Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:11:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237835.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_SRR6237835 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237835.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:11:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237835.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,942,211
Mapped reads	1,475,520 / 75.97%
Unmapped reads	466,691 / 24.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,882 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	54,991 / 2.83%
Duplication rate	2.76%
Clipped reads	810,959 / 41.75%

2.2. ACGT Content

Number/percentage of A's	26,062,253 / 27.65%
Number/percentage of C's	18,228,118 / 19.34%
Number/percentage of T's	28,560,002 / 30.3%
Number/percentage of G's	21,328,853 / 22.63%
Number/percentage of N's	87,480 / 0.09%
GC Percentage	41.96%

2.3. Coverage

Mean	0.0305

Standard Deviation	0.3029

2.4. Mapping Quality

Mean Mapping Quality	45.5

2.5. Mismatches and indels

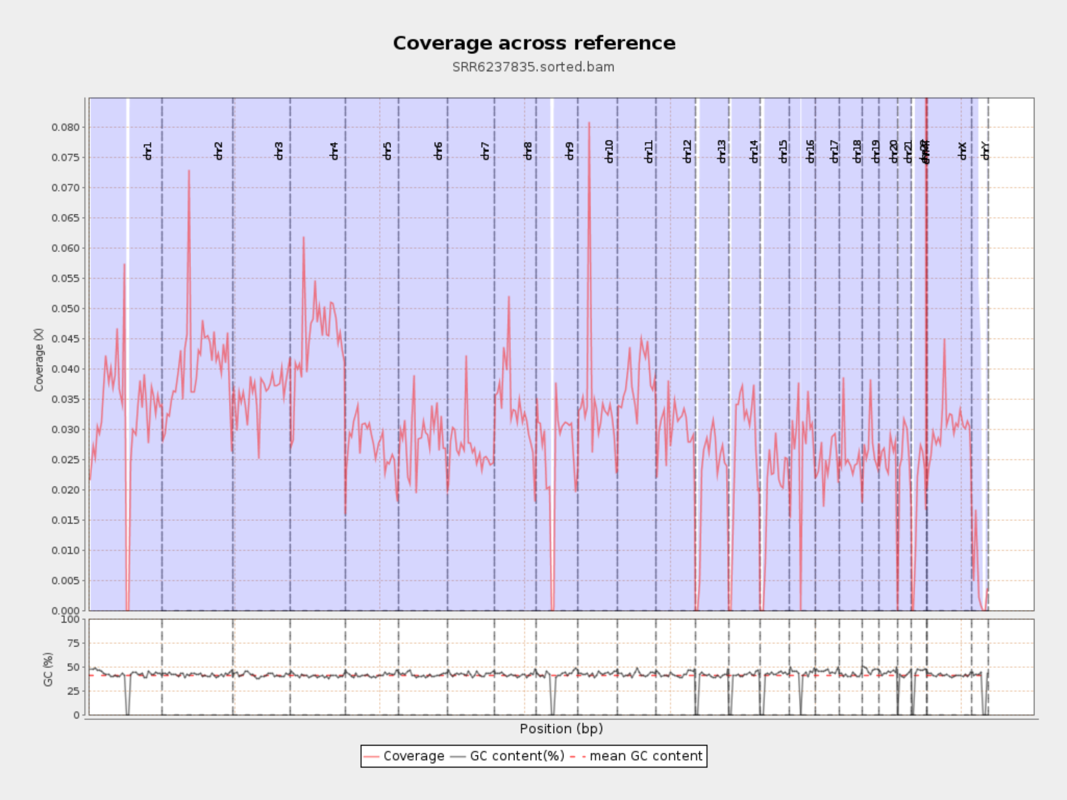
General error rate	0.79%
Mismatches	726,384
Insertions	7,334
Mapped reads with at least one insertion	0.49%
Deletions	21,306
Mapped reads with at least one deletion	1.43%
Homopolymer indels	46.03%

2.6. Chromosome stats

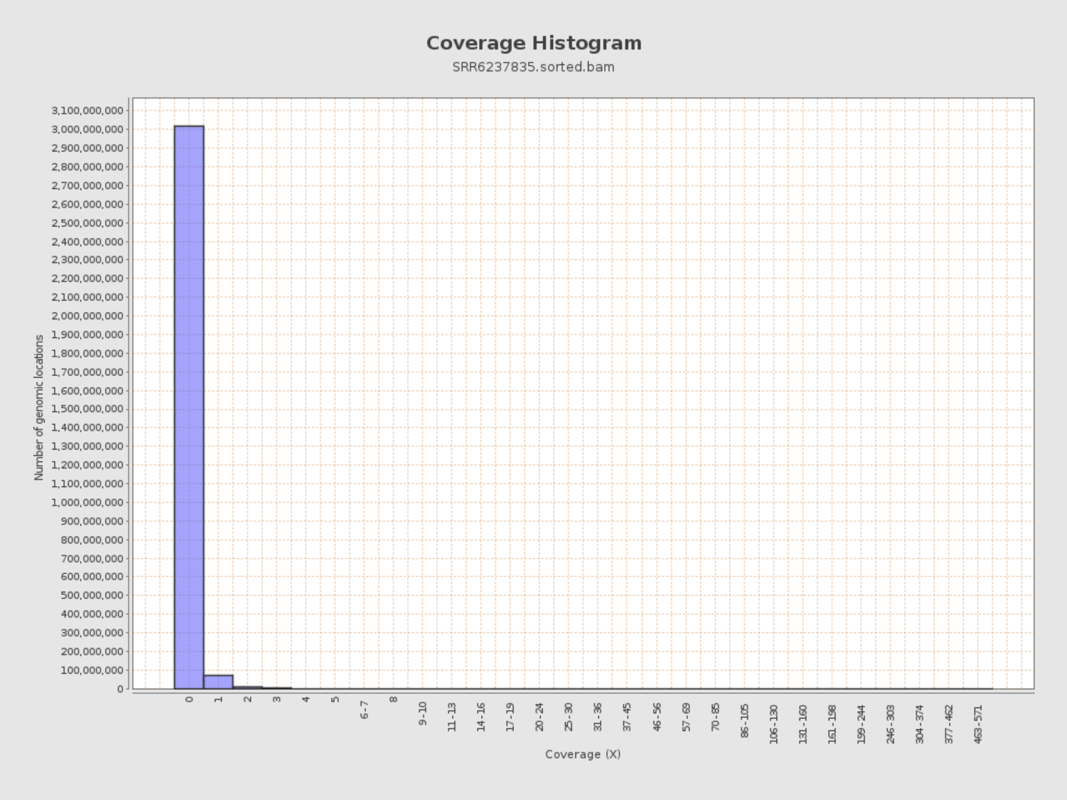
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8086213	0.0324	0.5046
chr2	243199373	9883138	0.0406	0.3581
chr3	198022430	7143369	0.0361	0.2256
chr4	191154276	8606620	0.045	0.2674
chr5	180915260	4987100	0.0276	0.1926
chr6	171115067	4895295	0.0286	0.2311
chr7	159138663	4295777	0.027	0.272

chr8	146364022	4932151	0.0337	0.322
chr9	141213431	3599500	0.0255	0.3212
chr10	135534747	4711678	0.0348	0.4358
chr11	135006516	5133987	0.038	0.3003
chr12	133851895	4047318	0.0302	0.2066
chr13	115169878	2531348	0.022	0.1692
chr14	107349540	2866903	0.0267	0.2221
chr15	102531392	1948959	0.019	0.1569
chr16	90354753	2461315	0.0272	0.2348
chr17	81195210	1982886	0.0244	0.2001
chr18	78077248	1995210	0.0256	0.5421
chr19	59128983	1609795	0.0272	0.3477
chr20	63025520	1594978	0.0253	0.1935
chr21	48129895	1138244	0.0236	0.2081
chr22	51304566	869855	0.017	0.1494
chrMT	16571	20136	1.2151	1.2653
chrX	155270560	4691861	0.0302	0.2299
chrY	59373566	268689	0.0045	0.1399

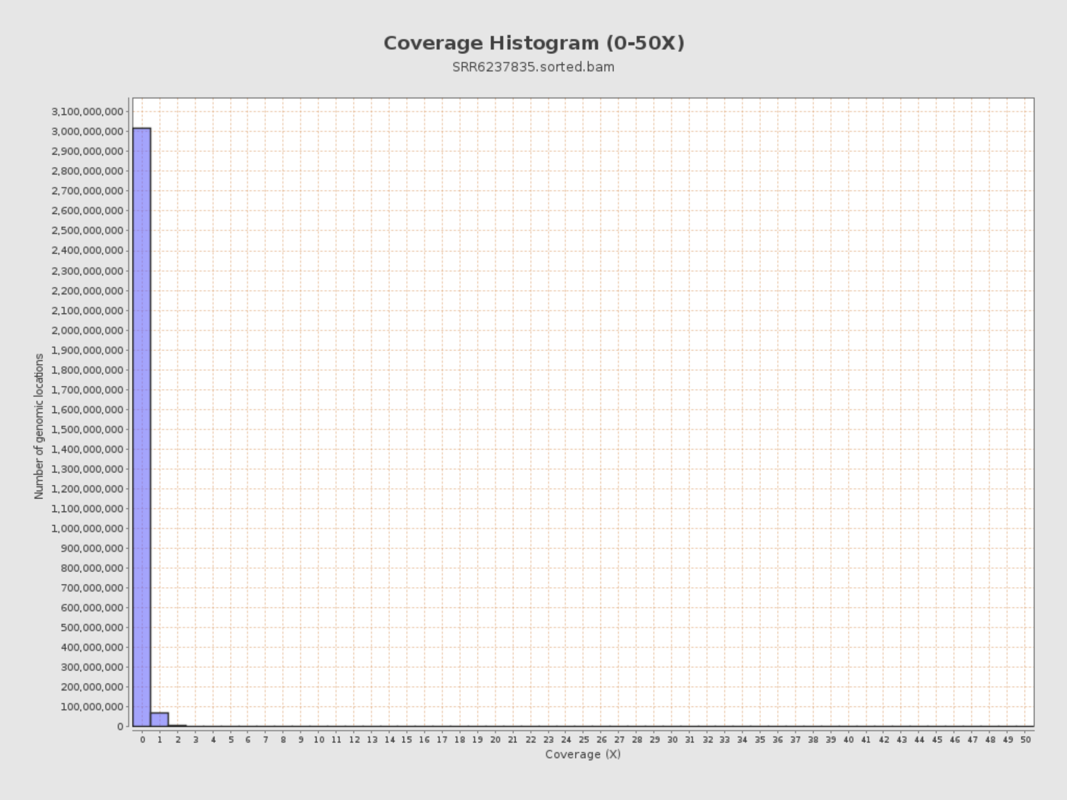
3. Results : Coverage across reference



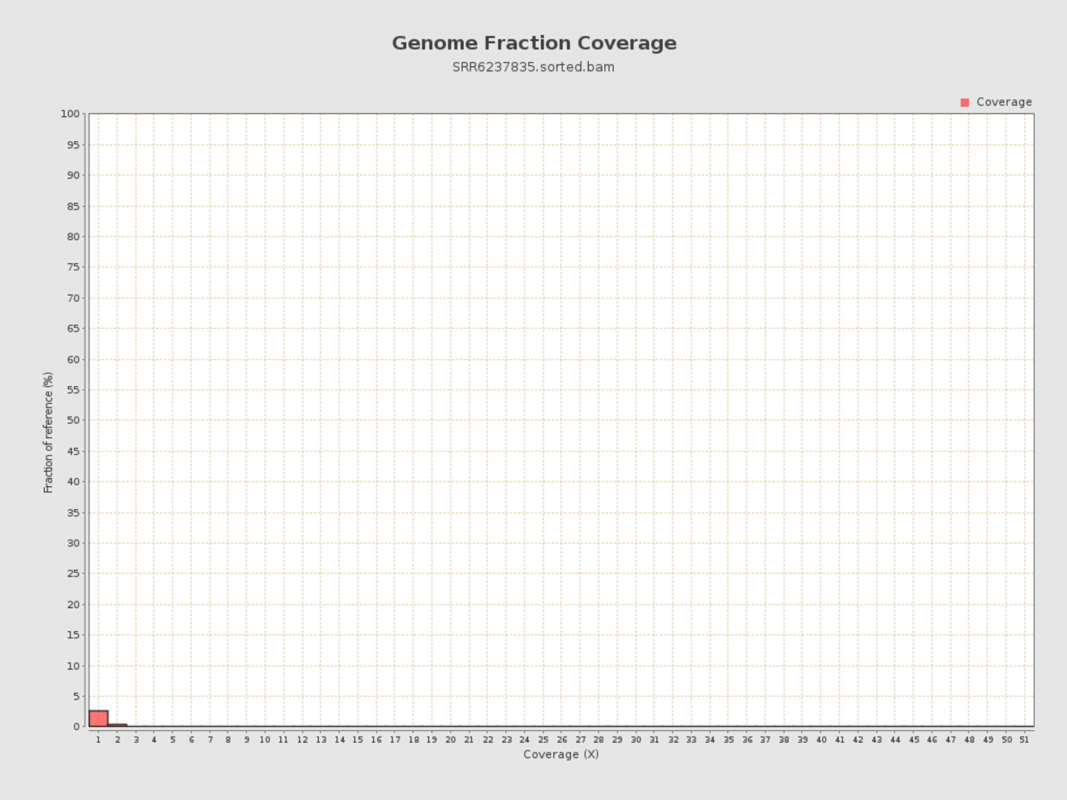
4. Results : Coverage Histogram



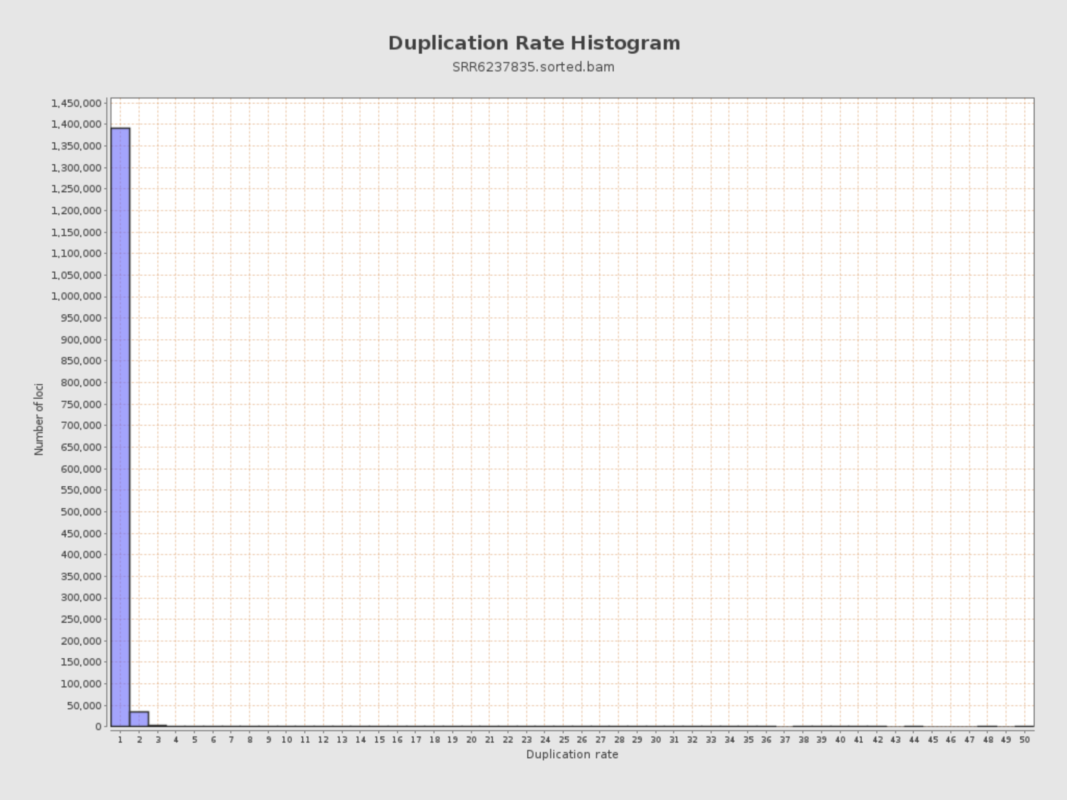
5. Results : Coverage Histogram (0-50X)



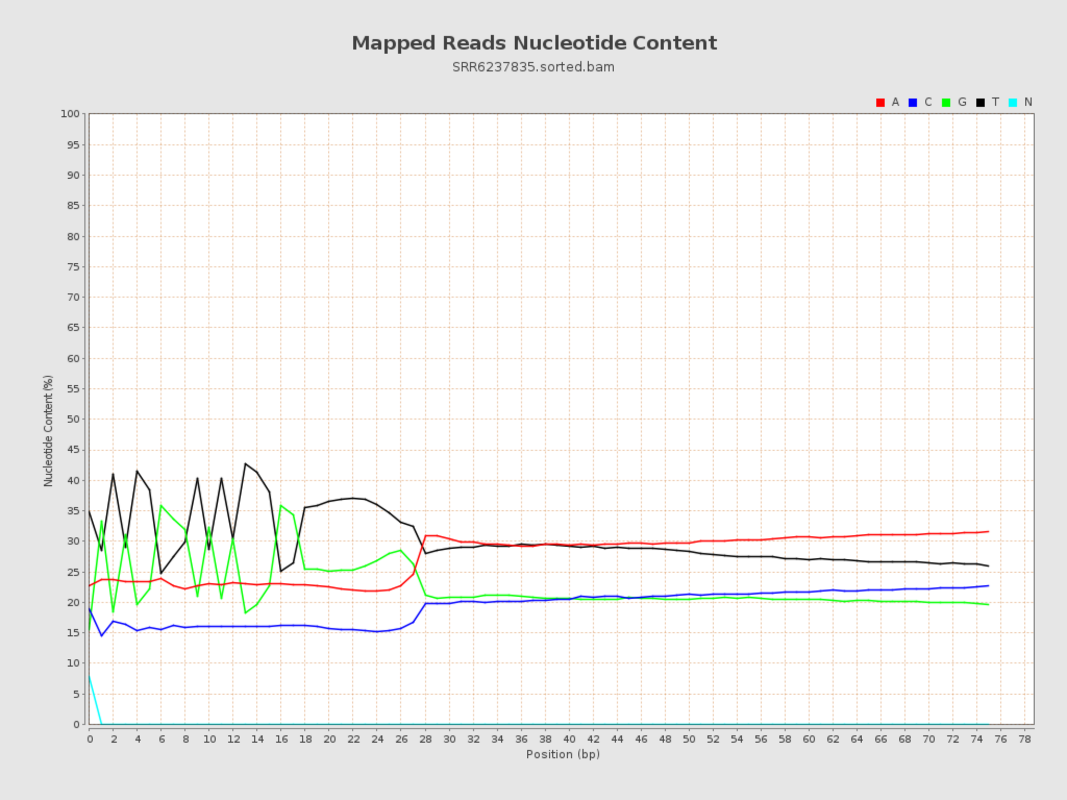
6. Results : Genome Fraction Coverage



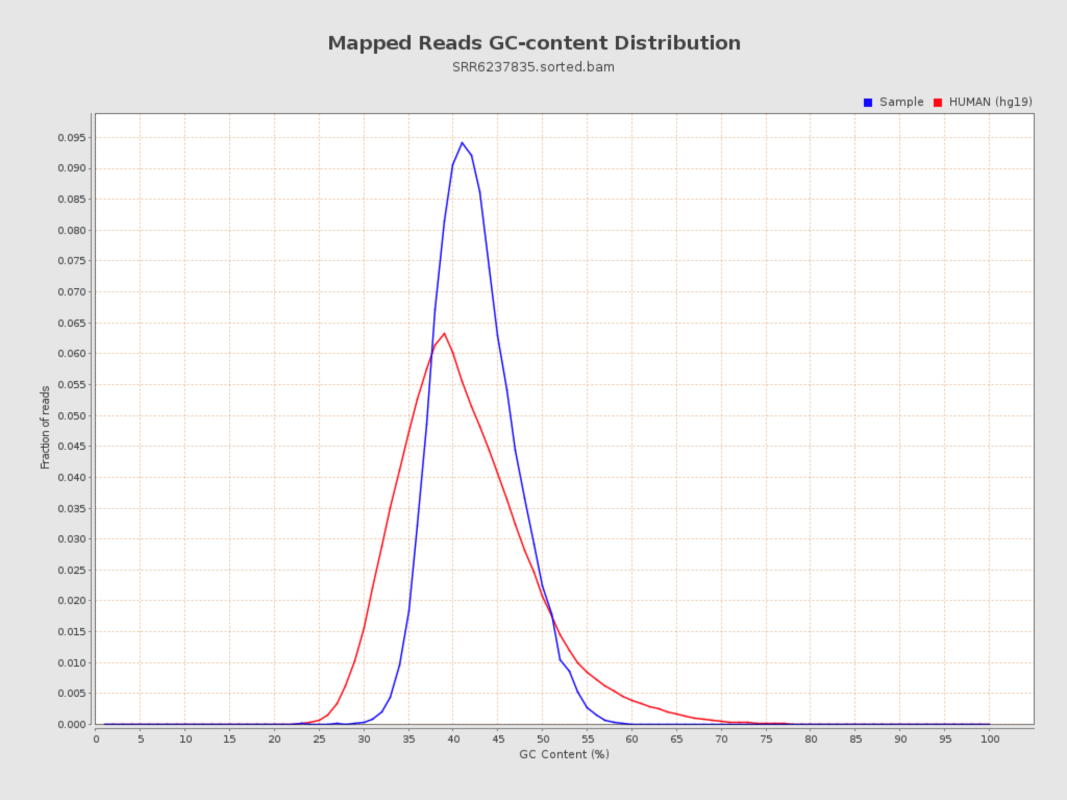
7. Results : Duplication Rate Histogram



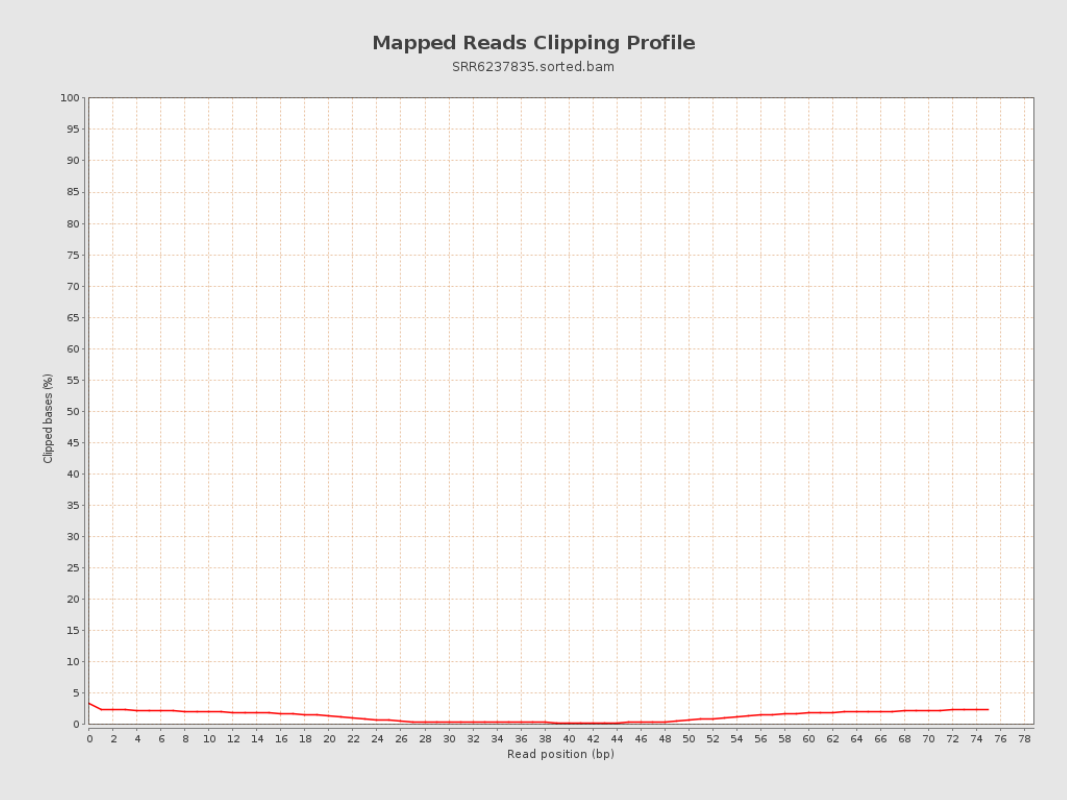
8. Results : Mapped Reads Nucleotide Content



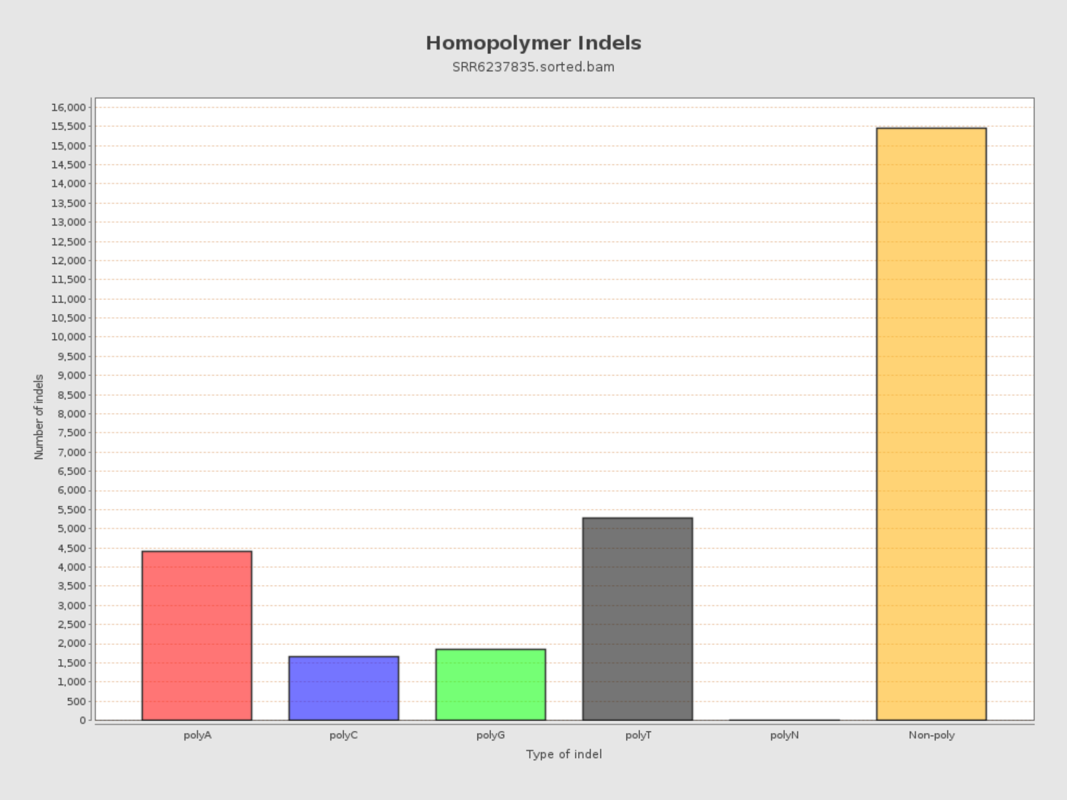
9. Results : Mapped Reads GC-content Distribution



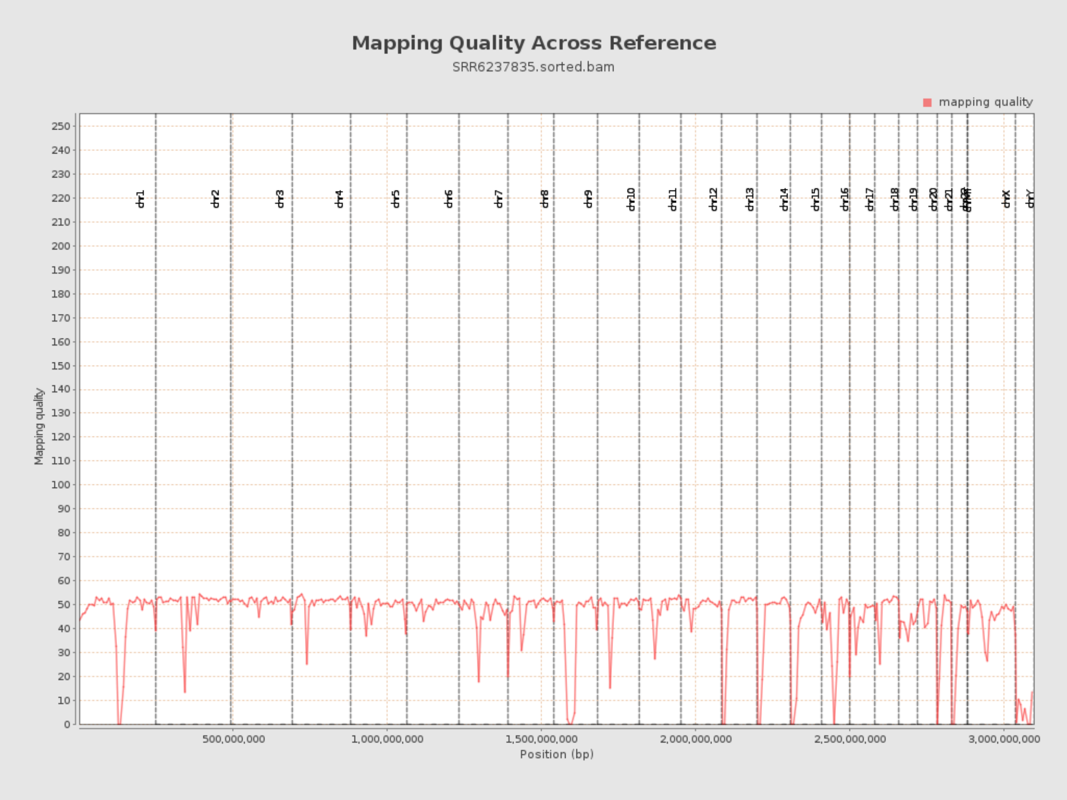
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram