Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:14:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237335.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_SRR6237335 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237335.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:14:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237335.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,431,655
Mapped reads	3,042,343 / 88.66%
Unmapped reads	389,312 / 11.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,079 / 0.85%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	1,302,943 / 37.97%
Duplication rate	26.55%
Clipped reads	2,307,242 / 67.23%

2.2. ACGT Content

Number/percentage of A's	44,502,060 / 24.92%
Number/percentage of C's	30,370,933 / 17.01%
Number/percentage of T's	60,402,888 / 33.83%
Number/percentage of G's	43,279,213 / 24.24%
Number/percentage of N's	16,917 / 0.01%
GC Percentage	41.24%

2.3. Coverage

Mean	0.0577

Standard Deviation	1.0078

2.4. Mapping Quality

Mean Mapping Quality	40.29

2.5. Mismatches and indels

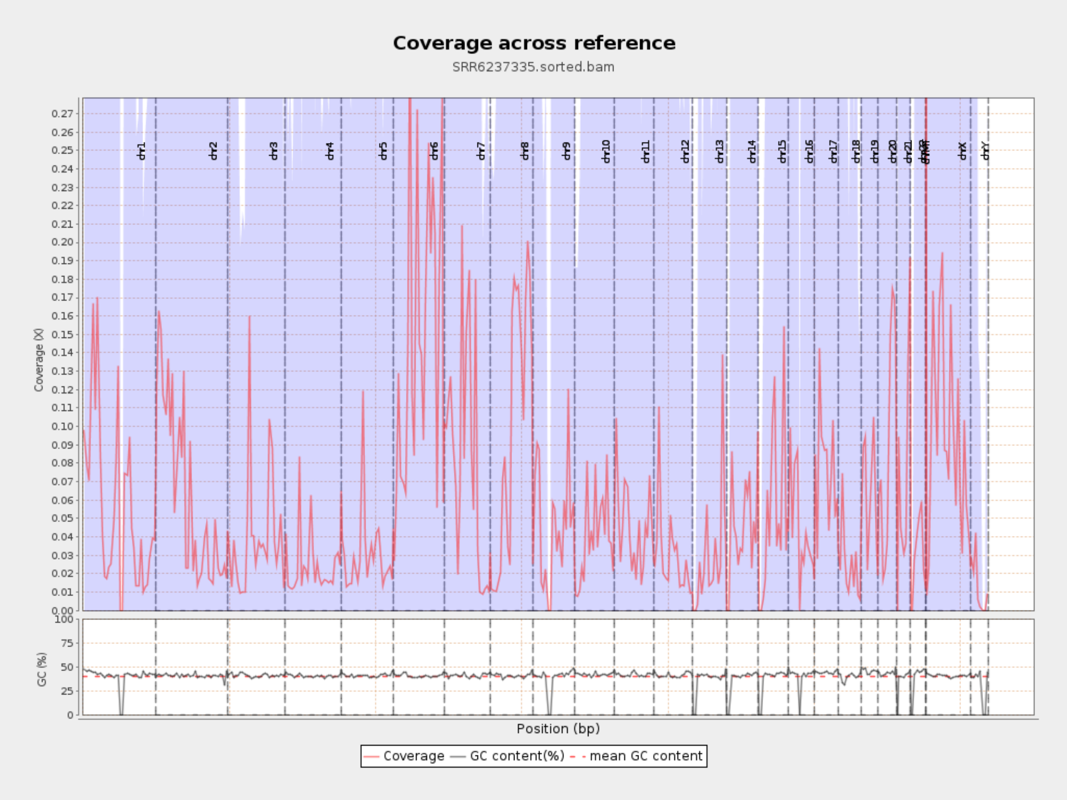
General error rate	0.71%
Mismatches	1,236,928
Insertions	12,131
Mapped reads with at least one insertion	0.39%
Deletions	63,480
Mapped reads with at least one deletion	2.06%
Homopolymer indels	40.63%

2.6. Chromosome stats

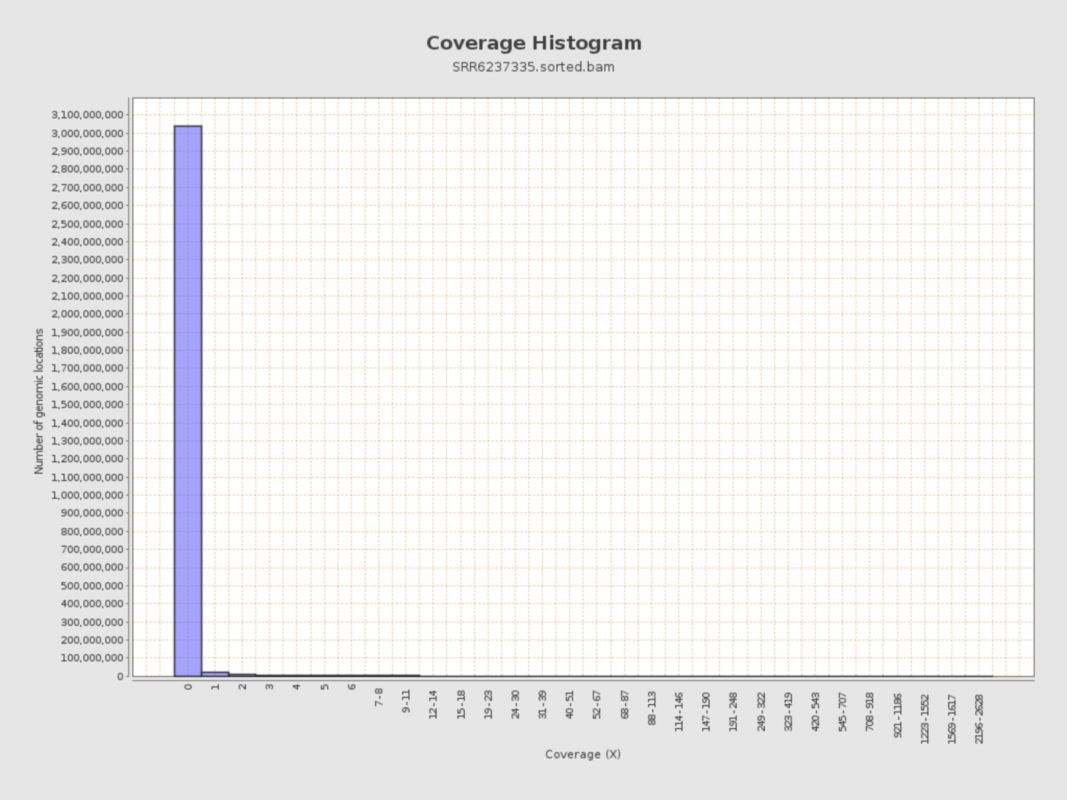
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14189716	0.0569	0.6876
chr2	243199373	15270773	0.0628	1.4788
chr3	198022430	7877944	0.0398	0.4893
chr4	191154276	4566948	0.0239	0.3853
chr5	180915260	5420909	0.03	0.427
chr6	171115067	25883833	0.1513	2.1429
chr7	159138663	13056650	0.082	1.4512

chr8	146364022	14717721	0.1006	1.1771
chr9	141213431	6564675	0.0465	0.6489
chr10	135534747	5401048	0.0398	0.6031
chr11	135006516	6054767	0.0448	0.807
chr12	133851895	4056571	0.0303	0.4427
chr13	115169878	3410481	0.0296	0.5192
chr14	107349540	4591818	0.0428	0.5192
chr15	102531392	5240658	0.0511	0.603
chr16	90354753	4032284	0.0446	0.6403
chr17	81195210	6353412	0.0782	0.9141
chr18	78077248	1986931	0.0254	2.3253
chr19	59128983	3786174	0.064	0.7182
chr20	63025520	5801456	0.092	0.77
chr21	48129895	3589651	0.0746	0.6861
chr22	51304566	1612455	0.0314	0.4263
chrMT	16571	12116	0.7312	2.3351
chrX	155270560	14437556	0.093	0.8209
chrY	59373566	765302	0.0129	0.3417

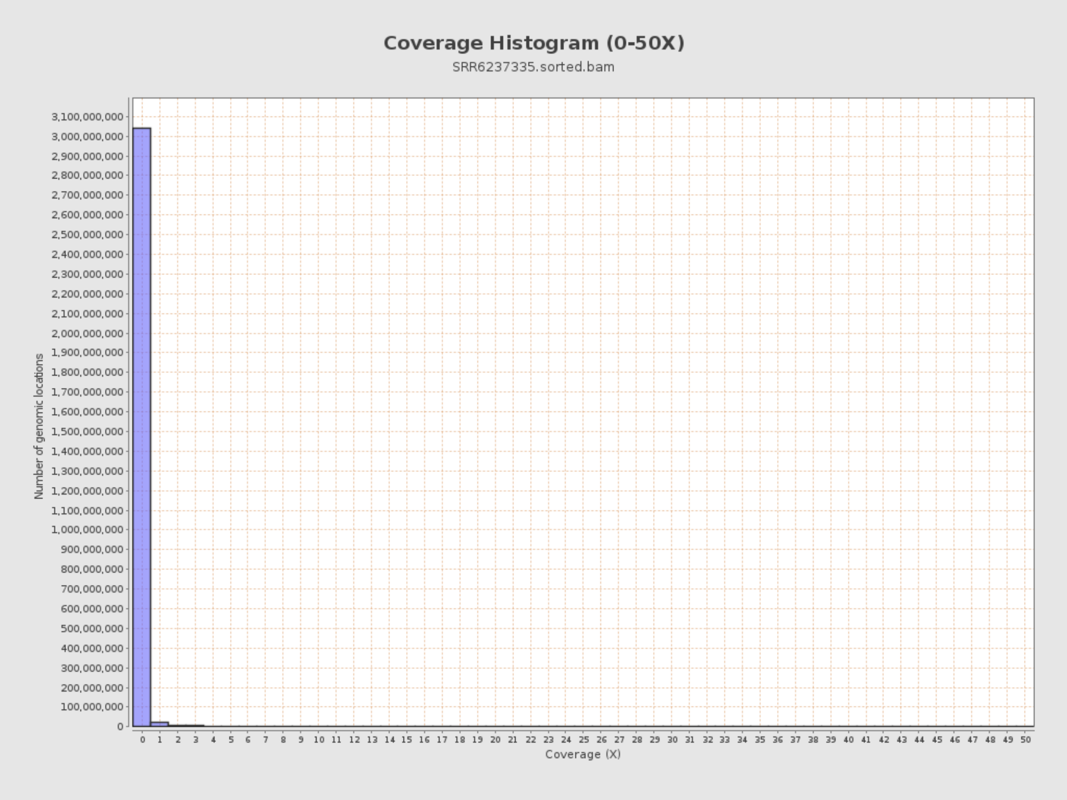
3. Results : Coverage across reference



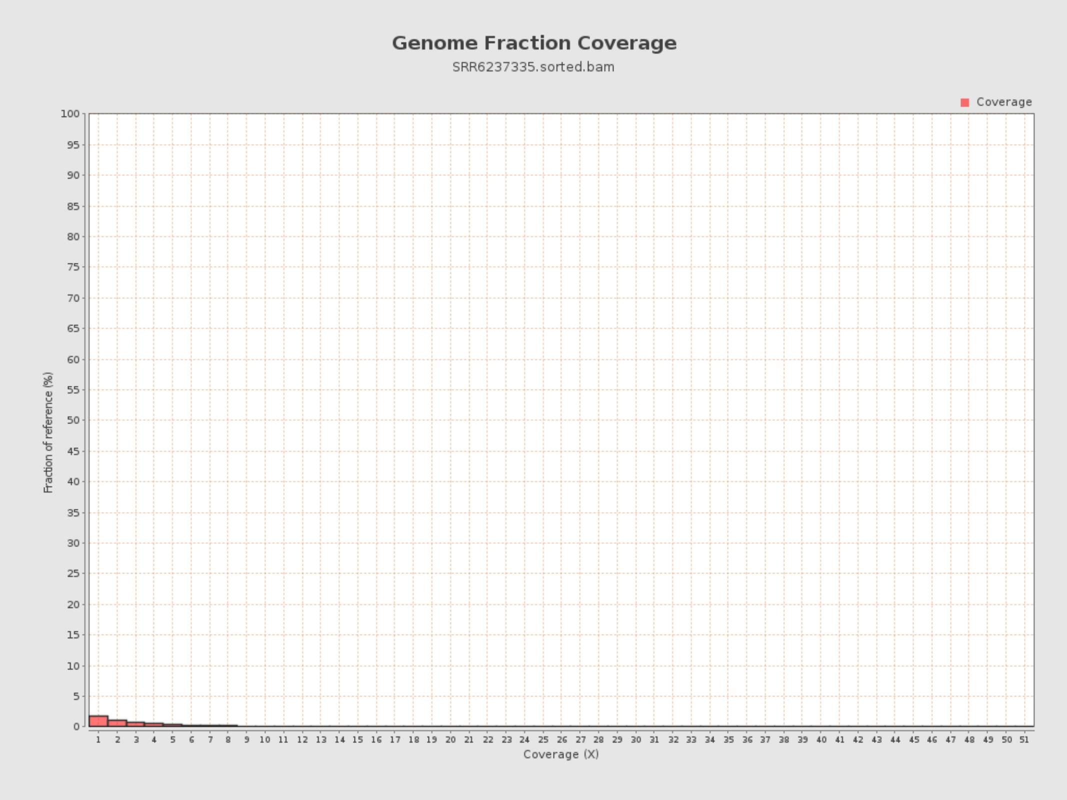
4. Results : Coverage Histogram



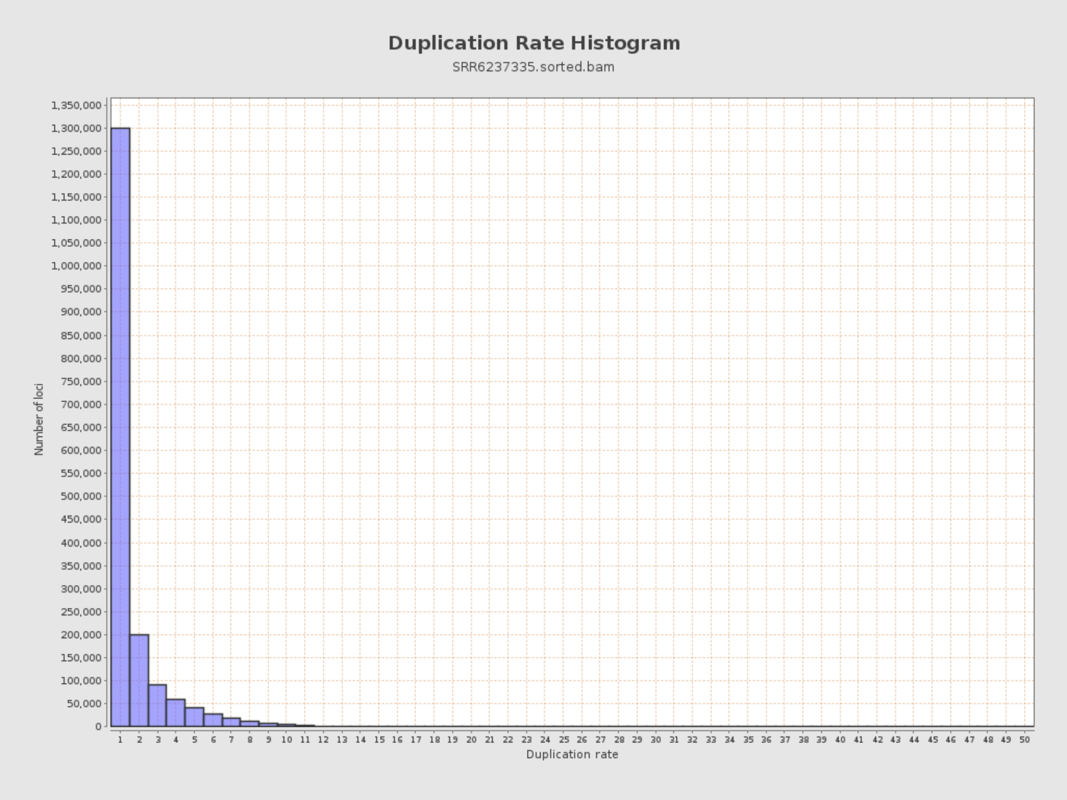
5. Results : Coverage Histogram (0-50X)



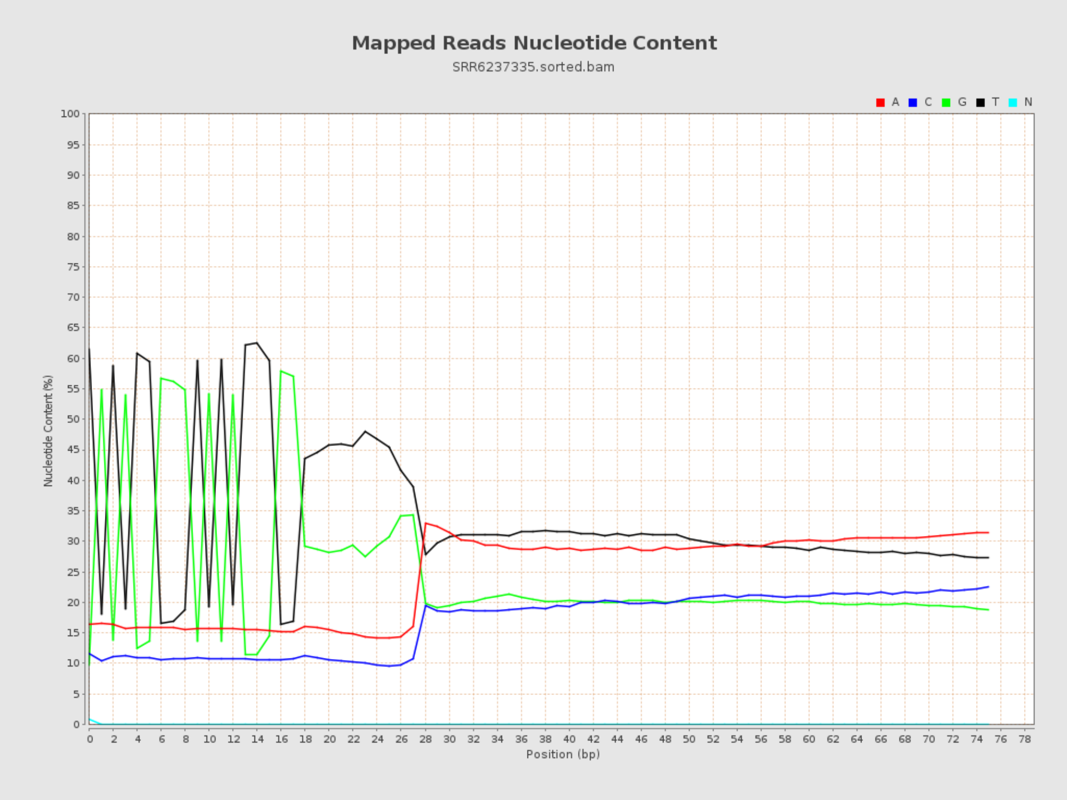
6. Results : Genome Fraction Coverage



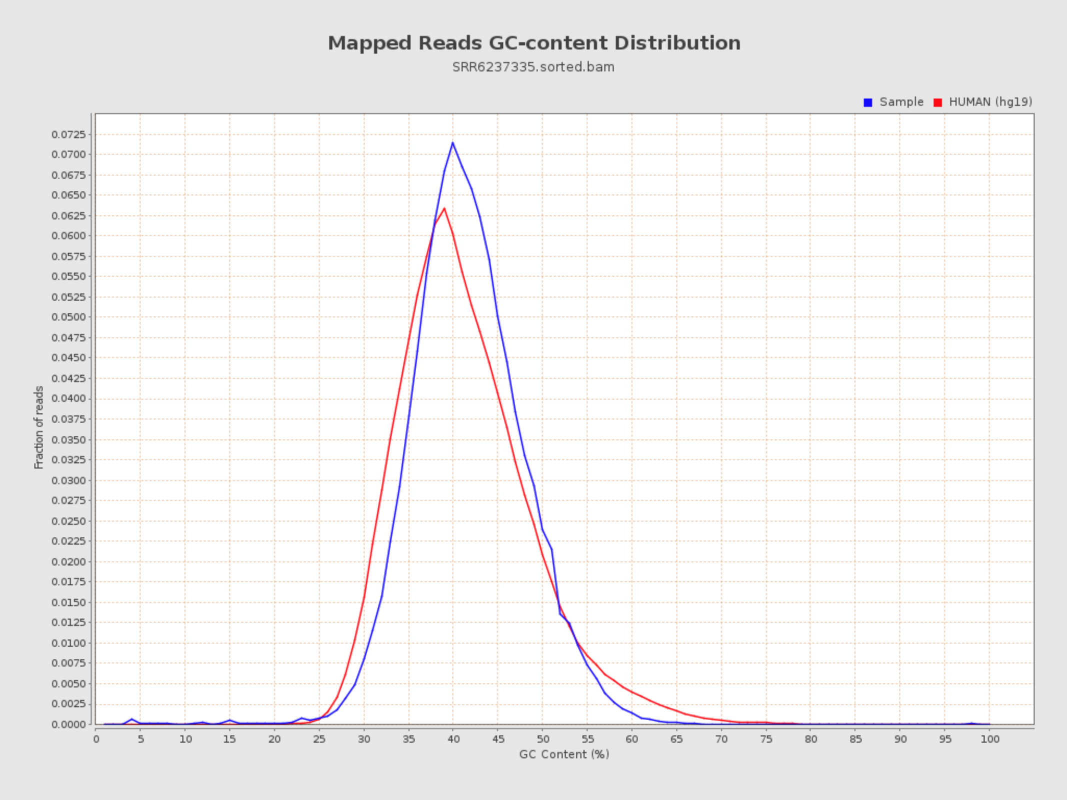
7. Results : Duplication Rate Histogram



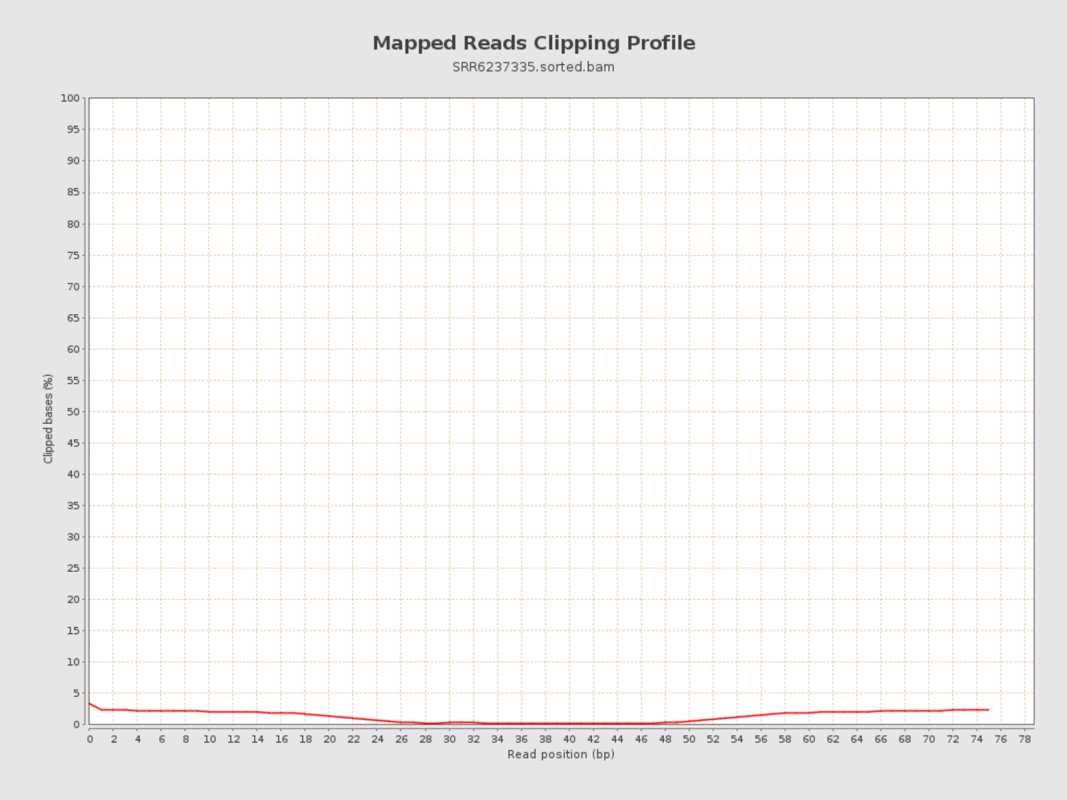
8. Results : Mapped Reads Nucleotide Content



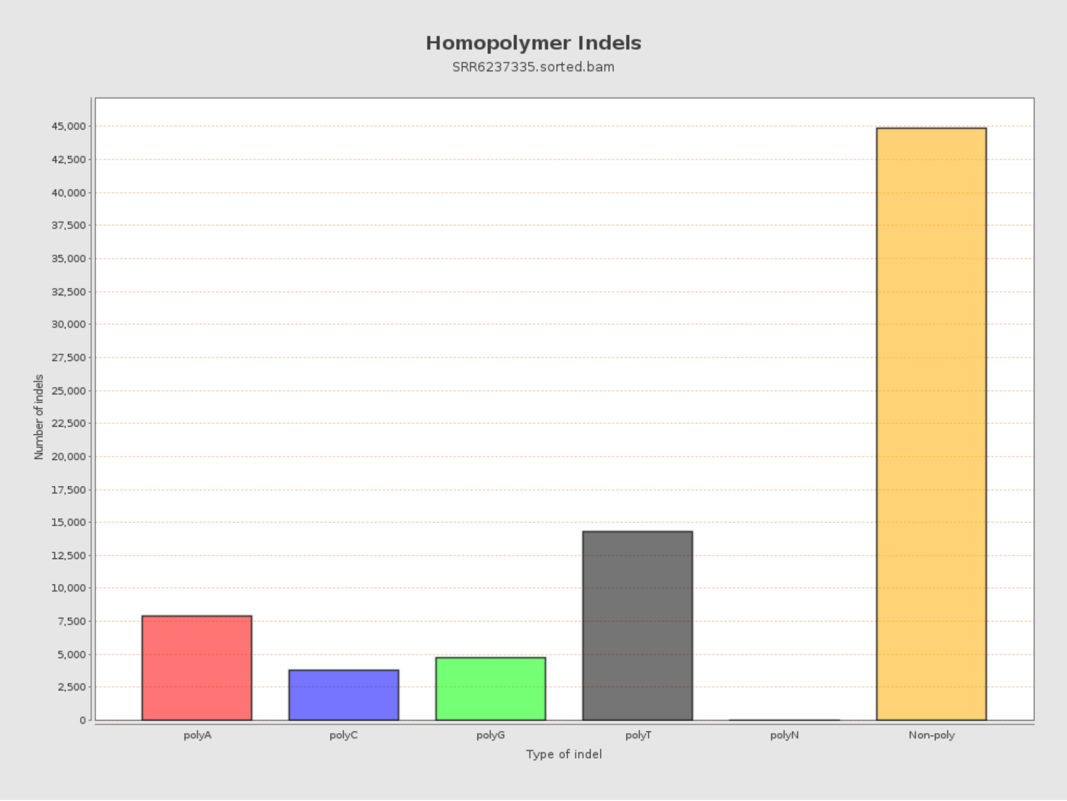
9. Results : Mapped Reads GC-content Distribution



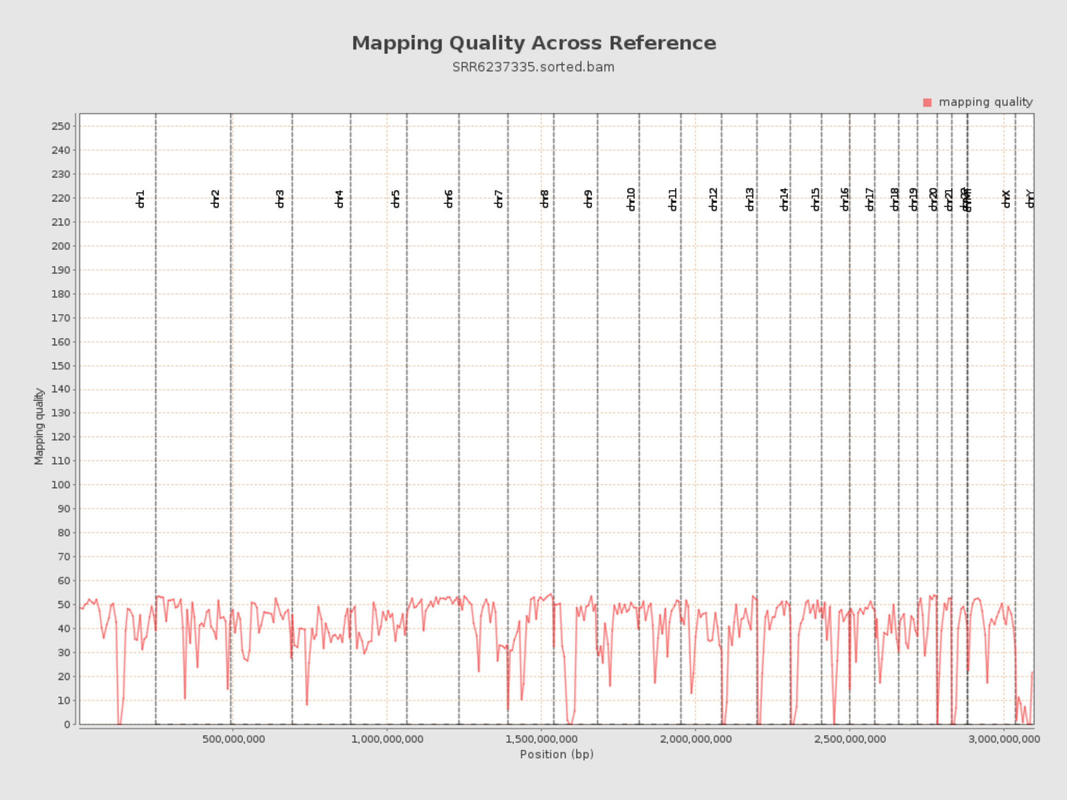
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram