Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:02:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238332.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_SRR6238332 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238332.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:02:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238332.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,354,806
Mapped reads	2,083,121 / 88.46%
Unmapped reads	271,685 / 11.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,919 / 1.19%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	143,791 / 6.11%
Duplication rate	5.09%
Clipped reads	1,019,696 / 43.3%

2.2. ACGT Content

Number/percentage of A's	38,511,299 / 27.93%
Number/percentage of C's	26,389,408 / 19.14%
Number/percentage of T's	42,655,954 / 30.94%
Number/percentage of G's	30,310,581 / 21.98%
Number/percentage of N's	19,952 / 0.01%
GC Percentage	41.12%

2.3. Coverage

Mean	0.0446

Standard Deviation	0.4805

2.4. Mapping Quality

Mean Mapping Quality	44.94

2.5. Mismatches and indels

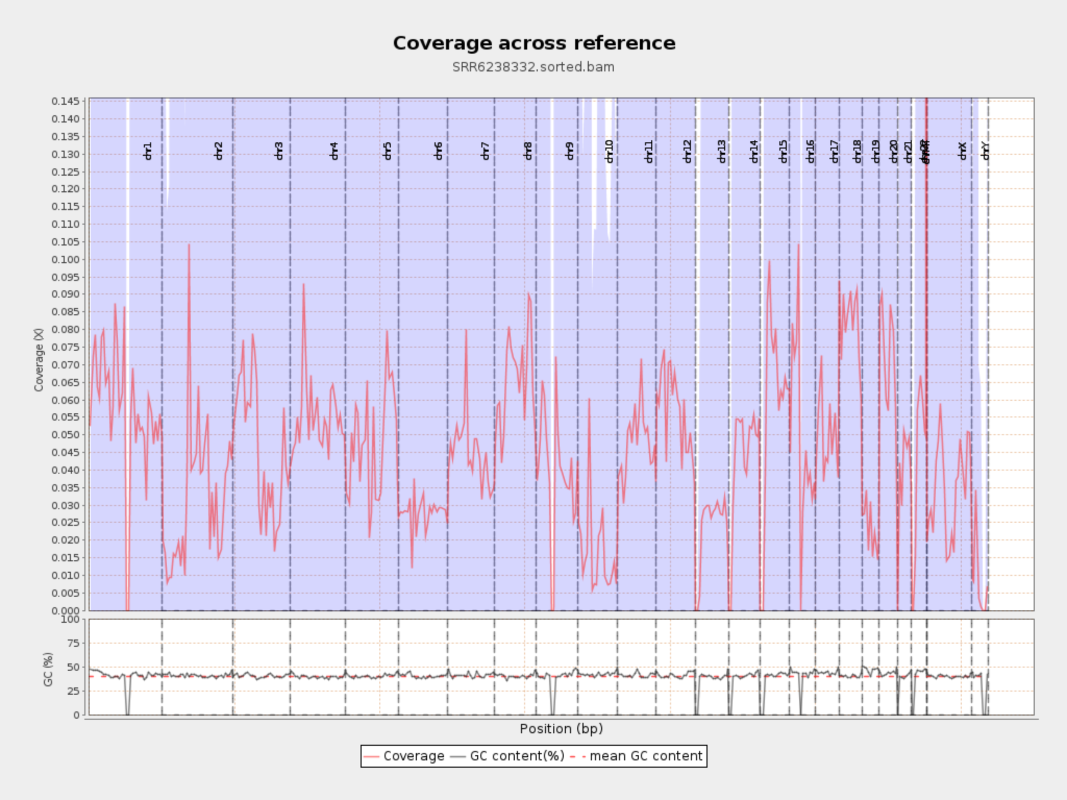
General error rate	0.89%
Mismatches	1,200,179
Insertions	11,744
Mapped reads with at least one insertion	0.56%
Deletions	37,773
Mapped reads with at least one deletion	1.79%
Homopolymer indels	45.89%

2.6. Chromosome stats

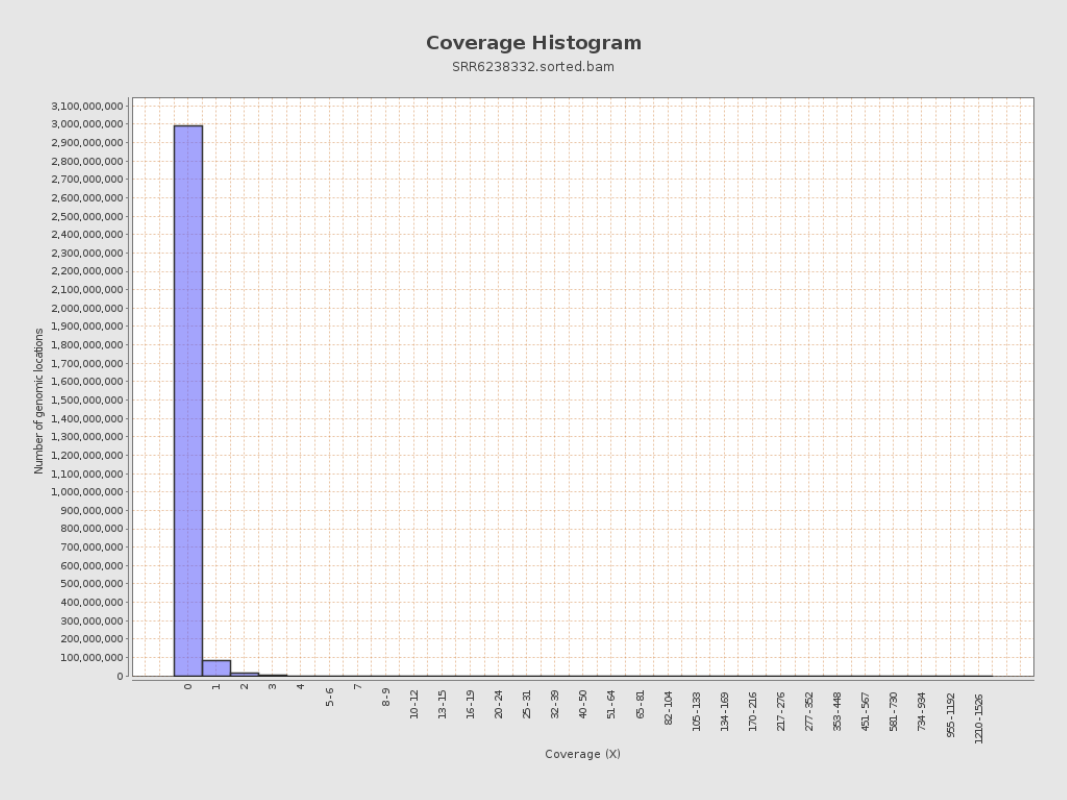
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14234736	0.0571	0.6185
chr2	243199373	7698186	0.0317	0.6492
chr3	198022430	9240802	0.0467	0.2728
chr4	191154276	10528759	0.0551	0.3559
chr5	180915260	8727817	0.0482	0.2827
chr6	171115067	4746215	0.0277	0.246
chr7	159138663	7212610	0.0453	0.5169

chr8	146364022	9639443	0.0659	0.9651
chr9	141213431	5549569	0.0393	0.5578
chr10	135534747	2262476	0.0167	0.3792
chr11	135006516	6445328	0.0477	0.4016
chr12	133851895	7625343	0.057	0.3273
chr13	115169878	2709513	0.0235	0.19
chr14	107349540	4589926	0.0428	0.3234
chr15	102531392	6116640	0.0597	0.3123
chr16	90354753	4503193	0.0498	0.3226
chr17	81195210	3994312	0.0492	0.3482
chr18	78077248	6408498	0.0821	1.01
chr19	59128983	1372394	0.0232	0.5111
chr20	63025520	4523001	0.0718	0.3464
chr21	48129895	1870014	0.0389	0.3155
chr22	51304566	2036584	0.0397	0.2495
chrMT	16571	25035	1.5108	1.9456
chrX	155270560	5430113	0.035	0.279
chrY	59373566	461398	0.0078	0.3302

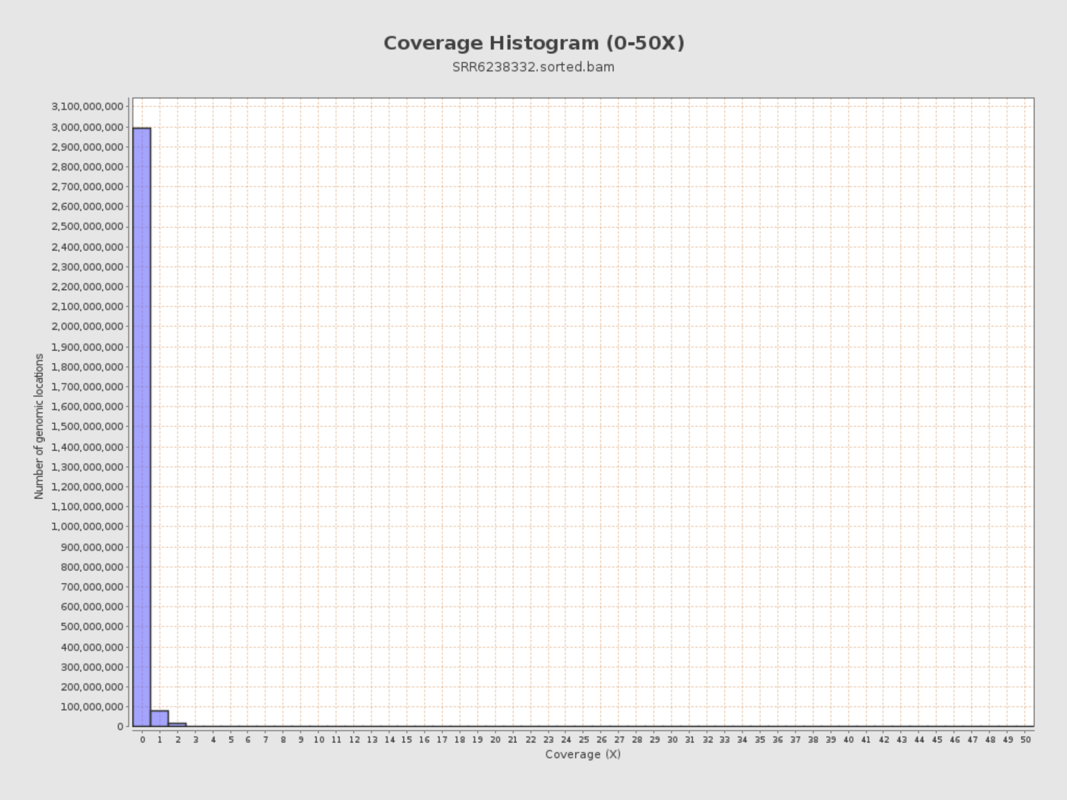
3. Results : Coverage across reference



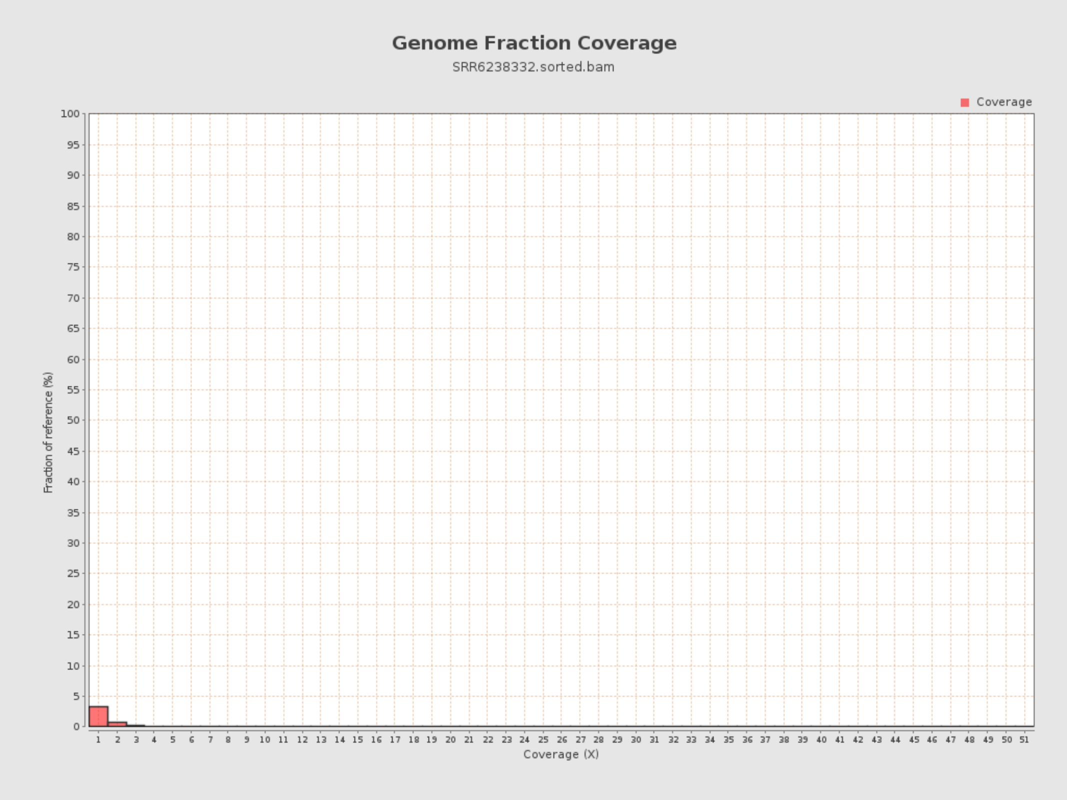
4. Results : Coverage Histogram



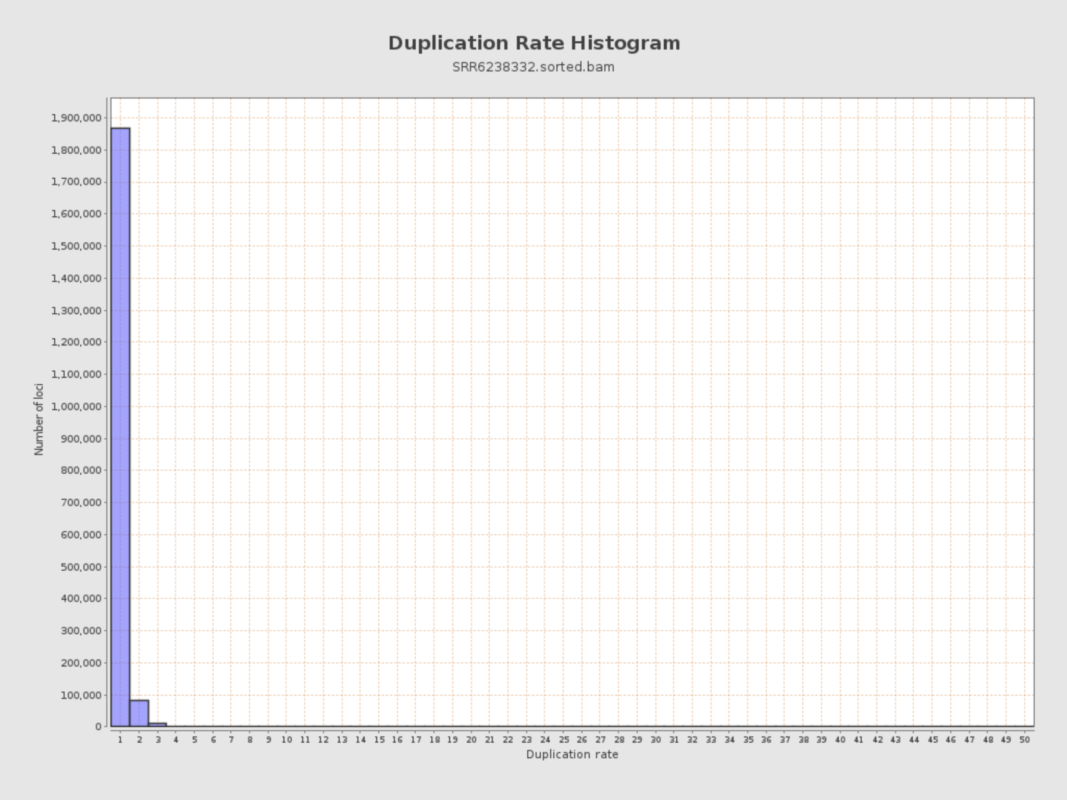
5. Results : Coverage Histogram (0-50X)



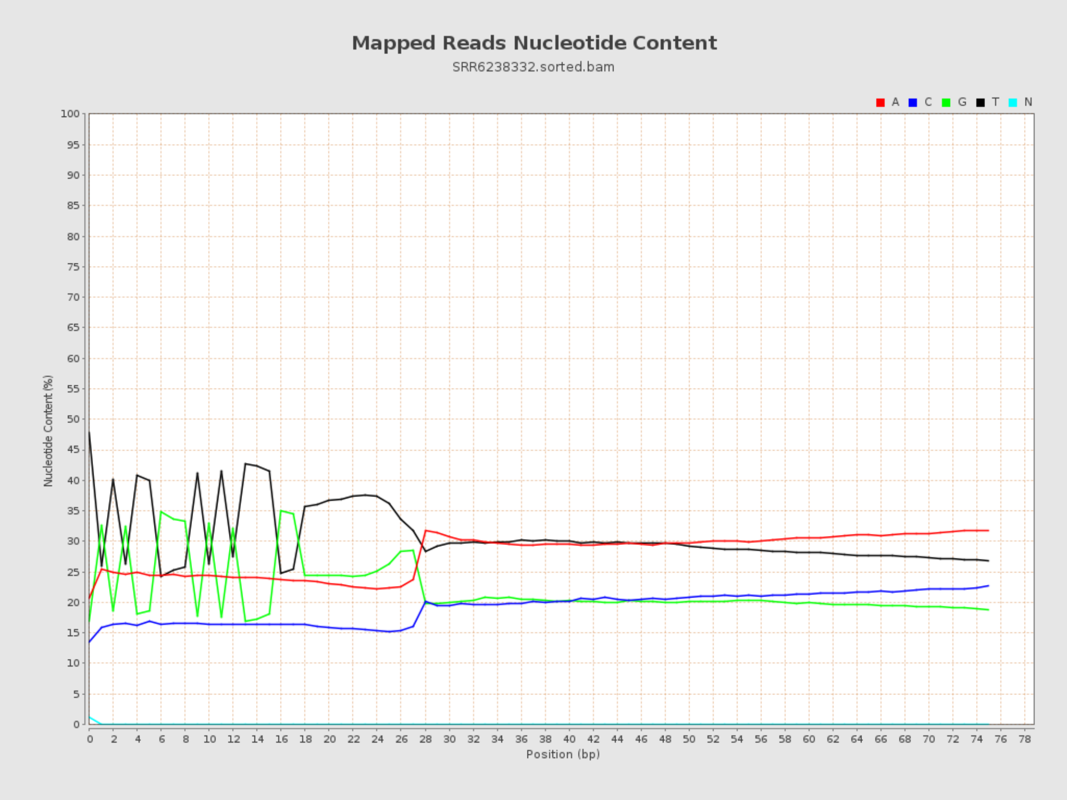
6. Results : Genome Fraction Coverage



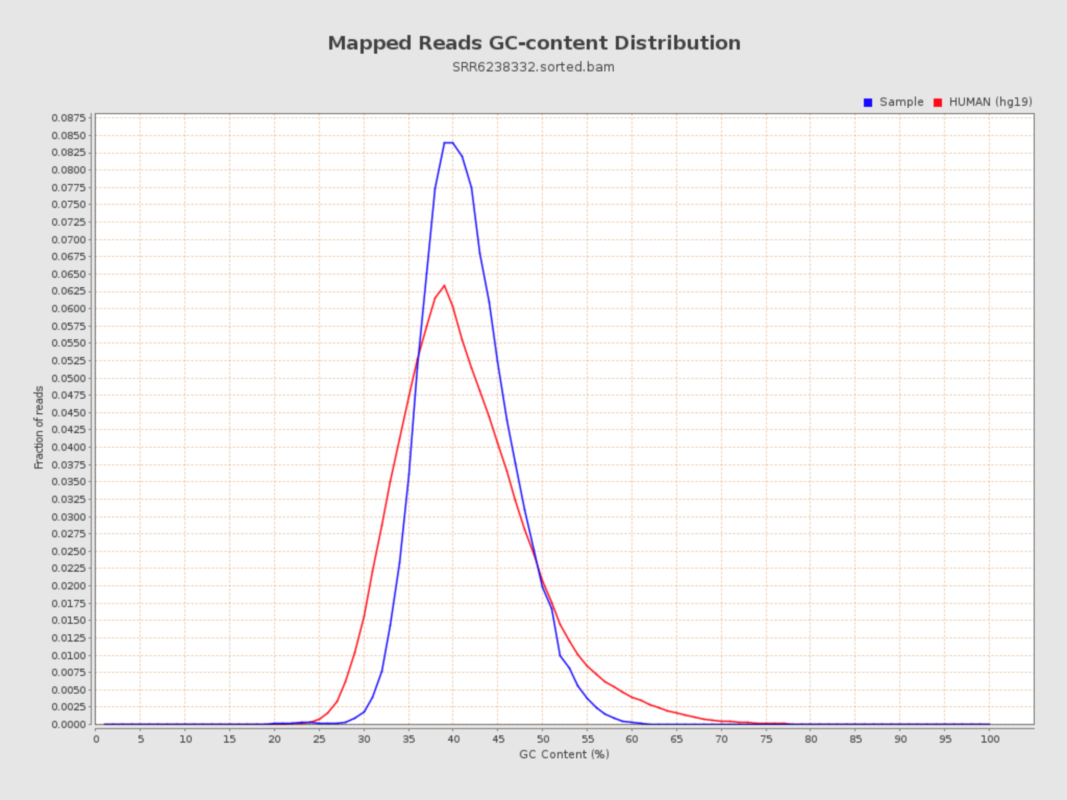
7. Results : Duplication Rate Histogram



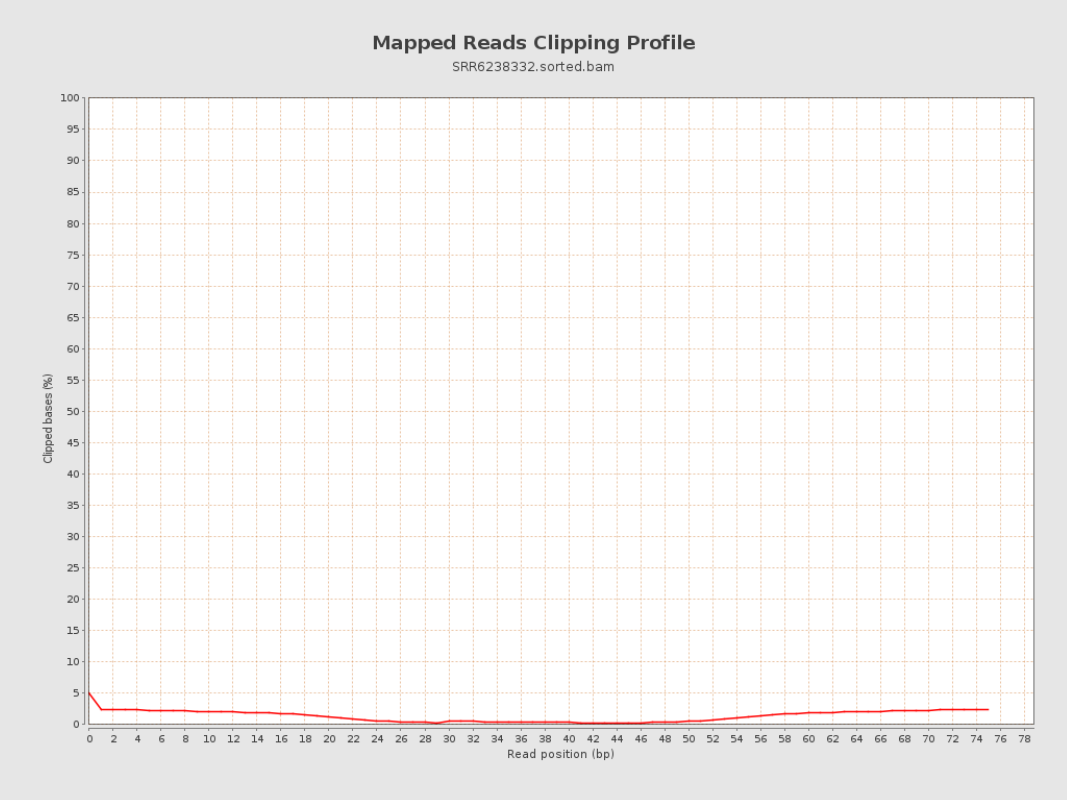
8. Results : Mapped Reads Nucleotide Content



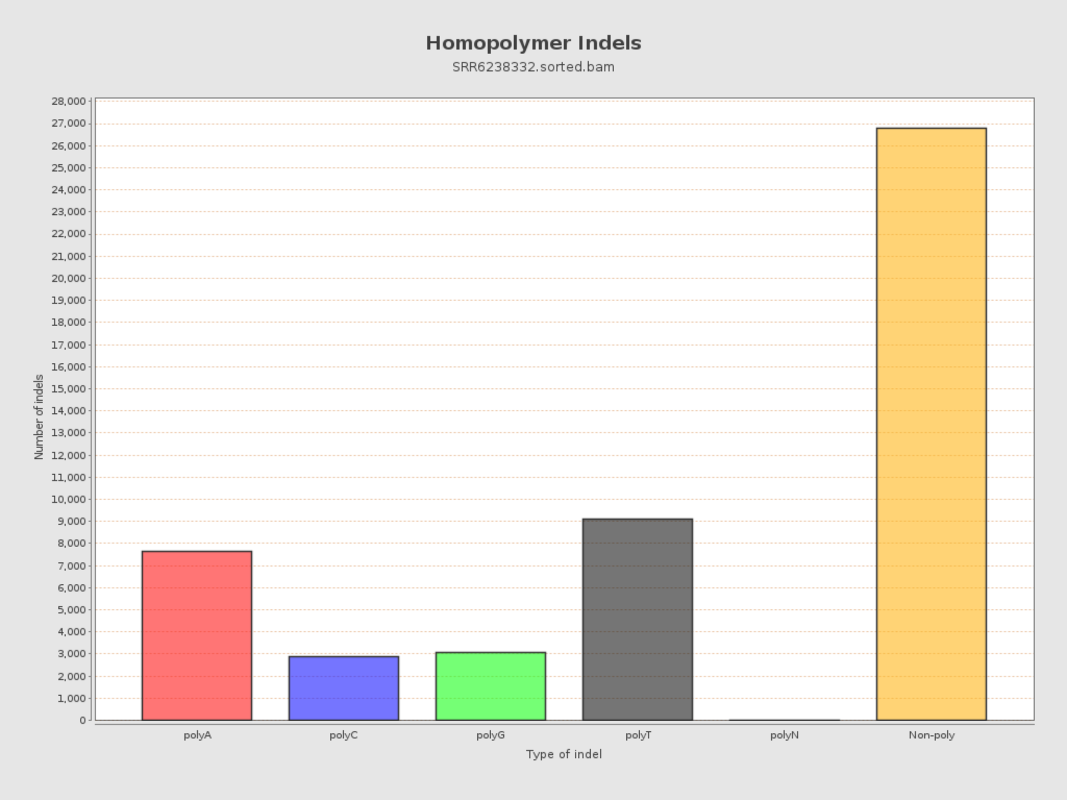
9. Results : Mapped Reads GC-content Distribution



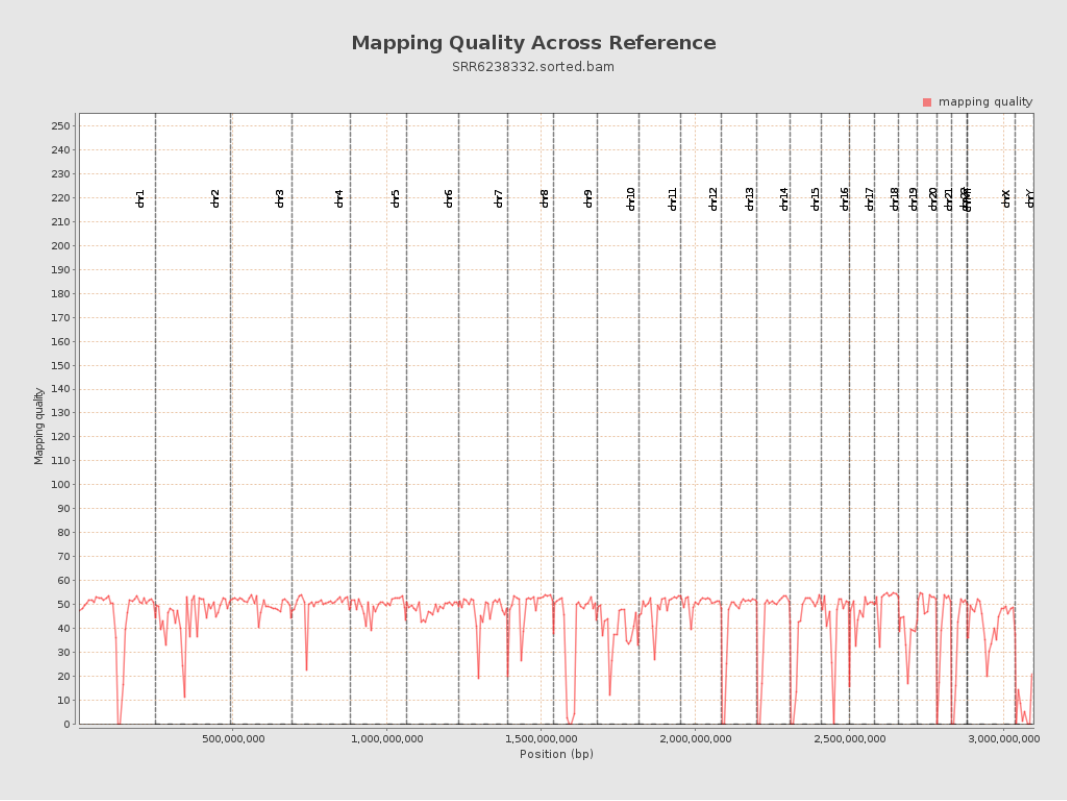
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram