Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:29:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237289.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_SRR6237289 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237289.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:29:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237289.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,073,428
Mapped reads	2,655,467 / 86.4%
Unmapped reads	417,961 / 13.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,182 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	181,688 / 5.91%
Duplication rate	5.31%
Clipped reads	1,212,994 / 39.47%

2.2. ACGT Content

Number/percentage of A's	48,560,227 / 27.47%
Number/percentage of C's	32,844,184 / 18.58%
Number/percentage of T's	55,661,323 / 31.48%
Number/percentage of G's	39,735,044 / 22.47%
Number/percentage of N's	2,803 / 0%
GC Percentage	41.05%

2.3. Coverage

Mean	0.0571

Standard Deviation	0.5429

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

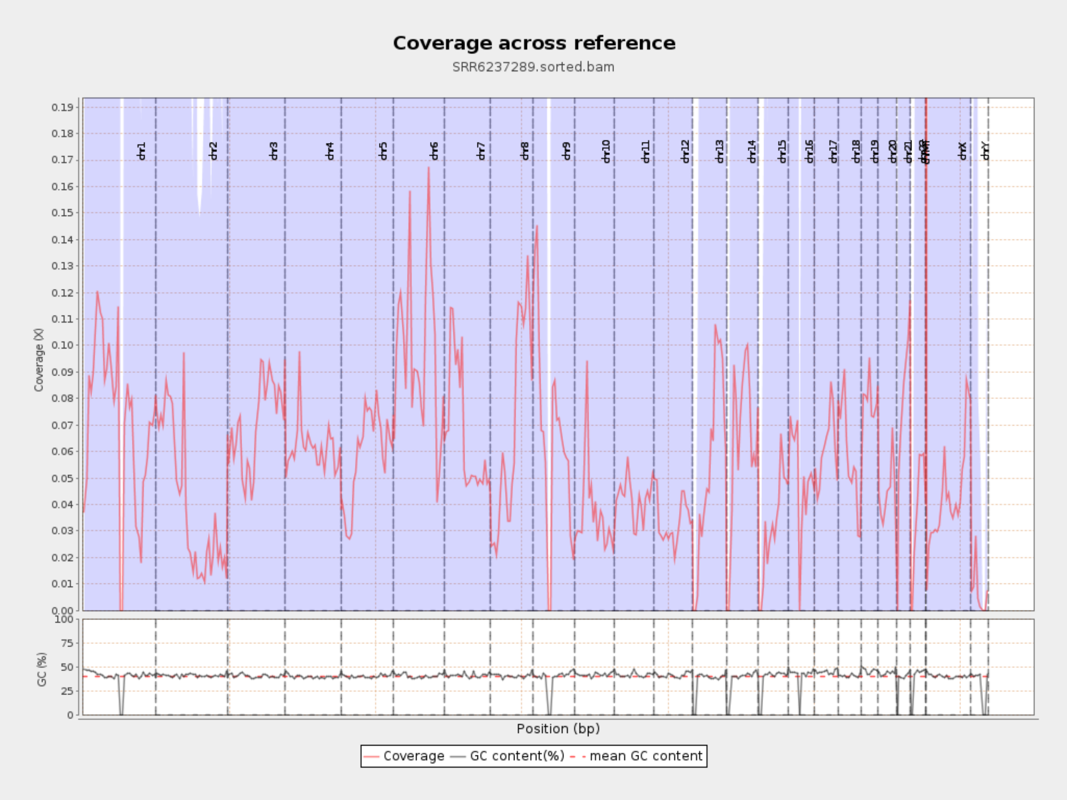
General error rate	0.79%
Mismatches	1,374,432
Insertions	13,597
Mapped reads with at least one insertion	0.51%
Deletions	40,711
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.17%

2.6. Chromosome stats

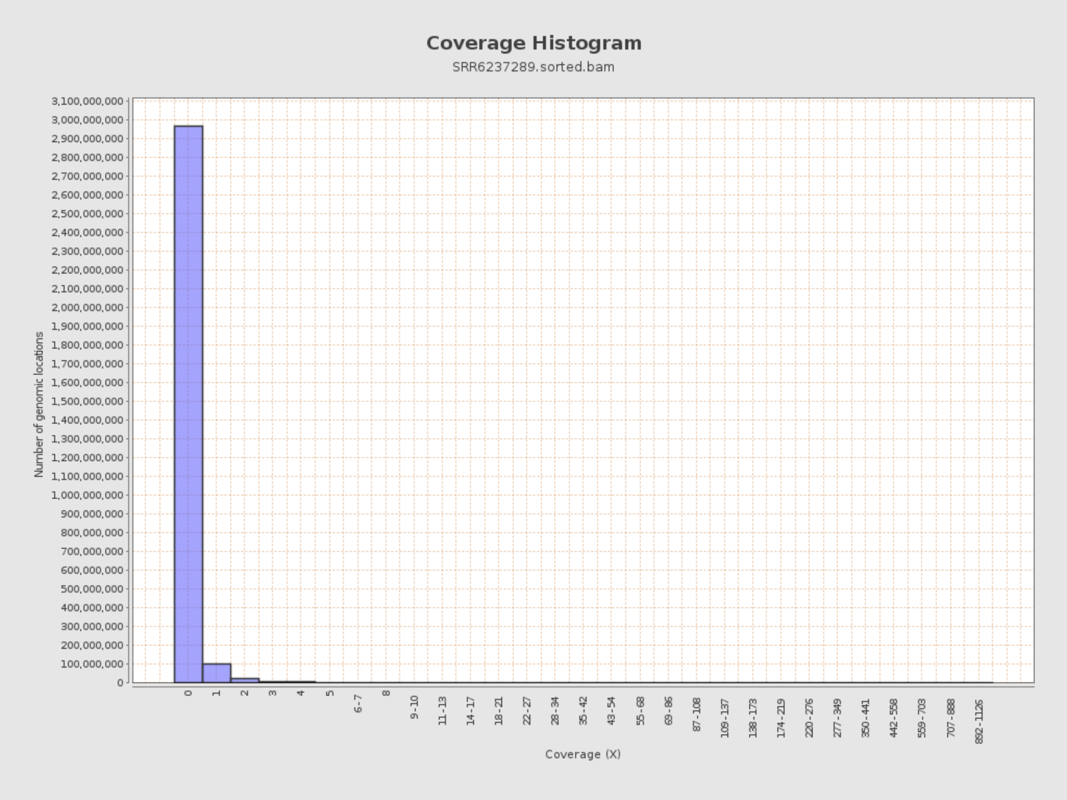
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17666629	0.0709	1.0291
chr2	243199373	9906850	0.0407	0.5899
chr3	198022430	13966325	0.0705	0.3373
chr4	191154276	11816155	0.0618	0.3818
chr5	180915260	10732209	0.0593	0.3148
chr6	171115067	16790070	0.0981	0.5816
chr7	159138663	10680550	0.0671	0.7581

chr8	146364022	10122667	0.0692	0.6449
chr9	141213431	9224382	0.0653	0.5494
chr10	135534747	4986708	0.0368	0.466
chr11	135006516	5702462	0.0422	0.4207
chr12	133851895	4543735	0.0339	0.263
chr13	115169878	6349277	0.0551	0.3
chr14	107349540	6809520	0.0634	0.3687
chr15	102531392	3137178	0.0306	0.2411
chr16	90354753	4446171	0.0492	0.326
chr17	81195210	5009362	0.0617	0.3433
chr18	78077248	4624847	0.0592	0.9388
chr19	59128983	4661625	0.0788	0.6557
chr20	63025520	2819050	0.0447	0.2821
chr21	48129895	3684715	0.0766	0.4047
chr22	51304566	1935354	0.0377	0.2433
chrMT	16571	101706	6.1376	5.1772
chrX	155270560	6729796	0.0433	0.3042
chrY	59373566	428142	0.0072	0.2349

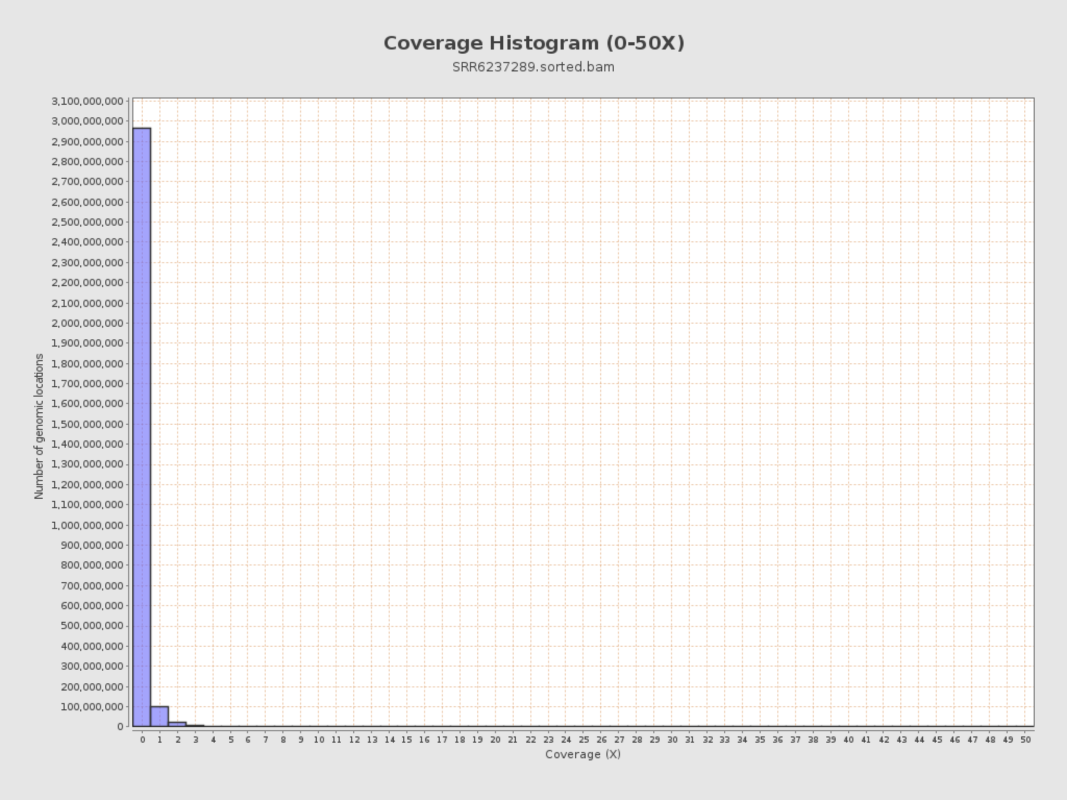
3. Results : Coverage across reference



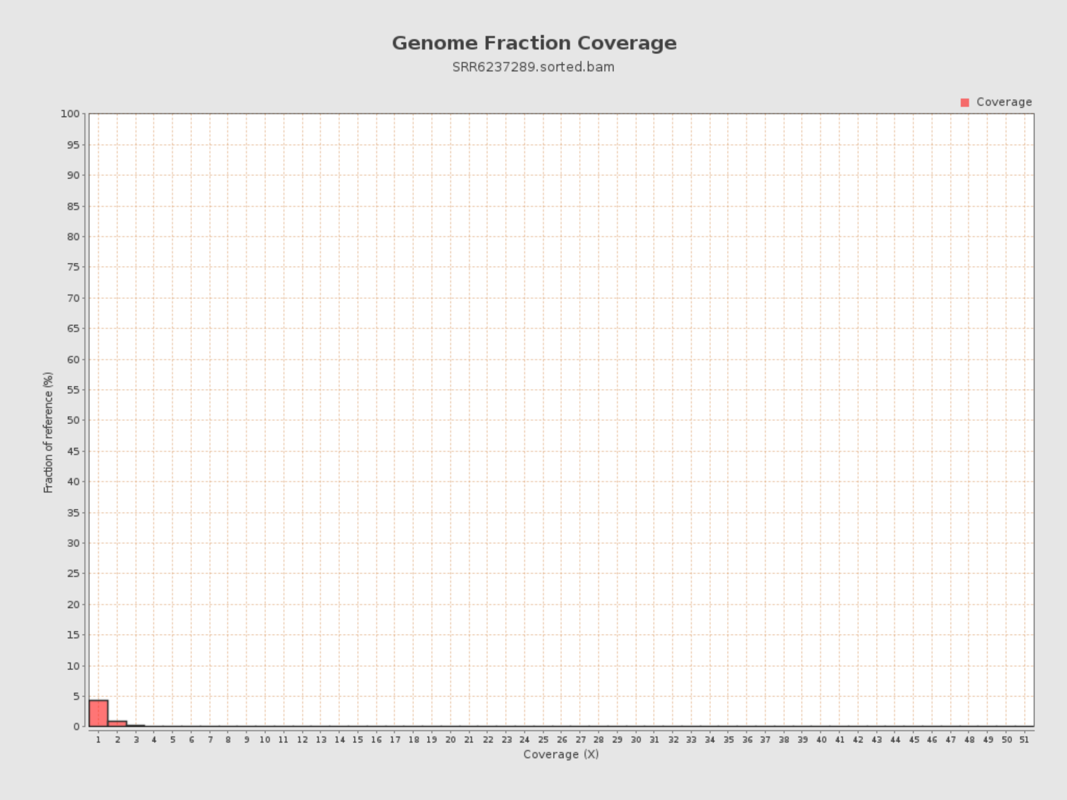
4. Results : Coverage Histogram



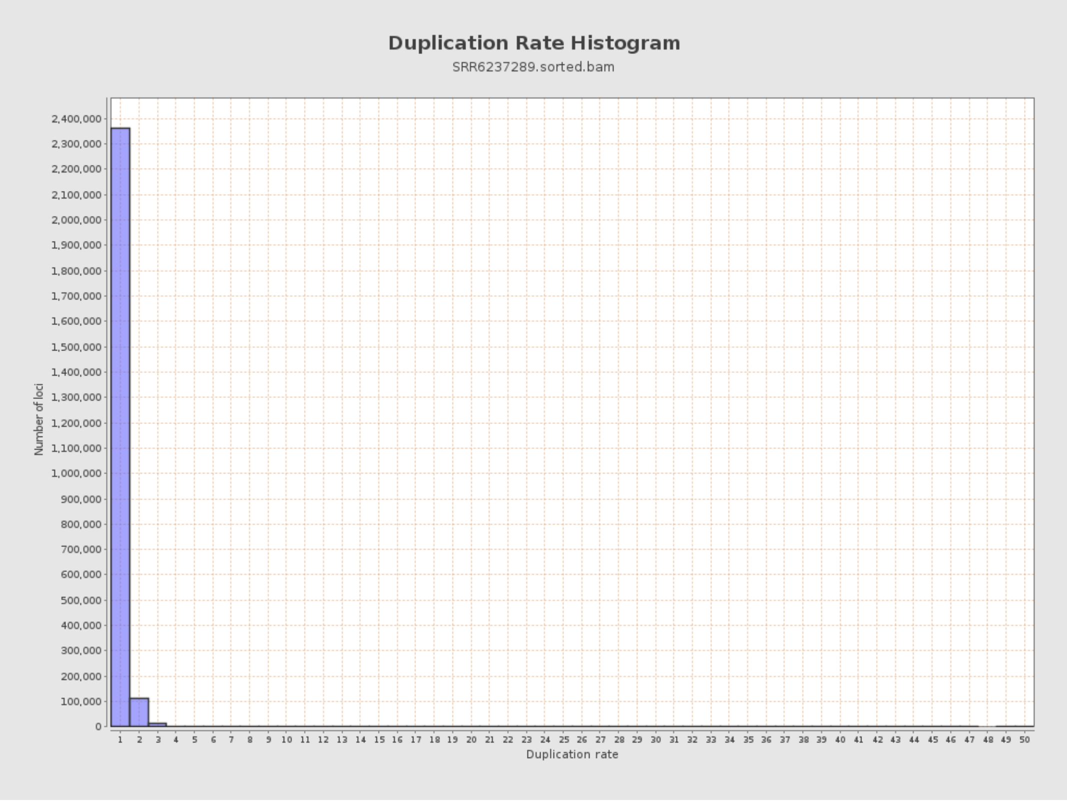
5. Results : Coverage Histogram (0-50X)



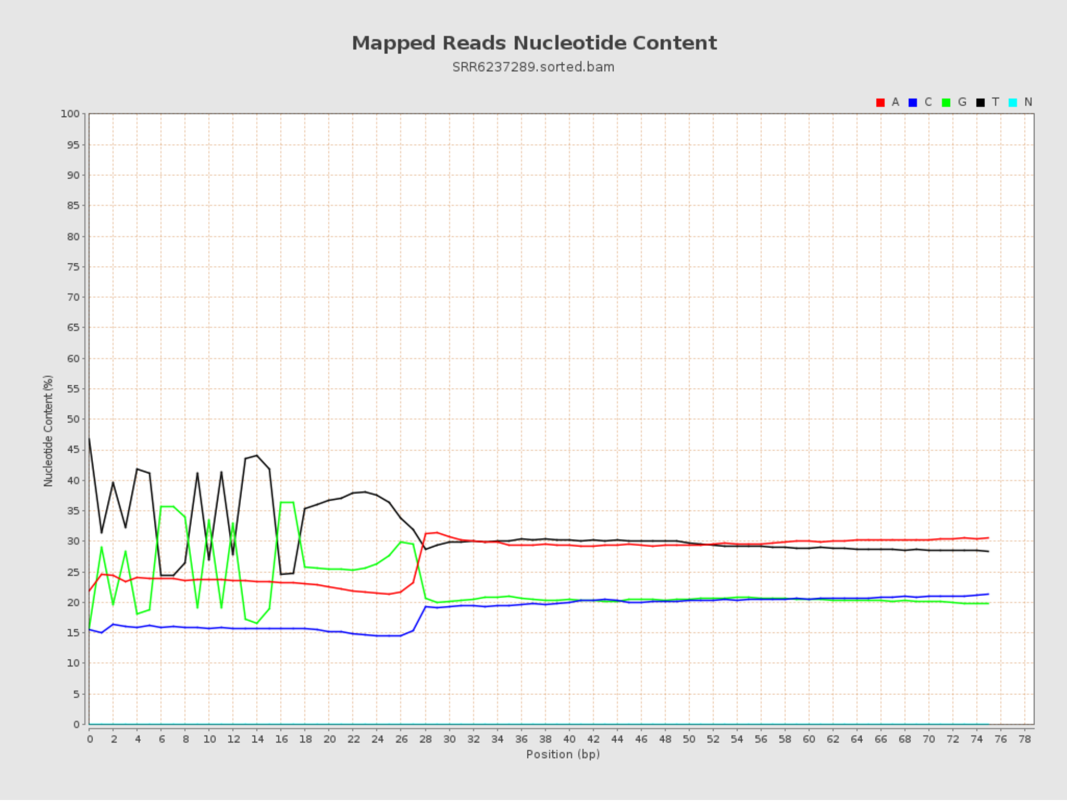
6. Results : Genome Fraction Coverage



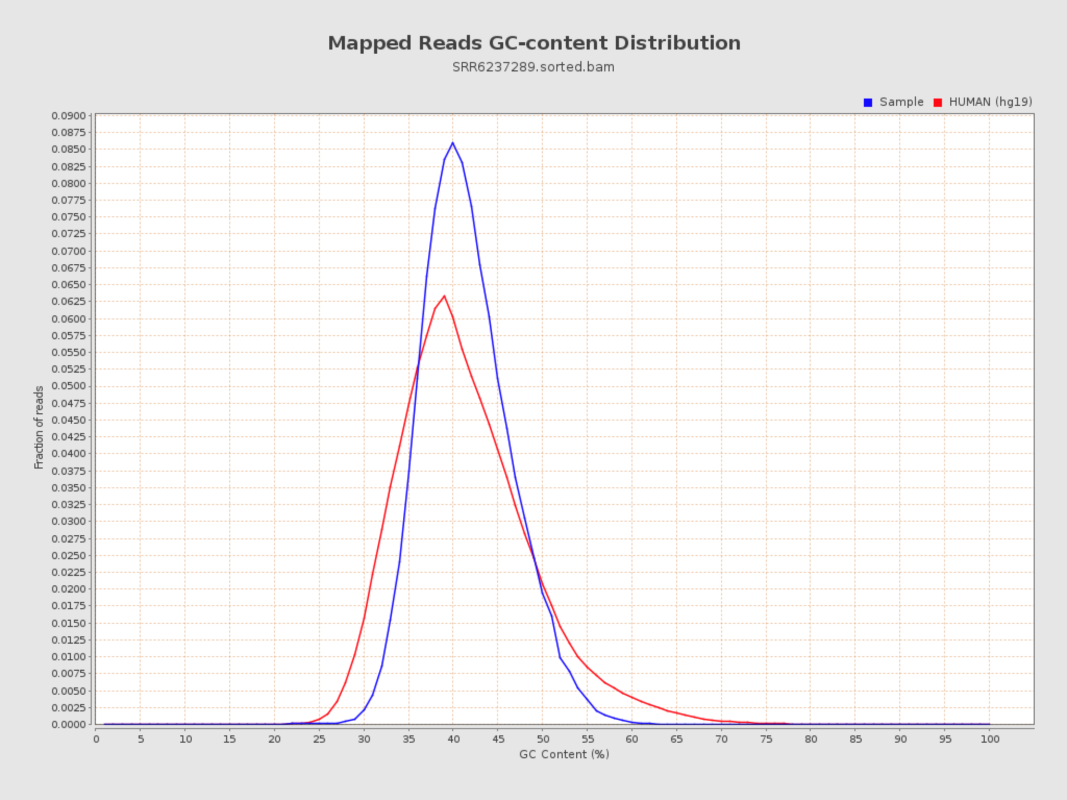
7. Results : Duplication Rate Histogram



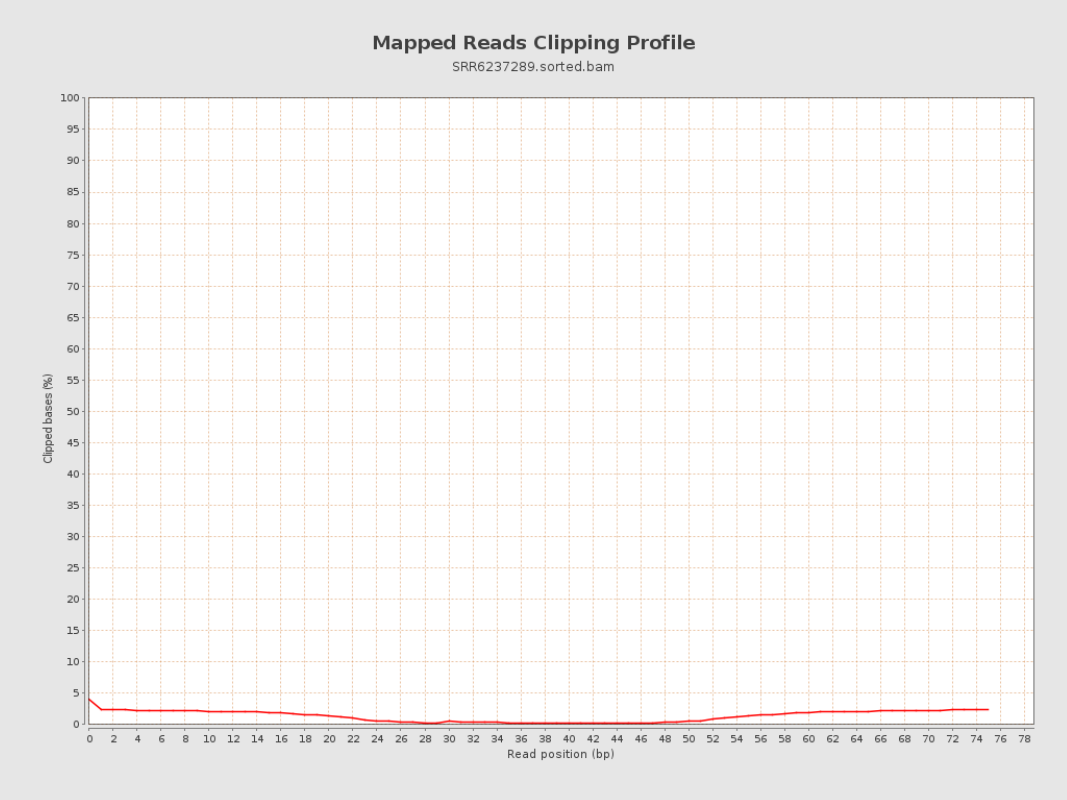
8. Results : Mapped Reads Nucleotide Content



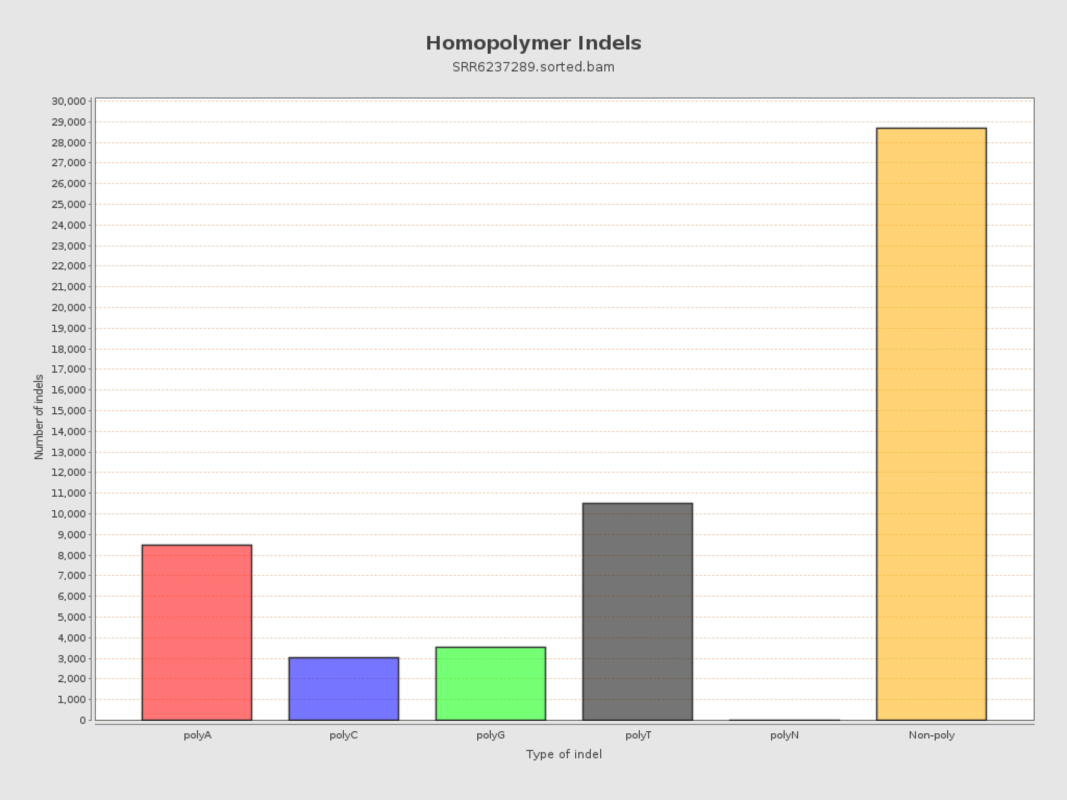
9. Results : Mapped Reads GC-content Distribution



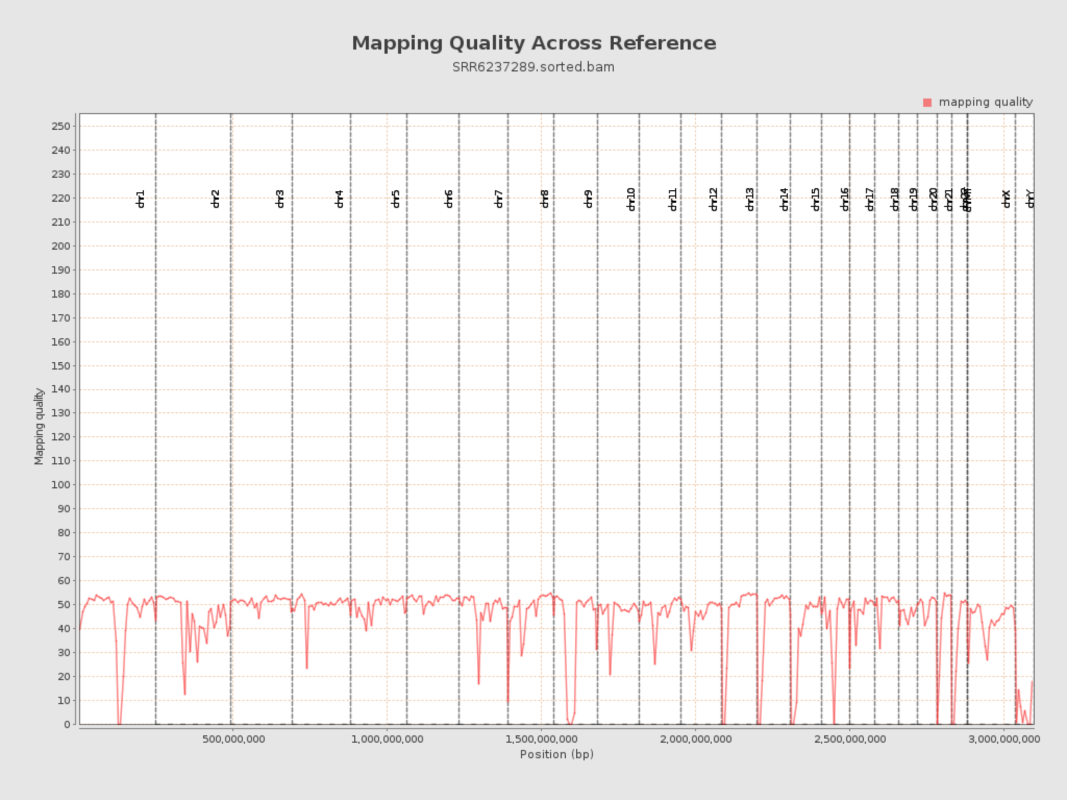
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram