Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:59:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237577.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_SRR6237577 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237577.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:59:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237577.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,122,646
Mapped reads	1,619,197 / 76.28%
Unmapped reads	503,449 / 23.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,878 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	80,977 / 3.81%
Duplication rate	3.52%
Clipped reads	1,098,498 / 51.75%

2.2. ACGT Content

Number/percentage of A's	26,006,712 / 26.48%
Number/percentage of C's	18,846,208 / 19.19%
Number/percentage of T's	28,606,173 / 29.13%
Number/percentage of G's	24,581,921 / 25.03%
Number/percentage of N's	167,088 / 0.17%
GC Percentage	44.22%

2.3. Coverage

Mean	0.0317

Standard Deviation	0.2817

2.4. Mapping Quality

Mean Mapping Quality	40.33

2.5. Mismatches and indels

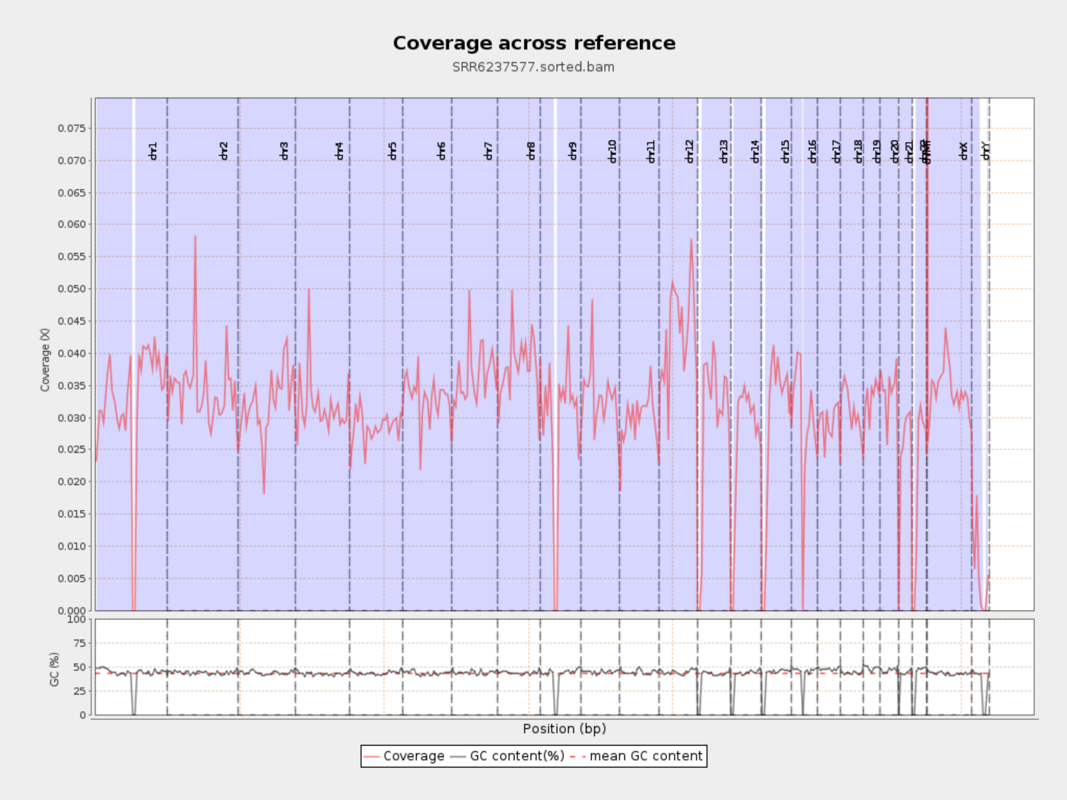
General error rate	0.99%
Mismatches	957,800
Insertions	8,895
Mapped reads with at least one insertion	0.54%
Deletions	30,793
Mapped reads with at least one deletion	1.88%
Homopolymer indels	44.74%

2.6. Chromosome stats

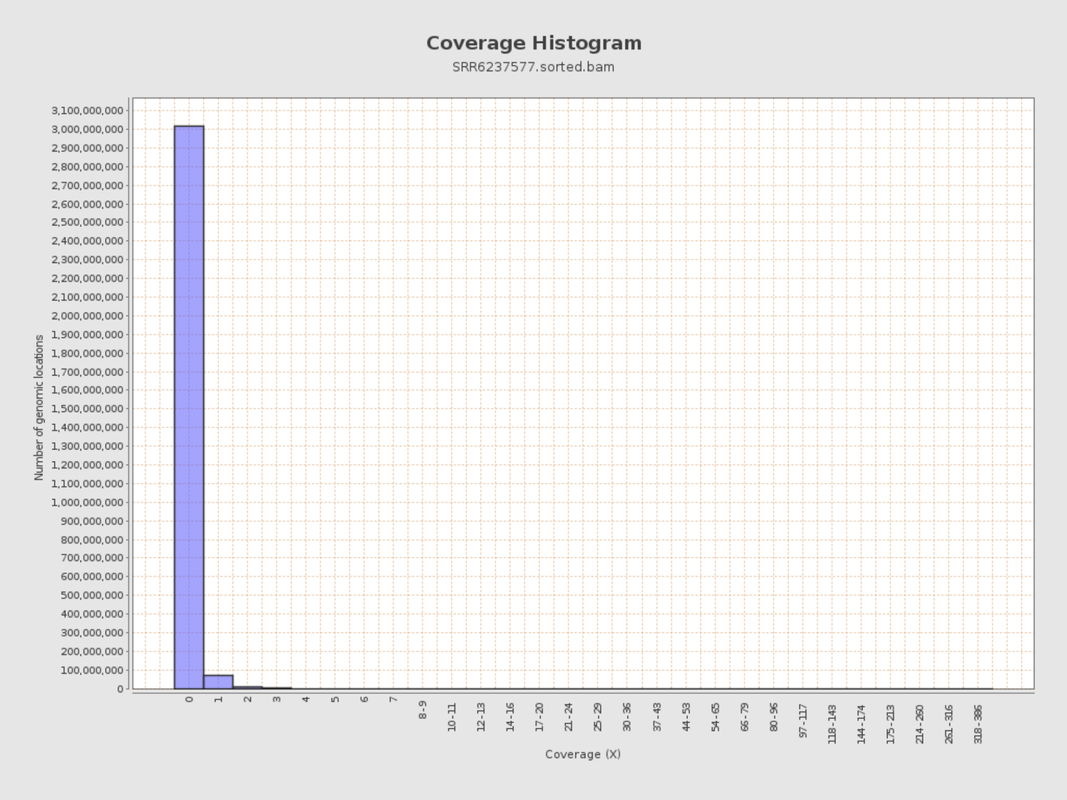
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8177607	0.0328	0.3191
chr2	243199373	8363443	0.0344	0.3859
chr3	198022430	6363800	0.0321	0.2293
chr4	191154276	6079492	0.0318	0.2406
chr5	180915260	5181855	0.0286	0.2086
chr6	171115067	5646758	0.033	0.2481
chr7	159138663	5799318	0.0364	0.3895

chr8	146364022	5544113	0.0379	0.2937
chr9	141213431	4095454	0.029	0.3086
chr10	135534747	4502656	0.0332	0.2842
chr11	135006516	4073562	0.0302	0.2749
chr12	133851895	5803978	0.0434	0.2735
chr13	115169878	3322524	0.0288	0.2152
chr14	107349540	2810706	0.0262	0.2269
chr15	102531392	2971709	0.029	0.2207
chr16	90354753	2615351	0.0289	0.244
chr17	81195210	2373151	0.0292	0.2243
chr18	78077248	2443750	0.0313	0.4115
chr19	59128983	1943714	0.0329	0.2858
chr20	63025520	2133408	0.0338	0.2368
chr21	48129895	1206203	0.0251	0.2155
chr22	51304566	1037560	0.0202	0.1833
chrMT	16571	90493	5.4609	4.659
chrX	155270560	5332710	0.0343	0.2513
chrY	59373566	345876	0.0058	0.1438

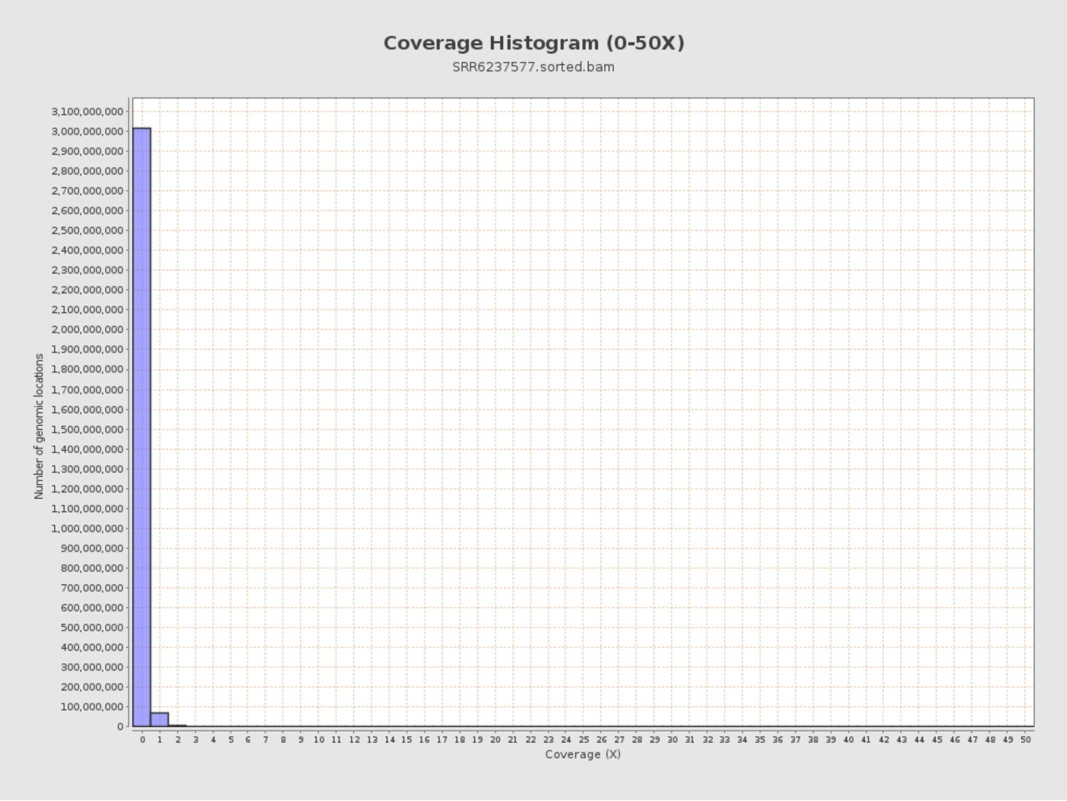
3. Results : Coverage across reference



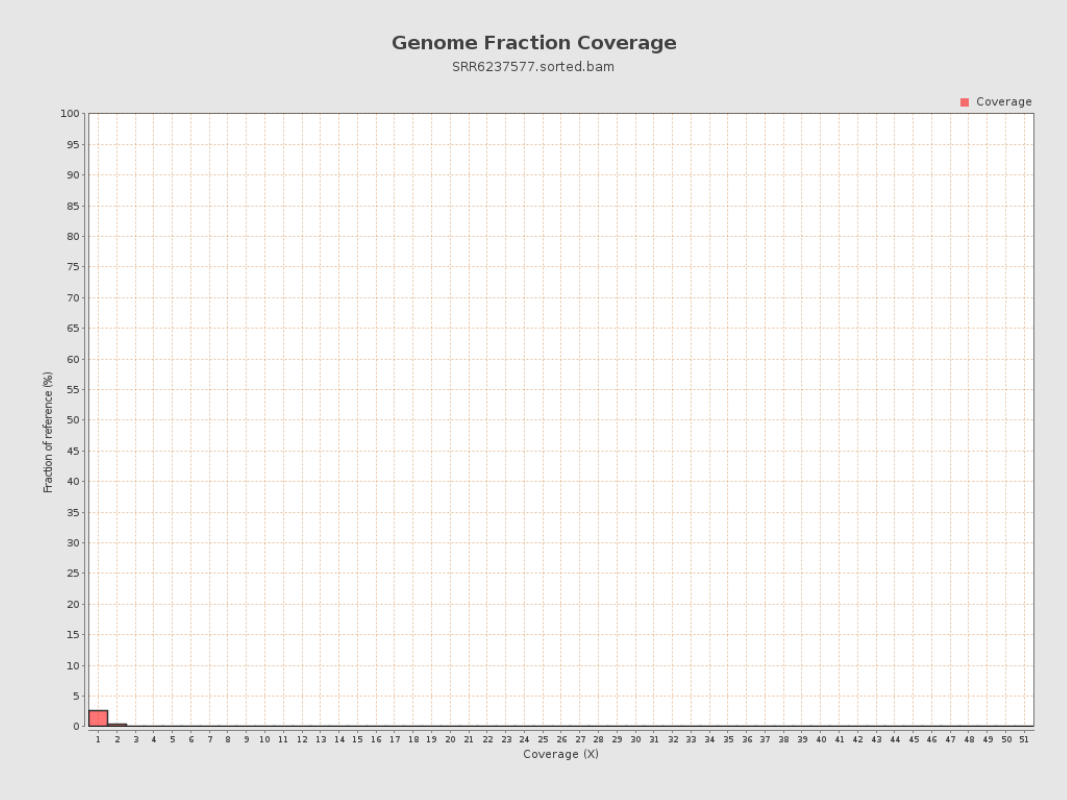
4. Results : Coverage Histogram



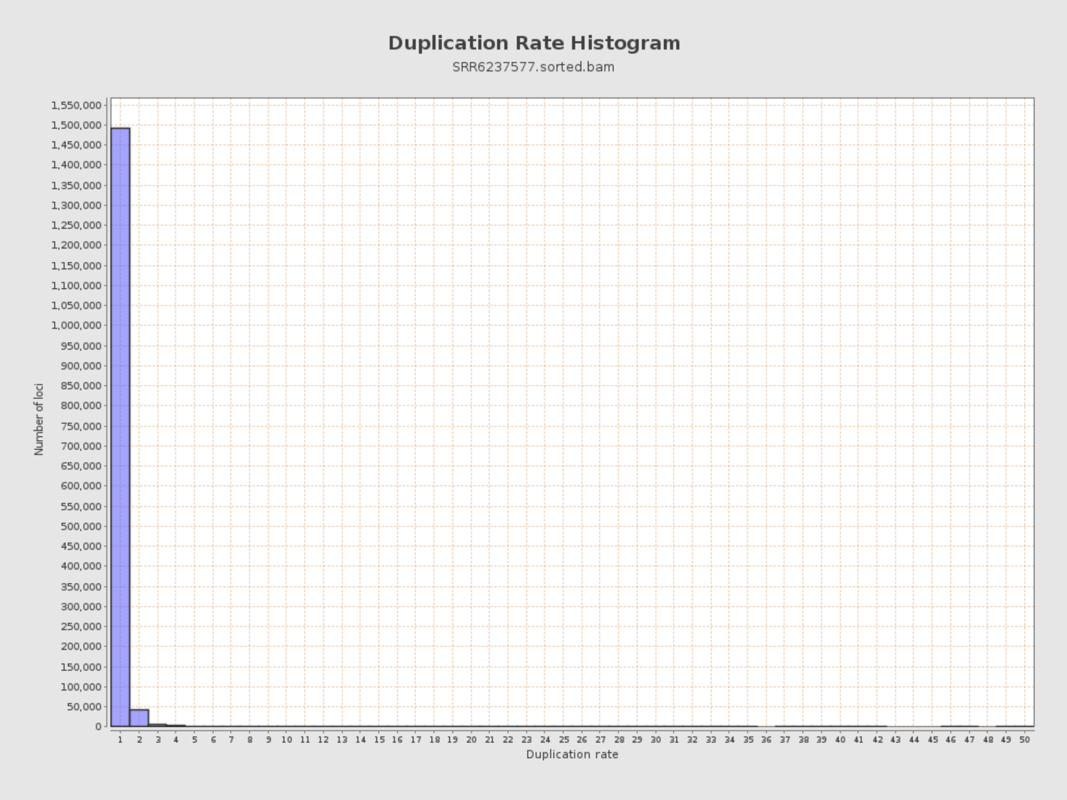
5. Results : Coverage Histogram (0-50X)



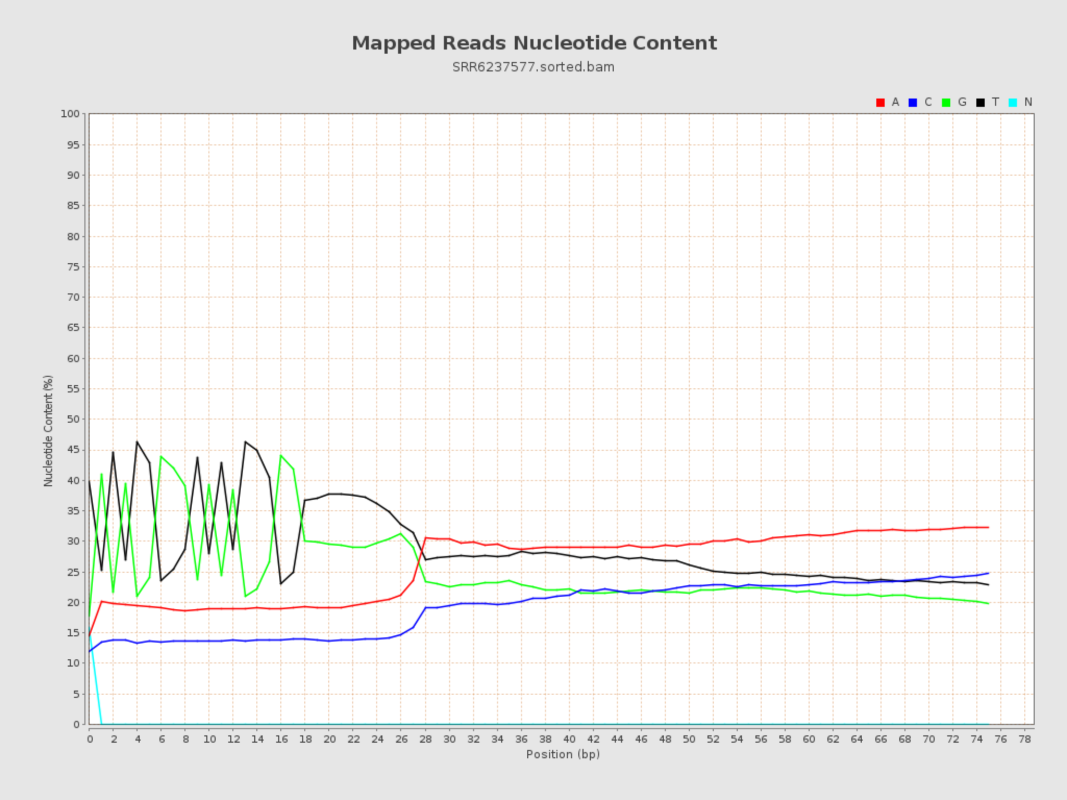
6. Results : Genome Fraction Coverage



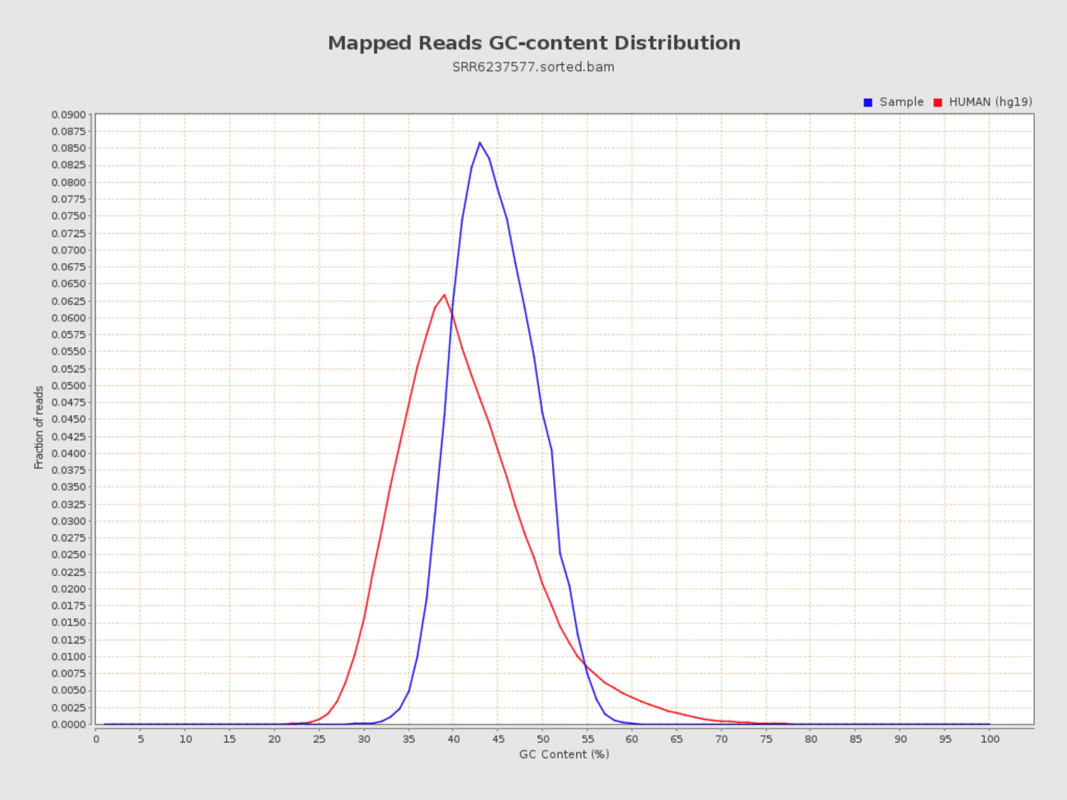
7. Results : Duplication Rate Histogram



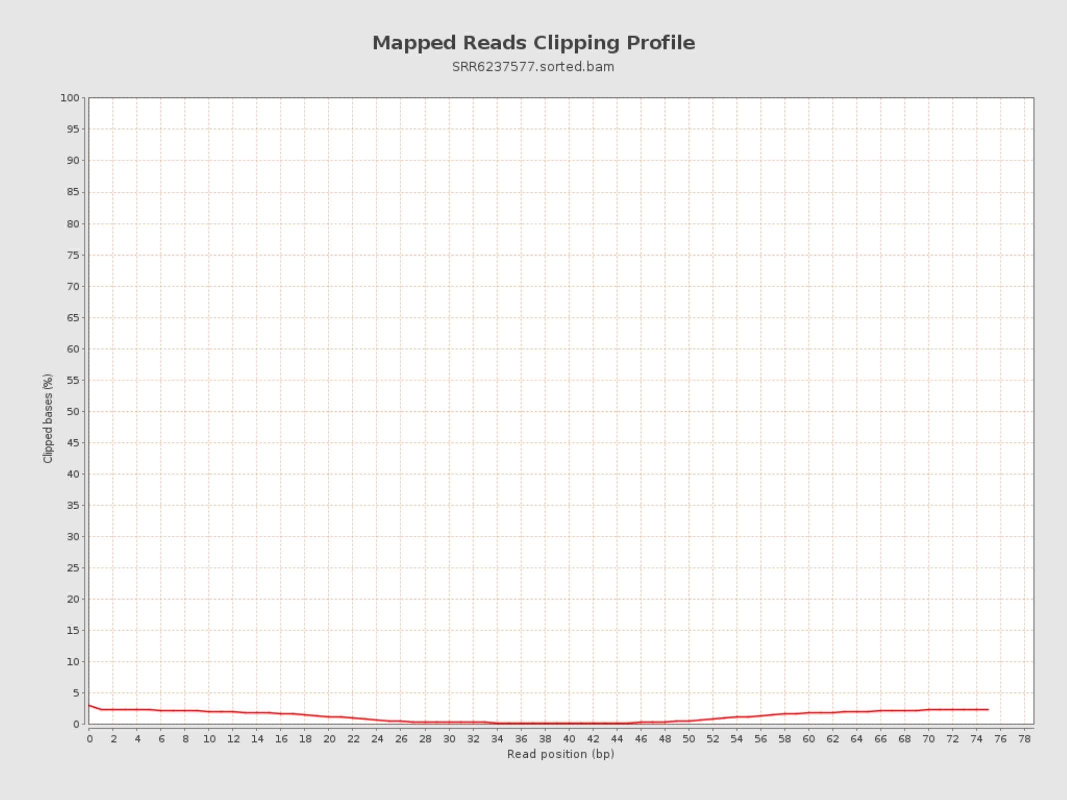
8. Results : Mapped Reads Nucleotide Content



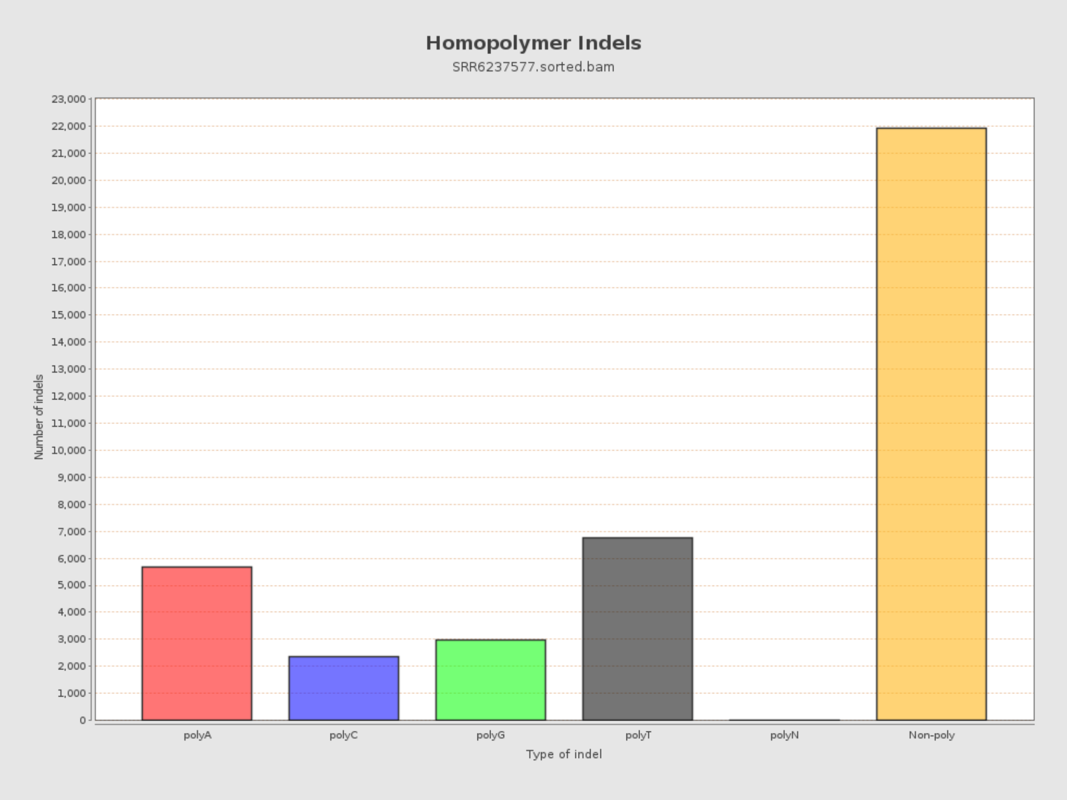
9. Results : Mapped Reads GC-content Distribution



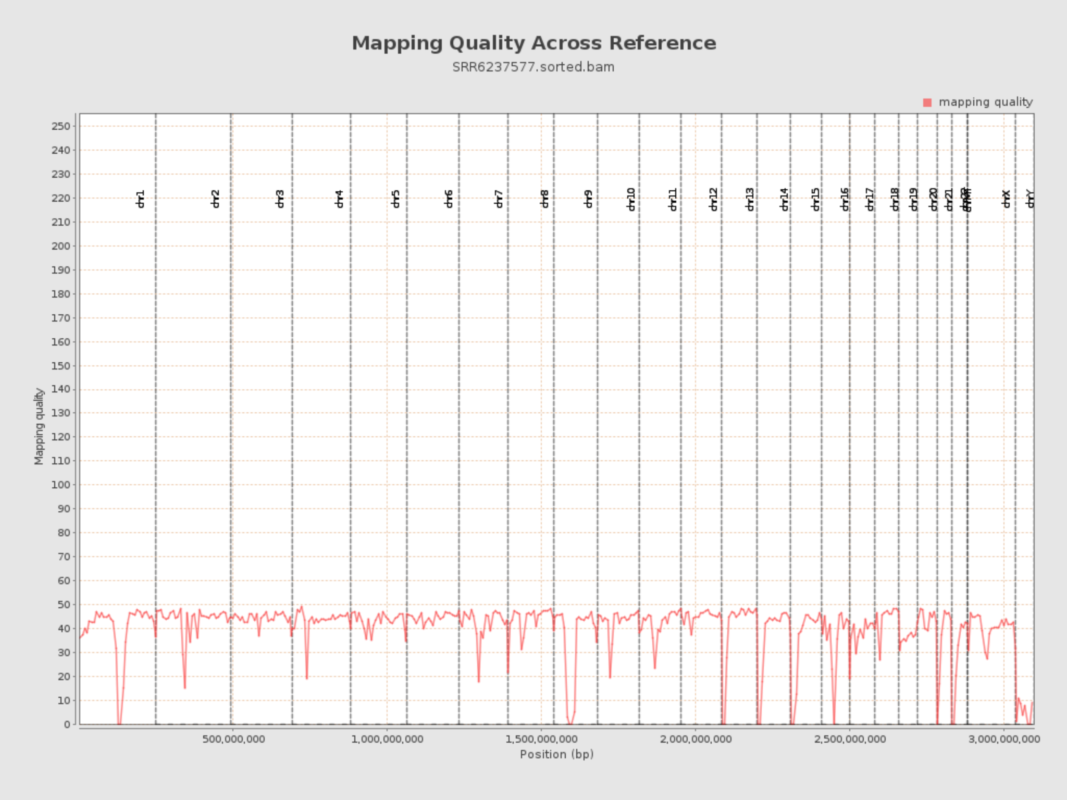
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram