Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:01:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237813.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_SRR6237813 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237813.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:01:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237813.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,519,138
Mapped reads	1,416,926 / 93.27%
Unmapped reads	102,212 / 6.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,519 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	37,059 / 2.44%
Duplication rate	1.52%
Clipped reads	323,243 / 21.28%

2.2. ACGT Content

Number/percentage of A's	31,176,388 / 30.28%
Number/percentage of C's	20,656,843 / 20.06%
Number/percentage of T's	30,022,427 / 29.15%
Number/percentage of G's	20,949,174 / 20.34%
Number/percentage of N's	171,951 / 0.17%
GC Percentage	40.4%

2.3. Coverage

Mean	0.0333

Standard Deviation	0.4092

2.4. Mapping Quality

Mean Mapping Quality	47.83

2.5. Mismatches and indels

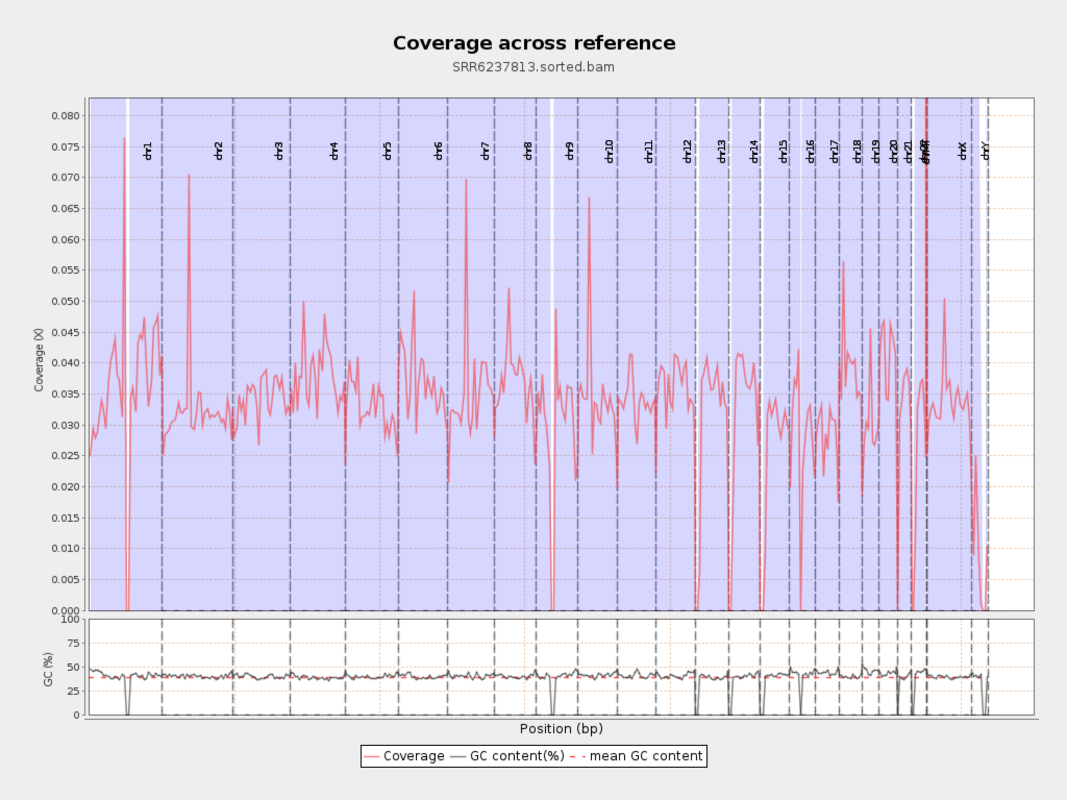
General error rate	0.91%
Mismatches	923,818
Insertions	8,217
Mapped reads with at least one insertion	0.58%
Deletions	25,609
Mapped reads with at least one deletion	1.79%
Homopolymer indels	47.09%

2.6. Chromosome stats

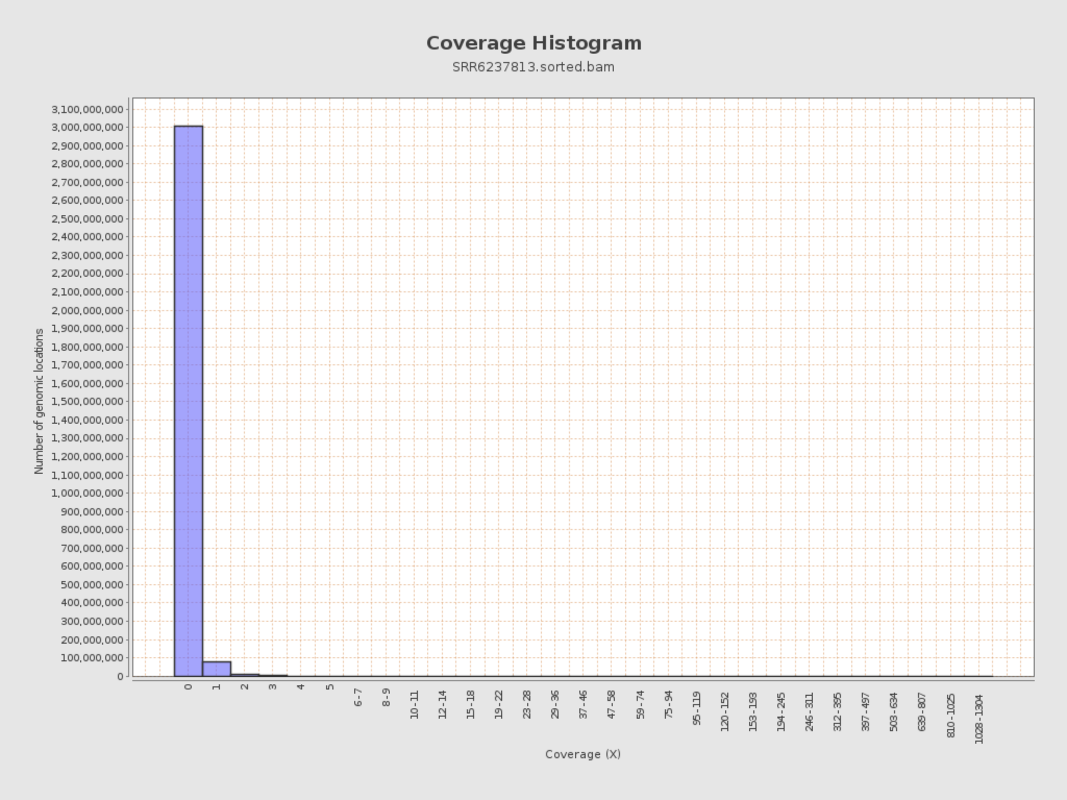
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9003842	0.0361	0.9483
chr2	243199373	7893002	0.0325	0.3566
chr3	198022430	6765819	0.0342	0.2095
chr4	191154276	7265793	0.038	0.2341
chr5	180915260	5982472	0.0331	0.2072
chr6	171115067	6379575	0.0373	0.2621
chr7	159138663	5660057	0.0356	0.5283

chr8	146364022	5409244	0.037	0.3421
chr9	141213431	4168971	0.0295	0.3667
chr10	135534747	4711612	0.0348	0.362
chr11	135006516	4550715	0.0337	0.3305
chr12	133851895	4866944	0.0364	0.2205
chr13	115169878	3490730	0.0303	0.1935
chr14	107349540	3381737	0.0315	0.2149
chr15	102531392	2589680	0.0253	0.1765
chr16	90354753	2551673	0.0282	0.2437
chr17	81195210	2292749	0.0282	0.2289
chr18	78077248	3087845	0.0395	0.7876
chr19	59128983	1790273	0.0303	0.5138
chr20	63025520	2580440	0.0409	0.2397
chr21	48129895	1520274	0.0316	0.2229
chr22	51304566	1210720	0.0236	0.1708
chrMT	16571	133253	8.0413	5.0309
chrX	155270560	5249489	0.0338	0.2307
chrY	59373566	486249	0.0082	0.1675

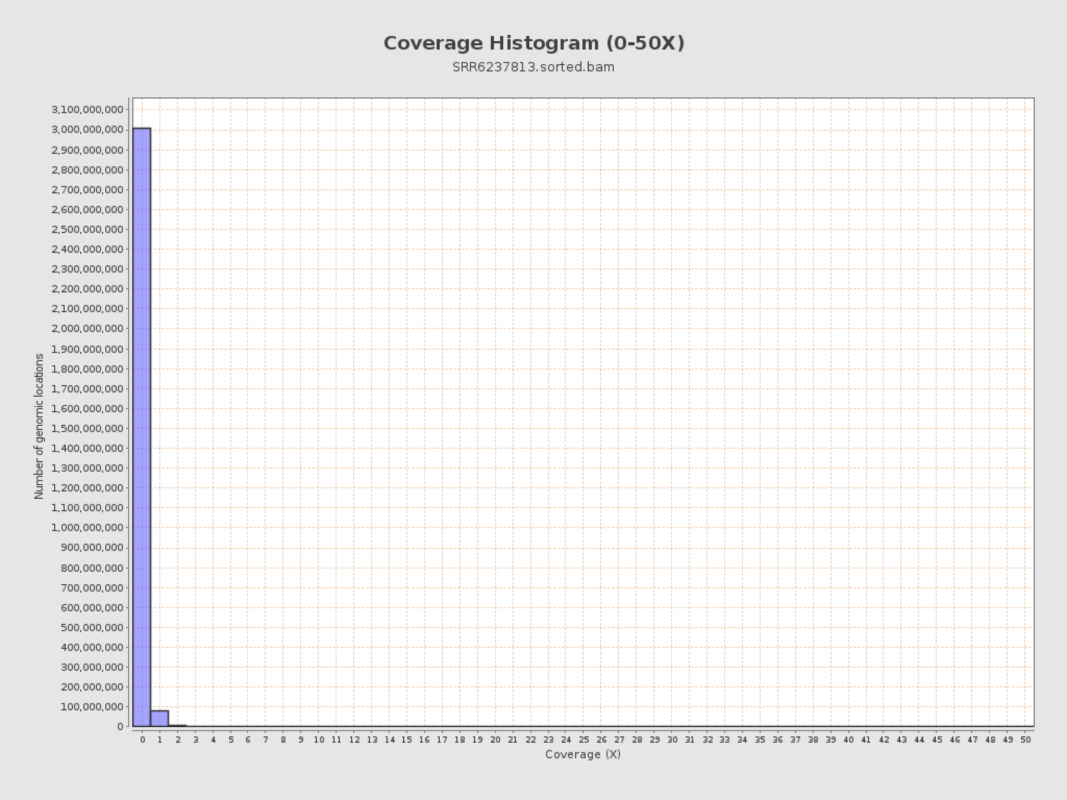
3. Results : Coverage across reference



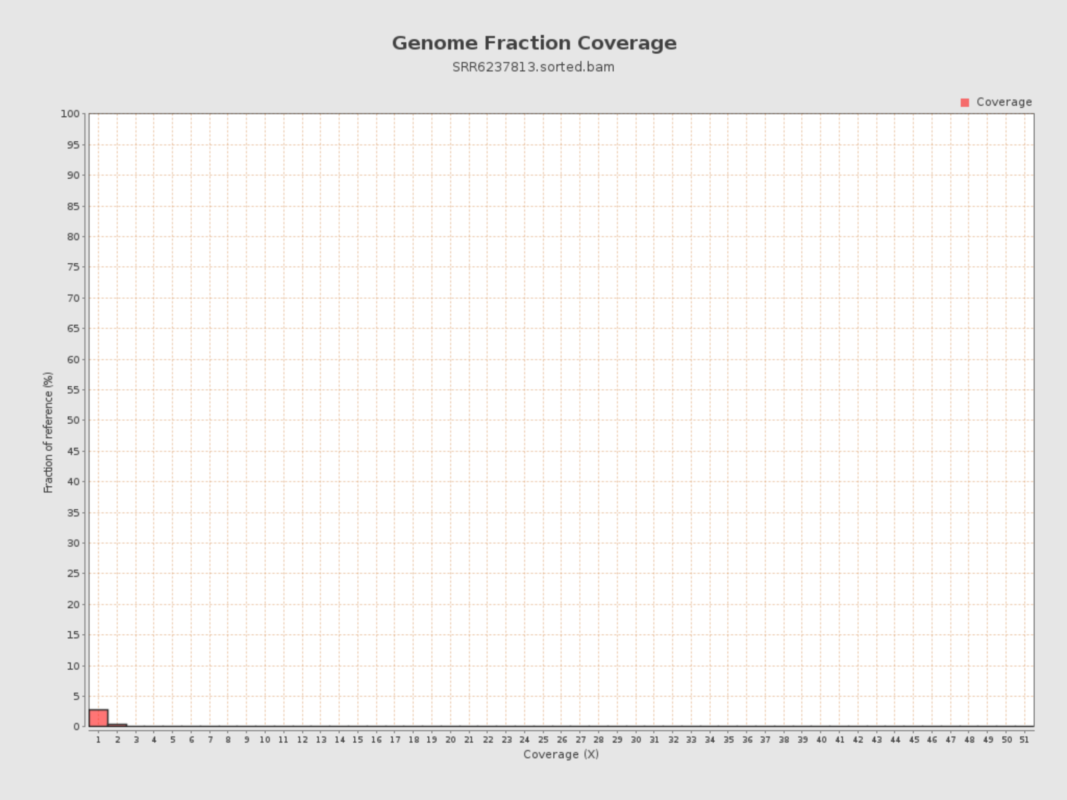
4. Results : Coverage Histogram



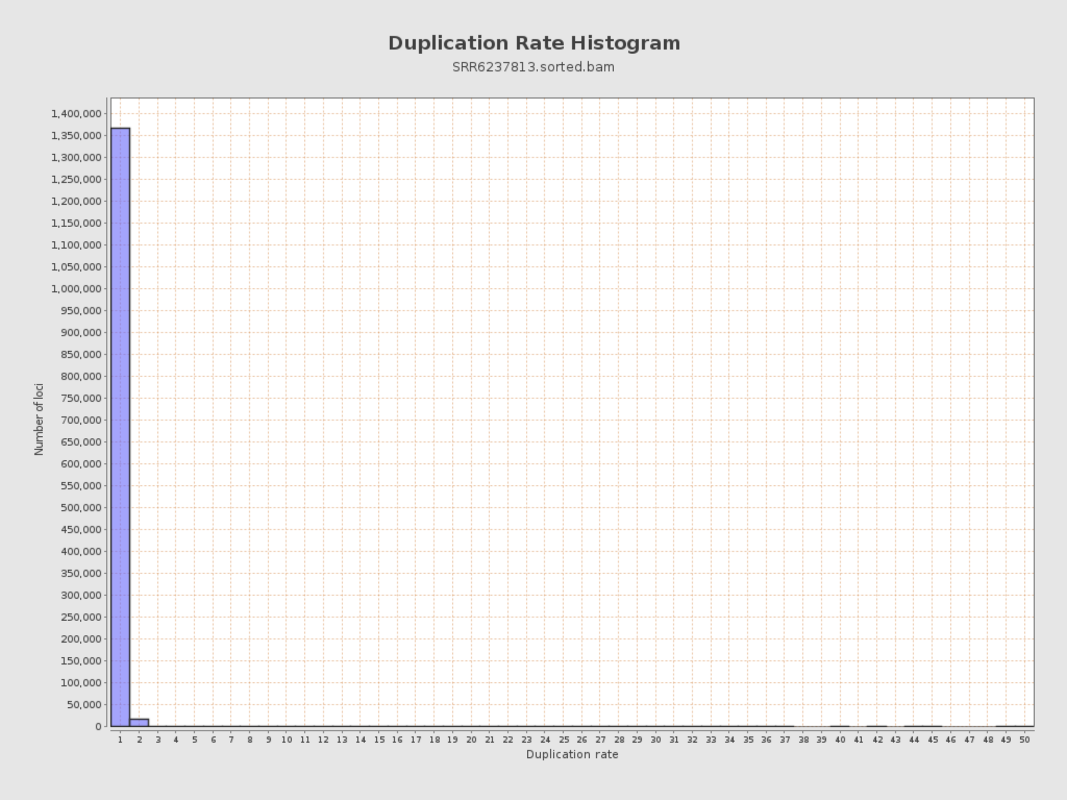
5. Results : Coverage Histogram (0-50X)



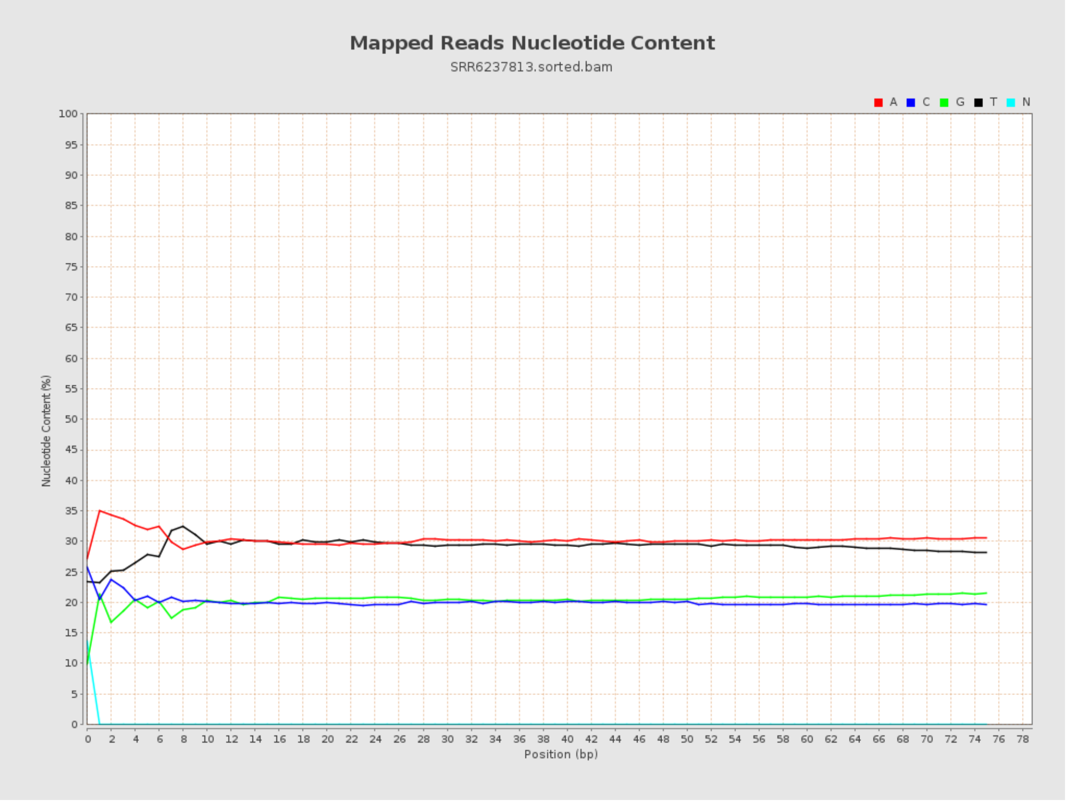
6. Results : Genome Fraction Coverage



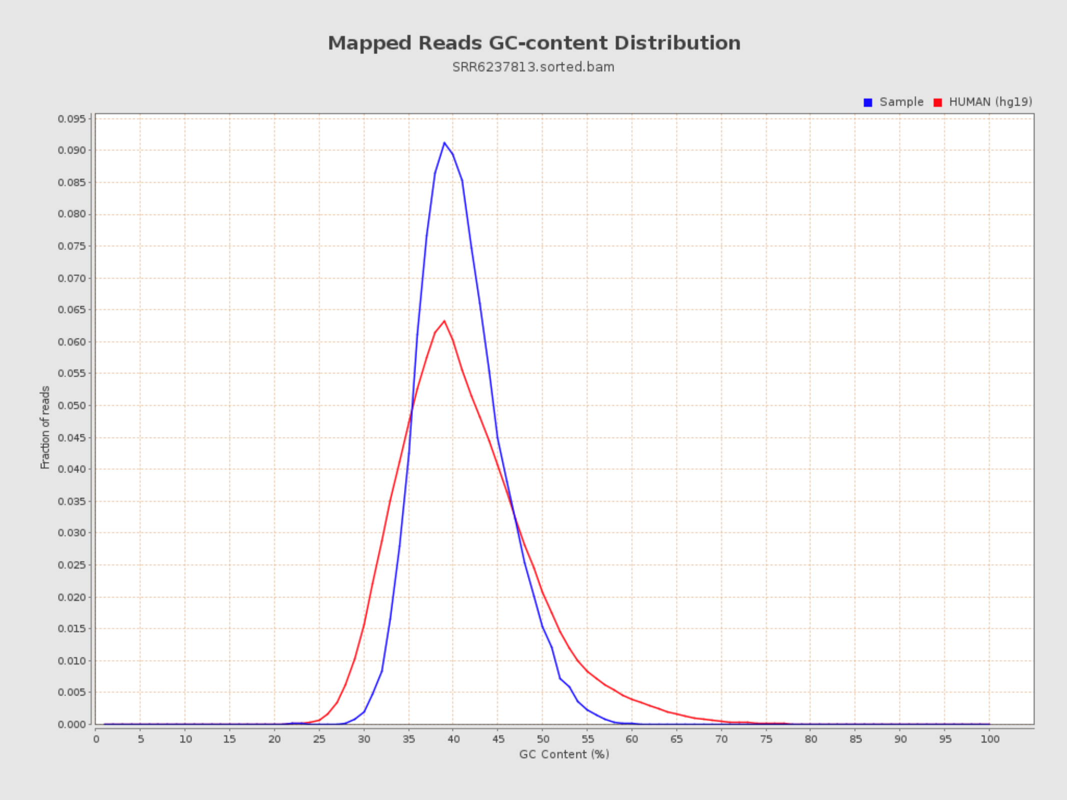
7. Results : Duplication Rate Histogram



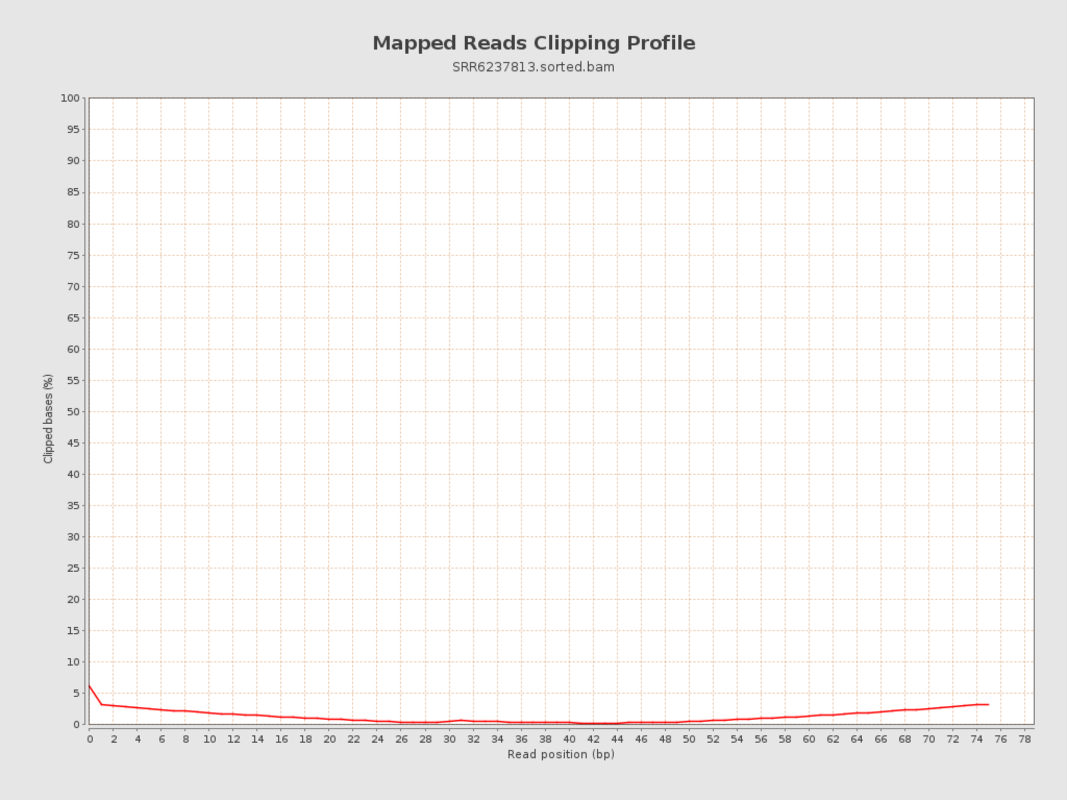
8. Results : Mapped Reads Nucleotide Content



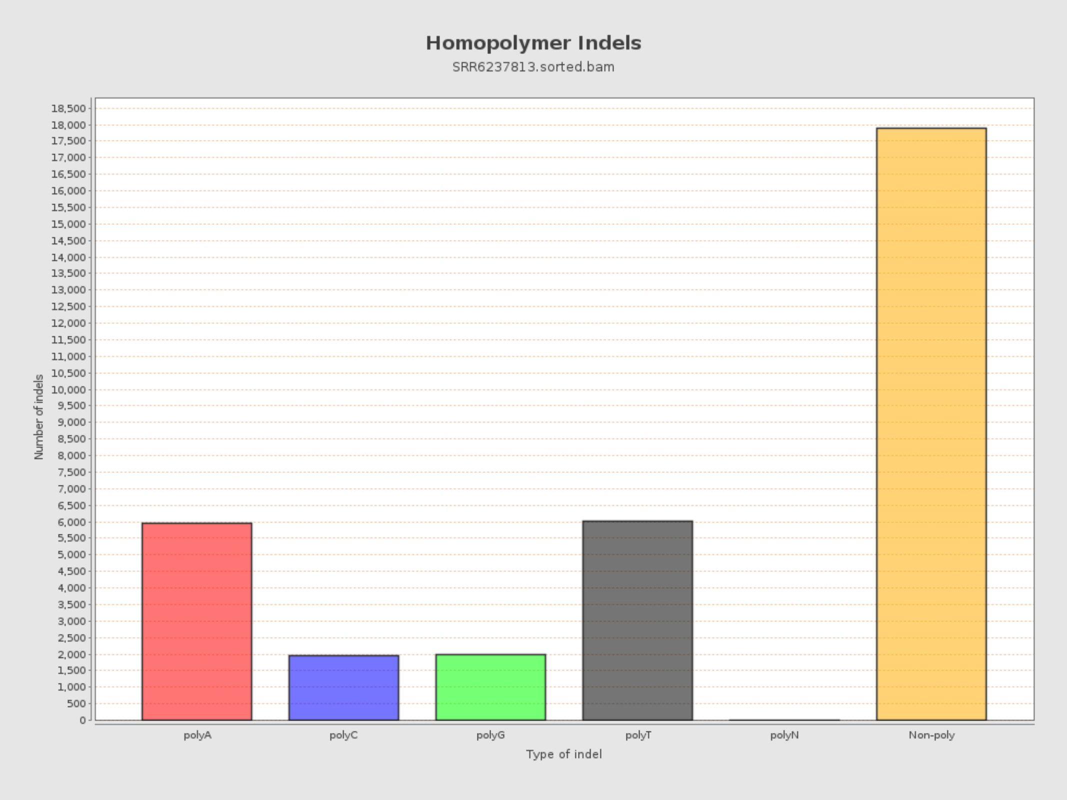
9. Results : Mapped Reads GC-content Distribution



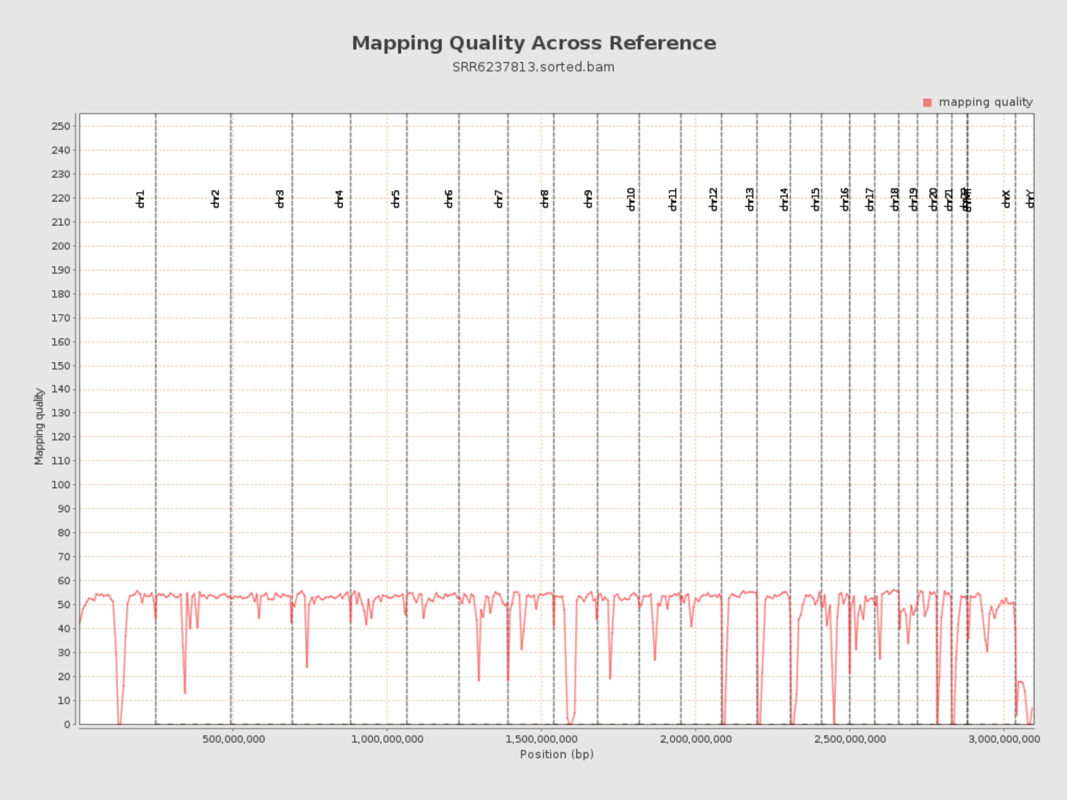
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram