Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:39:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237292.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_SRR6237292 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237292.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:39:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237292.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,503,472
Mapped reads	2,285,707 / 91.3%
Unmapped reads	217,765 / 8.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,161 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	96,535 / 3.86%
Duplication rate	3.35%
Clipped reads	832,480 / 33.25%

2.2. ACGT Content

Number/percentage of A's	44,239,561 / 28.27%
Number/percentage of C's	29,114,470 / 18.6%
Number/percentage of T's	49,414,958 / 31.58%
Number/percentage of G's	33,726,830 / 21.55%
Number/percentage of N's	2,549 / 0%
GC Percentage	40.15%

2.3. Coverage

Mean	0.0506

Standard Deviation	0.4064

2.4. Mapping Quality

Mean Mapping Quality	46.16

2.5. Mismatches and indels

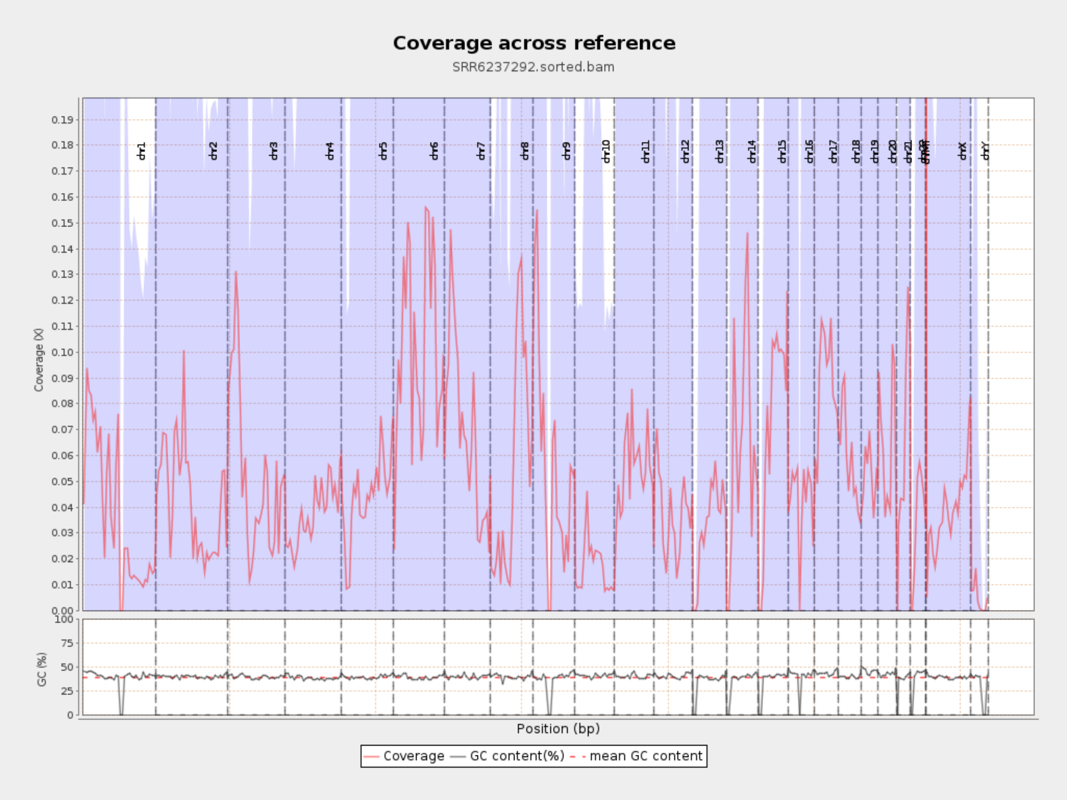
General error rate	0.73%
Mismatches	1,125,008
Insertions	11,534
Mapped reads with at least one insertion	0.5%
Deletions	36,016
Mapped reads with at least one deletion	1.56%
Homopolymer indels	49.18%

2.6. Chromosome stats

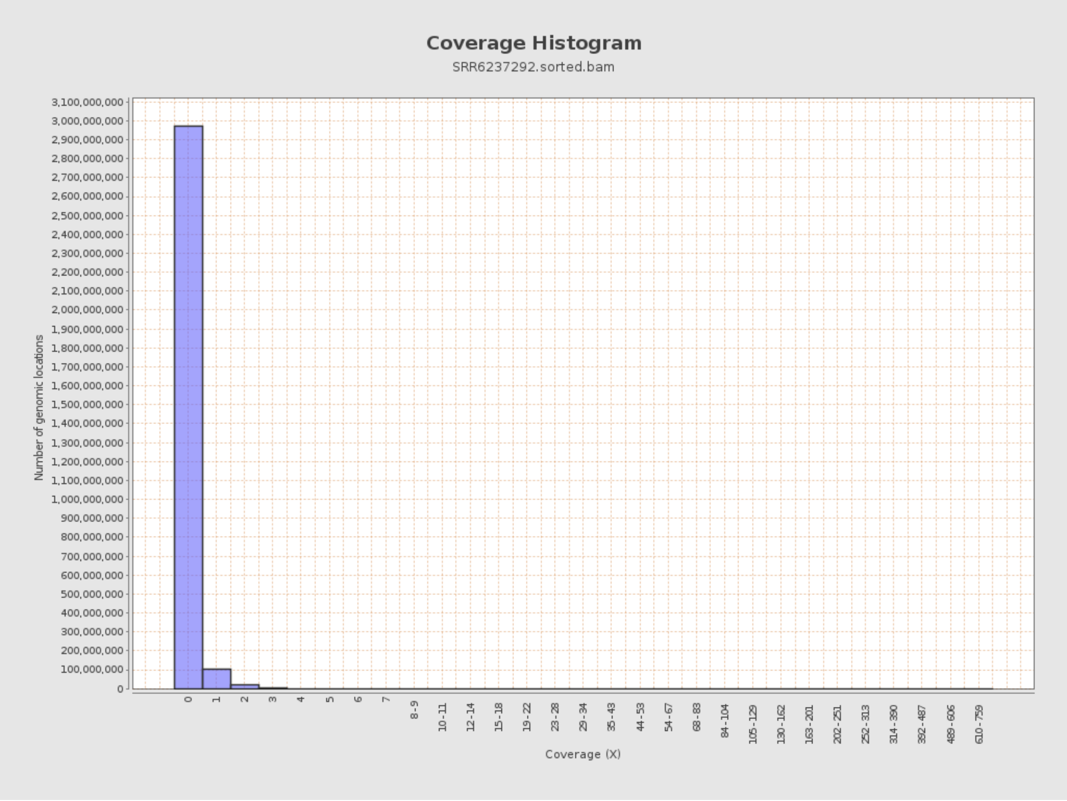
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9083195	0.0364	0.6473
chr2	243199373	10401413	0.0428	0.4788
chr3	198022430	10417996	0.0526	0.273
chr4	191154276	7153014	0.0374	0.2443
chr5	180915260	8165144	0.0451	0.2565
chr6	171115067	17455116	0.102	0.4629
chr7	159138663	10984319	0.069	0.5104

chr8	146364022	7972642	0.0545	0.5403
chr9	141213431	7876398	0.0558	0.4523
chr10	135534747	2289084	0.0169	0.2332
chr11	135006516	7319662	0.0542	0.361
chr12	133851895	5153991	0.0385	0.2408
chr13	115169878	3817886	0.0332	0.2147
chr14	107349540	6947567	0.0647	0.3238
chr15	102531392	7324329	0.0714	0.3224
chr16	90354753	3773821	0.0418	0.2689
chr17	81195210	7199642	0.0887	0.3807
chr18	78077248	4621996	0.0592	0.7649
chr19	59128983	3138648	0.0531	0.4631
chr20	63025520	4212957	0.0668	0.3124
chr21	48129895	3146584	0.0654	0.3289
chr22	51304566	1776284	0.0346	0.2169
chrMT	16571	52128	3.1457	2.6035
chrX	155270560	5980537	0.0385	0.2569
chrY	59373566	297597	0.005	0.1375

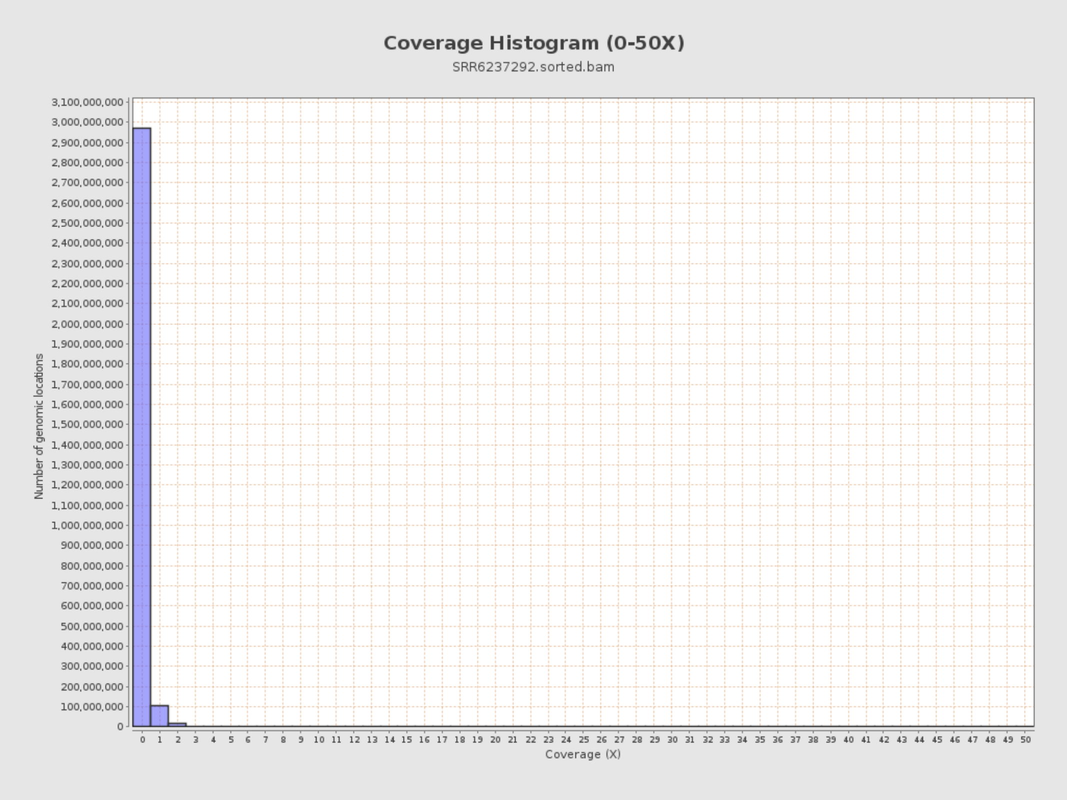
3. Results : Coverage across reference



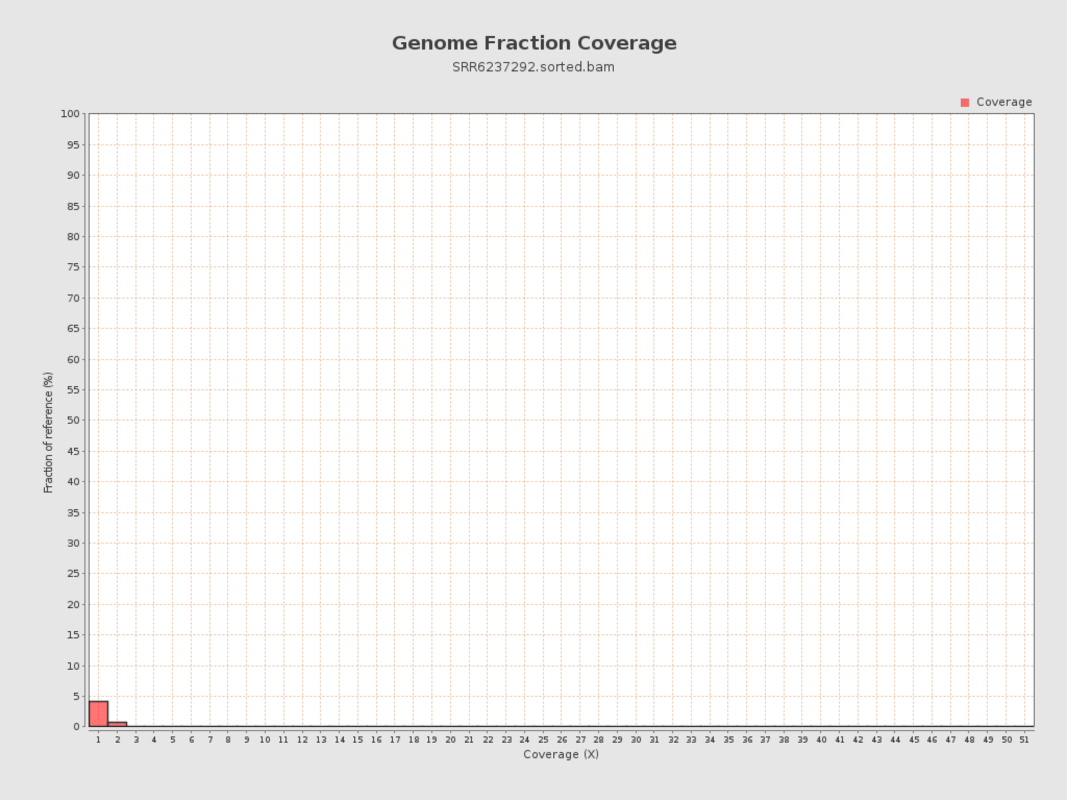
4. Results : Coverage Histogram



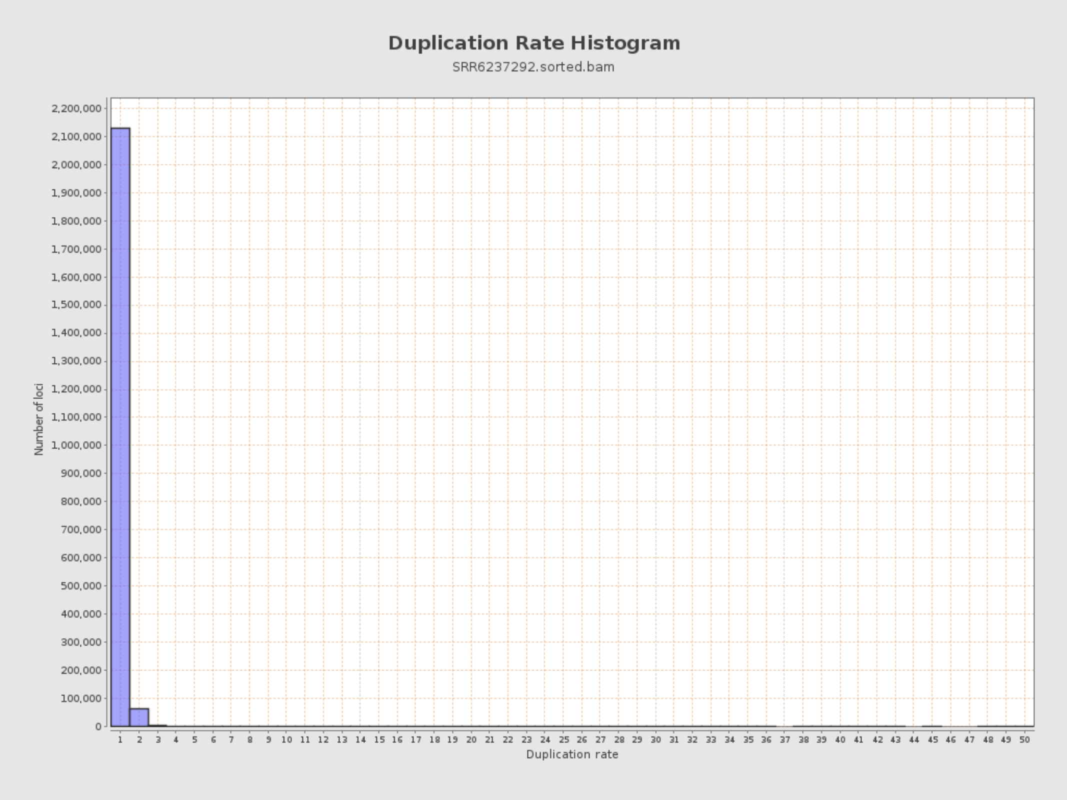
5. Results : Coverage Histogram (0-50X)



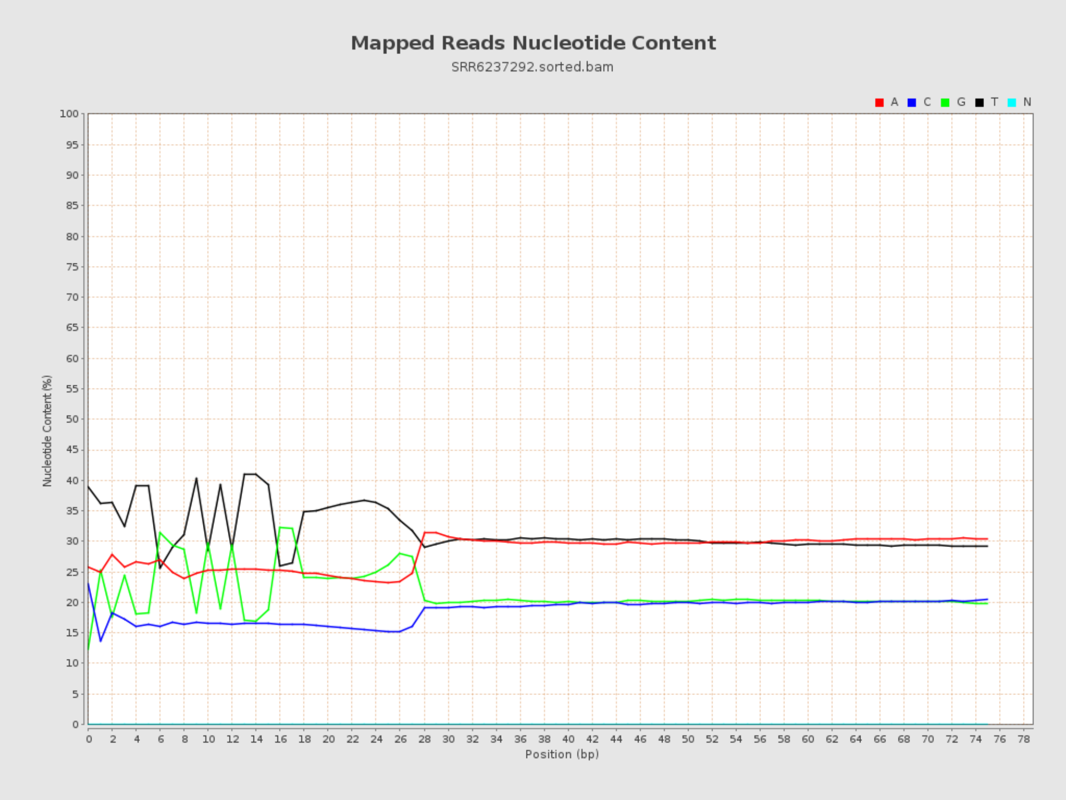
6. Results : Genome Fraction Coverage



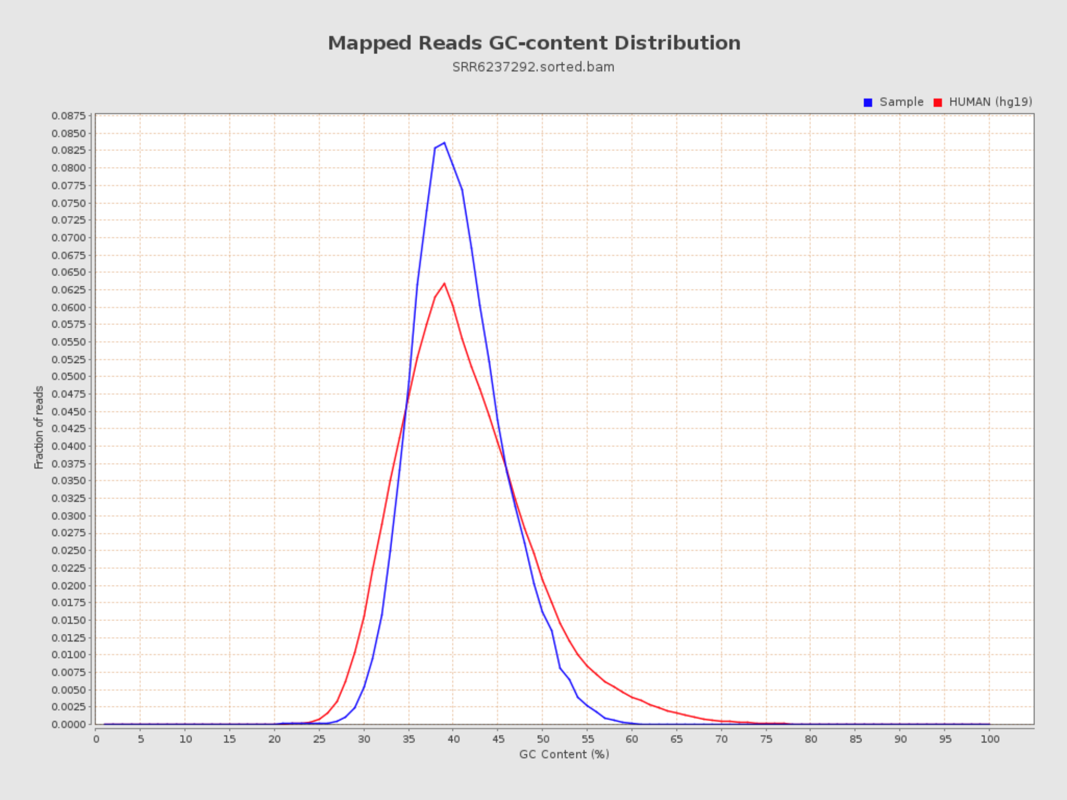
7. Results : Duplication Rate Histogram



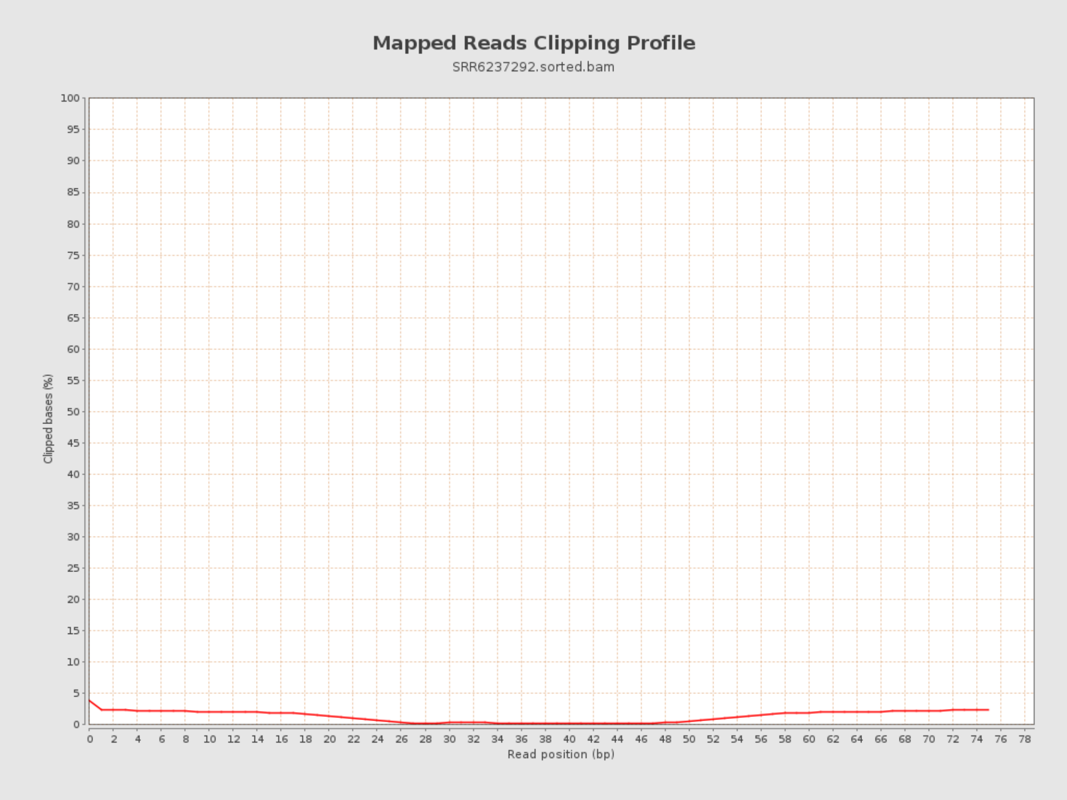
8. Results : Mapped Reads Nucleotide Content



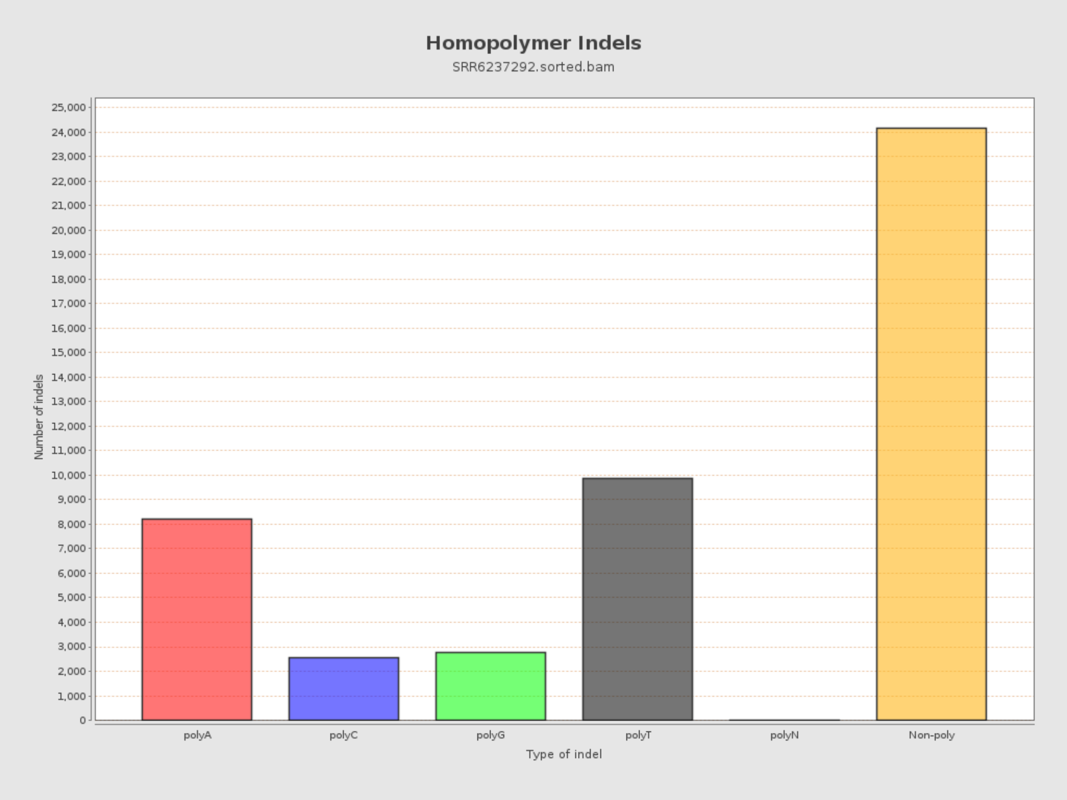
9. Results : Mapped Reads GC-content Distribution



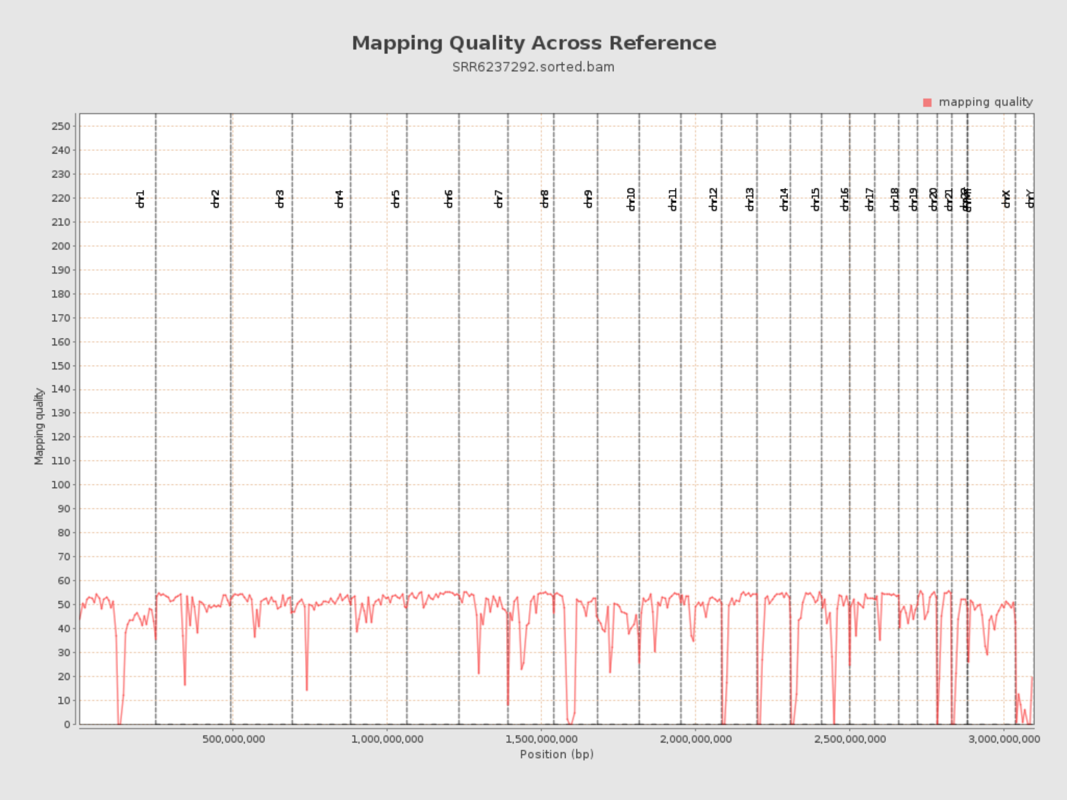
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram