Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:26:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237338.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_SRR6237338 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237338.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:26:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237338.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,346,975
Mapped reads	3,081,990 / 92.08%
Unmapped reads	264,985 / 7.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,034 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	351,569 / 10.5%
Duplication rate	9.54%
Clipped reads	1,861,942 / 55.63%

2.2. ACGT Content

Number/percentage of A's	50,722,757 / 26.44%
Number/percentage of C's	32,533,982 / 16.96%
Number/percentage of T's	64,583,207 / 33.66%
Number/percentage of G's	43,992,470 / 22.93%
Number/percentage of N's	20,835 / 0.01%
GC Percentage	39.89%

2.3. Coverage

Mean	0.062

Standard Deviation	0.639

2.4. Mapping Quality

Mean Mapping Quality	42.56

2.5. Mismatches and indels

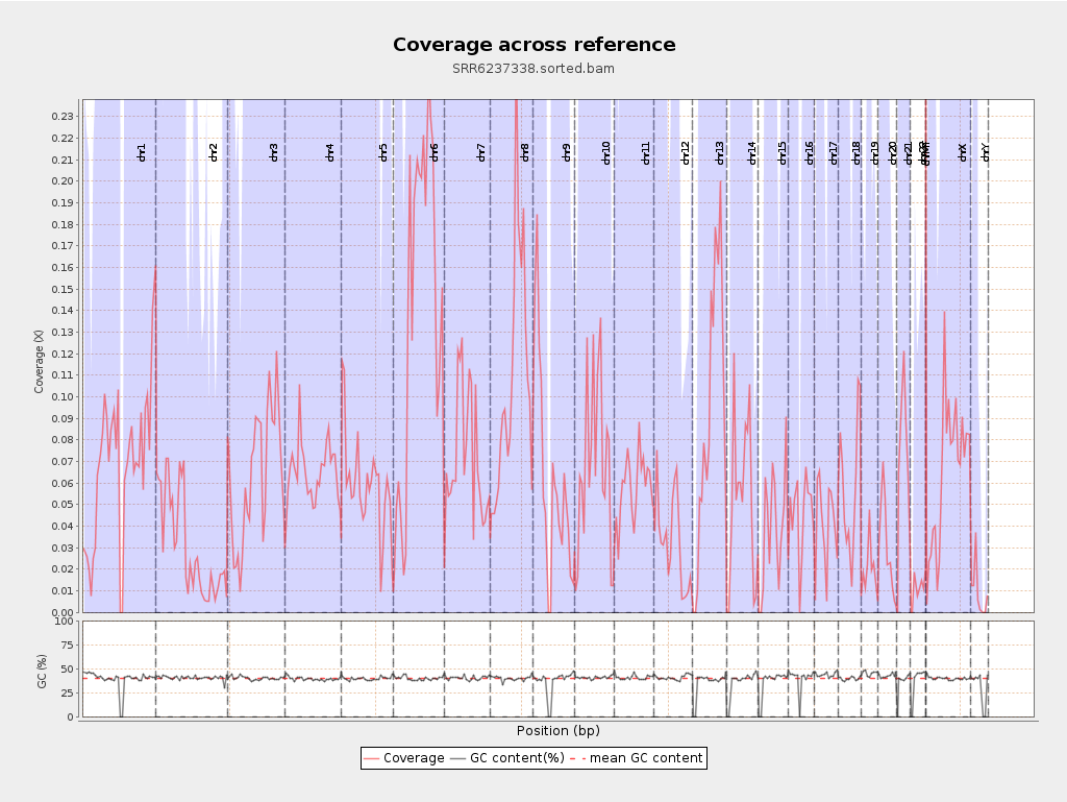
General error rate	0.63%
Mismatches	1,181,779
Insertions	13,208
Mapped reads with at least one insertion	0.43%
Deletions	64,897
Mapped reads with at least one deletion	2.08%
Homopolymer indels	42.73%

2.6. Chromosome stats

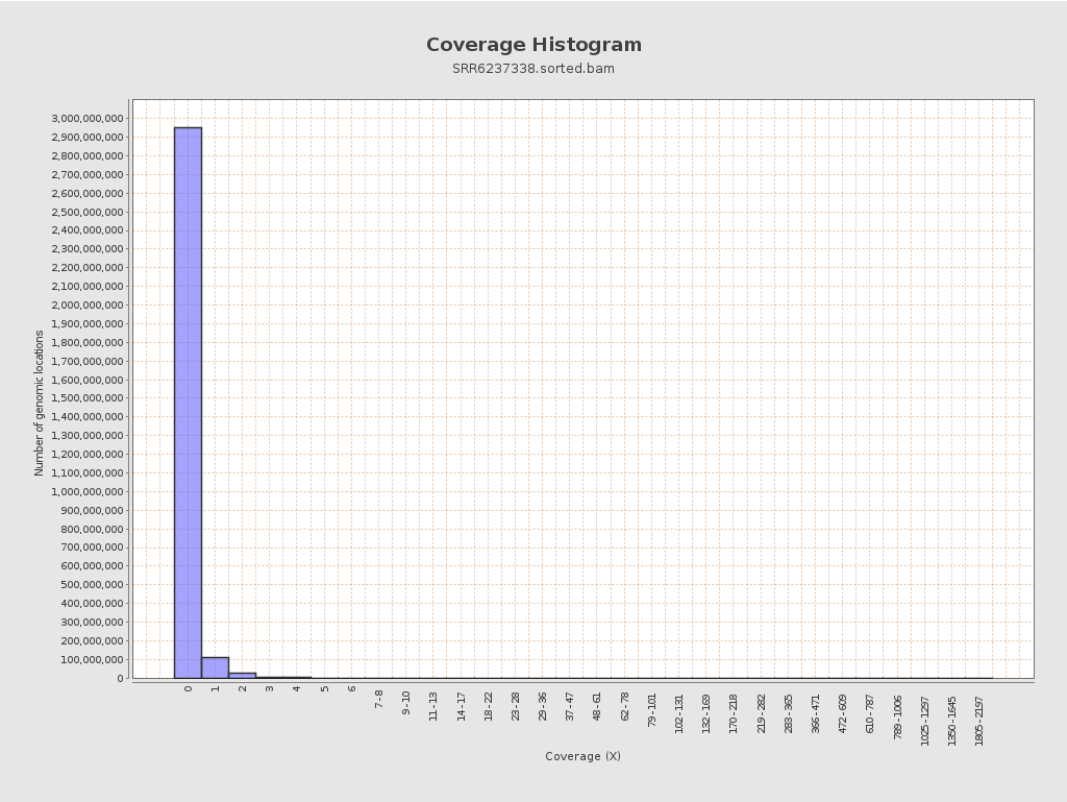
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17249097	0.0692	0.6785
chr2	243199373	7504684	0.0309	1.0656
chr3	198022430	12530815	0.0633	0.3225
chr4	191154276	12563486	0.0657	0.3924
chr5	180915260	10531687	0.0582	0.3128
chr6	171115067	24318934	0.1421	0.7709
chr7	159138663	11465452	0.072	0.8755

chr8	146364022	15971969	0.1091	1.3517
chr9	141213431	8692608	0.0616	0.4298
chr10	135534747	9149923	0.0675	0.611
chr11	135006516	7738347	0.0573	0.3858
chr12	133851895	4282249	0.032	0.2541
chr13	115169878	10712343	0.093	0.4365
chr14	107349540	5623994	0.0524	0.3184
chr15	102531392	3972685	0.0387	0.2917
chr16	90354753	3997233	0.0442	0.329
chr17	81195210	3310979	0.0408	0.3712
chr18	78077248	4495181	0.0576	1.0695
chr19	59128983	1211689	0.0205	0.5002
chr20	63025520	2005702	0.0318	0.2433
chr21	48129895	3447923	0.0716	0.3833
chr22	51304566	533227	0.0104	0.1247
chrMT	16571	4231	0.2553	0.6143
chrX	155270560	10086278	0.065	0.385
chrY	59373566	566563	0.0095	0.2948

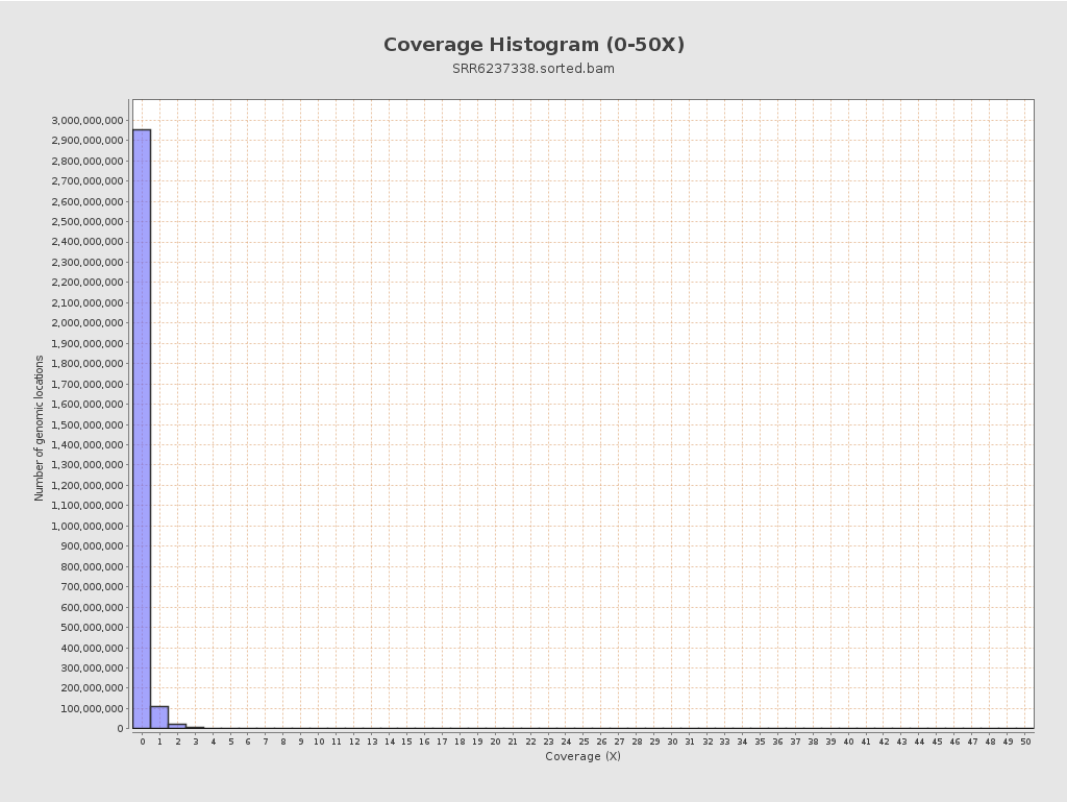
3. Results : Coverage across reference



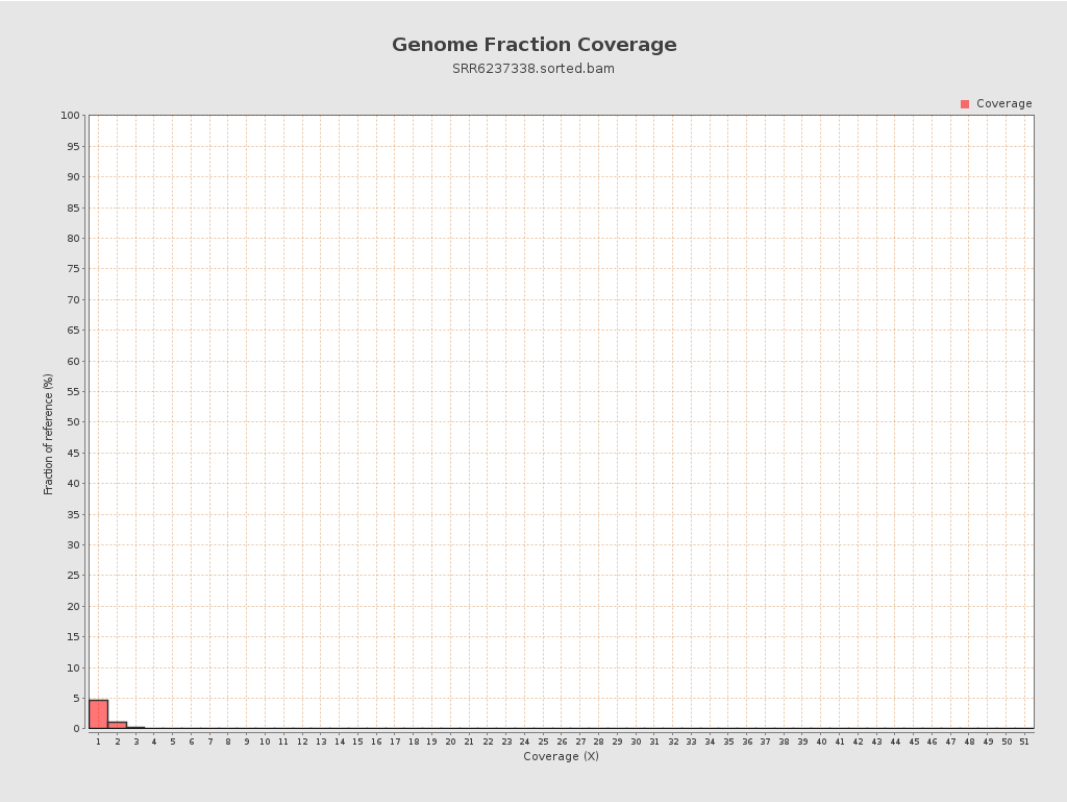
4. Results : Coverage Histogram



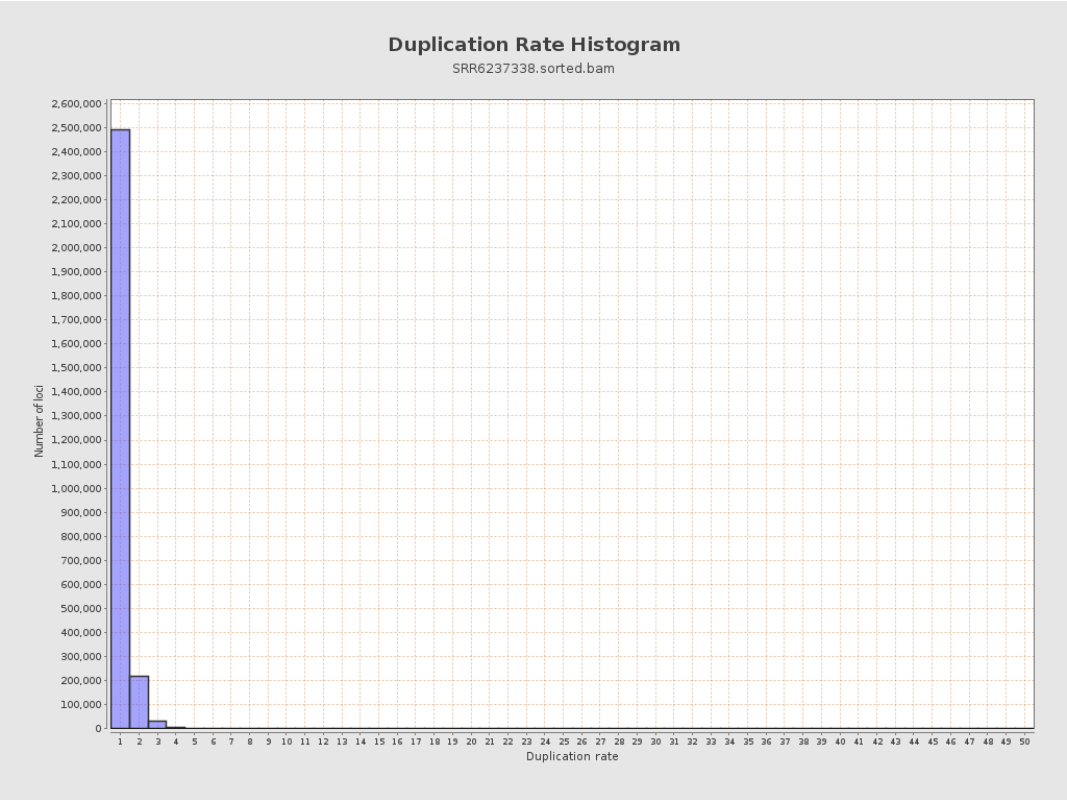
5. Results : Coverage Histogram (0-50X)



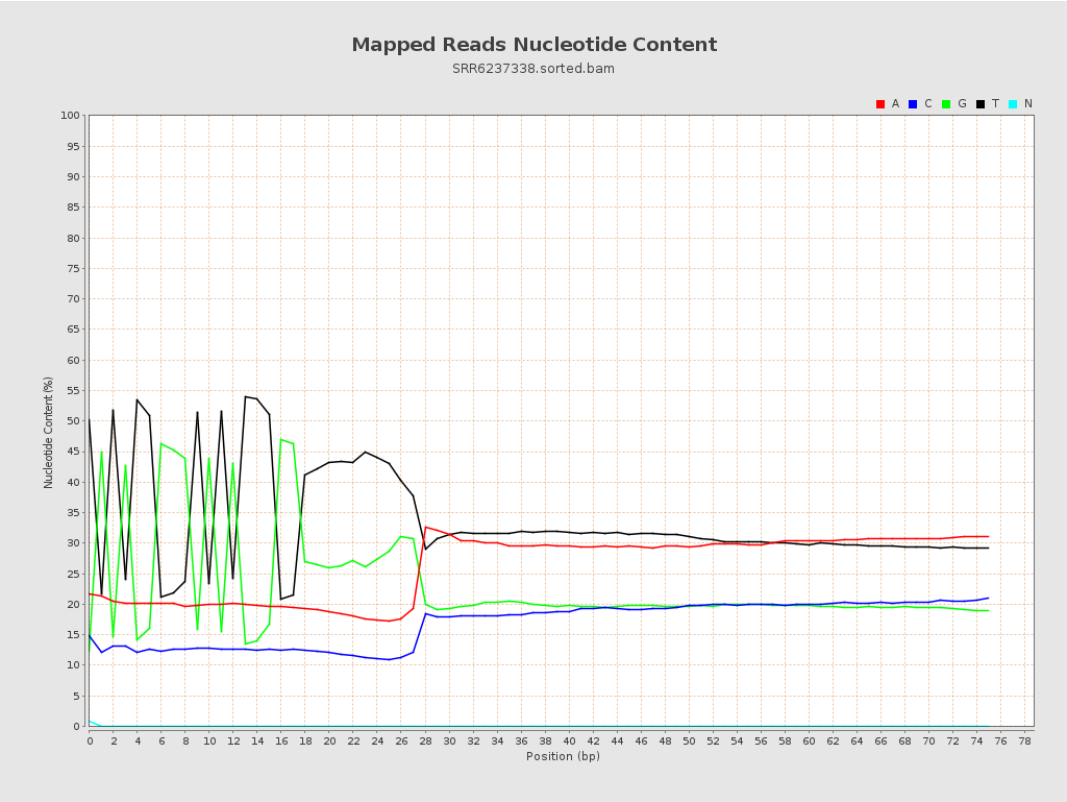
6. Results : Genome Fraction Coverage



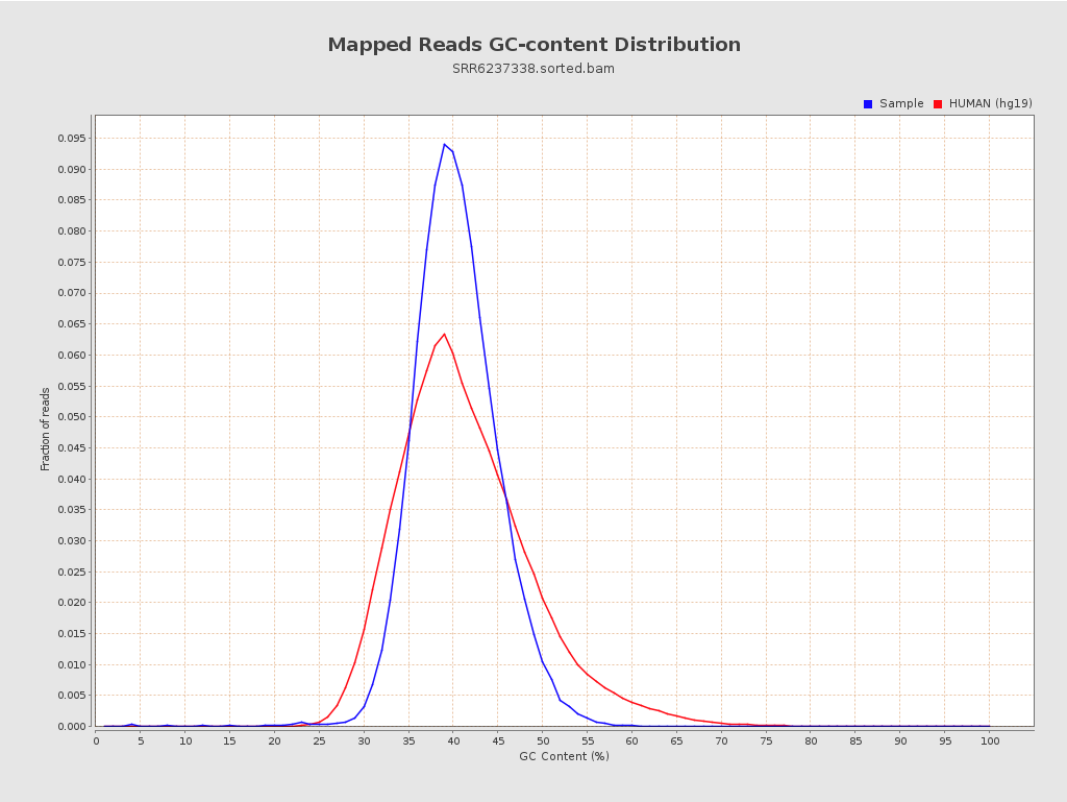
7. Results : Duplication Rate Histogram



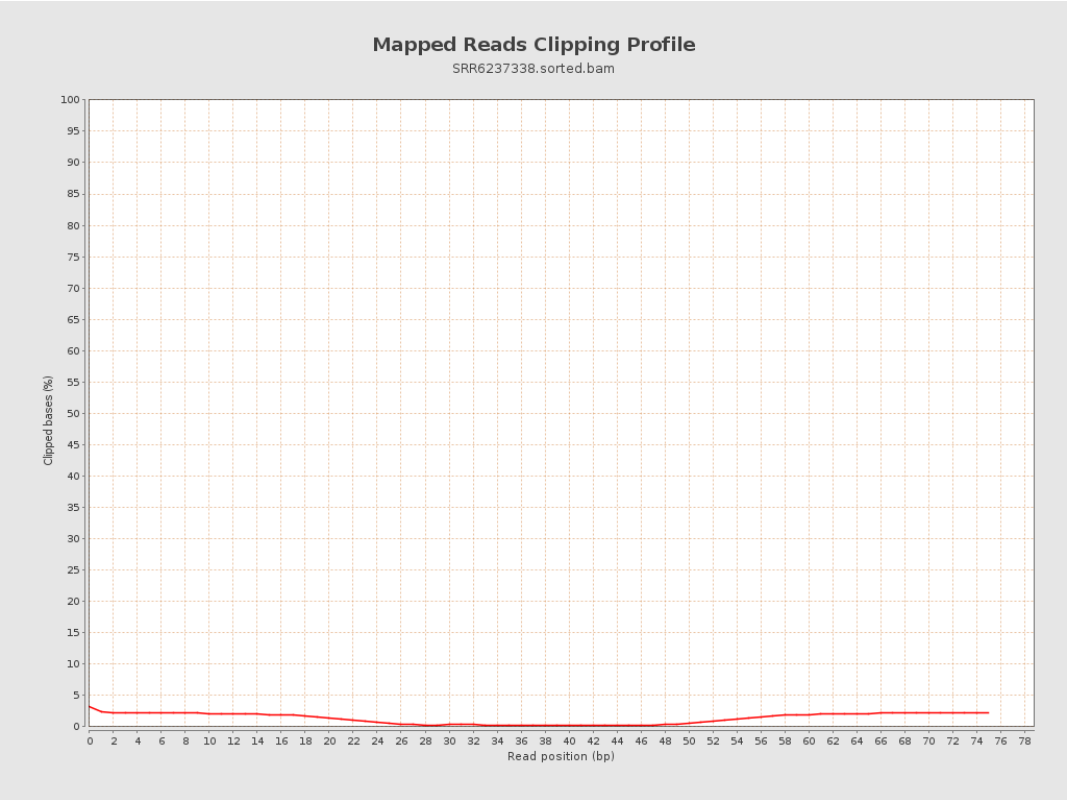
8. Results : Mapped Reads Nucleotide Content



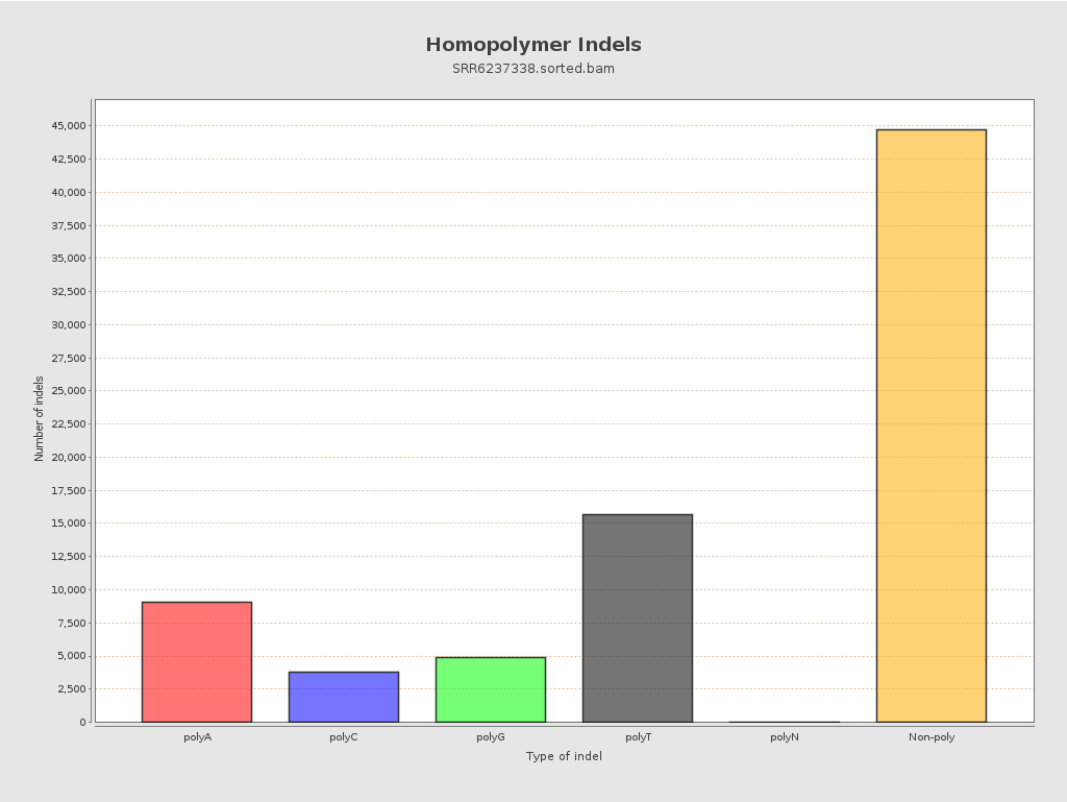
9. Results : Mapped Reads GC-content Distribution



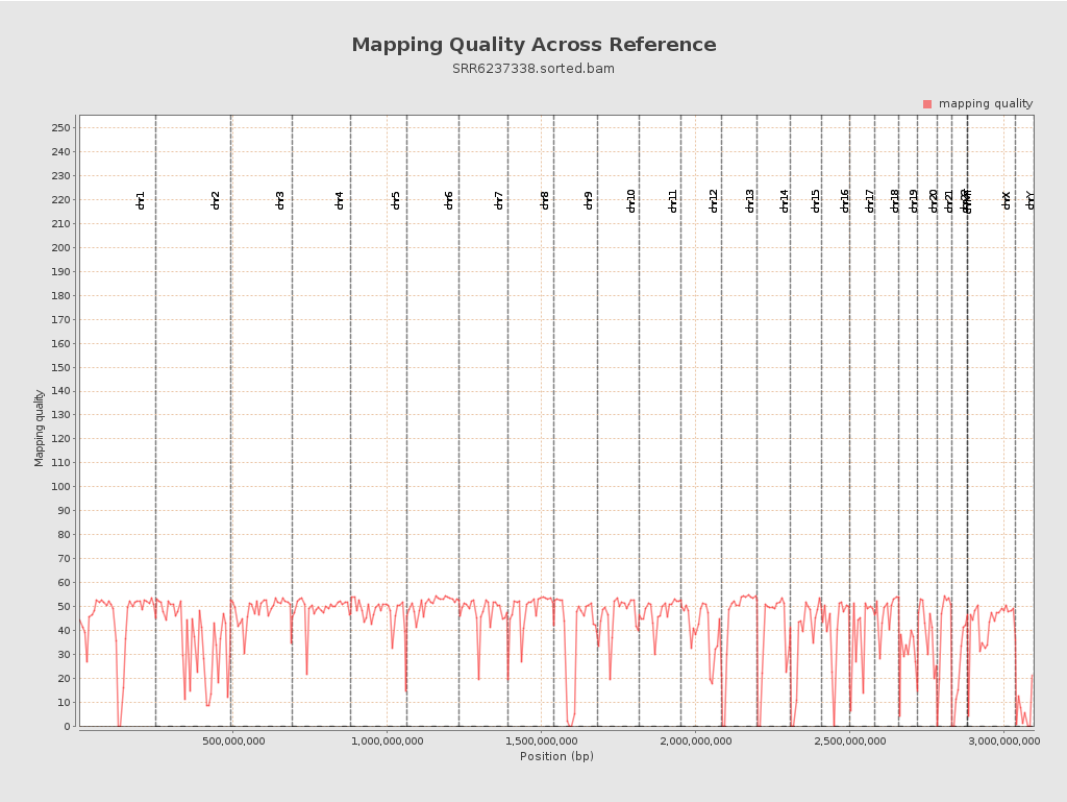
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram