Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:53:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237278.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_SRR6237278 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237278.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:53:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237278.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,647,657
Mapped reads	2,258,852 / 85.32%
Unmapped reads	388,805 / 14.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,882 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	133,104 / 5.03%
Duplication rate	4.33%
Clipped reads	854,325 / 32.27%

2.2. ACGT Content

Number/percentage of A's	44,878,638 / 29.08%
Number/percentage of C's	28,444,621 / 18.43%
Number/percentage of T's	48,677,250 / 31.54%
Number/percentage of G's	32,341,831 / 20.95%
Number/percentage of N's	2,662 / 0%
GC Percentage	39.38%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.5329

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

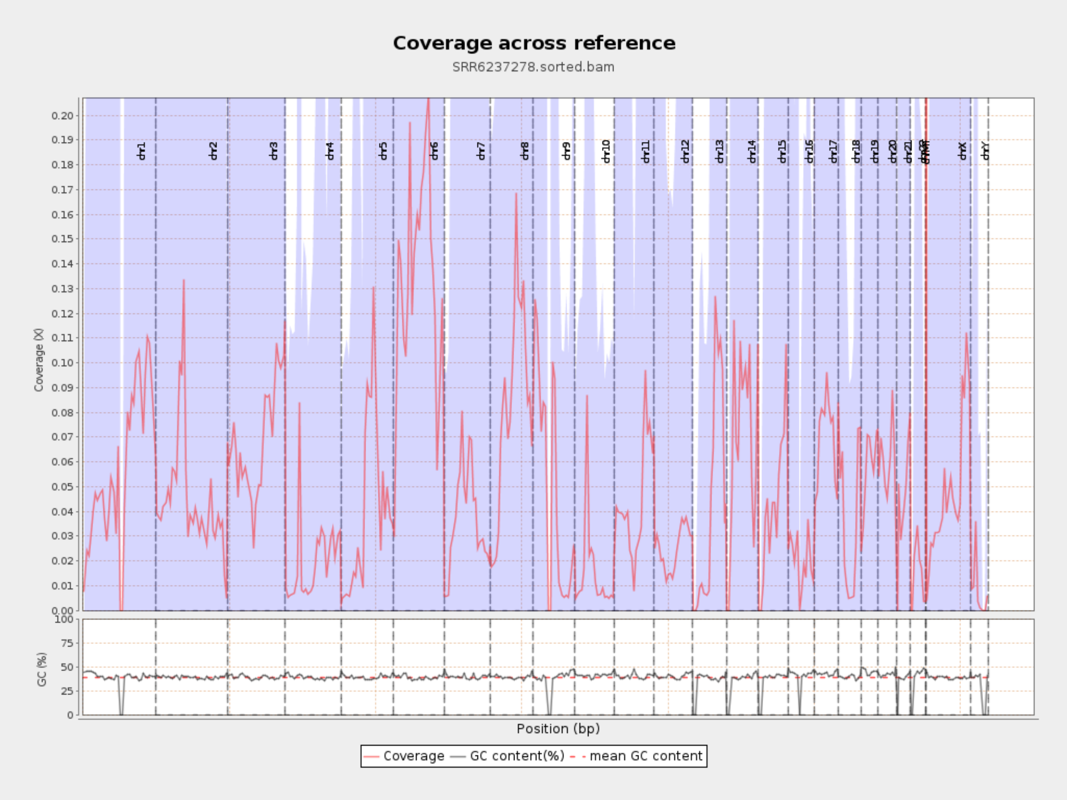
General error rate	0.84%
Mismatches	1,257,590
Insertions	13,757
Mapped reads with at least one insertion	0.6%
Deletions	47,806
Mapped reads with at least one deletion	2.09%
Homopolymer indels	45.37%

2.6. Chromosome stats

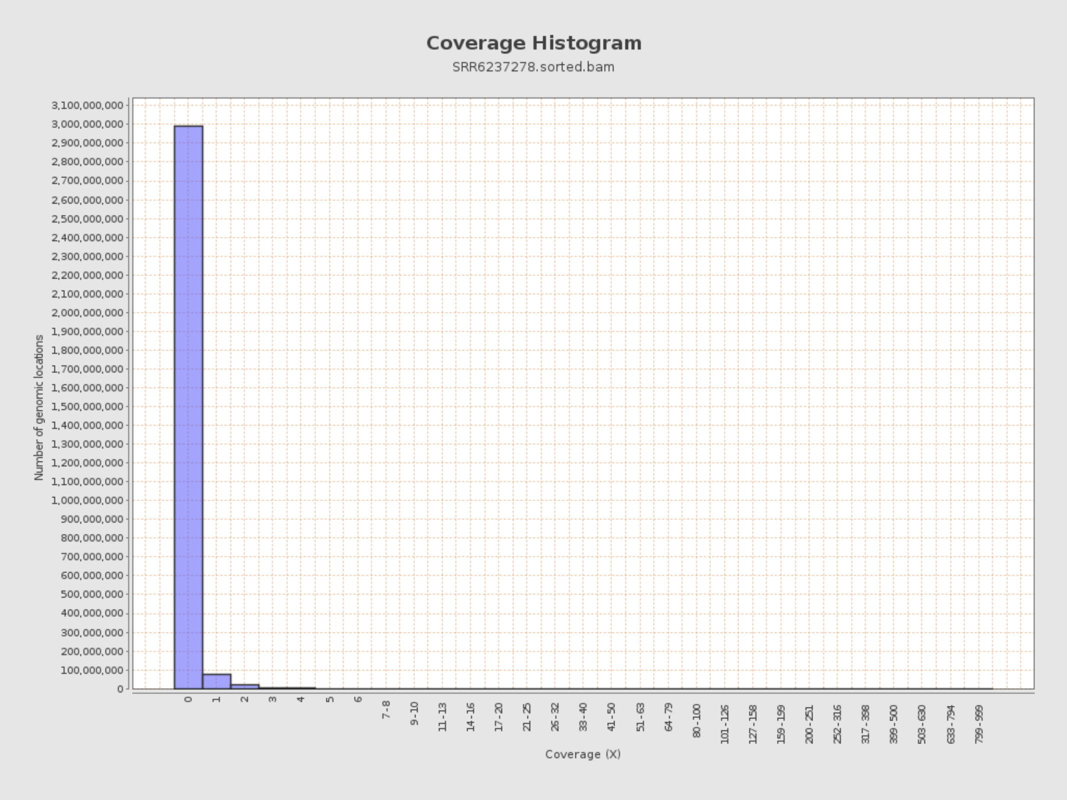
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14171789	0.0569	0.847
chr2	243199373	11026275	0.0453	0.6466
chr3	198022430	13567842	0.0685	0.353
chr4	191154276	3825808	0.02	0.3916
chr5	180915260	7451546	0.0412	0.2876
chr6	171115067	23002448	0.1344	0.7995
chr7	159138663	5925657	0.0372	0.4941

chr8	146364022	12217730	0.0835	0.5732
chr9	141213431	6889982	0.0488	0.5959
chr10	135534747	2005176	0.0148	0.5678
chr11	135006516	5974276	0.0443	0.3736
chr12	133851895	3366369	0.0251	0.2357
chr13	115169878	4961722	0.0431	0.281
chr14	107349540	7184518	0.0669	0.3894
chr15	102531392	4360245	0.0425	0.2758
chr16	90354753	1793820	0.0199	0.3043
chr17	81195210	5702082	0.0702	0.455
chr18	78077248	2681878	0.0343	1.0984
chr19	59128983	3445261	0.0583	0.4738
chr20	63025520	3863761	0.0613	0.3509
chr21	48129895	2240288	0.0465	0.4302
chr22	51304566	764638	0.0149	0.1574
chrMT	16571	109360	6.5995	4.8672
chrX	155270560	7417039	0.0478	0.3298
chrY	59373566	480935	0.0081	0.3916

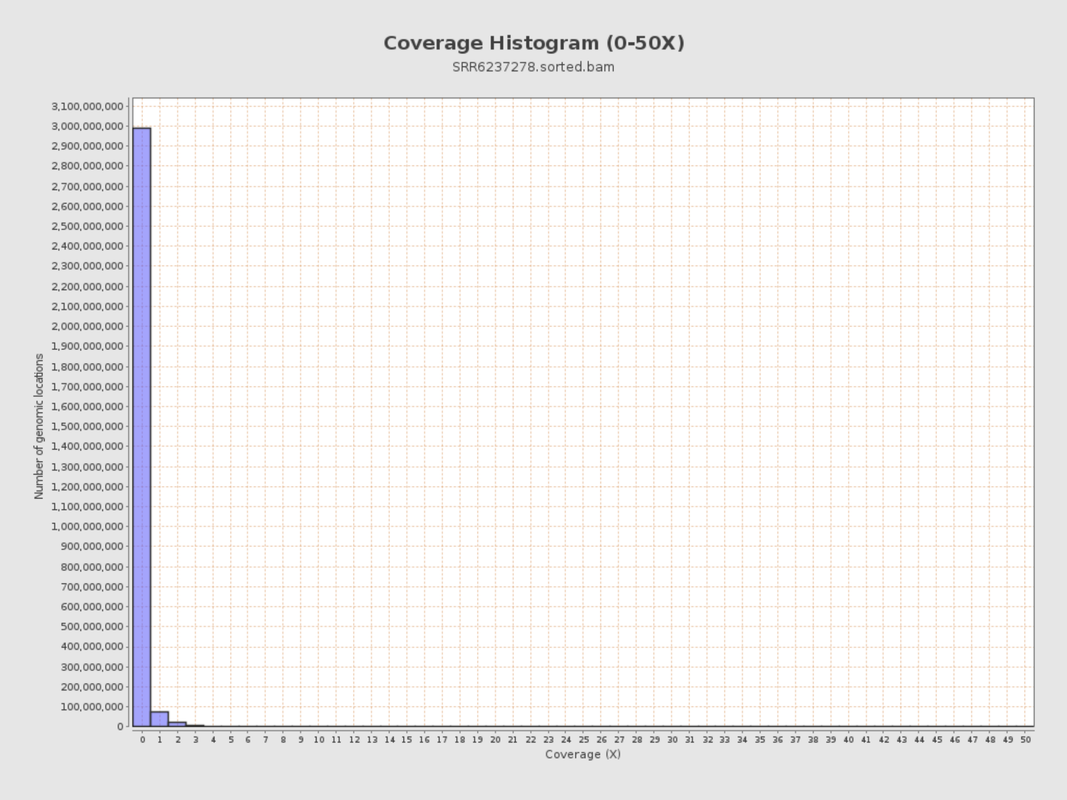
3. Results : Coverage across reference



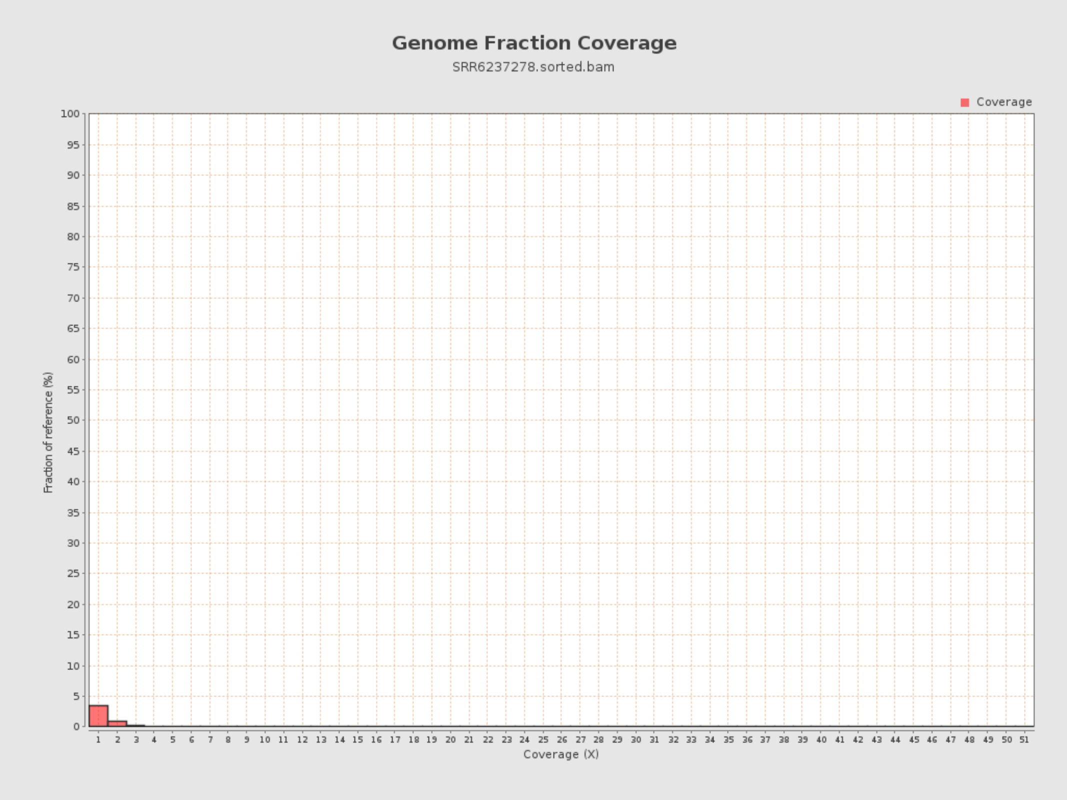
4. Results : Coverage Histogram



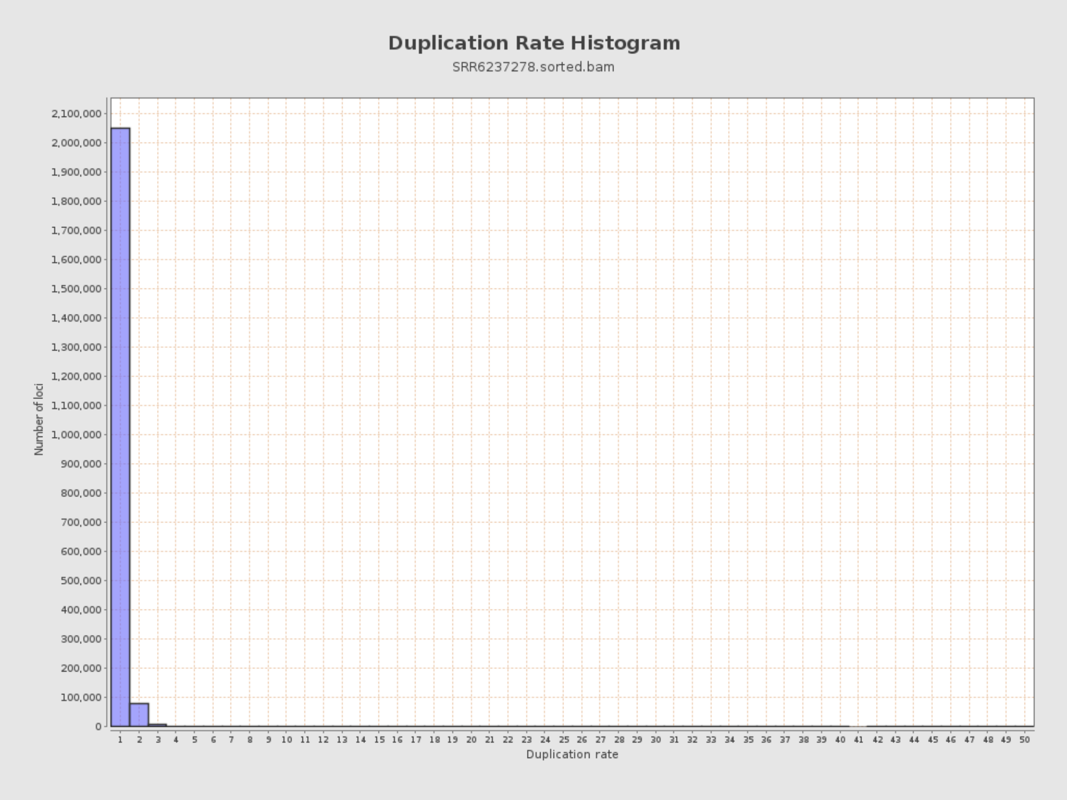
5. Results : Coverage Histogram (0-50X)



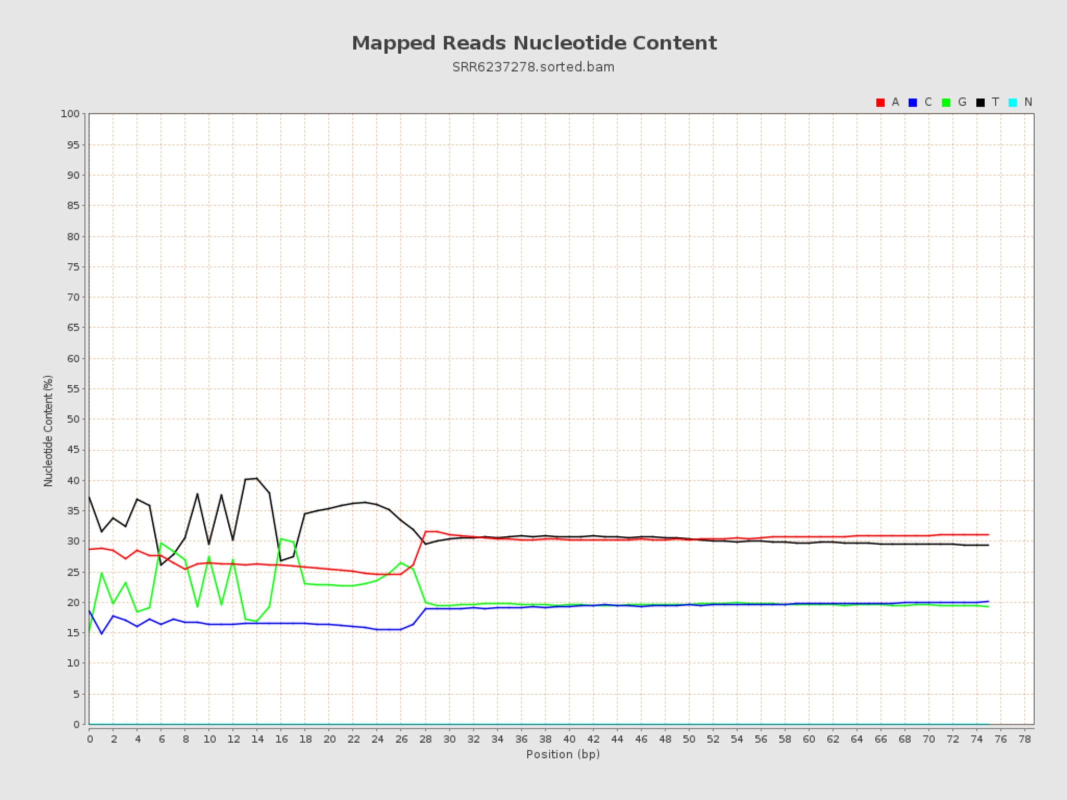
6. Results : Genome Fraction Coverage



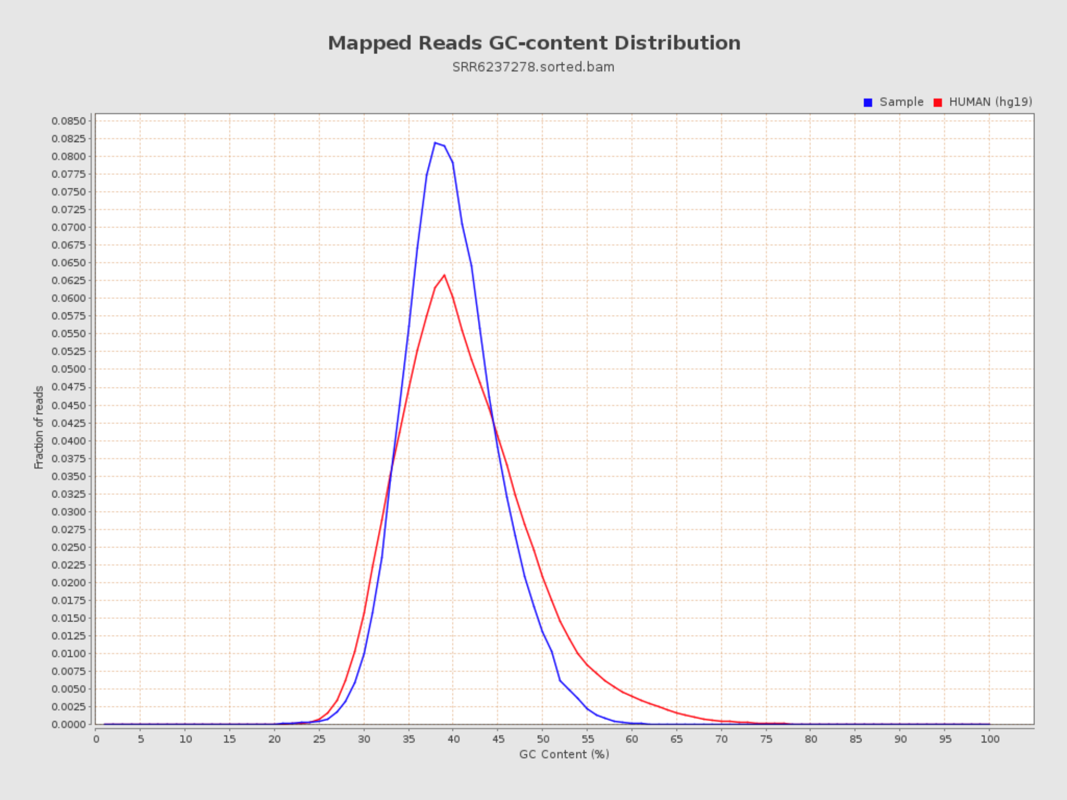
7. Results : Duplication Rate Histogram



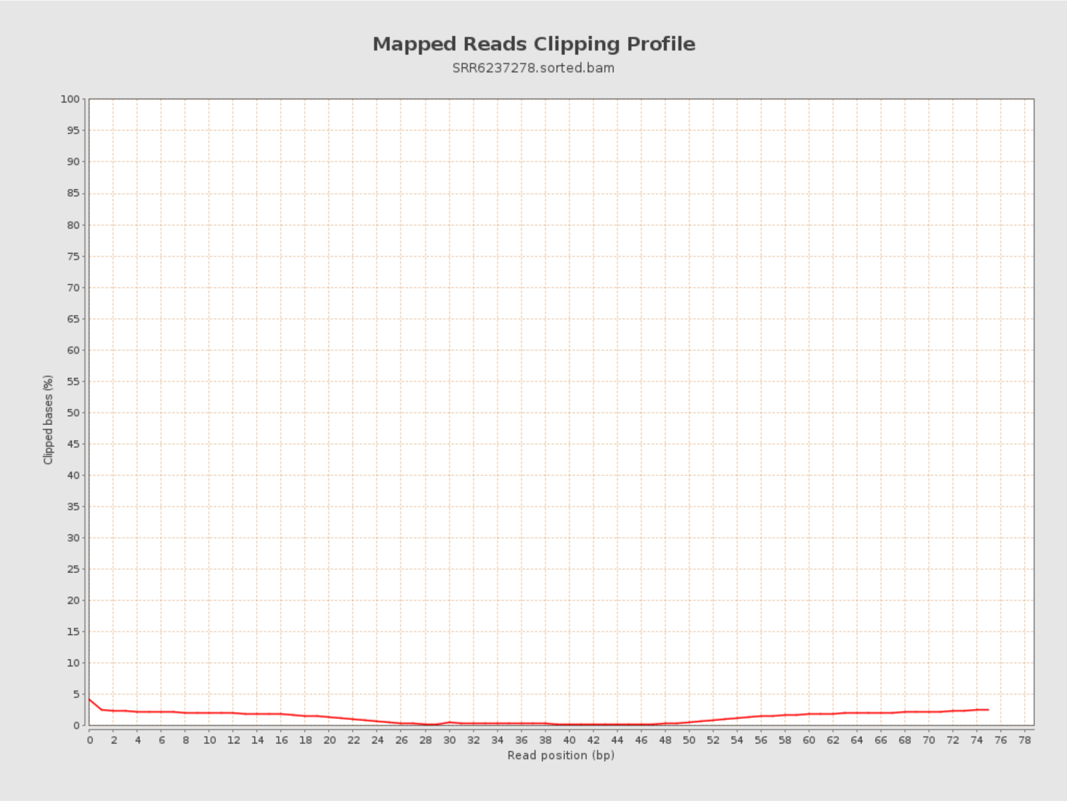
8. Results : Mapped Reads Nucleotide Content



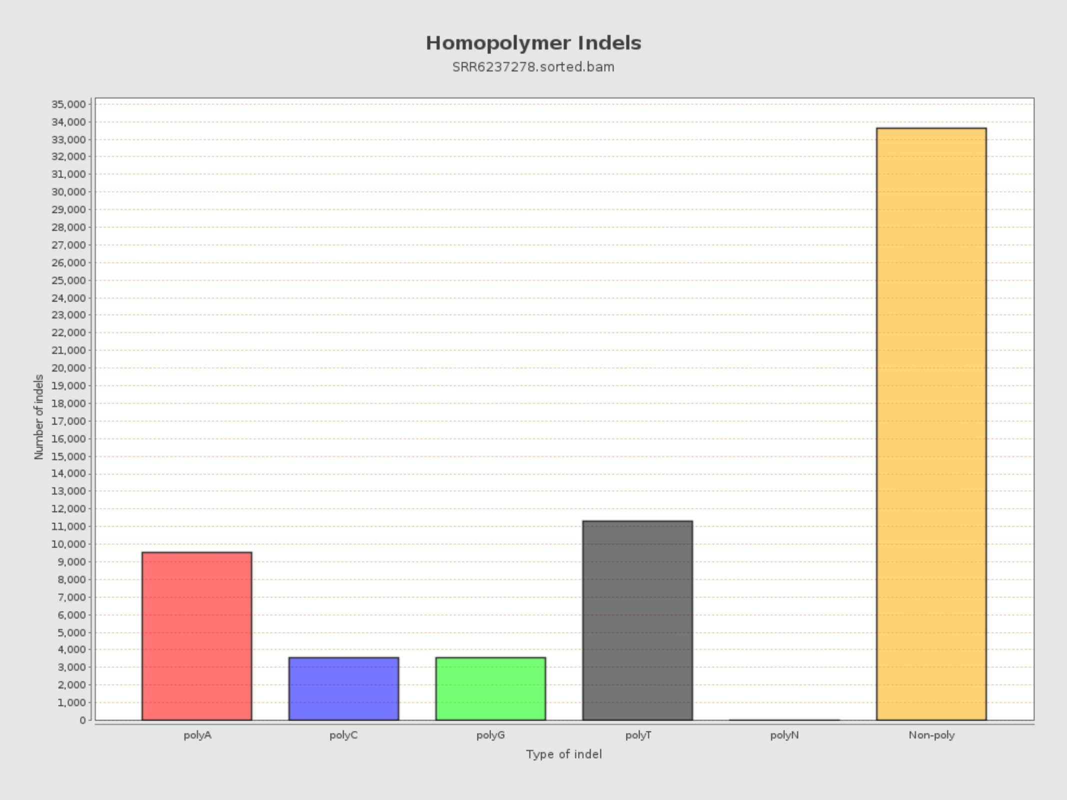
9. Results : Mapped Reads GC-content Distribution



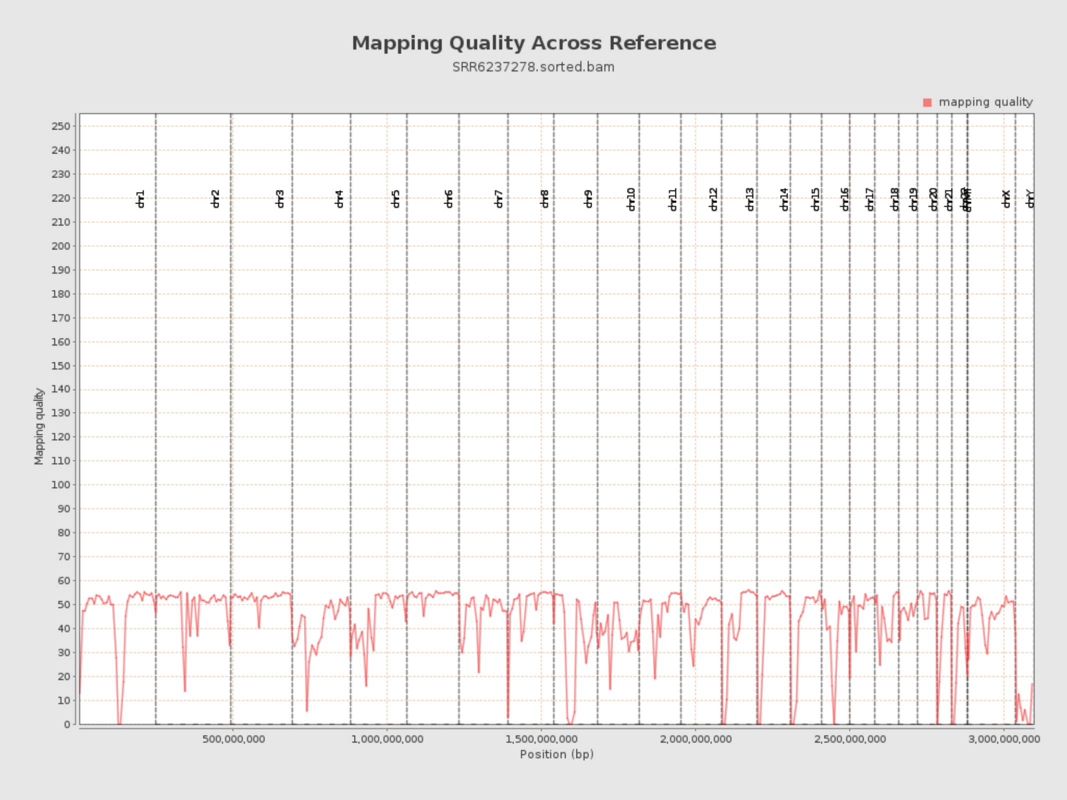
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram