Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:24:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237322.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_SRR6237322 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237322.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:24:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237322.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,335,862
Mapped reads	3,003,176 / 90.03%
Unmapped reads	332,686 / 9.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,756 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	641,002 / 19.22%
Duplication rate	17.04%
Clipped reads	2,057,839 / 61.69%

2.2. ACGT Content

Number/percentage of A's	45,326,124 / 24.97%
Number/percentage of C's	31,538,374 / 17.38%
Number/percentage of T's	60,766,998 / 33.48%
Number/percentage of G's	43,844,961 / 24.16%
Number/percentage of N's	18,589 / 0.01%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0587

Standard Deviation	0.7432

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

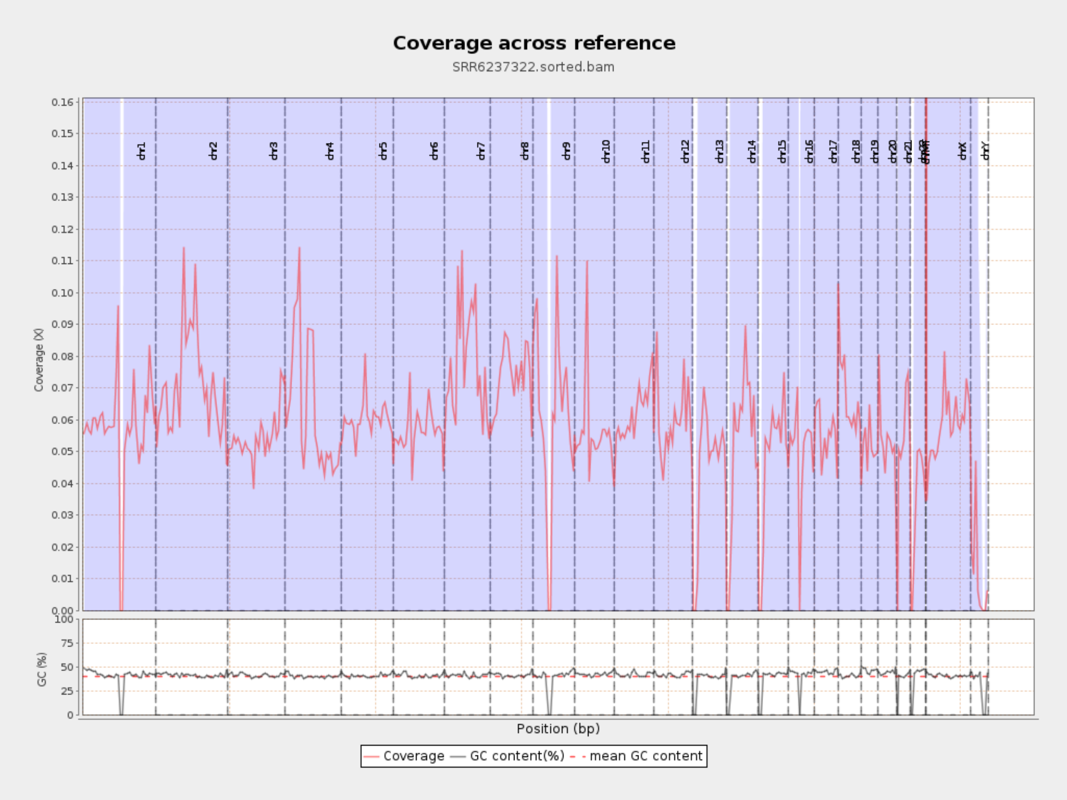
General error rate	0.62%
Mismatches	1,106,375
Insertions	12,111
Mapped reads with at least one insertion	0.4%
Deletions	53,011
Mapped reads with at least one deletion	1.74%
Homopolymer indels	41.86%

2.6. Chromosome stats

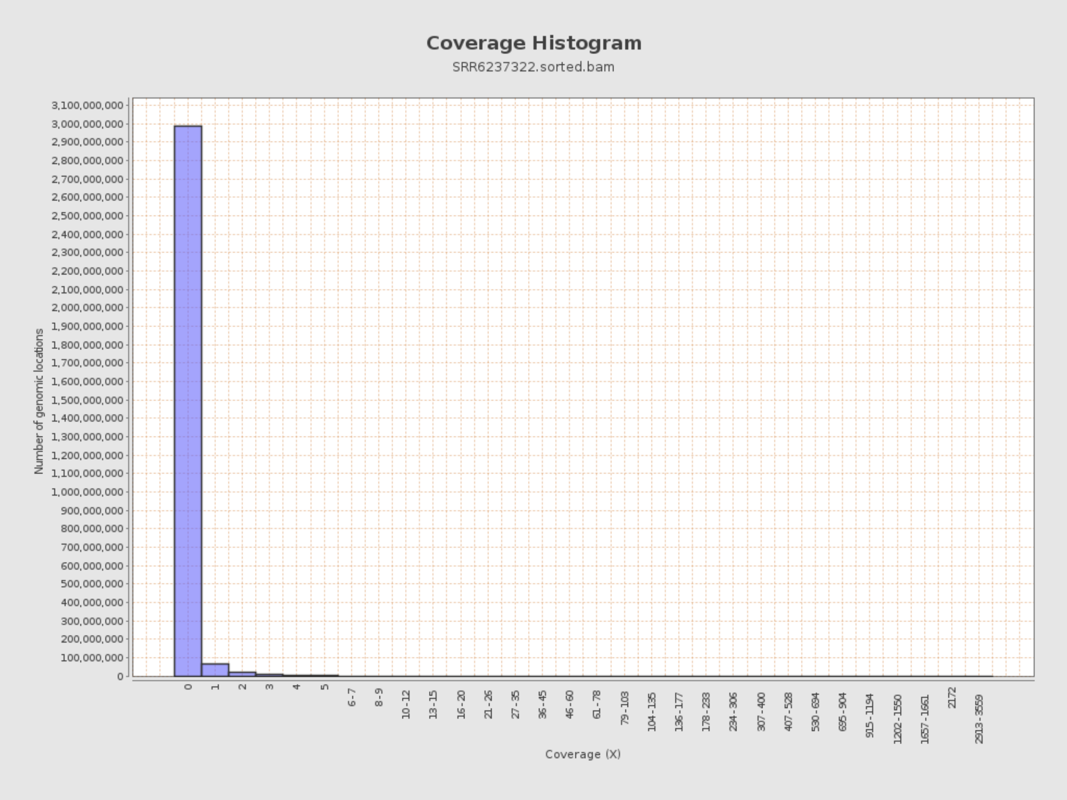
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14249743	0.0572	0.9515
chr2	243199373	17426518	0.0717	1.6886
chr3	198022430	10779305	0.0544	0.3648
chr4	191154276	11995109	0.0628	0.439
chr5	180915260	10863782	0.06	0.3856
chr6	171115067	9738721	0.0569	0.6293
chr7	159138663	12390292	0.0779	0.769

chr8	146364022	10730350	0.0733	0.8231
chr9	141213431	8625069	0.0611	0.4722
chr10	135534747	7579697	0.0559	0.5721
chr11	135006516	8360246	0.0619	0.443
chr12	133851895	8073512	0.0603	0.3856
chr13	115169878	5177334	0.045	0.4073
chr14	107349540	5723288	0.0533	0.3744
chr15	102531392	4736874	0.0462	0.396
chr16	90354753	4378370	0.0485	0.3782
chr17	81195210	4562298	0.0562	0.3948
chr18	78077248	5274466	0.0676	1.2961
chr19	59128983	3062227	0.0518	0.6422
chr20	63025520	3362886	0.0534	0.3729
chr21	48129895	2560352	0.0532	0.3921
chr22	51304566	1705326	0.0332	0.2739
chrMT	16571	534929	32.281	19.25
chrX	155270560	9038559	0.0582	0.4077
chrY	59373566	657223	0.0111	0.5273

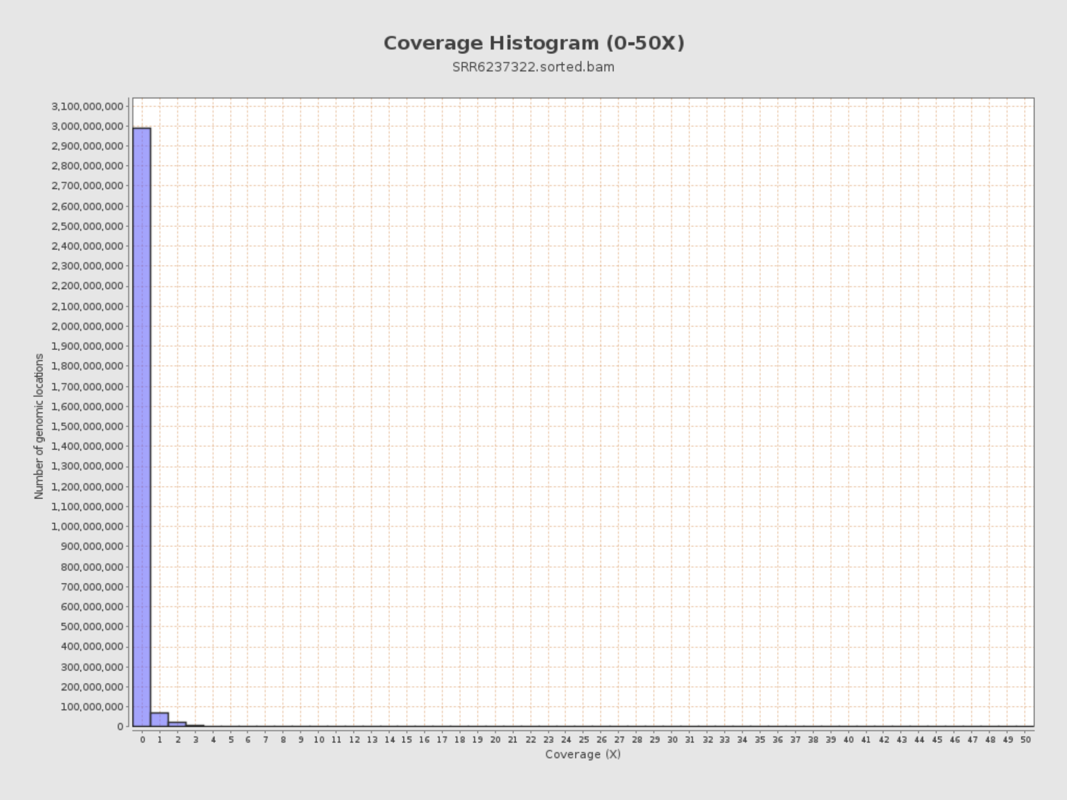
3. Results : Coverage across reference



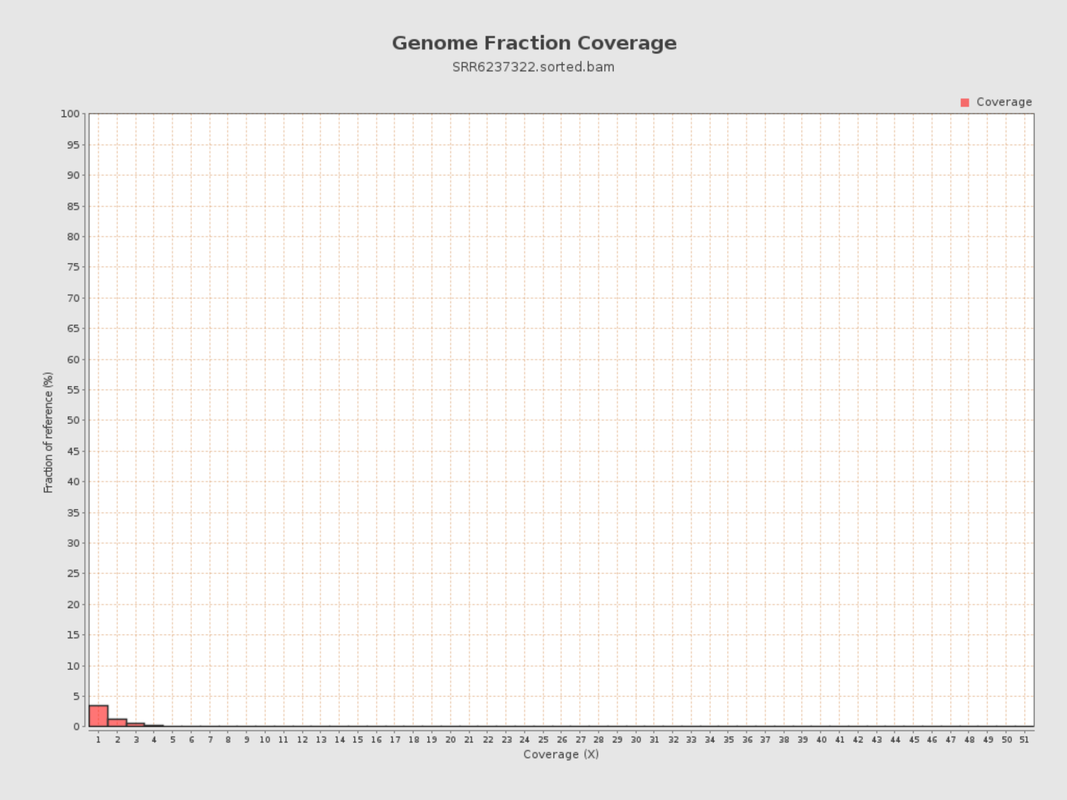
4. Results : Coverage Histogram



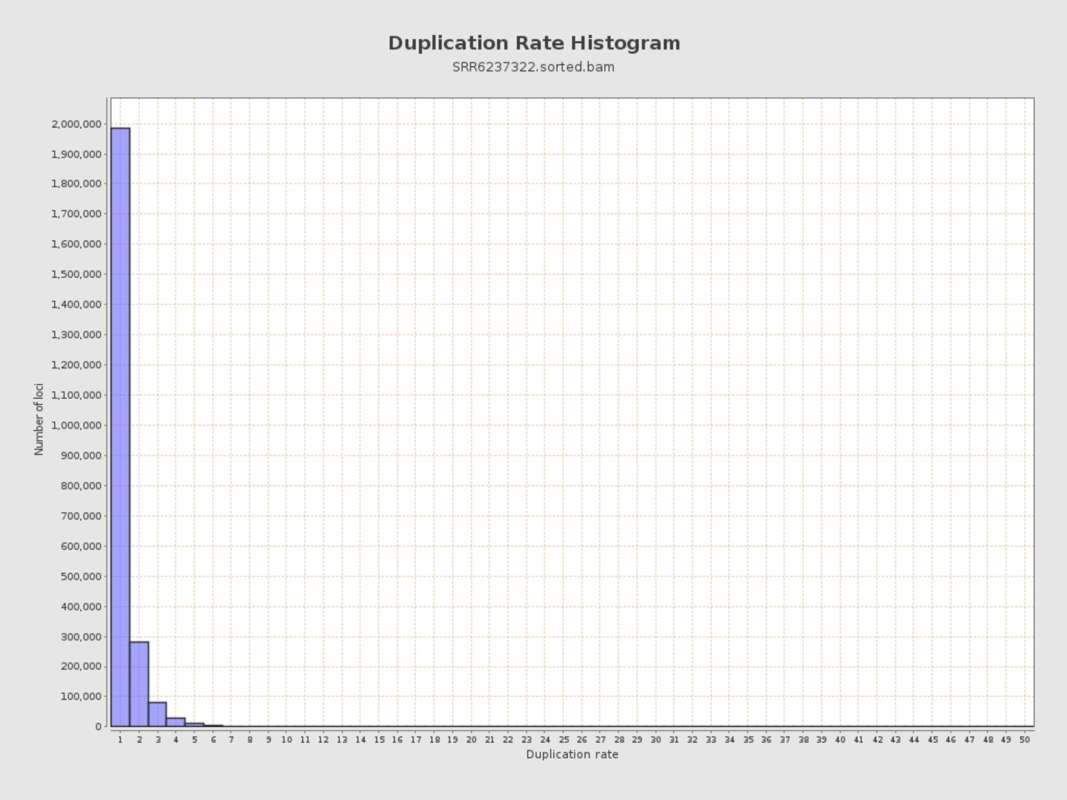
5. Results : Coverage Histogram (0-50X)



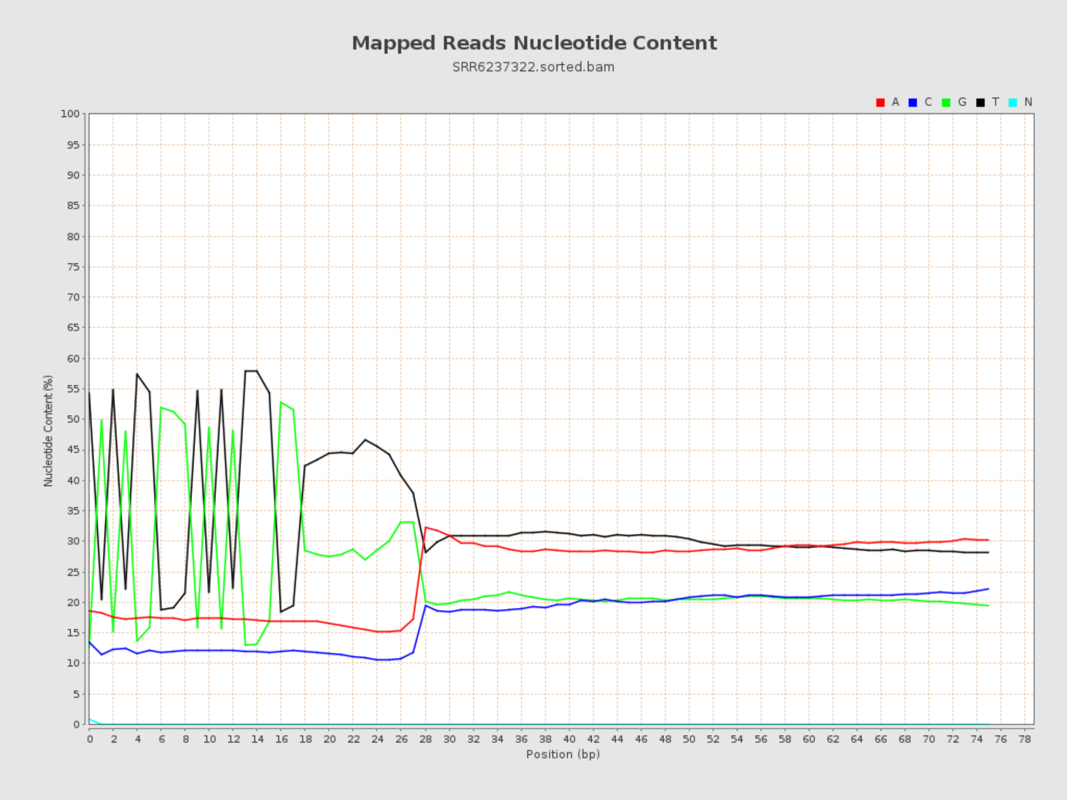
6. Results : Genome Fraction Coverage



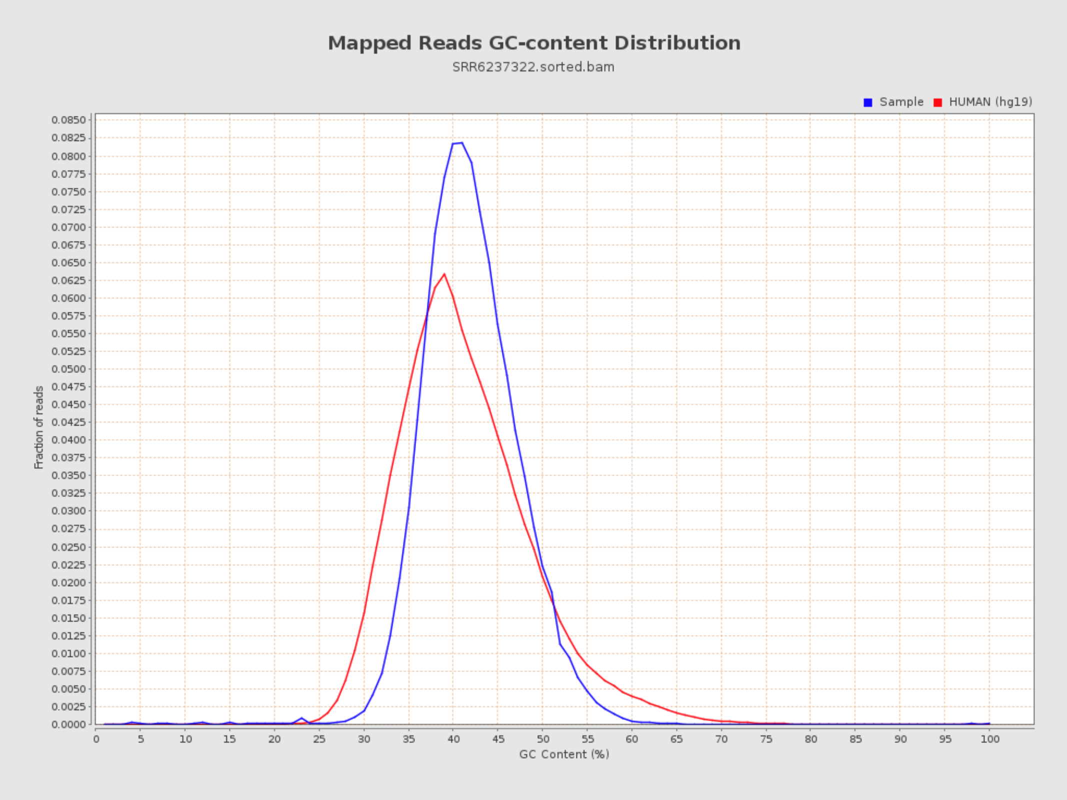
7. Results : Duplication Rate Histogram



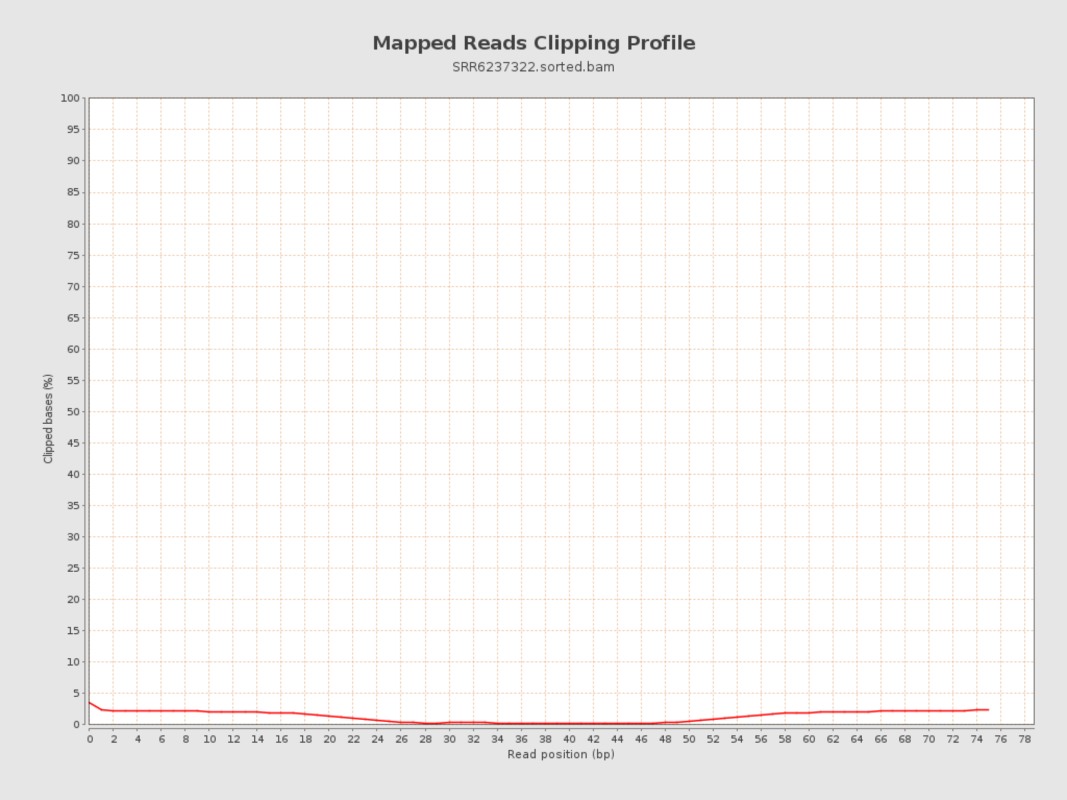
8. Results : Mapped Reads Nucleotide Content



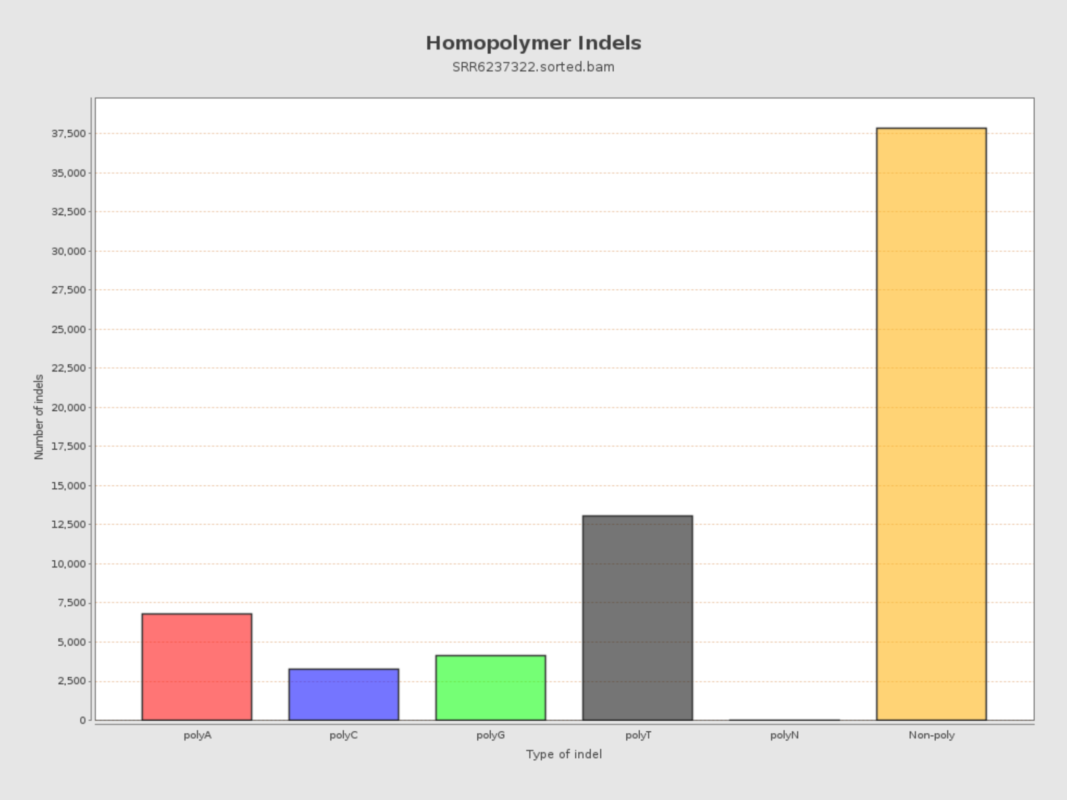
9. Results : Mapped Reads GC-content Distribution



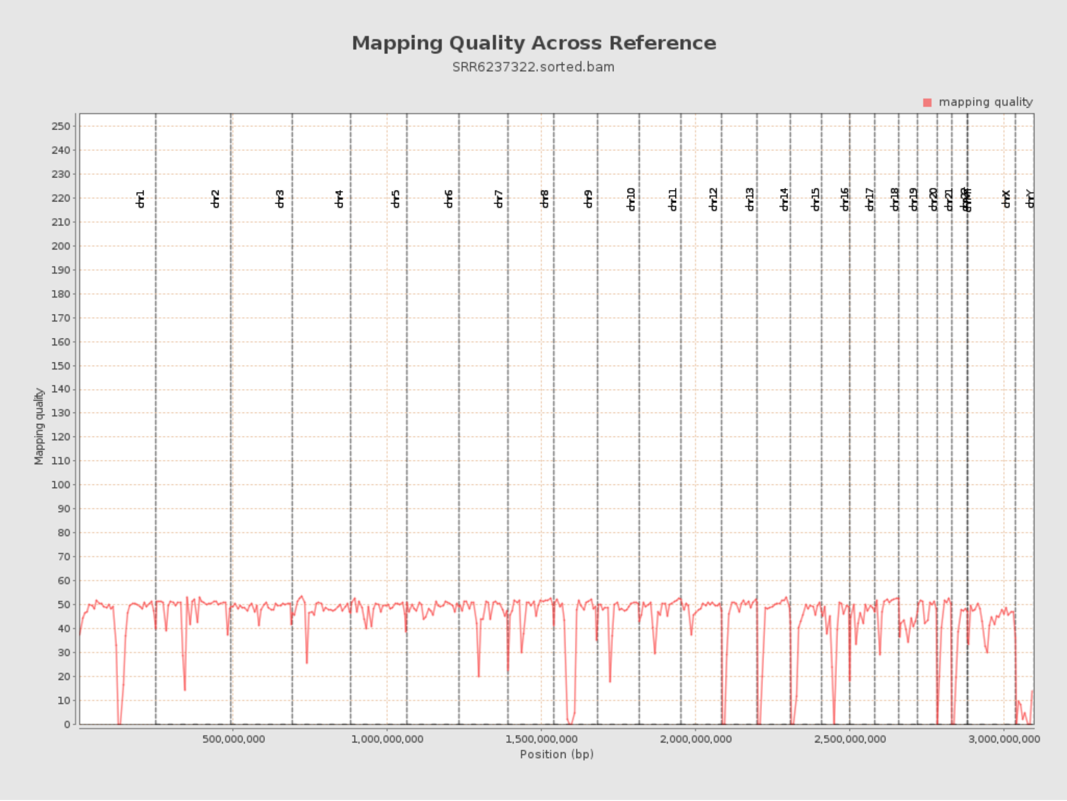
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram