Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:22:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237858.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_SRR6237858 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237858.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:22:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237858.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,498,110
Mapped reads	2,957,321 / 84.54%
Unmapped reads	540,789 / 15.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,018 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	142,545 / 4.07%
Duplication rate	3.01%
Clipped reads	1,500,284 / 42.89%

2.2. ACGT Content

Number/percentage of A's	55,021,024 / 28.48%
Number/percentage of C's	36,705,515 / 19%
Number/percentage of T's	59,357,565 / 30.73%
Number/percentage of G's	41,914,197 / 21.7%
Number/percentage of N's	178,661 / 0.09%
GC Percentage	40.7%

2.3. Coverage

Mean	0.0624

Standard Deviation	0.7599

2.4. Mapping Quality

Mean Mapping Quality	43.37

2.5. Mismatches and indels

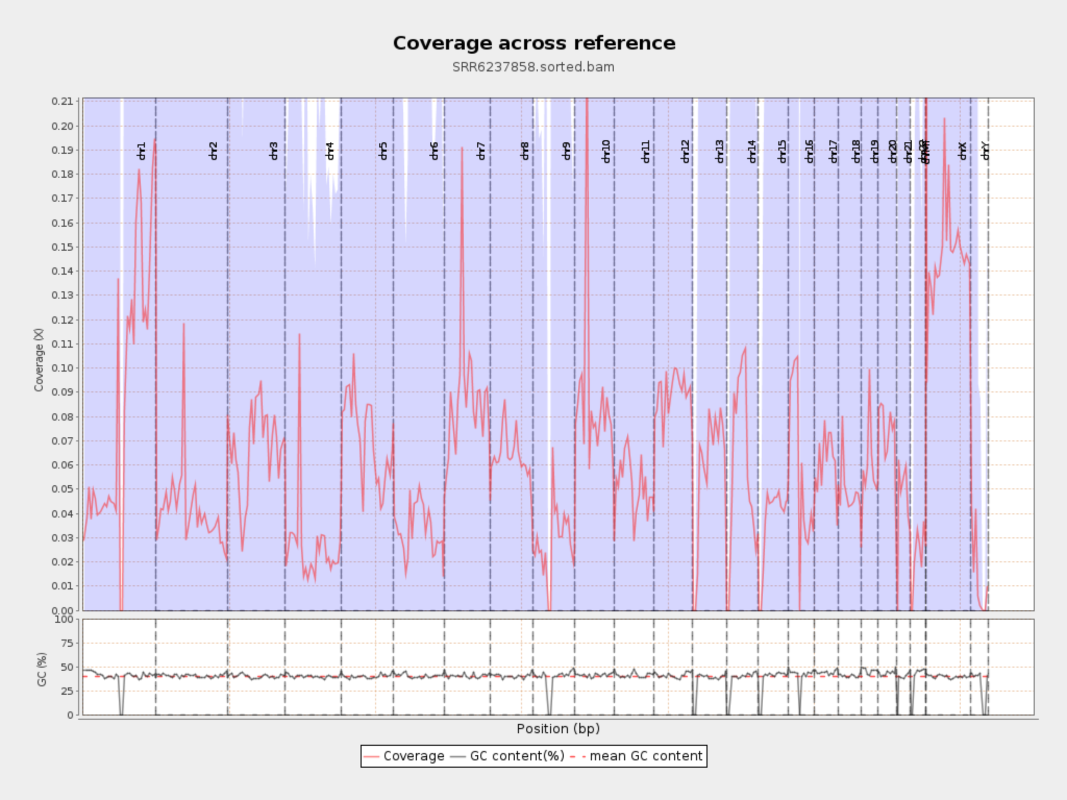
General error rate	0.87%
Mismatches	1,652,764
Insertions	17,798
Mapped reads with at least one insertion	0.6%
Deletions	46,494
Mapped reads with at least one deletion	1.55%
Homopolymer indels	45.6%

2.6. Chromosome stats

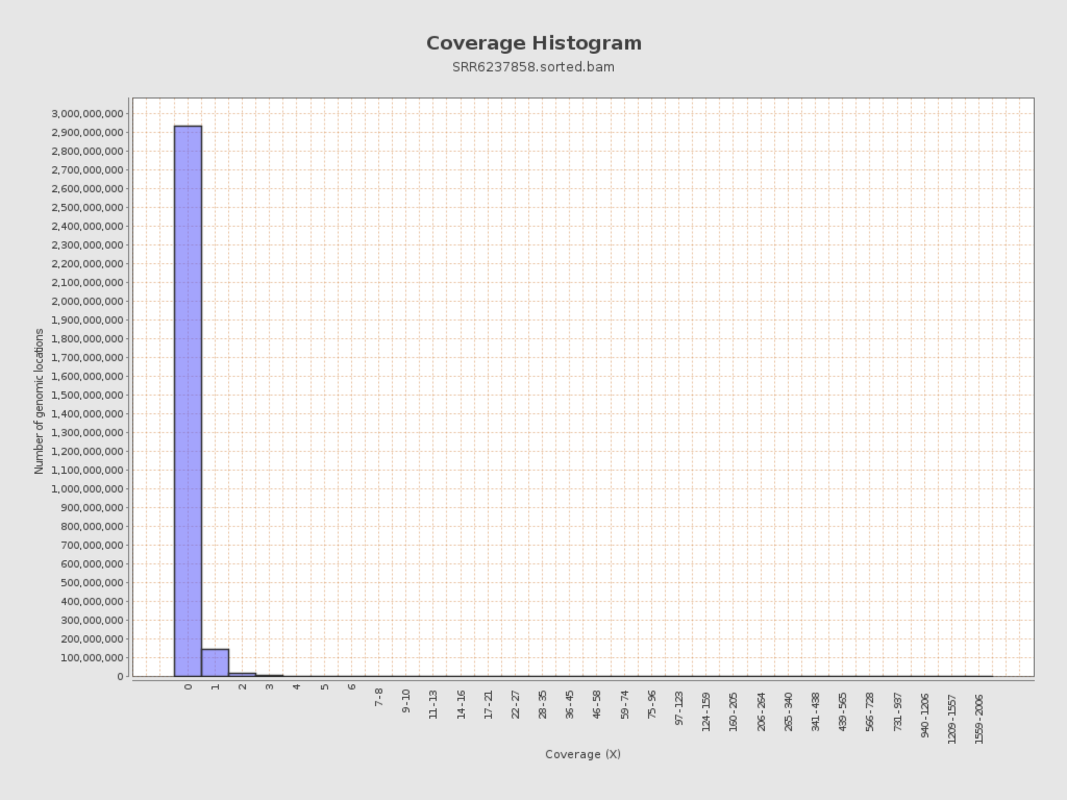
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21375963	0.0858	1.5751
chr2	243199373	10097315	0.0415	0.6366
chr3	198022430	13352523	0.0674	0.3811
chr4	191154276	5096932	0.0267	0.3233
chr5	180915260	12899642	0.0713	0.3042
chr6	171115067	5756251	0.0336	0.2636
chr7	159138663	13995451	0.0879	1.3818

chr8	146364022	9345125	0.0638	0.7397
chr9	141213431	4023821	0.0285	0.4845
chr10	135534747	11970164	0.0883	1.3574
chr11	135006516	6988963	0.0518	0.4617
chr12	133851895	12019985	0.0898	0.3442
chr13	115169878	6779314	0.0589	0.2685
chr14	107349540	6432146	0.0599	0.3195
chr15	102531392	3715544	0.0362	0.2127
chr16	90354753	5138715	0.0569	0.3971
chr17	81195210	5053972	0.0622	0.451
chr18	78077248	3891206	0.0498	1.0862
chr19	59128983	3559564	0.0602	1.0381
chr20	63025520	4736978	0.0752	0.3409
chr21	48129895	2216656	0.0461	0.3087
chr22	51304566	1100233	0.0214	0.1651
chrMT	16571	165218	9.9703	6.8295
chrX	155270560	22741512	0.1465	0.5517
chrY	59373566	803713	0.0135	0.3062

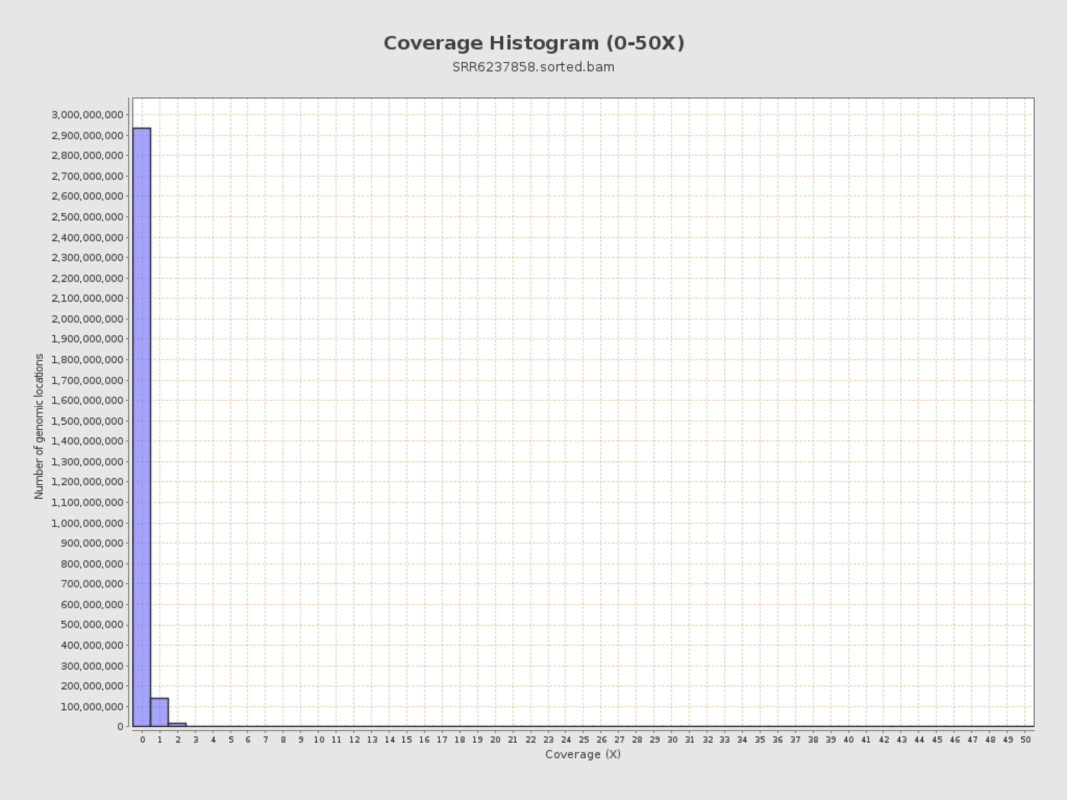
3. Results : Coverage across reference



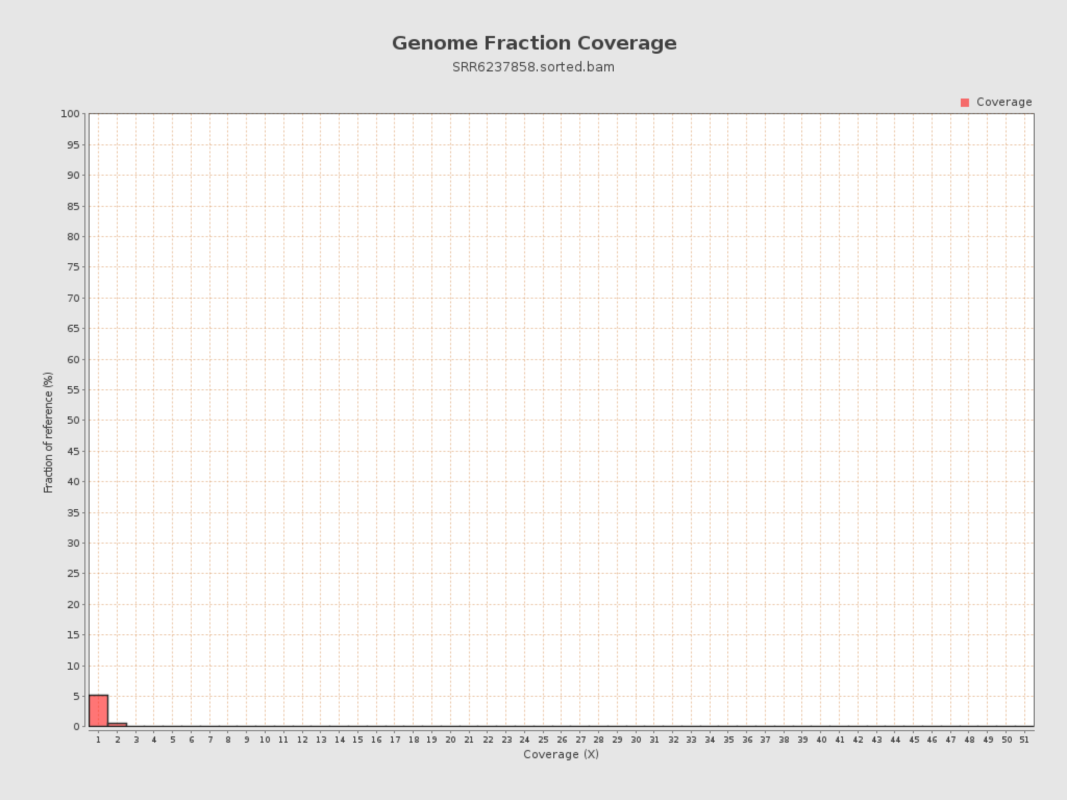
4. Results : Coverage Histogram



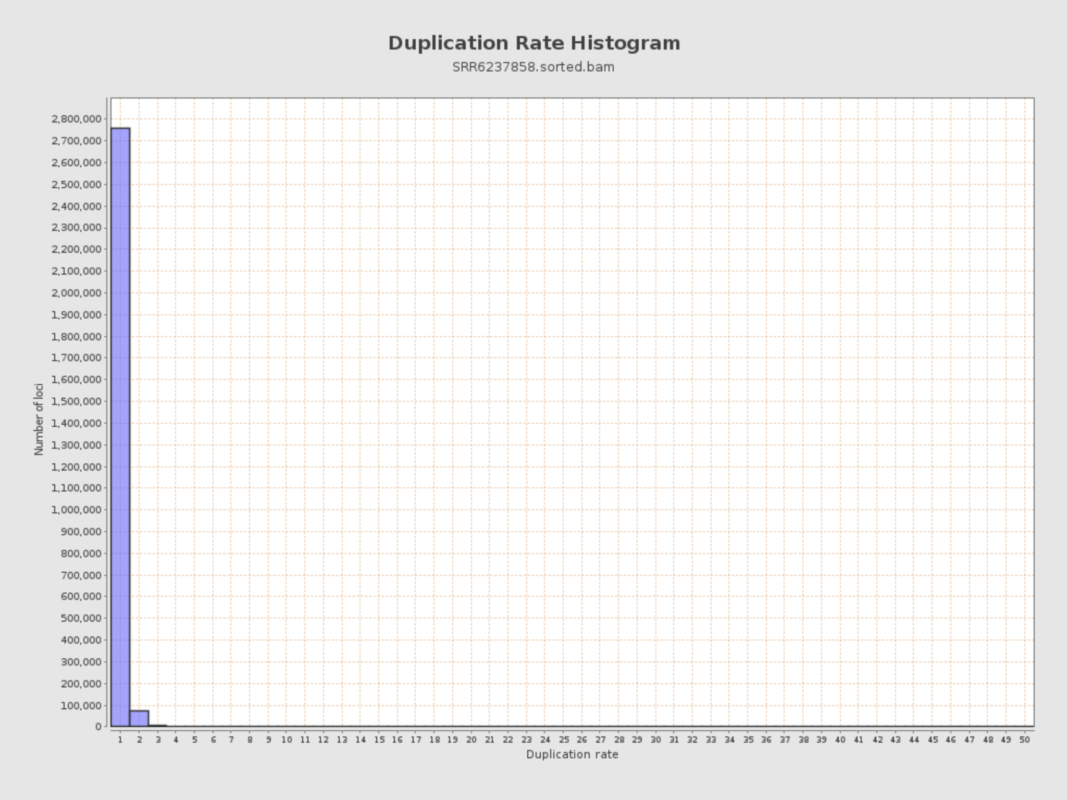
5. Results : Coverage Histogram (0-50X)



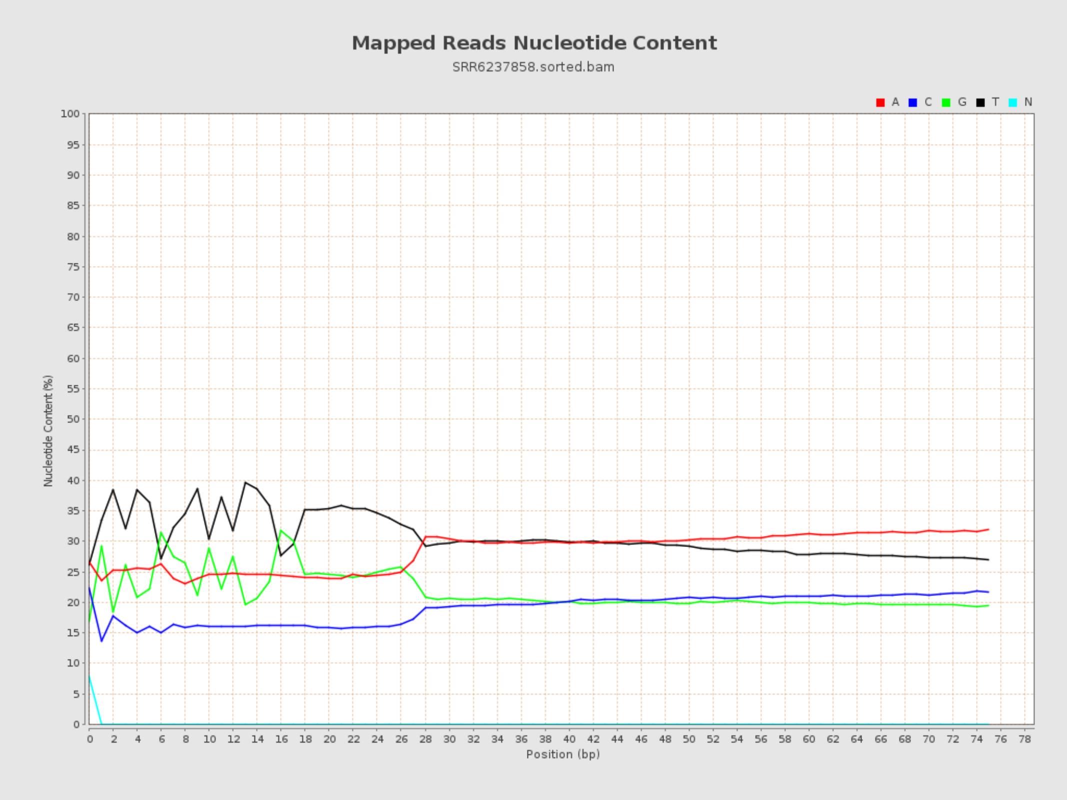
6. Results : Genome Fraction Coverage



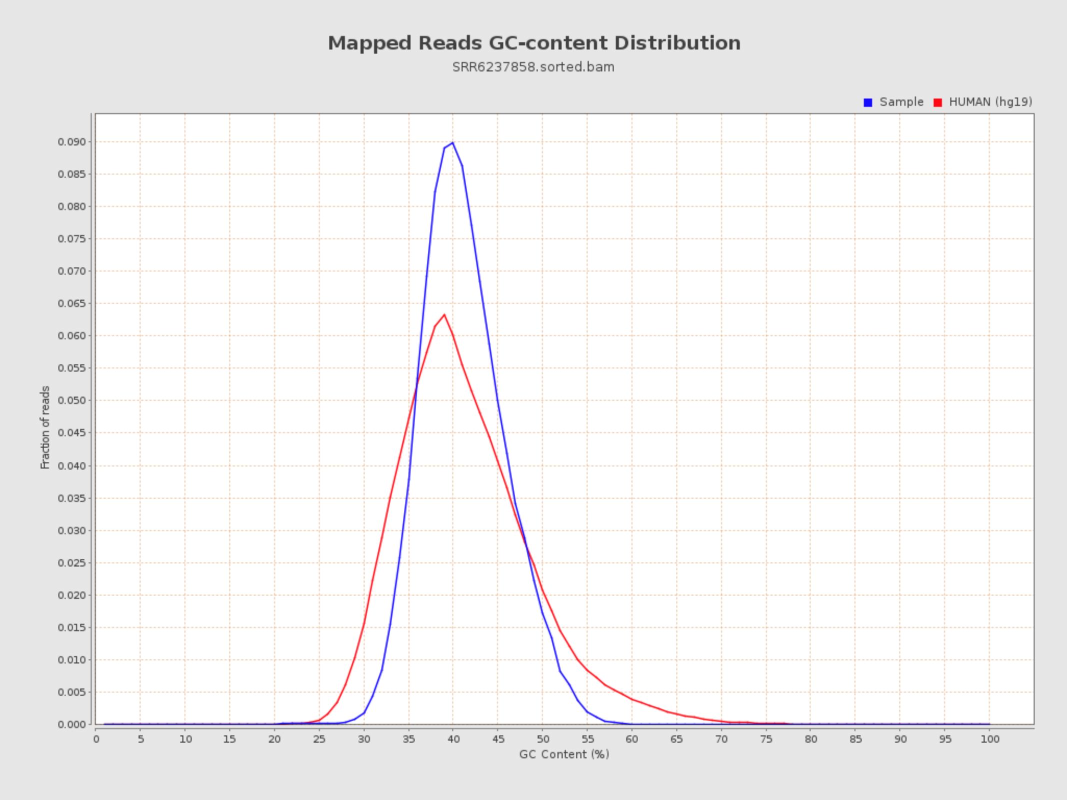
7. Results : Duplication Rate Histogram



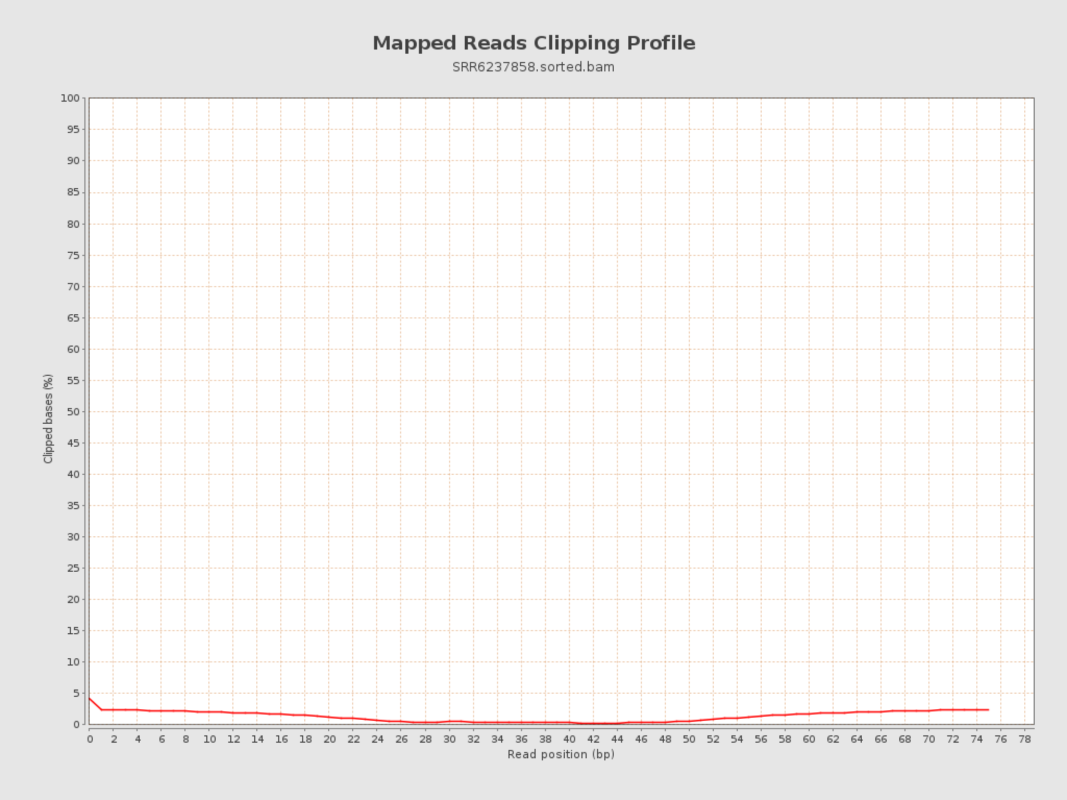
8. Results : Mapped Reads Nucleotide Content



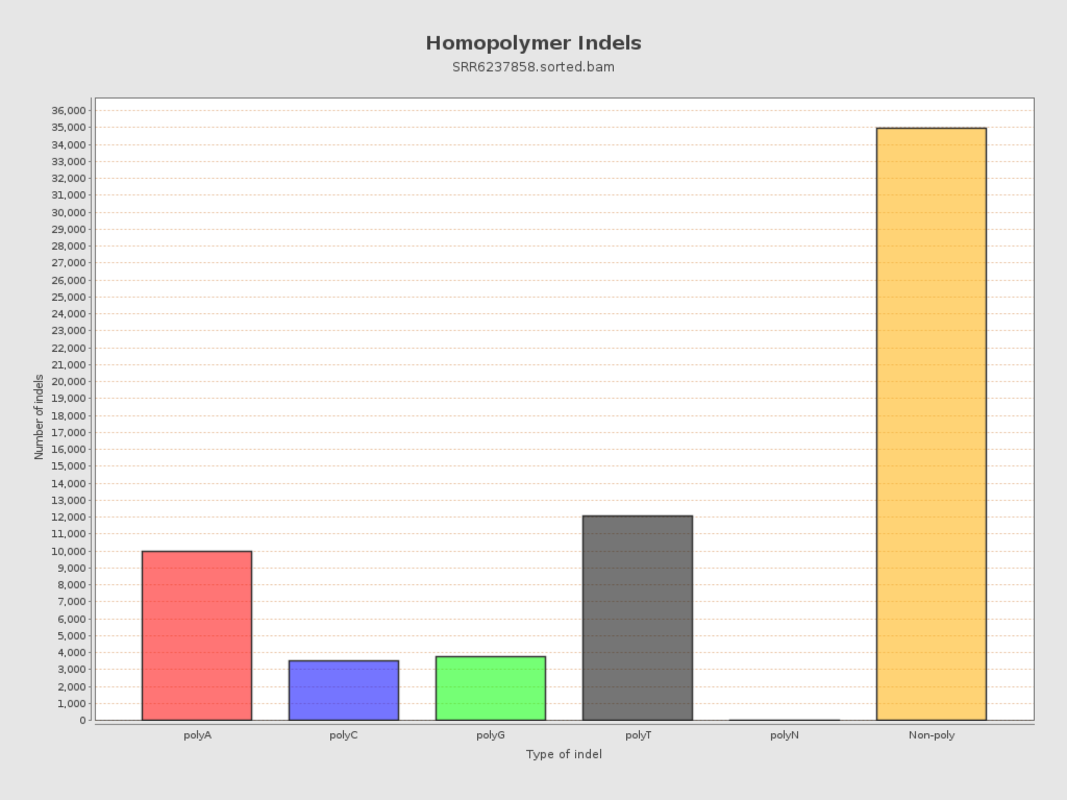
9. Results : Mapped Reads GC-content Distribution



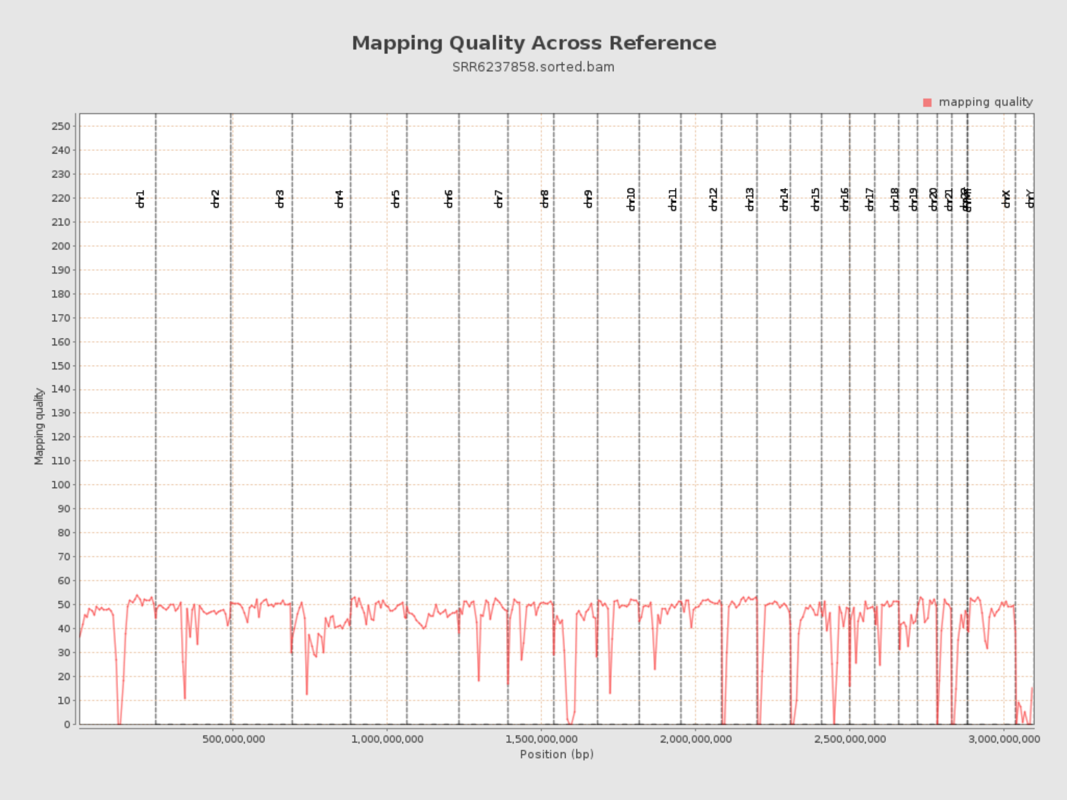
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram