Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:18:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237838.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_SRR6237838 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237838.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:18:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237838.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,795,675
Mapped reads	1,574,276 / 87.67%
Unmapped reads	221,399 / 12.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,618 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	50,653 / 2.82%
Duplication rate	2.03%
Clipped reads	822,495 / 45.8%

2.2. ACGT Content

Number/percentage of A's	28,242,795 / 27.69%
Number/percentage of C's	19,131,277 / 18.75%
Number/percentage of T's	30,395,416 / 29.8%
Number/percentage of G's	24,142,109 / 23.67%
Number/percentage of N's	95,331 / 0.09%
GC Percentage	42.42%

2.3. Coverage

Mean	0.033

Standard Deviation	0.3637

2.4. Mapping Quality

Mean Mapping Quality	43.65

2.5. Mismatches and indels

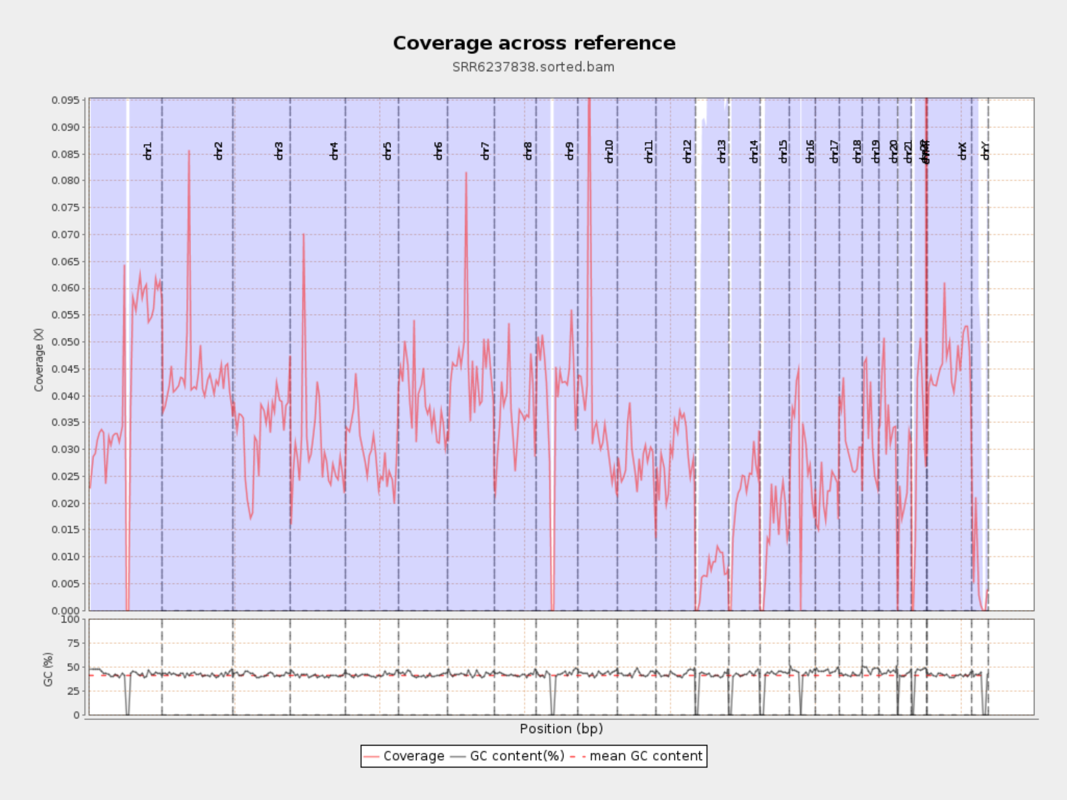
General error rate	0.83%
Mismatches	825,645
Insertions	9,058
Mapped reads with at least one insertion	0.57%
Deletions	25,024
Mapped reads with at least one deletion	1.57%
Homopolymer indels	45.75%

2.6. Chromosome stats

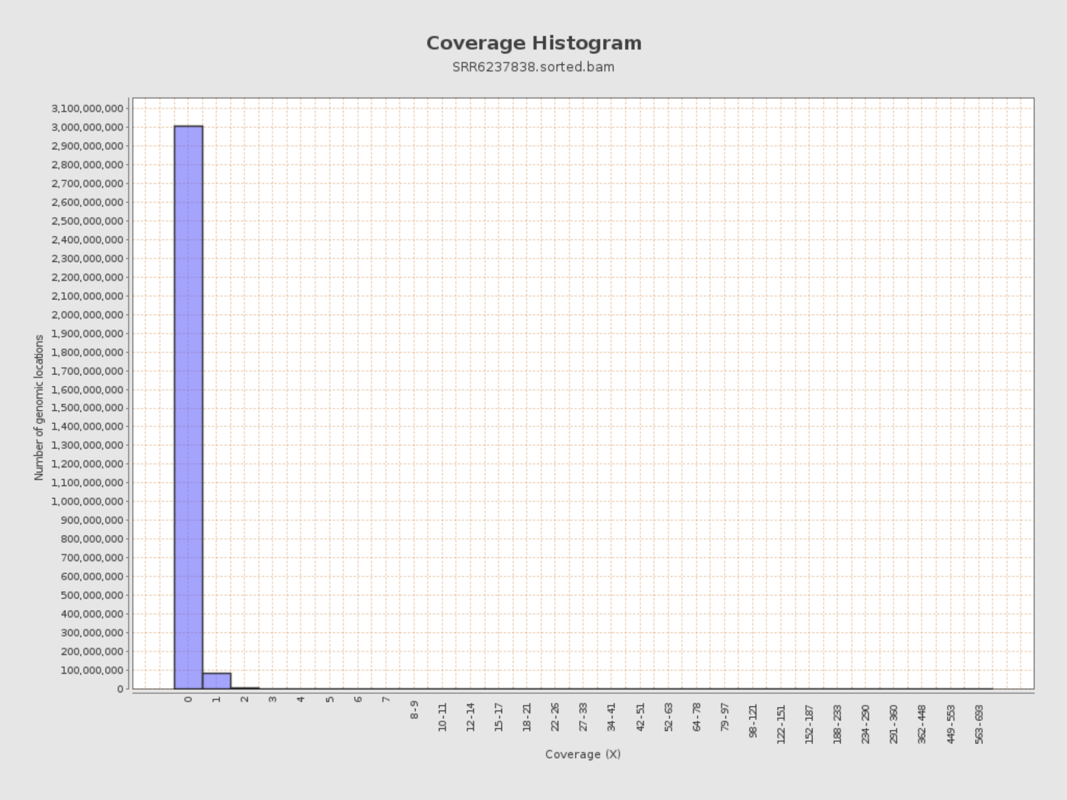
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10369487	0.0416	0.6207
chr2	243199373	10688330	0.0439	0.4306
chr3	198022430	6675049	0.0337	0.2113
chr4	191154276	5761860	0.0301	0.251
chr5	180915260	5374477	0.0297	0.1875
chr6	171115067	6655203	0.0389	0.2658
chr7	159138663	7286501	0.0458	0.574

chr8	146364022	5297808	0.0362	0.3021
chr9	141213431	5538848	0.0392	0.3736
chr10	135534747	5129922	0.0378	0.6127
chr11	135006516	3738408	0.0277	0.2551
chr12	133851895	3905201	0.0292	0.196
chr13	115169878	815172	0.0071	0.0888
chr14	107349540	2239741	0.0209	0.2304
chr15	102531392	1493582	0.0146	0.1309
chr16	90354753	2603932	0.0288	0.2498
chr17	81195210	1723469	0.0212	0.1987
chr18	78077248	2447797	0.0314	0.5902
chr19	59128983	2036590	0.0344	0.457
chr20	63025520	2275433	0.0361	0.2217
chr21	48129895	1035454	0.0215	0.225
chr22	51304566	1425900	0.0278	0.1818
chrMT	16571	44979	2.7143	2.5031
chrX	155270560	7146908	0.046	0.2712
chrY	59373566	339098	0.0057	0.2161

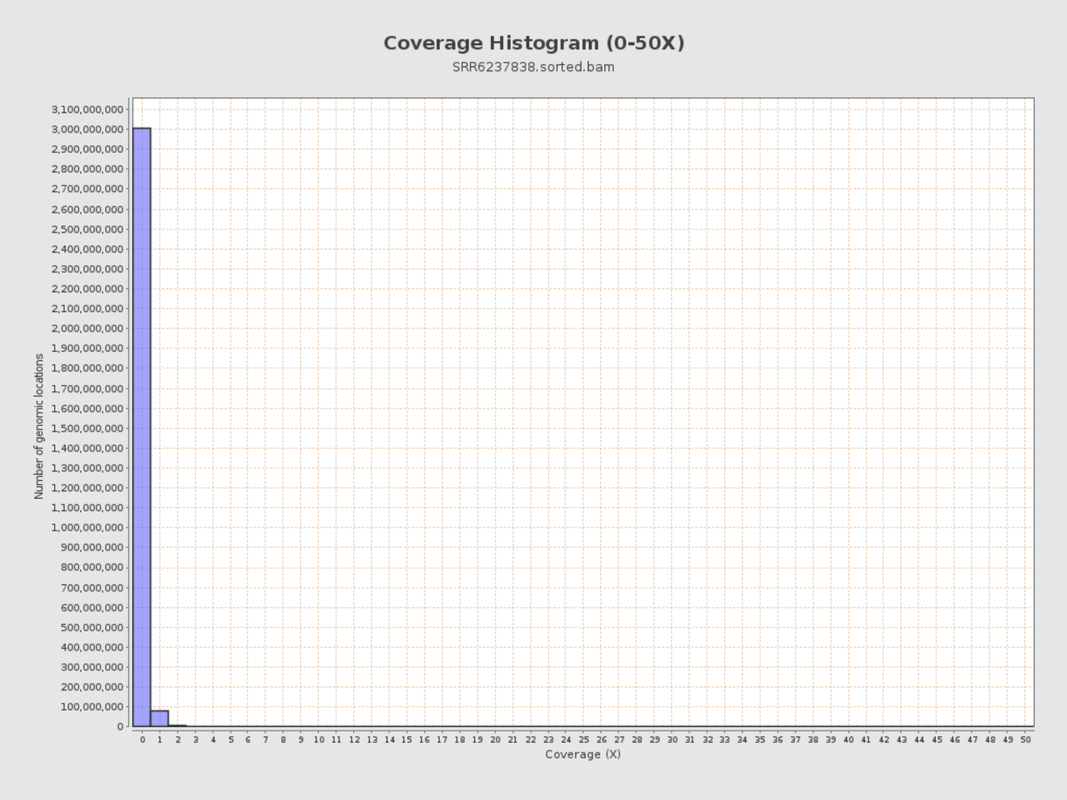
3. Results : Coverage across reference



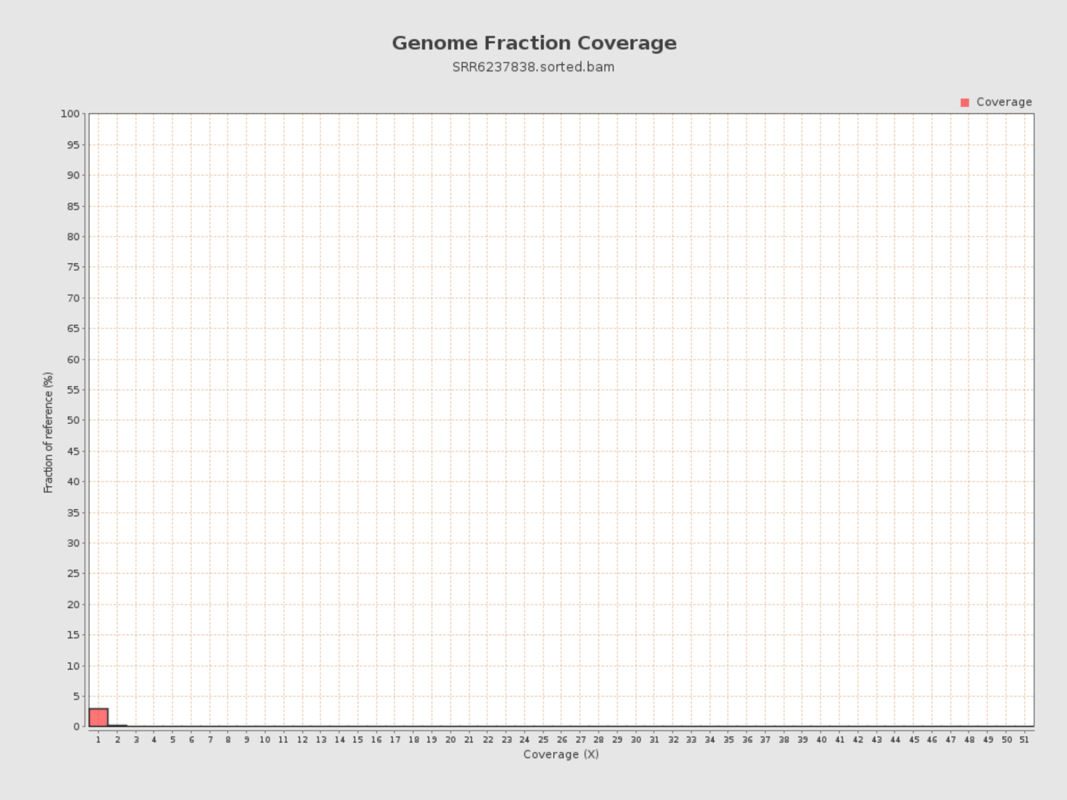
4. Results : Coverage Histogram



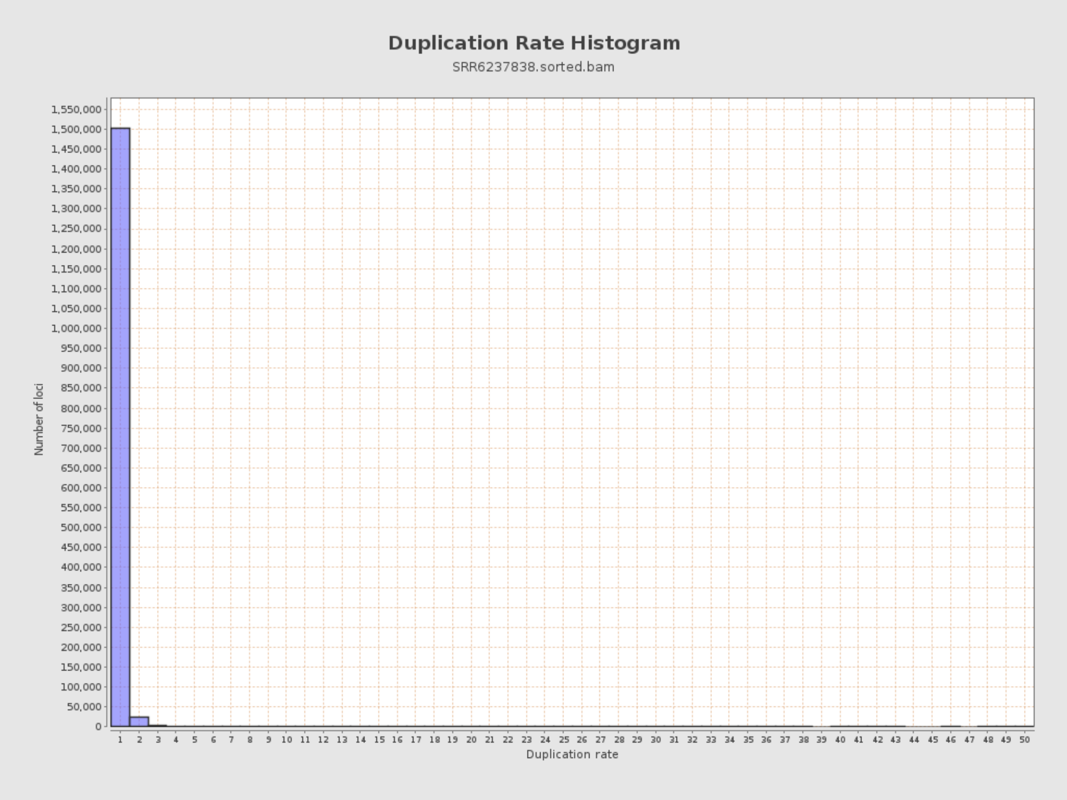
5. Results : Coverage Histogram (0-50X)



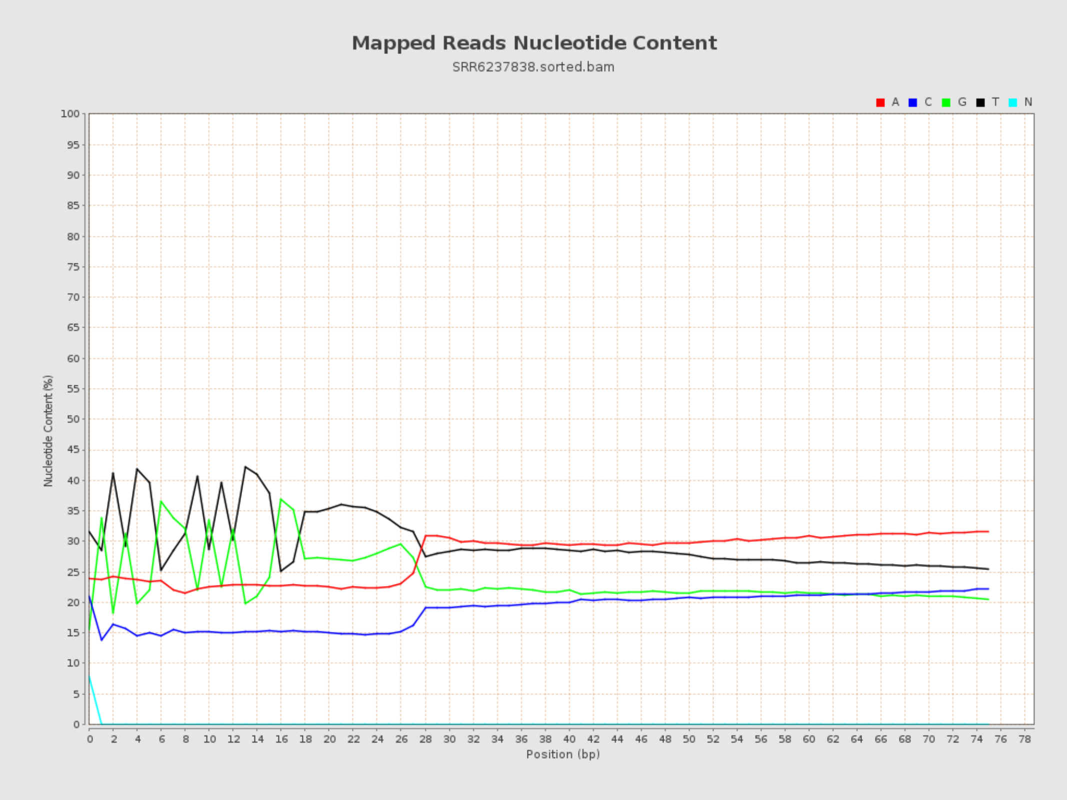
6. Results : Genome Fraction Coverage



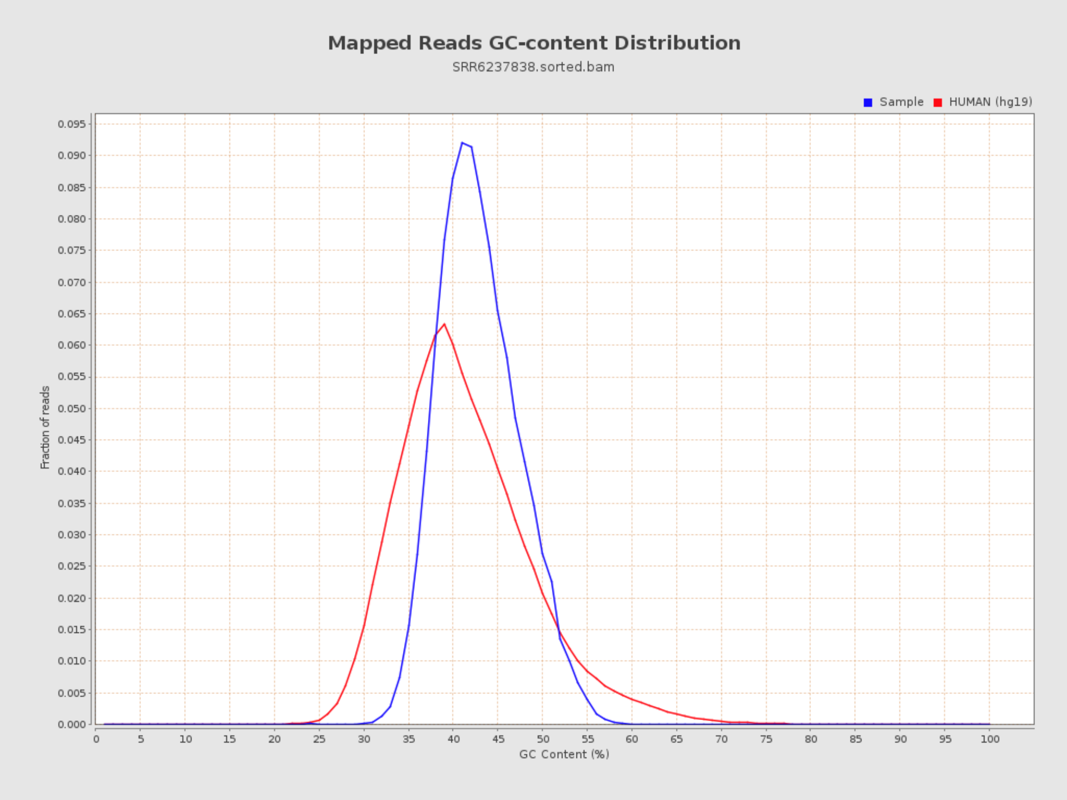
7. Results : Duplication Rate Histogram



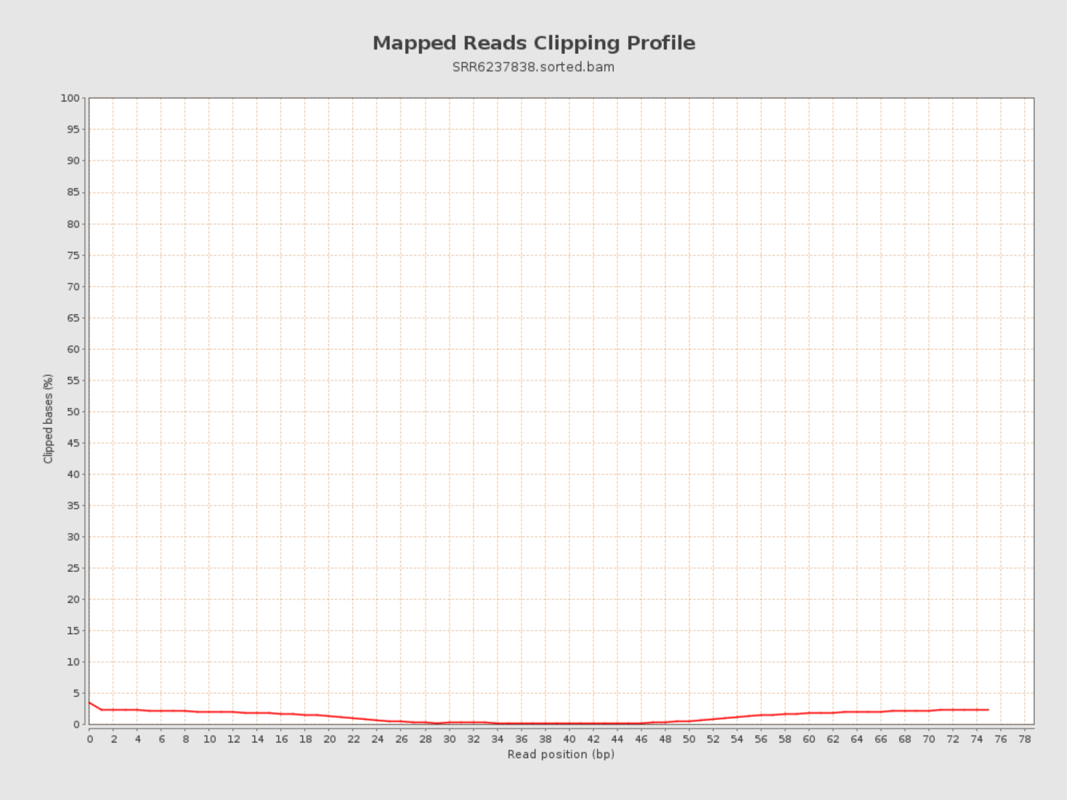
8. Results : Mapped Reads Nucleotide Content



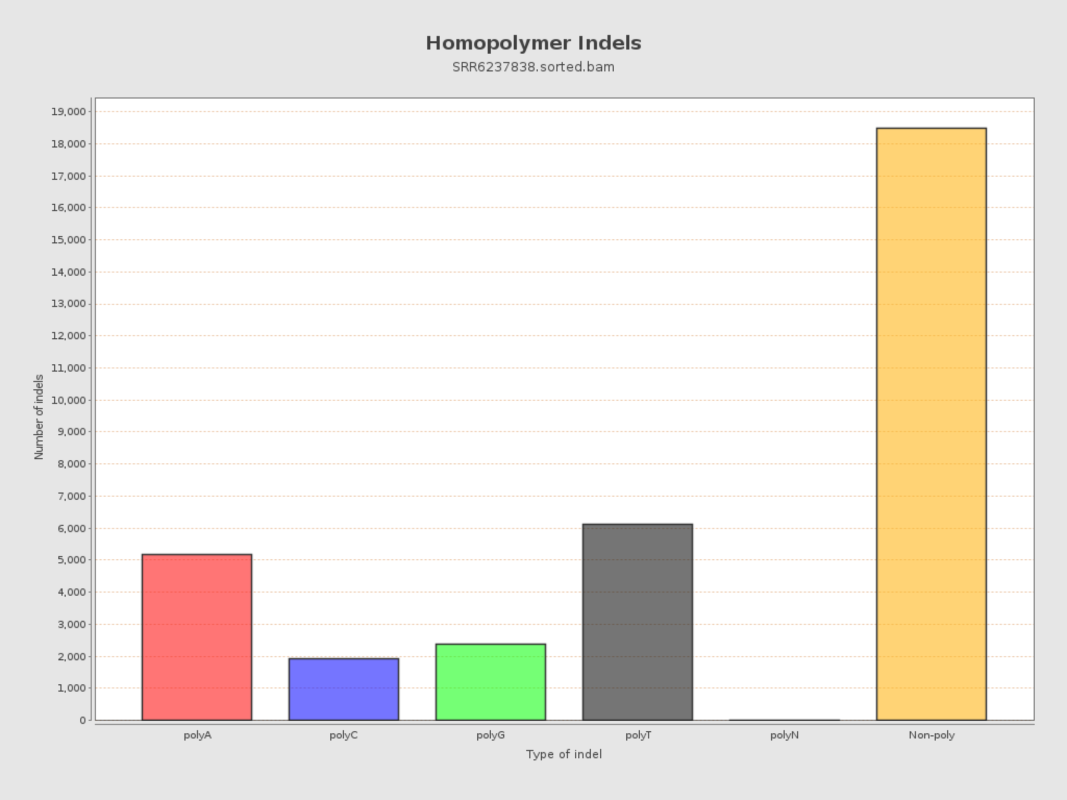
9. Results : Mapped Reads GC-content Distribution



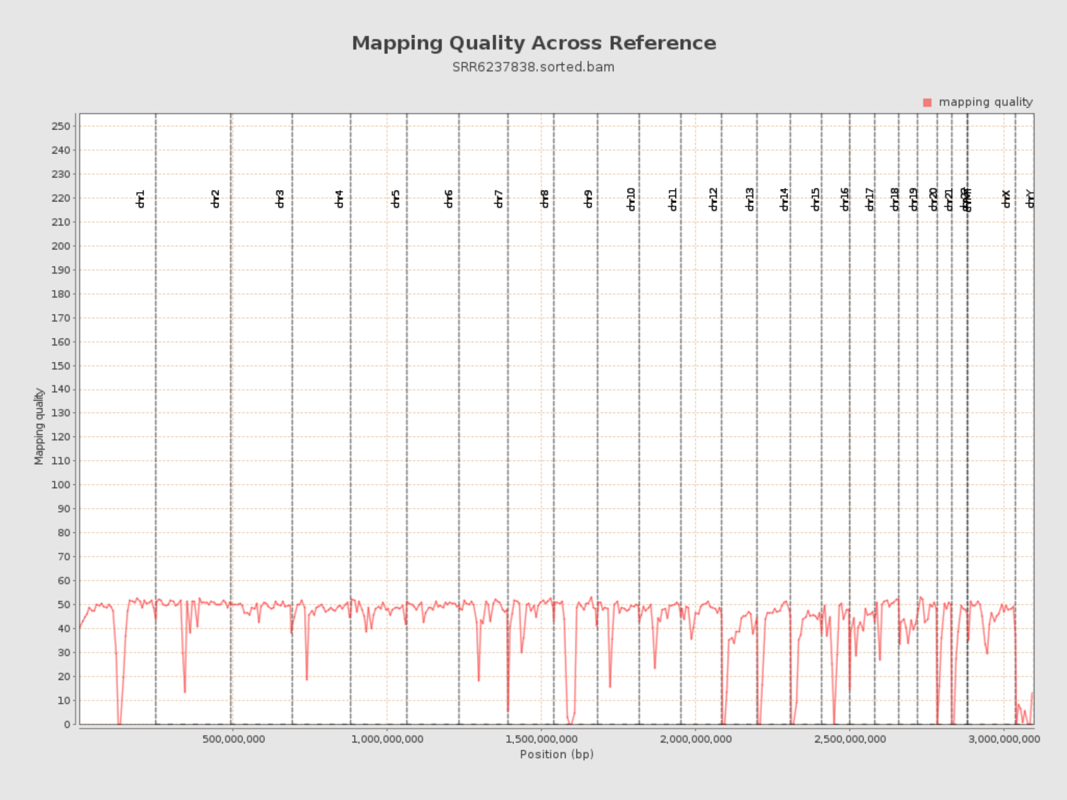
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram