Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:32:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013218.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_SRR6013218 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013218.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:32:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013218.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,890,674
Mapped reads	1,429,768 / 75.62%
Unmapped reads	460,906 / 24.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,394 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	107,676 / 5.7%
Duplication rate	6.37%
Clipped reads	845,992 / 44.75%

2.2. ACGT Content

Number/percentage of A's	23,534,792 / 26.16%
Number/percentage of C's	16,152,996 / 17.95%
Number/percentage of T's	29,009,665 / 32.24%
Number/percentage of G's	21,280,571 / 23.65%
Number/percentage of N's	1,194 / 0%
GC Percentage	41.6%

2.3. Coverage

Mean	0.0291

Standard Deviation	0.2681

2.4. Mapping Quality

Mean Mapping Quality	43.52

2.5. Mismatches and indels

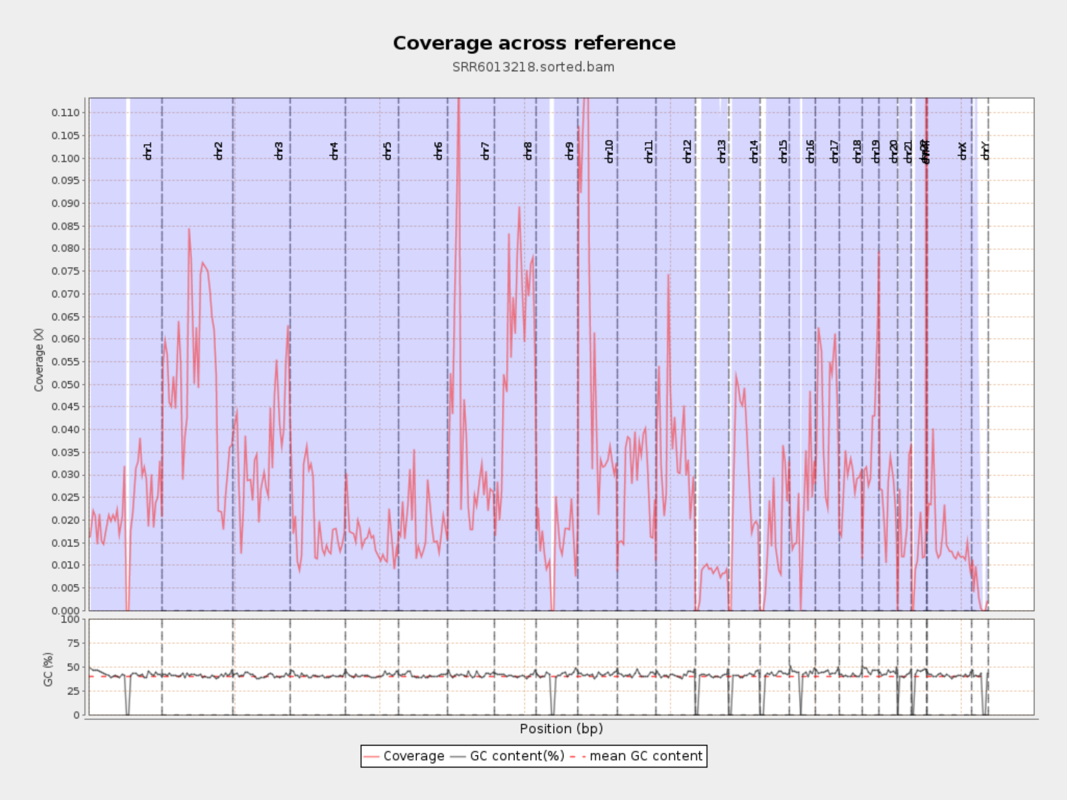
General error rate	0.8%
Mismatches	709,722
Insertions	5,663
Mapped reads with at least one insertion	0.39%
Deletions	24,268
Mapped reads with at least one deletion	1.68%
Homopolymer indels	45.95%

2.6. Chromosome stats

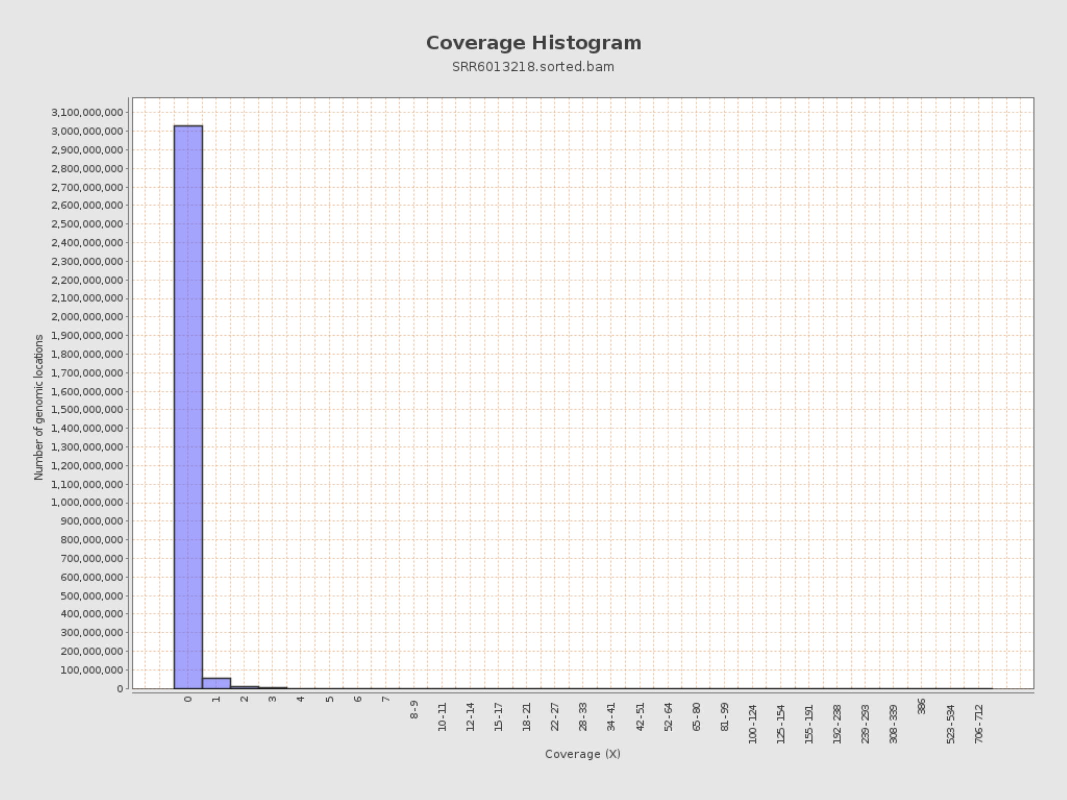
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5441666	0.0218	0.3031
chr2	243199373	12610009	0.0519	0.4324
chr3	198022430	6971981	0.0352	0.2361
chr4	191154276	3582804	0.0187	0.1769
chr5	180915260	2846410	0.0157	0.157
chr6	171115067	3276356	0.0191	0.2433
chr7	159138663	6205915	0.039	0.3228

chr8	146364022	8583588	0.0586	0.3553
chr9	141213431	2051336	0.0145	0.2109
chr10	135534747	8061780	0.0595	0.3818
chr11	135006516	3853088	0.0285	0.2453
chr12	133851895	4935746	0.0369	0.2452
chr13	115169878	854311	0.0074	0.1061
chr14	107349540	3160345	0.0294	0.2239
chr15	102531392	1705946	0.0166	0.1662
chr16	90354753	2032979	0.0225	0.1906
chr17	81195210	3637627	0.0448	0.3133
chr18	78077248	2198368	0.0282	0.3314
chr19	59128983	2291779	0.0388	0.3009
chr20	63025520	1522146	0.0242	0.1972
chr21	48129895	981256	0.0204	0.1849
chr22	51304566	541746	0.0106	0.1248
chrMT	16571	12772	0.7707	1.2221
chrX	155270560	2454990	0.0158	0.1708
chrY	59373566	205051	0.0035	0.0765

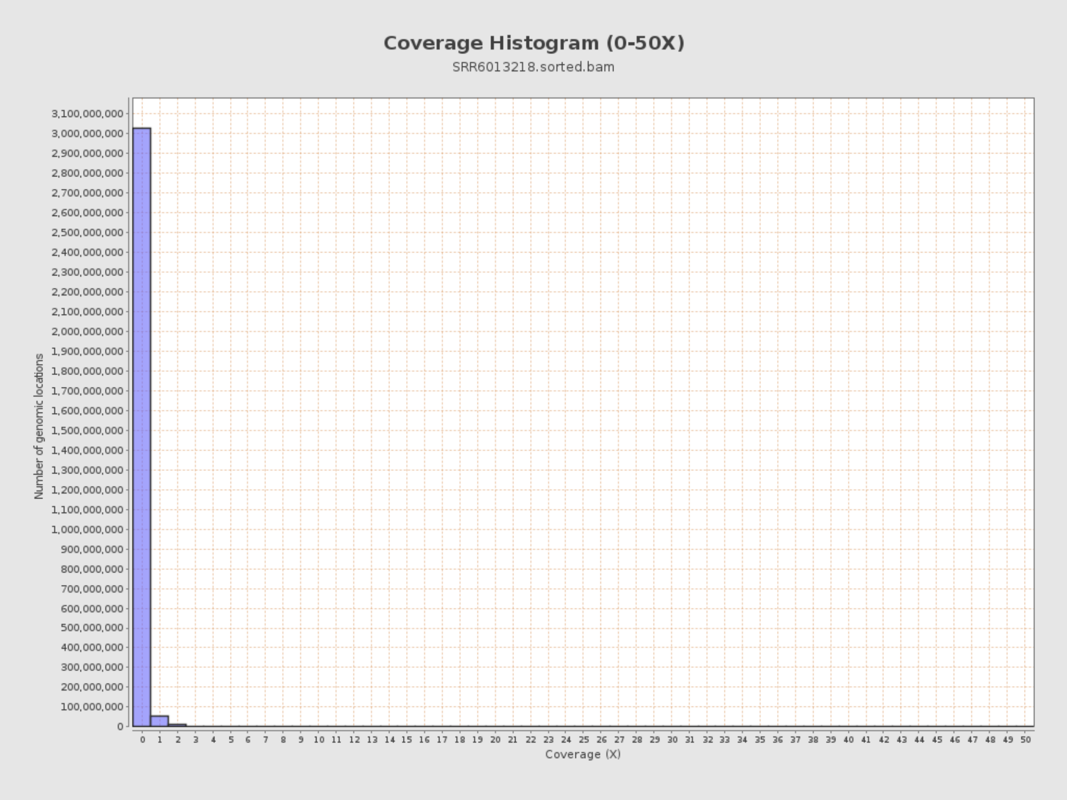
3. Results : Coverage across reference



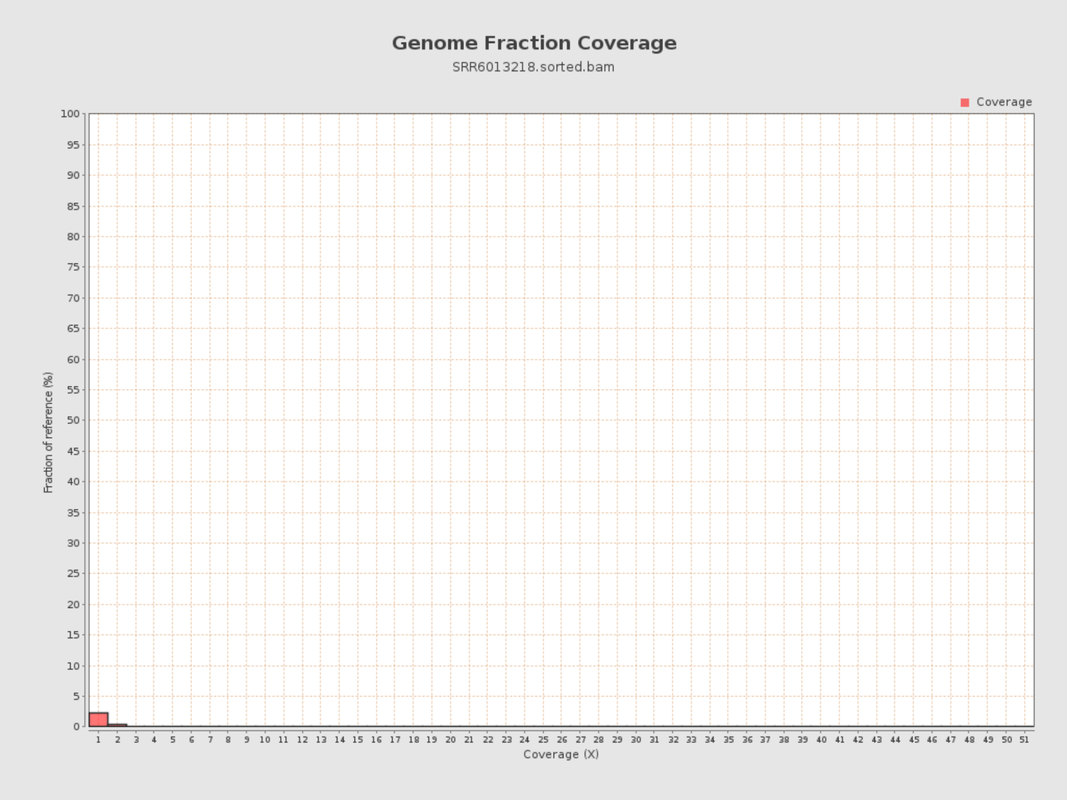
4. Results : Coverage Histogram



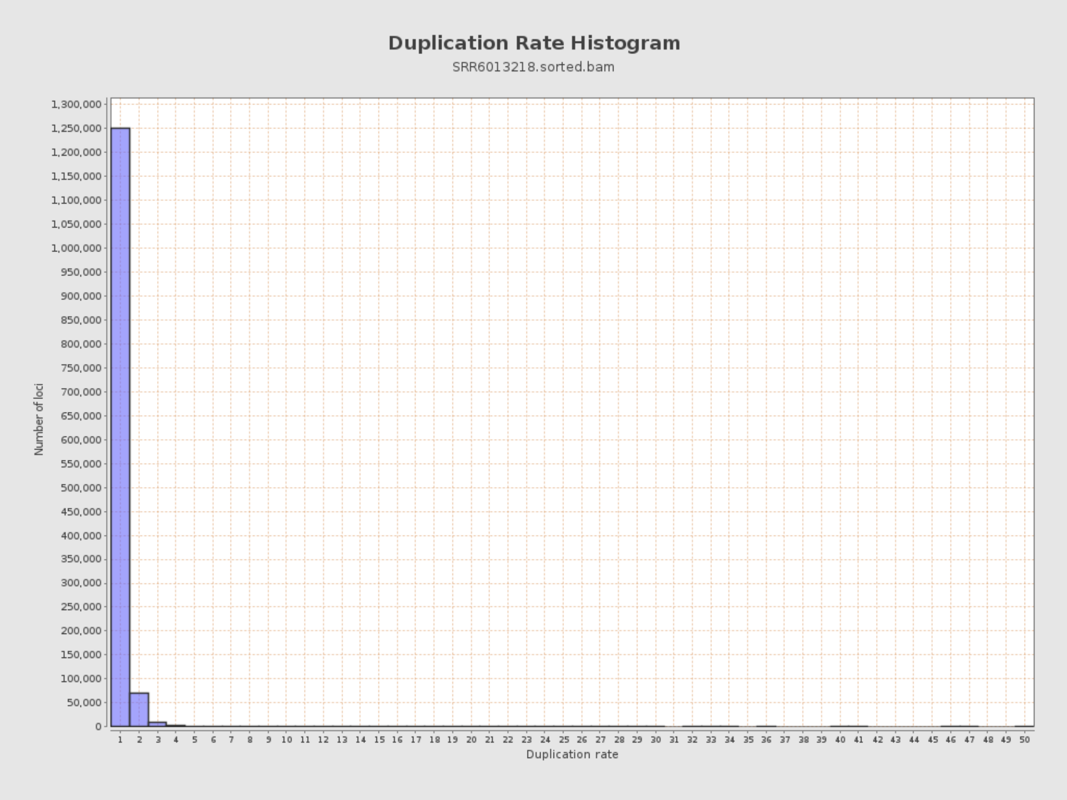
5. Results : Coverage Histogram (0-50X)



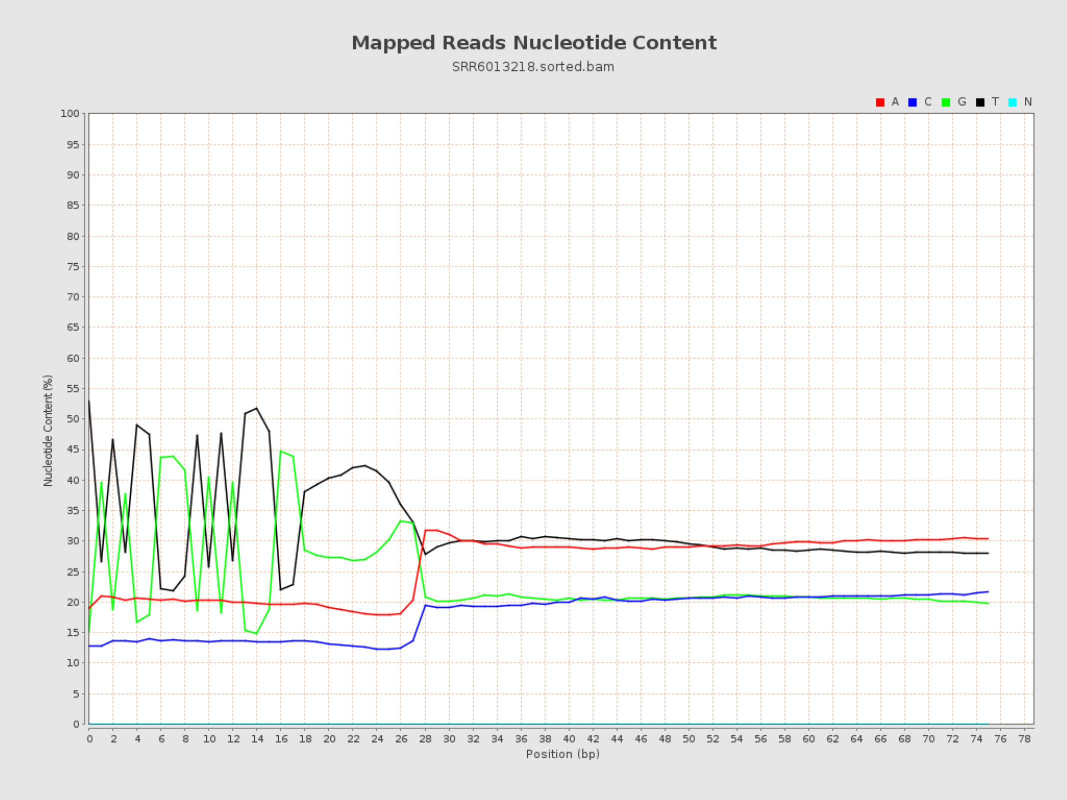
6. Results : Genome Fraction Coverage



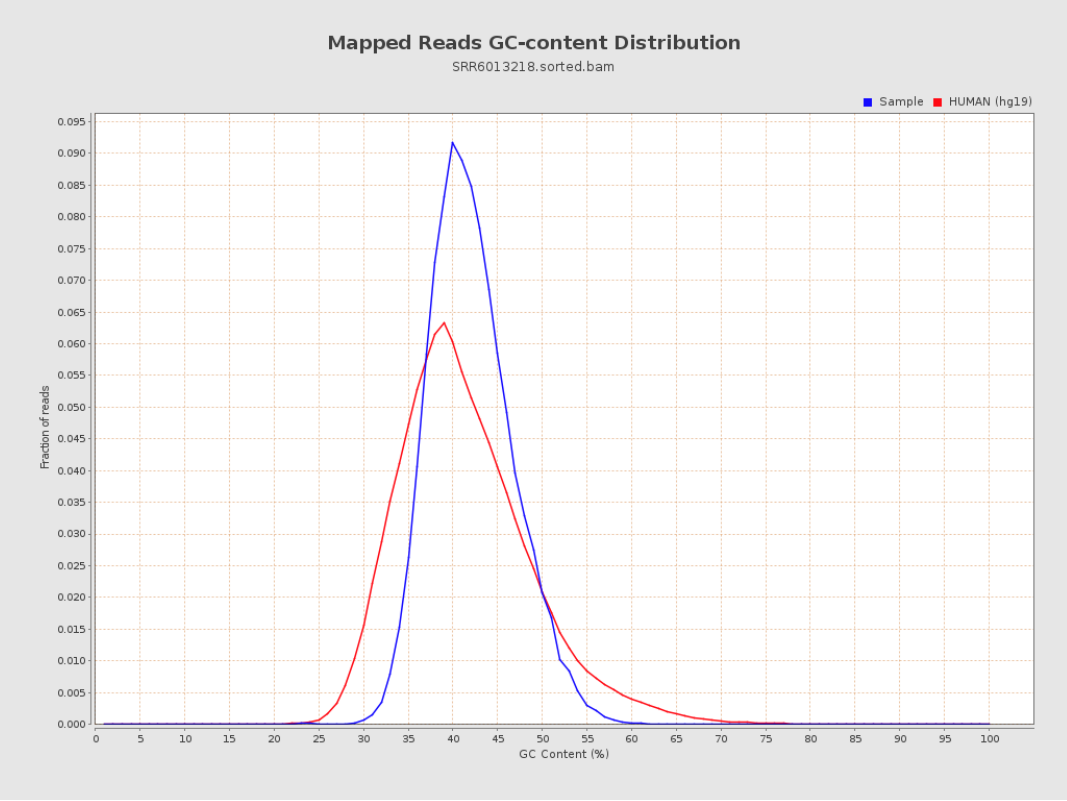
7. Results : Duplication Rate Histogram



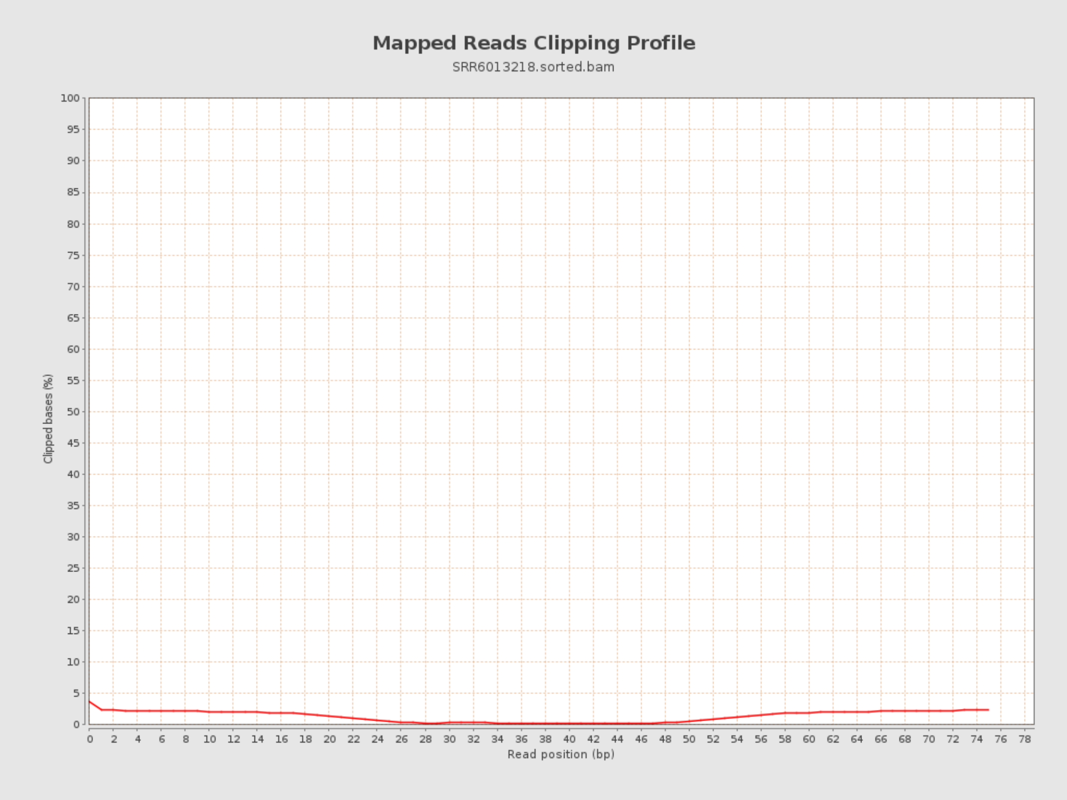
8. Results : Mapped Reads Nucleotide Content



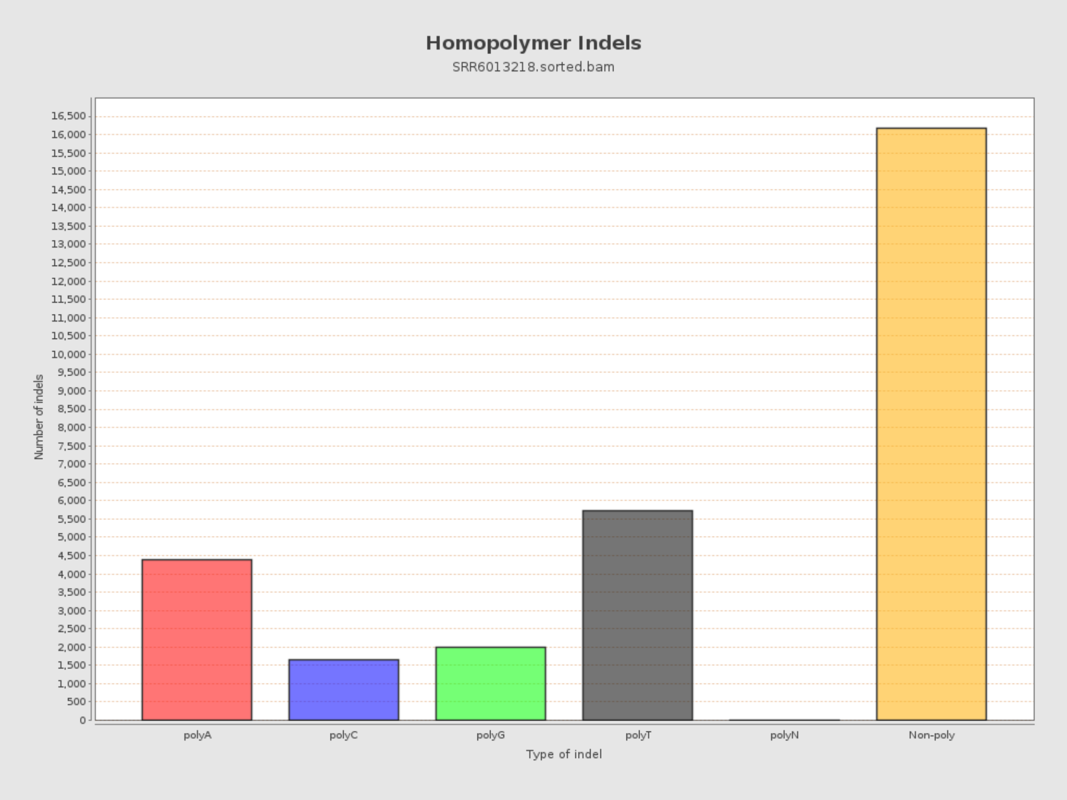
9. Results : Mapped Reads GC-content Distribution



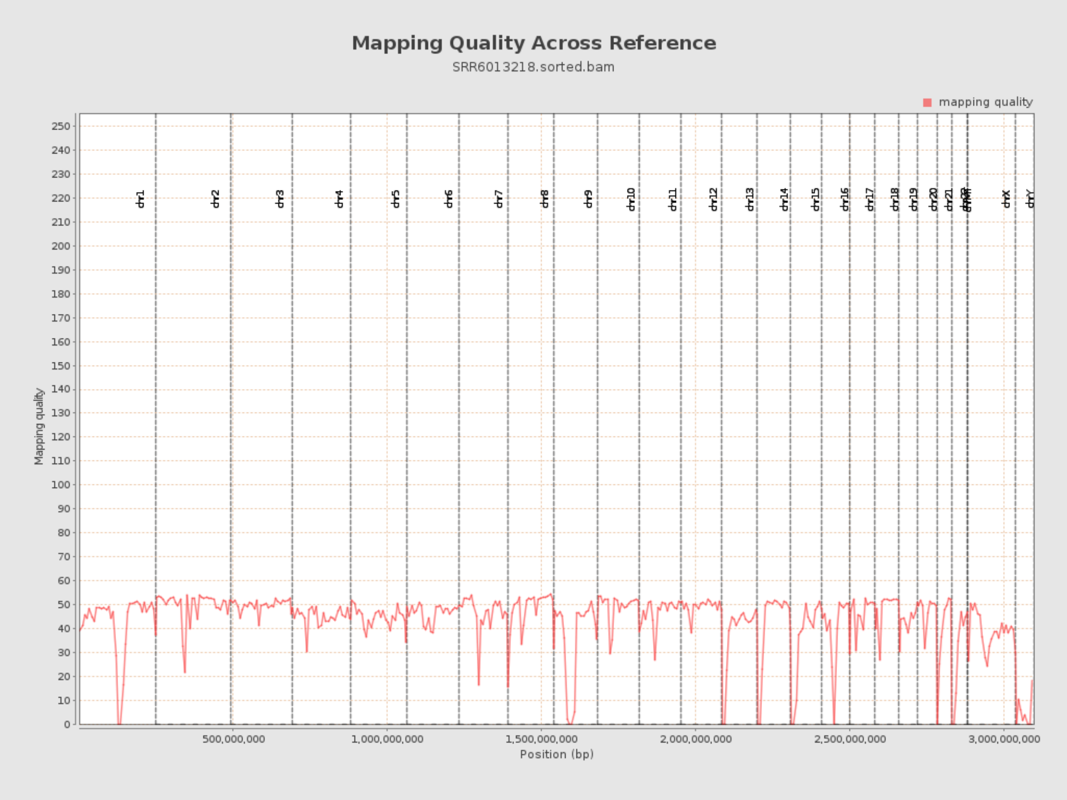
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram