Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:30:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013262.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_SRR6013262 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013262.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:30:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013262.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,764,128
Mapped reads	1,498,576 / 84.95%
Unmapped reads	265,552 / 15.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,362 / 0.81%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	119,649 / 6.78%
Duplication rate	6.26%
Clipped reads	666,829 / 37.8%

2.2. ACGT Content

Number/percentage of A's	27,680,009 / 27.61%
Number/percentage of C's	18,475,854 / 18.43%
Number/percentage of T's	32,001,558 / 31.93%
Number/percentage of G's	22,057,472 / 22.01%
Number/percentage of N's	21,345 / 0.02%
GC Percentage	40.44%

2.3. Coverage

Mean	0.0324

Standard Deviation	0.3997

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

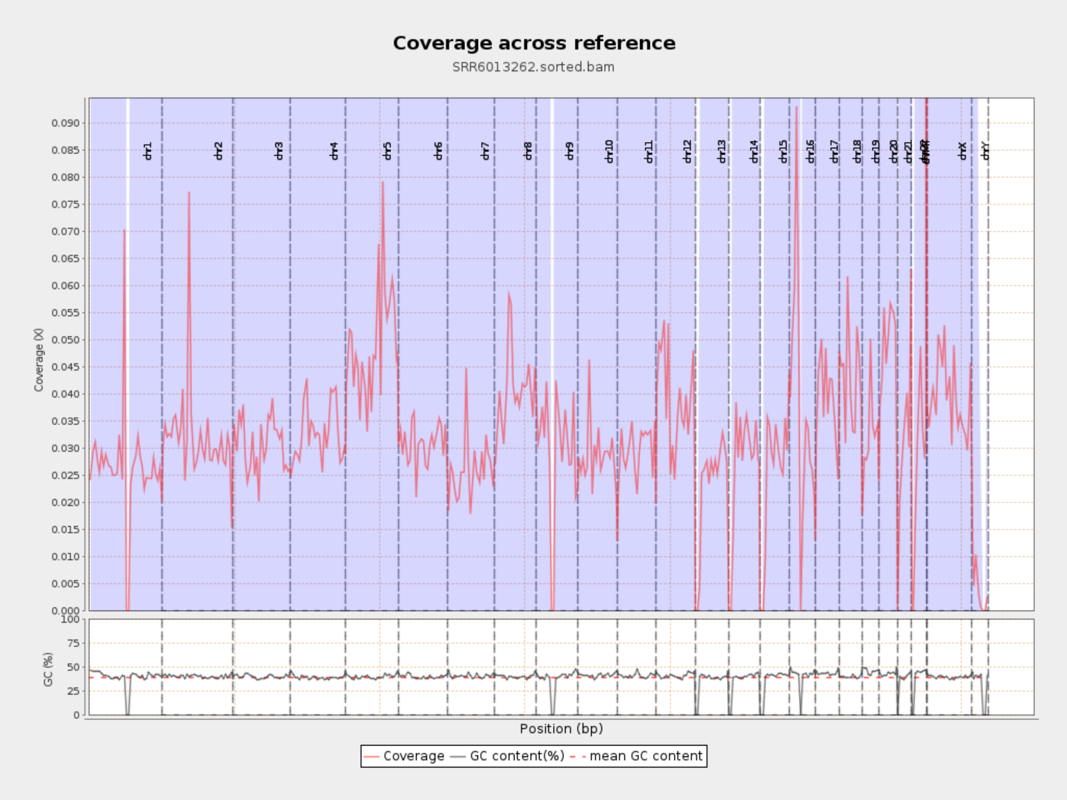
General error rate	0.83%
Mismatches	815,760
Insertions	7,225
Mapped reads with at least one insertion	0.48%
Deletions	21,148
Mapped reads with at least one deletion	1.4%
Homopolymer indels	47.87%

2.6. Chromosome stats

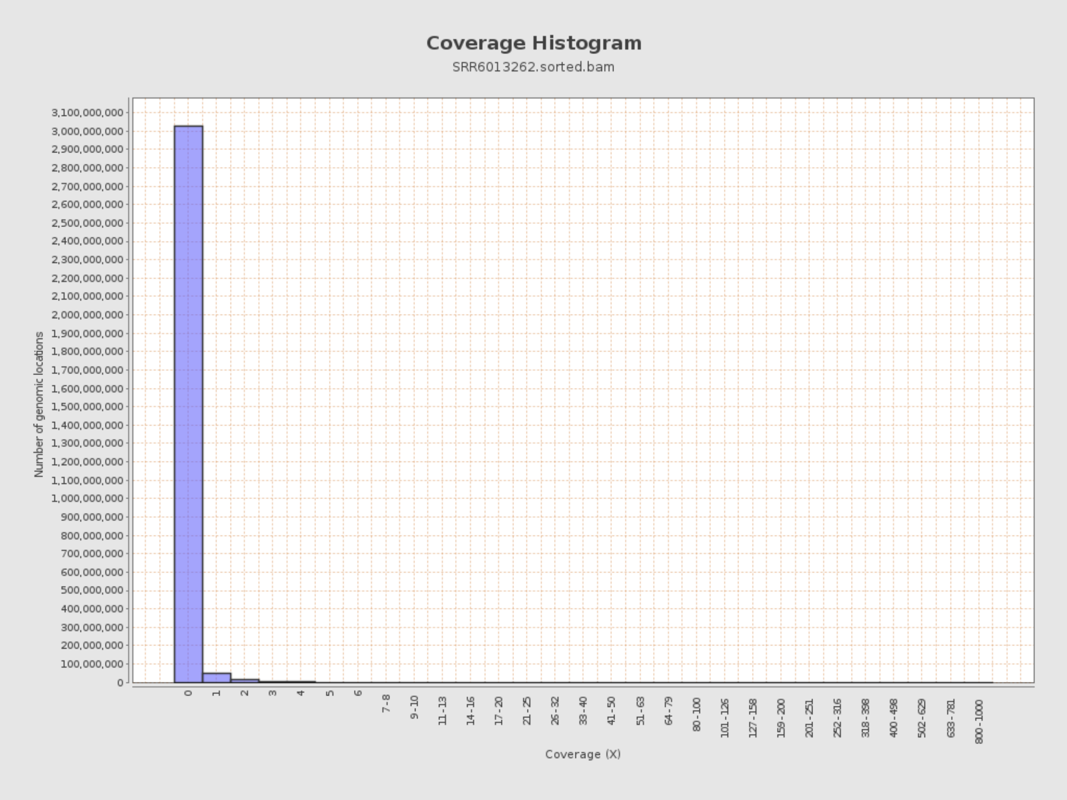
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6563474	0.0263	0.8362
chr2	243199373	7827153	0.0322	0.515
chr3	198022430	6096369	0.0308	0.2405
chr4	191154276	6222905	0.0326	0.2508
chr5	180915260	8877611	0.0491	0.3048
chr6	171115067	5261544	0.0307	0.2708
chr7	159138663	4140390	0.026	0.3543

chr8	146364022	5948548	0.0406	0.4451
chr9	141213431	4148440	0.0294	0.3545
chr10	135534747	3887678	0.0287	0.3104
chr11	135006516	3958990	0.0293	0.2964
chr12	133851895	5214328	0.039	0.2732
chr13	115169878	2612696	0.0227	0.209
chr14	107349540	2837330	0.0264	0.2307
chr15	102531392	2568915	0.0251	0.2177
chr16	90354753	3442899	0.0381	0.2732
chr17	81195210	3128419	0.0385	0.335
chr18	78077248	3358852	0.043	0.5301
chr19	59128983	1931245	0.0327	0.6161
chr20	63025520	3091645	0.0491	0.3084
chr21	48129895	1473203	0.0306	0.2465
chr22	51304566	1290443	0.0252	0.2099
chrMT	16571	13730	0.8286	1.1167
chrX	155270560	6148862	0.0396	0.2951
chrY	59373566	225601	0.0038	0.0907

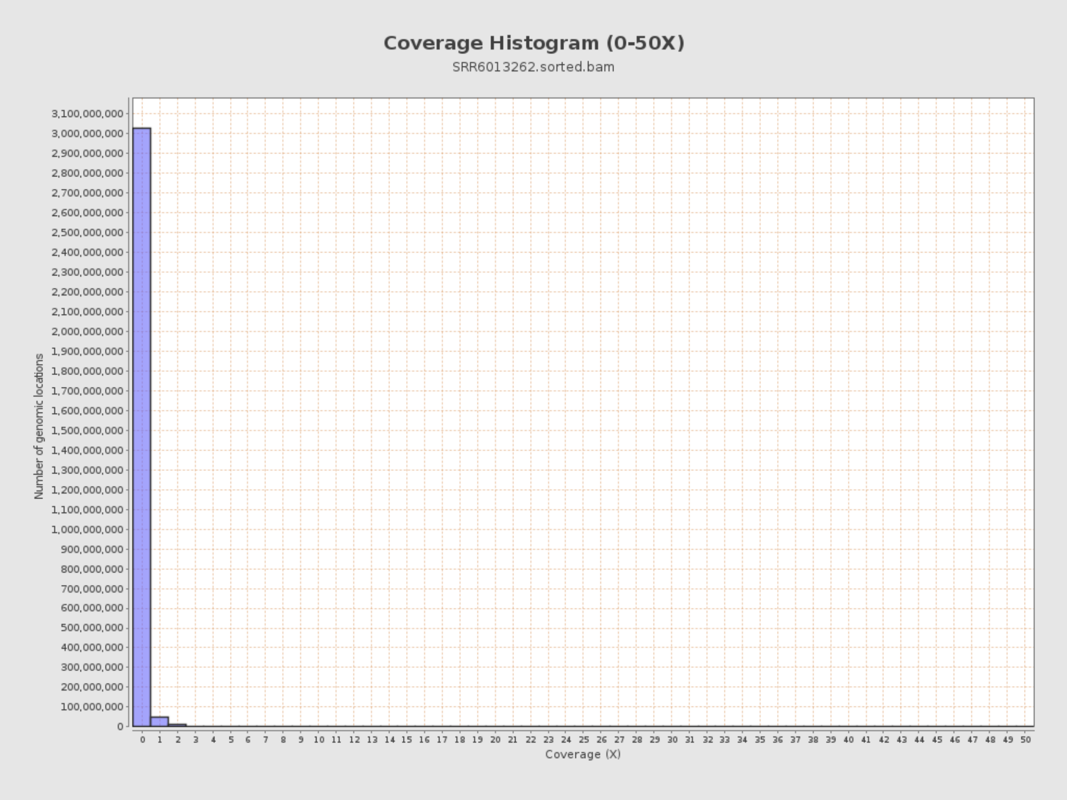
3. Results : Coverage across reference



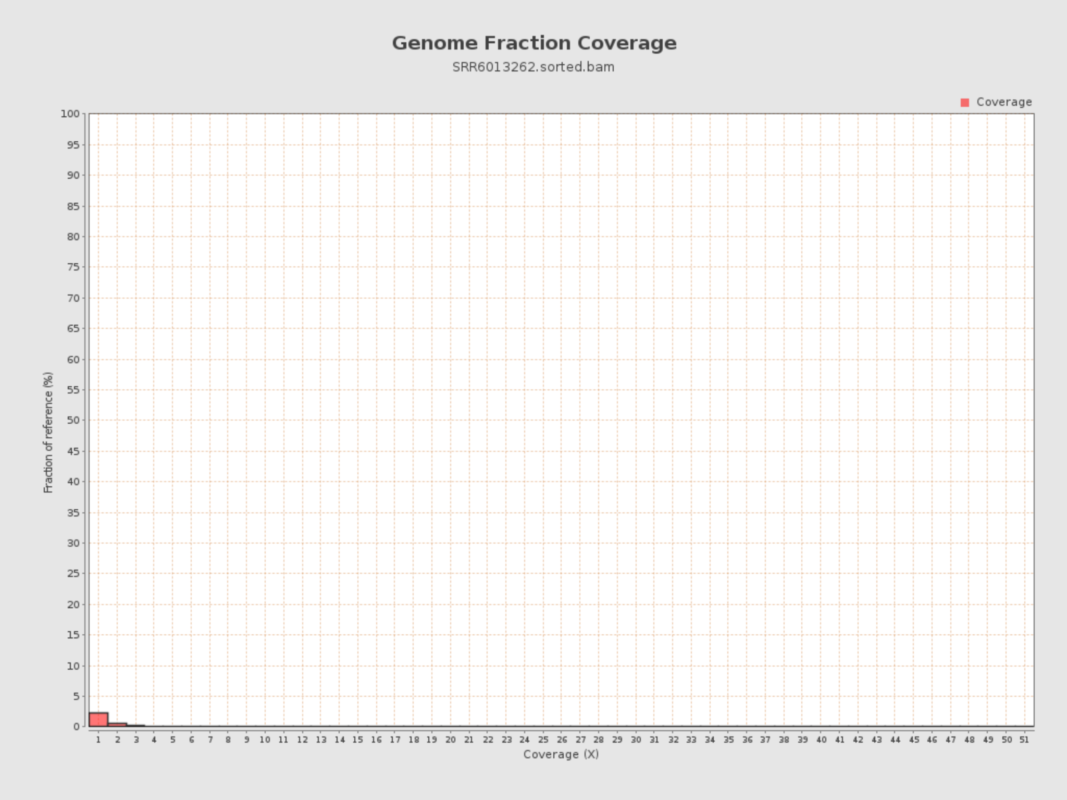
4. Results : Coverage Histogram



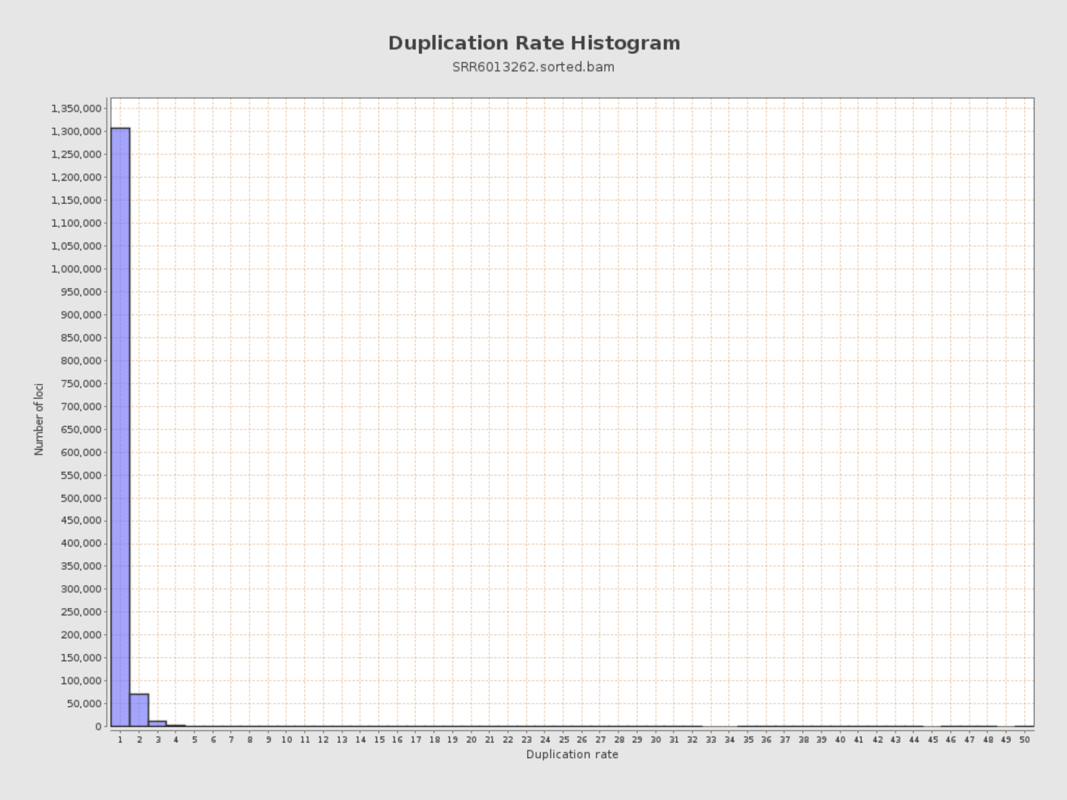
5. Results : Coverage Histogram (0-50X)



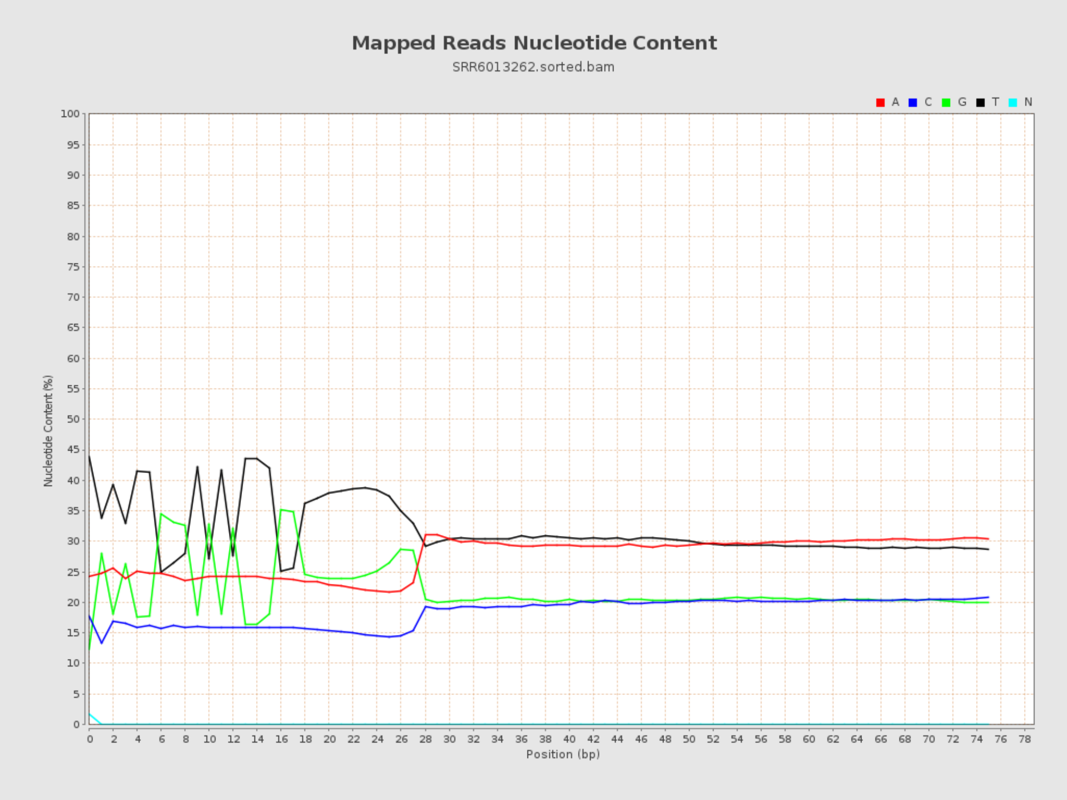
6. Results : Genome Fraction Coverage



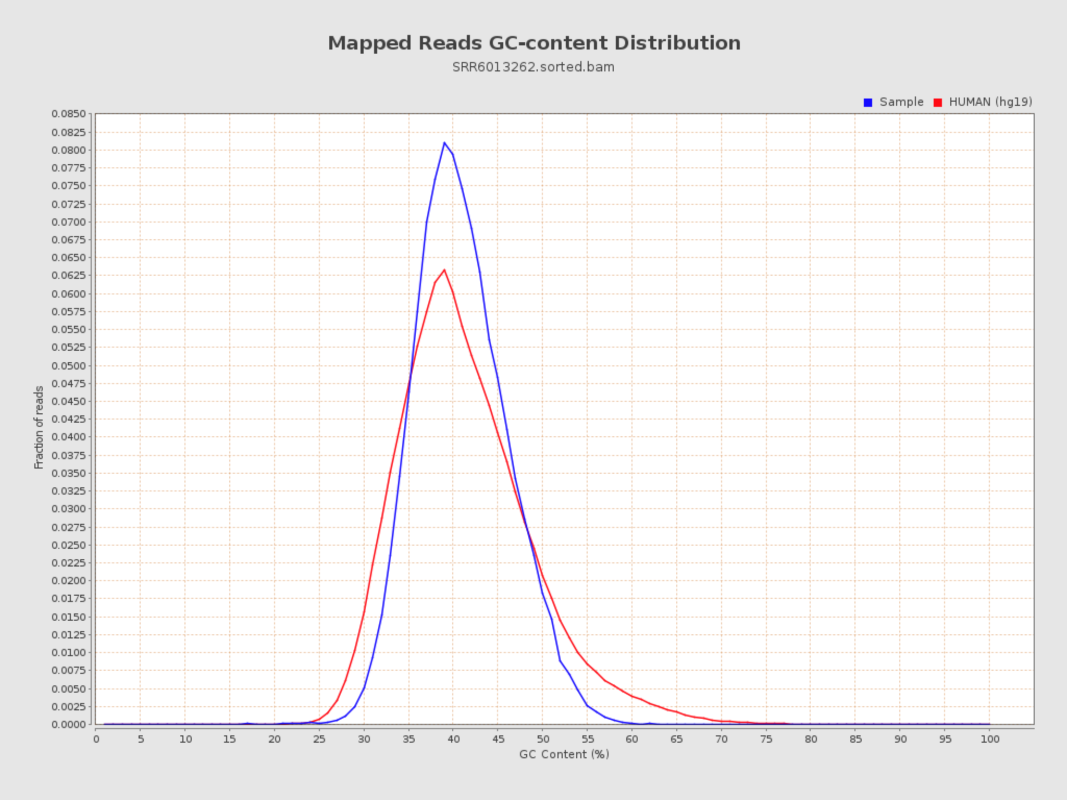
7. Results : Duplication Rate Histogram



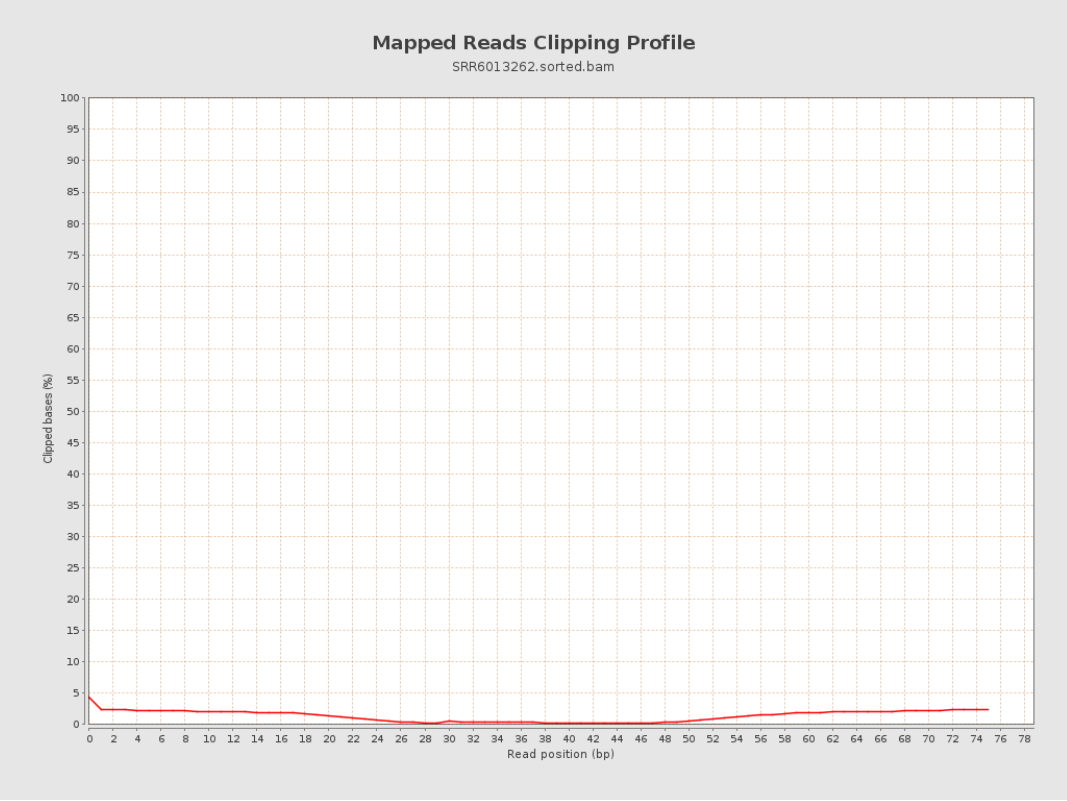
8. Results : Mapped Reads Nucleotide Content



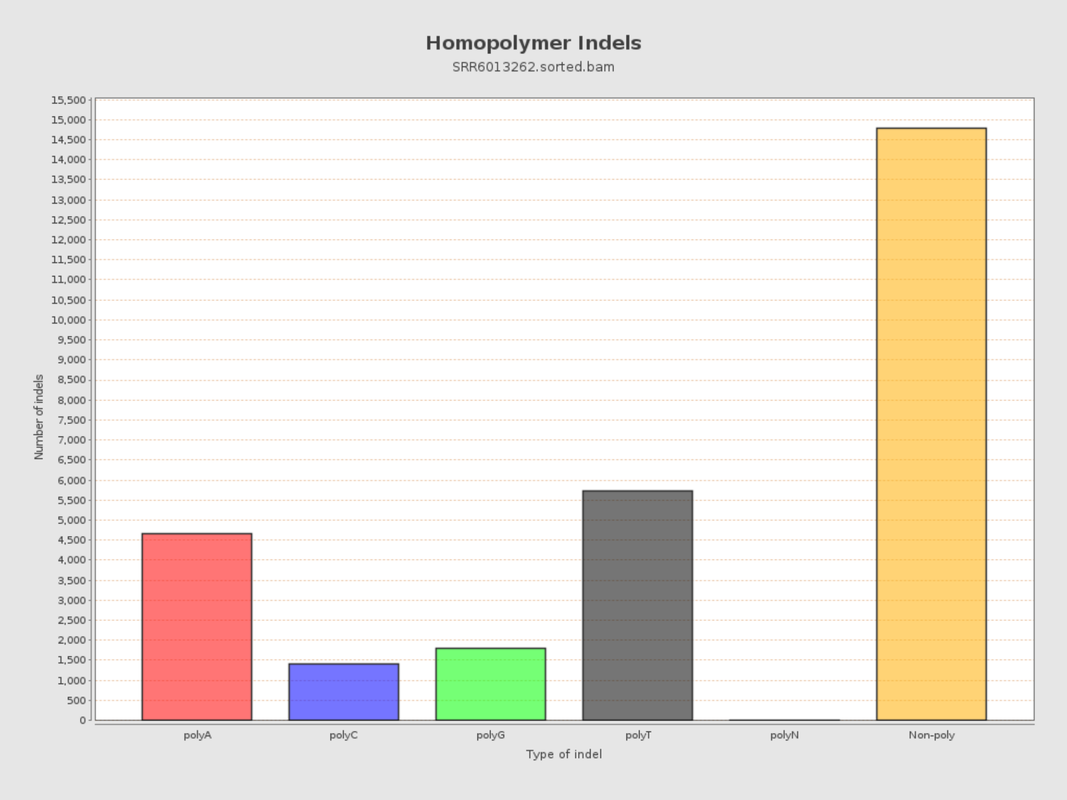
9. Results : Mapped Reads GC-content Distribution



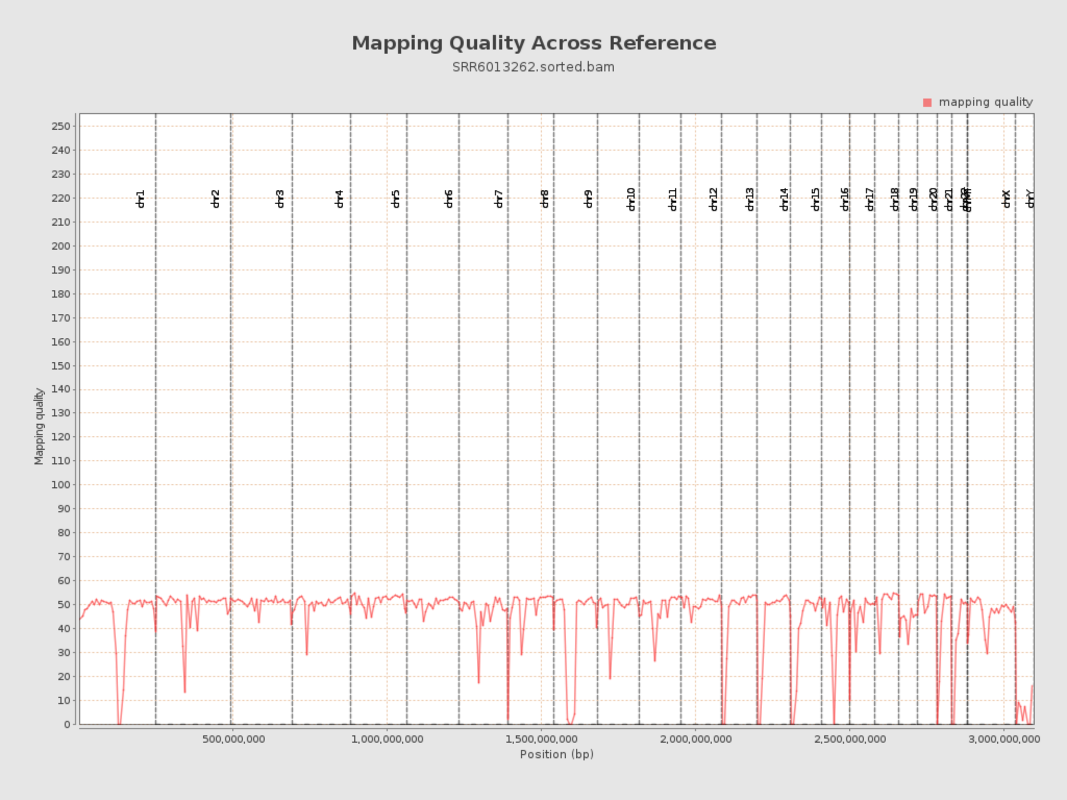
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram