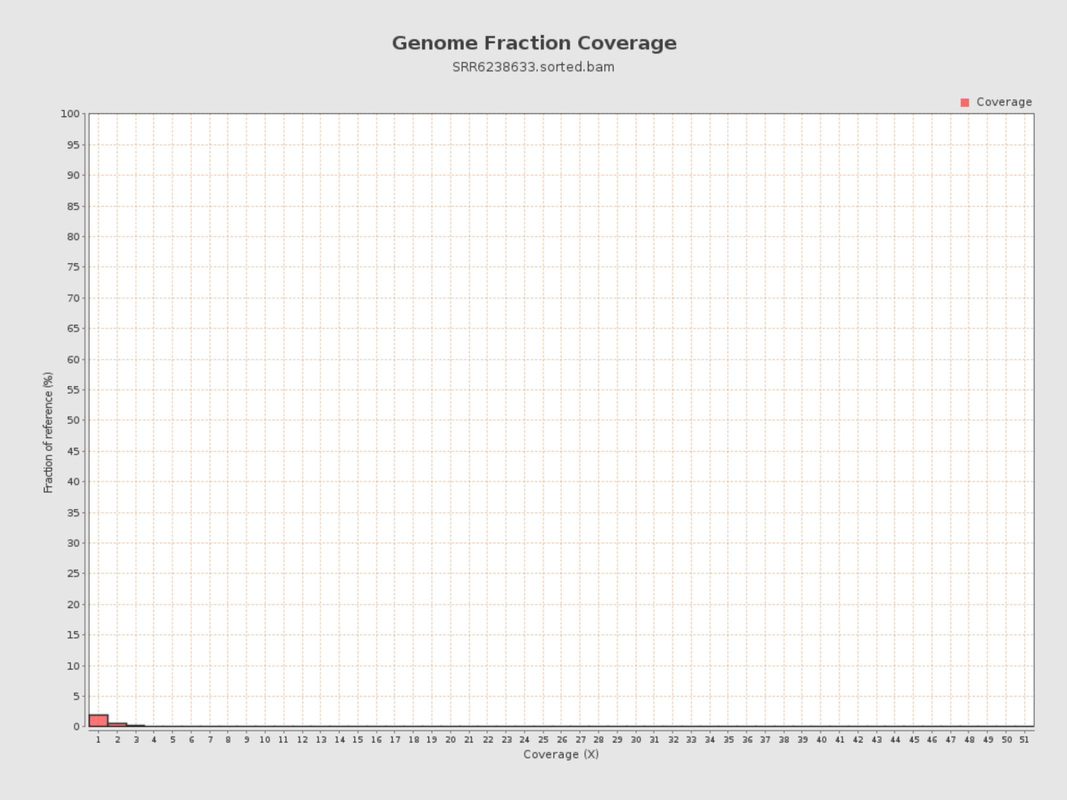
4. Results : Coverage Histogram



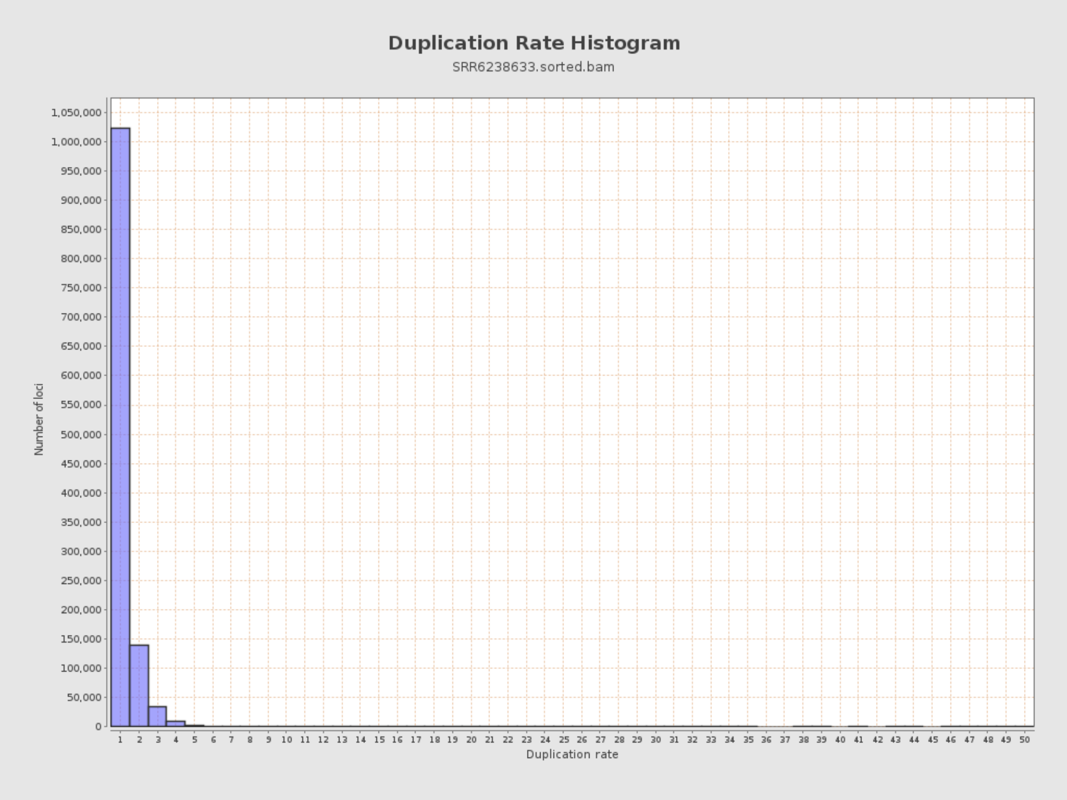
5. Results : Coverage Histogram (0-50X)



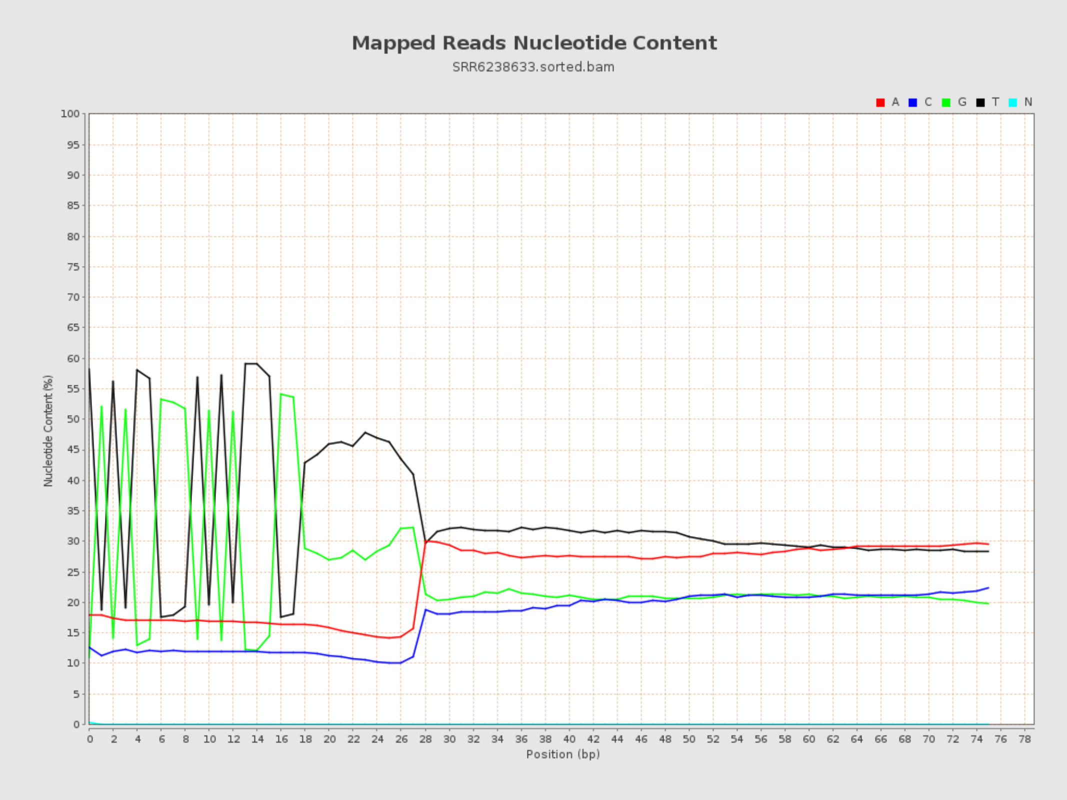
6. Results : Genome Fraction Coverage



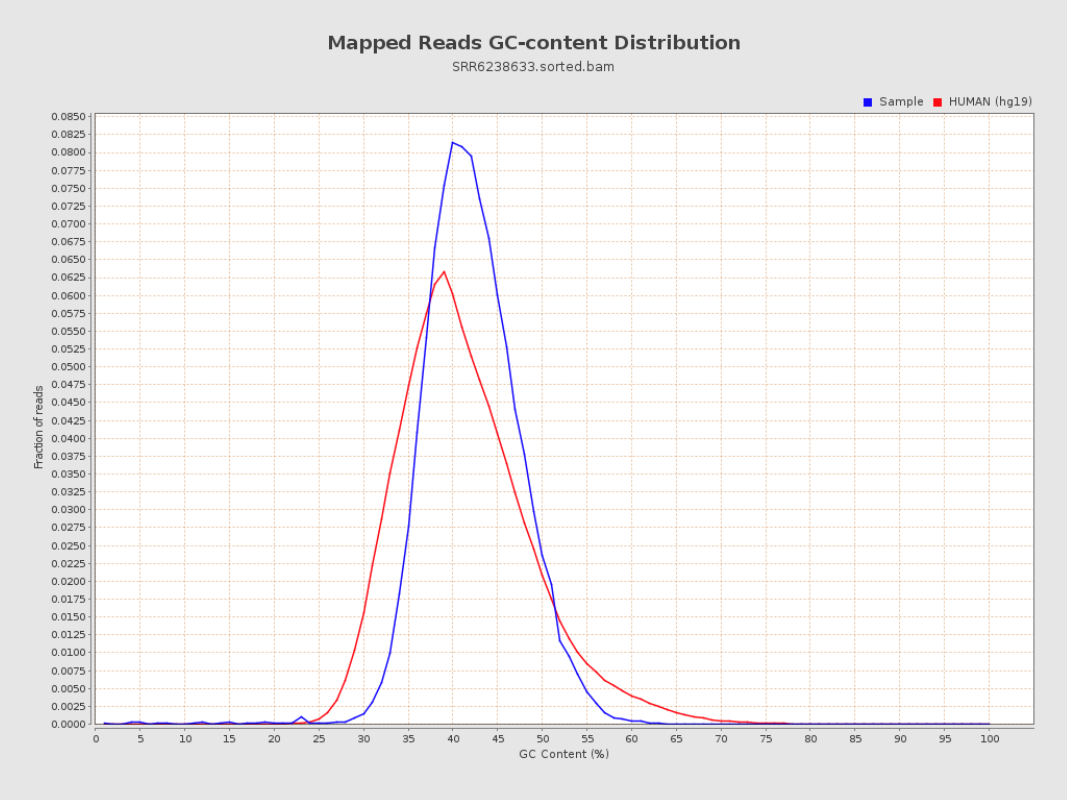
7. Results : Duplication Rate Histogram



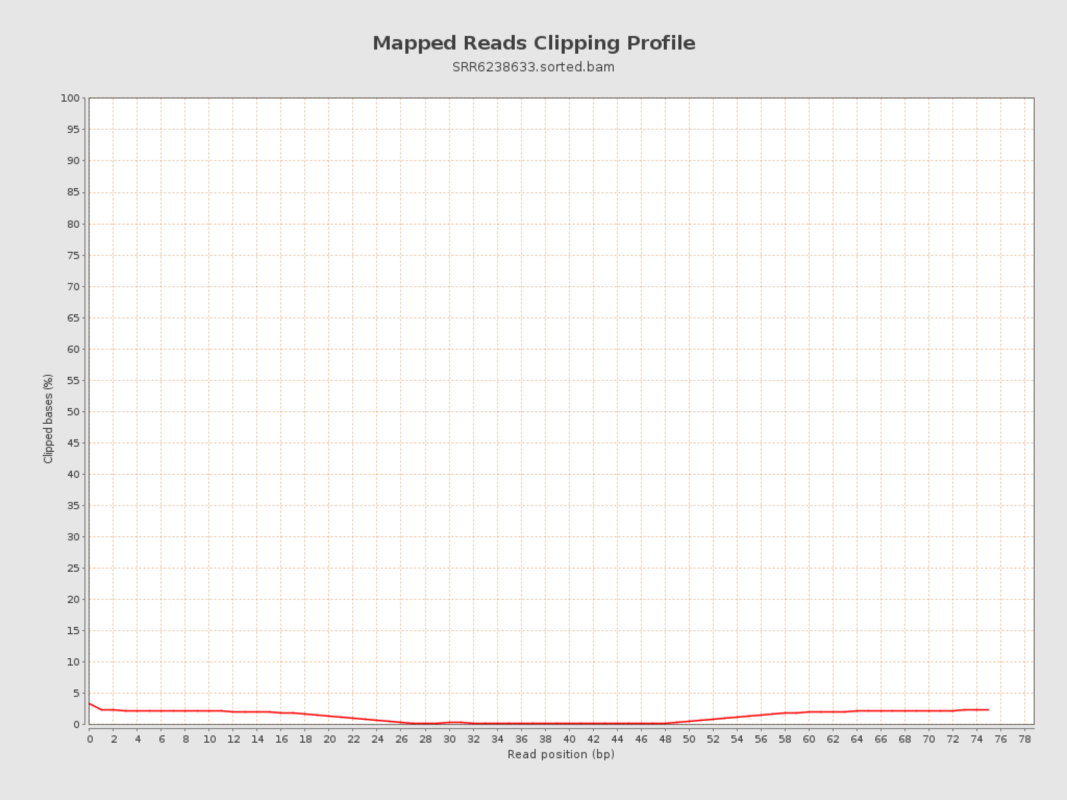
8. Results : Mapped Reads Nucleotide Content



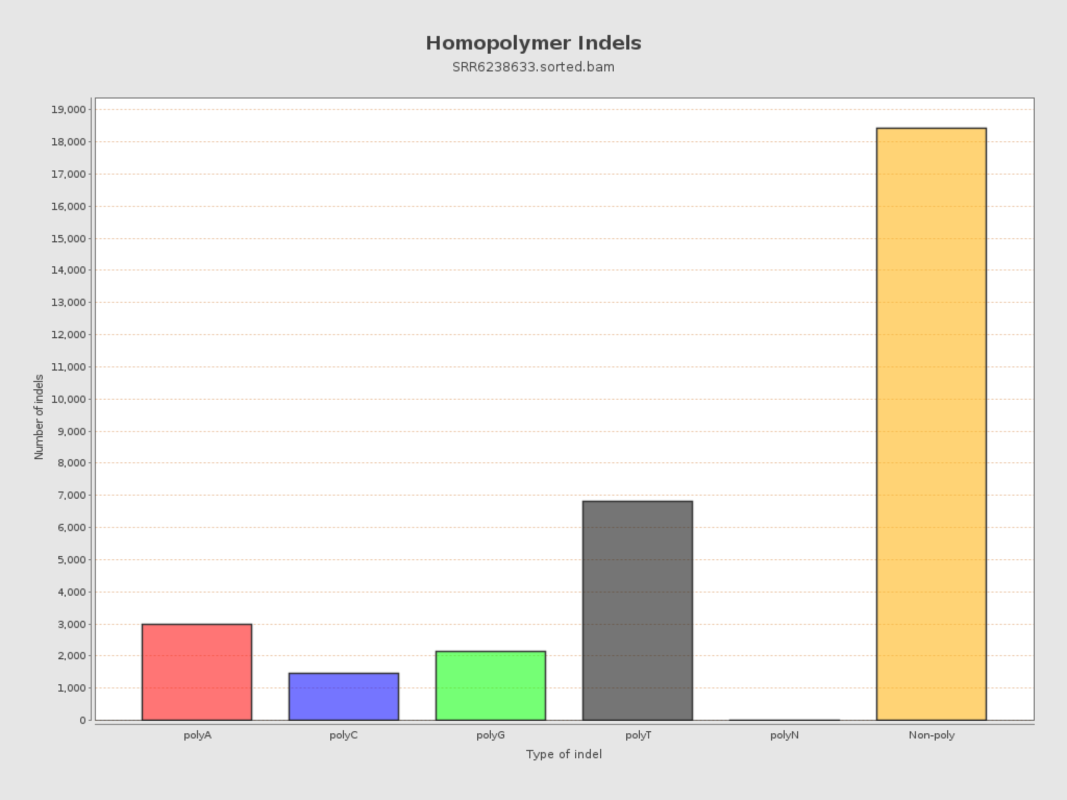
9. Results : Mapped Reads GC-content Distribution



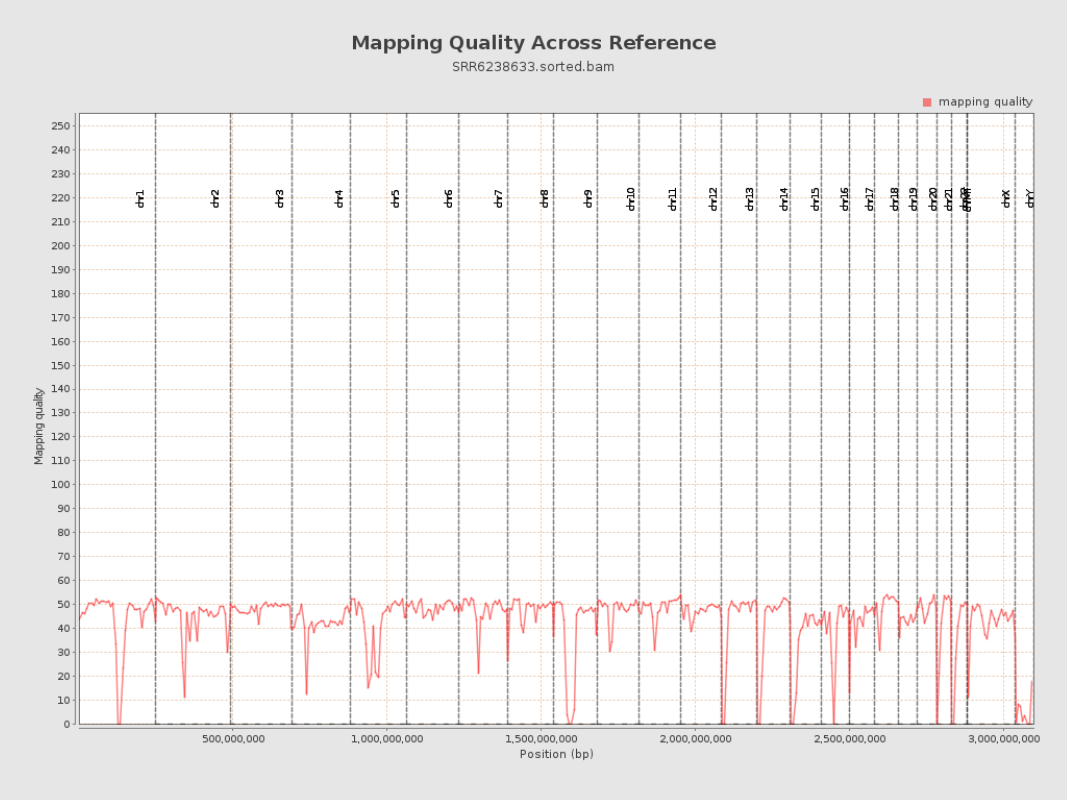
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram