Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:16:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238673.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_SRR6238673 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238673.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:16:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238673.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,619,276
Mapped reads	3,225,418 / 89.12%
Unmapped reads	393,858 / 10.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,652 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	1,118,703 / 30.91%
Duplication rate	20.13%
Clipped reads	2,034,078 / 56.2%

2.2. ACGT Content

Number/percentage of A's	50,251,612 / 25.19%
Number/percentage of C's	35,164,258 / 17.63%
Number/percentage of T's	66,981,927 / 33.58%
Number/percentage of G's	47,048,880 / 23.59%
Number/percentage of N's	10,202 / 0.01%
GC Percentage	41.22%

2.3. Coverage

Mean	0.0645

Standard Deviation	1.0226

2.4. Mapping Quality

Mean Mapping Quality	39.02

2.5. Mismatches and indels

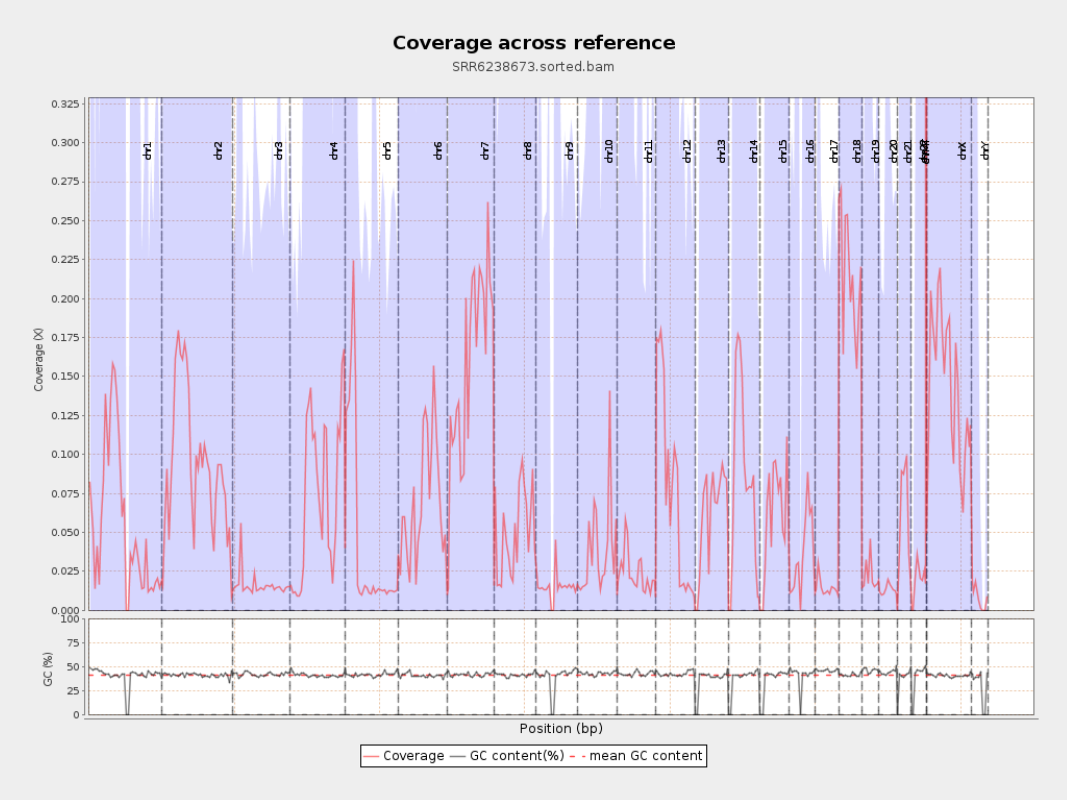
General error rate	0.59%
Mismatches	1,154,500
Insertions	12,228
Mapped reads with at least one insertion	0.38%
Deletions	56,377
Mapped reads with at least one deletion	1.73%
Homopolymer indels	41.72%

2.6. Chromosome stats

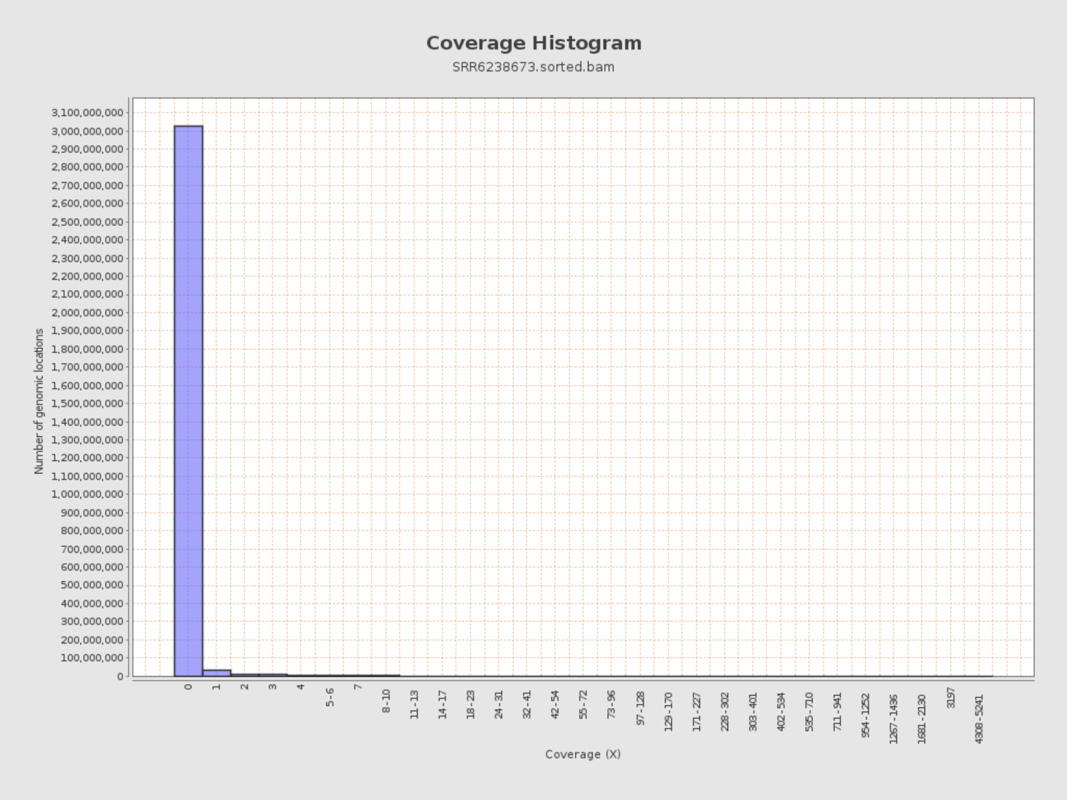
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13550799	0.0544	0.66
chr2	243199373	22917508	0.0942	2.3974
chr3	198022430	3205901	0.0162	0.2982
chr4	191154276	14283619	0.0747	0.6597
chr5	180915260	8057685	0.0445	0.5137
chr6	171115067	11736325	0.0686	0.9318
chr7	159138663	25851274	0.1624	1.7492

chr8	146364022	7316714	0.05	0.7011
chr9	141213431	2098546	0.0149	0.401
chr10	135534747	5202381	0.0384	0.5317
chr11	135006516	3252970	0.0241	0.3856
chr12	133851895	9884653	0.0738	0.6675
chr13	115169878	7111529	0.0617	0.7376
chr14	107349540	9031693	0.0841	0.7182
chr15	102531392	6196201	0.0604	0.726
chr16	90354753	3324342	0.0368	0.4956
chr17	81195210	1152810	0.0142	0.2564
chr18	78077248	16594843	0.2125	2.0932
chr19	59128983	1339230	0.0226	0.4873
chr20	63025520	851933	0.0135	0.2777
chr21	48129895	2783264	0.0578	0.5884
chr22	51304566	979071	0.0191	0.3156
chrMT	16571	99499	6.0044	6.6659
chrX	155270560	22270963	0.1434	0.9415
chrY	59373566	456645	0.0077	0.33

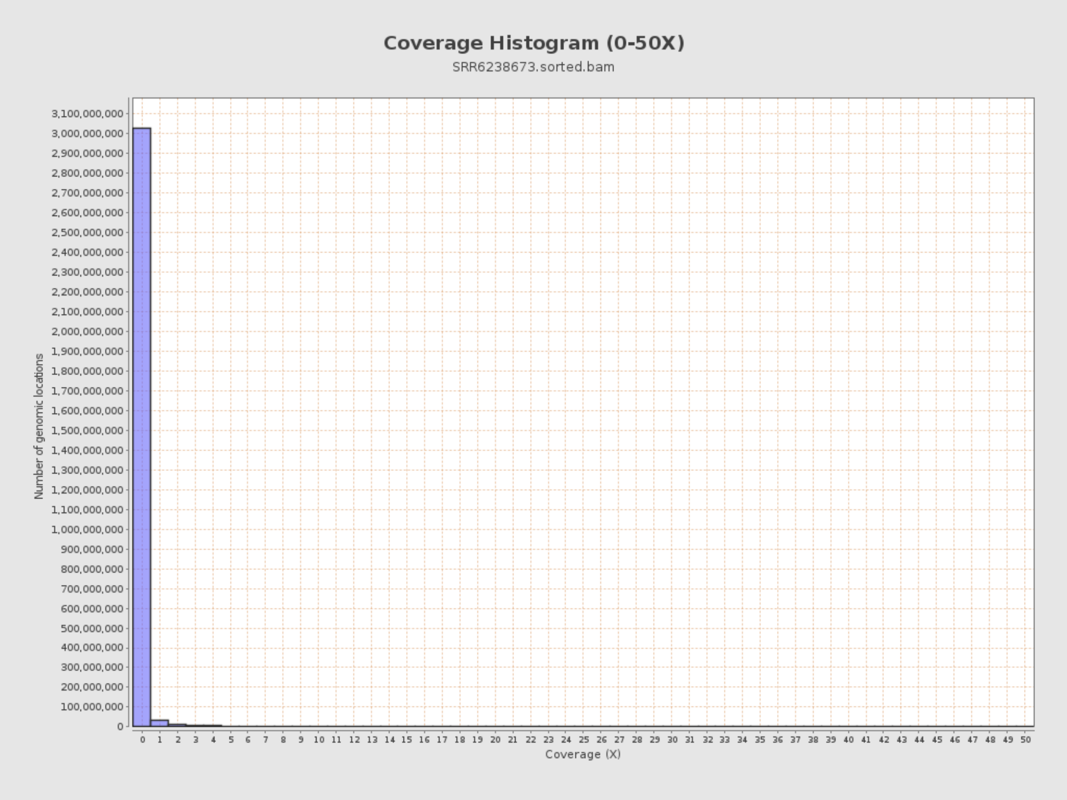
3. Results : Coverage across reference



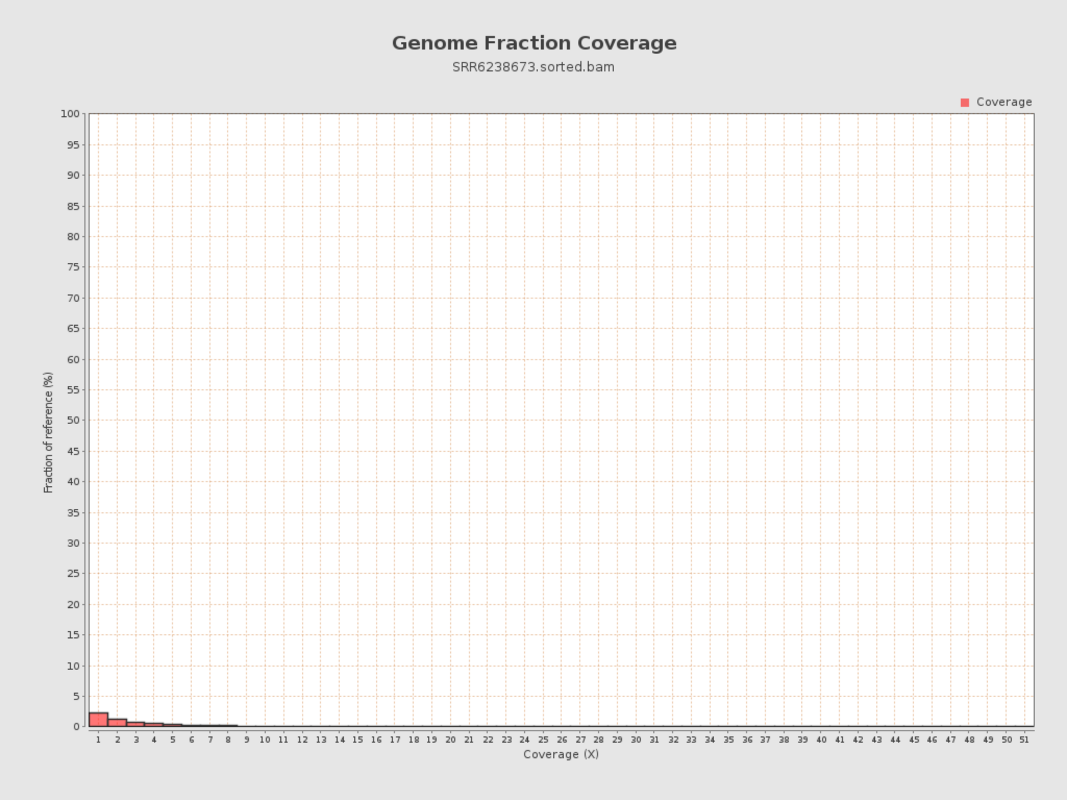
4. Results : Coverage Histogram



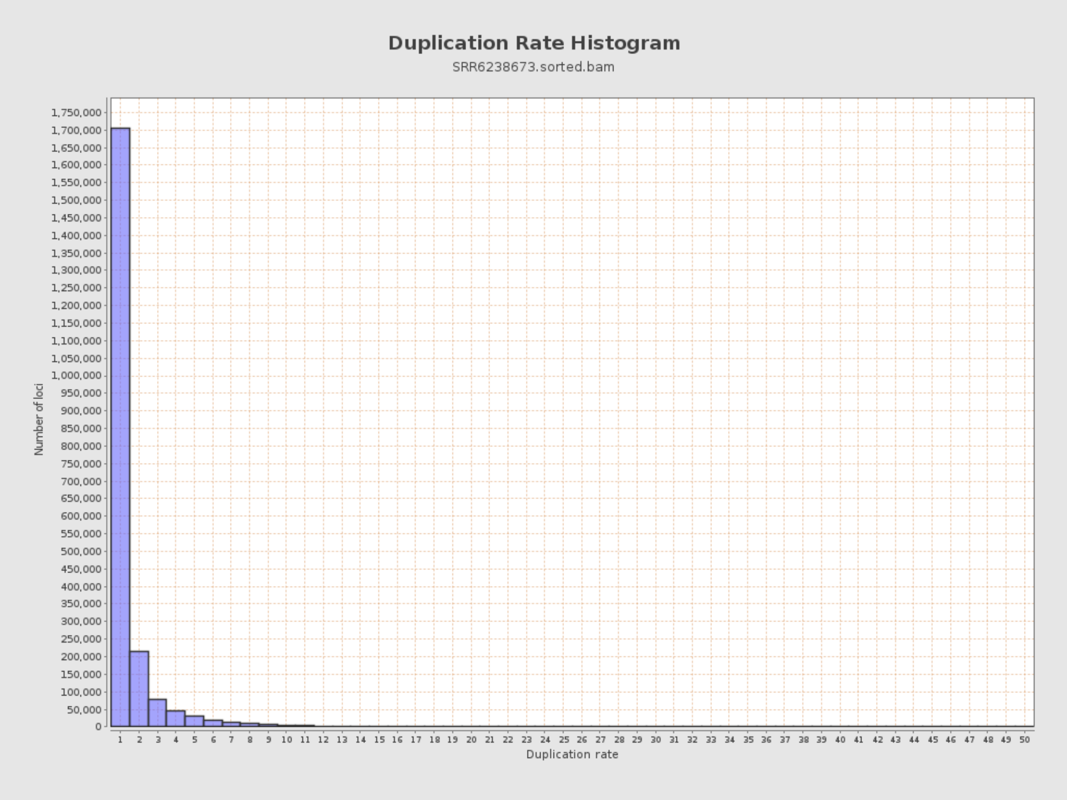
5. Results : Coverage Histogram (0-50X)



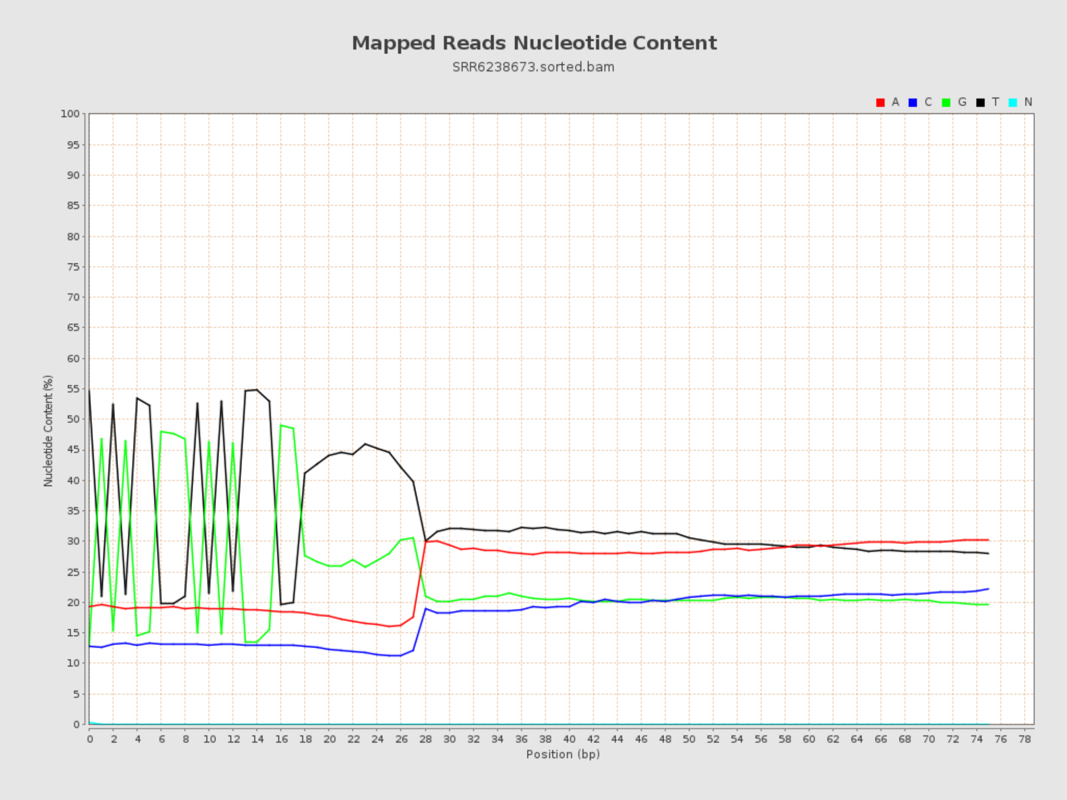
6. Results : Genome Fraction Coverage



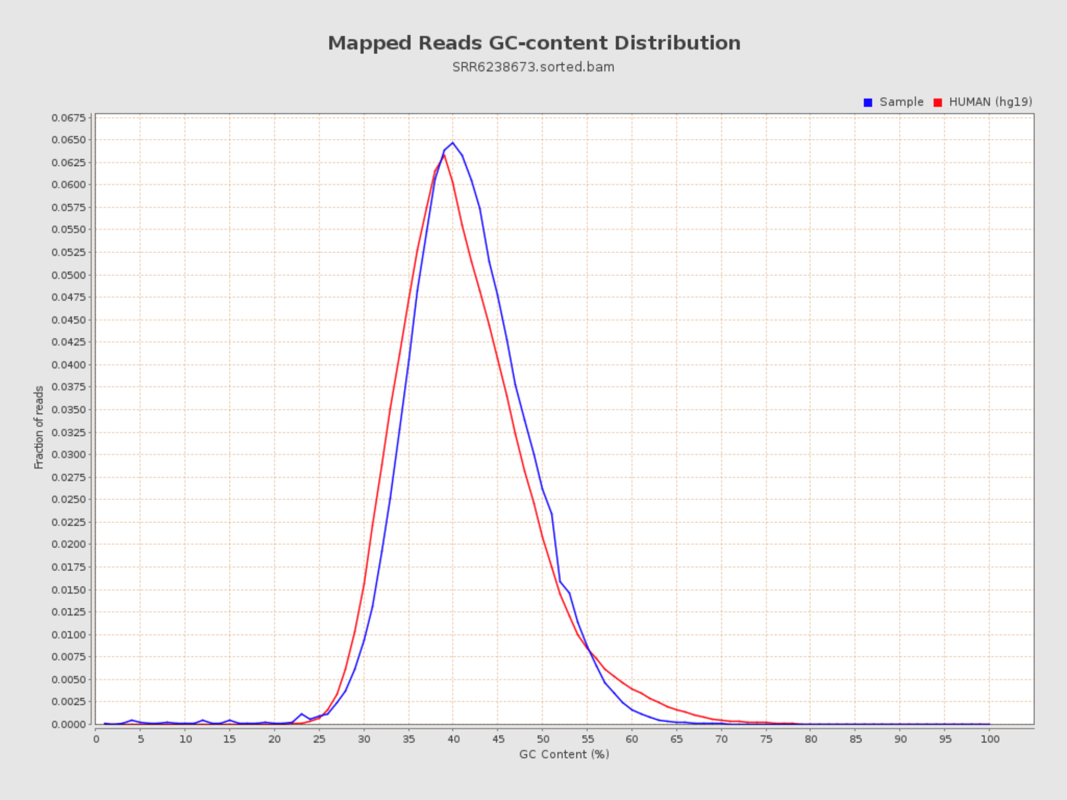
7. Results : Duplication Rate Histogram



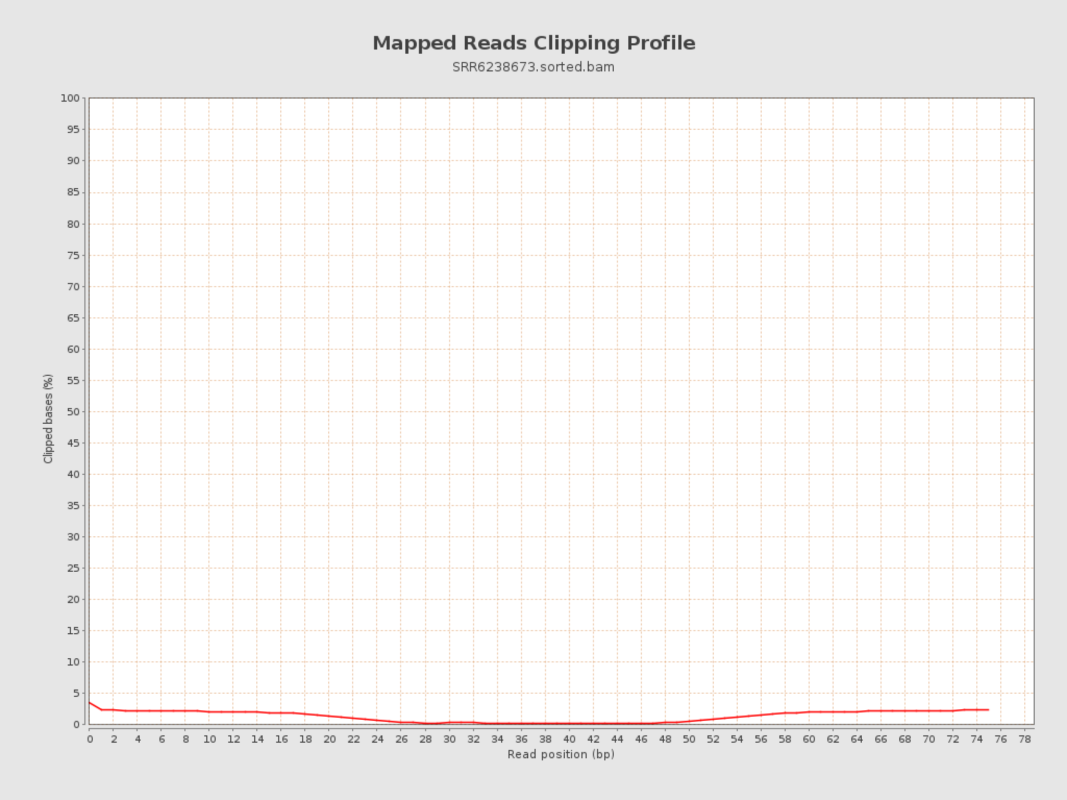
8. Results : Mapped Reads Nucleotide Content



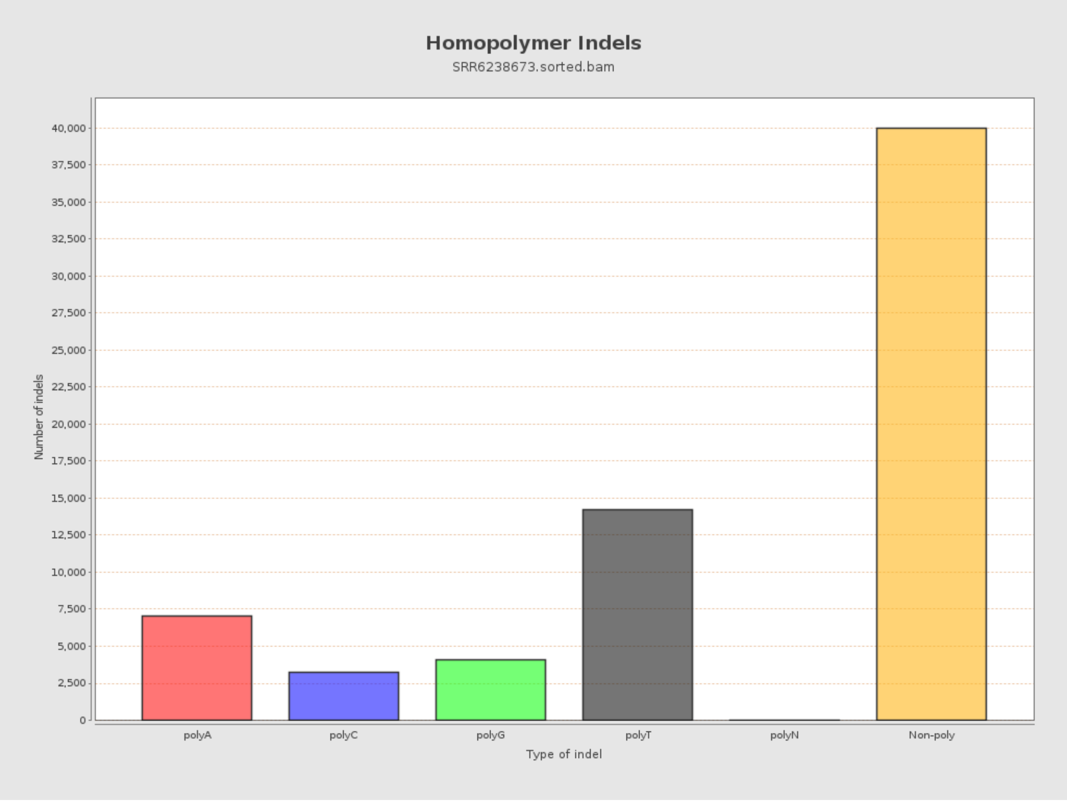
9. Results : Mapped Reads GC-content Distribution



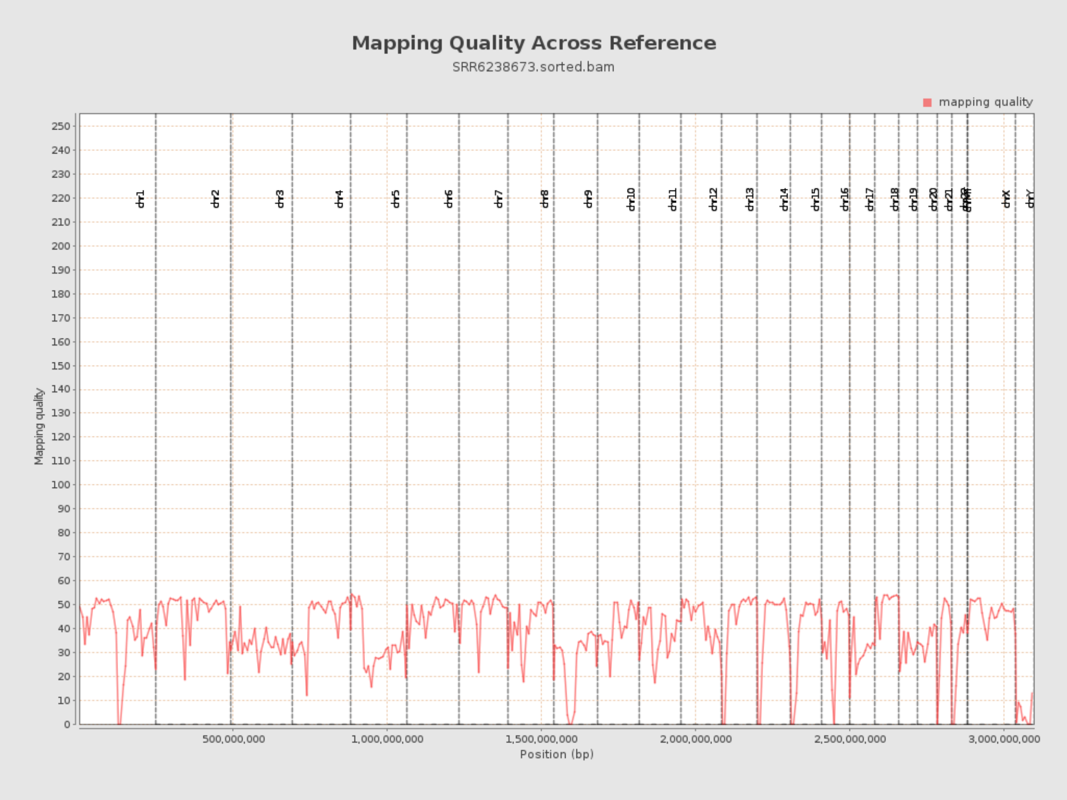
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram