Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:19:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237584.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_SRR6237584 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237584.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:19:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237584.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,918,513
Mapped reads	1,557,287 / 81.17%
Unmapped reads	361,226 / 18.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,798 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	70,377 / 3.67%
Duplication rate	3.11%
Clipped reads	952,369 / 49.64%

2.2. ACGT Content

Number/percentage of A's	25,327,968 / 25.78%
Number/percentage of C's	18,912,127 / 19.25%
Number/percentage of T's	29,338,044 / 29.87%
Number/percentage of G's	24,634,420 / 25.08%
Number/percentage of N's	17,546 / 0.02%
GC Percentage	44.33%

2.3. Coverage

Mean	0.0317

Standard Deviation	0.2978

2.4. Mapping Quality

Mean Mapping Quality	39.77

2.5. Mismatches and indels

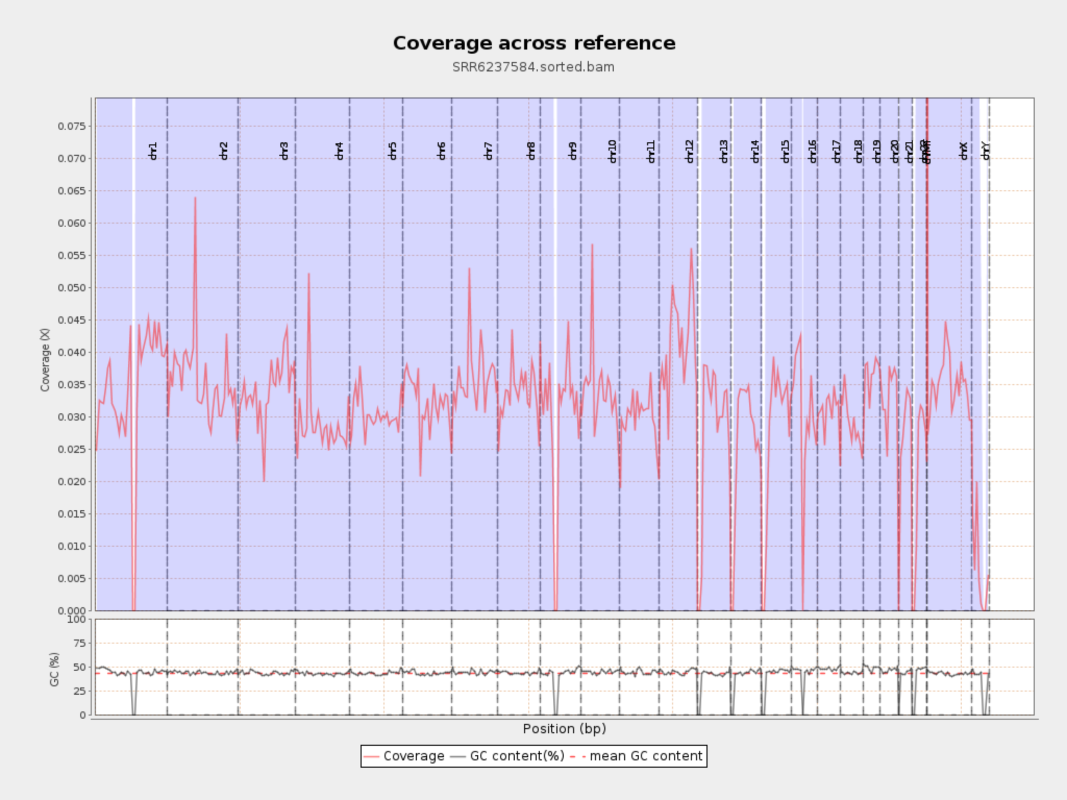
General error rate	0.94%
Mismatches	908,873
Insertions	9,247
Mapped reads with at least one insertion	0.59%
Deletions	33,190
Mapped reads with at least one deletion	2.1%
Homopolymer indels	45.58%

2.6. Chromosome stats

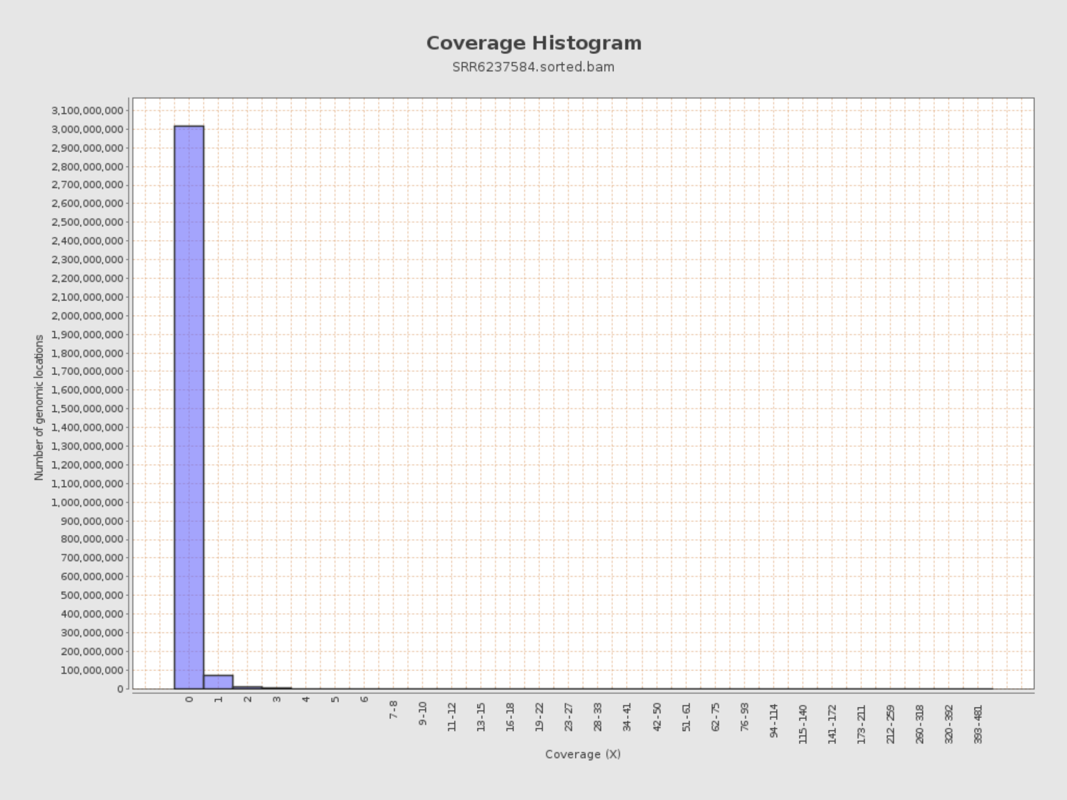
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8505796	0.0341	0.3957
chr2	243199373	8667144	0.0356	0.4203
chr3	198022430	6744974	0.0341	0.2287
chr4	191154276	5513639	0.0288	0.236
chr5	180915260	5524683	0.0305	0.21
chr6	171115067	5512337	0.0322	0.2422
chr7	159138663	5761431	0.0362	0.4224

chr8	146364022	4911137	0.0336	0.2739
chr9	141213431	4196781	0.0297	0.3054
chr10	135534747	4629925	0.0342	0.3202
chr11	135006516	4084055	0.0303	0.3086
chr12	133851895	5538734	0.0414	0.2613
chr13	115169878	3166949	0.0275	0.2071
chr14	107349540	2753650	0.0257	0.2319
chr15	102531392	2775348	0.0271	0.2101
chr16	90354753	2723435	0.0301	0.2453
chr17	81195210	2513072	0.031	0.2352
chr18	78077248	2275457	0.0291	0.4231
chr19	59128983	2152226	0.0364	0.3324
chr20	63025520	2081793	0.033	0.2278
chr21	48129895	1290951	0.0268	0.233
chr22	51304566	1050799	0.0205	0.1789
chrMT	16571	85951	5.1868	4.3677
chrX	155270560	5456946	0.0351	0.2462
chrY	59373566	367344	0.0062	0.1617

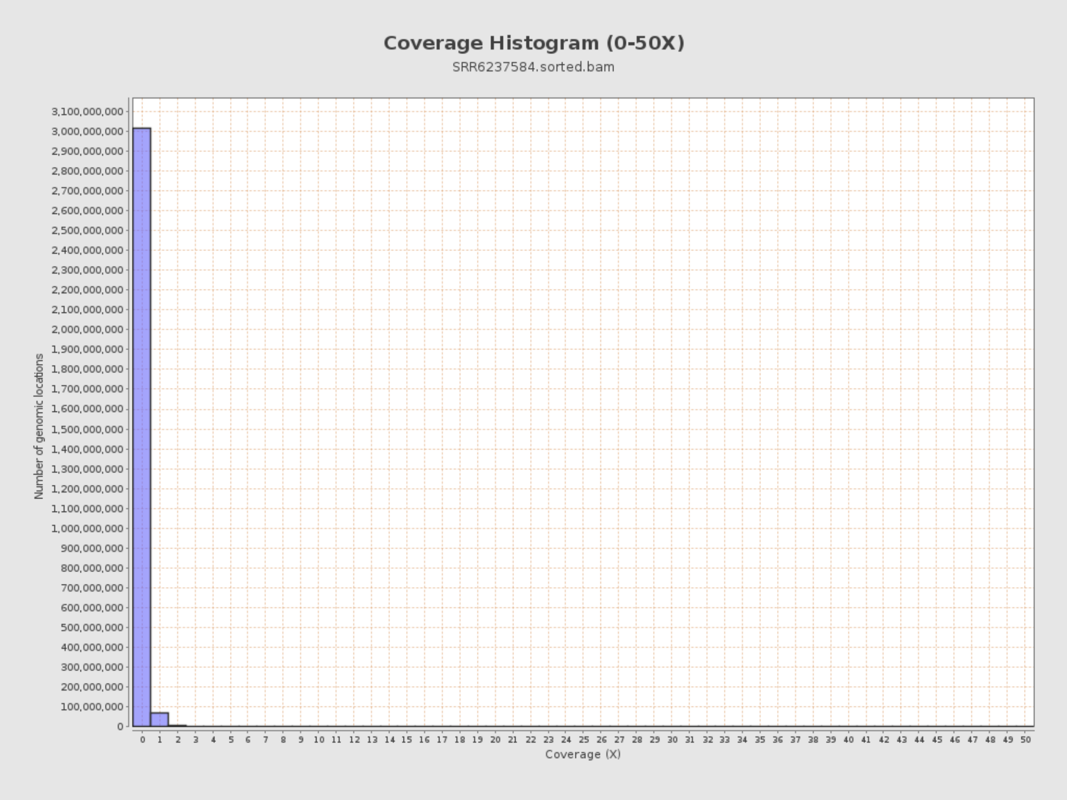
3. Results : Coverage across reference



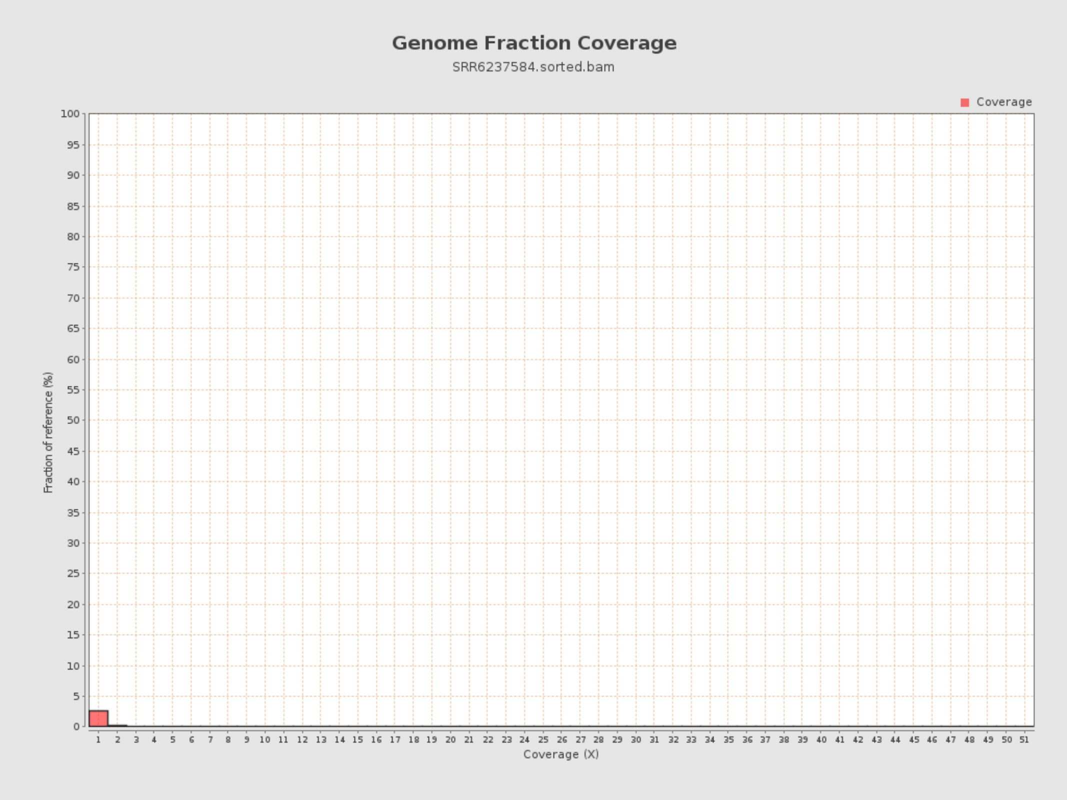
4. Results : Coverage Histogram



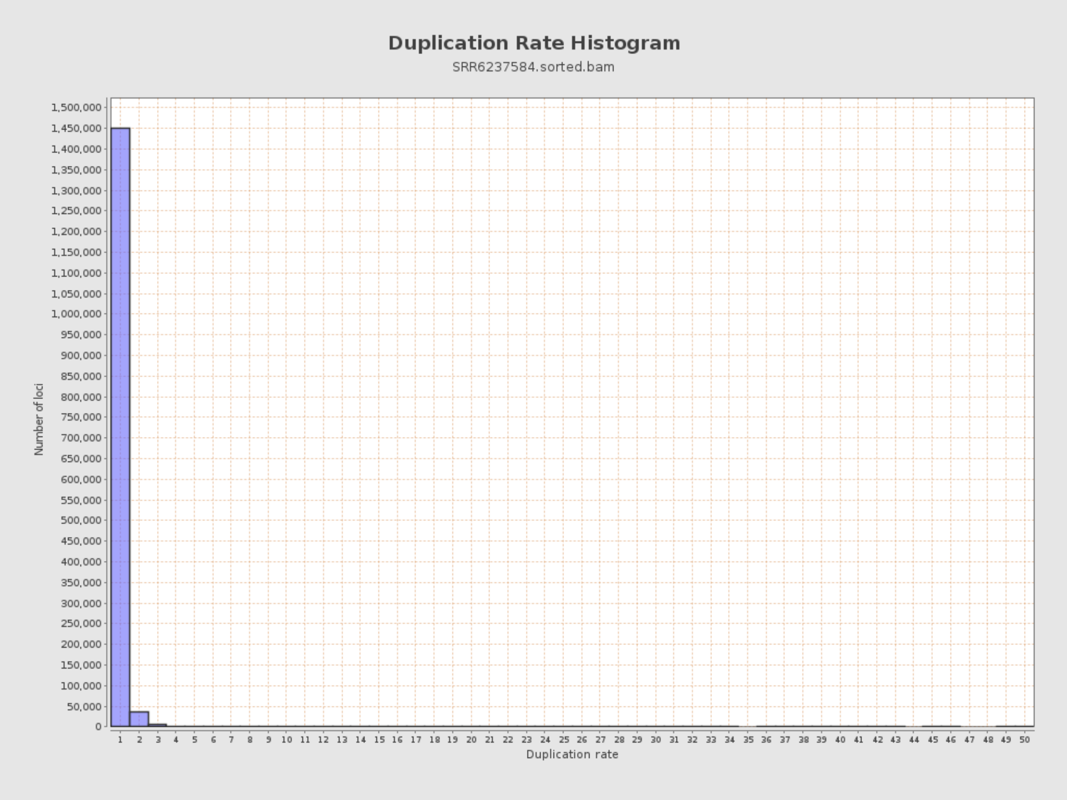
5. Results : Coverage Histogram (0-50X)



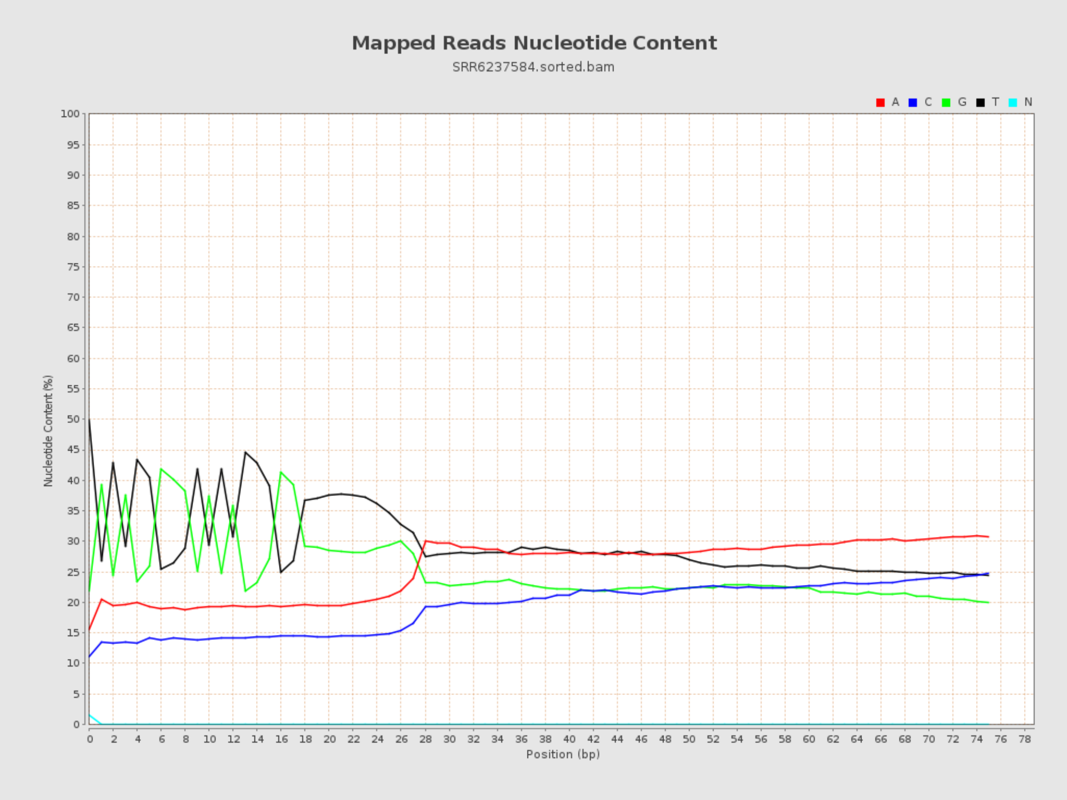
6. Results : Genome Fraction Coverage



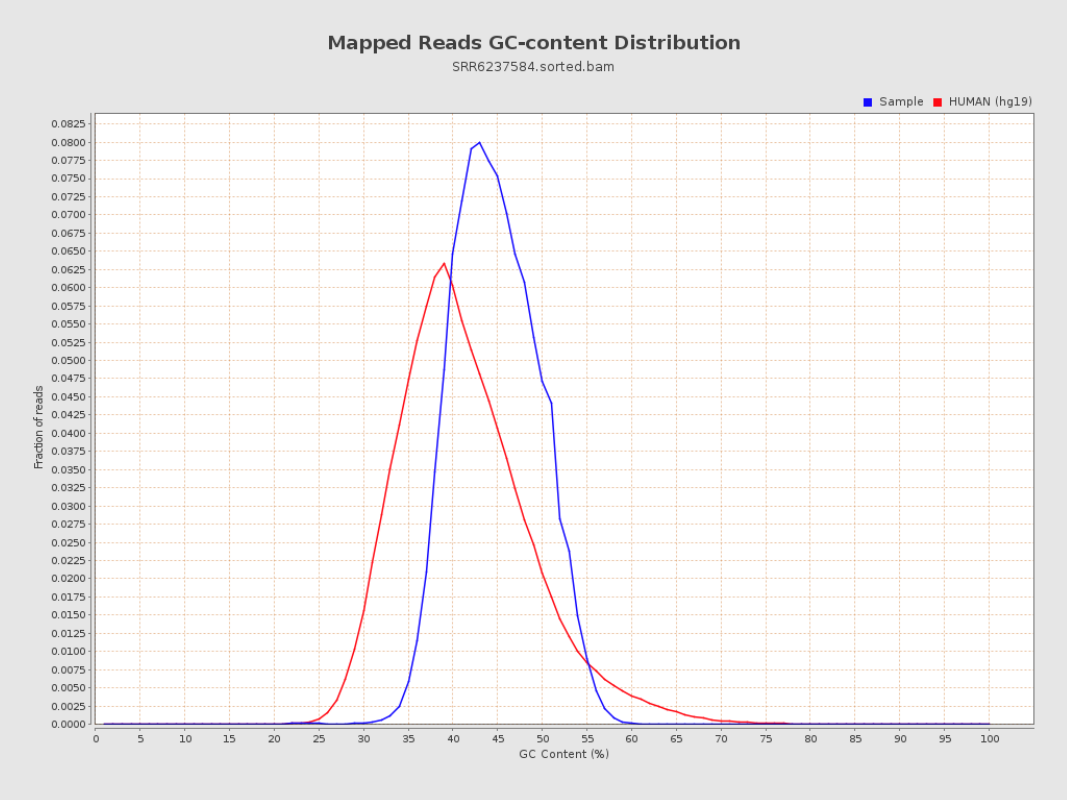
7. Results : Duplication Rate Histogram



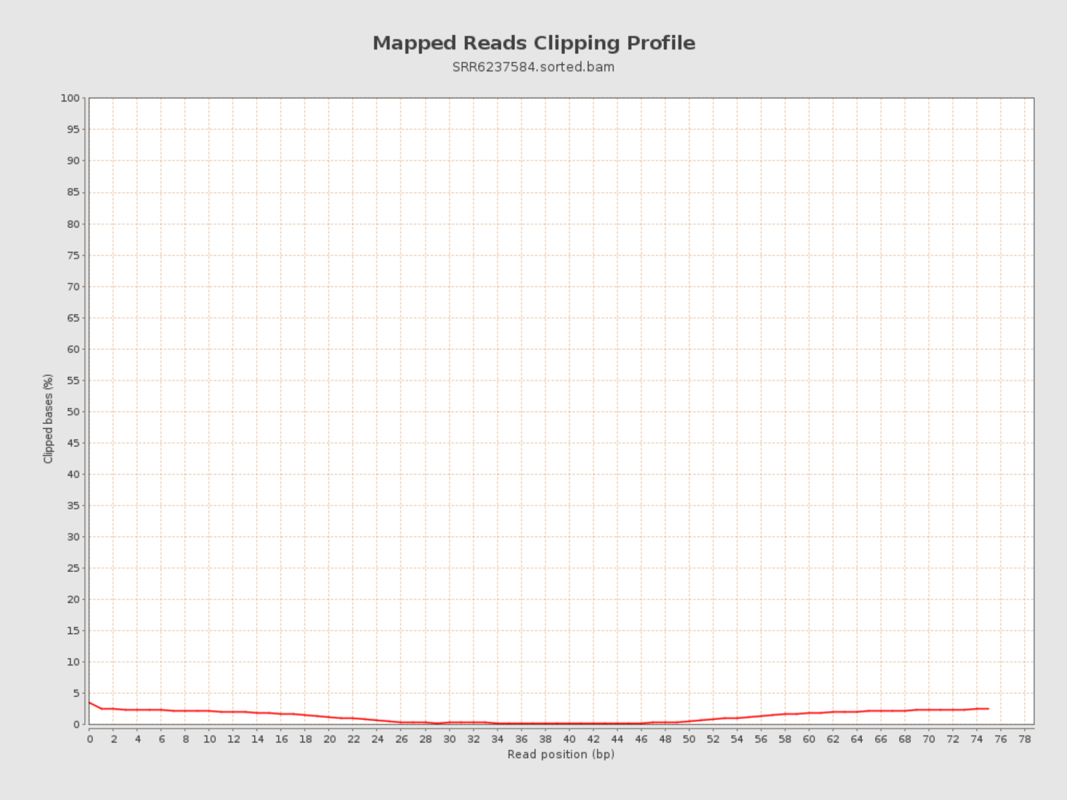
8. Results : Mapped Reads Nucleotide Content



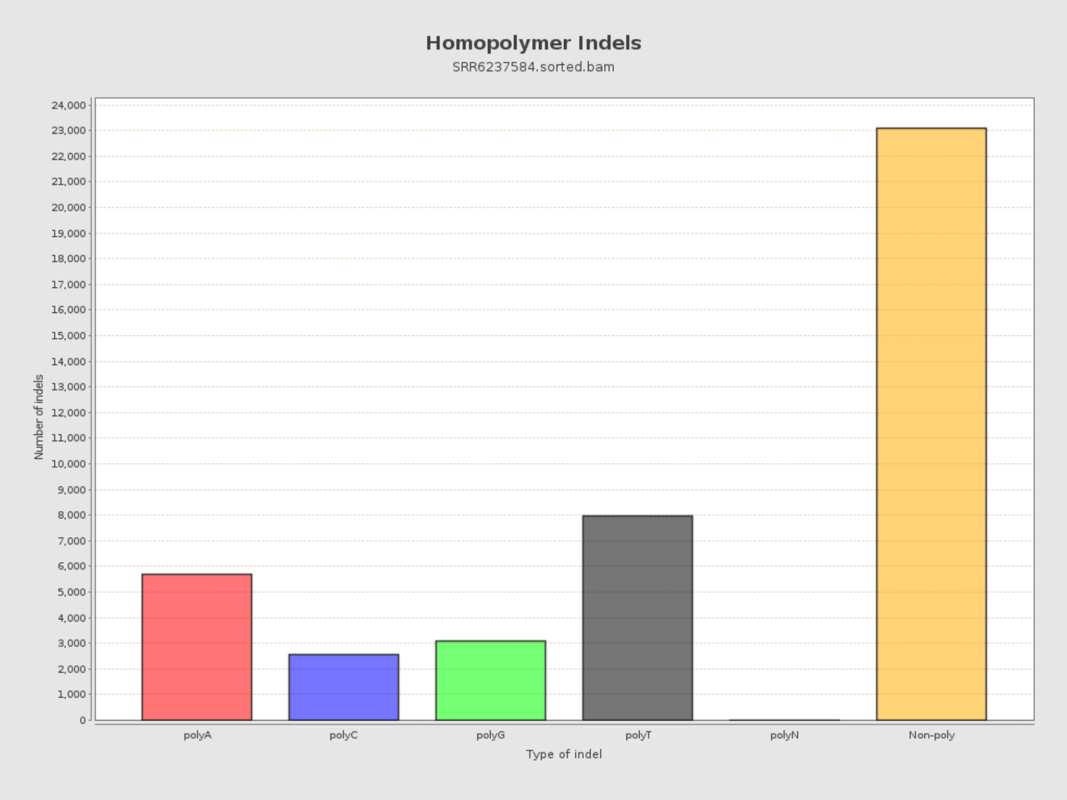
9. Results : Mapped Reads GC-content Distribution



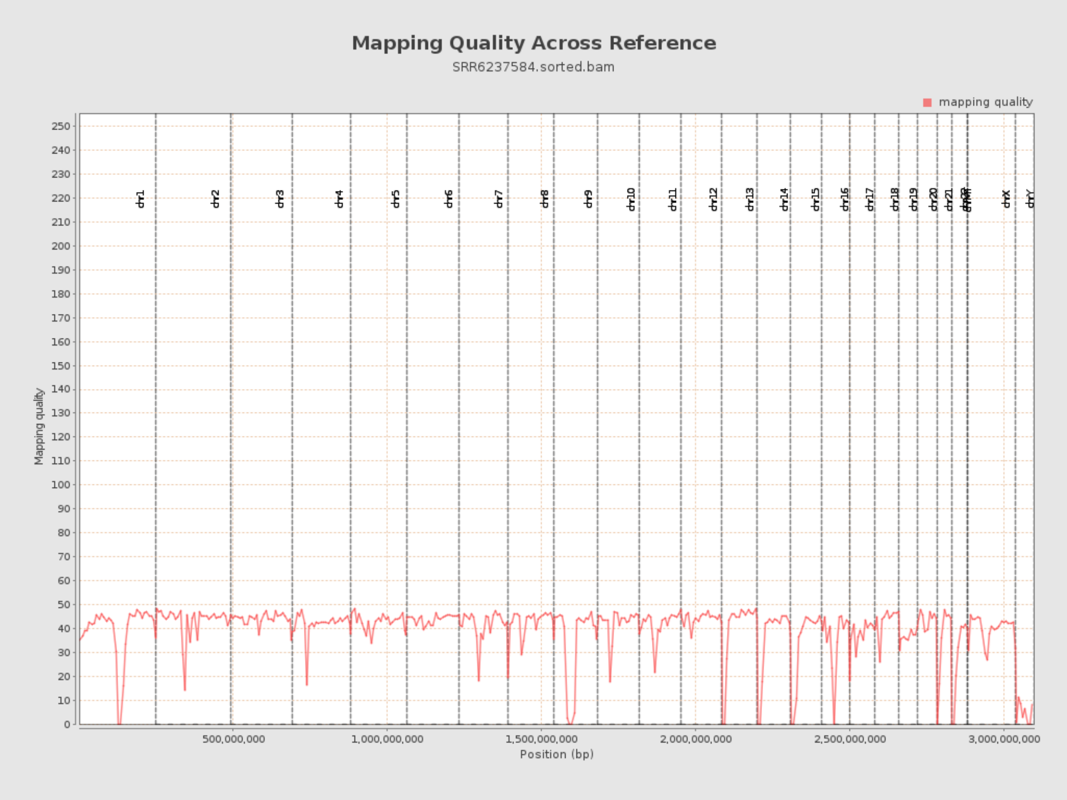
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram