Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:53:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237829.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_SRR6237829 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237829.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:53:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237829.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,589,255
Mapped reads	1,418,672 / 89.27%
Unmapped reads	170,583 / 10.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,211 / 0.96%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	248,745 / 15.65%
Duplication rate	11.77%
Clipped reads	583,900 / 36.74%

2.2. ACGT Content

Number/percentage of A's	27,040,690 / 28.33%
Number/percentage of C's	17,176,660 / 17.99%
Number/percentage of T's	30,884,997 / 32.36%
Number/percentage of G's	20,192,479 / 21.15%
Number/percentage of N's	160,313 / 0.17%
GC Percentage	39.15%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.4627

2.4. Mapping Quality

Mean Mapping Quality	46.86

2.5. Mismatches and indels

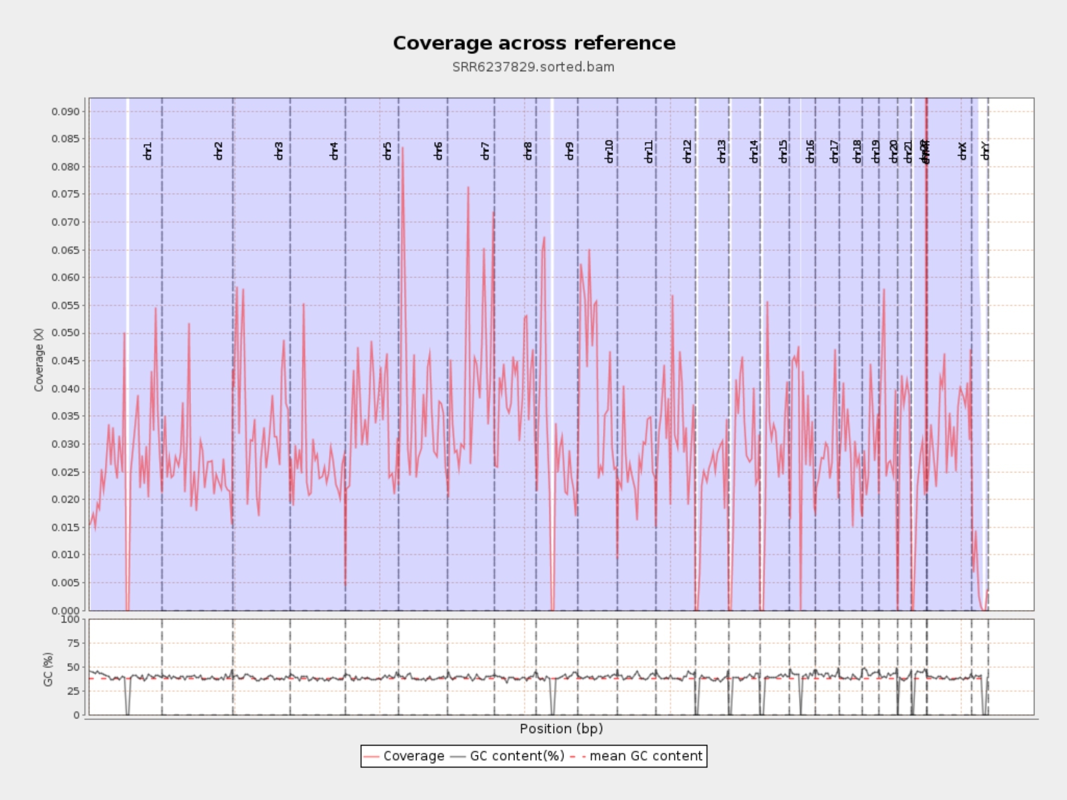
General error rate	0.88%
Mismatches	823,922
Insertions	7,334
Mapped reads with at least one insertion	0.51%
Deletions	27,450
Mapped reads with at least one deletion	1.91%
Homopolymer indels	46.28%

2.6. Chromosome stats

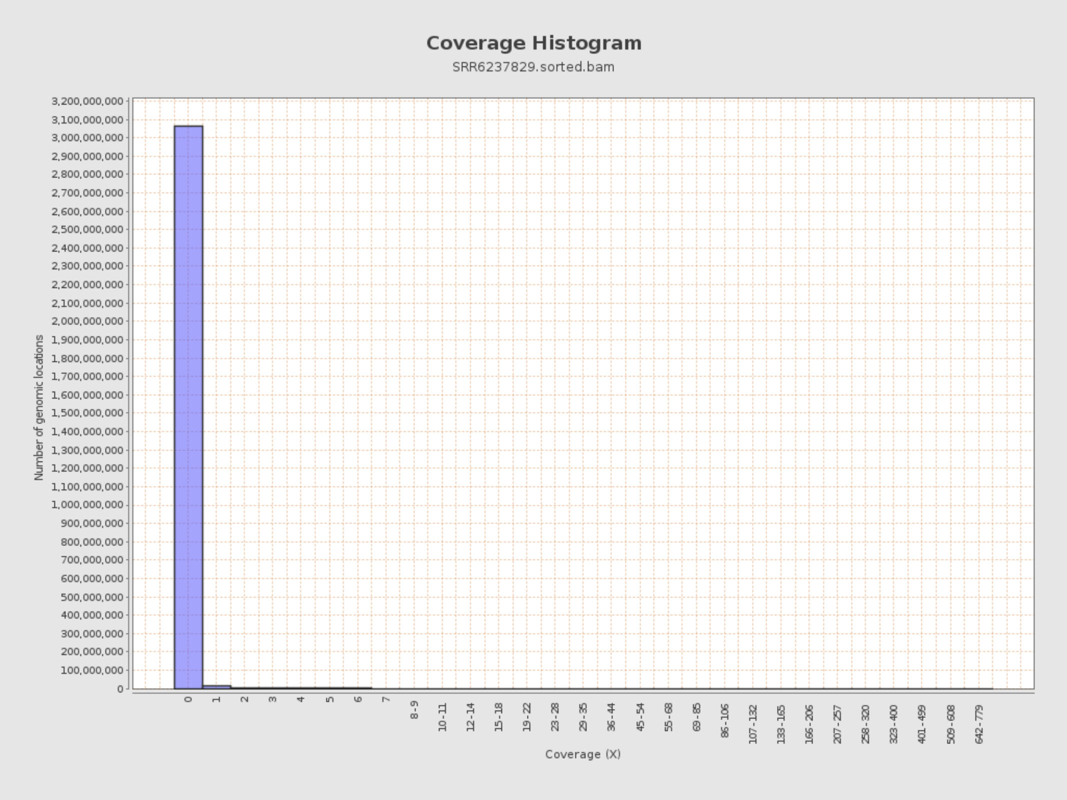
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6624664	0.0266	0.6074
chr2	243199373	6359058	0.0261	0.4366
chr3	198022430	6889589	0.0348	0.422
chr4	191154276	5044611	0.0264	0.3765
chr5	180915260	6239435	0.0345	0.4354
chr6	171115067	6282026	0.0367	0.4569
chr7	159138663	6661658	0.0419	0.5308

chr8	146364022	5790042	0.0396	0.6567
chr9	141213431	4058117	0.0287	0.4196
chr10	135534747	5728414	0.0423	0.5513
chr11	135006516	3581495	0.0265	0.39
chr12	133851895	4515642	0.0337	0.4247
chr13	115169878	2549064	0.0221	0.3385
chr14	107349540	2983871	0.0278	0.3937
chr15	102531392	2841721	0.0277	0.384
chr16	90354753	2946241	0.0326	0.4117
chr17	81195210	2297112	0.0283	0.38
chr18	78077248	2237072	0.0287	0.6585
chr19	59128983	1776436	0.03	0.4925
chr20	63025520	2161531	0.0343	0.4333
chr21	48129895	1537797	0.032	0.4091
chr22	51304566	926811	0.0181	0.2863
chrMT	16571	9780	0.5902	1.3093
chrX	155270560	5192929	0.0334	0.4228
chrY	59373566	269004	0.0045	0.1436

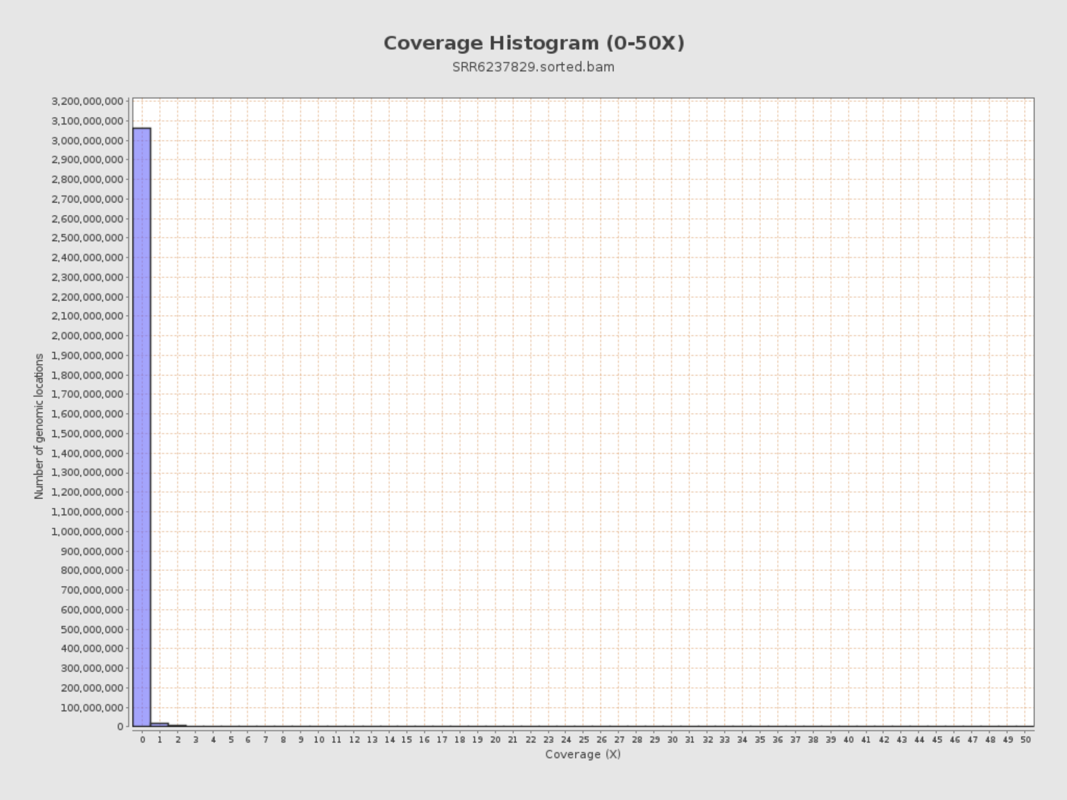
3. Results : Coverage across reference



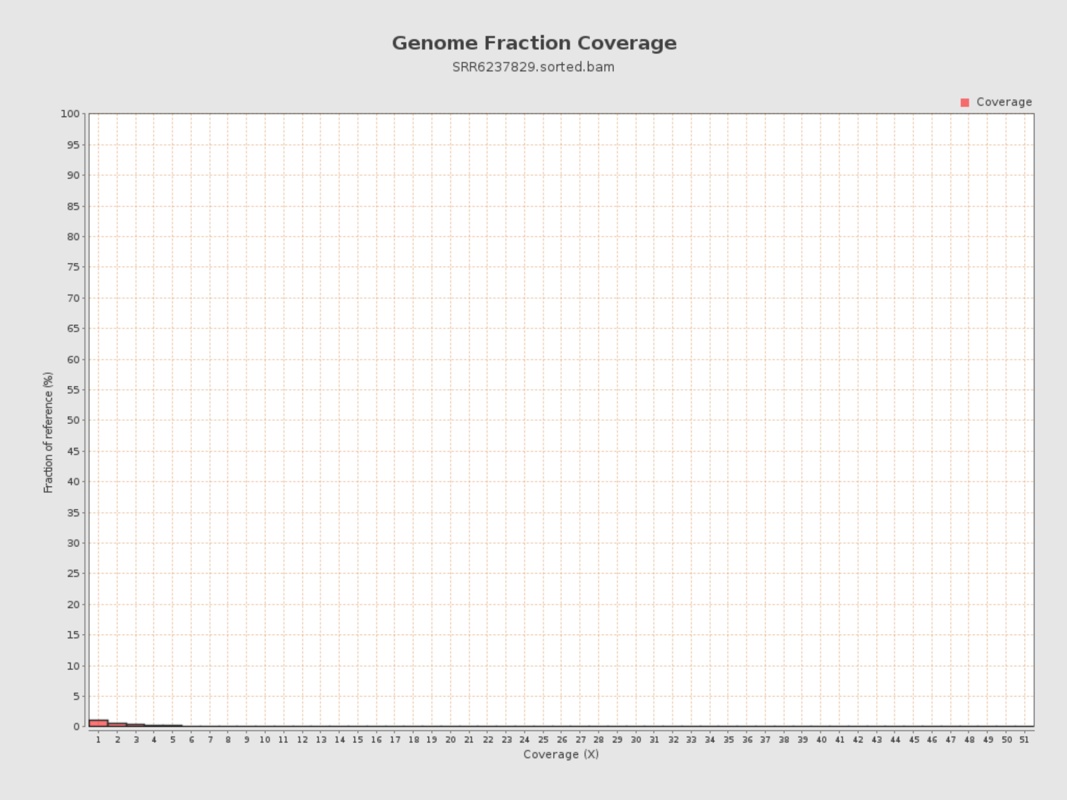
4. Results : Coverage Histogram



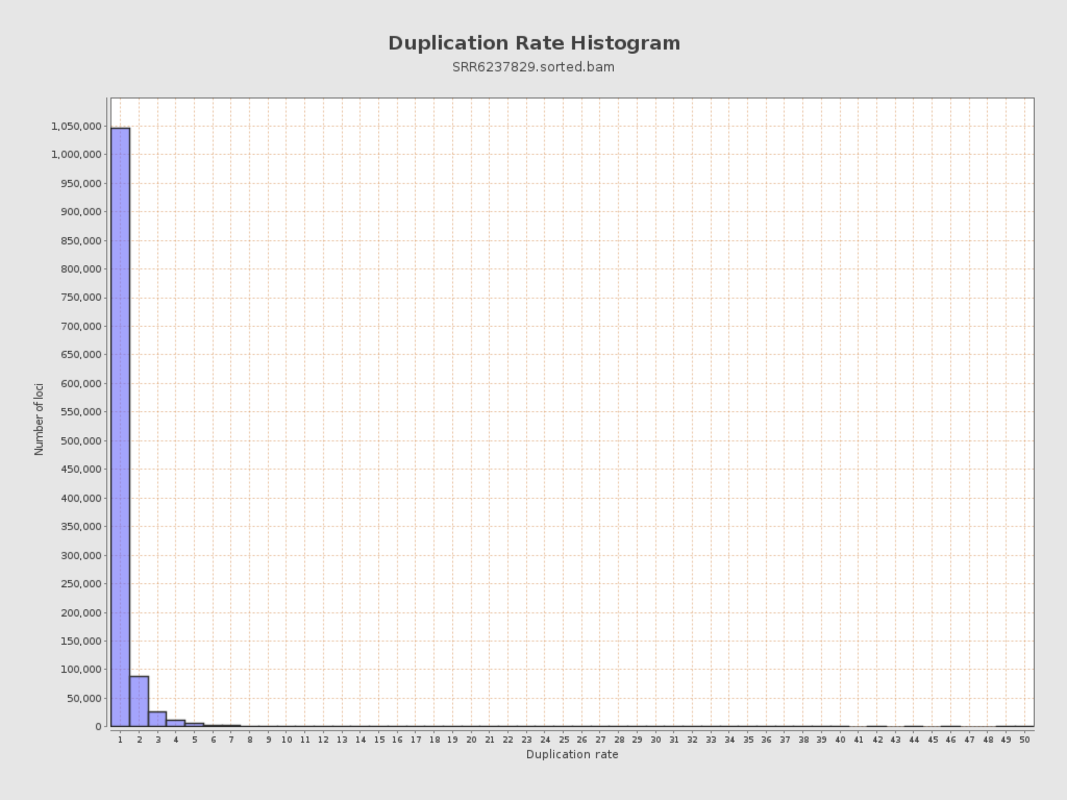
5. Results : Coverage Histogram (0-50X)



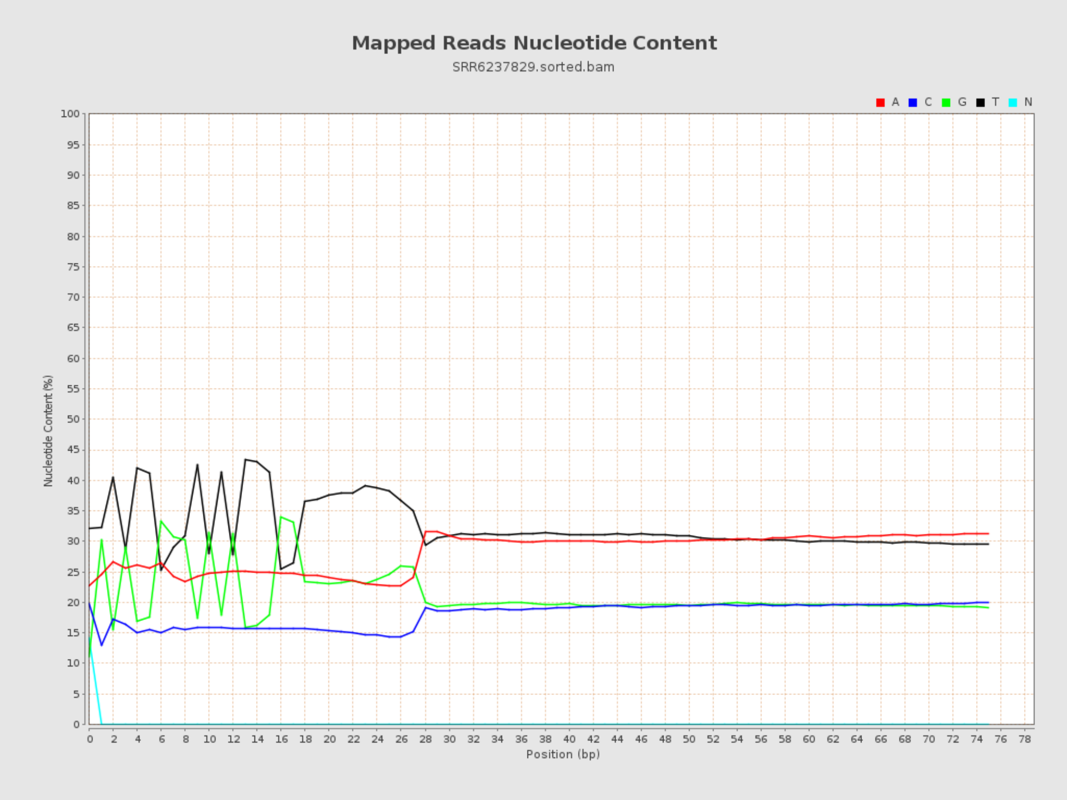
6. Results : Genome Fraction Coverage



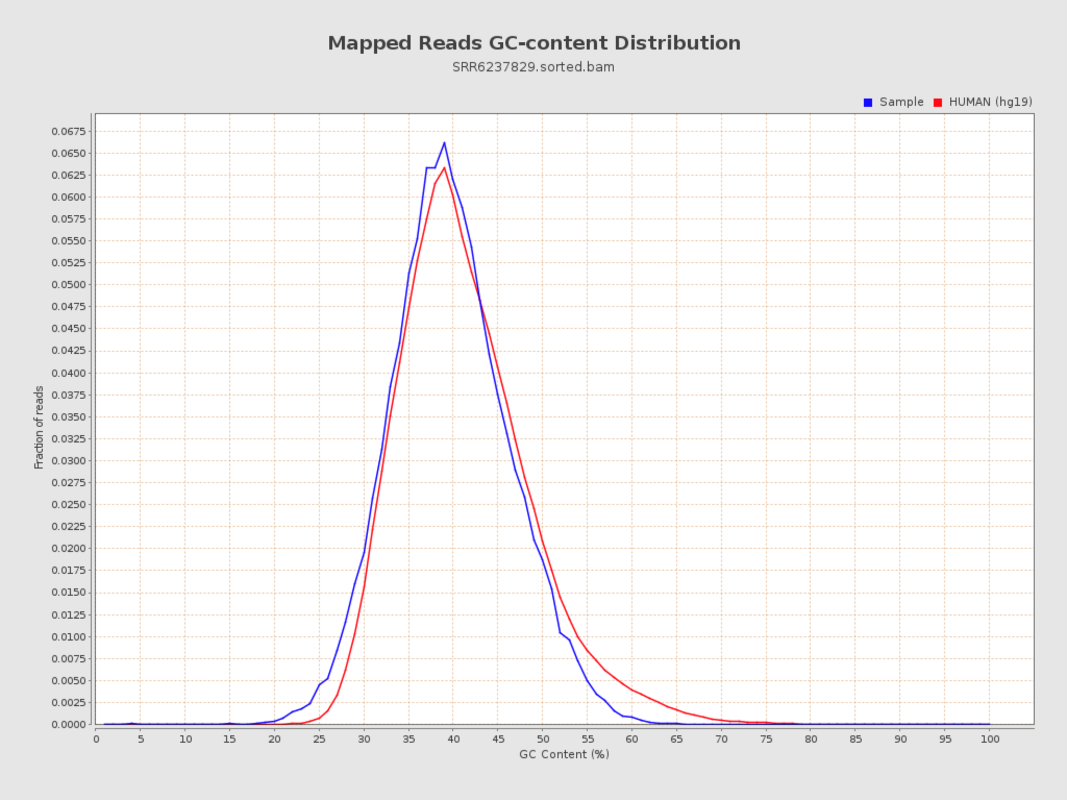
7. Results : Duplication Rate Histogram



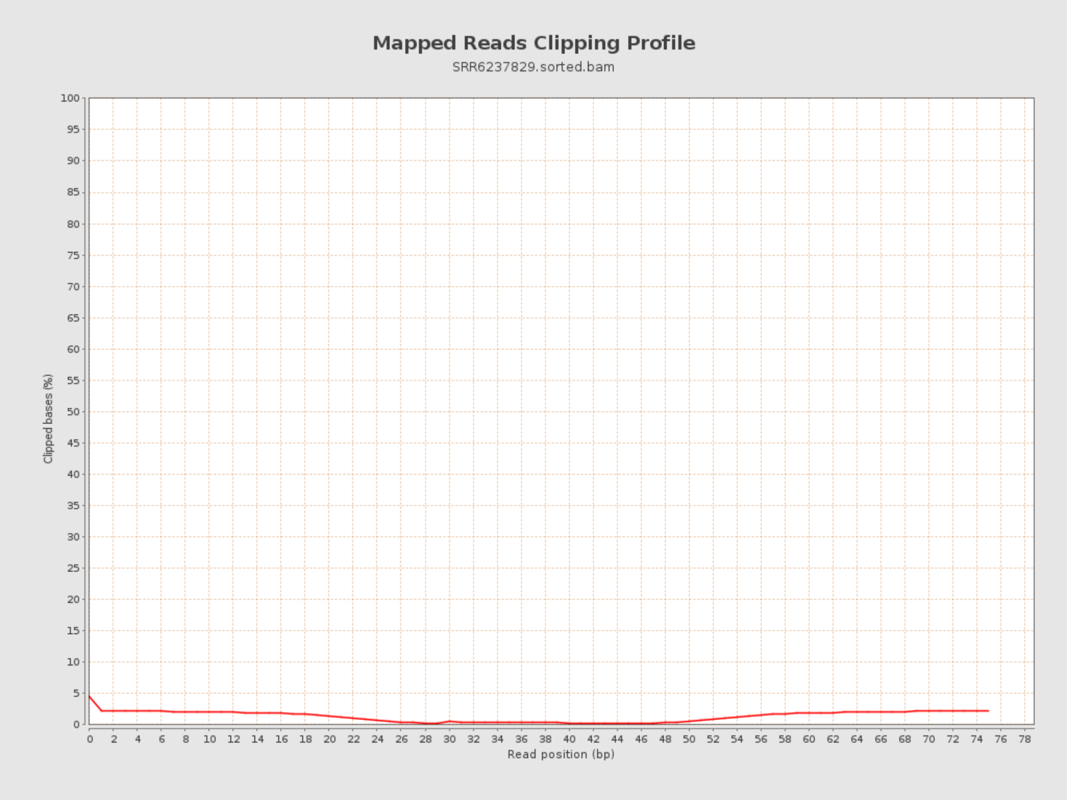
8. Results : Mapped Reads Nucleotide Content



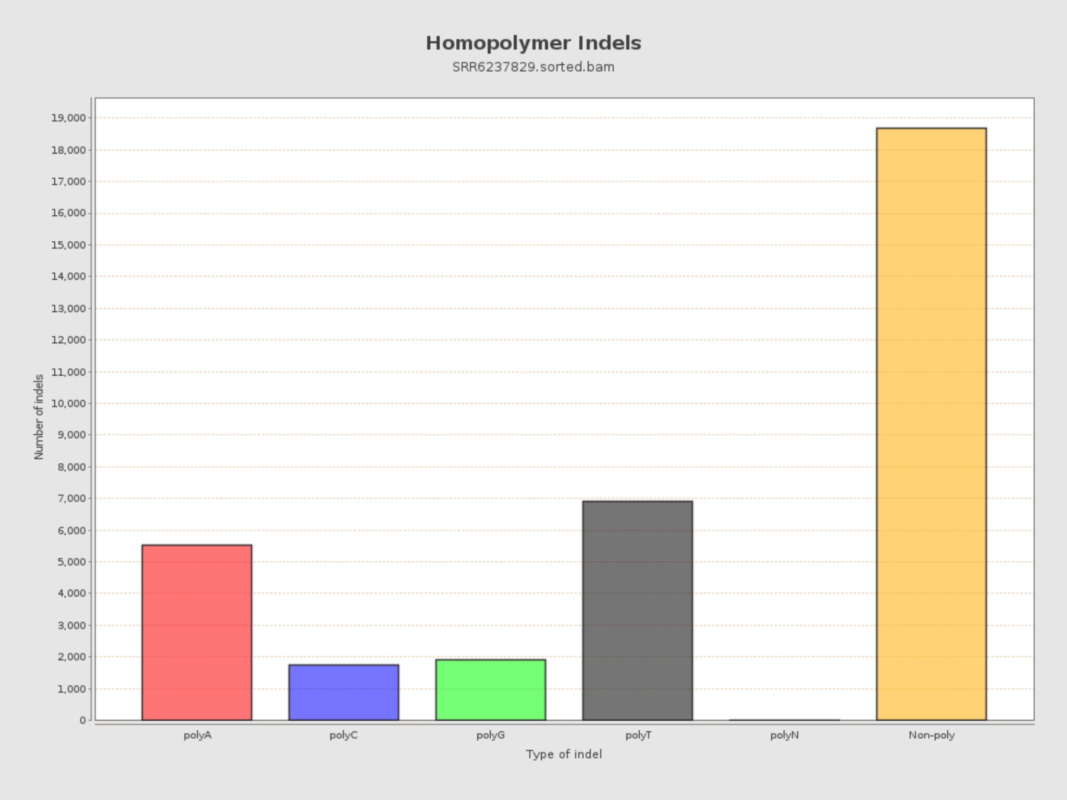
9. Results : Mapped Reads GC-content Distribution



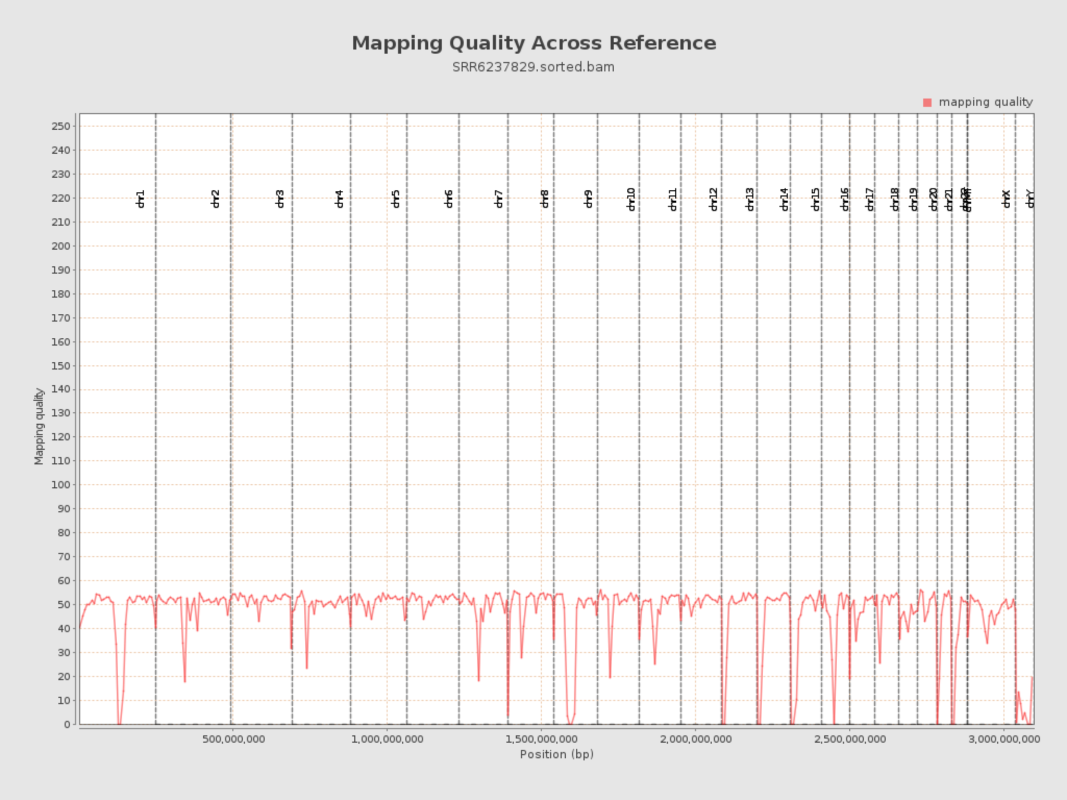
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram