Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:02:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013170.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_SRR6013170 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013170.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:02:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013170.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,812,769
Mapped reads	1,219,147 / 67.25%
Unmapped reads	593,622 / 32.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,671 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	220,599 / 12.17%
Duplication rate	13.15%
Clipped reads	758,134 / 41.82%

2.2. ACGT Content

Number/percentage of A's	20,641,272 / 27.17%
Number/percentage of C's	13,554,466 / 17.84%
Number/percentage of T's	24,492,257 / 32.24%
Number/percentage of G's	17,163,571 / 22.59%
Number/percentage of N's	112,647 / 0.15%
GC Percentage	40.44%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.33

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

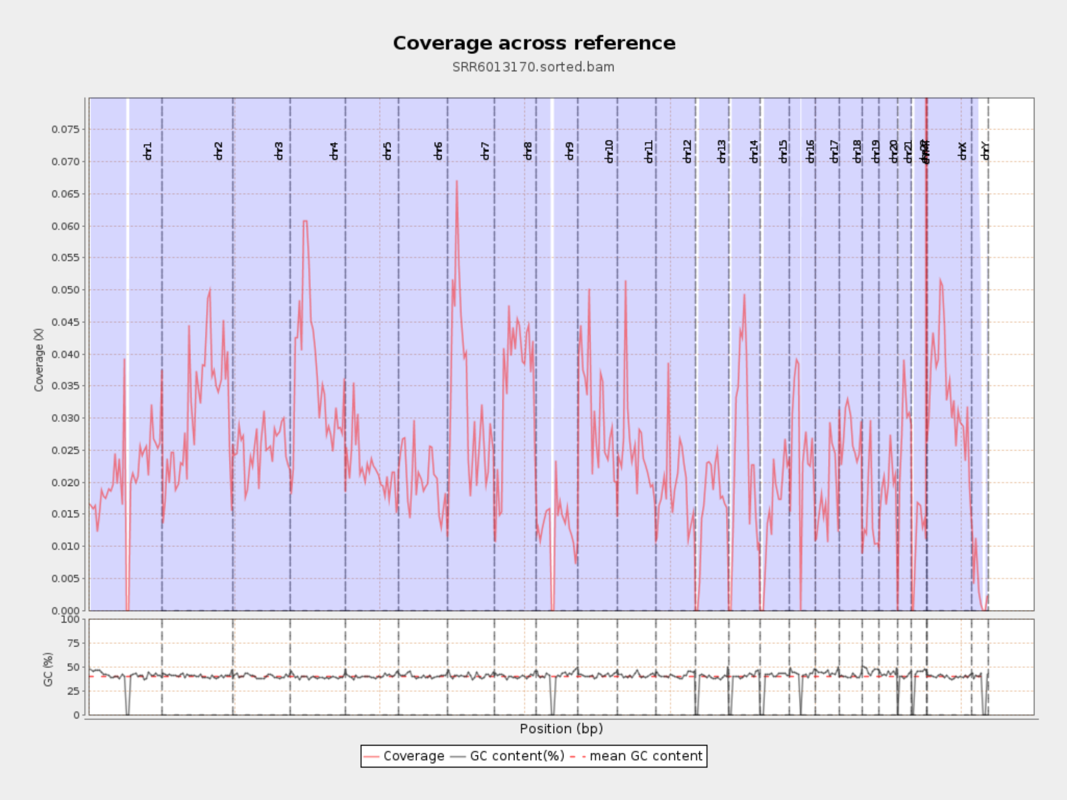
General error rate	1.14%
Mismatches	860,379
Insertions	5,283
Mapped reads with at least one insertion	0.43%
Deletions	43,166
Mapped reads with at least one deletion	3.46%
Homopolymer indels	43%

2.6. Chromosome stats

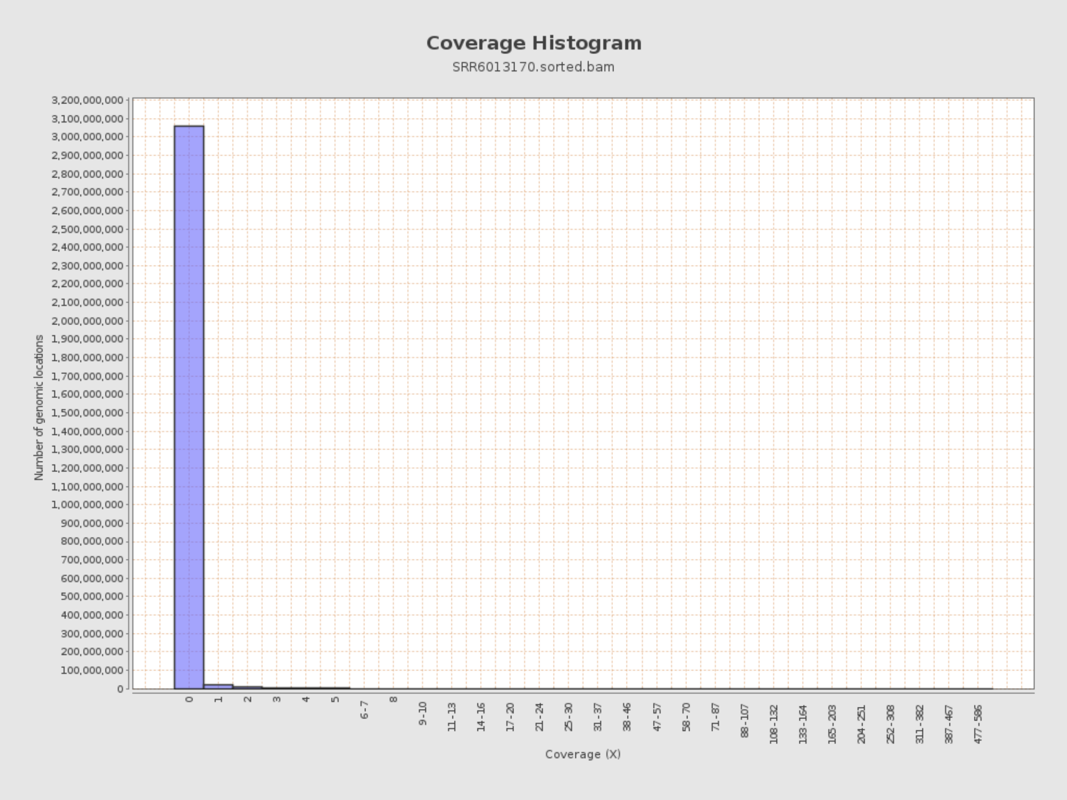
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5100322	0.0205	0.4766
chr2	243199373	7510182	0.0309	0.3754
chr3	198022430	5013211	0.0253	0.2801
chr4	191154276	7039904	0.0368	0.3544
chr5	180915260	4027453	0.0223	0.259
chr6	171115067	3502993	0.0205	0.2757
chr7	159138663	5255629	0.033	0.4025

chr8	146364022	5150021	0.0352	0.4672
chr9	141213431	1757388	0.0124	0.2142
chr10	135534747	4229341	0.0312	0.3585
chr11	135006516	3371290	0.025	0.2858
chr12	133851895	2593286	0.0194	0.2376
chr13	115169878	1868885	0.0162	0.2225
chr14	107349540	2631741	0.0245	0.2879
chr15	102531392	1591917	0.0155	0.2147
chr16	90354753	2295299	0.0254	0.2886
chr17	81195210	1452363	0.0179	0.2308
chr18	78077248	2127065	0.0272	0.4227
chr19	59128983	893820	0.0151	0.3656
chr20	63025520	1243539	0.0197	0.251
chr21	48129895	1284444	0.0267	0.2956
chr22	51304566	554138	0.0108	0.1737
chrMT	16571	50544	3.0501	3.4493
chrX	155270560	5268041	0.0339	0.3339
chrY	59373566	227212	0.0038	0.1023

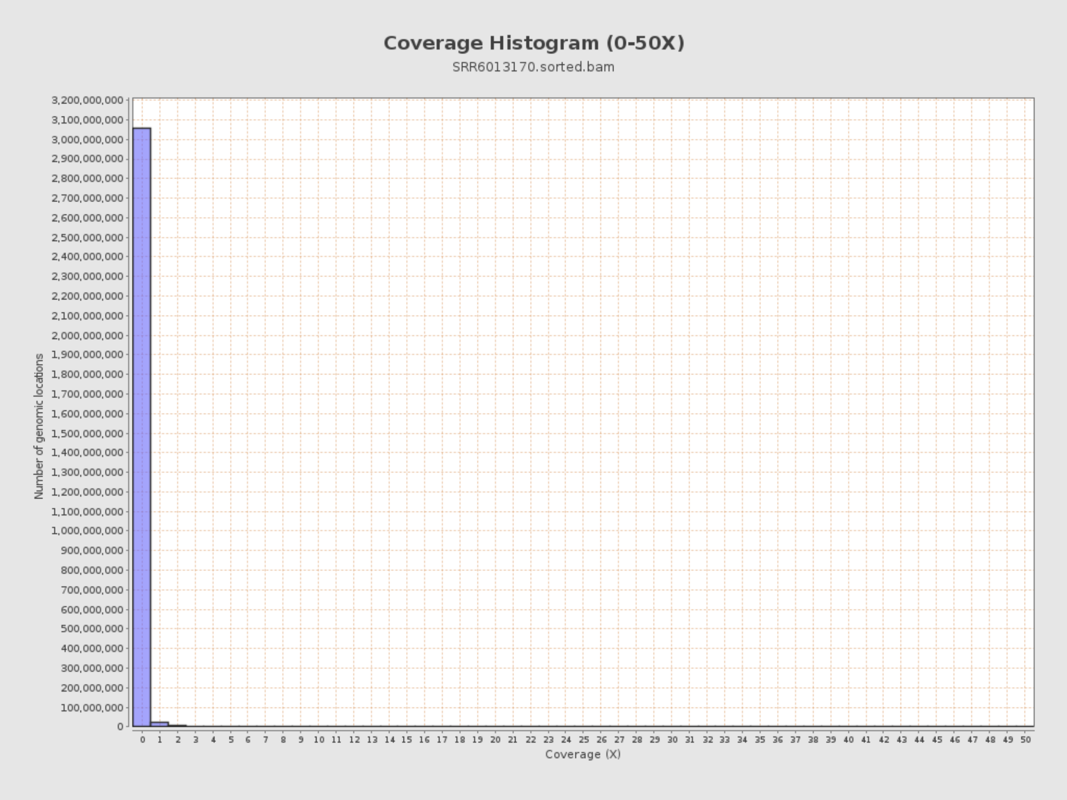
3. Results : Coverage across reference



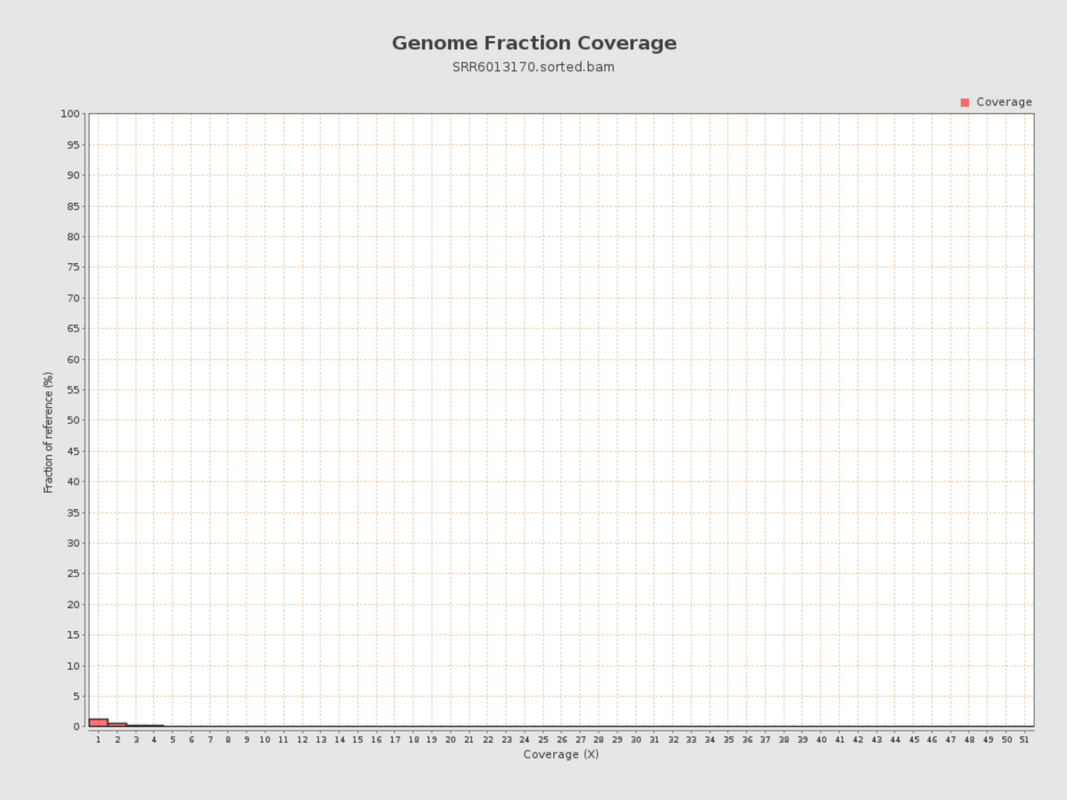
4. Results : Coverage Histogram



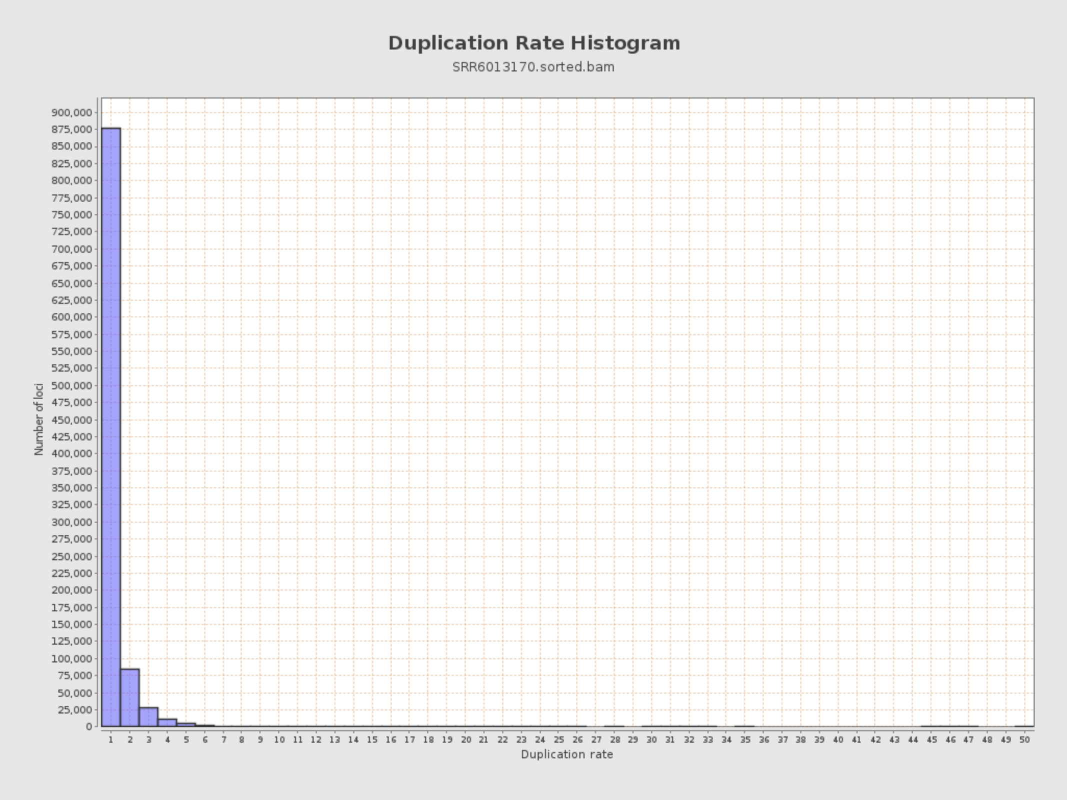
5. Results : Coverage Histogram (0-50X)



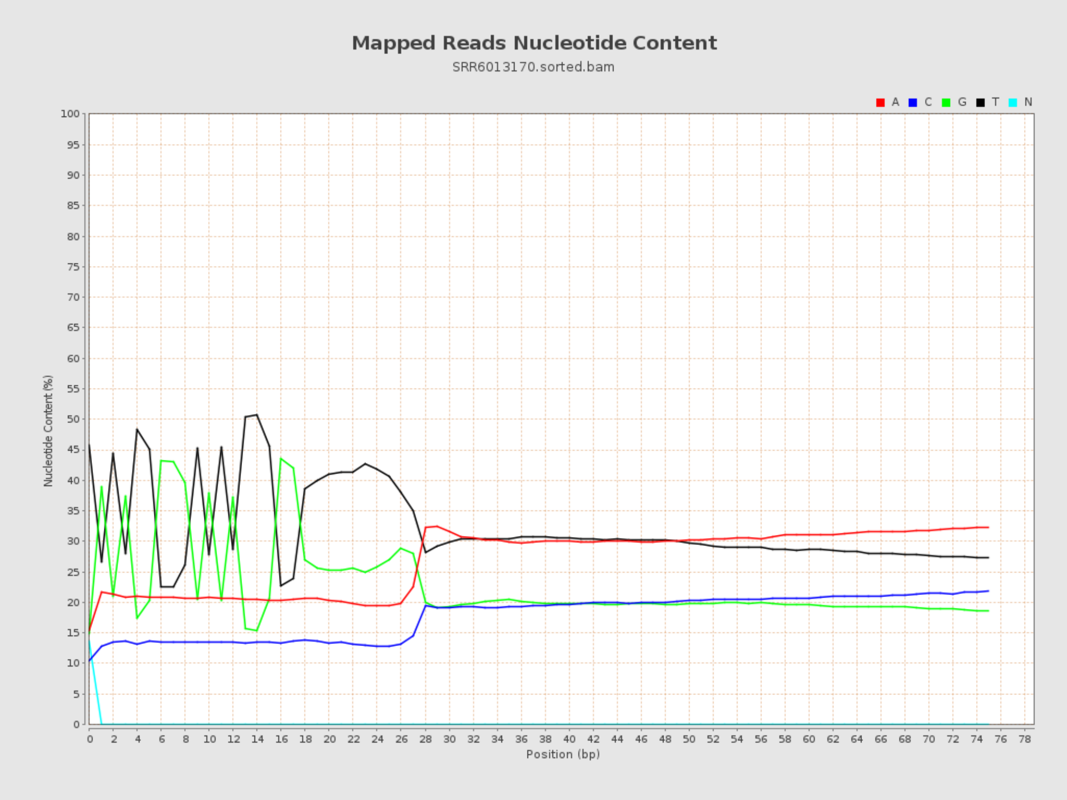
6. Results : Genome Fraction Coverage



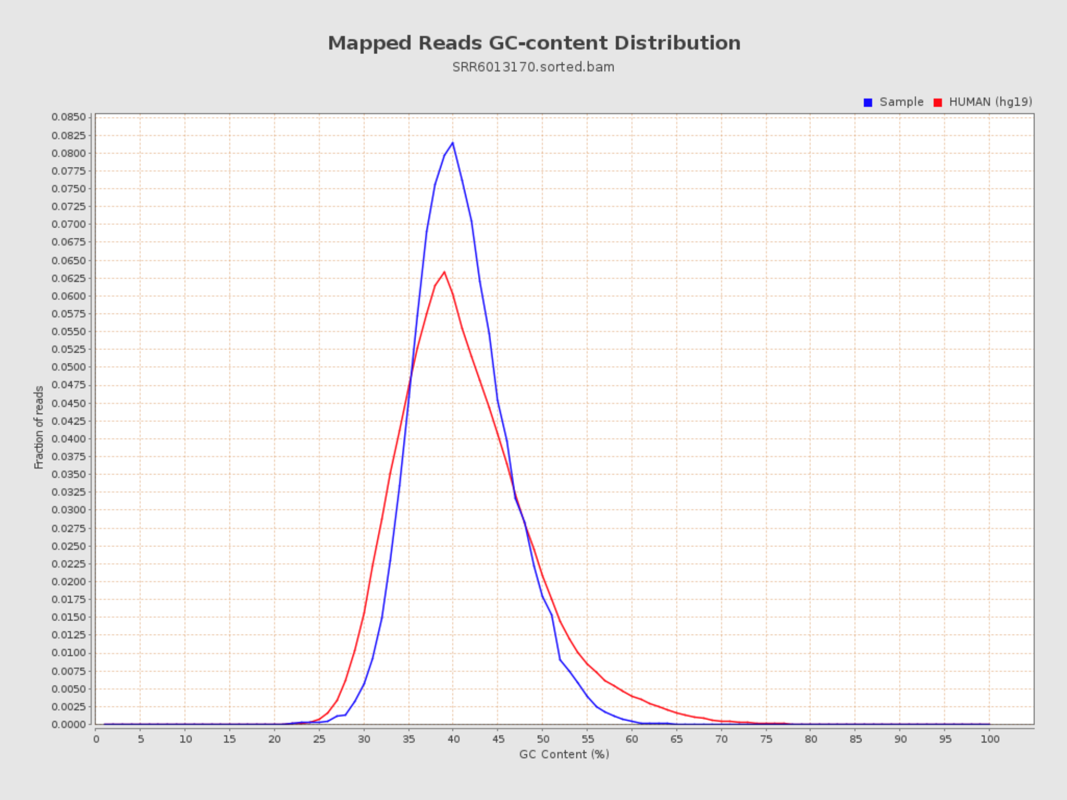
7. Results : Duplication Rate Histogram



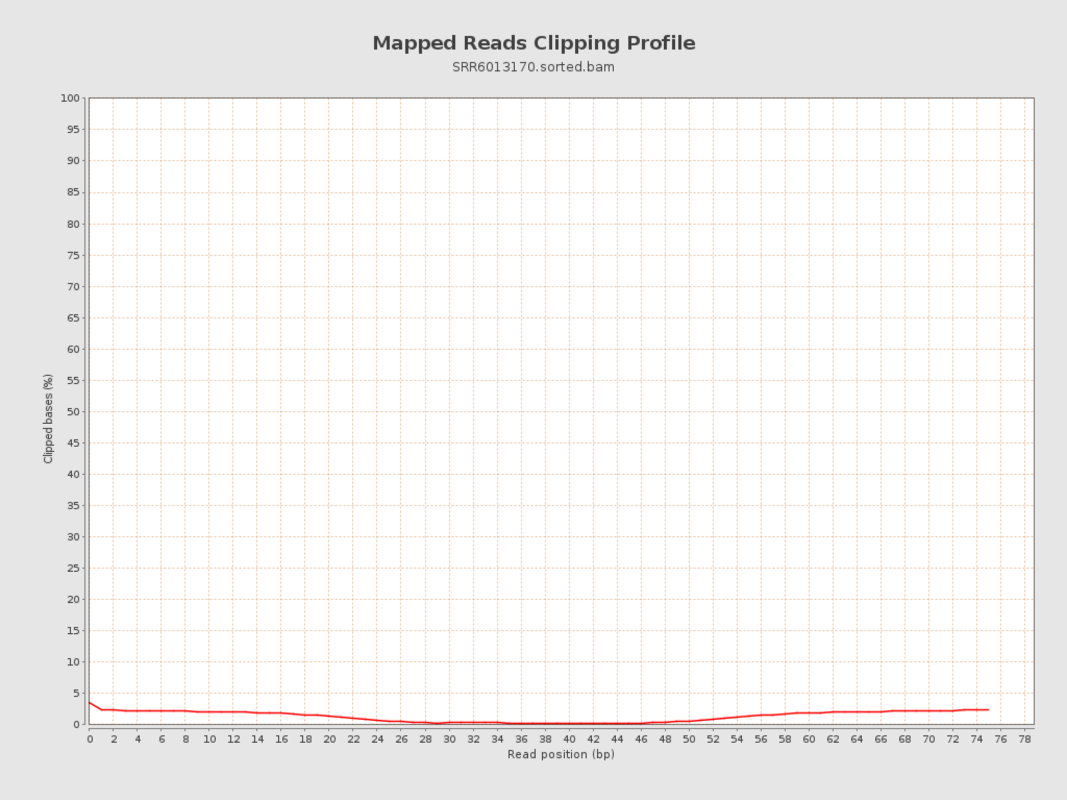
8. Results : Mapped Reads Nucleotide Content



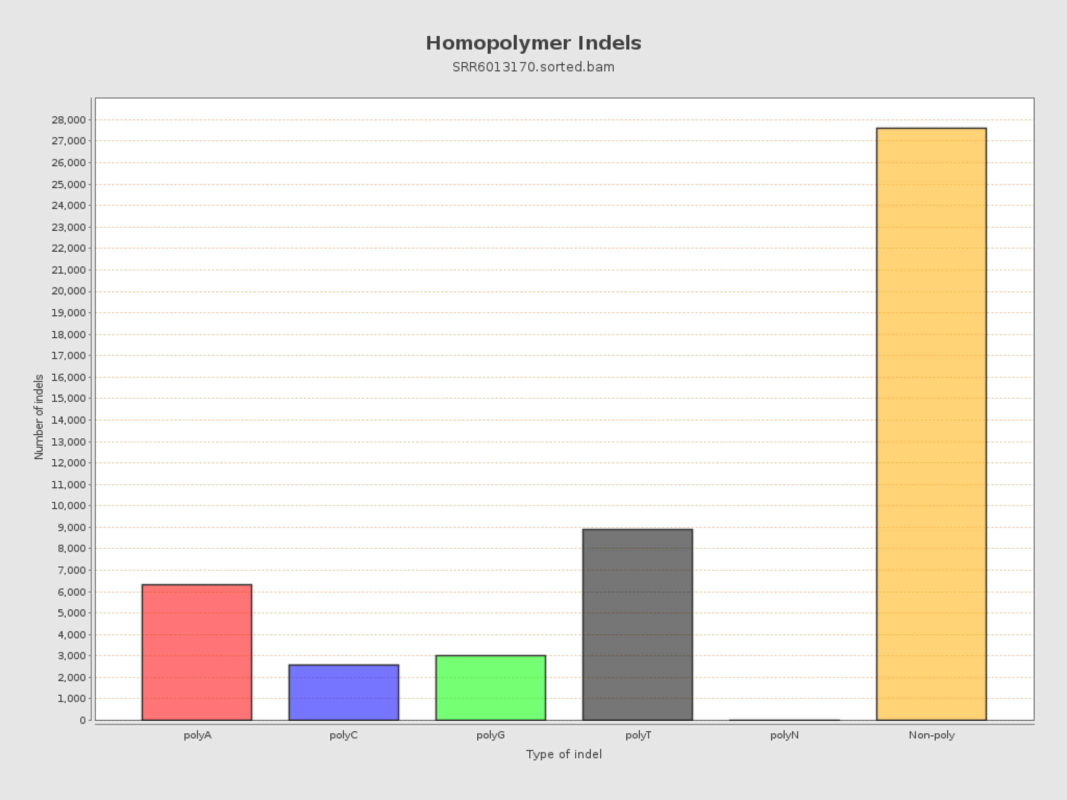
9. Results : Mapped Reads GC-content Distribution



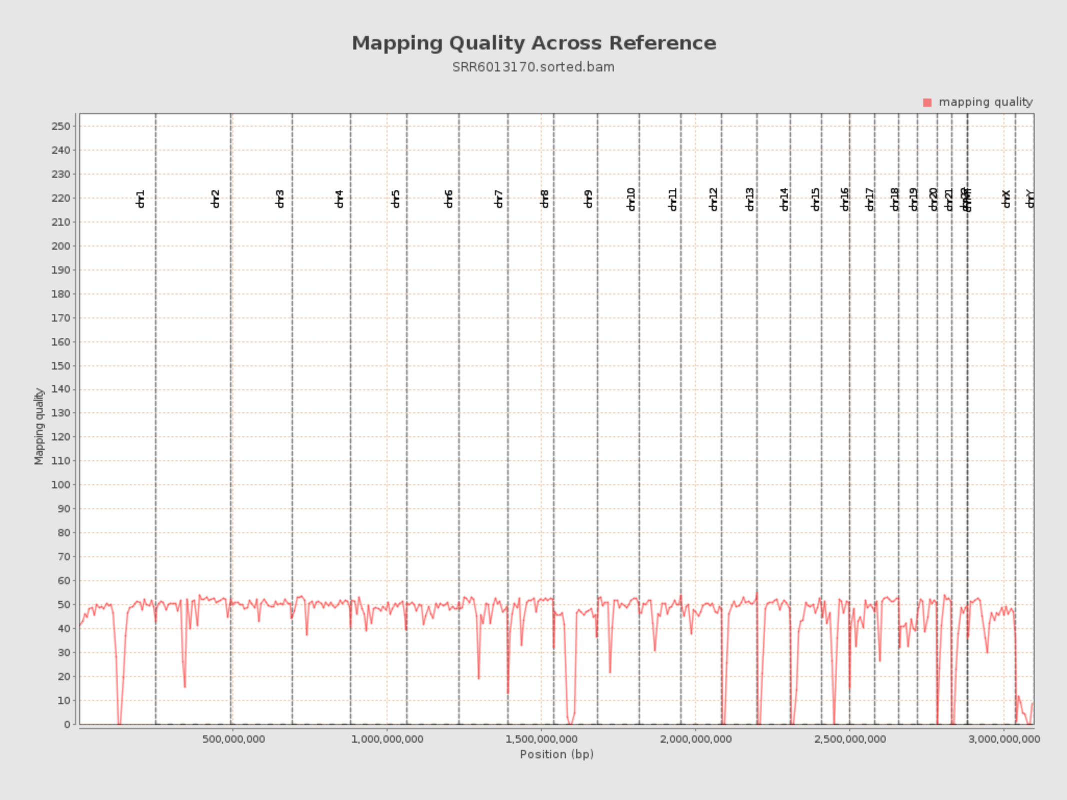
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram