Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:02:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237832.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_SRR6237832 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237832.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:02:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237832.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,689,851
Mapped reads	2,264,380 / 84.18%
Unmapped reads	425,471 / 15.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,430 / 1.02%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	442,770 / 16.46%
Duplication rate	13.75%
Clipped reads	830,117 / 30.86%

2.2. ACGT Content

Number/percentage of A's	44,497,907 / 28.57%
Number/percentage of C's	29,556,220 / 18.98%
Number/percentage of T's	48,197,946 / 30.95%
Number/percentage of G's	33,214,490 / 21.33%
Number/percentage of N's	266,728 / 0.17%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0503

Standard Deviation	0.8906

2.4. Mapping Quality

Mean Mapping Quality	46.85

2.5. Mismatches and indels

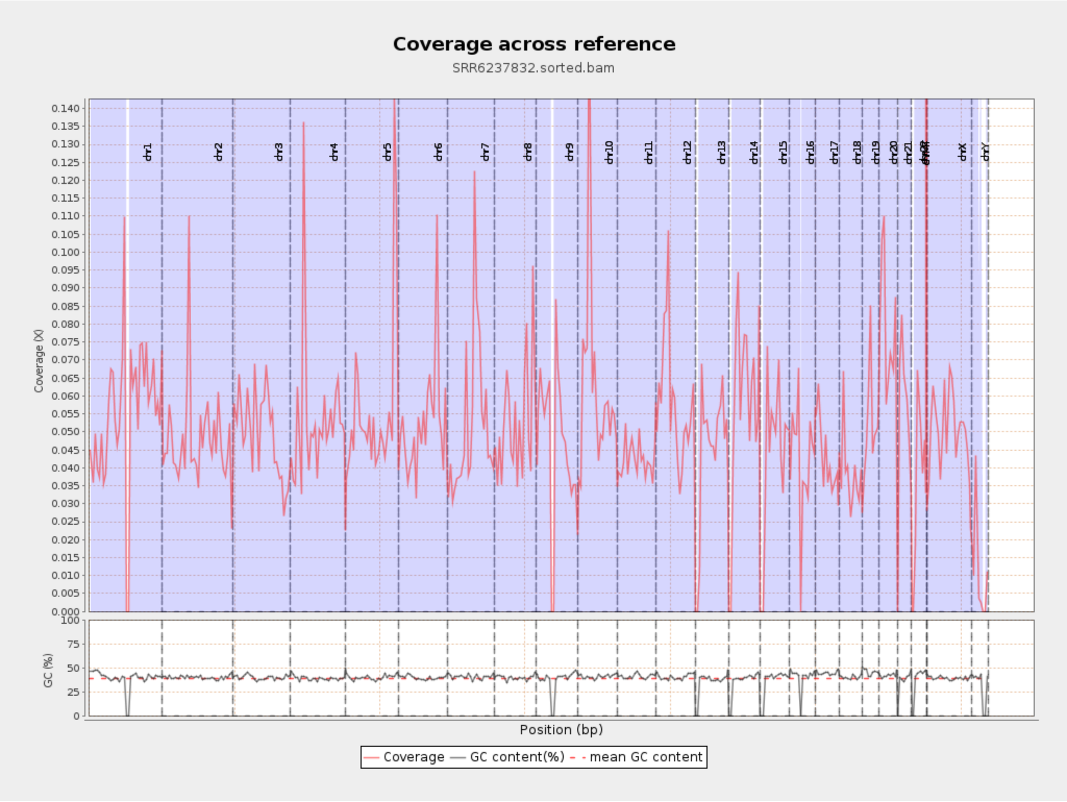
General error rate	0.94%
Mismatches	1,427,619
Insertions	13,236
Mapped reads with at least one insertion	0.58%
Deletions	48,195
Mapped reads with at least one deletion	2.09%
Homopolymer indels	44.91%

2.6. Chromosome stats

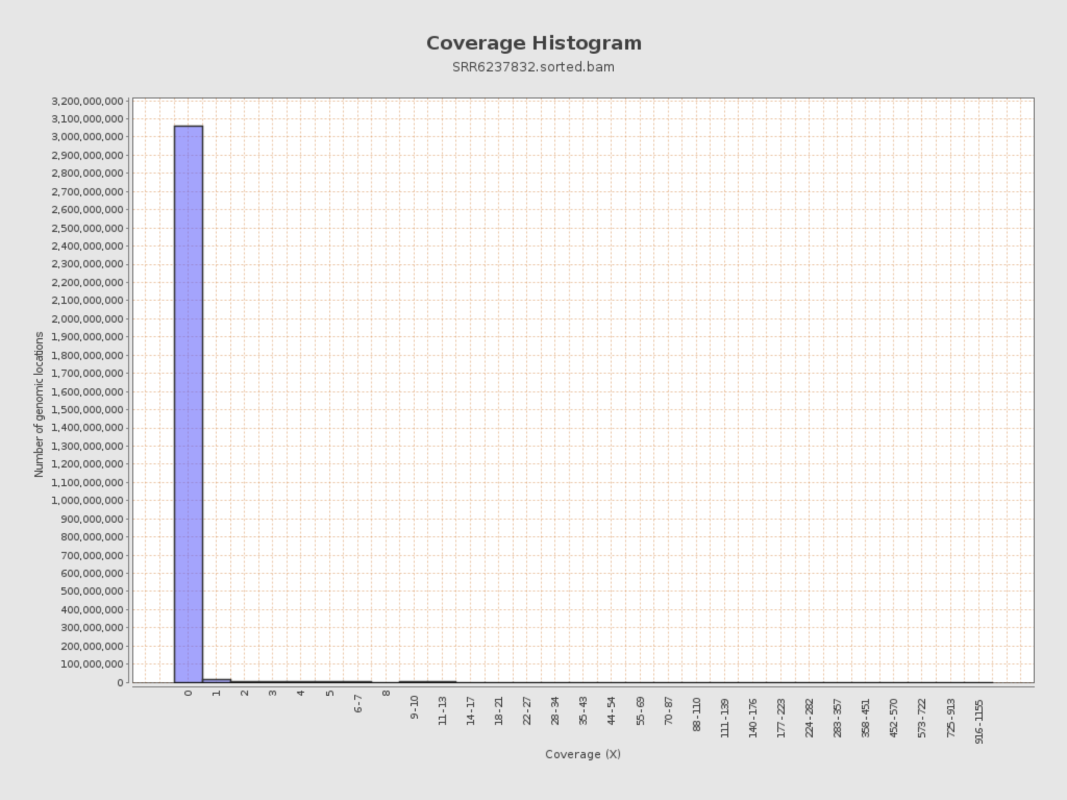
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13660301	0.0548	1.2445
chr2	243199373	11650010	0.0479	0.8991
chr3	198022430	9834742	0.0497	0.7682
chr4	191154276	10061497	0.0526	0.8562
chr5	180915260	10253018	0.0567	0.8219
chr6	171115067	8889034	0.0519	0.8364
chr7	159138663	8288006	0.0521	0.927

chr8	146364022	7727920	0.0528	1.1204
chr9	141213431	6678796	0.0473	0.85
chr10	135534747	8486597	0.0626	1.0674
chr11	135006516	5700866	0.0422	0.7474
chr12	133851895	7765780	0.058	0.7957
chr13	115169878	5080256	0.0441	0.7079
chr14	107349540	6071626	0.0566	0.7917
chr15	102531392	4450698	0.0434	0.7075
chr16	90354753	3829020	0.0424	0.705
chr17	81195210	3455555	0.0426	0.7219
chr18	78077248	3019924	0.0387	1.2
chr19	59128983	3105249	0.0525	0.9482
chr20	63025520	4949341	0.0785	0.9243
chr21	48129895	2664057	0.0554	0.7879
chr22	51304566	1798480	0.0351	0.6162
chrMT	16571	40359	2.4355	4.5771
chrX	155270560	7724209	0.0497	0.7698
chrY	59373566	636017	0.0107	0.4427

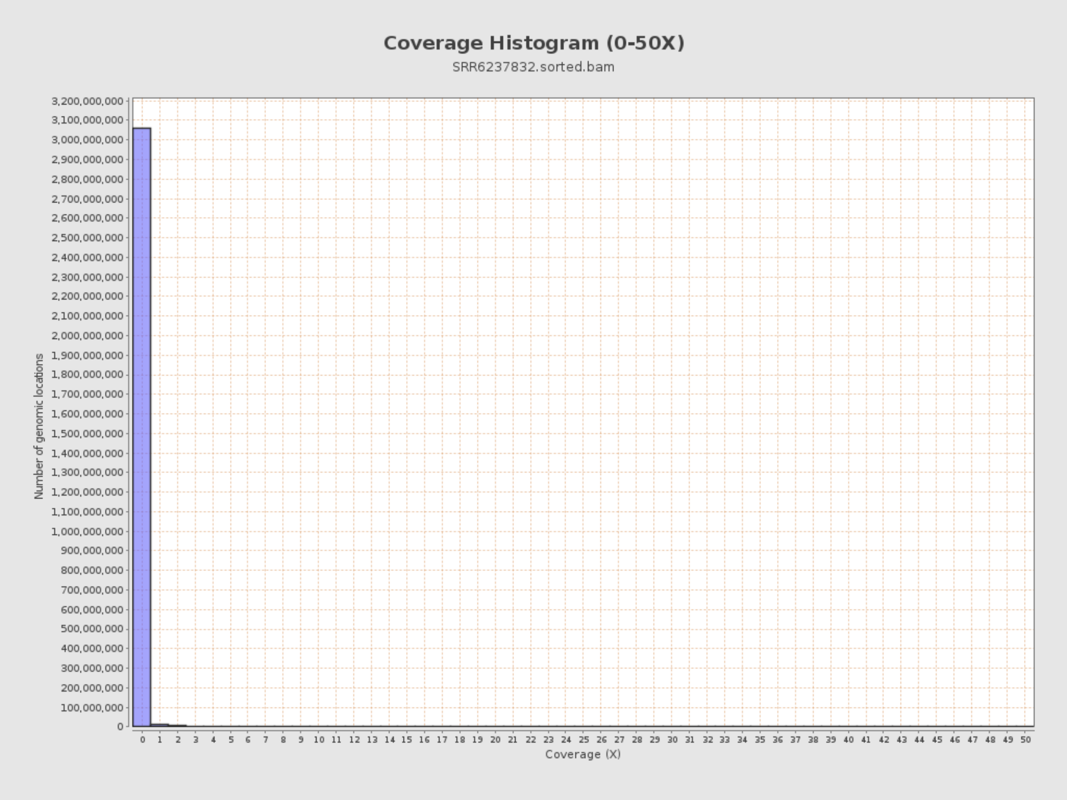
3. Results : Coverage across reference



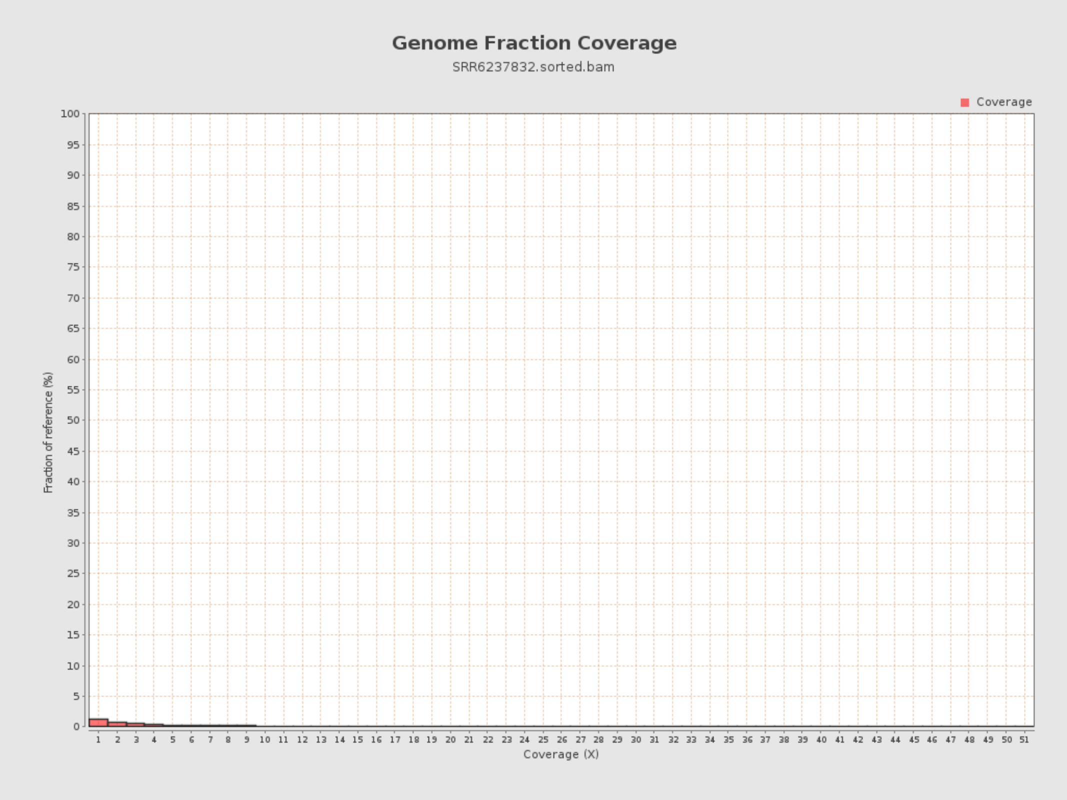
4. Results : Coverage Histogram



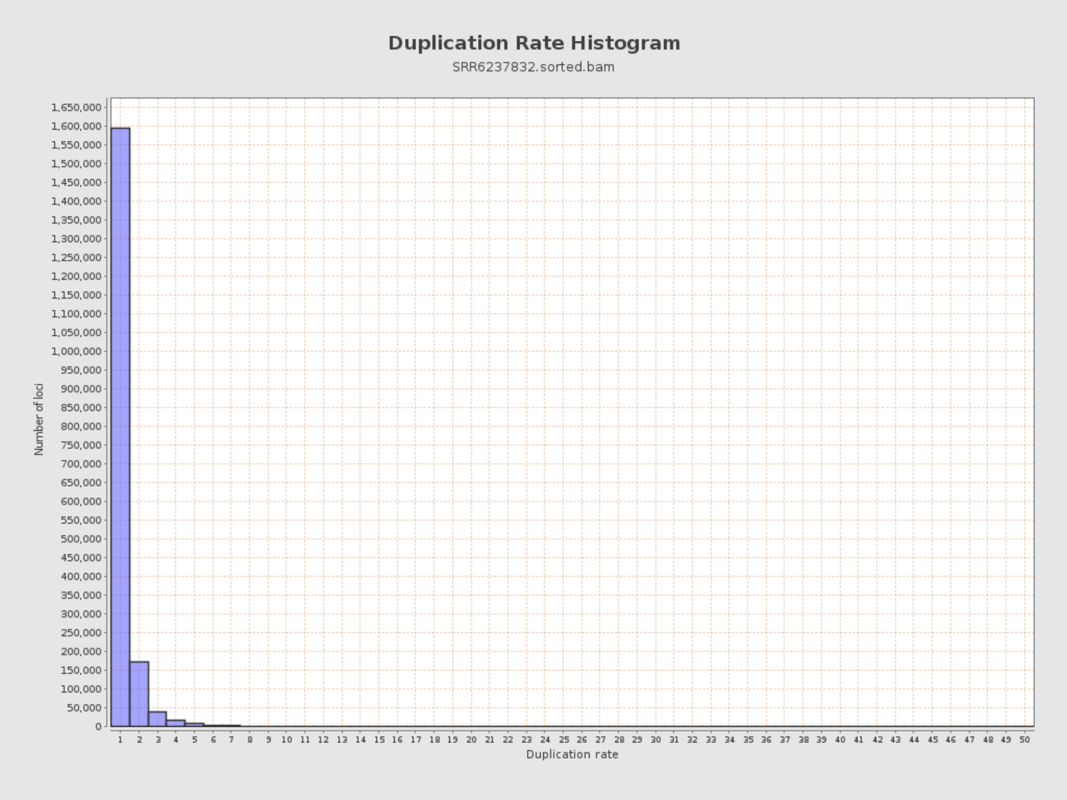
5. Results : Coverage Histogram (0-50X)



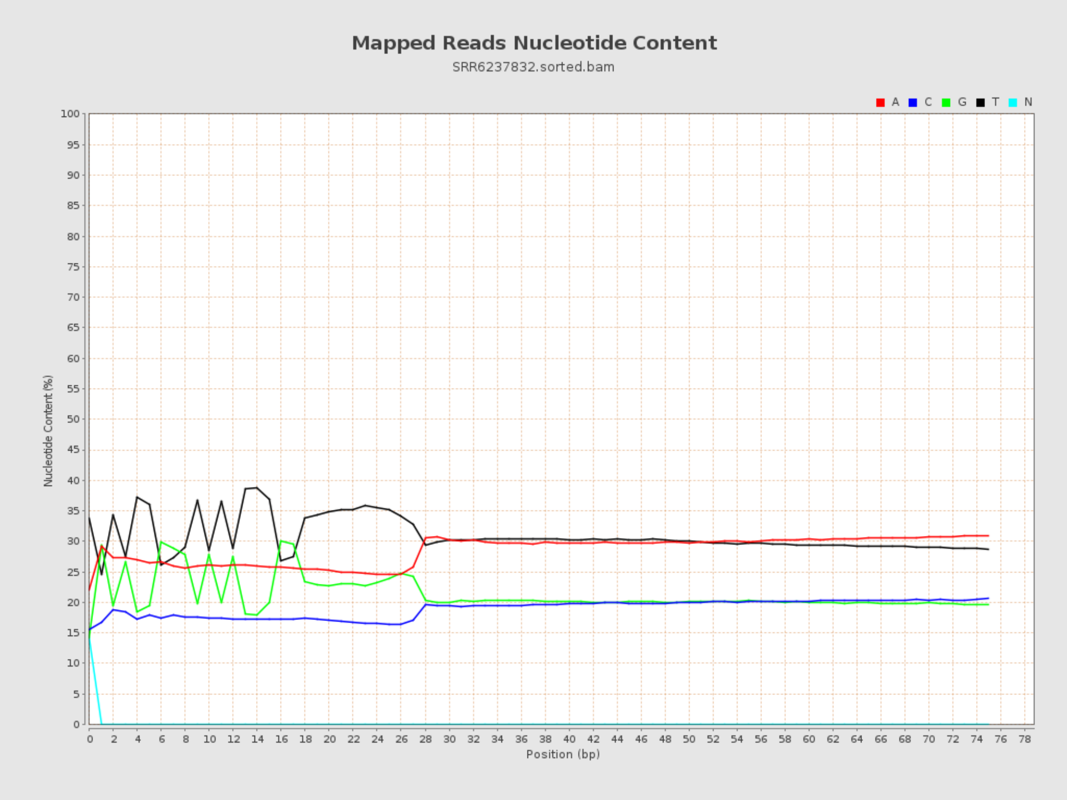
6. Results : Genome Fraction Coverage



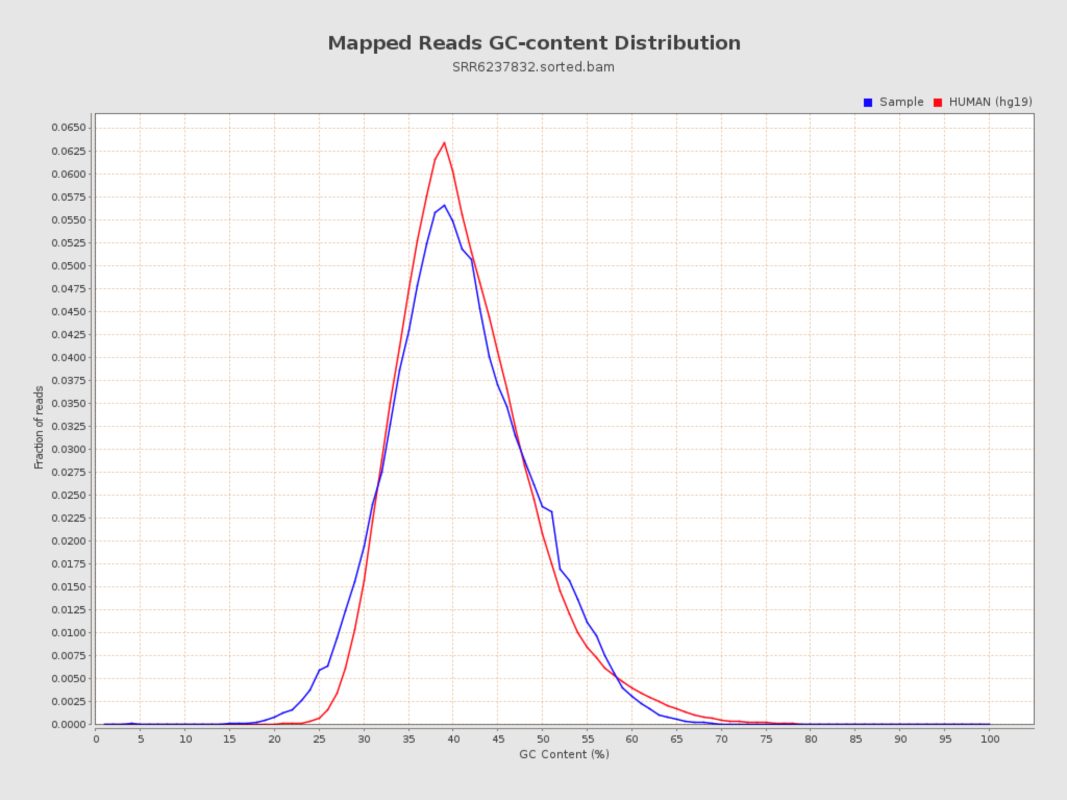
7. Results : Duplication Rate Histogram



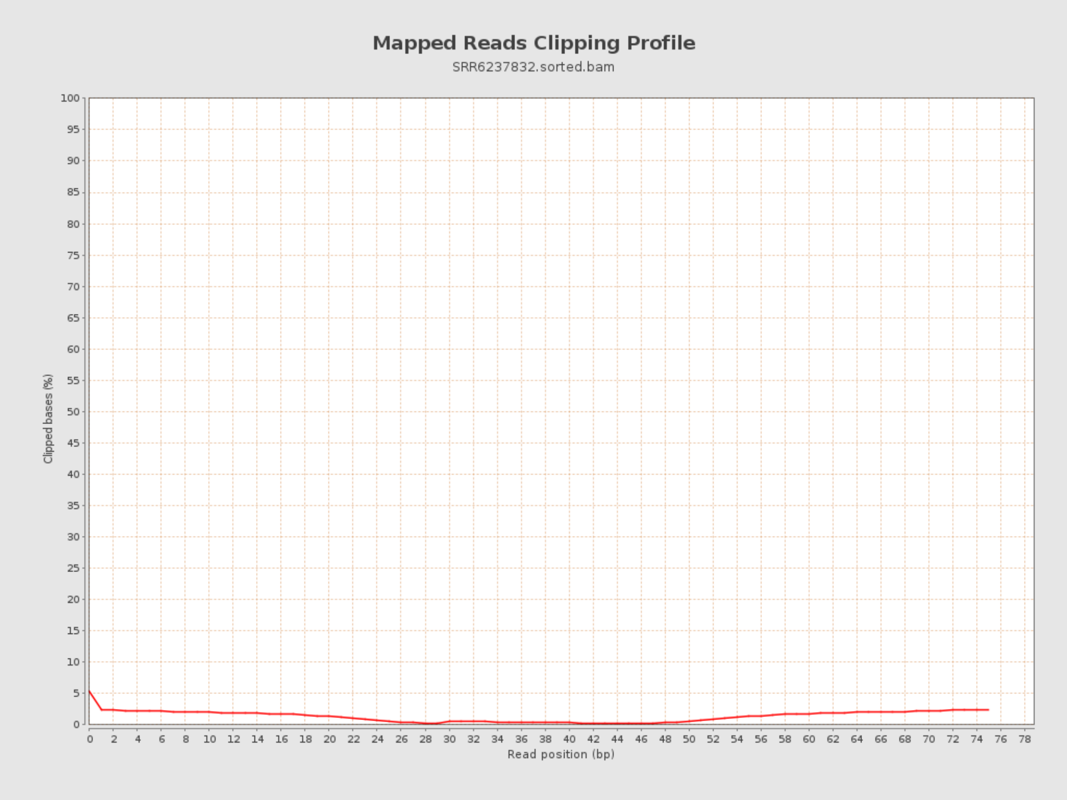
8. Results : Mapped Reads Nucleotide Content



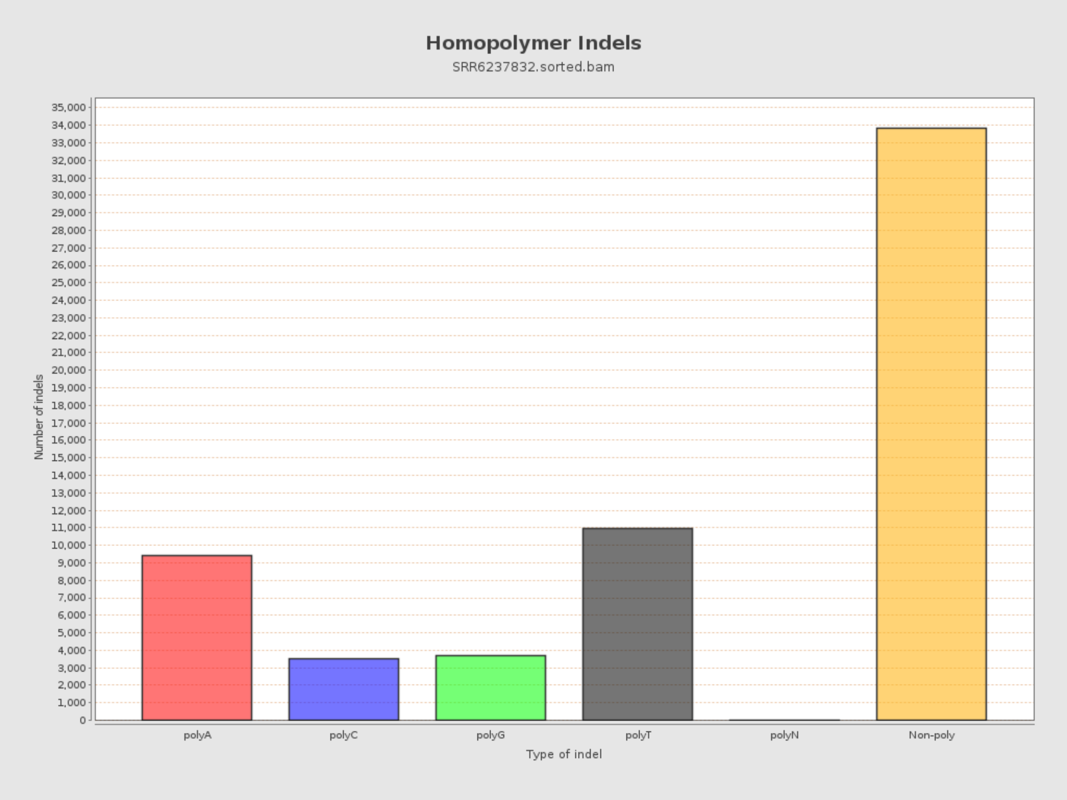
9. Results : Mapped Reads GC-content Distribution



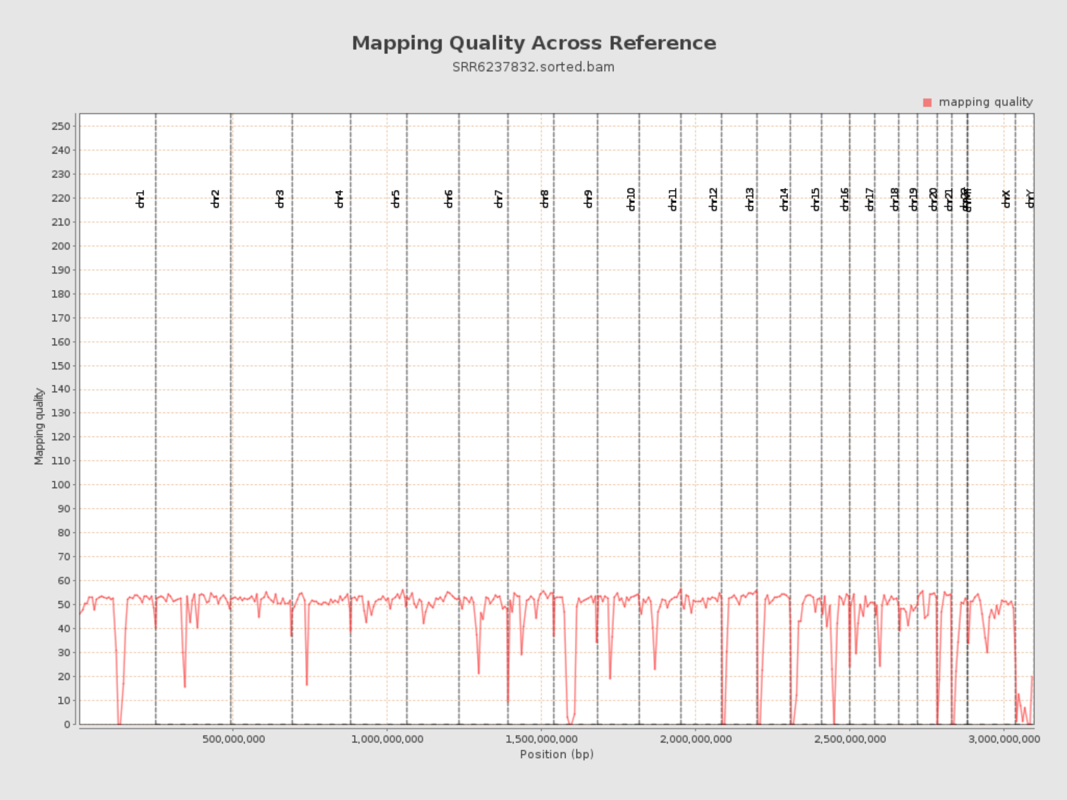
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram