Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:46:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237866.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_SRR6237866 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237866.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:45:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237866.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,689,431
Mapped reads	3,023,468 / 81.95%
Unmapped reads	665,963 / 18.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,200 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	97,664 / 2.65%
Duplication rate	1.92%
Clipped reads	1,466,091 / 39.74%

2.2. ACGT Content

Number/percentage of A's	55,857,069 / 28.06%
Number/percentage of C's	37,818,076 / 19%
Number/percentage of T's	62,403,155 / 31.35%
Number/percentage of G's	42,953,114 / 21.58%
Number/percentage of N's	37,048 / 0.02%
GC Percentage	40.57%

2.3. Coverage

Mean	0.0643

Standard Deviation	0.5754

2.4. Mapping Quality

Mean Mapping Quality	45.62

2.5. Mismatches and indels

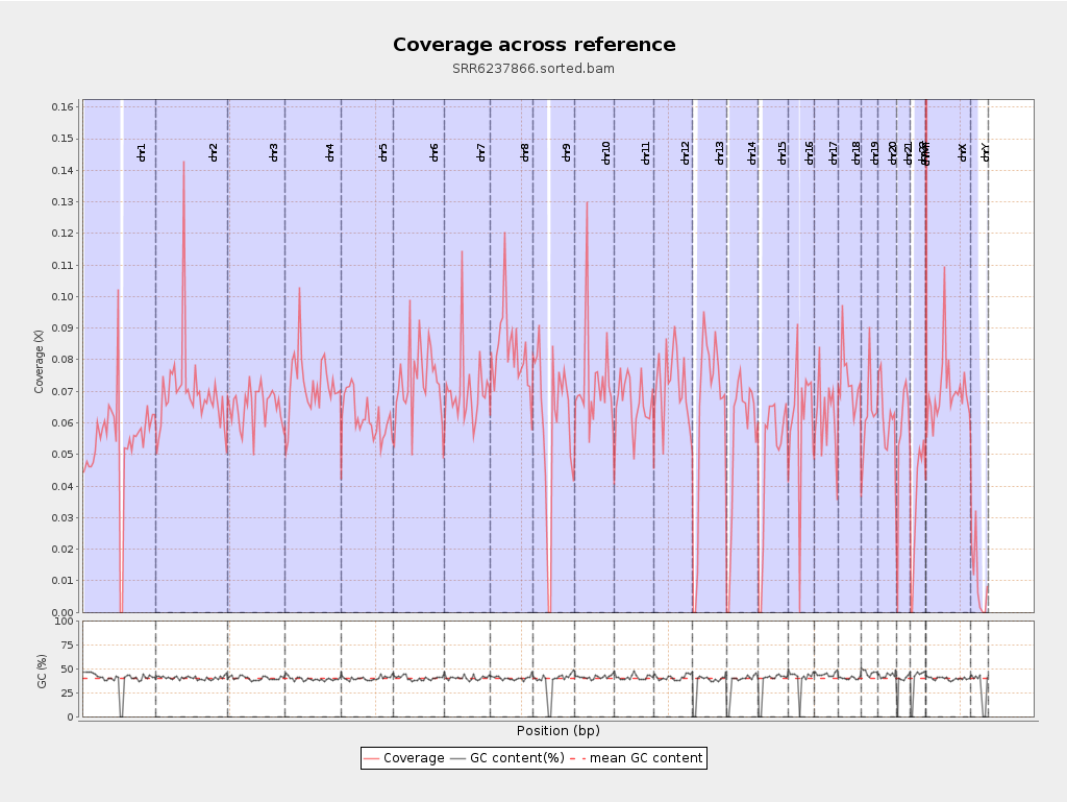
General error rate	0.89%
Mismatches	1,730,997
Insertions	17,218
Mapped reads with at least one insertion	0.56%
Deletions	50,817
Mapped reads with at least one deletion	1.66%
Homopolymer indels	46.59%

2.6. Chromosome stats

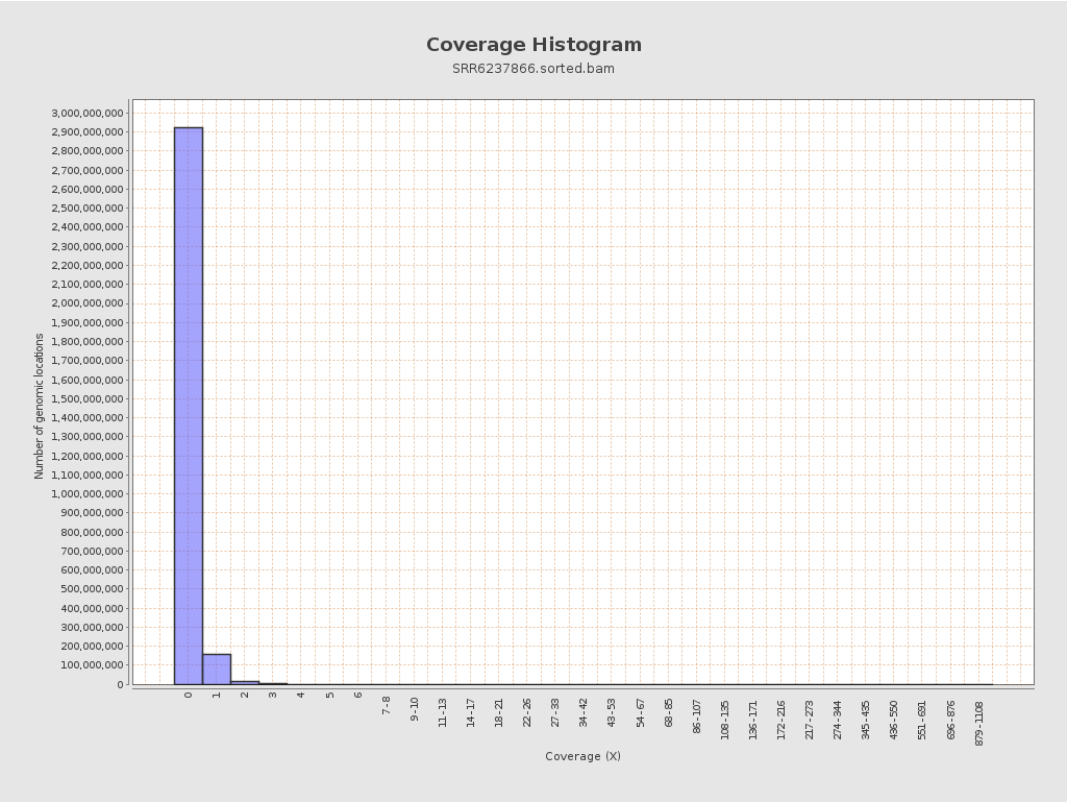
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13412431	0.0538	0.9643
chr2	243199373	16948325	0.0697	0.7211
chr3	198022430	12927207	0.0653	0.2868
chr4	191154276	13830796	0.0724	0.3484
chr5	180915260	11179908	0.0618	0.2806
chr6	171115067	12584681	0.0735	0.4361
chr7	159138663	11100305	0.0698	0.7757

chr8	146364022	12066029	0.0824	0.6891
chr9	141213431	8499377	0.0602	0.605
chr10	135534747	9797742	0.0723	0.6408
chr11	135006516	8945159	0.0663	0.5636
chr12	133851895	9643386	0.072	0.3093
chr13	115169878	7347783	0.0638	0.2753
chr14	107349540	5990266	0.0558	0.3715
chr15	102531392	4969911	0.0485	0.2441
chr16	90354753	5458654	0.0604	0.3762
chr17	81195210	5087550	0.0627	0.3892
chr18	78077248	5740746	0.0735	1.2238
chr19	59128983	3732954	0.0631	0.7638
chr20	63025520	3889129	0.0617	0.3079
chr21	48129895	2730167	0.0567	0.3277
chr22	51304566	1793849	0.035	0.203
chrMT	16571	51377	3.1004	2.4981
chrX	155270560	10848463	0.0699	0.4276
chrY	59373566	576351	0.0097	0.2432

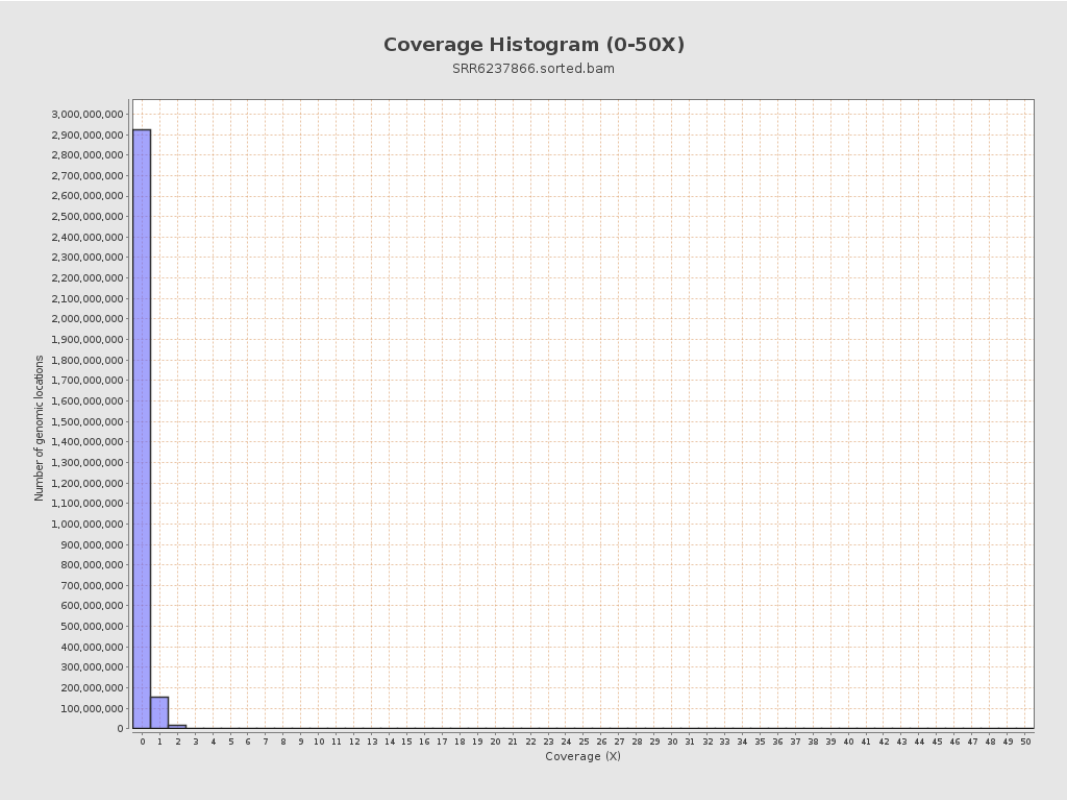
3. Results : Coverage across reference



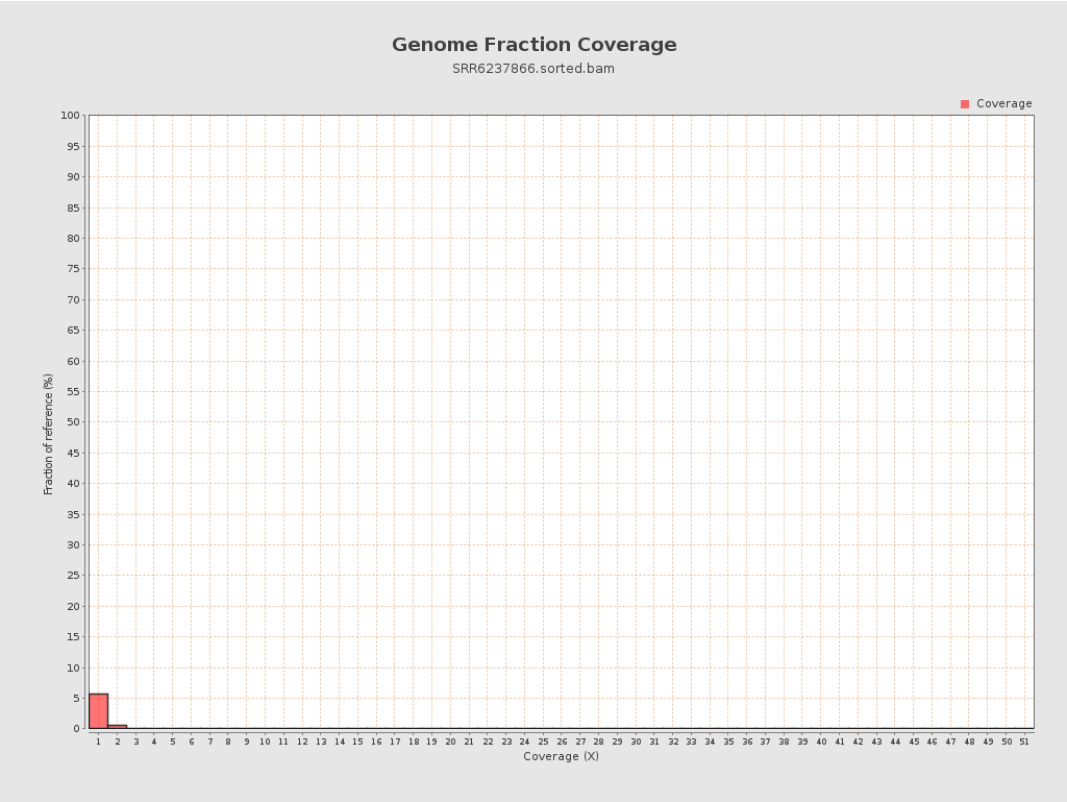
4. Results : Coverage Histogram



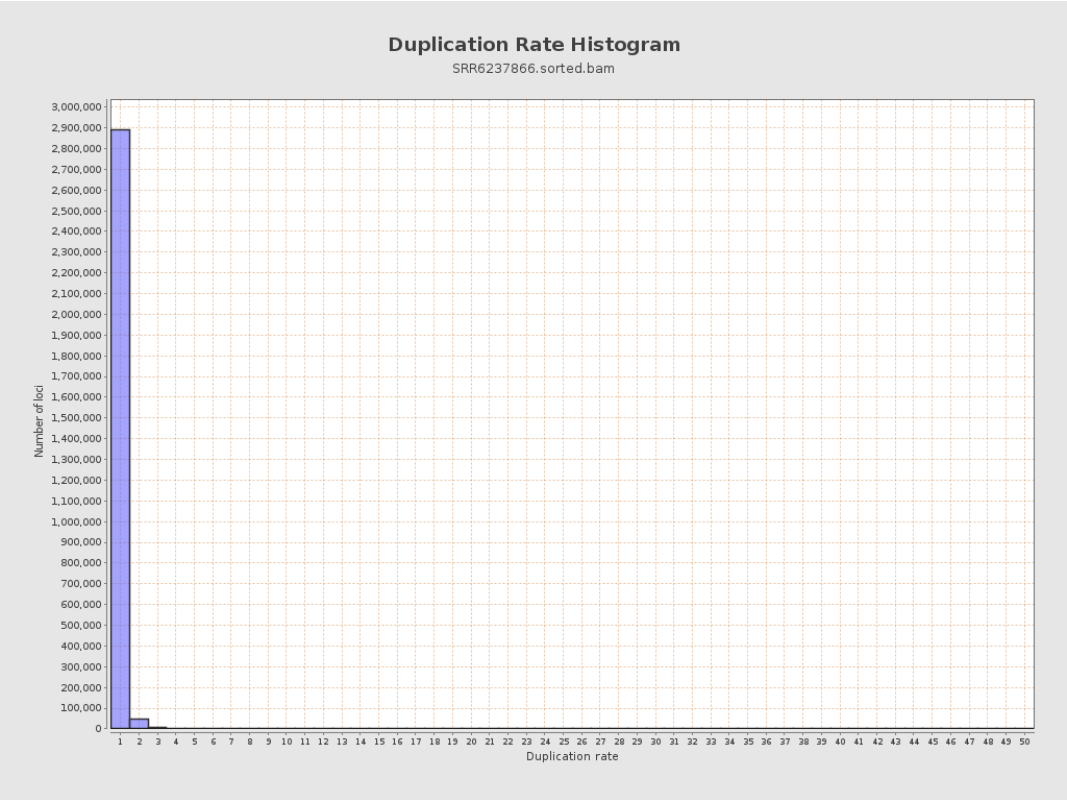
5. Results : Coverage Histogram (0-50X)



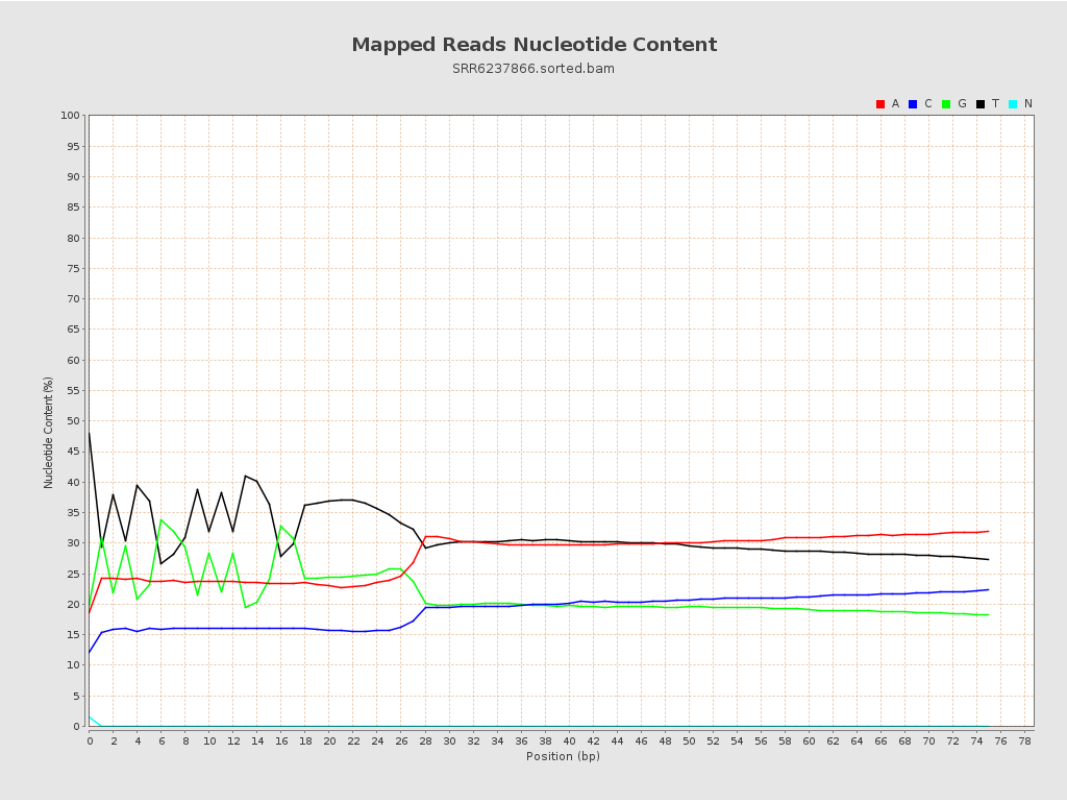
6. Results : Genome Fraction Coverage



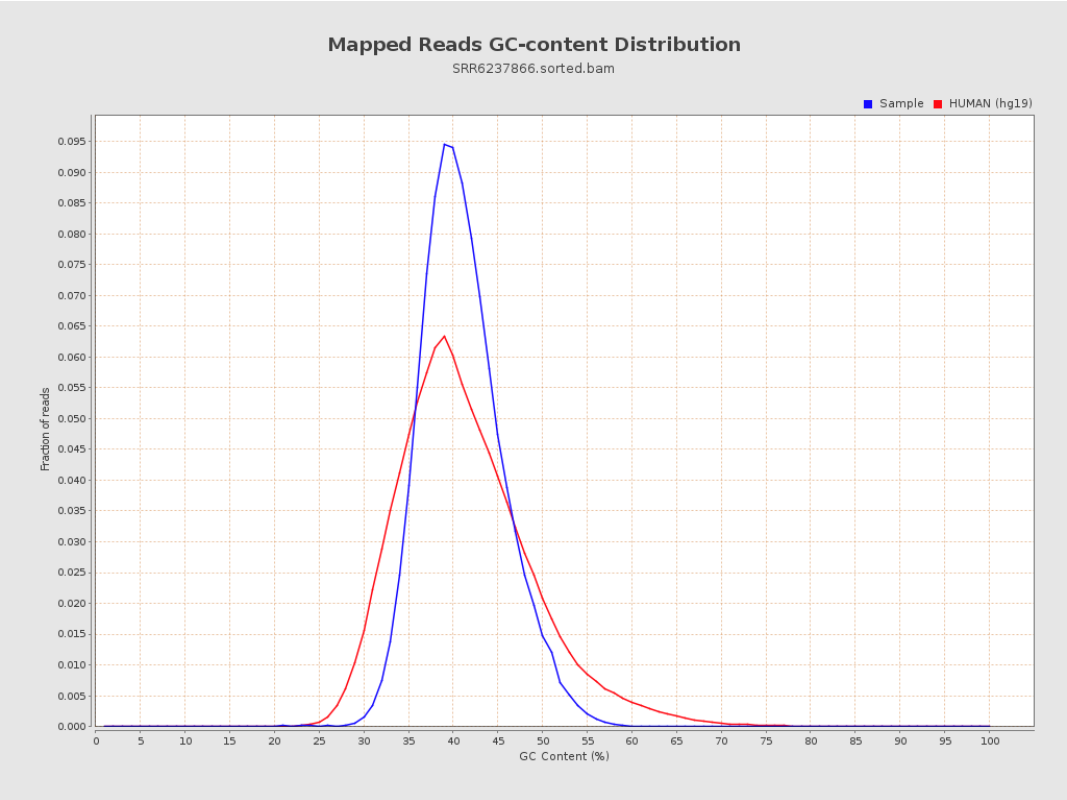
7. Results : Duplication Rate Histogram



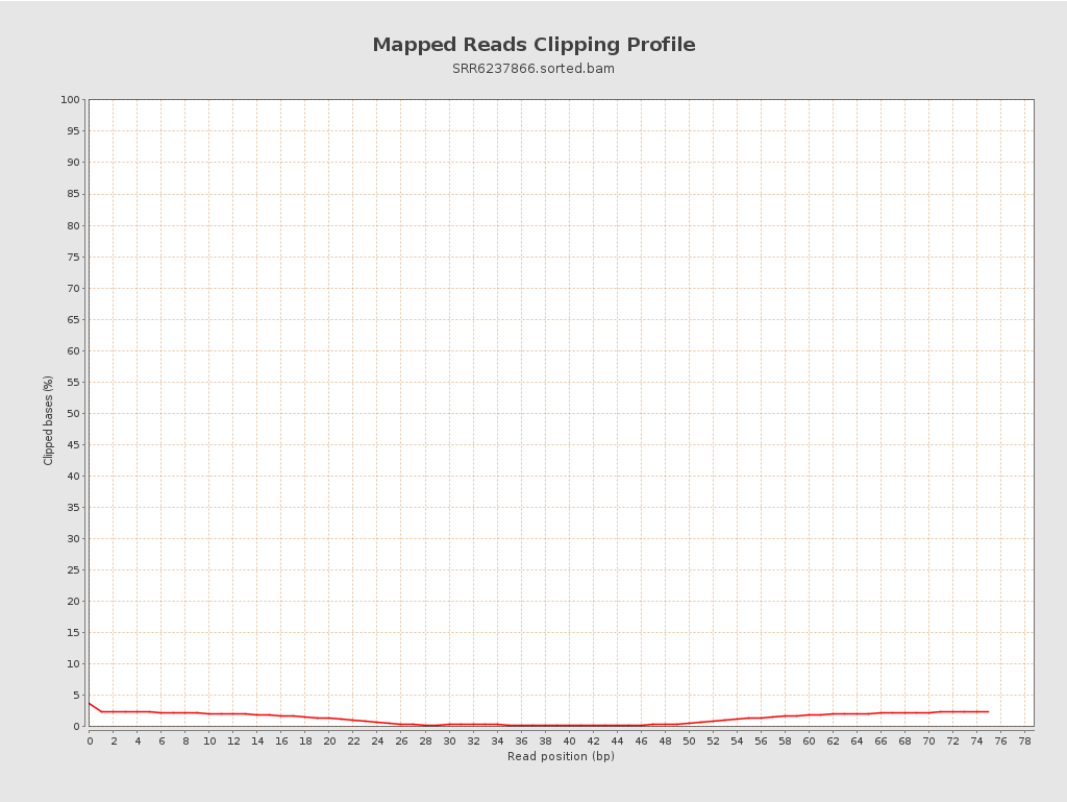
8. Results : Mapped Reads Nucleotide Content



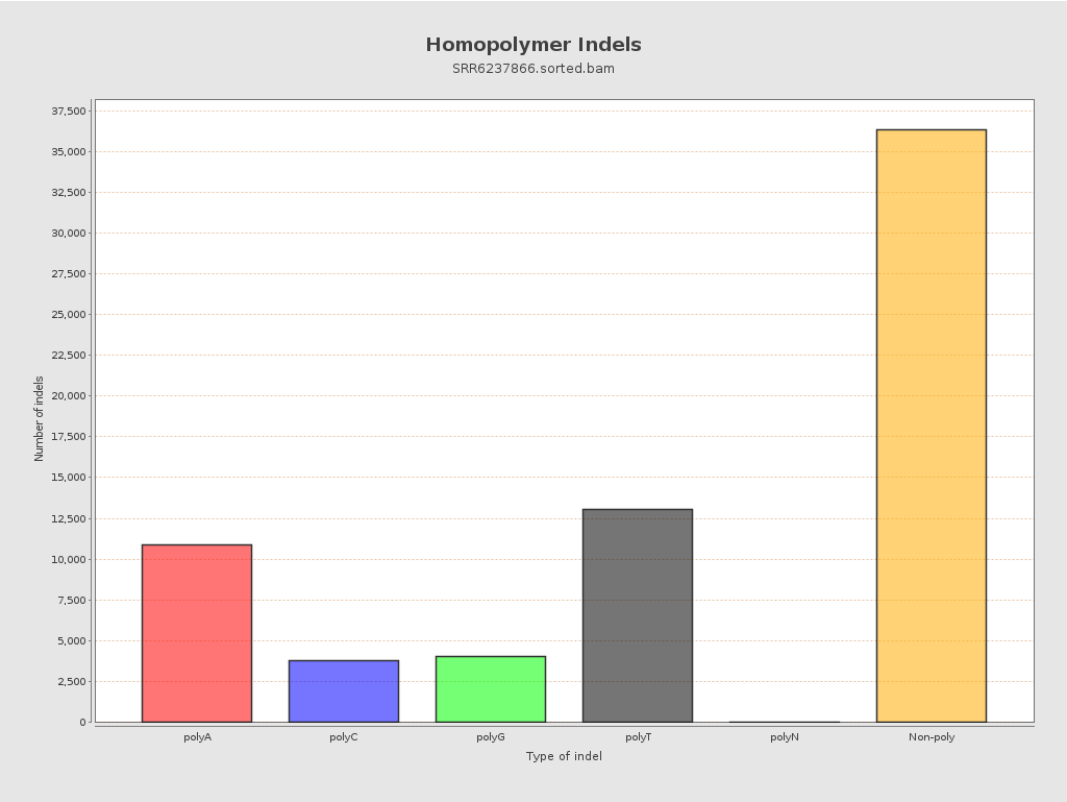
9. Results : Mapped Reads GC-content Distribution



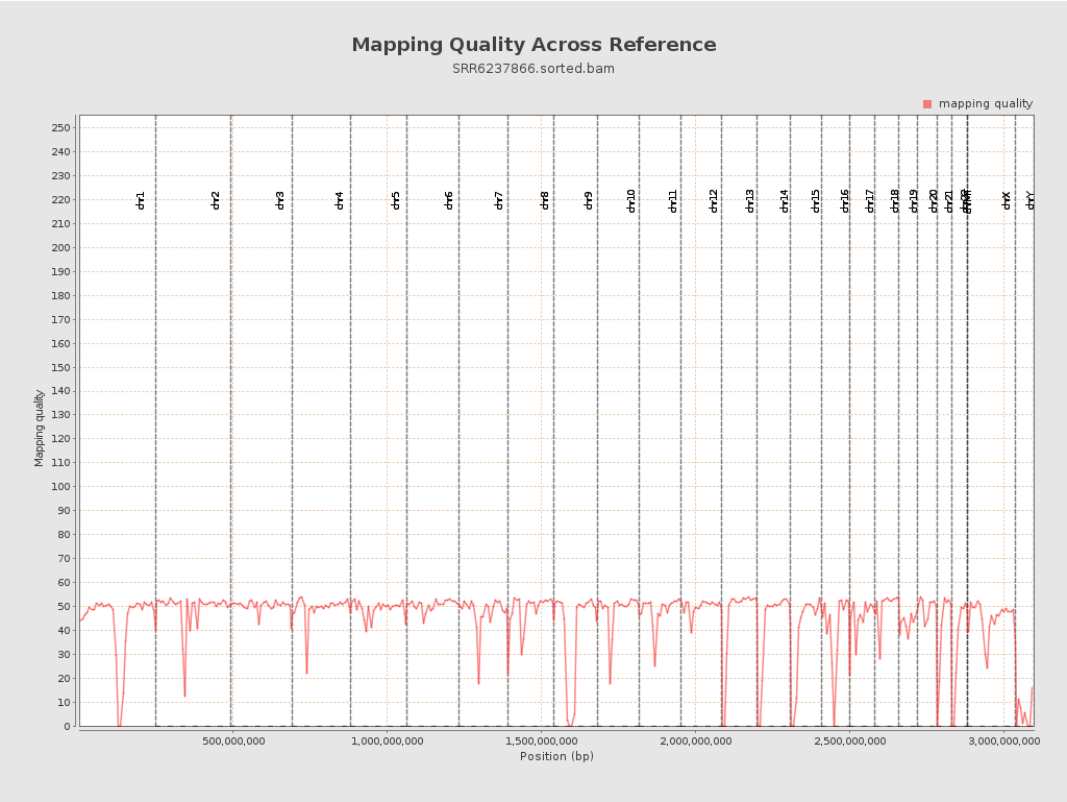
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram