Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:09:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237798.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_SRR6237798 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237798.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:09:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237798.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,904,478
Mapped reads	3,400,272 / 87.09%
Unmapped reads	504,206 / 12.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,211 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	548,903 / 14.06%
Duplication rate	12.5%
Clipped reads	964,017 / 24.69%

2.2. ACGT Content

Number/percentage of A's	71,290,374 / 29.58%
Number/percentage of C's	46,522,962 / 19.3%
Number/percentage of T's	73,471,190 / 30.48%
Number/percentage of G's	49,322,282 / 20.46%
Number/percentage of N's	405,646 / 0.17%
GC Percentage	39.77%

2.3. Coverage

Mean	0.0779

Standard Deviation	1.1686

2.4. Mapping Quality

Mean Mapping Quality	47.86

2.5. Mismatches and indels

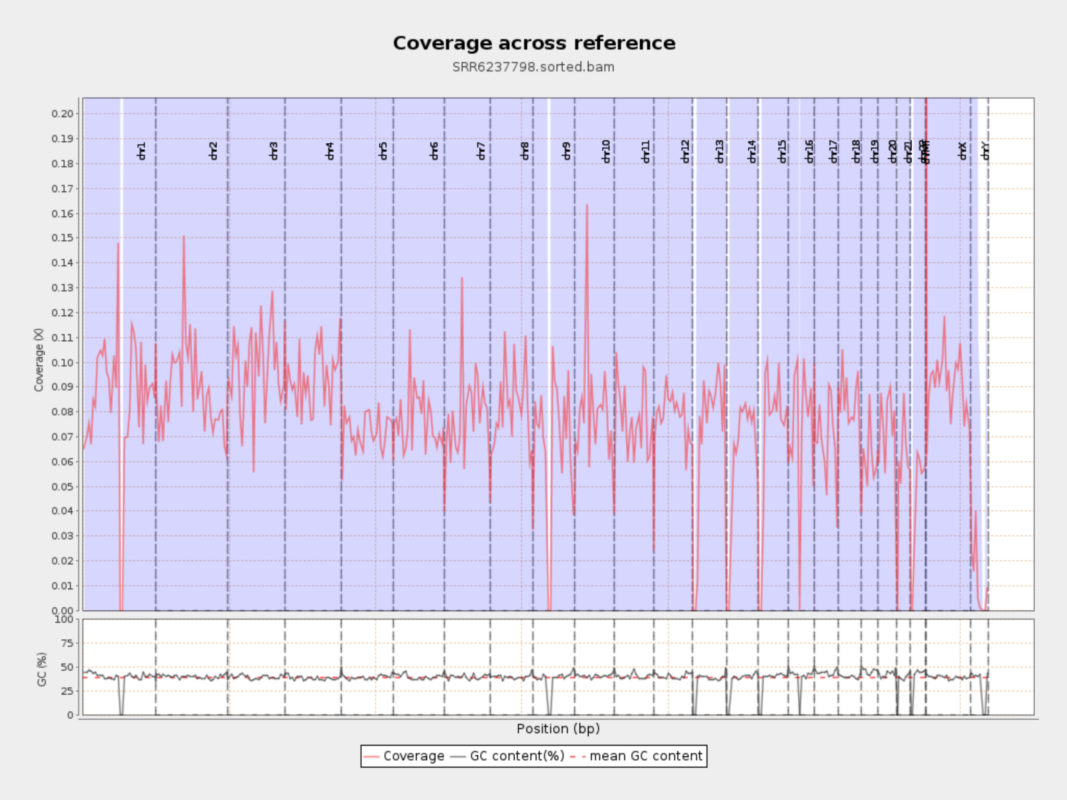
General error rate	0.83%
Mismatches	1,968,185
Insertions	18,065
Mapped reads with at least one insertion	0.53%
Deletions	55,647
Mapped reads with at least one deletion	1.62%
Homopolymer indels	47.89%

2.6. Chromosome stats

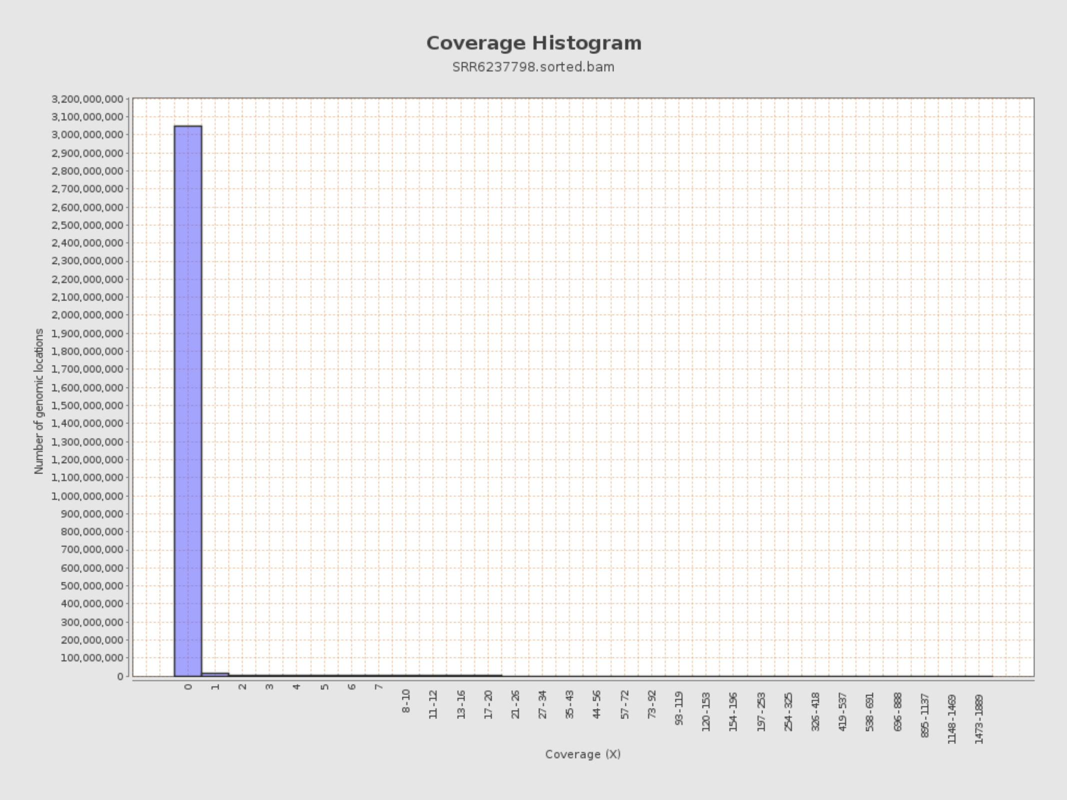
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21272404	0.0853	1.8451
chr2	243199373	21643836	0.089	1.1845
chr3	198022430	19259306	0.0973	1.1624
chr4	191154276	17930762	0.0938	1.1102
chr5	180915260	13031510	0.072	0.9503
chr6	171115067	13191591	0.0771	1.0299
chr7	159138663	12543318	0.0788	1.2711

chr8	146364022	12040538	0.0823	1.243
chr9	141213431	9562060	0.0677	1.032
chr10	135534747	10980450	0.081	1.2404
chr11	135006516	10371429	0.0768	1.0699
chr12	133851895	10541900	0.0788	1.0155
chr13	115169878	8042578	0.0698	0.9605
chr14	107349540	6741999	0.0628	0.94
chr15	102531392	7131882	0.0696	0.9463
chr16	90354753	6542443	0.0724	0.9842
chr17	81195210	5629836	0.0693	0.9318
chr18	78077248	6619158	0.0848	1.6287
chr19	59128983	3635410	0.0615	1.1749
chr20	63025520	4675126	0.0742	1.0073
chr21	48129895	2780546	0.0578	0.8224
chr22	51304566	2151136	0.0419	0.683
chrMT	16571	24761	1.4942	3.3628
chrX	155270560	14092286	0.0908	1.0945
chrY	59373566	676396	0.0114	0.3682

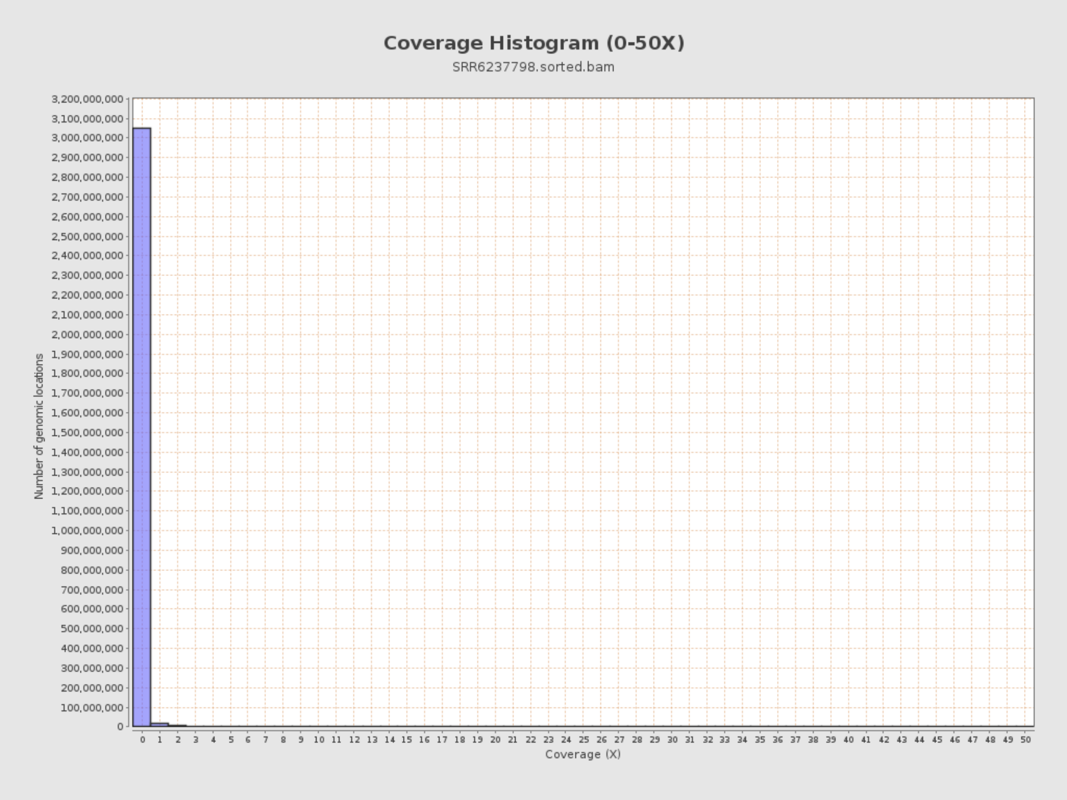
3. Results : Coverage across reference



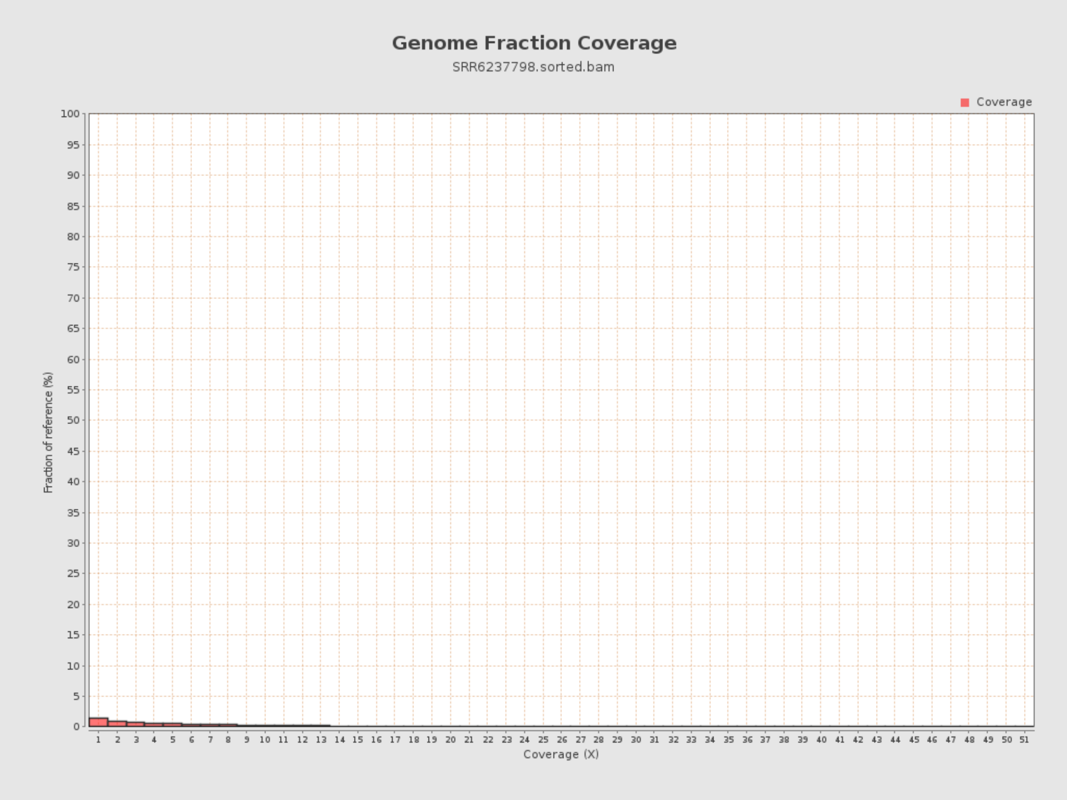
4. Results : Coverage Histogram



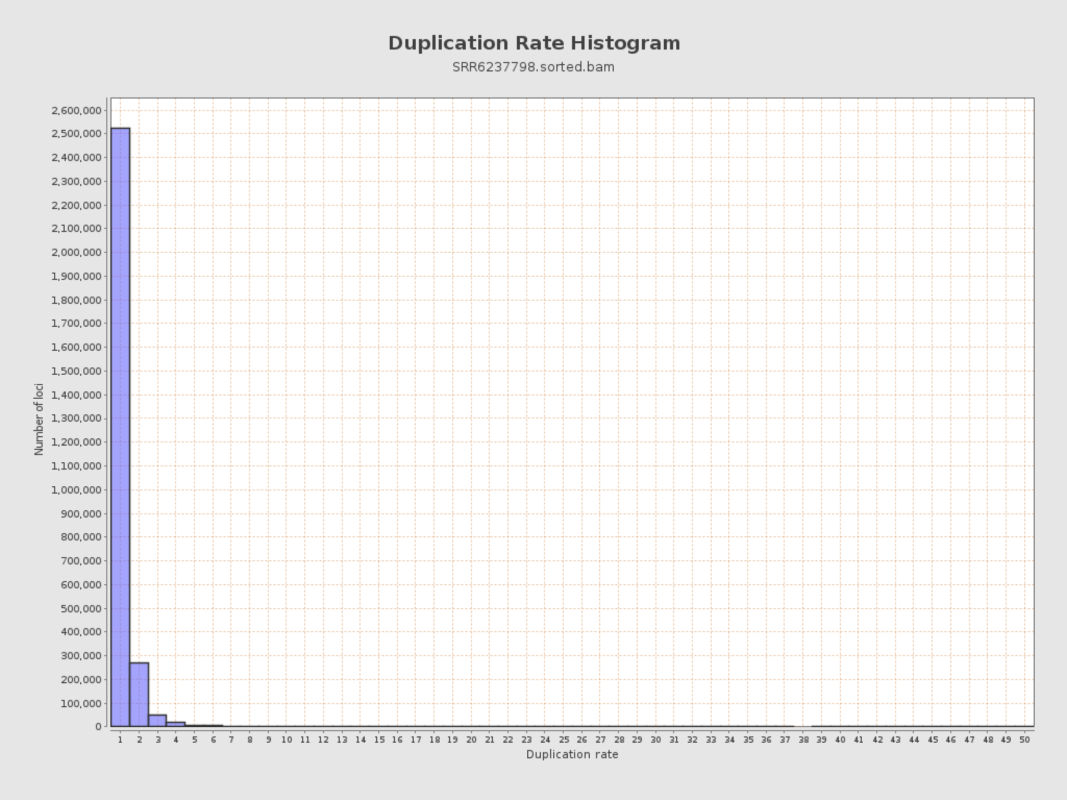
5. Results : Coverage Histogram (0-50X)



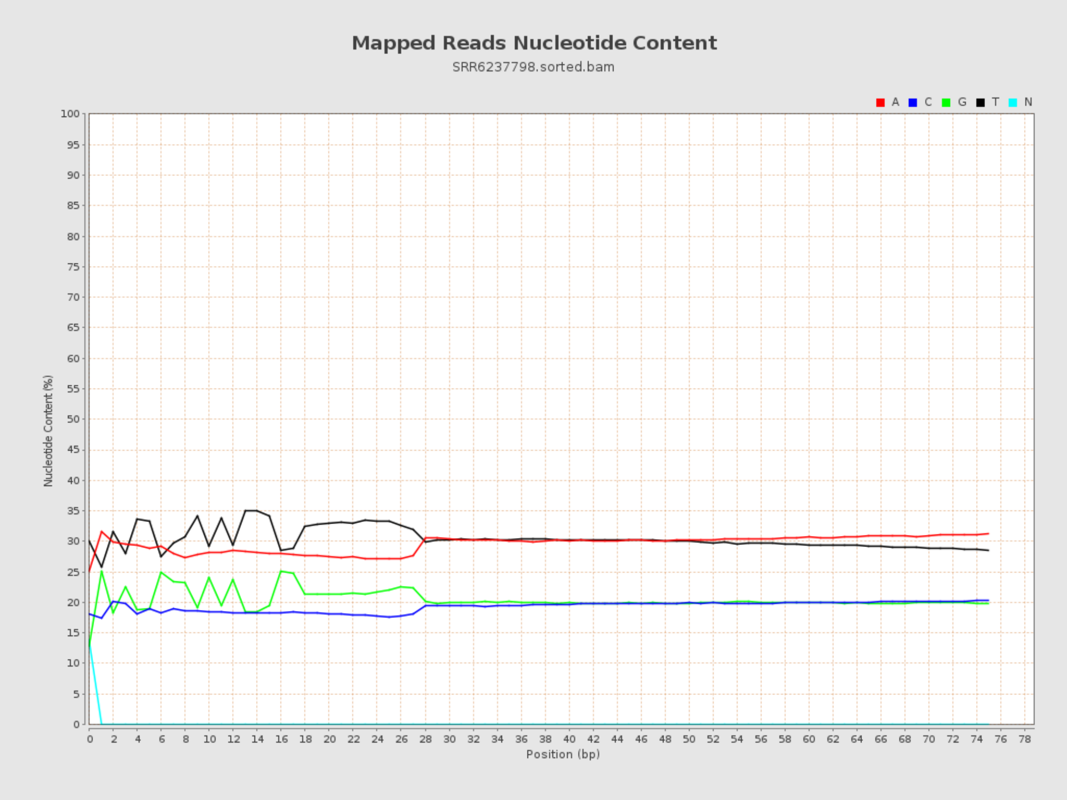
6. Results : Genome Fraction Coverage



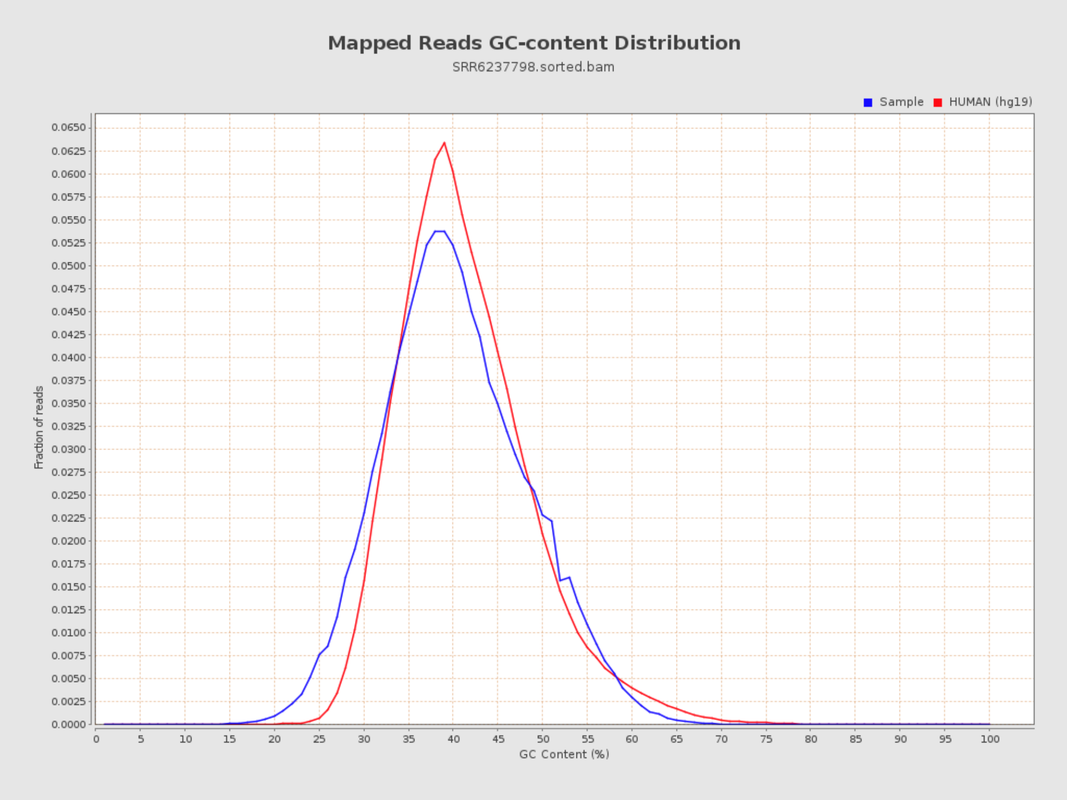
7. Results : Duplication Rate Histogram



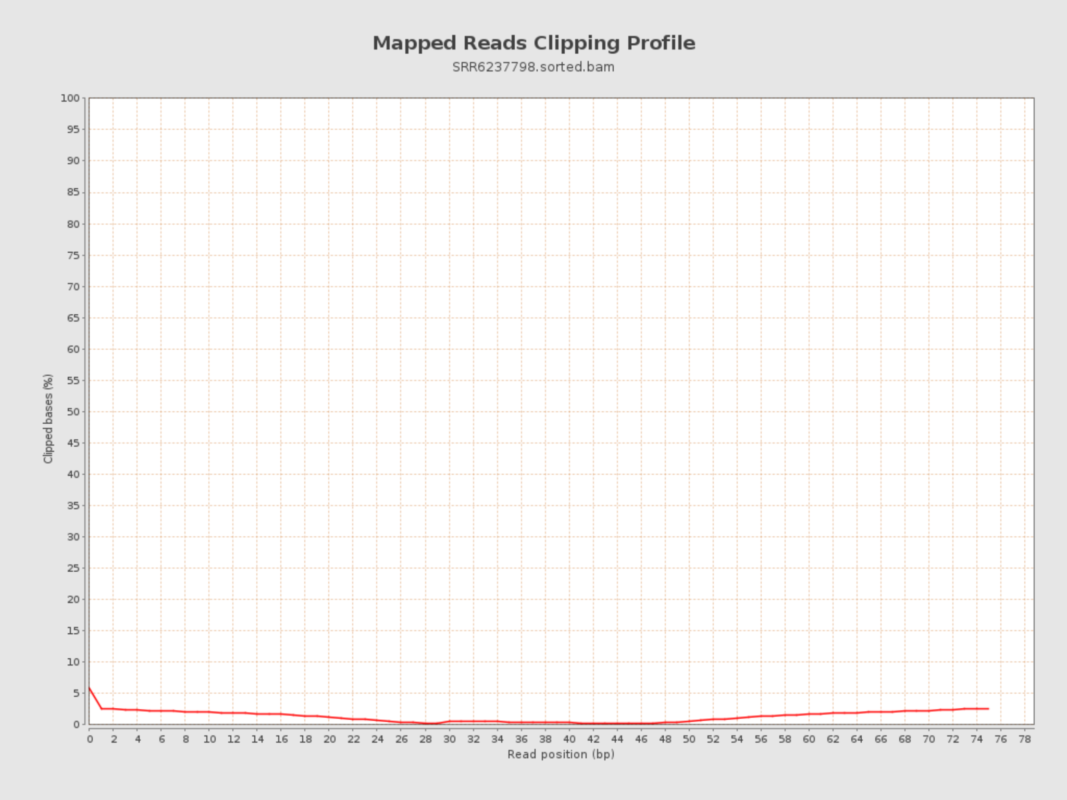
8. Results : Mapped Reads Nucleotide Content



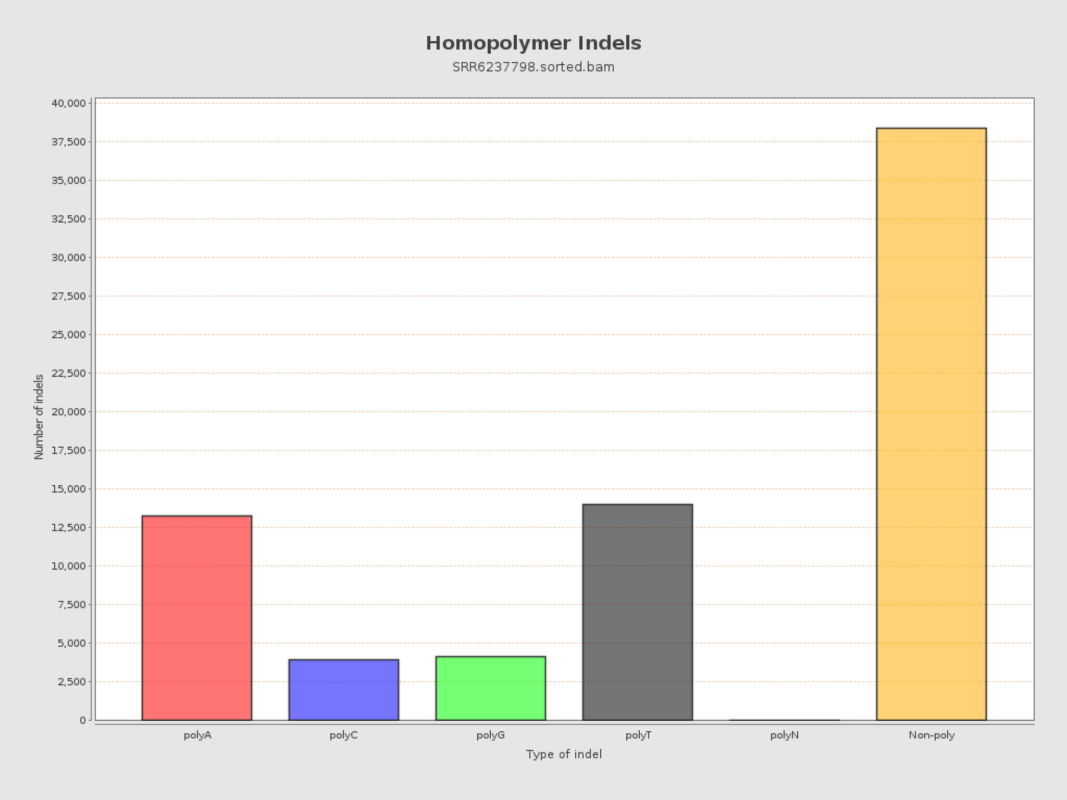
9. Results : Mapped Reads GC-content Distribution



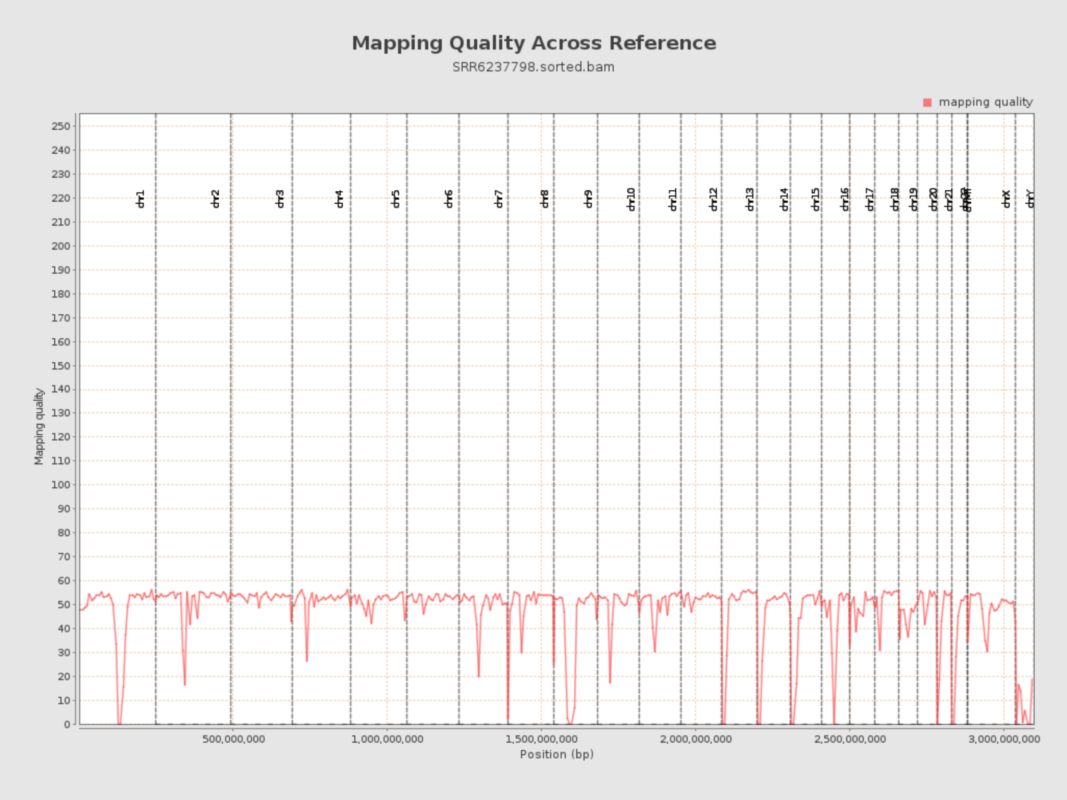
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram