Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:05:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238333.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_SRR6238333 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238333.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:05:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238333.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,729,116
Mapped reads	1,445,425 / 83.59%
Unmapped reads	283,691 / 16.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,774 / 1.2%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	90,369 / 5.23%
Duplication rate	5.16%
Clipped reads	865,261 / 50.04%

2.2. ACGT Content

Number/percentage of A's	25,980,224 / 28.25%
Number/percentage of C's	17,358,677 / 18.88%
Number/percentage of T's	28,701,914 / 31.21%
Number/percentage of G's	19,904,060 / 21.64%
Number/percentage of N's	20,533 / 0.02%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0297

Standard Deviation	0.2932

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

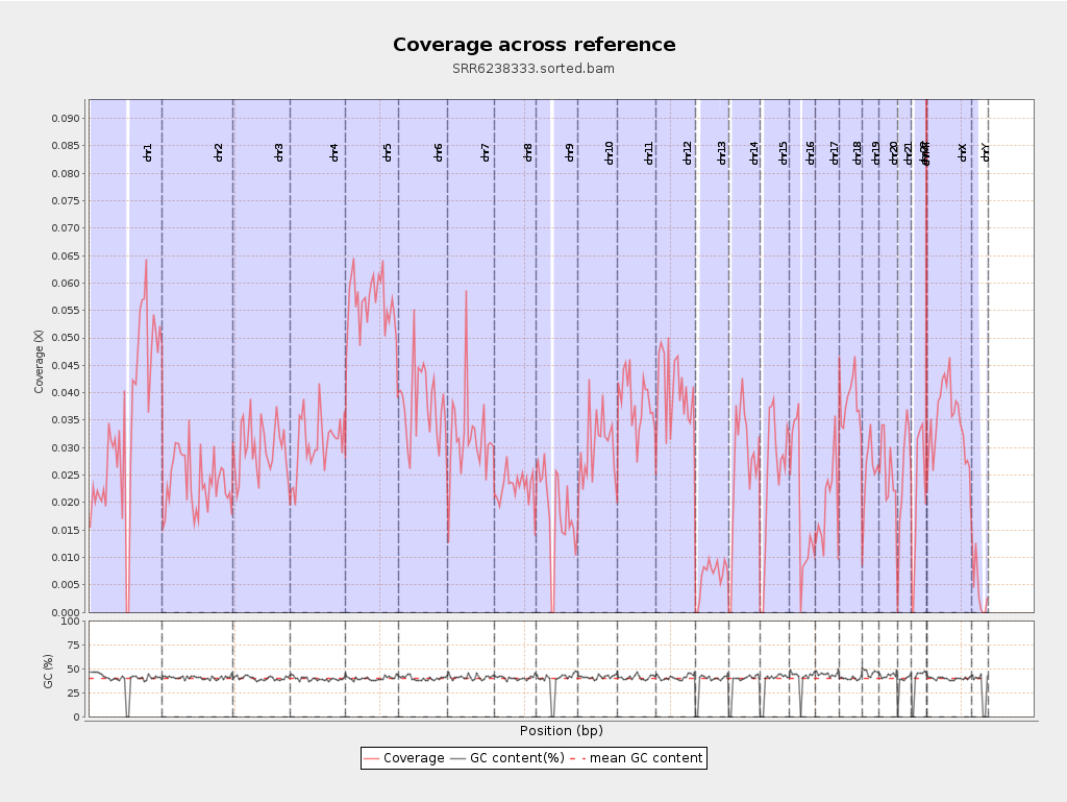
General error rate	0.92%
Mismatches	836,555
Insertions	7,150
Mapped reads with at least one insertion	0.49%
Deletions	28,152
Mapped reads with at least one deletion	1.92%
Homopolymer indels	45.22%

2.6. Chromosome stats

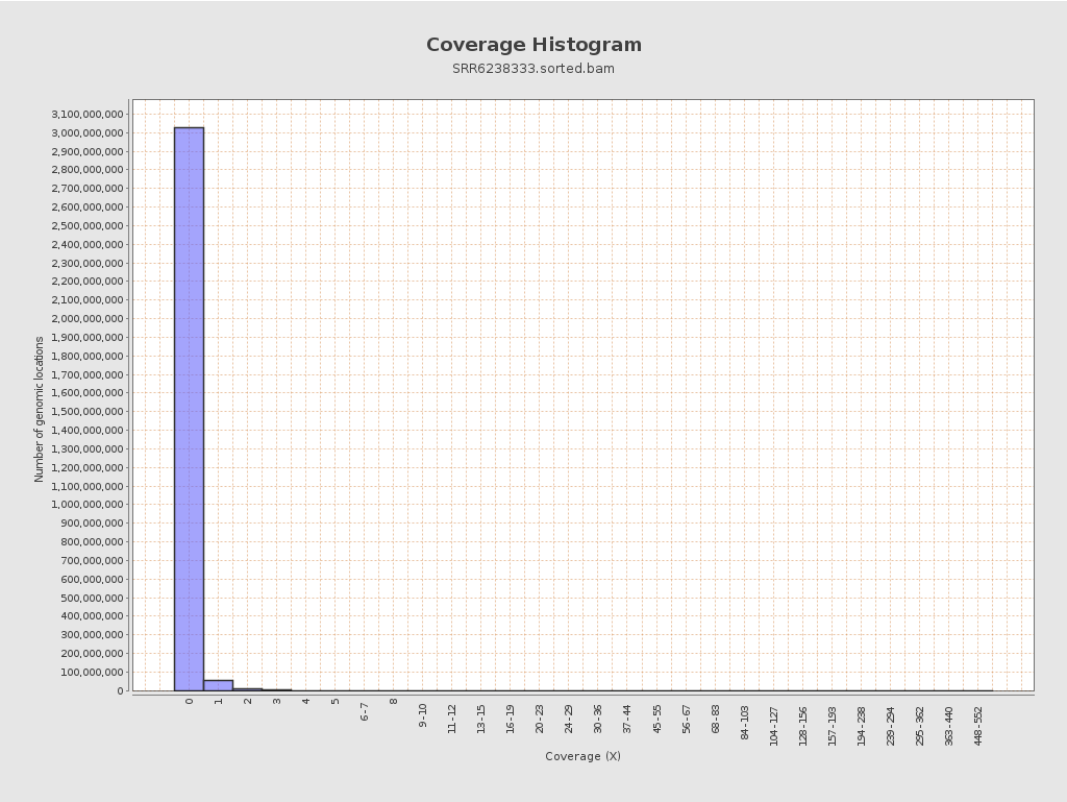
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8522343	0.0342	0.4678
chr2	243199373	5796849	0.0238	0.3189
chr3	198022430	5889531	0.0297	0.215
chr4	191154276	5879105	0.0308	0.2241
chr5	180915260	10186134	0.0563	0.3006
chr6	171115067	6488751	0.0379	0.3066
chr7	159138663	5126746	0.0322	0.4517

chr8	146364022	3323795	0.0227	0.3275
chr9	141213431	2548594	0.018	0.2057
chr10	135534747	4097705	0.0302	0.2699
chr11	135006516	5139648	0.0381	0.299
chr12	133851895	5397482	0.0403	0.2525
chr13	115169878	770002	0.0067	0.1045
chr14	107349540	2892004	0.0269	0.2183
chr15	102531392	2573589	0.0251	0.2273
chr16	90354753	1719221	0.019	0.1765
chr17	81195210	1602006	0.0197	0.1808
chr18	78077248	3016520	0.0386	0.3536
chr19	59128983	1552144	0.0263	0.3541
chr20	63025520	1603156	0.0254	0.2001
chr21	48129895	1180639	0.0245	0.1969
chr22	51304566	1092364	0.0213	0.1817
chrMT	16571	3796	0.2291	0.5728
chrX	155270560	5371495	0.0346	0.2467
chrY	59373566	238153	0.004	0.1176

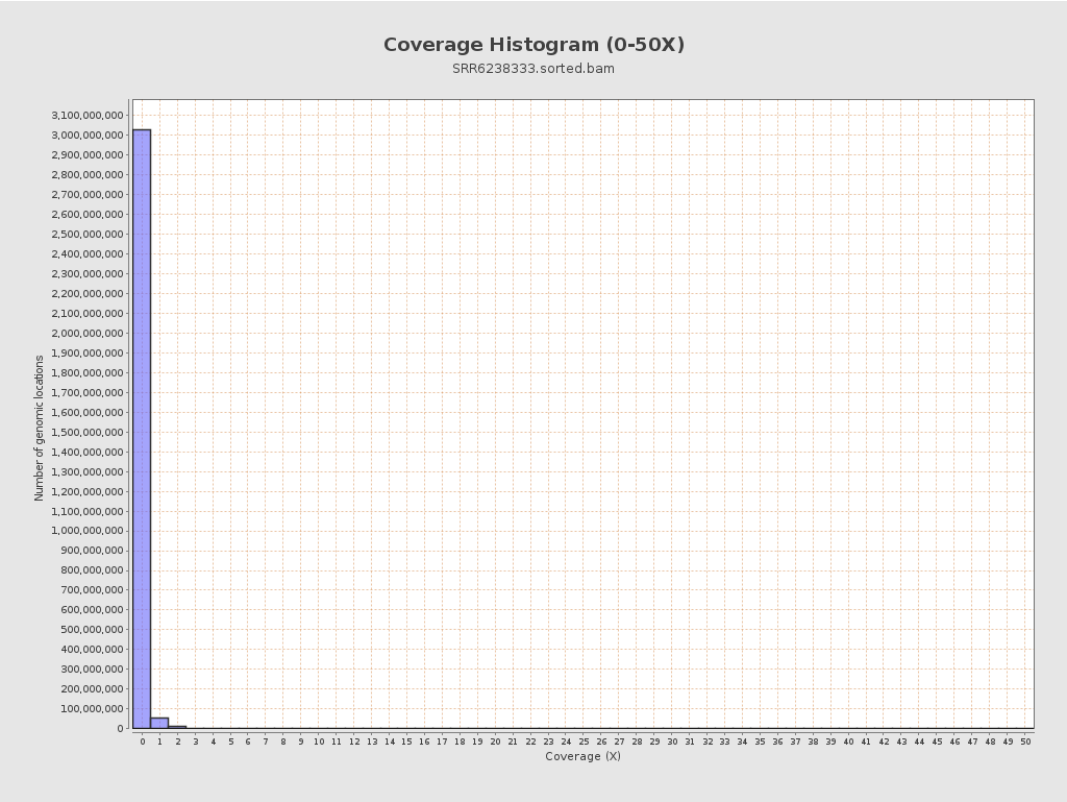
3. Results : Coverage across reference



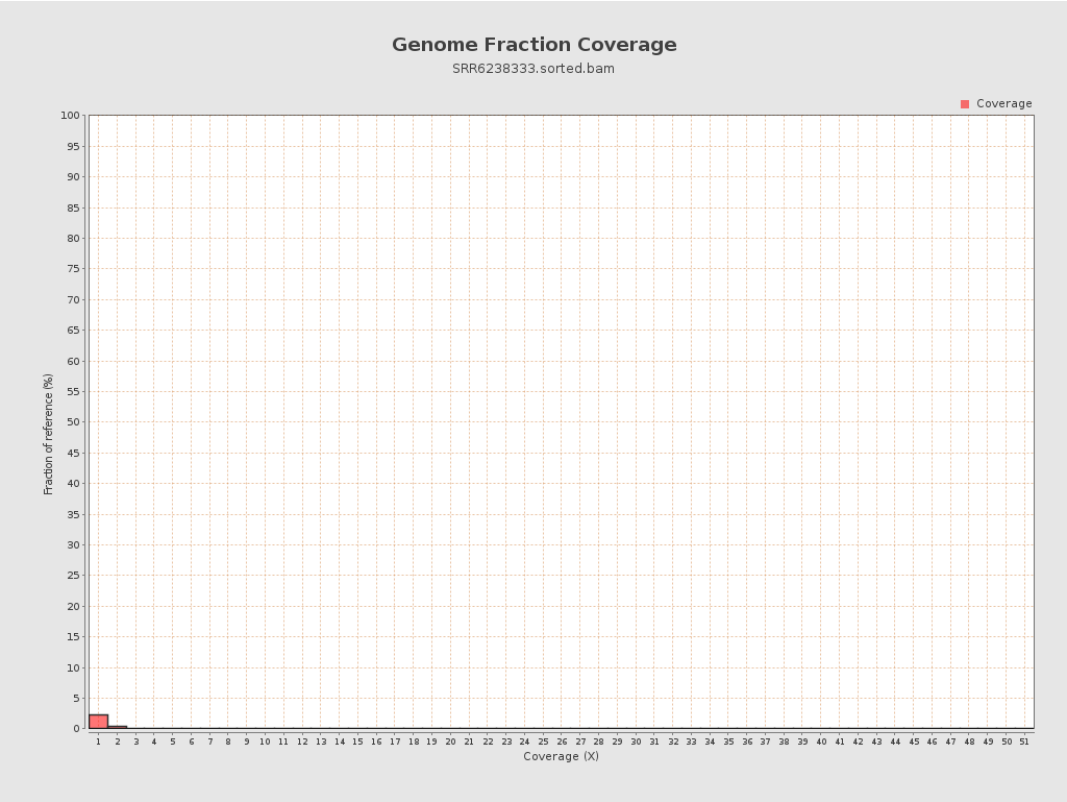
4. Results : Coverage Histogram



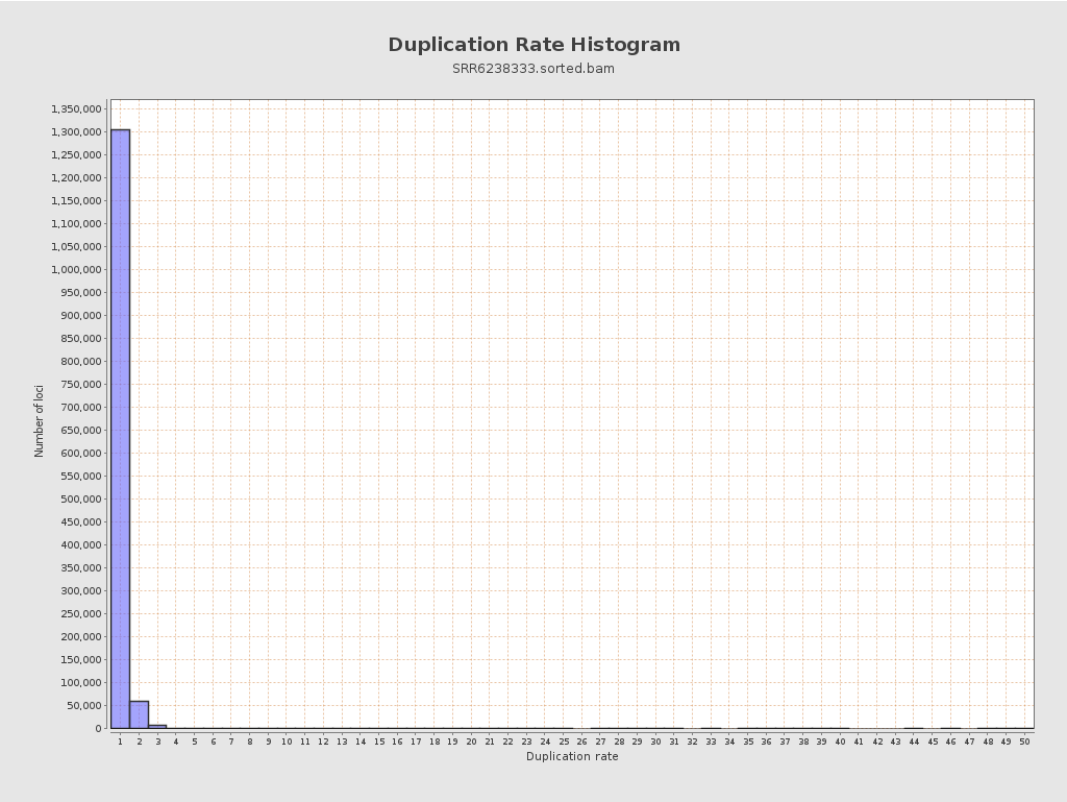
5. Results : Coverage Histogram (0-50X)



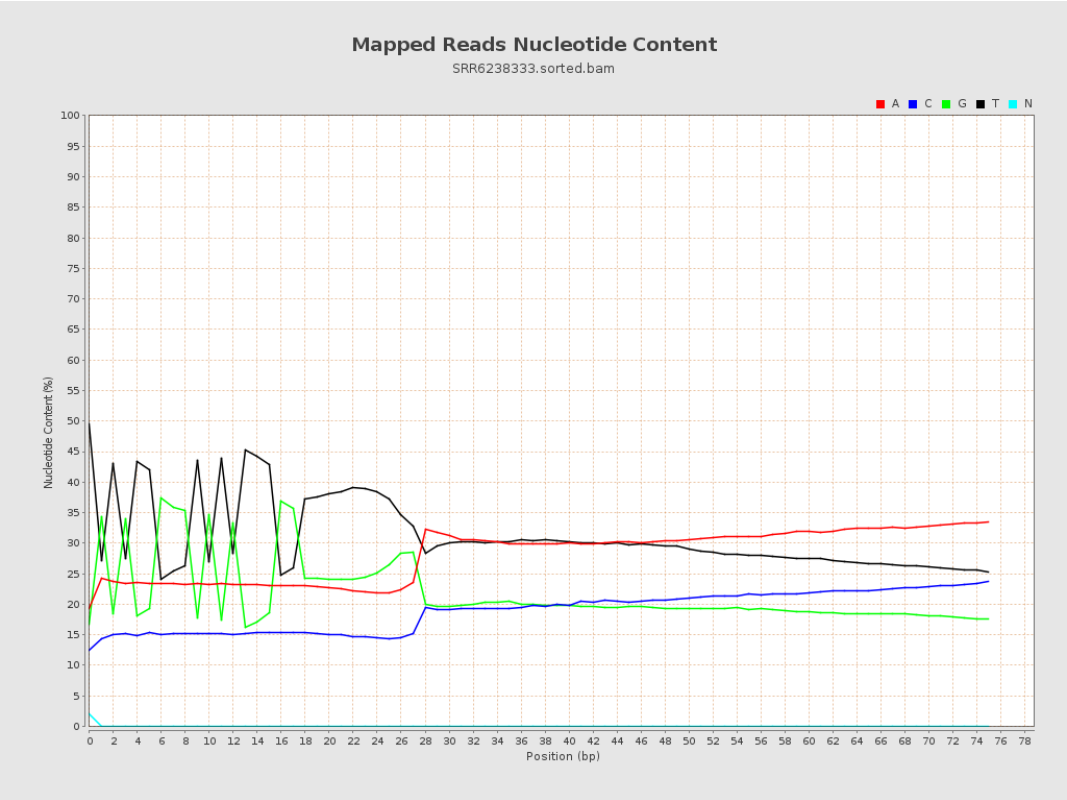
6. Results : Genome Fraction Coverage



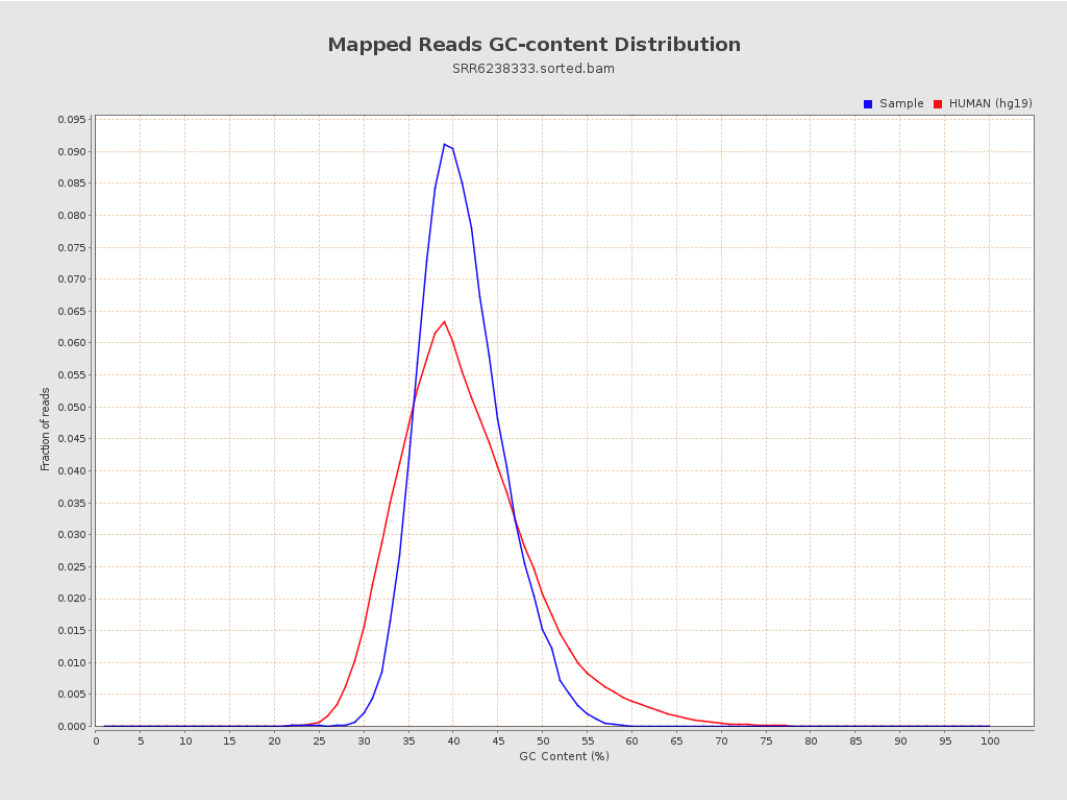
7. Results : Duplication Rate Histogram



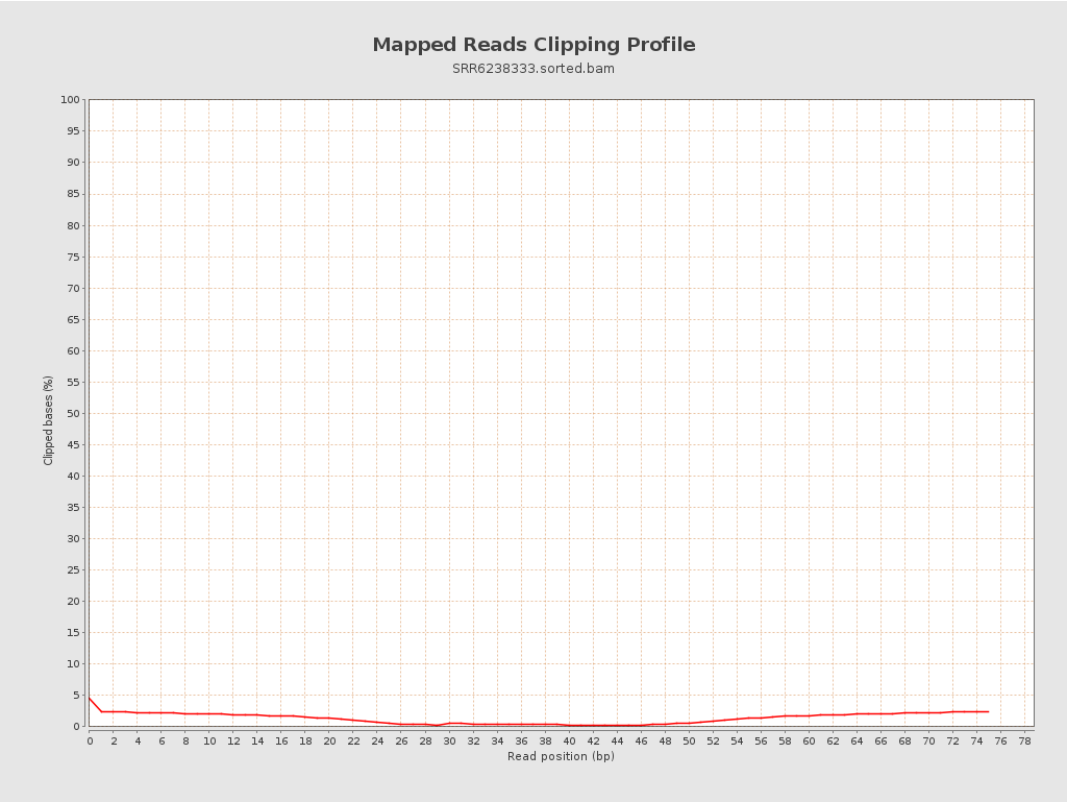
8. Results : Mapped Reads Nucleotide Content



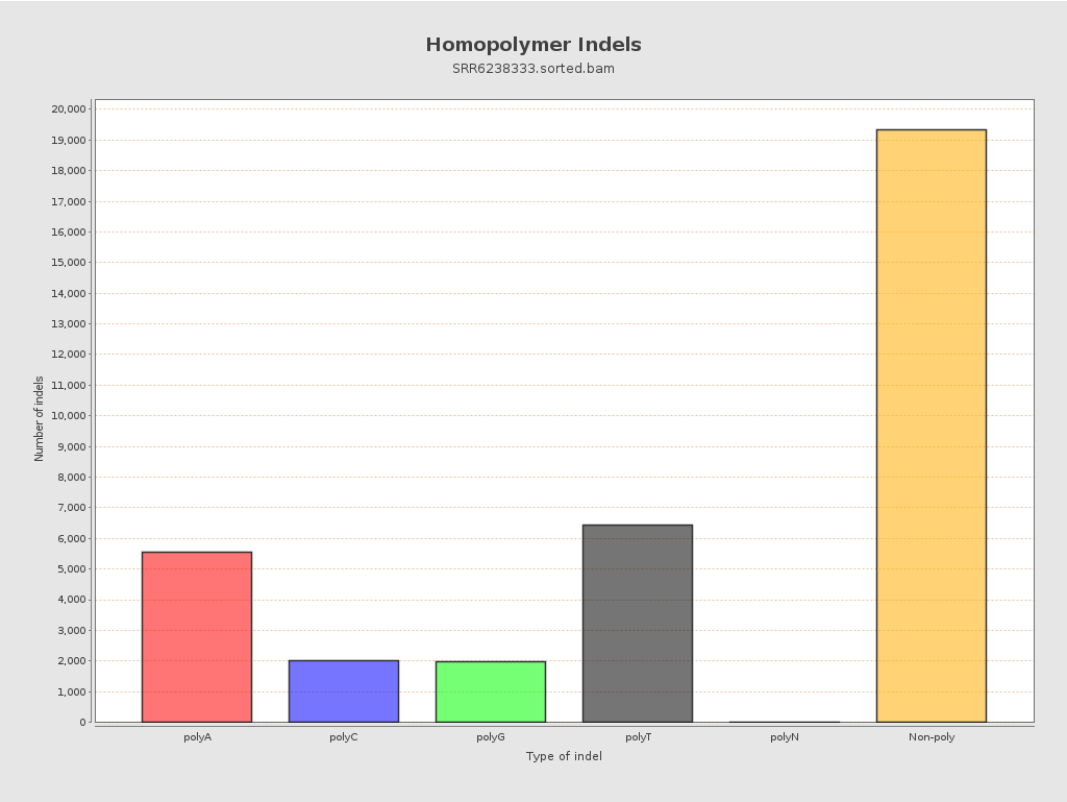
9. Results : Mapped Reads GC-content Distribution



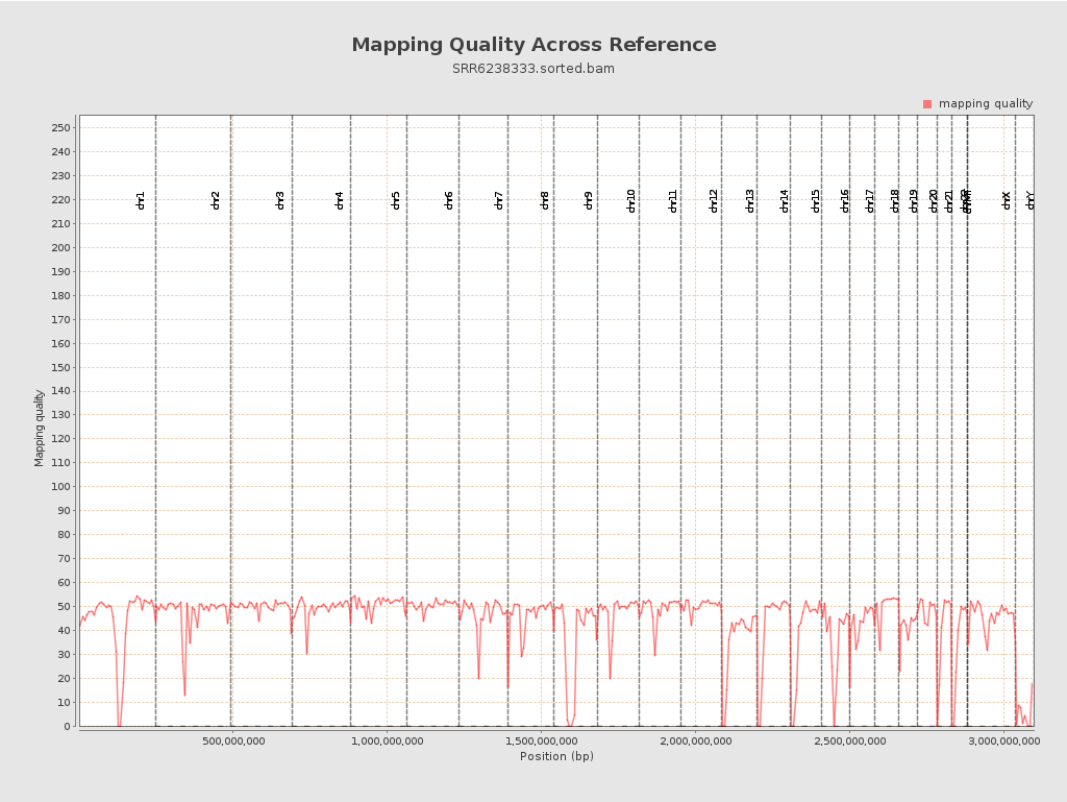
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram