Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:58:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237851.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_SRR6237851 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237851.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:58:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237851.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,127,604
Mapped reads	1,754,974 / 82.49%
Unmapped reads	372,630 / 17.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,924 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	87,918 / 4.13%
Duplication rate	4.01%
Clipped reads	900,105 / 42.31%

2.2. ACGT Content

Number/percentage of A's	30,769,374 / 27.19%
Number/percentage of C's	19,769,312 / 17.47%
Number/percentage of T's	36,660,333 / 32.4%
Number/percentage of G's	25,849,057 / 22.85%
Number/percentage of N's	98,181 / 0.09%
GC Percentage	40.32%

2.3. Coverage

Mean	0.0366

Standard Deviation	0.3713

2.4. Mapping Quality

Mean Mapping Quality	46.46

2.5. Mismatches and indels

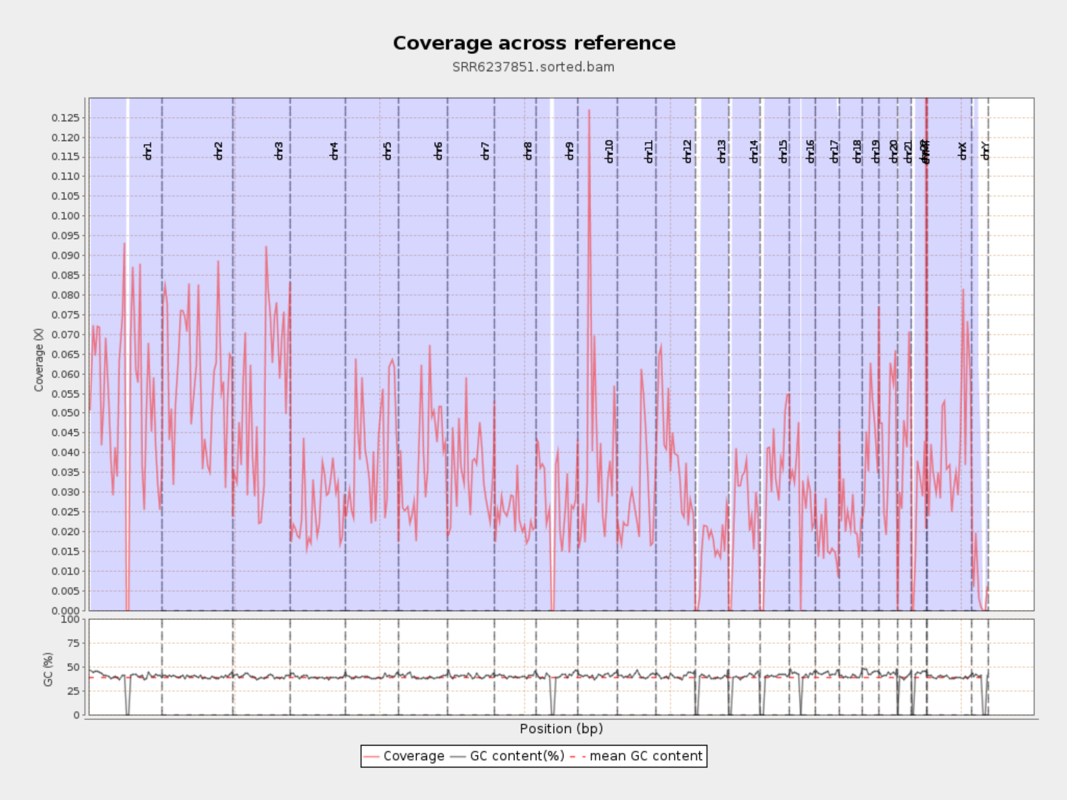
General error rate	0.77%
Mismatches	854,012
Insertions	8,765
Mapped reads with at least one insertion	0.5%
Deletions	31,051
Mapped reads with at least one deletion	1.75%
Homopolymer indels	47.66%

2.6. Chromosome stats

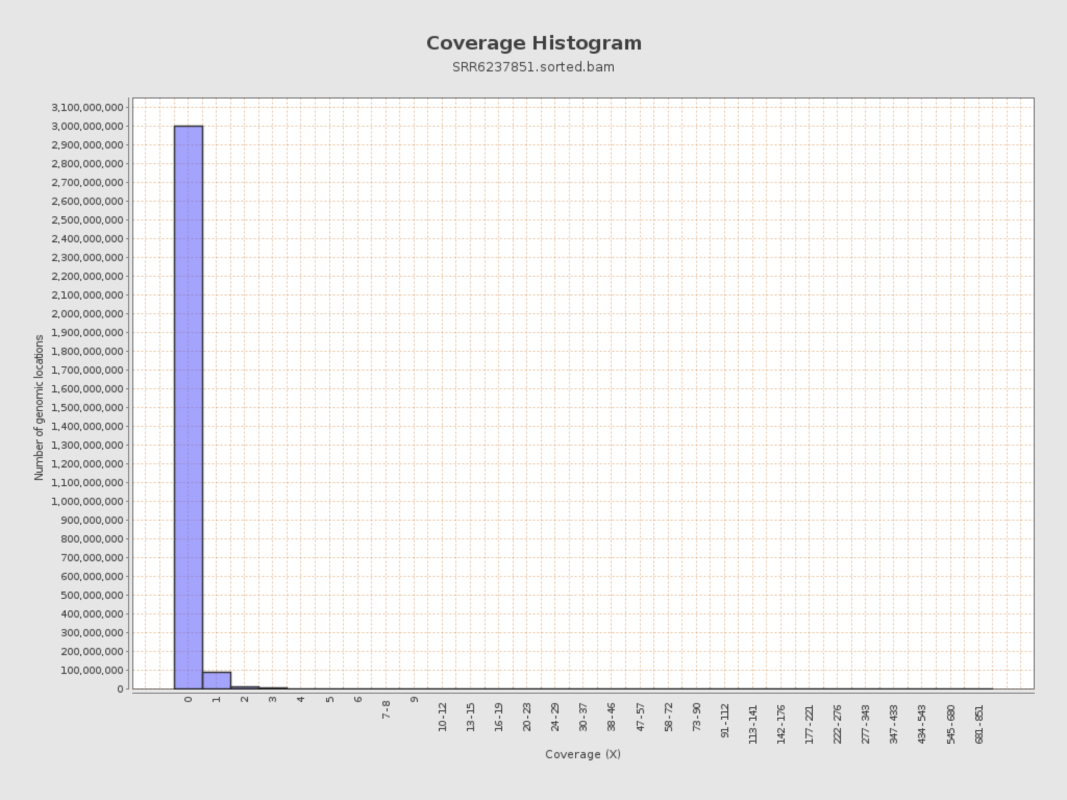
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12979611	0.0521	0.764
chr2	243199373	14472805	0.0595	0.352
chr3	198022430	10670535	0.0539	0.3048
chr4	191154276	4955514	0.0259	0.2049
chr5	180915260	7393611	0.0409	0.2281
chr6	171115067	6417685	0.0375	0.2408
chr7	159138663	5572579	0.035	0.3724

chr8	146364022	3472853	0.0237	0.2462
chr9	141213431	3705012	0.0262	0.2606
chr10	135534747	5337403	0.0394	0.7464
chr11	135006516	3889547	0.0288	0.2493
chr12	133851895	5199253	0.0388	0.223
chr13	115169878	1796904	0.0156	0.1402
chr14	107349540	2655158	0.0247	0.186
chr15	102531392	3393797	0.0331	0.2041
chr16	90354753	2647515	0.0293	0.2447
chr17	81195210	1379016	0.017	0.1644
chr18	78077248	1856168	0.0238	0.513
chr19	59128983	2597600	0.0439	0.4907
chr20	63025520	2782231	0.0441	0.2384
chr21	48129895	1938883	0.0403	0.2411
chr22	51304566	1251542	0.0244	0.1742
chrMT	16571	29261	1.7658	1.7392
chrX	155270560	6470310	0.0417	0.2743
chrY	59373566	332617	0.0056	0.1542

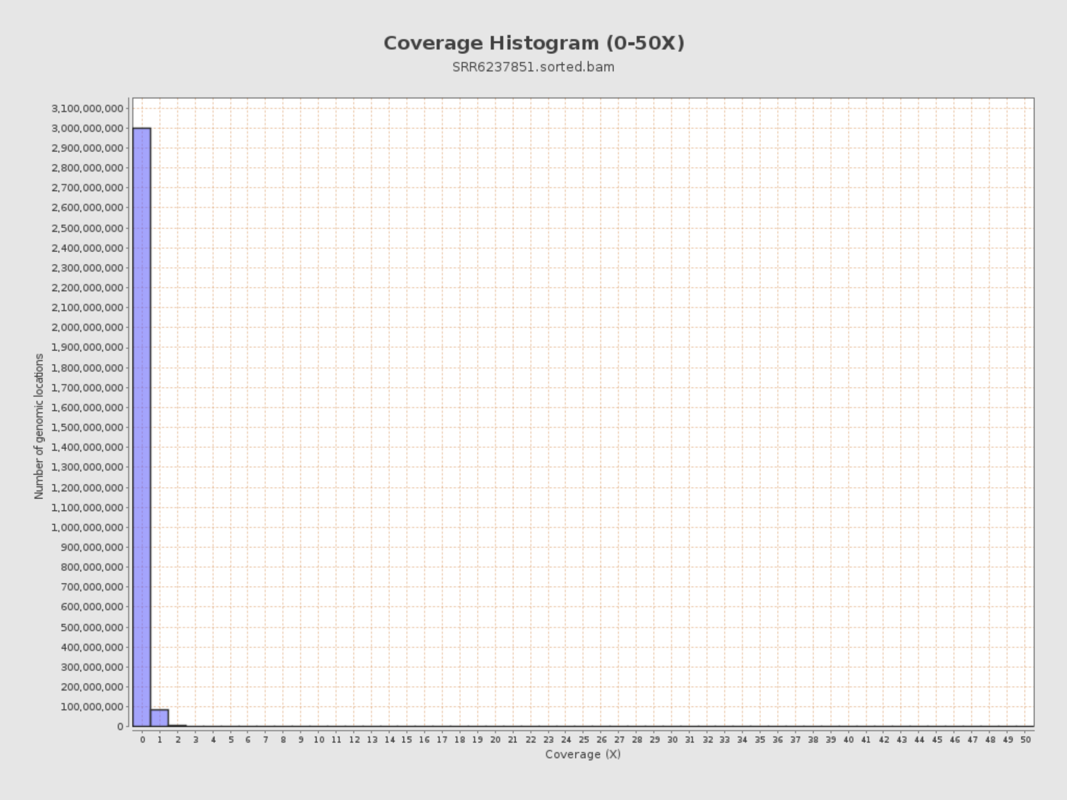
3. Results : Coverage across reference



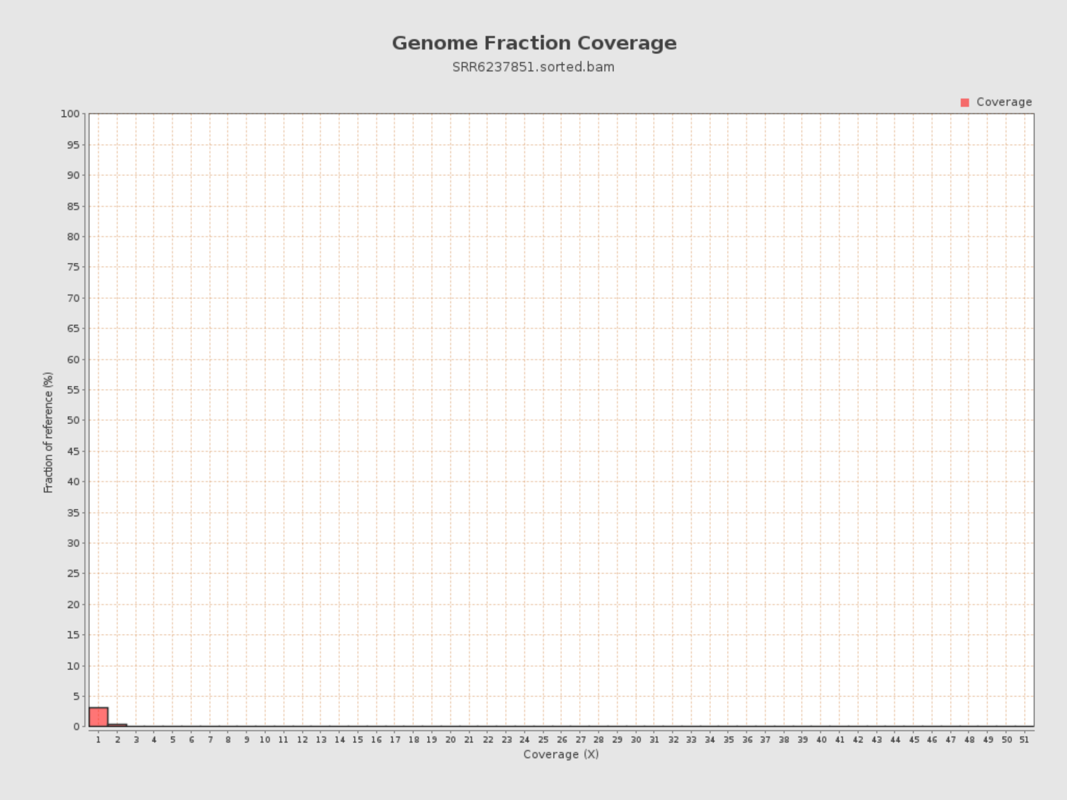
4. Results : Coverage Histogram



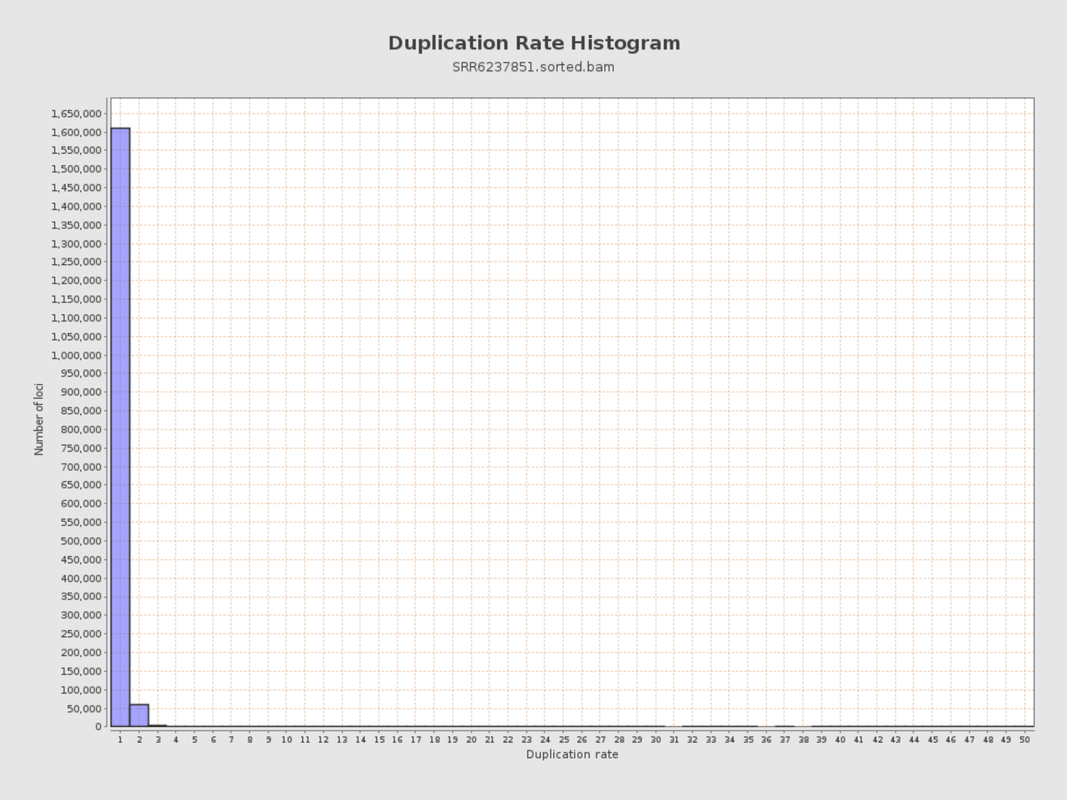
5. Results : Coverage Histogram (0-50X)



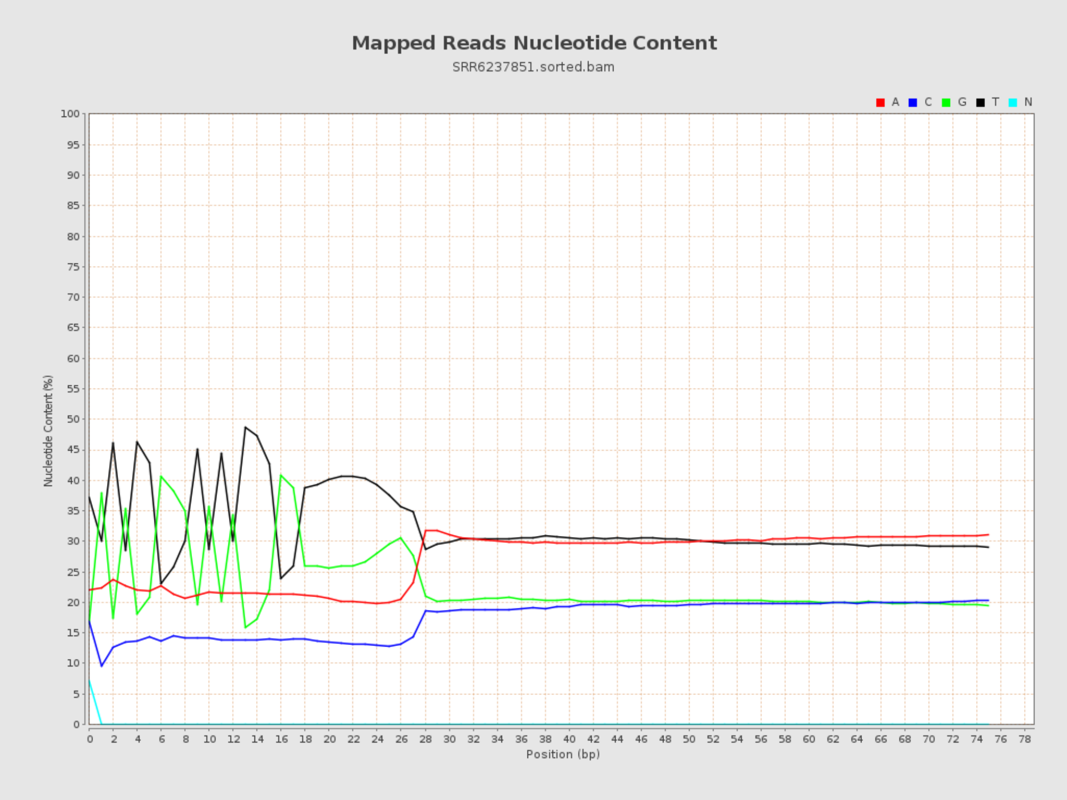
6. Results : Genome Fraction Coverage



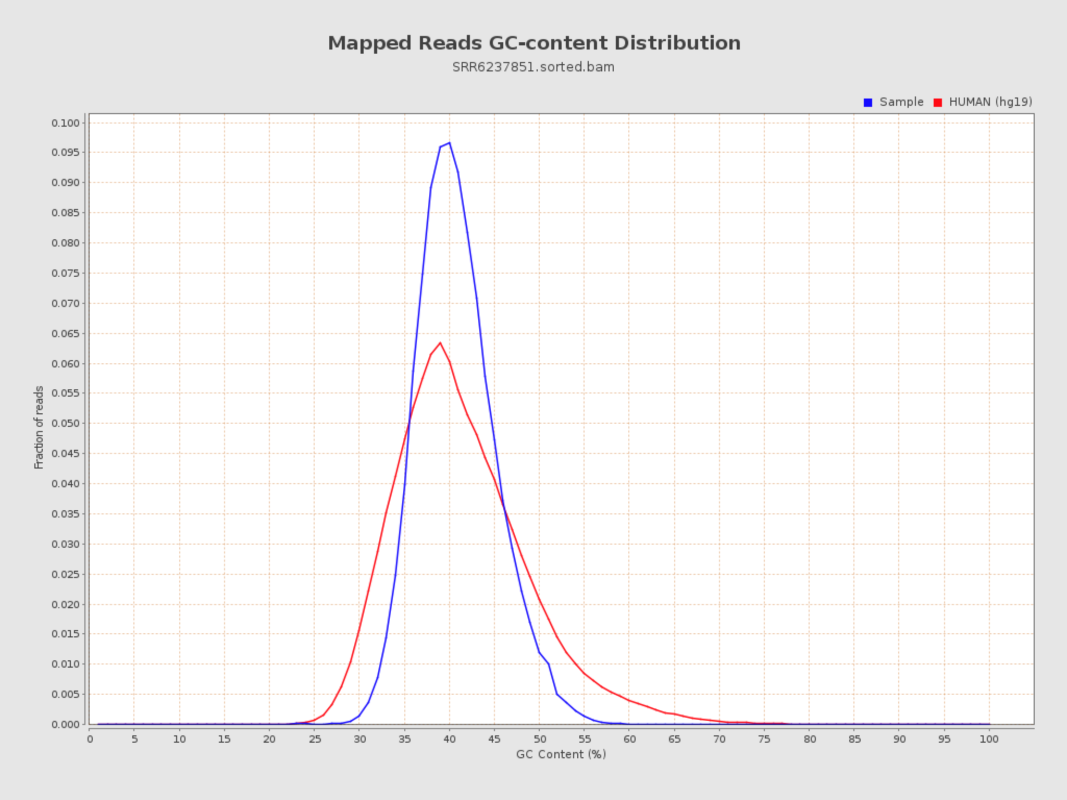
7. Results : Duplication Rate Histogram



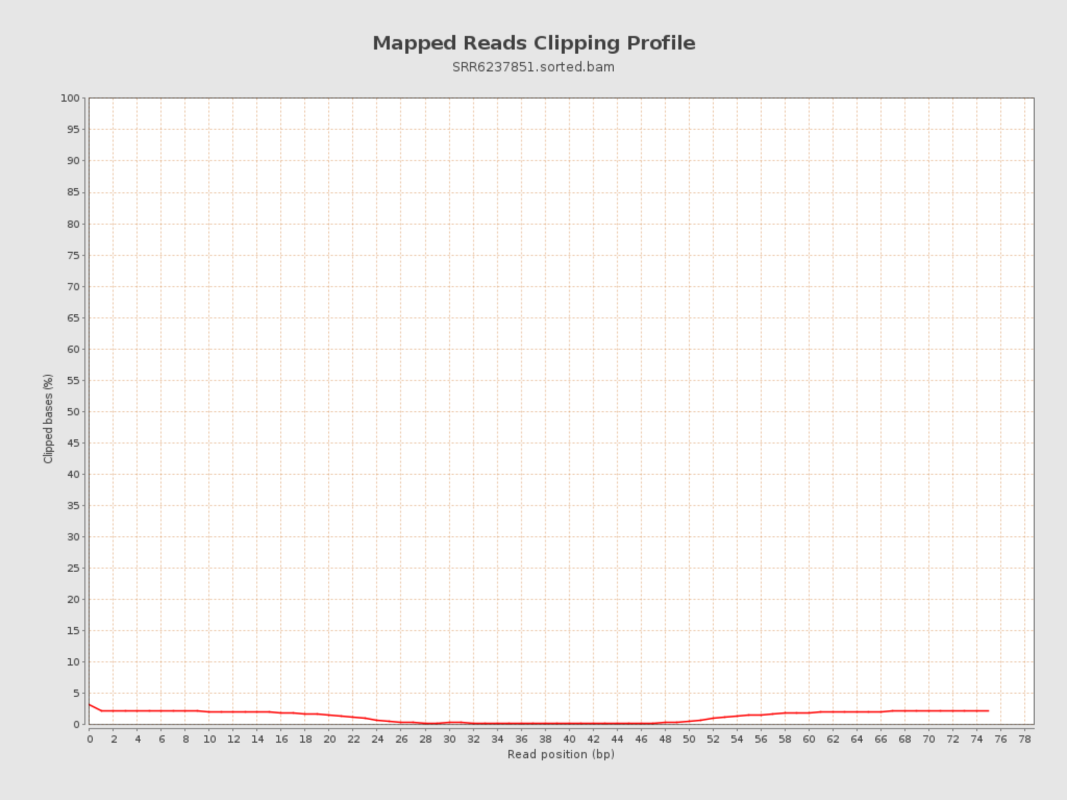
8. Results : Mapped Reads Nucleotide Content



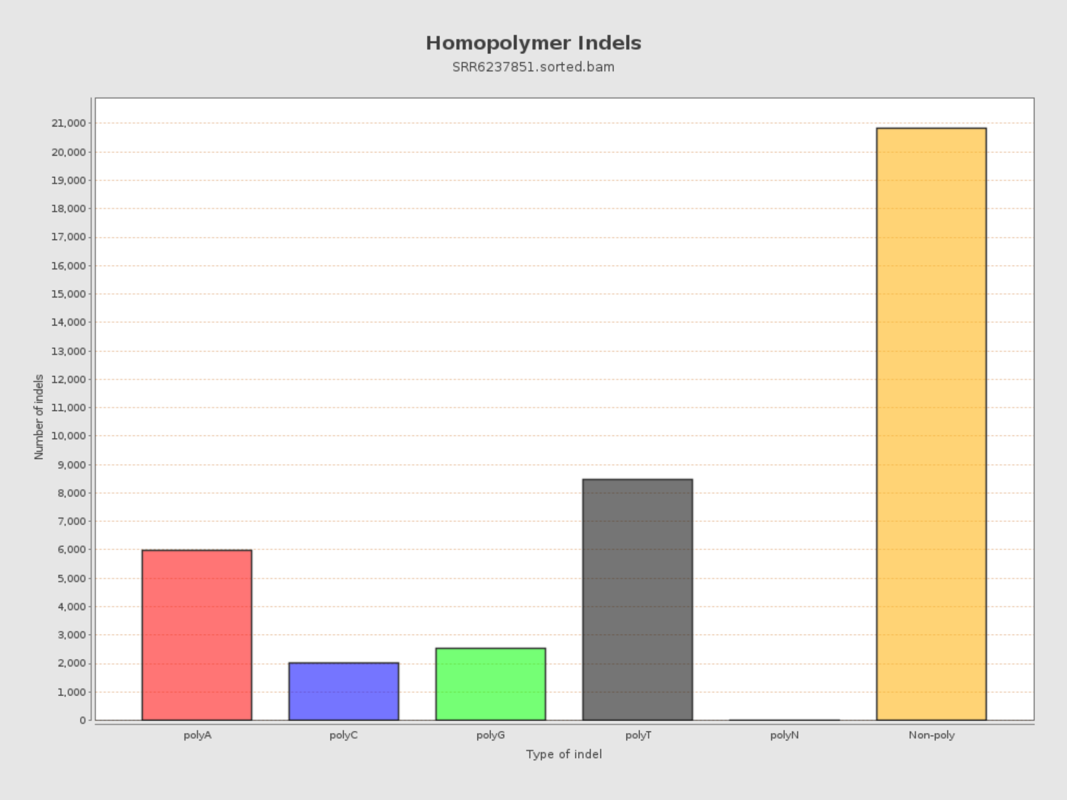
9. Results : Mapped Reads GC-content Distribution



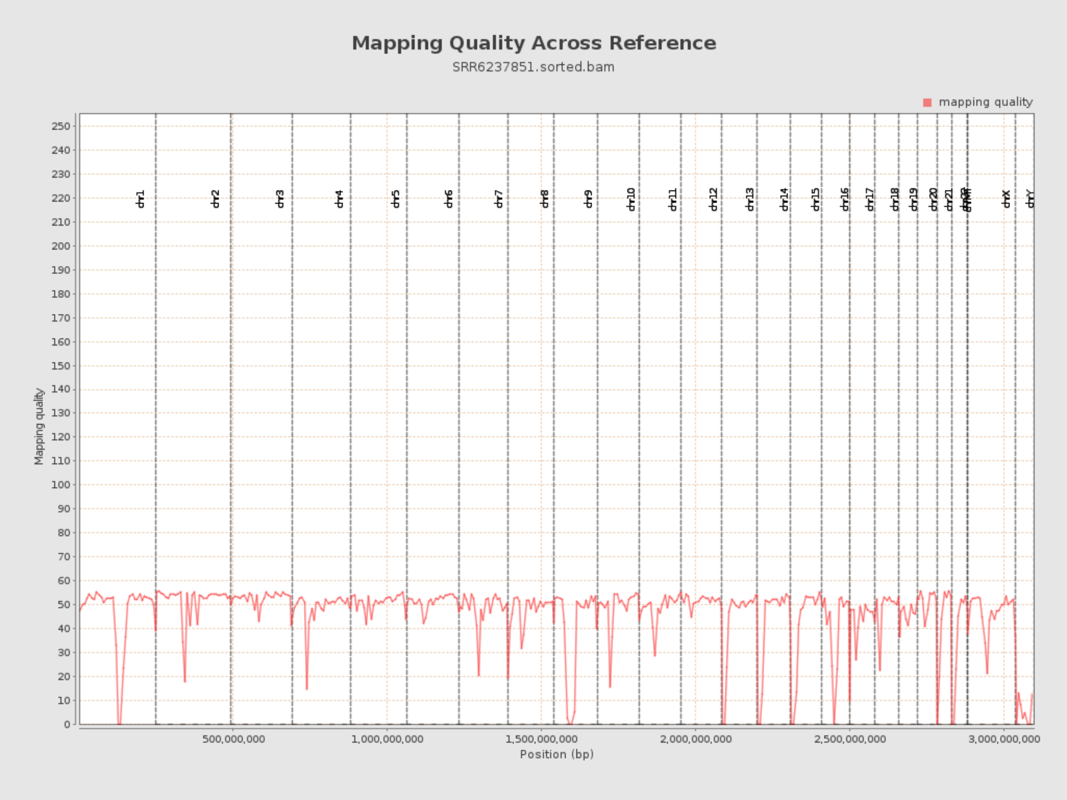
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram