Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:34:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237787.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_SRR6237787 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237787.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:34:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237787.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,870,549
Mapped reads	2,522,220 / 87.87%
Unmapped reads	348,329 / 12.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,068 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	158,179 / 5.51%
Duplication rate	4.46%
Clipped reads	1,408,822 / 49.08%

2.2. ACGT Content

Number/percentage of A's	42,684,928 / 26.53%
Number/percentage of C's	29,985,596 / 18.64%
Number/percentage of T's	50,434,043 / 31.35%
Number/percentage of G's	37,728,462 / 23.45%
Number/percentage of N's	39,112 / 0.02%
GC Percentage	42.09%

2.3. Coverage

Mean	0.052

Standard Deviation	0.5915

2.4. Mapping Quality

Mean Mapping Quality	43.66

2.5. Mismatches and indels

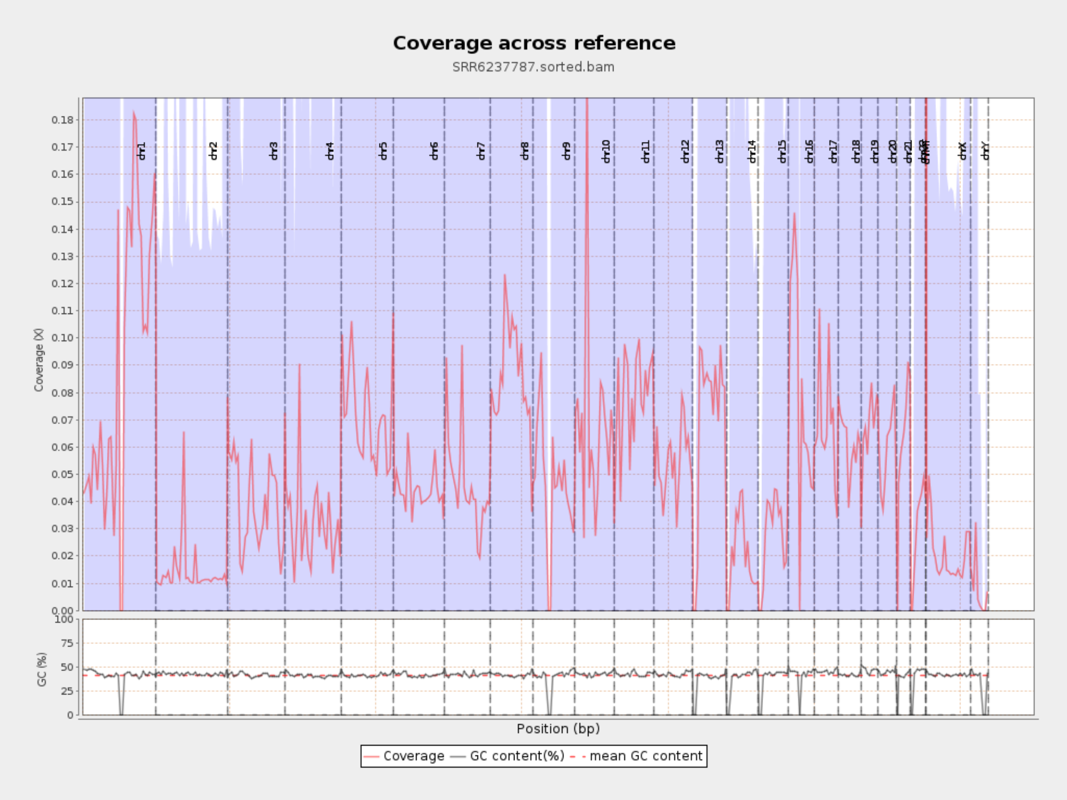
General error rate	0.9%
Mismatches	1,425,628
Insertions	13,133
Mapped reads with at least one insertion	0.52%
Deletions	59,594
Mapped reads with at least one deletion	2.33%
Homopolymer indels	44.89%

2.6. Chromosome stats

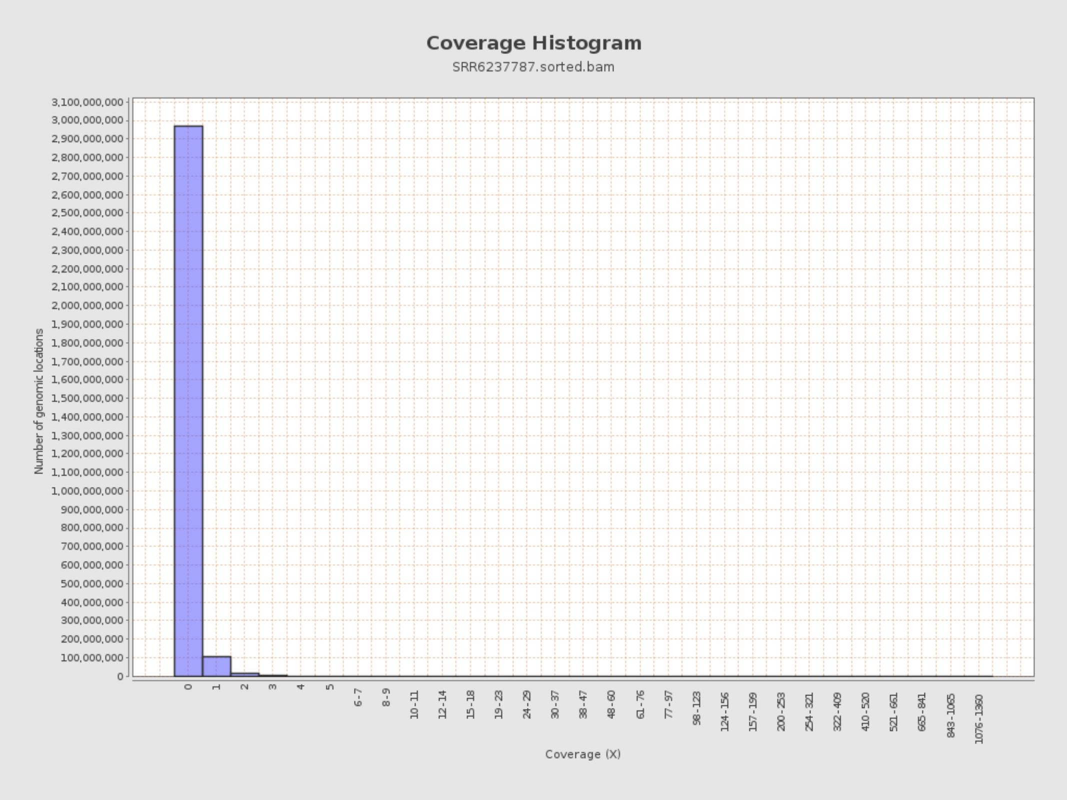
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21963497	0.0881	1.2546
chr2	243199373	3547207	0.0146	0.4499
chr3	198022430	7876334	0.0398	0.3131
chr4	191154276	6179589	0.0323	0.3039
chr5	180915260	13173845	0.0728	0.3297
chr6	171115067	7640431	0.0447	0.2891
chr7	159138663	7467840	0.0469	0.7088

chr8	146364022	12639888	0.0864	0.5024
chr9	141213431	6637933	0.047	0.4103
chr10	135534747	9231799	0.0681	1.2283
chr11	135006516	10484705	0.0777	0.4475
chr12	133851895	7378164	0.0551	0.2914
chr13	115169878	8139721	0.0707	0.3215
chr14	107349540	2204608	0.0205	0.2386
chr15	102531392	2748766	0.0268	0.1981
chr16	90354753	7057817	0.0781	0.4551
chr17	81195210	5640646	0.0695	0.5775
chr18	78077248	4824774	0.0618	0.6657
chr19	59128983	4040717	0.0683	0.9601
chr20	63025520	3750564	0.0595	0.3208
chr21	48129895	3012337	0.0626	0.3486
chr22	51304566	1501668	0.0293	0.2074
chrMT	16571	143835	8.6799	5.2825
chrX	155270560	3210721	0.0207	0.2282
chrY	59373566	475333	0.008	0.2507

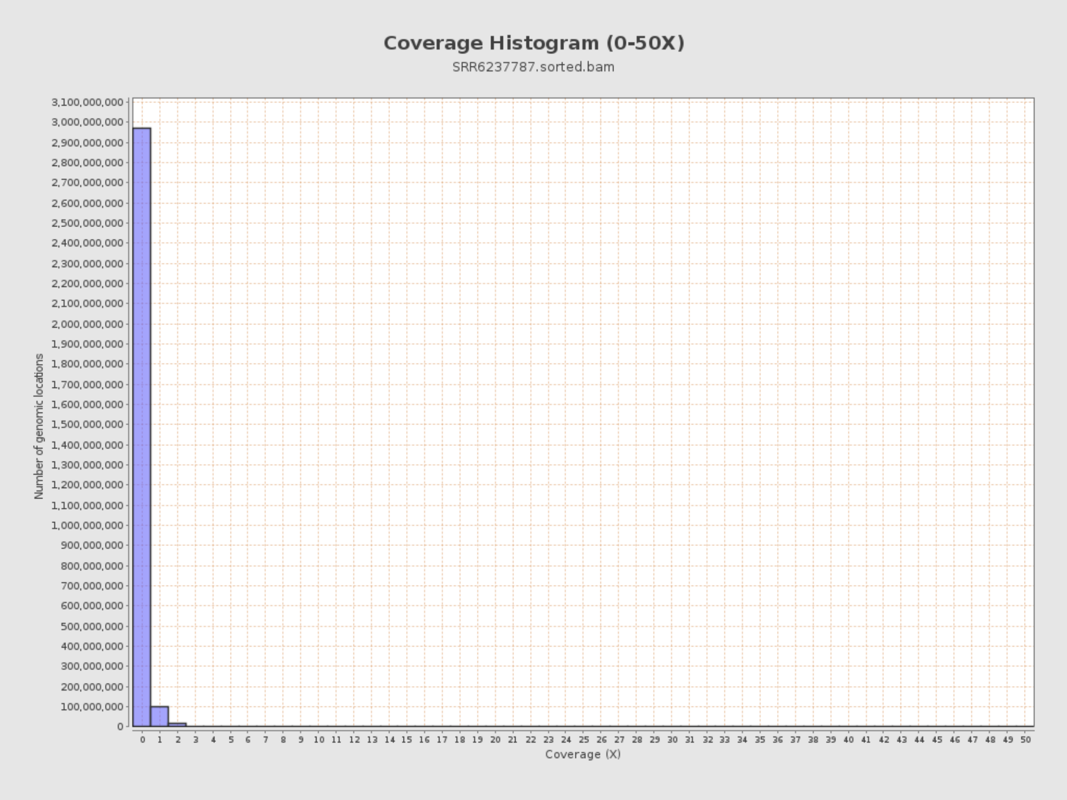
3. Results : Coverage across reference



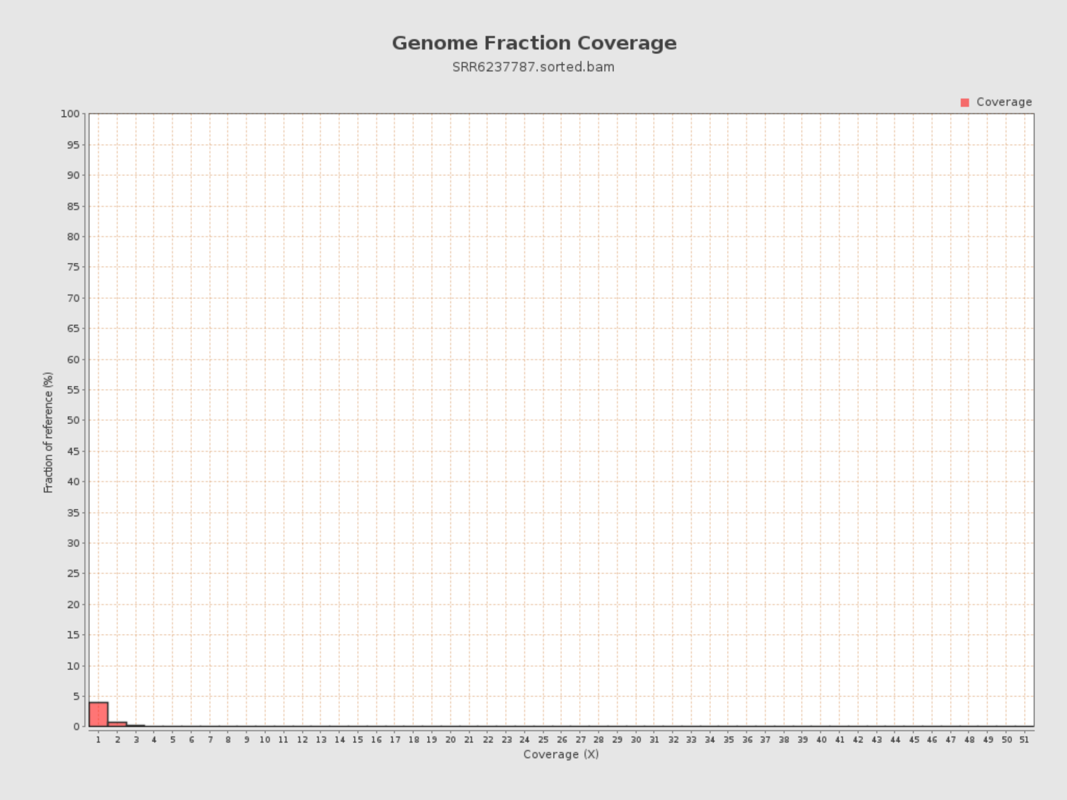
4. Results : Coverage Histogram



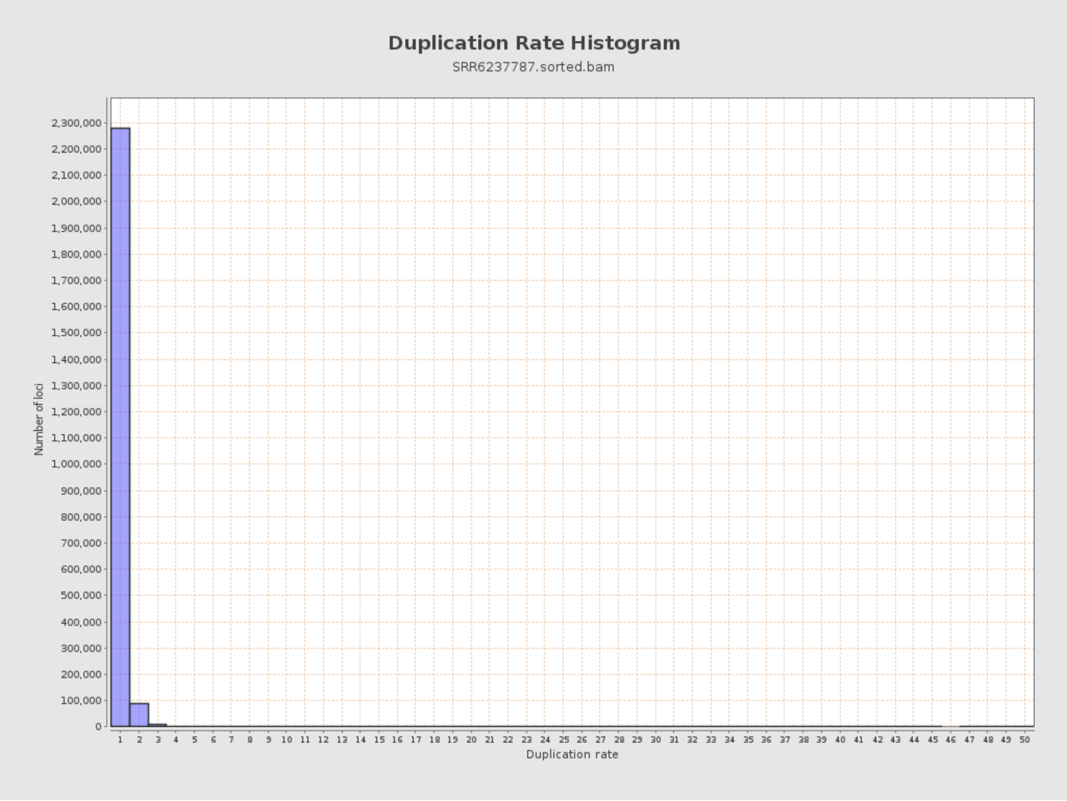
5. Results : Coverage Histogram (0-50X)



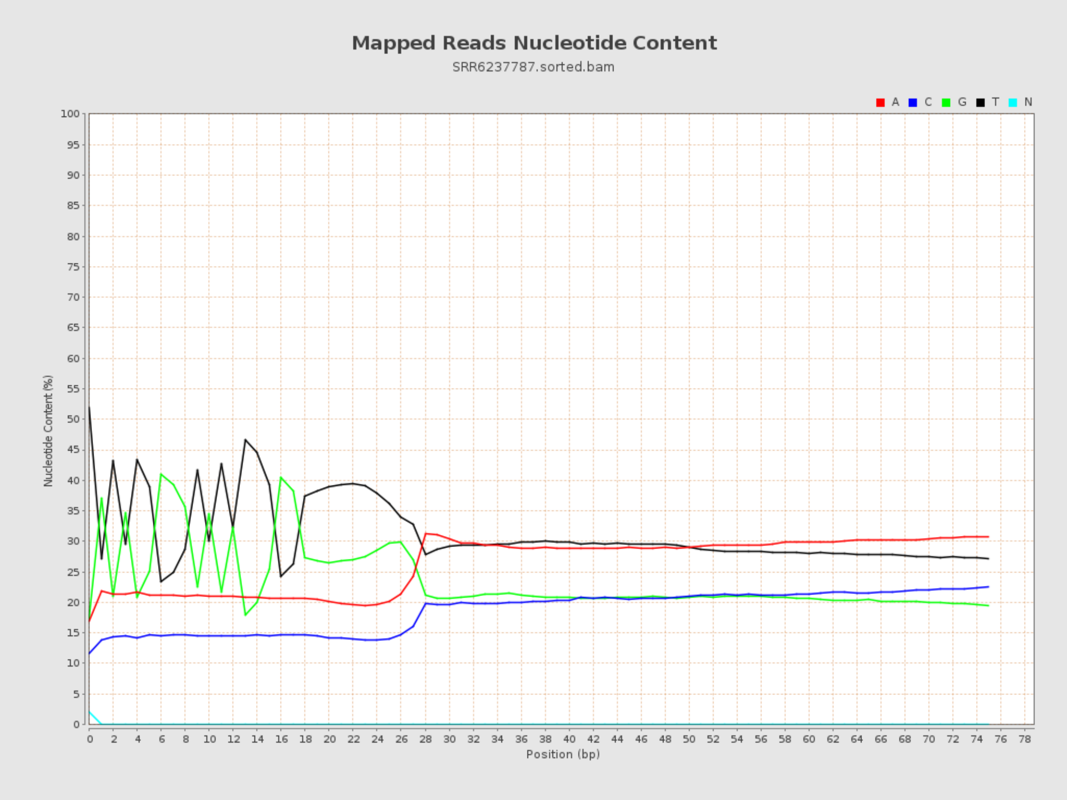
6. Results : Genome Fraction Coverage



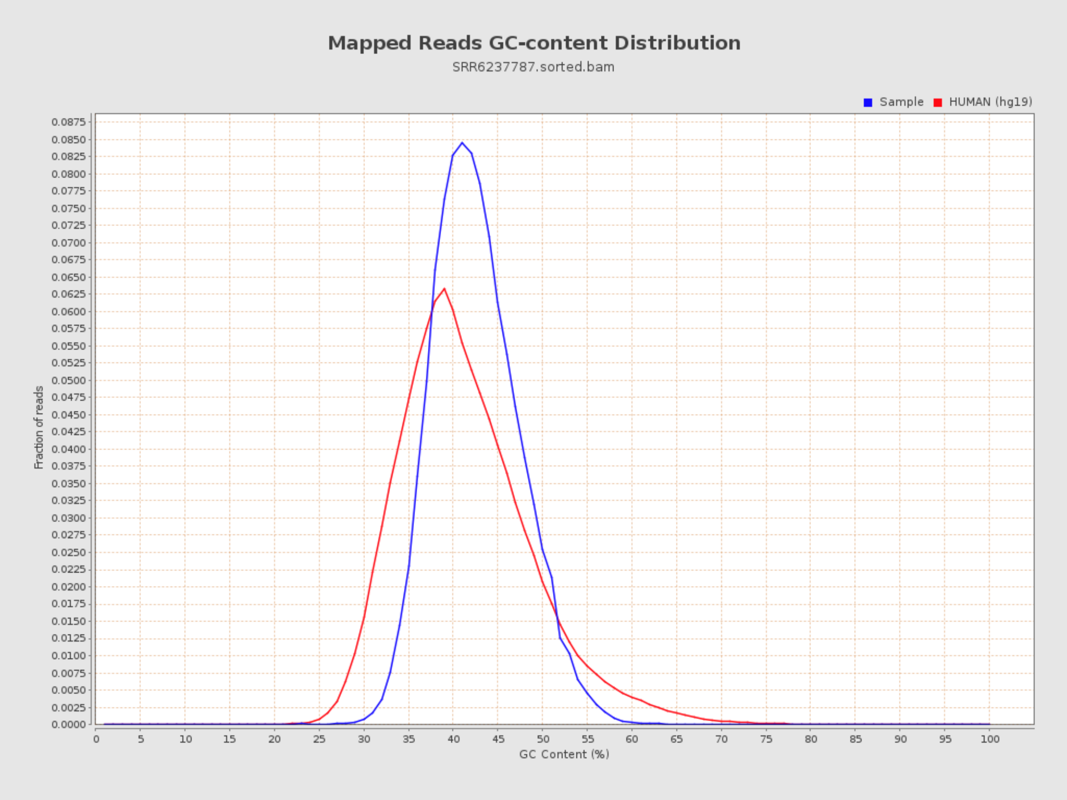
7. Results : Duplication Rate Histogram



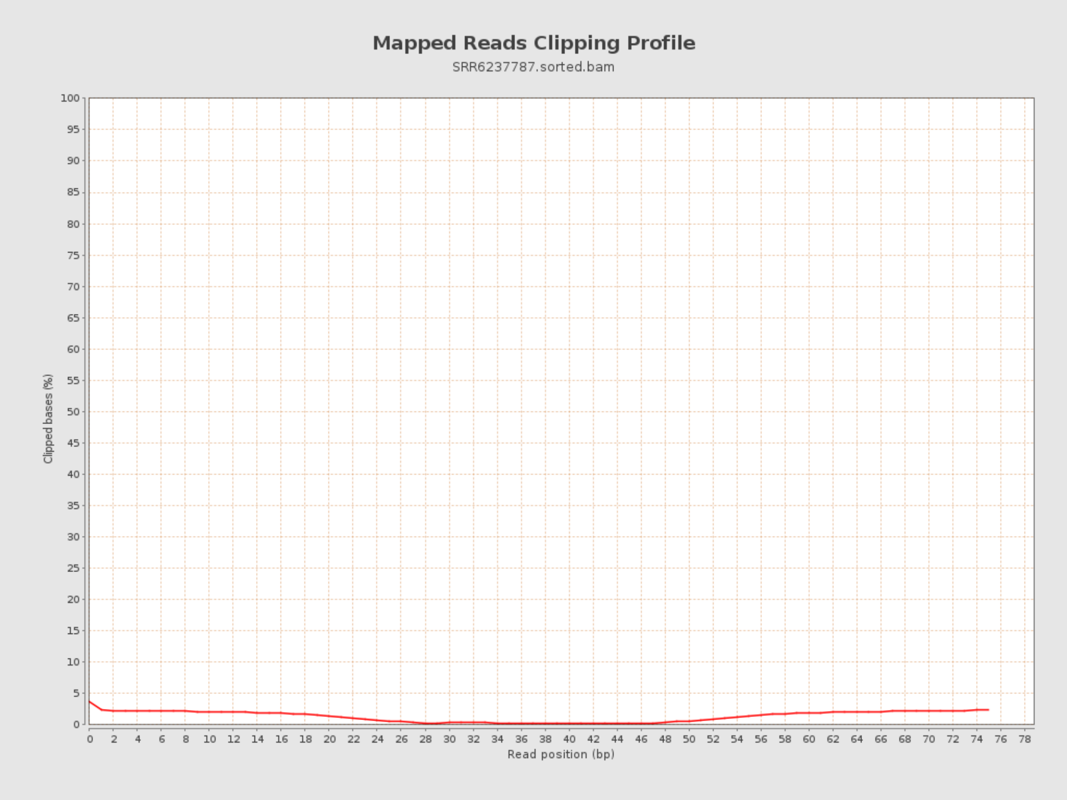
8. Results : Mapped Reads Nucleotide Content



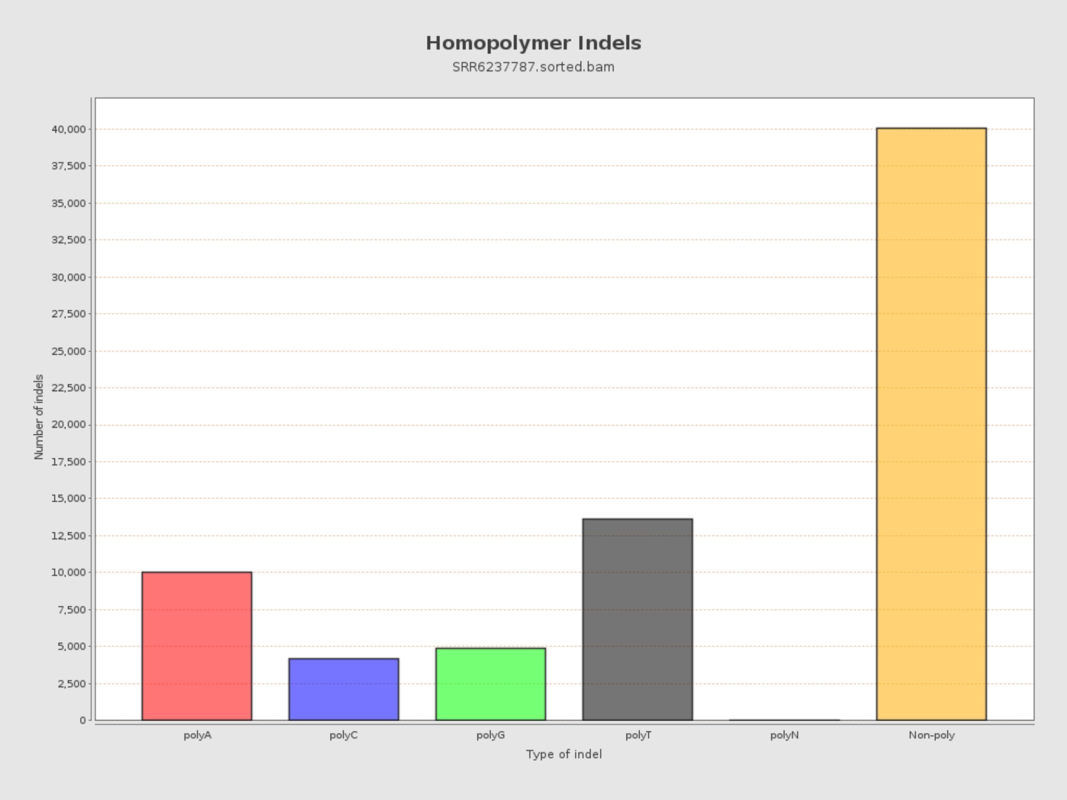
9. Results : Mapped Reads GC-content Distribution



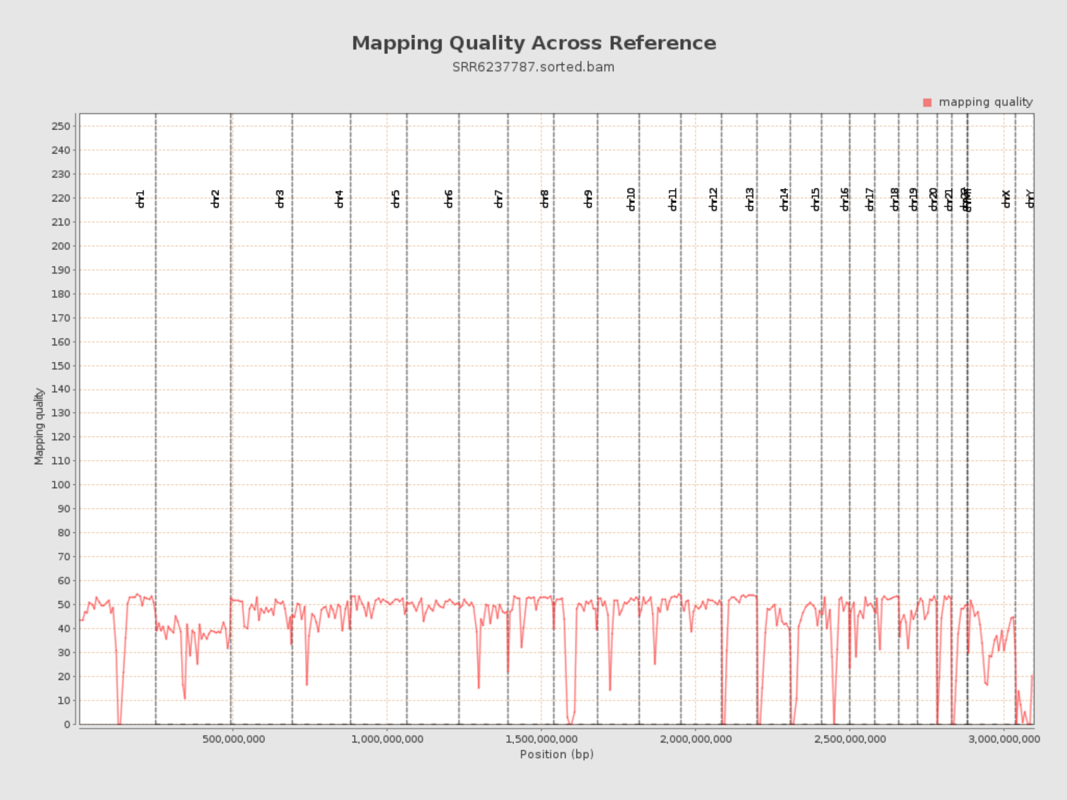
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram