Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:31:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237324.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_SRR6237324 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237324.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:31:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237324.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,752,156
Mapped reads	2,539,017 / 92.26%
Unmapped reads	213,139 / 7.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,511 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	589,543 / 21.42%
Duplication rate	18.39%
Clipped reads	1,603,175 / 58.25%

2.2. ACGT Content

Number/percentage of A's	40,949,861 / 26.02%
Number/percentage of C's	27,095,343 / 17.21%
Number/percentage of T's	52,743,504 / 33.51%
Number/percentage of G's	36,598,254 / 23.25%
Number/percentage of N's	16,701 / 0.01%
GC Percentage	40.47%

2.3. Coverage

Mean	0.0509

Standard Deviation	0.6479

2.4. Mapping Quality

Mean Mapping Quality	43.03

2.5. Mismatches and indels

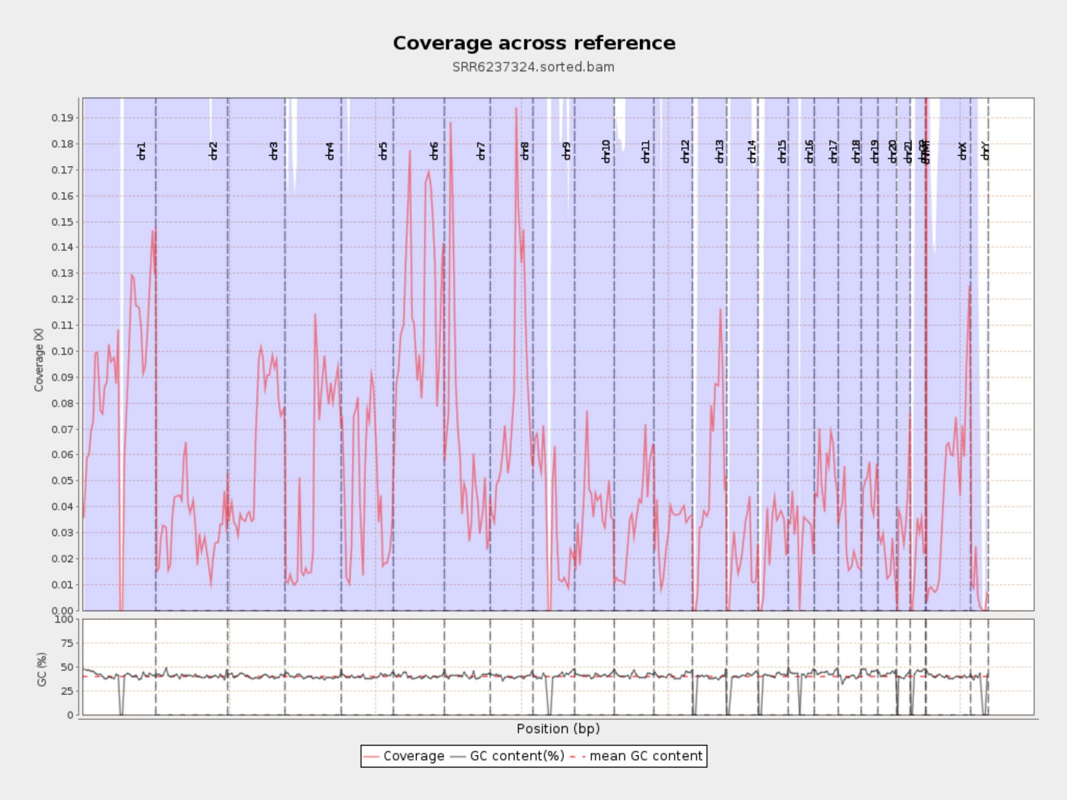
General error rate	0.56%
Mismatches	852,421
Insertions	10,580
Mapped reads with at least one insertion	0.41%
Deletions	40,359
Mapped reads with at least one deletion	1.57%
Homopolymer indels	43.02%

2.6. Chromosome stats

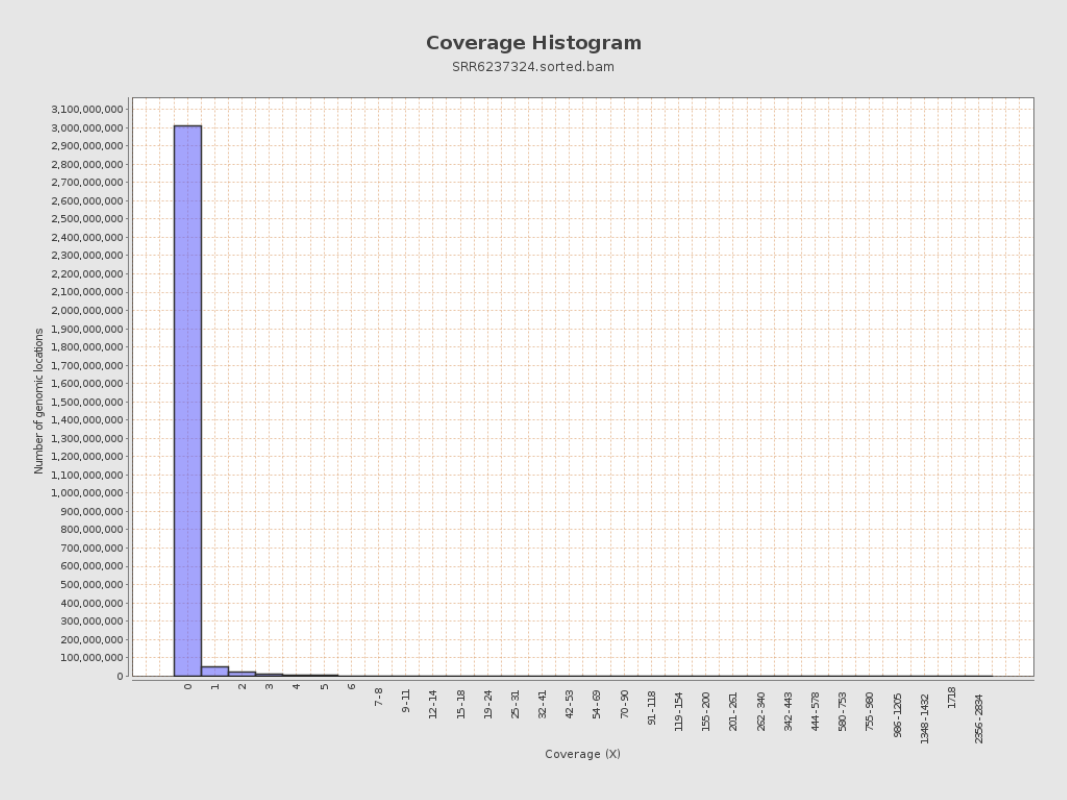
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22392314	0.0898	0.8576
chr2	243199373	7717214	0.0317	1.3459
chr3	198022430	12460483	0.0629	0.4183
chr4	191154276	9828135	0.0514	0.4059
chr5	180915260	8635722	0.0477	0.3682
chr6	171115067	20493955	0.1198	0.858
chr7	159138663	9721005	0.0611	0.4625

chr8	146364022	12230550	0.0836	0.7236
chr9	141213431	4834158	0.0342	0.3276
chr10	135534747	5359972	0.0395	0.43
chr11	135006516	4645006	0.0344	0.3264
chr12	133851895	4240742	0.0317	0.2996
chr13	115169878	6021270	0.0523	0.4478
chr14	107349540	2157179	0.0201	0.2389
chr15	102531392	2634987	0.0257	0.3302
chr16	90354753	2756880	0.0305	0.319
chr17	81195210	4416314	0.0544	0.3958
chr18	78077248	2127350	0.0272	1.4346
chr19	59128983	2779929	0.047	0.5685
chr20	63025520	1332264	0.0211	0.2399
chr21	48129895	1784255	0.0371	0.3408
chr22	51304566	1095275	0.0213	0.2305
chrMT	16571	69206	4.1763	5.0373
chrX	155270560	7320031	0.0471	0.3674
chrY	59373566	418795	0.0071	0.2584

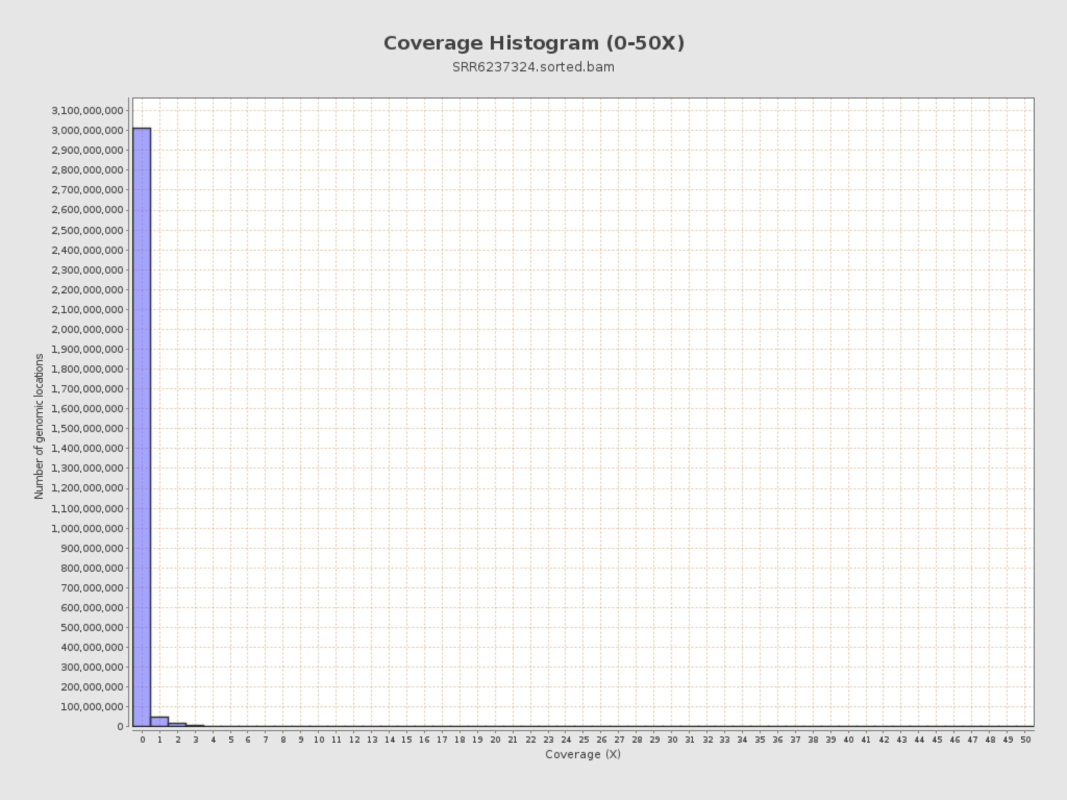
3. Results : Coverage across reference



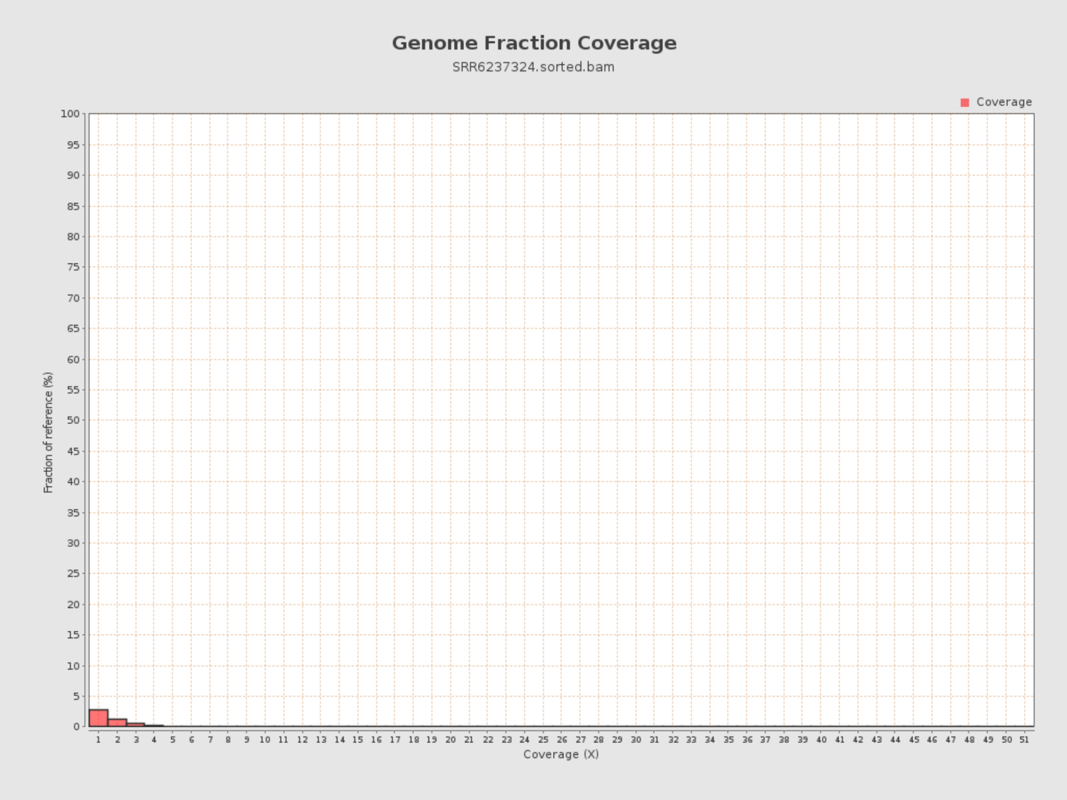
4. Results : Coverage Histogram



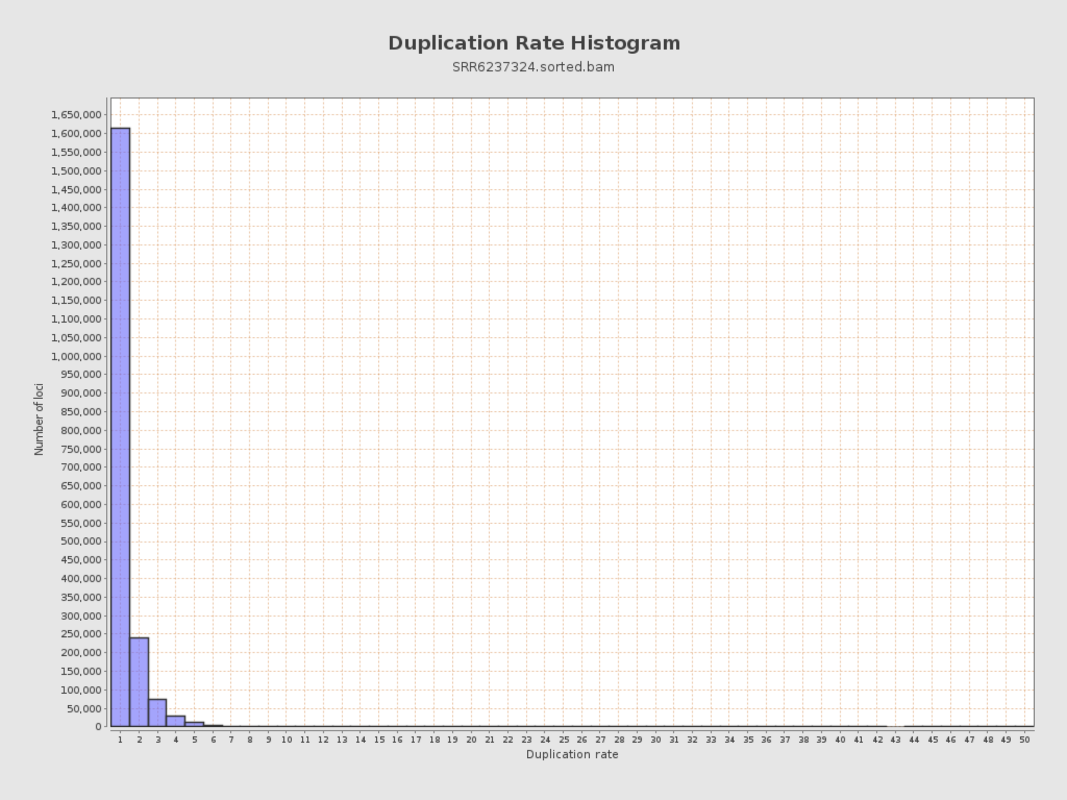
5. Results : Coverage Histogram (0-50X)



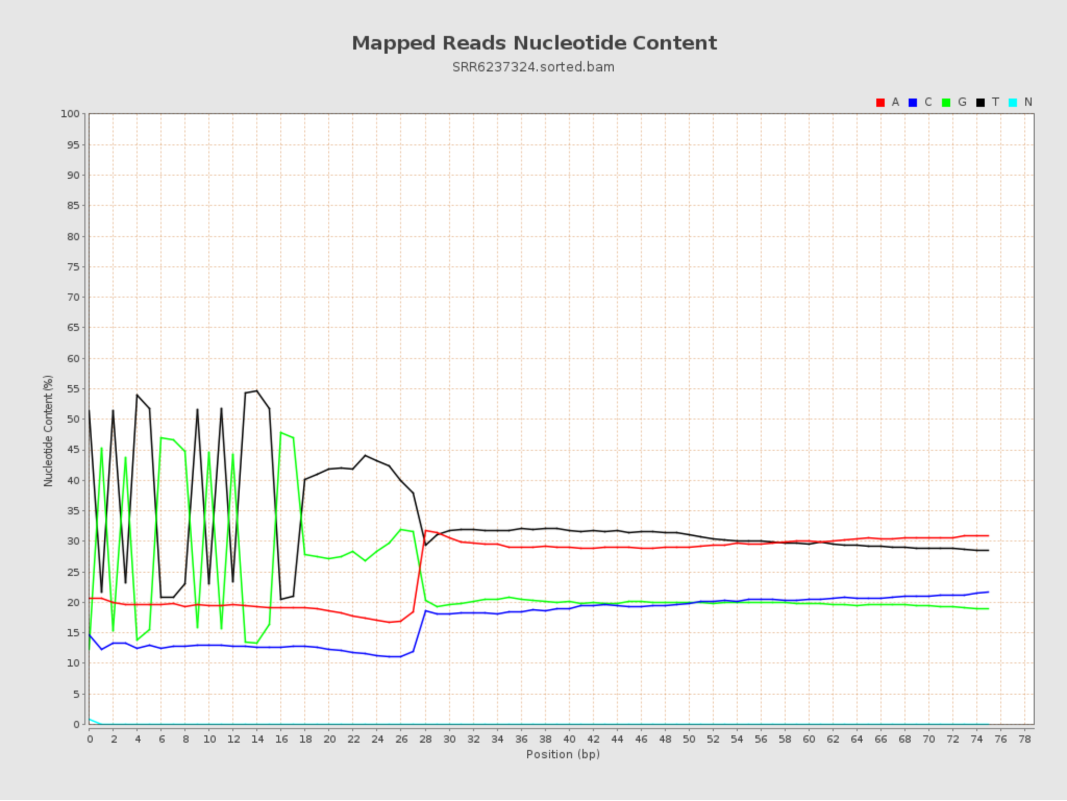
6. Results : Genome Fraction Coverage



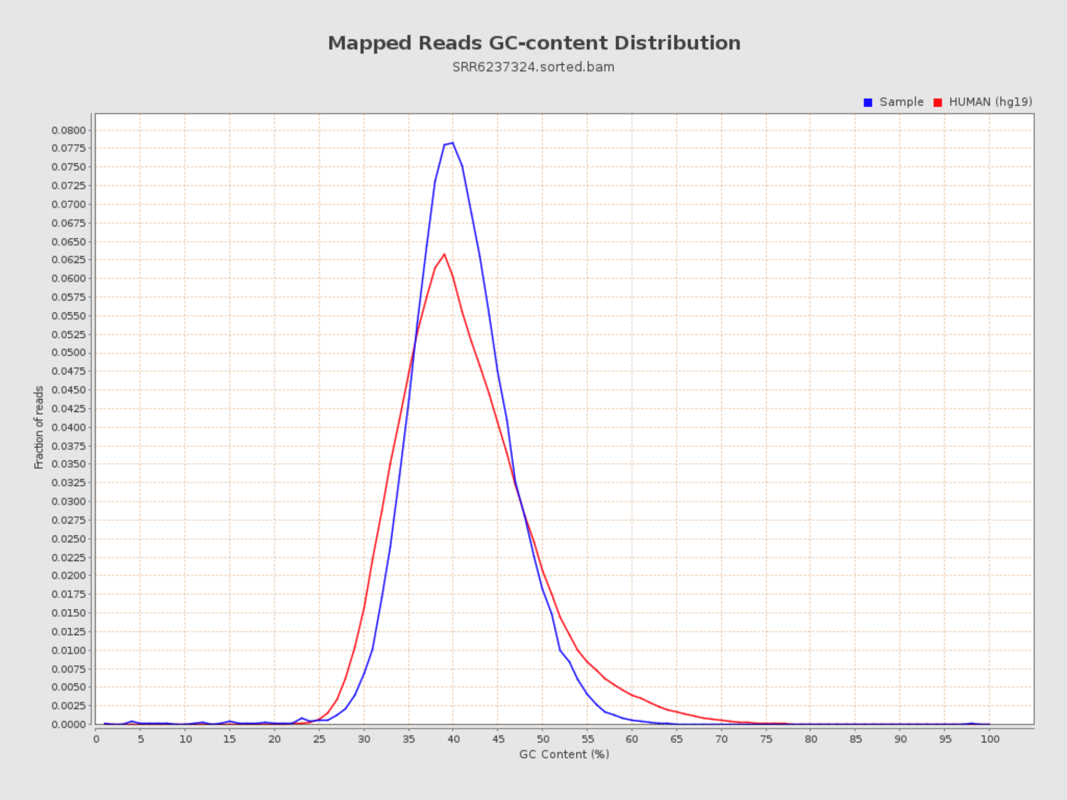
7. Results : Duplication Rate Histogram



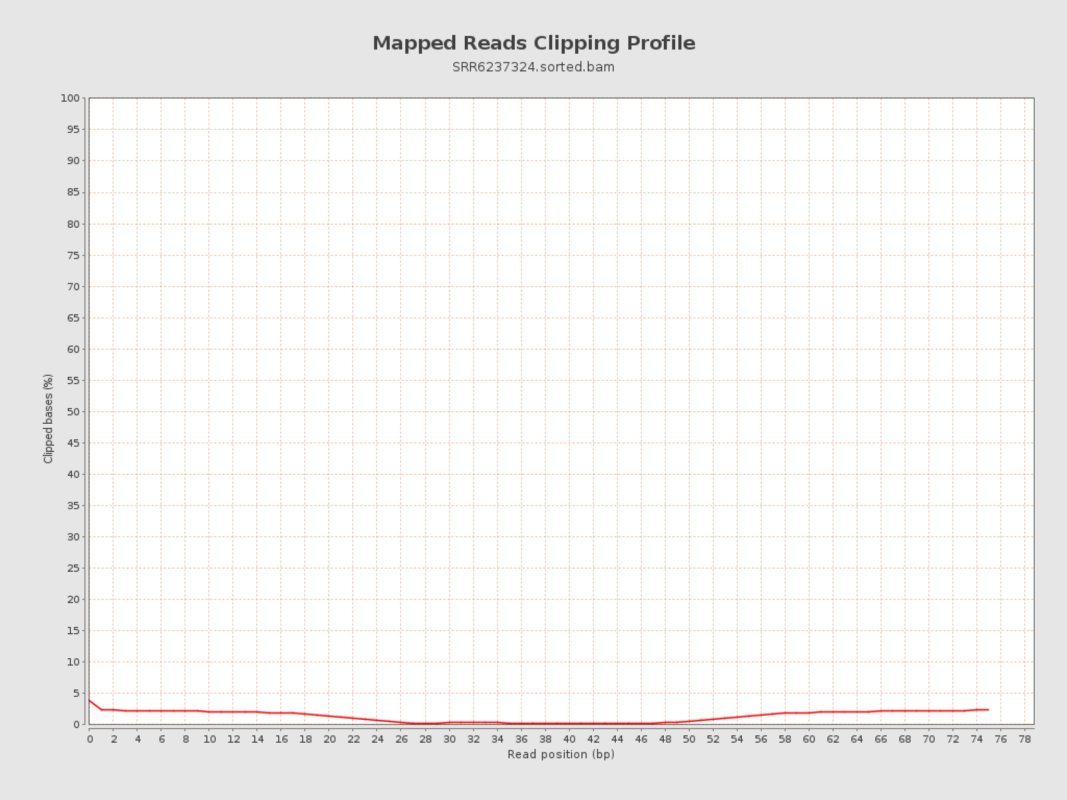
8. Results : Mapped Reads Nucleotide Content



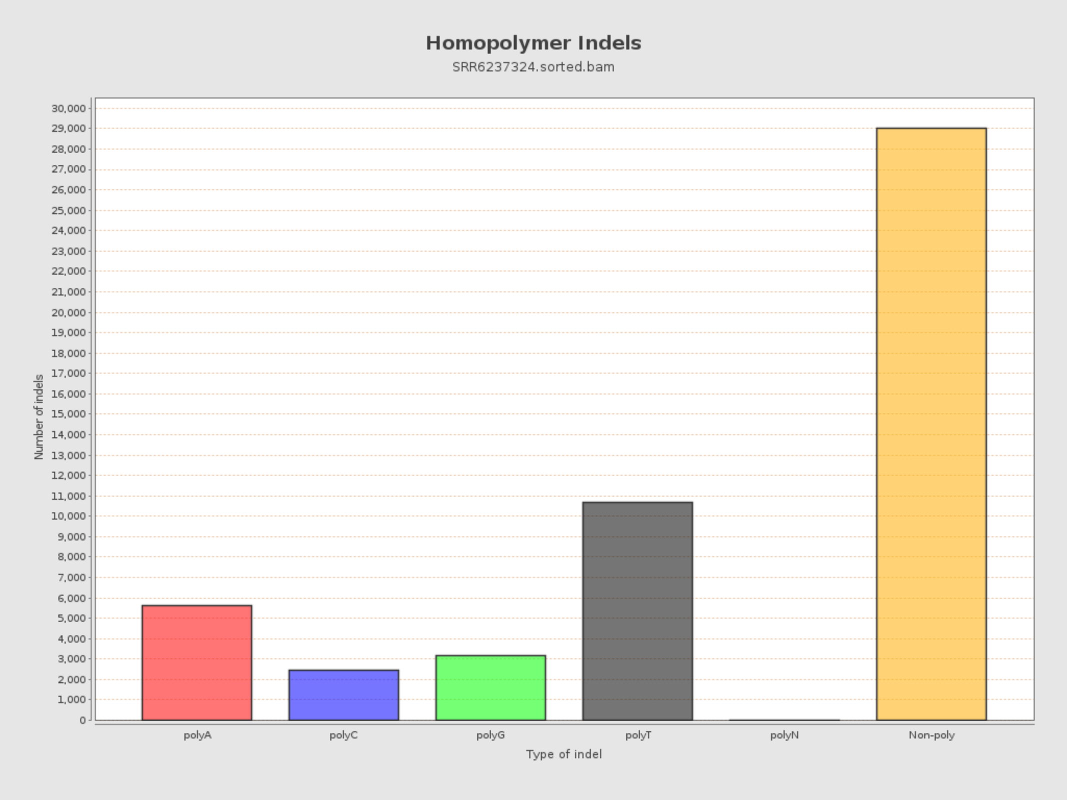
9. Results : Mapped Reads GC-content Distribution



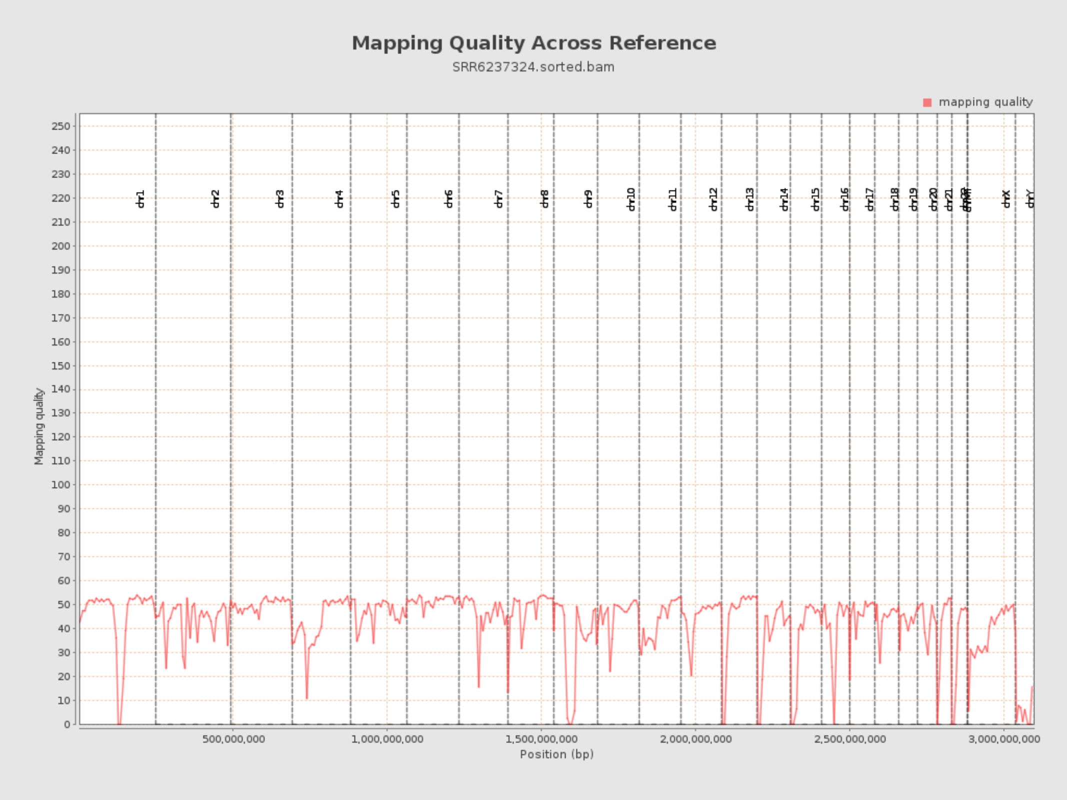
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram