Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:17:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237800.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_SRR6237800 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237800.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:17:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237800.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,081,258
Mapped reads	1,746,014 / 83.89%
Unmapped reads	335,244 / 16.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,441 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	367,058 / 17.64%
Duplication rate	12.83%
Clipped reads	766,740 / 36.84%

2.2. ACGT Content

Number/percentage of A's	32,257,321 / 27.71%
Number/percentage of C's	21,700,022 / 18.64%
Number/percentage of T's	36,506,200 / 31.36%
Number/percentage of G's	25,758,792 / 22.13%
Number/percentage of N's	188,430 / 0.16%
GC Percentage	40.77%

2.3. Coverage

Mean	0.0376

Standard Deviation	0.5718

2.4. Mapping Quality

Mean Mapping Quality	46.46

2.5. Mismatches and indels

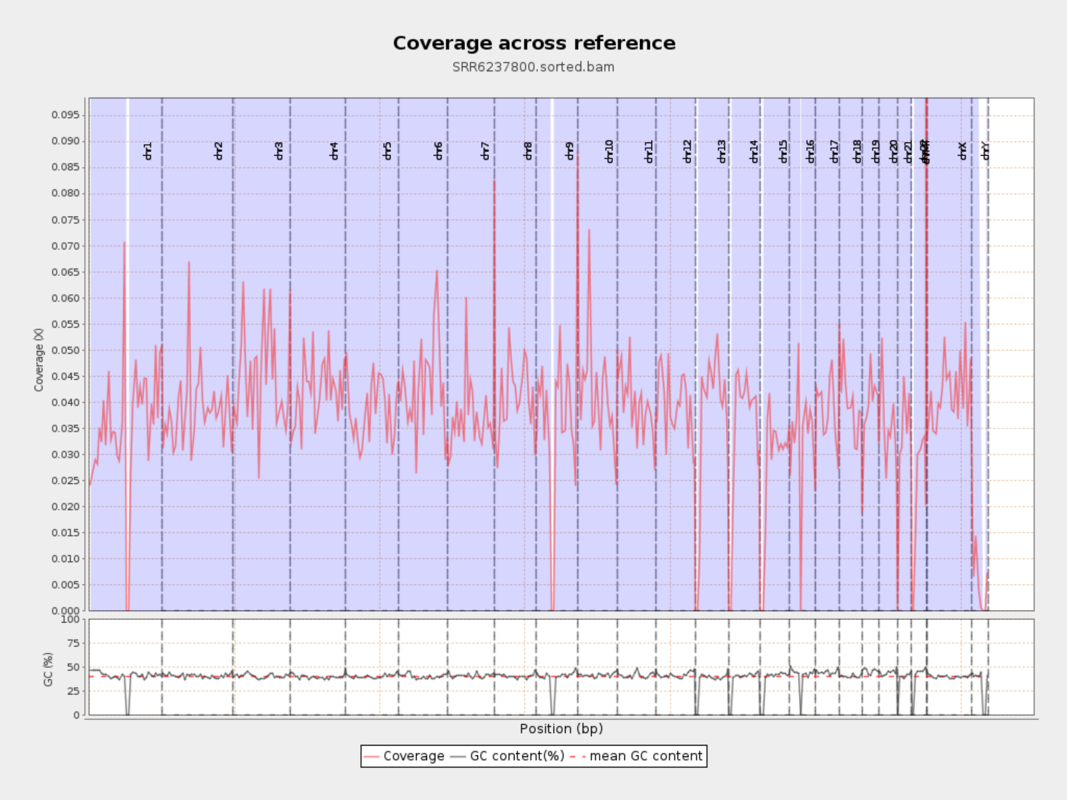
General error rate	0.85%
Mismatches	968,850
Insertions	8,165
Mapped reads with at least one insertion	0.46%
Deletions	29,063
Mapped reads with at least one deletion	1.65%
Homopolymer indels	47.23%

2.6. Chromosome stats

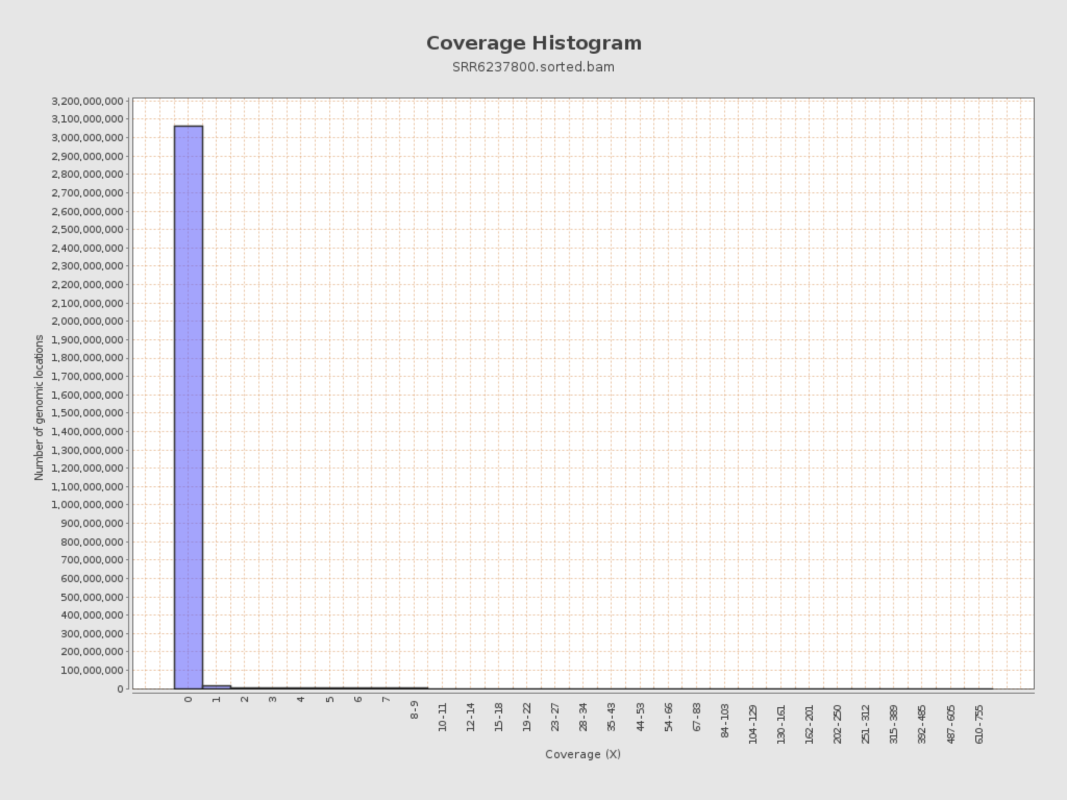
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8799563	0.0353	0.8118
chr2	243199373	9393927	0.0386	0.5948
chr3	198022430	8822840	0.0446	0.5702
chr4	191154276	8031480	0.042	0.555
chr5	180915260	6932733	0.0383	0.5172
chr6	171115067	7379454	0.0431	0.5669
chr7	159138663	5888613	0.037	0.5926

chr8	146364022	5991792	0.0409	0.5787
chr9	141213431	4990592	0.0353	0.5221
chr10	135534747	5633552	0.0416	0.6109
chr11	135006516	5331465	0.0395	0.5435
chr12	133851895	5285244	0.0395	0.5398
chr13	115169878	4220819	0.0366	0.5314
chr14	107349540	3670405	0.0342	0.4923
chr15	102531392	2789938	0.0272	0.4226
chr16	90354753	2982089	0.033	0.477
chr17	81195210	3101852	0.0382	0.532
chr18	78077248	3139172	0.0402	0.6474
chr19	59128983	2330852	0.0394	0.6481
chr20	63025520	2253683	0.0358	0.5088
chr21	48129895	1556318	0.0323	0.4703
chr22	51304566	1128513	0.022	0.3753
chrMT	16571	34699	2.094	3.3133
chrX	155270560	6440862	0.0415	0.5575
chrY	59373566	332248	0.0056	0.1703

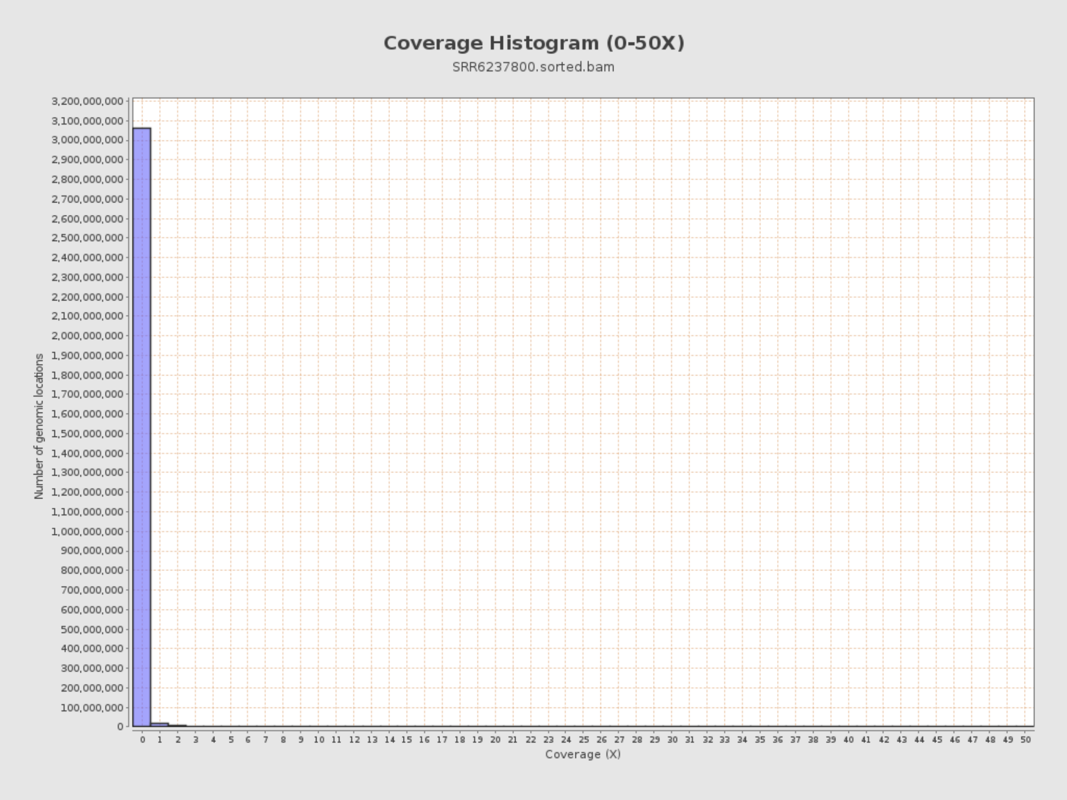
3. Results : Coverage across reference



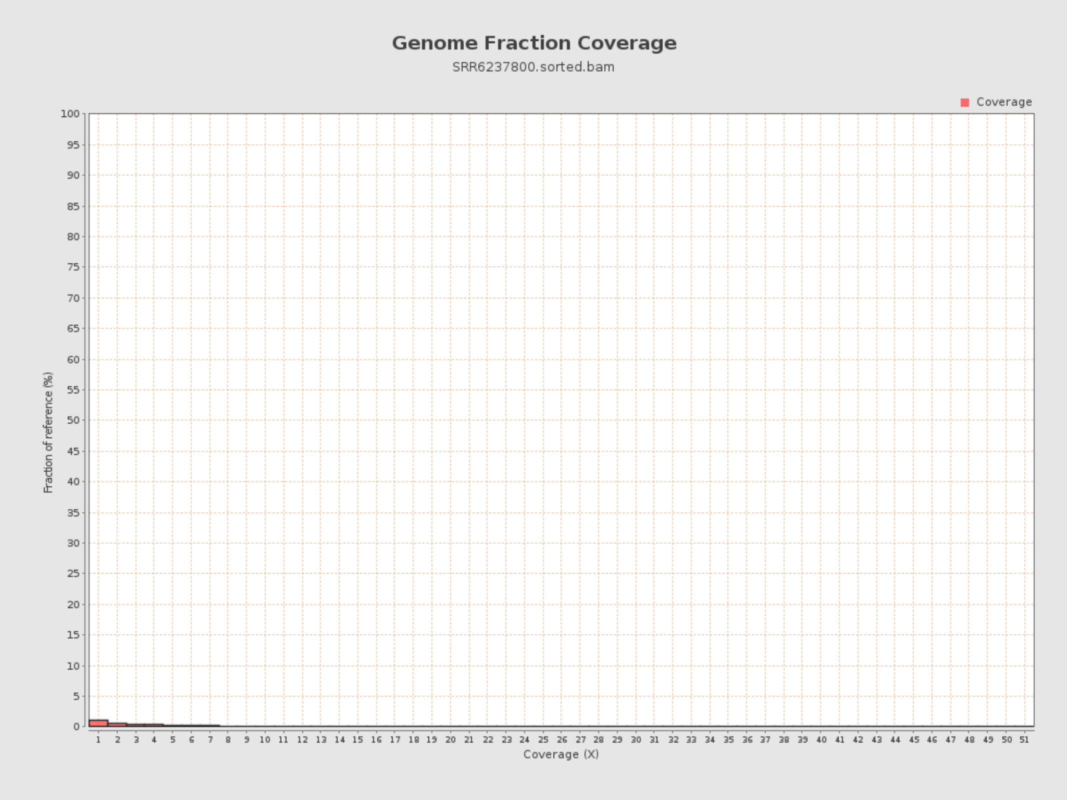
4. Results : Coverage Histogram



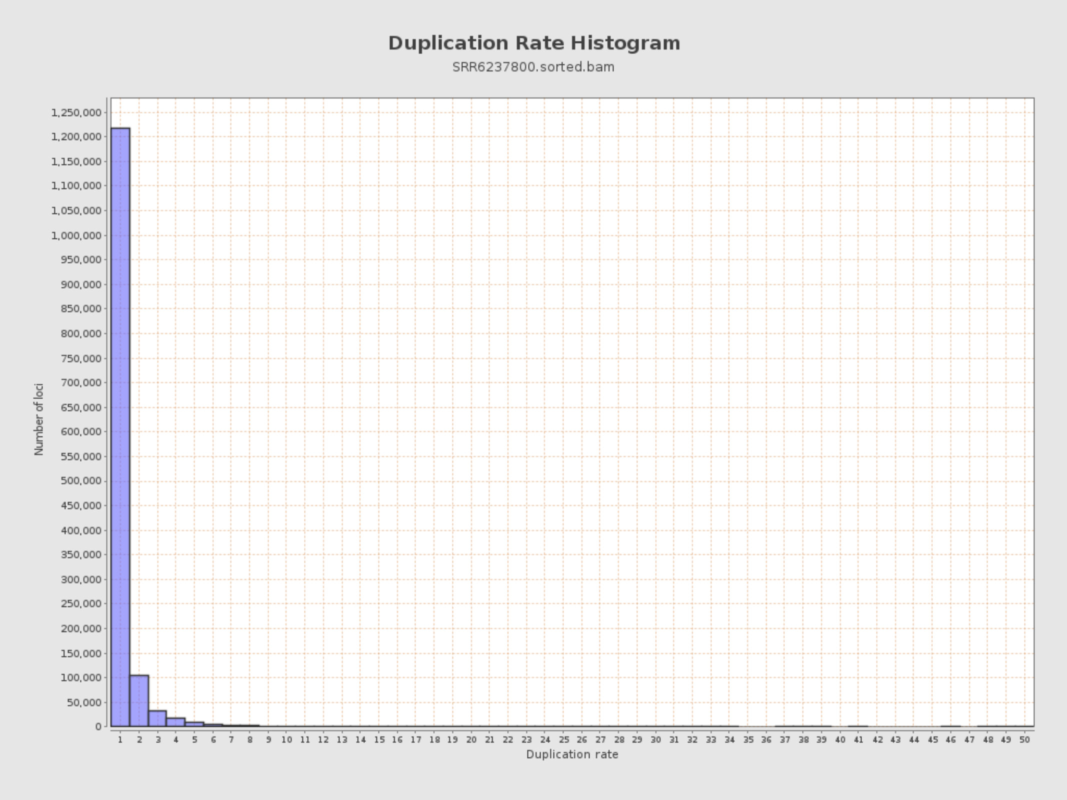
5. Results : Coverage Histogram (0-50X)



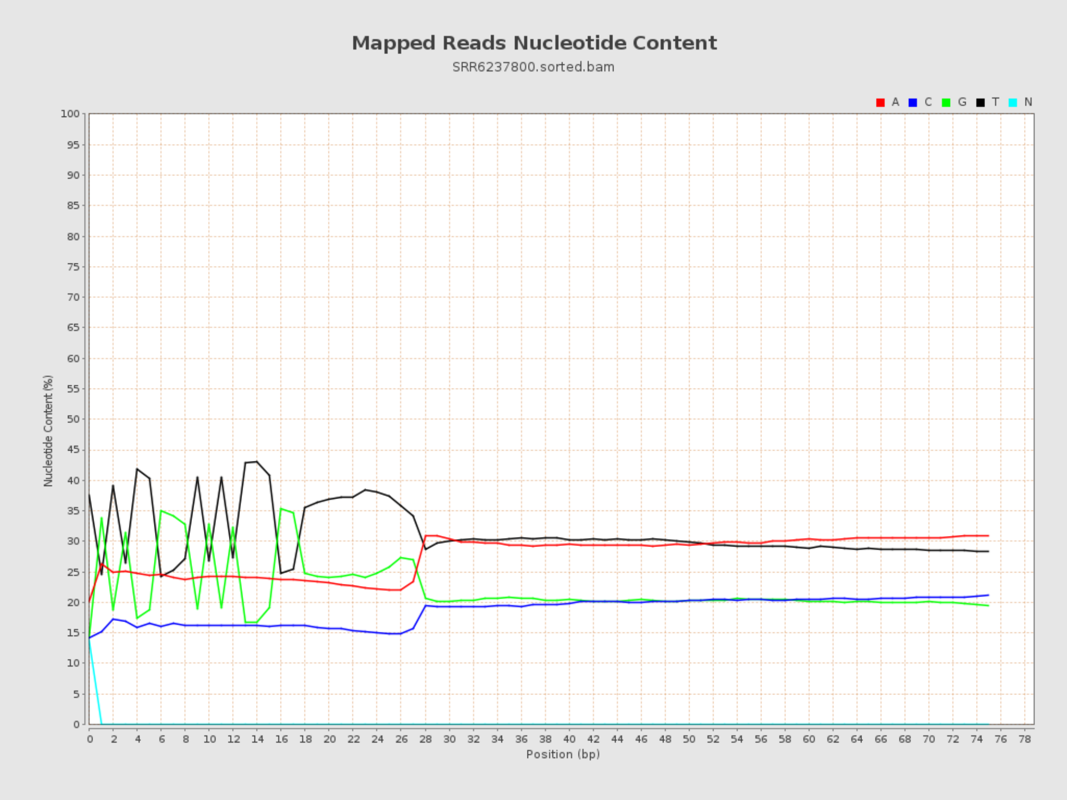
6. Results : Genome Fraction Coverage



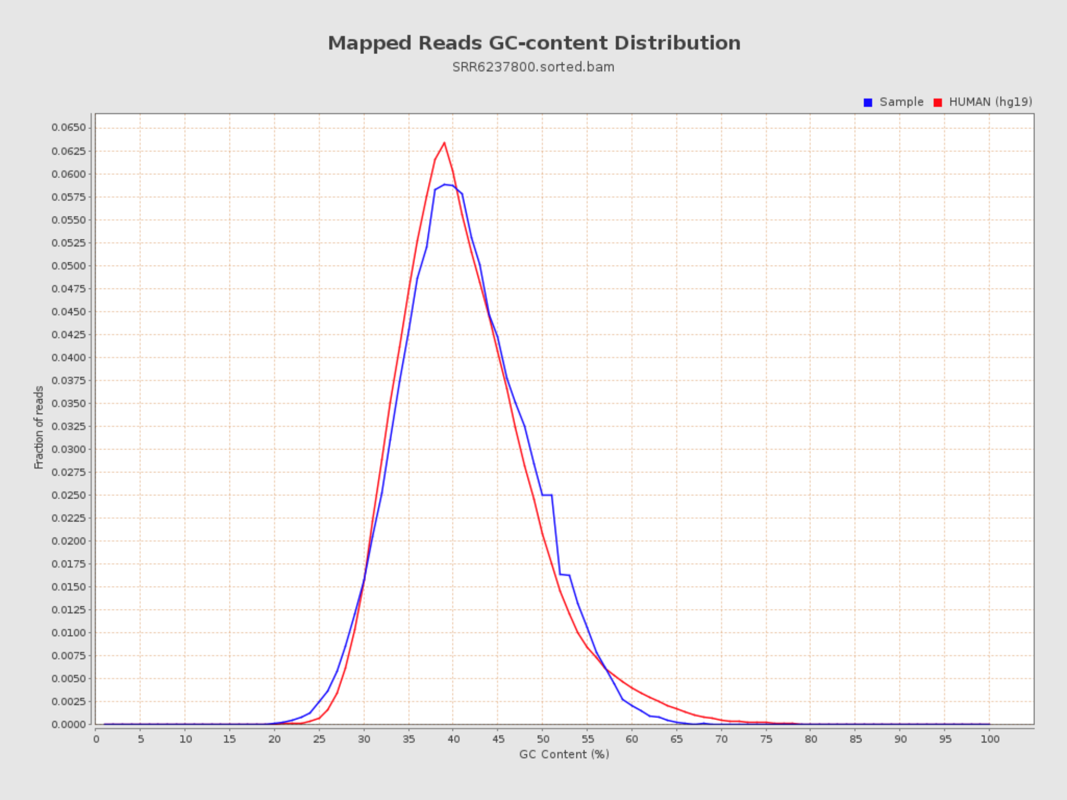
7. Results : Duplication Rate Histogram



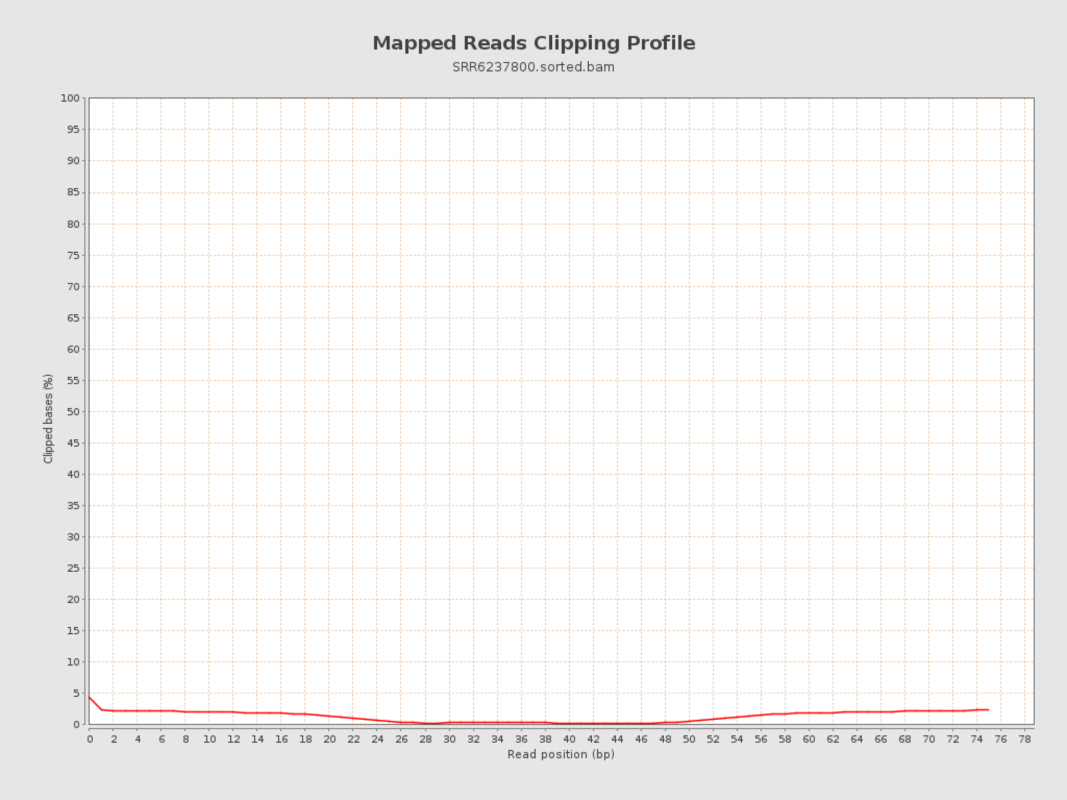
8. Results : Mapped Reads Nucleotide Content



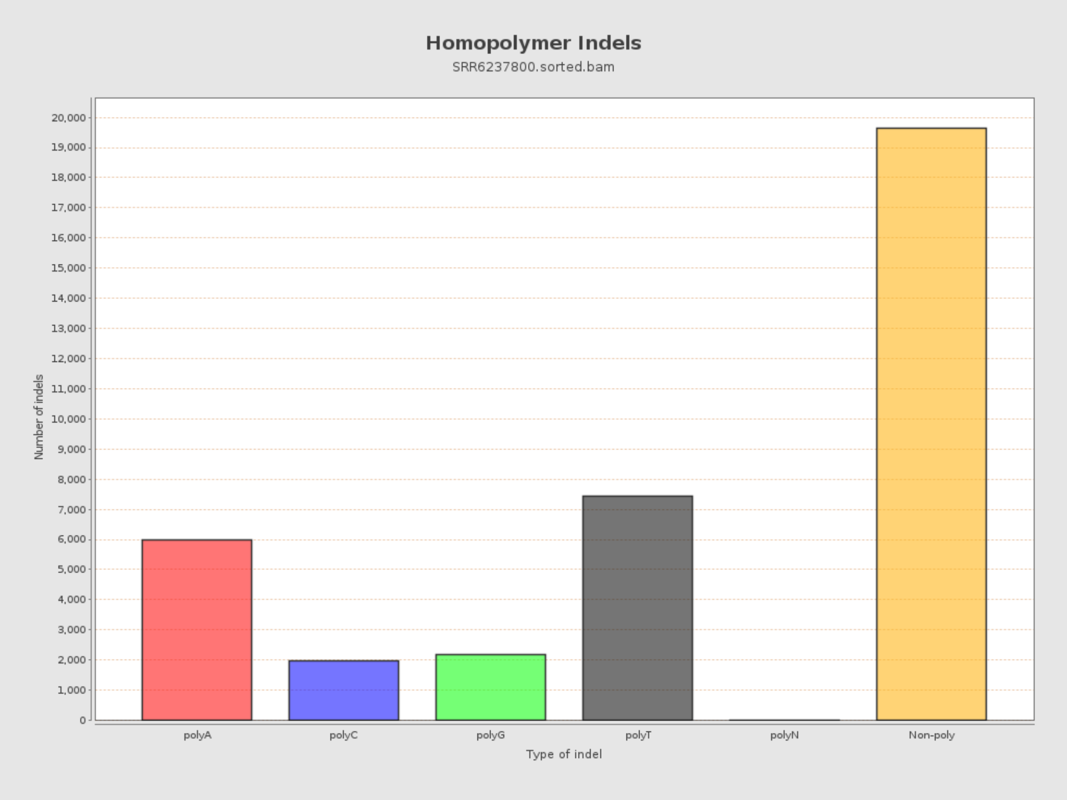
9. Results : Mapped Reads GC-content Distribution



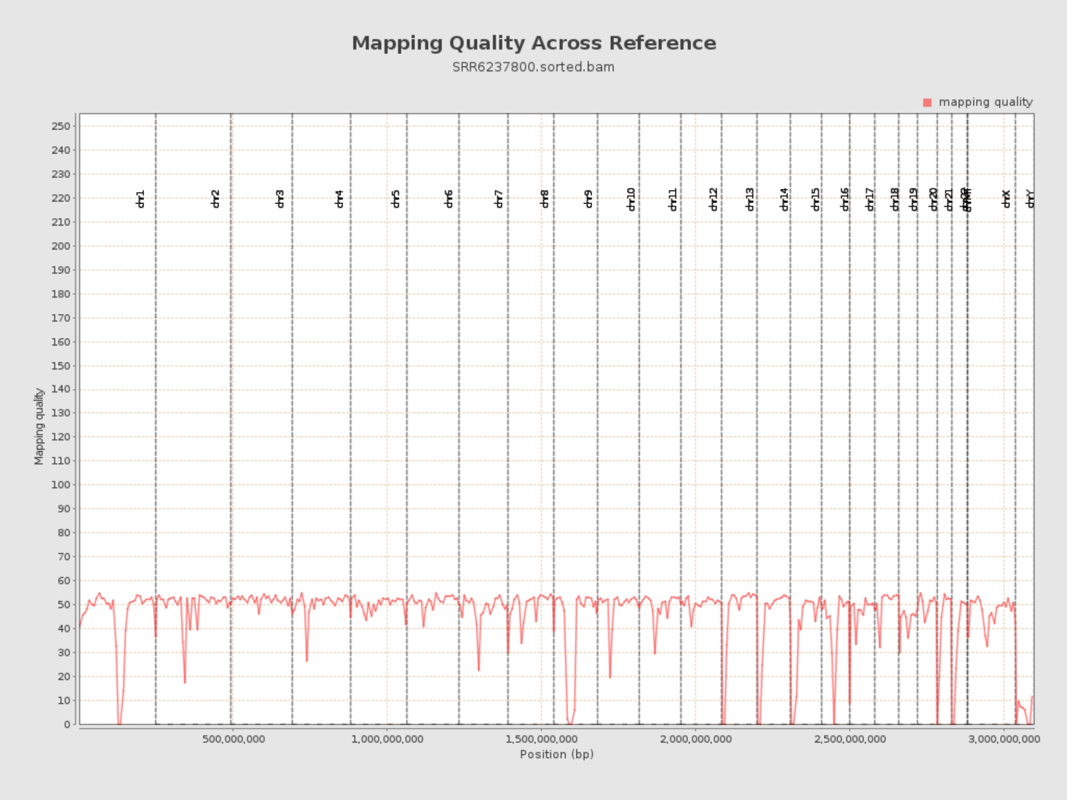
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram