Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:38:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013162.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_SRR6013162 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013162.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:38:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,813,089
Mapped reads	2,139,333 / 76.05%
Unmapped reads	673,756 / 23.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,838 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	642,821 / 22.85%
Duplication rate	15.51%
Clipped reads	1,147,979 / 40.81%

2.2. ACGT Content

Number/percentage of A's	35,531,171 / 25.82%
Number/percentage of C's	26,785,878 / 19.46%
Number/percentage of T's	41,991,329 / 30.51%
Number/percentage of G's	33,088,093 / 24.04%
Number/percentage of N's	215,939 / 0.16%
GC Percentage	43.51%

2.3. Coverage

Mean	0.0445

Standard Deviation	0.7037

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Mismatches and indels

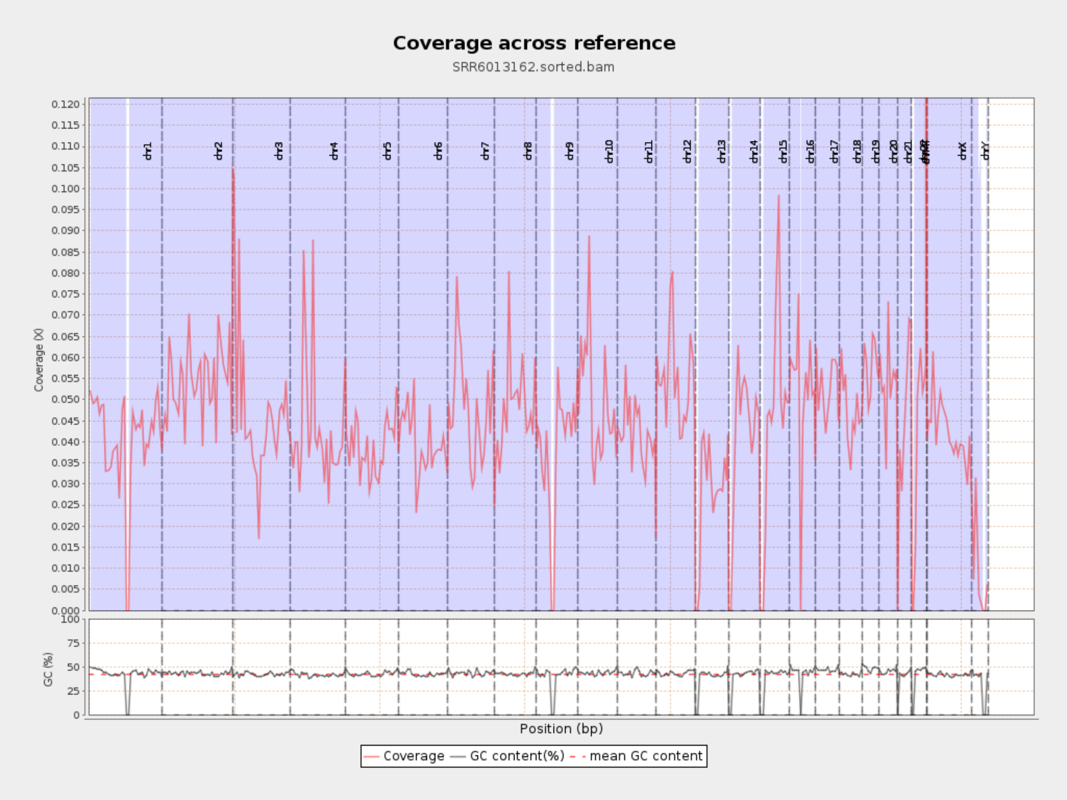
General error rate	0.96%
Mismatches	1,303,693
Insertions	10,709
Mapped reads with at least one insertion	0.5%
Deletions	44,077
Mapped reads with at least one deletion	2.03%
Homopolymer indels	45.03%

2.6. Chromosome stats

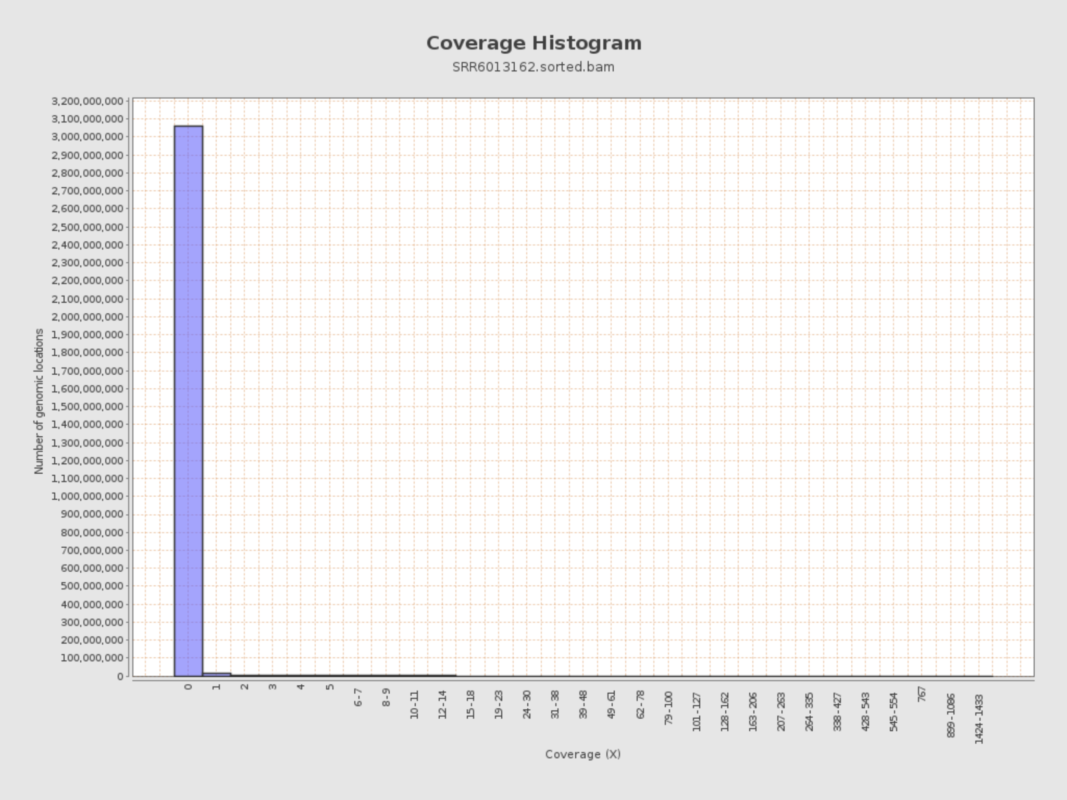
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10062553	0.0404	0.7441
chr2	243199373	13192261	0.0542	0.9454
chr3	198022430	9337735	0.0472	0.6703
chr4	191154276	8117392	0.0425	0.6393
chr5	180915260	7080737	0.0391	0.6048
chr6	171115067	6789126	0.0397	0.6362
chr7	159138663	7675390	0.0482	0.7056

chr8	146364022	7053290	0.0482	0.7138
chr9	141213431	5267477	0.0373	0.6052
chr10	135534747	6655288	0.0491	0.7219
chr11	135006516	5689199	0.0421	0.6391
chr12	133851895	7379447	0.0551	0.7345
chr13	115169878	3138150	0.0272	0.5019
chr14	107349540	4394227	0.0409	0.6081
chr15	102531392	4530835	0.0442	0.6455
chr16	90354753	4678066	0.0518	0.6895
chr17	81195210	4300771	0.053	0.701
chr18	78077248	3684835	0.0472	0.7799
chr19	59128983	3403925	0.0576	0.7776
chr20	63025520	3421514	0.0543	0.7261
chr21	48129895	2136831	0.0444	0.6515
chr22	51304566	1927565	0.0376	0.5958
chrMT	16571	720046	43.4522	41.4628
chrX	155270560	6555839	0.0422	0.6092
chrY	59373566	501373	0.0084	0.2748

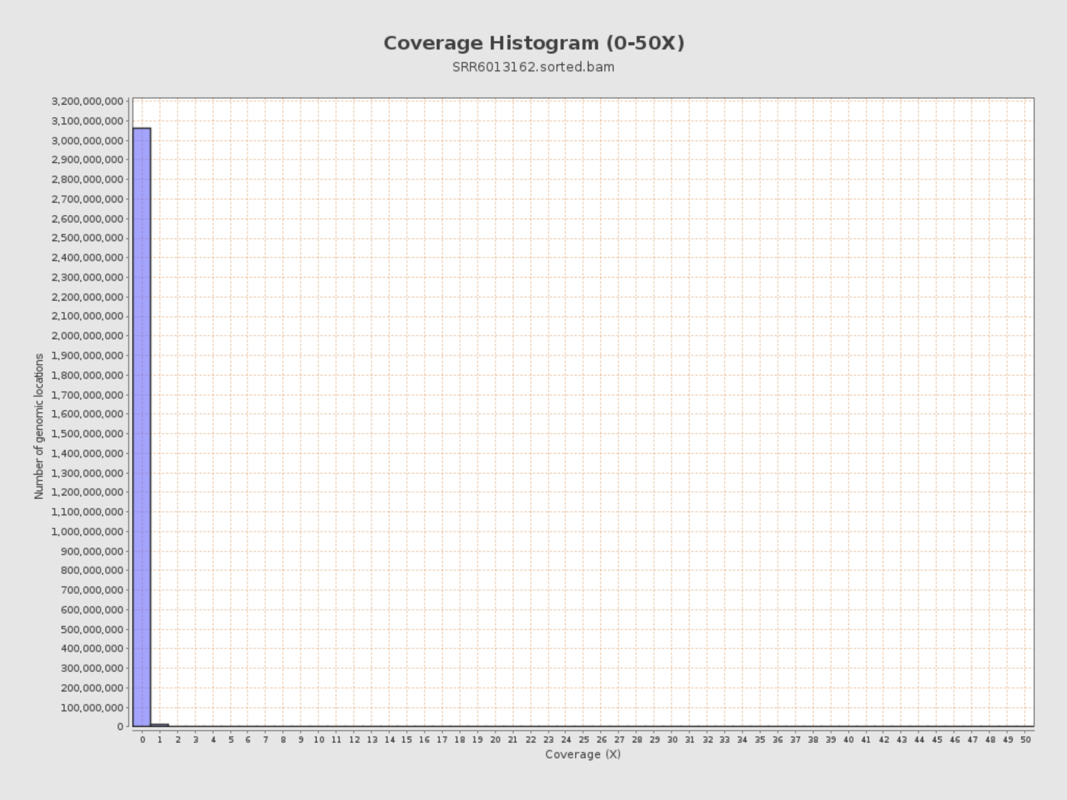
3. Results : Coverage across reference



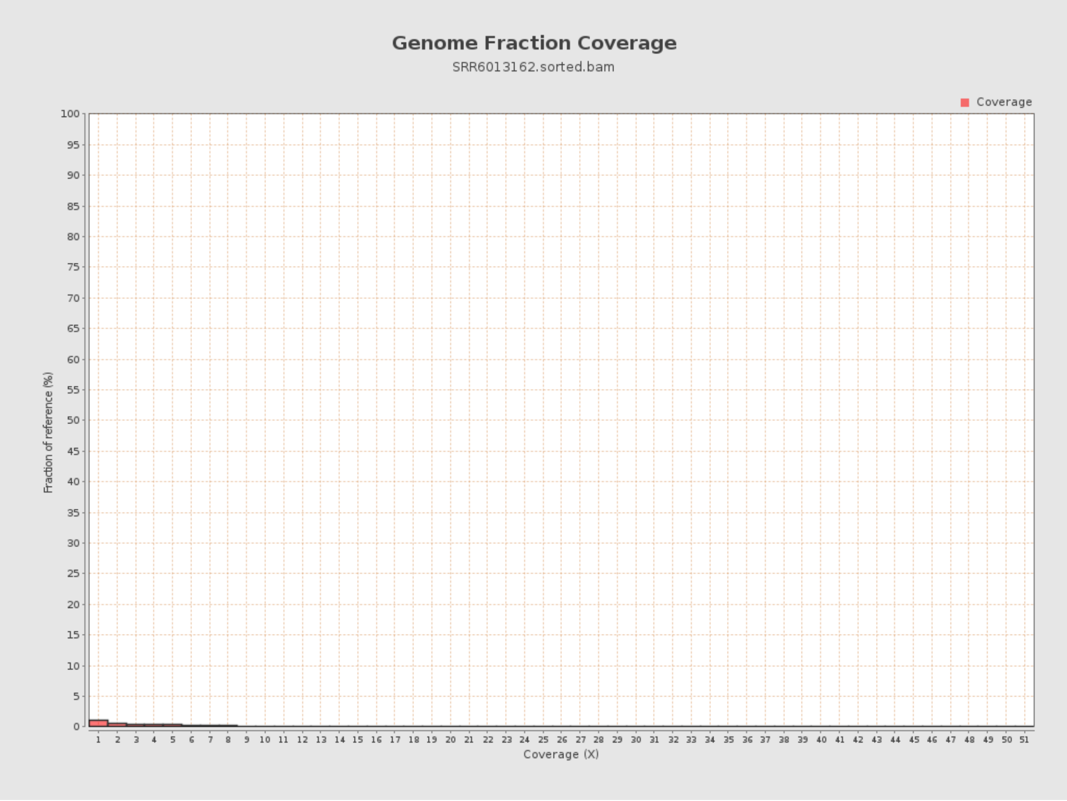
4. Results : Coverage Histogram



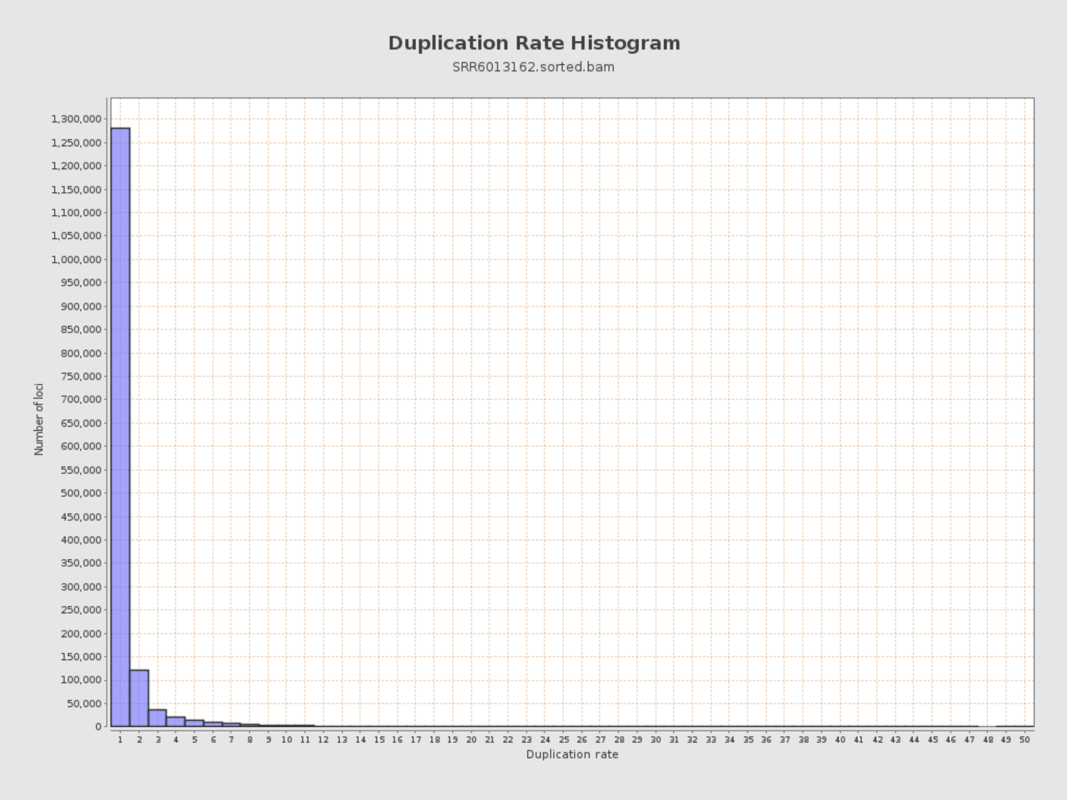
5. Results : Coverage Histogram (0-50X)



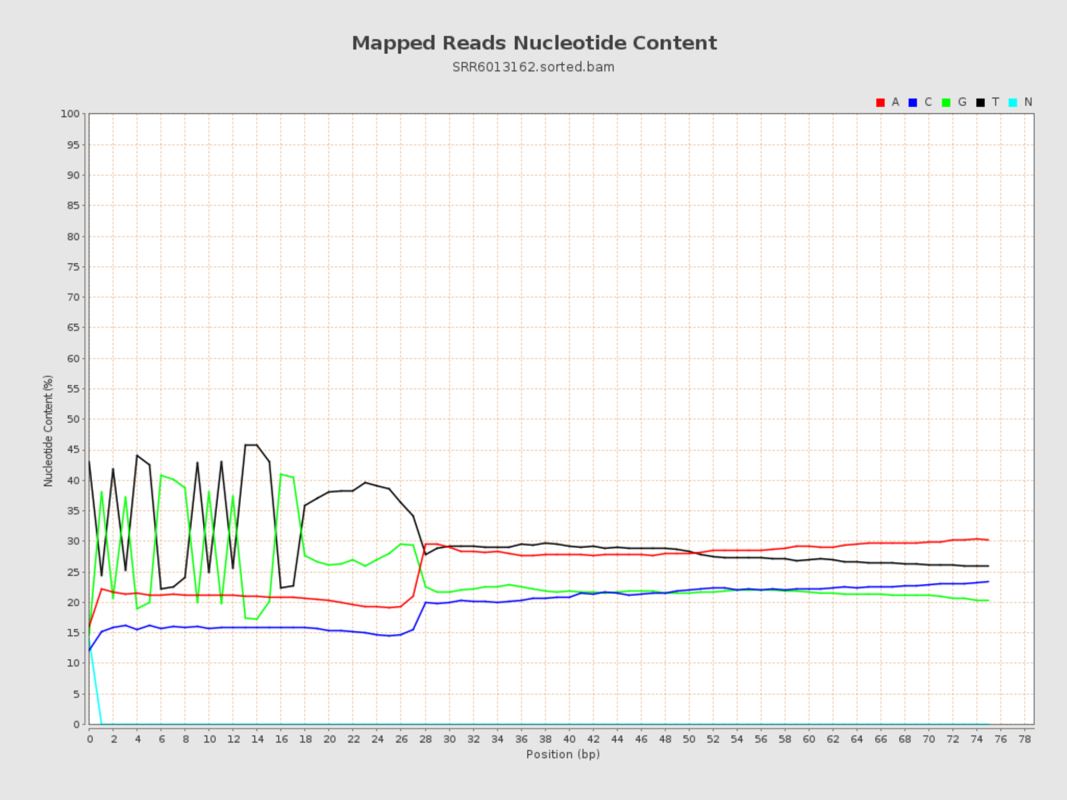
6. Results : Genome Fraction Coverage



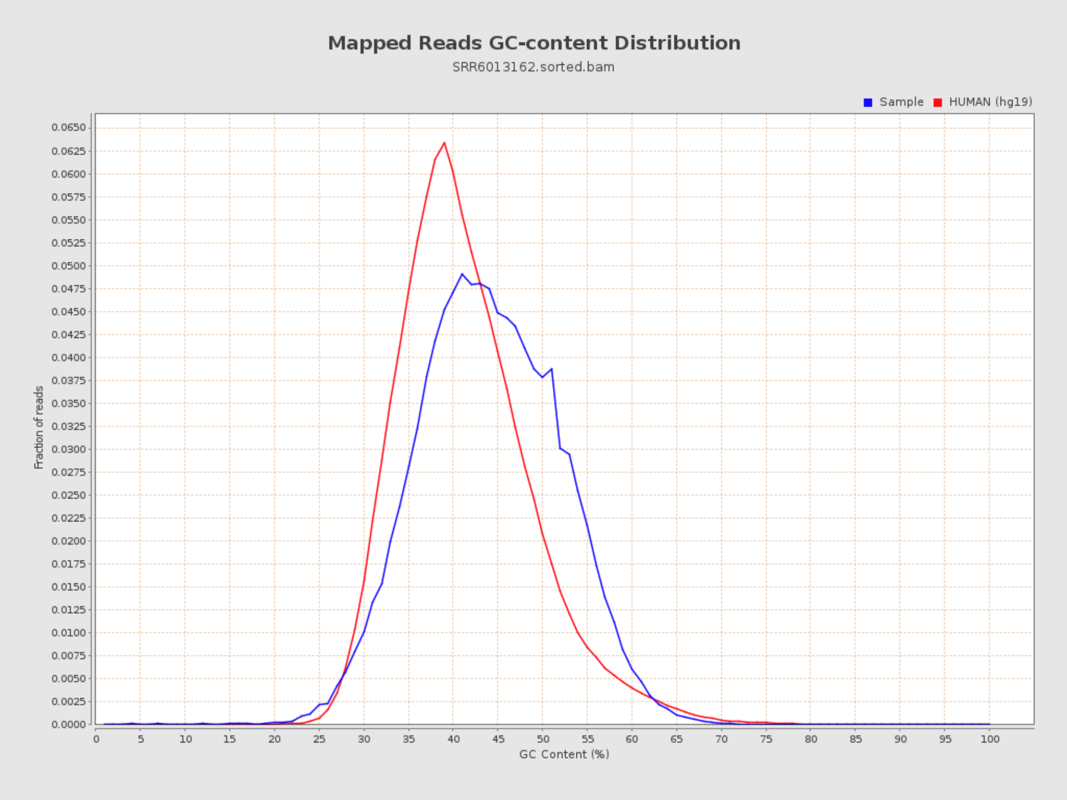
7. Results : Duplication Rate Histogram



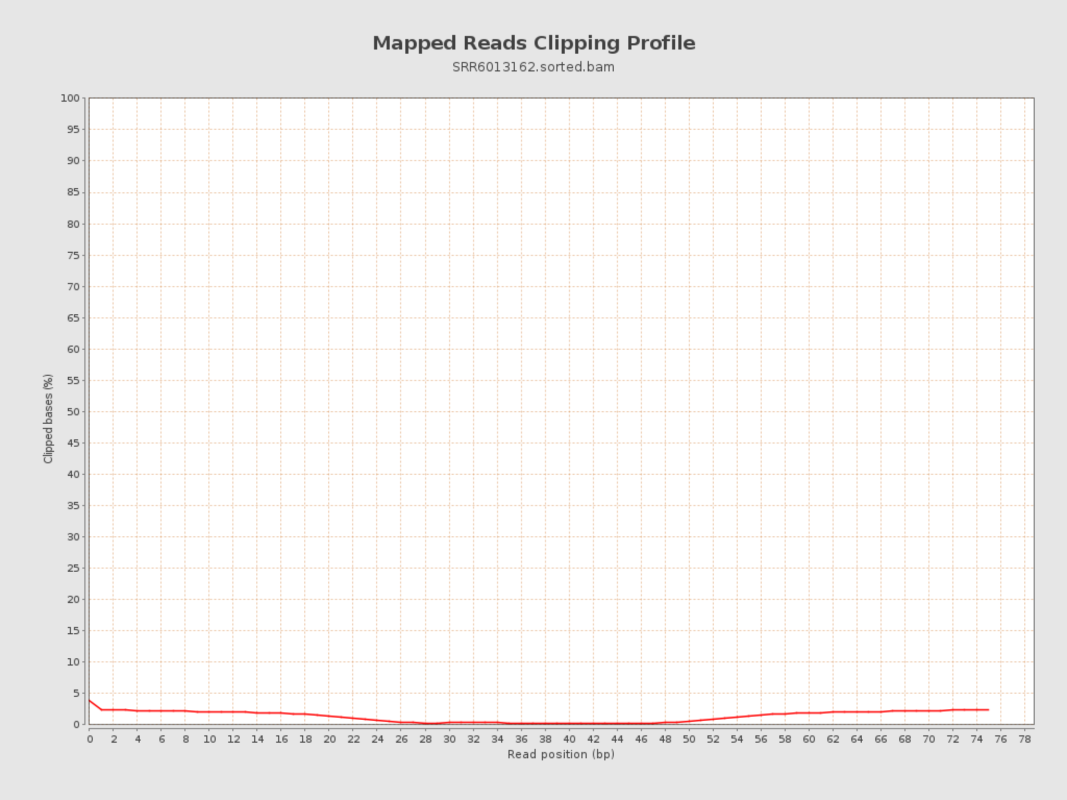
8. Results : Mapped Reads Nucleotide Content



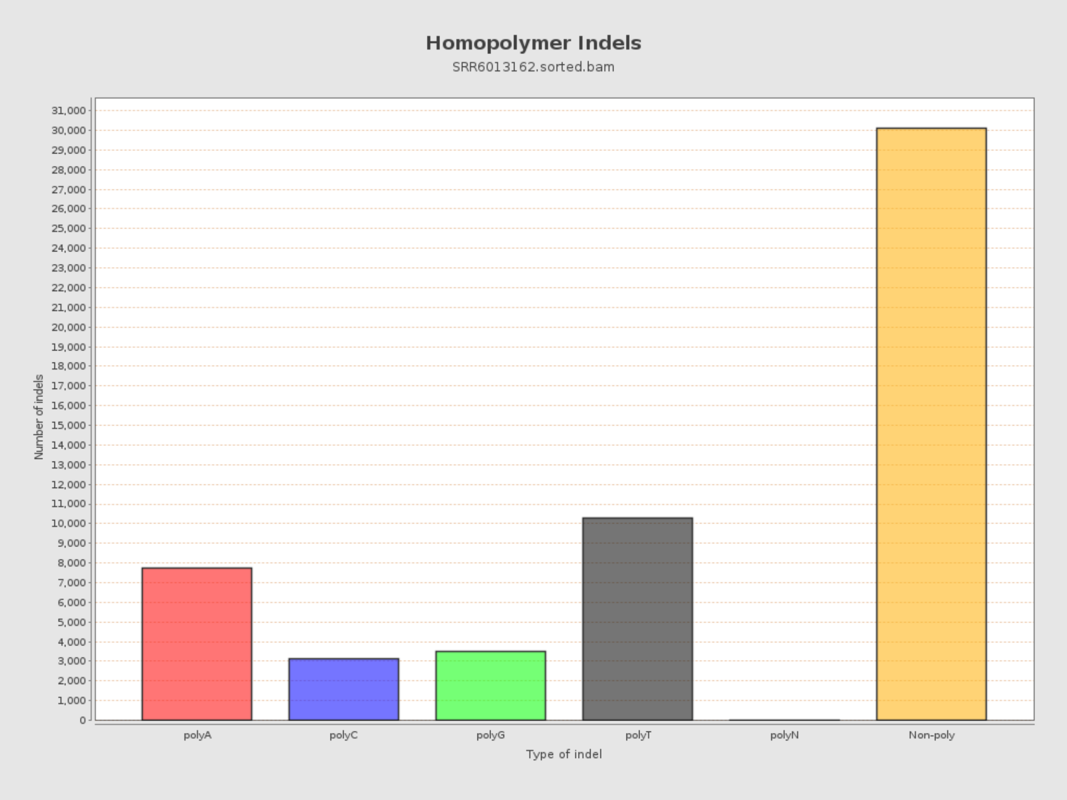
9. Results : Mapped Reads GC-content Distribution



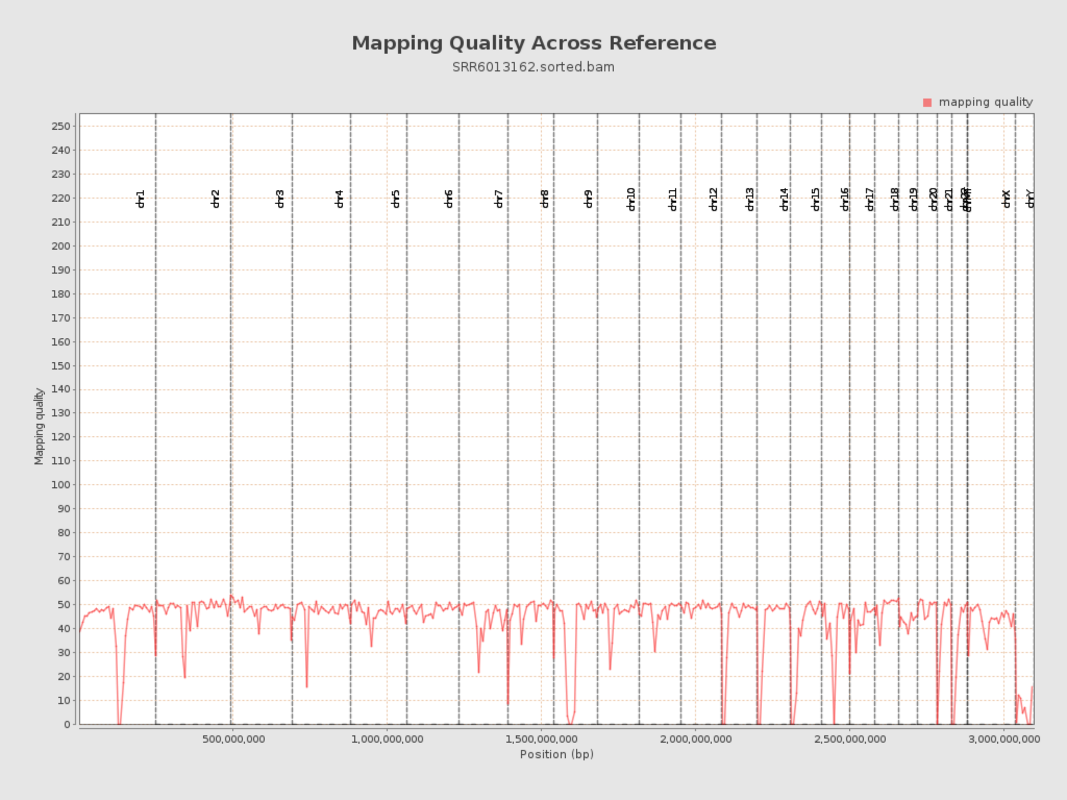
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram