Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:25:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238517.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_SRR6238517 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238517.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:25:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238517.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,586,694
Mapped reads	2,498,644 / 69.66%
Unmapped reads	1,088,050 / 30.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,079 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,027,995 / 28.66%
Duplication rate	21.18%
Clipped reads	1,605,379 / 44.76%

2.2. ACGT Content

Number/percentage of A's	38,030,529 / 24.79%
Number/percentage of C's	27,089,694 / 17.66%
Number/percentage of T's	51,240,012 / 33.4%
Number/percentage of G's	37,056,455 / 24.15%
Number/percentage of N's	10,133 / 0.01%
GC Percentage	41.81%

2.3. Coverage

Mean	0.0496

Standard Deviation	0.9479

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

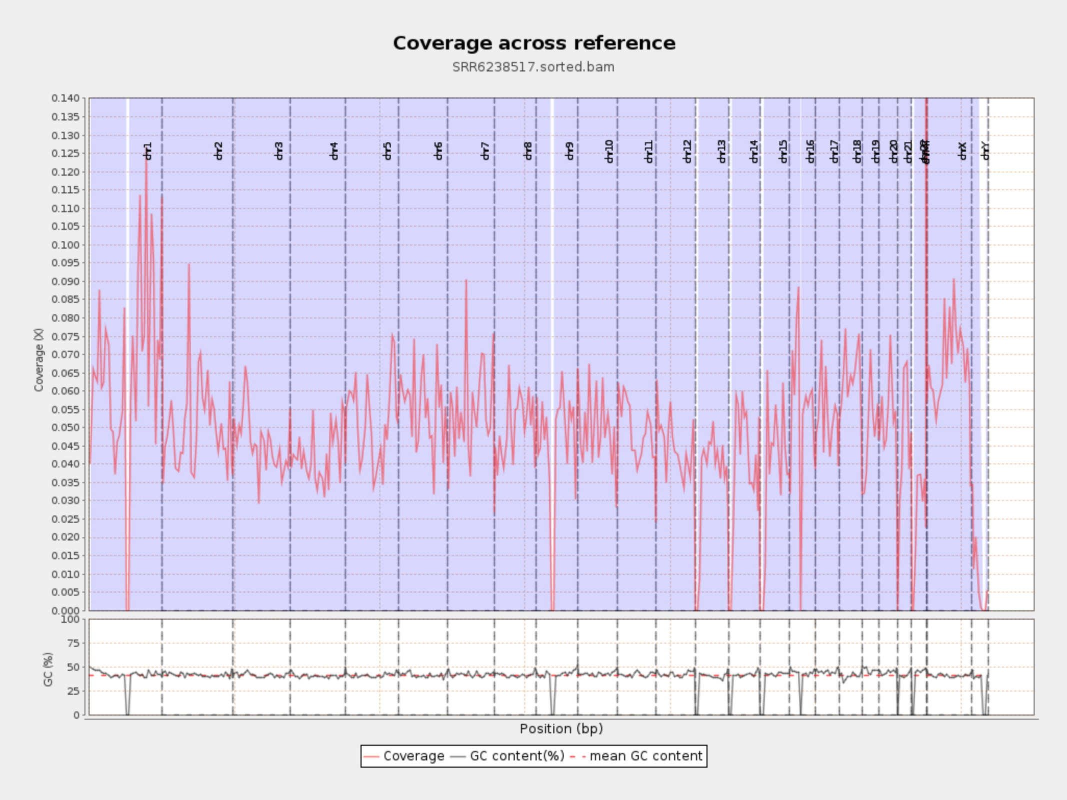
General error rate	0.6%
Mismatches	896,506
Insertions	9,540
Mapped reads with at least one insertion	0.38%
Deletions	37,689
Mapped reads with at least one deletion	1.5%
Homopolymer indels	41.99%

2.6. Chromosome stats

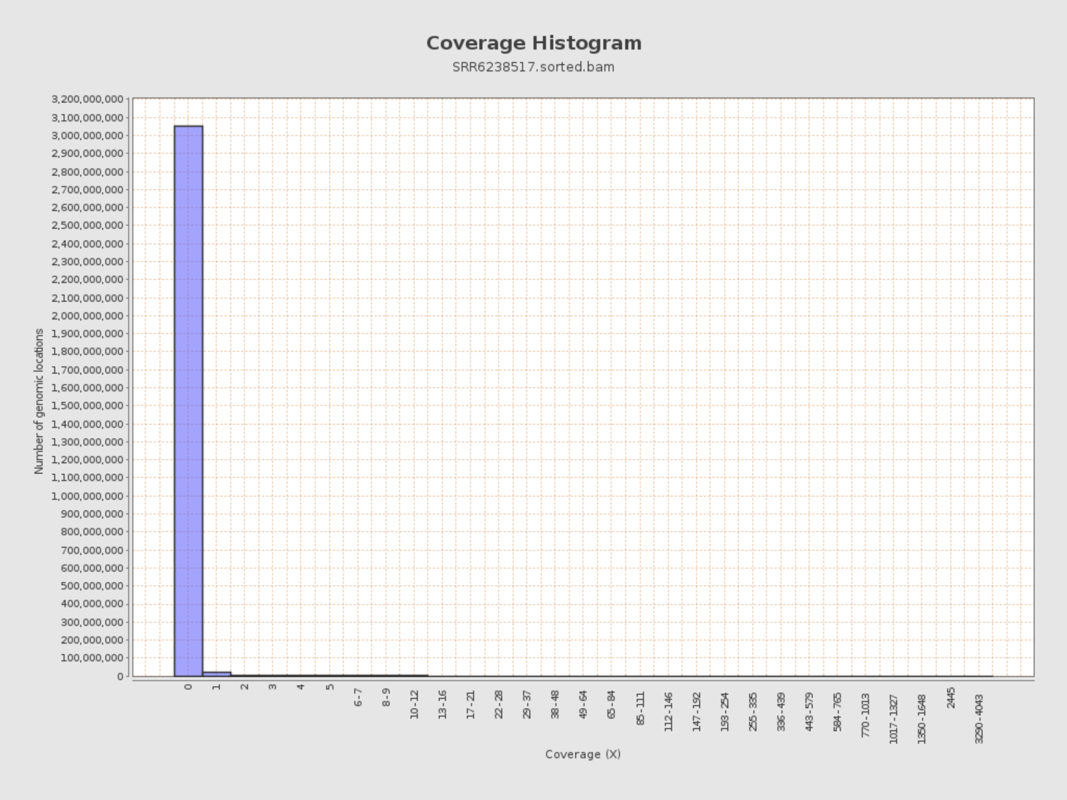
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16218120	0.0651	1.1982
chr2	243199373	12391763	0.051	1.8857
chr3	198022430	9015998	0.0455	0.6307
chr4	191154276	8085472	0.0423	0.6019
chr5	180915260	9359729	0.0517	0.6624
chr6	171115067	9496161	0.0555	0.8885
chr7	159138663	8894493	0.0559	0.8481

chr8	146364022	7364200	0.0503	0.7369
chr9	141213431	6264503	0.0444	0.6486
chr10	135534747	6697891	0.0494	0.6914
chr11	135006516	6651087	0.0493	0.6764
chr12	133851895	5984031	0.0447	0.6307
chr13	115169878	4073501	0.0354	0.6904
chr14	107349540	4055065	0.0378	0.5662
chr15	102531392	3831112	0.0374	0.6097
chr16	90354753	5034363	0.0557	0.7197
chr17	81195210	4322707	0.0532	0.7055
chr18	78077248	5045679	0.0646	2.1029
chr19	59128983	2922382	0.0494	0.8992
chr20	63025520	3401946	0.054	0.6983
chr21	48129895	2104522	0.0437	0.5908
chr22	51304566	1247205	0.0243	0.4649
chrMT	16571	38174	2.3037	4.555
chrX	155270560	10480530	0.0675	0.7601
chrY	59373566	510023	0.0086	0.3214

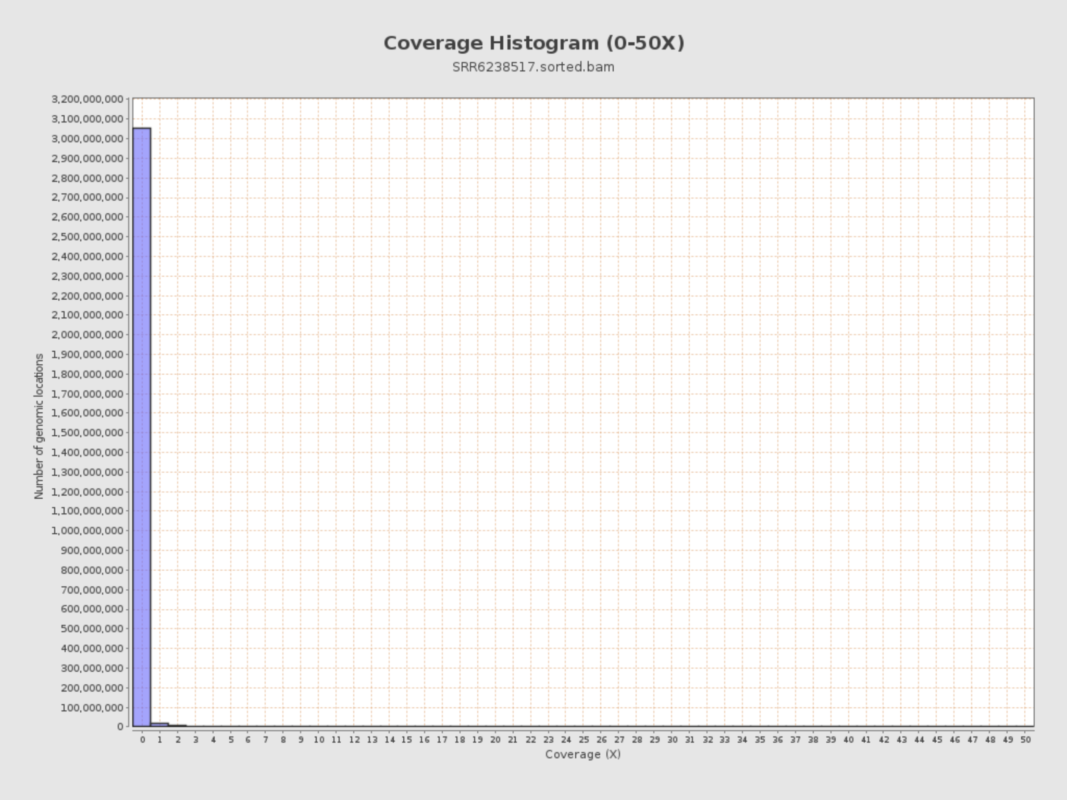
3. Results : Coverage across reference



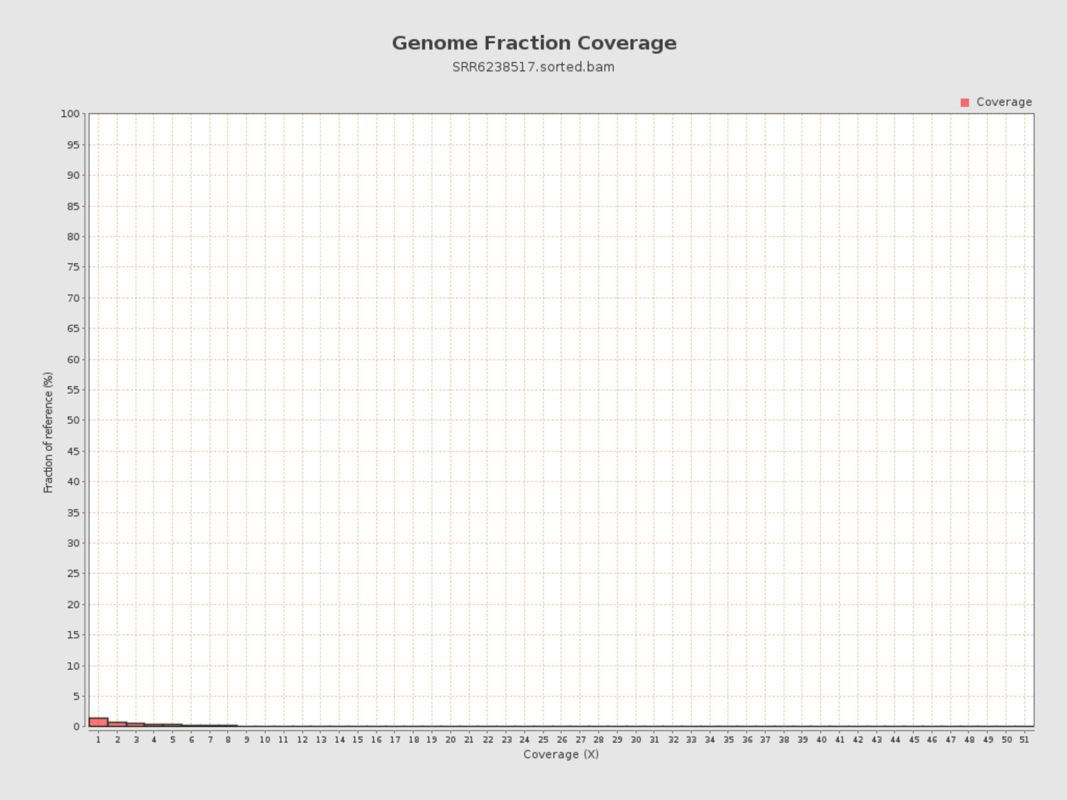
4. Results : Coverage Histogram



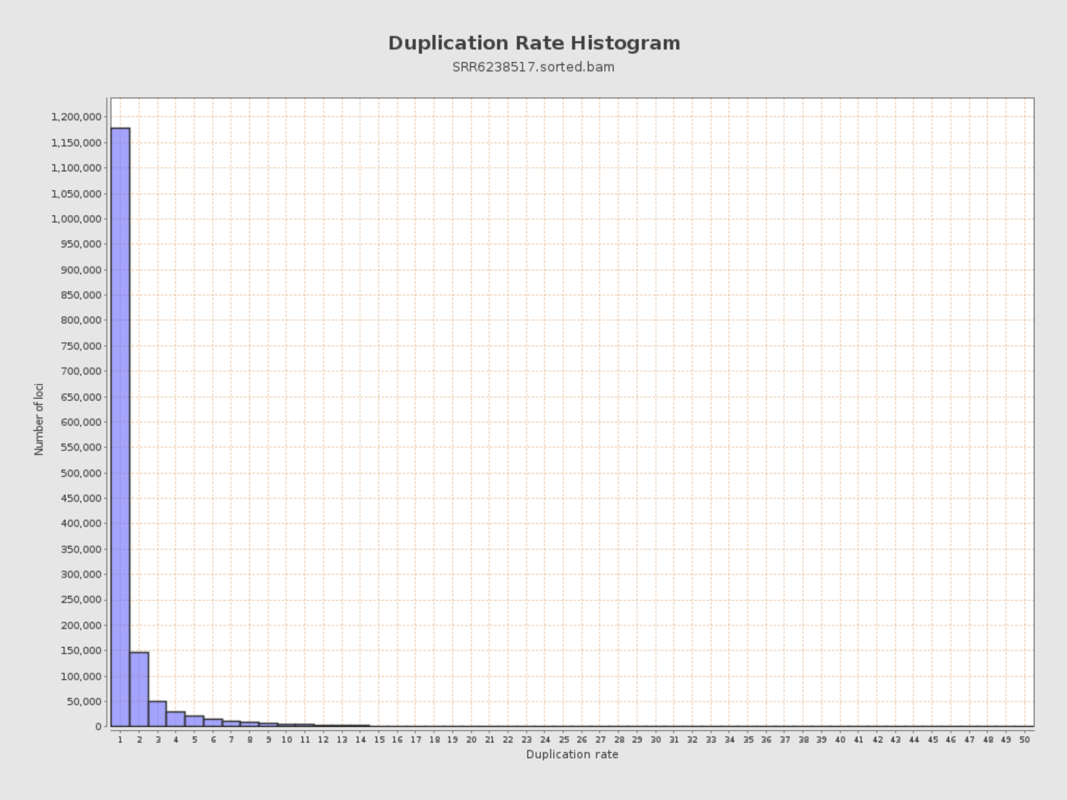
5. Results : Coverage Histogram (0-50X)



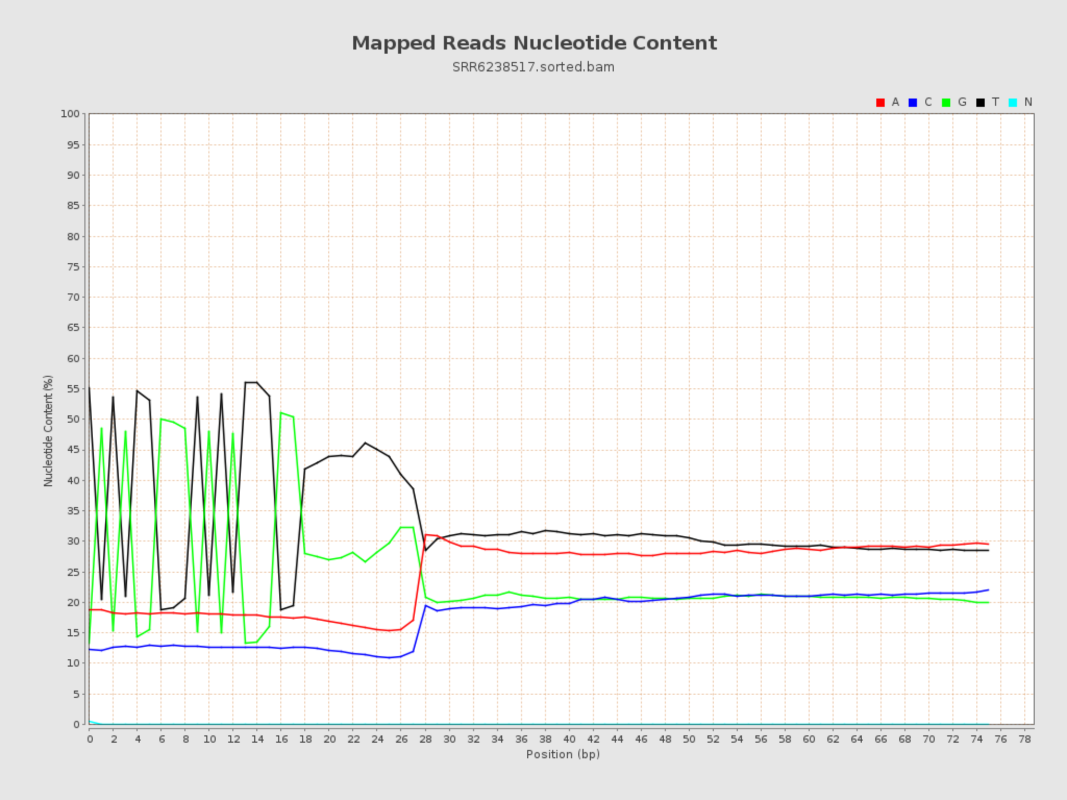
6. Results : Genome Fraction Coverage



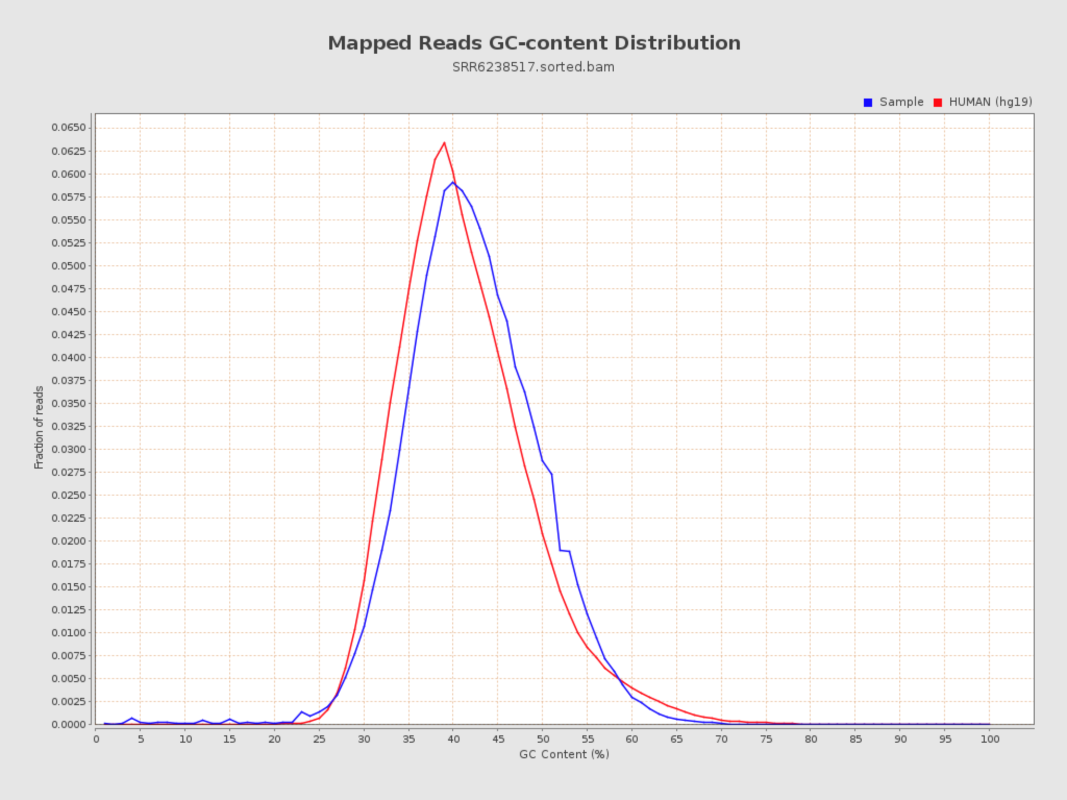
7. Results : Duplication Rate Histogram



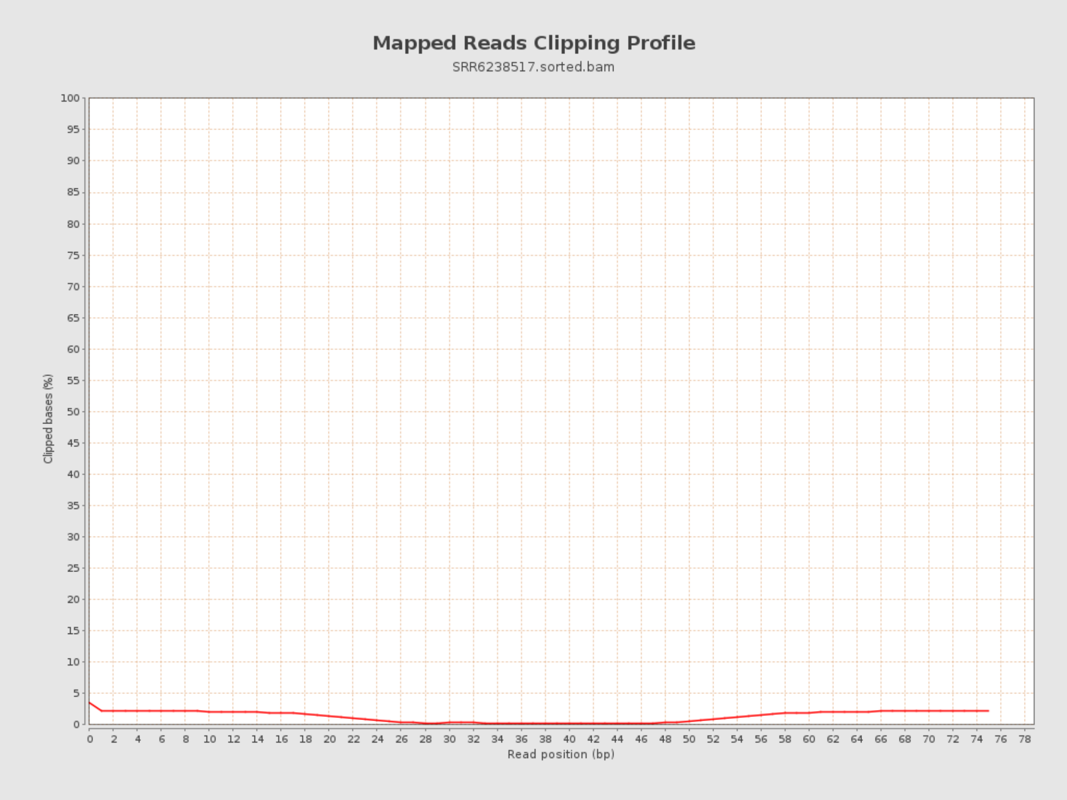
8. Results : Mapped Reads Nucleotide Content



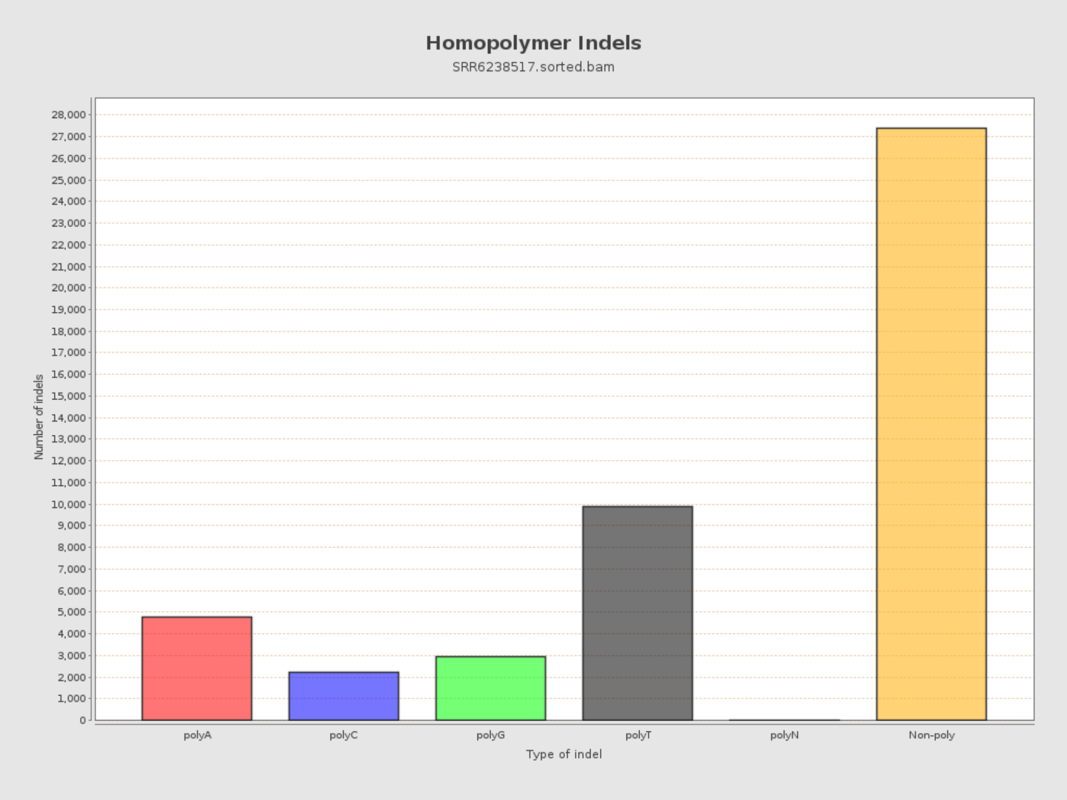
9. Results : Mapped Reads GC-content Distribution



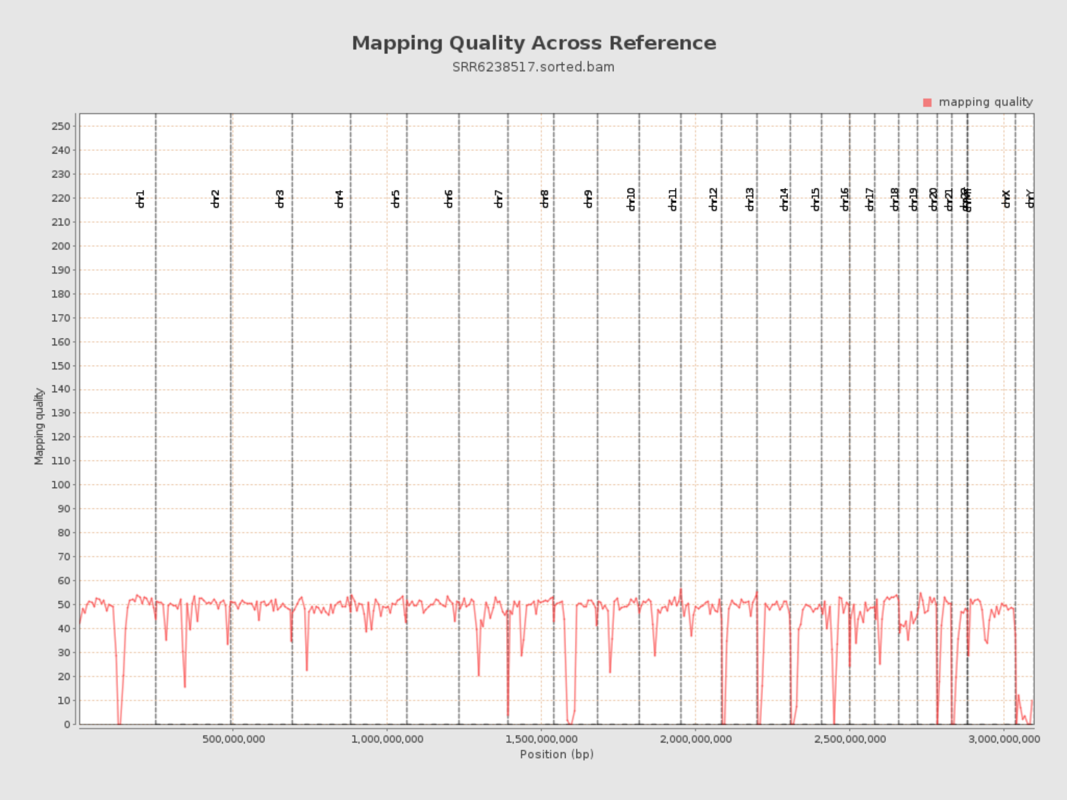
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram