Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:01:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237332.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_SRR6237332 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237332.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:01:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237332.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,310,853
Mapped reads	2,549,604 / 77.01%
Unmapped reads	761,249 / 22.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,279 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	795,790 / 24.04%
Duplication rate	22.34%
Clipped reads	1,887,144 / 57%

2.2. ACGT Content

Number/percentage of A's	38,986,734 / 25.83%
Number/percentage of C's	26,304,493 / 17.43%
Number/percentage of T's	50,359,487 / 33.37%
Number/percentage of G's	35,268,778 / 23.37%
Number/percentage of N's	15,168 / 0.01%
GC Percentage	40.79%

2.3. Coverage

Mean	0.0488

Standard Deviation	0.7992

2.4. Mapping Quality

Mean Mapping Quality	41.92

2.5. Mismatches and indels

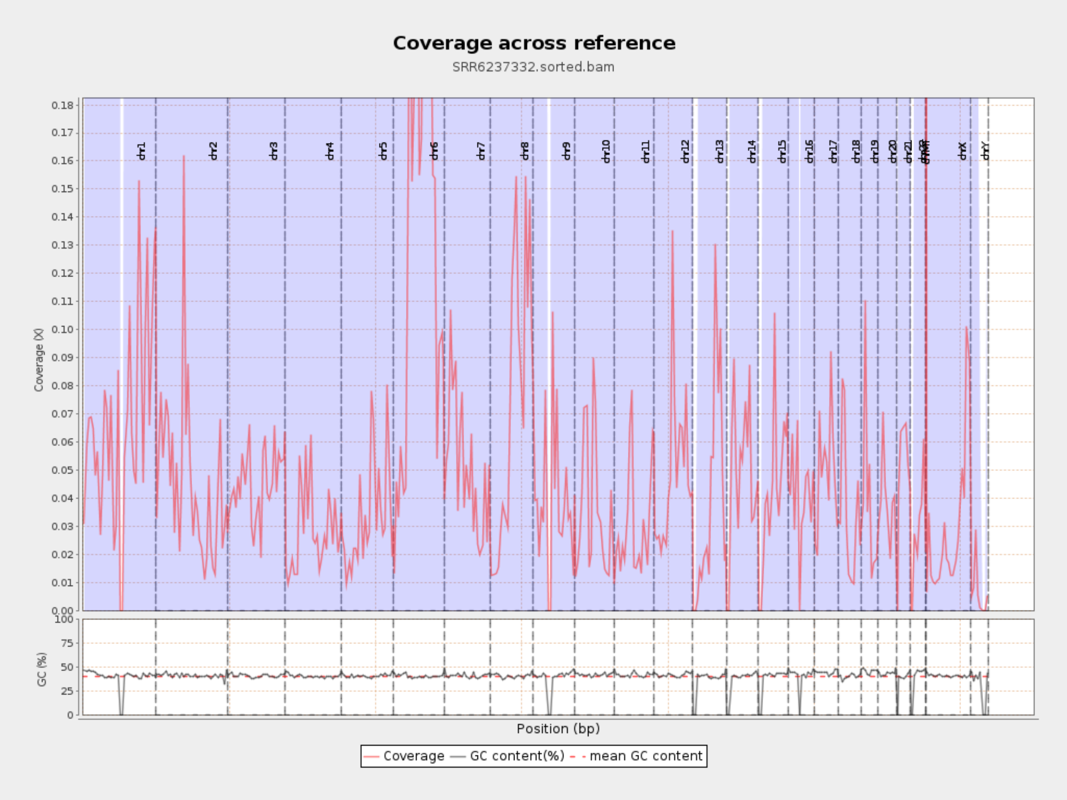
General error rate	0.74%
Mismatches	1,103,234
Insertions	10,209
Mapped reads with at least one insertion	0.4%
Deletions	62,184
Mapped reads with at least one deletion	2.4%
Homopolymer indels	40.35%

2.6. Chromosome stats

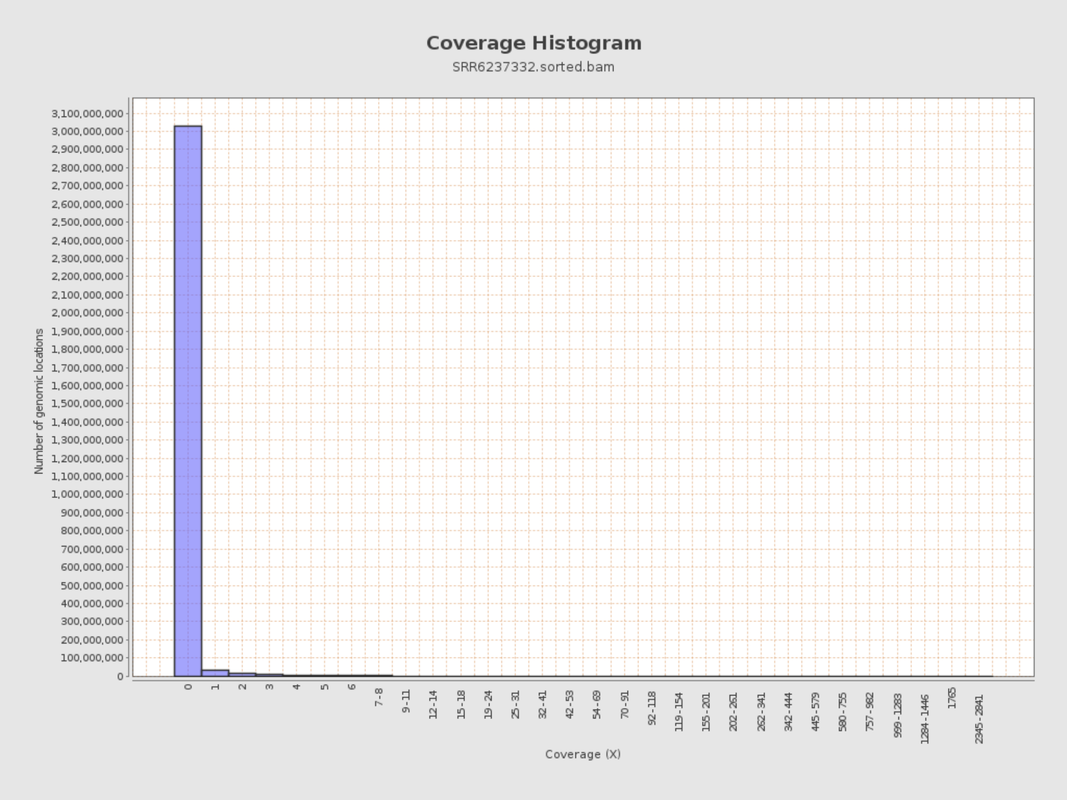
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16606893	0.0666	0.7505
chr2	243199373	11233264	0.0462	1.525
chr3	198022430	8902535	0.045	0.422
chr4	191154276	5444601	0.0285	0.361
chr5	180915260	5970078	0.033	0.3647
chr6	171115067	24805018	0.145	1.2531
chr7	159138663	8077582	0.0508	0.6593

chr8	146364022	10856230	0.0742	0.698
chr9	141213431	5495217	0.0389	0.7291
chr10	135534747	4849916	0.0358	0.4799
chr11	135006516	4088411	0.0303	0.5595
chr12	133851895	6582614	0.0492	0.4948
chr13	115169878	4440259	0.0386	0.479
chr14	107349540	5225516	0.0487	0.4934
chr15	102531392	4289640	0.0418	0.4379
chr16	90354753	3679573	0.0407	0.5046
chr17	81195210	4056805	0.05	0.4374
chr18	78077248	2790206	0.0357	2.2426
chr19	59128983	2324722	0.0393	0.7601
chr20	63025520	2489068	0.0395	0.4117
chr21	48129895	2460733	0.0511	0.4613
chr22	51304566	1436662	0.028	0.3131
chrMT	16571	15466	0.9333	1.8127
chrX	155270560	4518442	0.0291	0.4004
chrY	59373566	401211	0.0068	0.3132

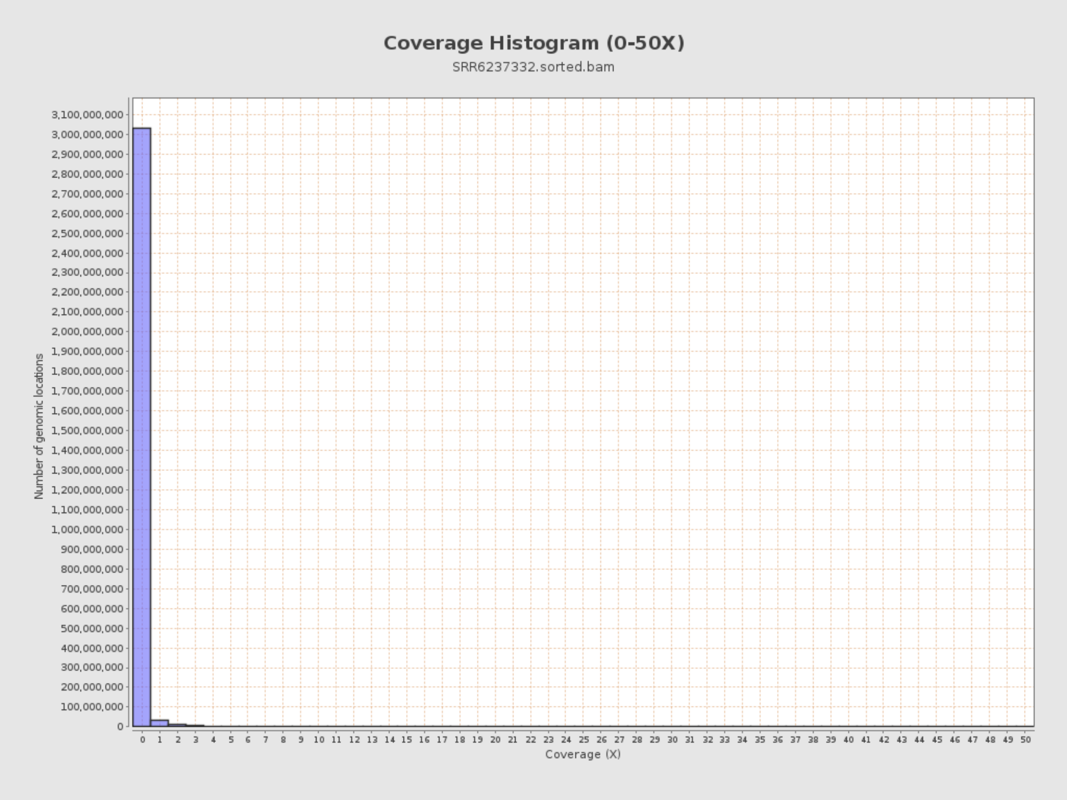
3. Results : Coverage across reference



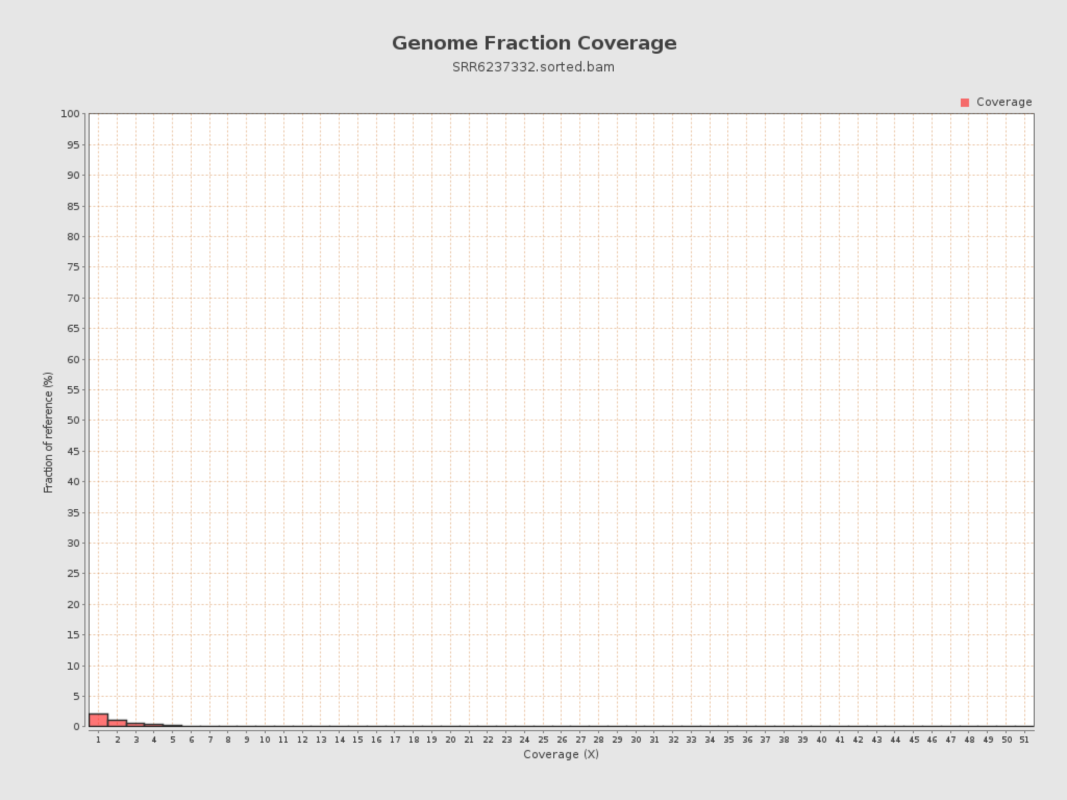
4. Results : Coverage Histogram



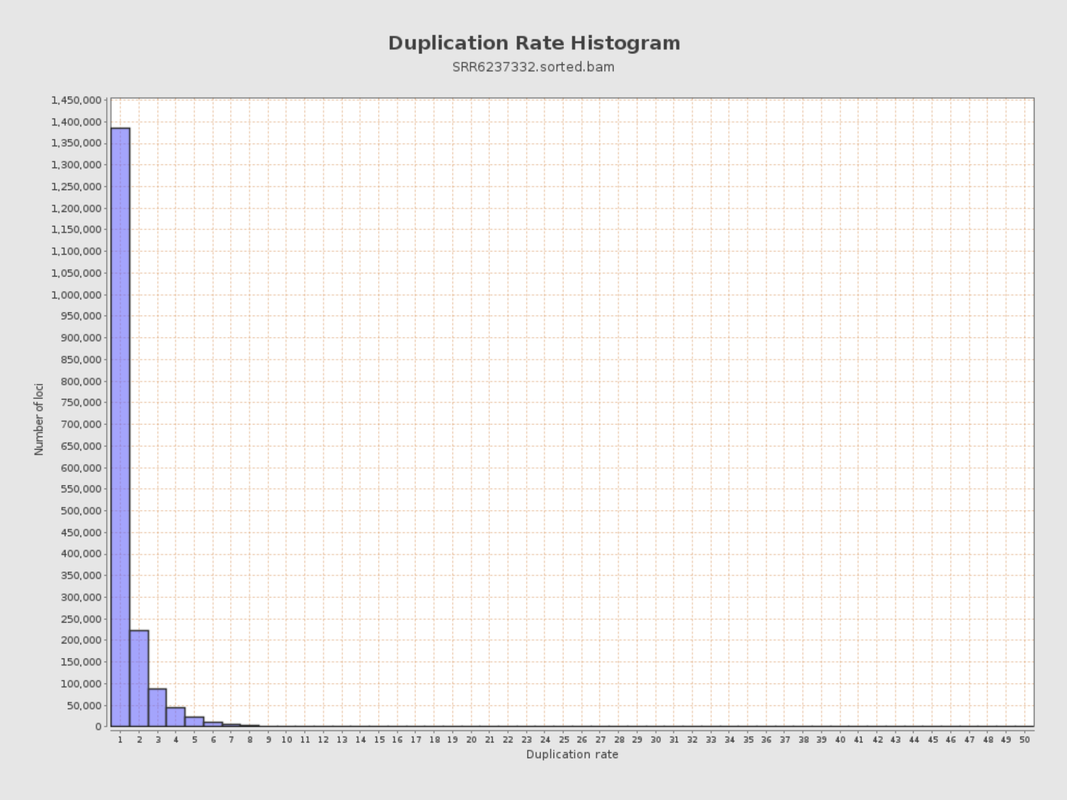
5. Results : Coverage Histogram (0-50X)



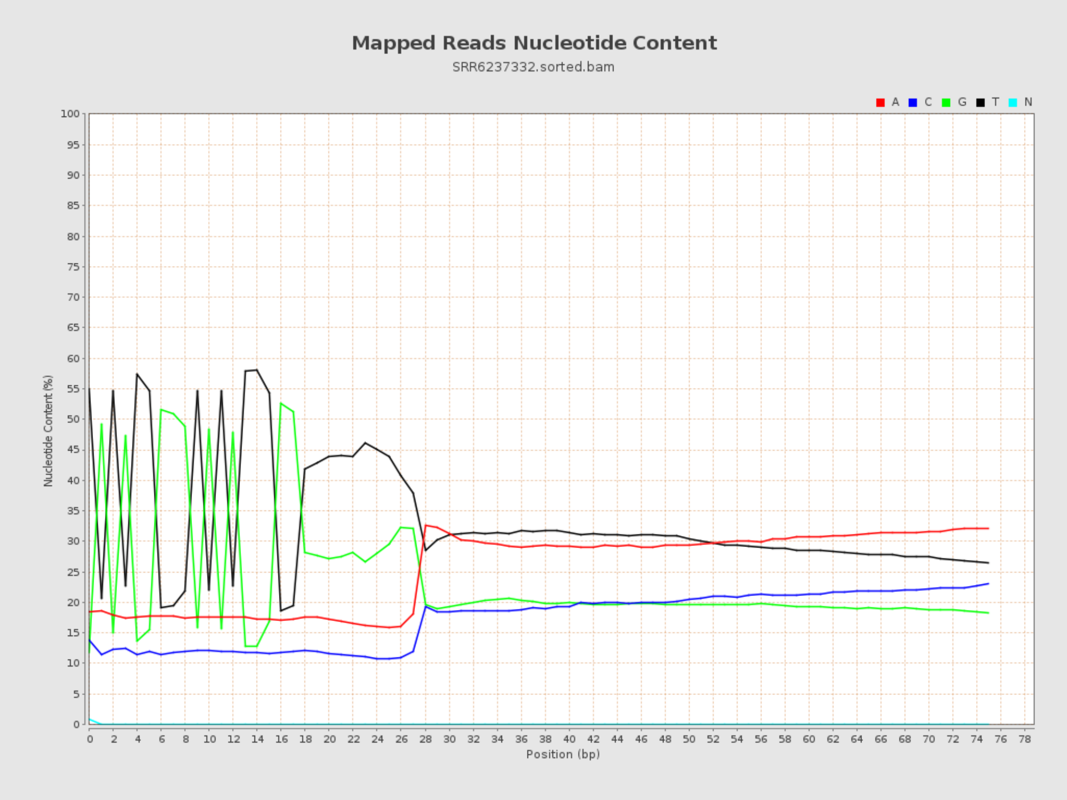
6. Results : Genome Fraction Coverage



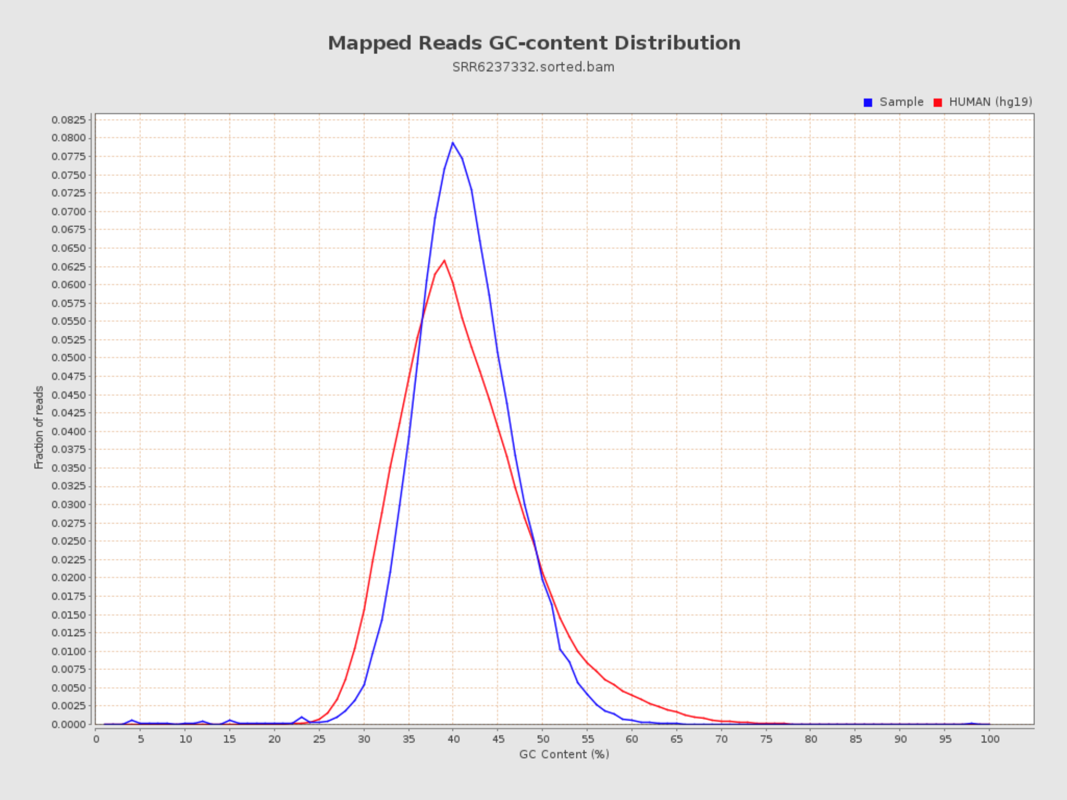
7. Results : Duplication Rate Histogram



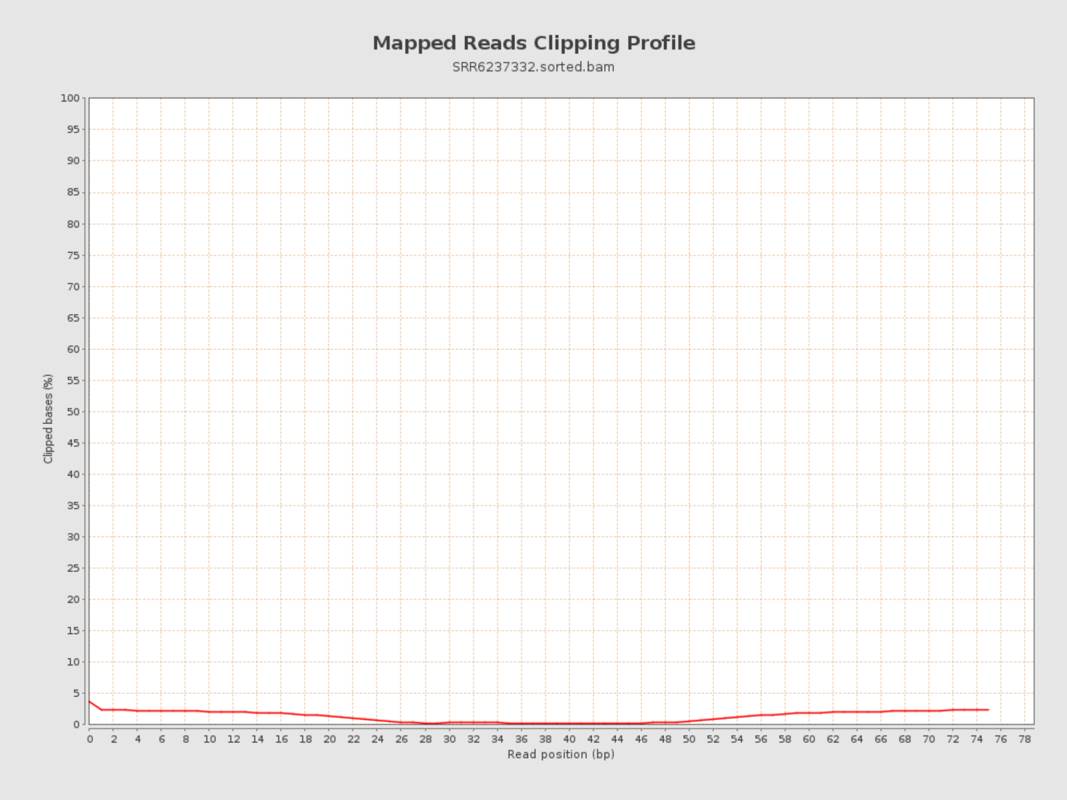
8. Results : Mapped Reads Nucleotide Content



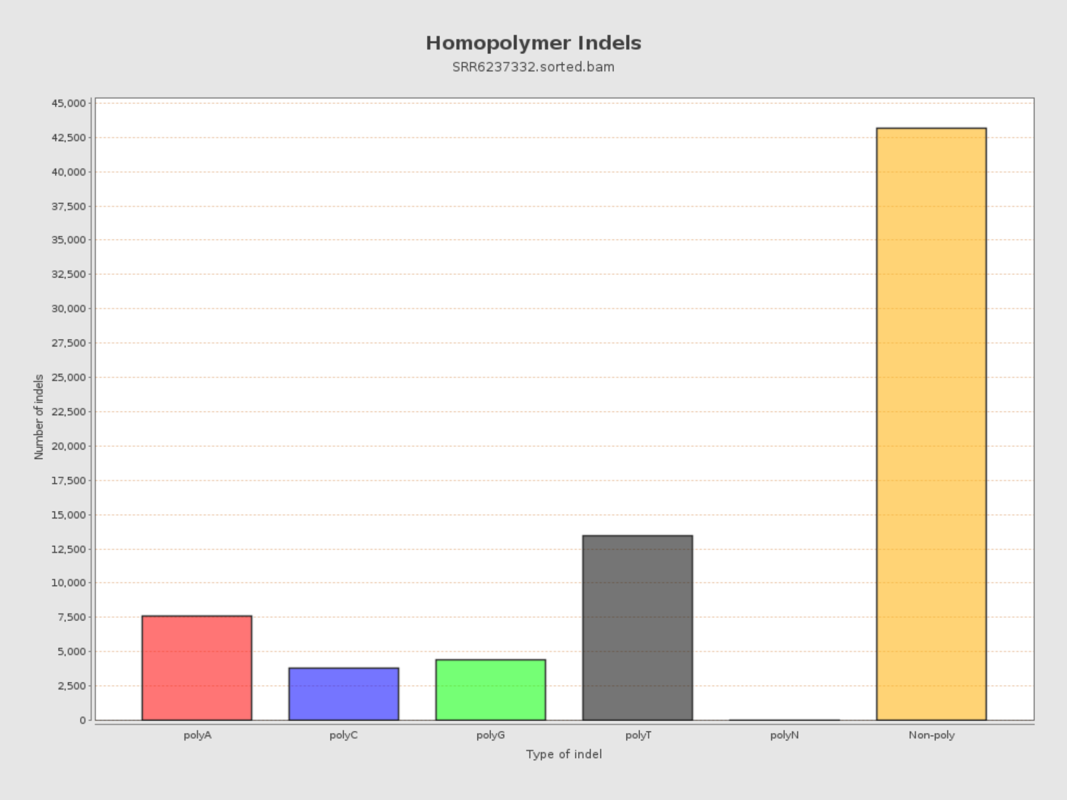
9. Results : Mapped Reads GC-content Distribution



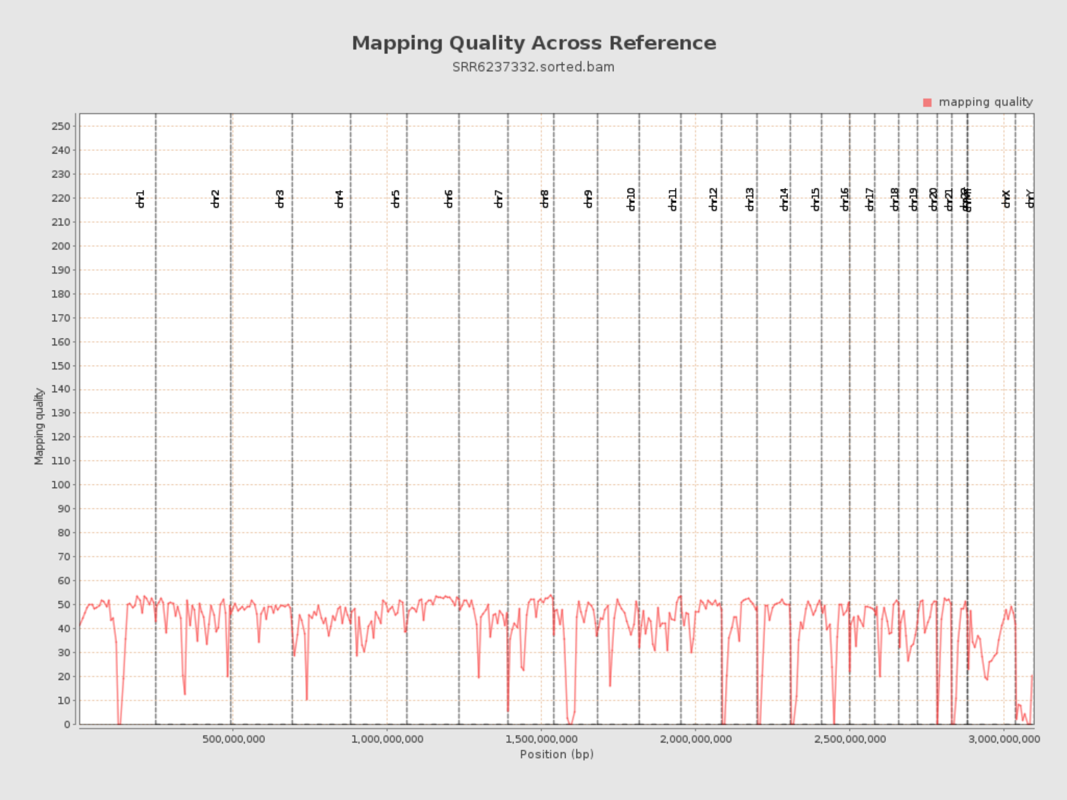
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram