Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:24:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013342.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_SRR6013342 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013342.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:24:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013342.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,063,716
Mapped reads	1,868,439 / 90.54%
Unmapped reads	195,277 / 9.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,751 / 0.42%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	62,734 / 3.04%
Duplication rate	2.71%
Clipped reads	819,813 / 39.73%

2.2. ACGT Content

Number/percentage of A's	33,668,708 / 27%
Number/percentage of C's	24,045,555 / 19.28%
Number/percentage of T's	38,330,166 / 30.73%
Number/percentage of G's	28,641,212 / 22.96%
Number/percentage of N's	32,626 / 0.03%
GC Percentage	42.24%

2.3. Coverage

Mean	0.0403

Standard Deviation	0.3058

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

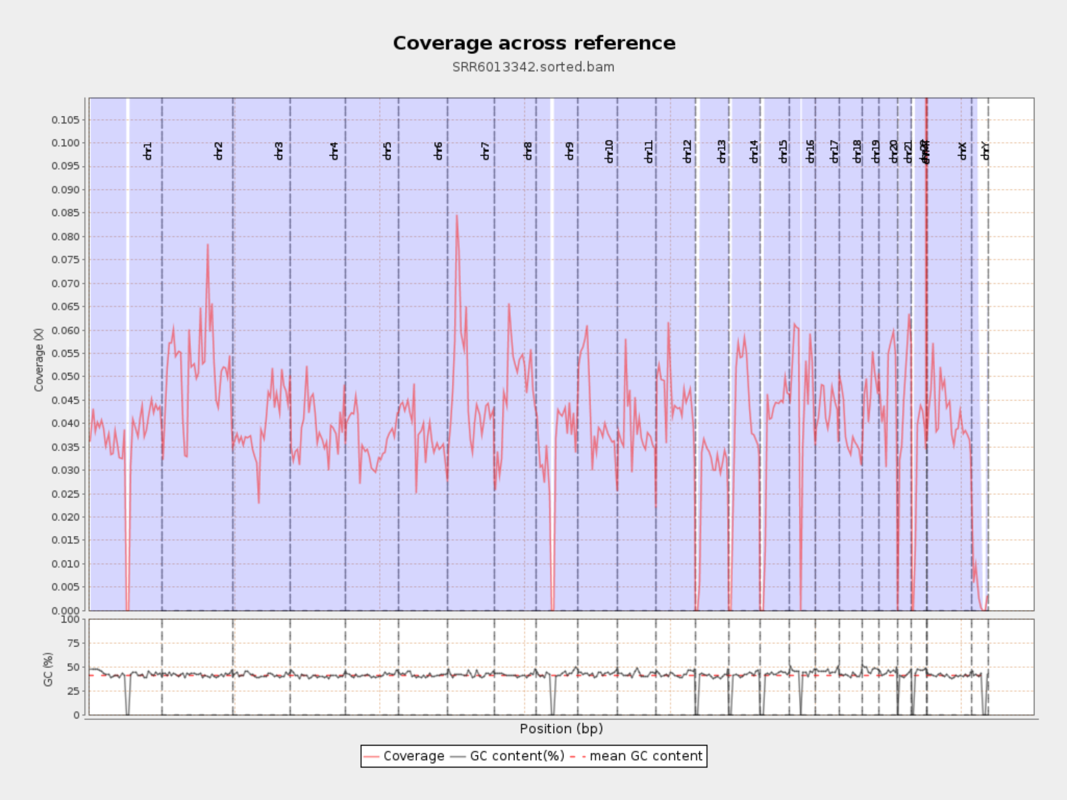
General error rate	0.77%
Mismatches	940,233
Insertions	8,361
Mapped reads with at least one insertion	0.44%
Deletions	28,659
Mapped reads with at least one deletion	1.52%
Homopolymer indels	46.17%

2.6. Chromosome stats

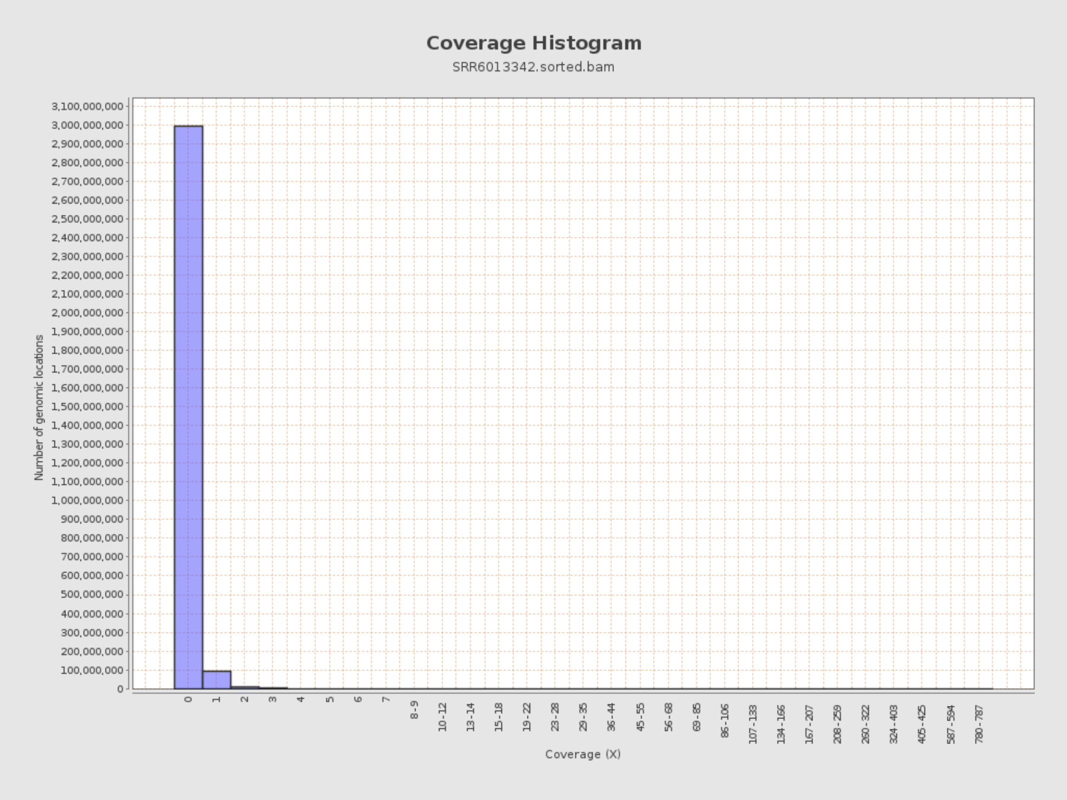
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9058443	0.0363	0.3342
chr2	243199373	12630742	0.0519	0.4447
chr3	198022430	7916603	0.04	0.2278
chr4	191154276	7385050	0.0386	0.2283
chr5	180915260	6556539	0.0362	0.2183
chr6	171115067	6509645	0.038	0.2654
chr7	159138663	7699826	0.0484	0.5121

chr8	146364022	6935174	0.0474	0.3111
chr9	141213431	4648423	0.0329	0.2627
chr10	135534747	5784782	0.0427	0.29
chr11	135006516	5226489	0.0387	0.2503
chr12	133851895	6161188	0.046	0.2483
chr13	115169878	3141521	0.0273	0.1956
chr14	107349540	4227873	0.0394	0.2341
chr15	102531392	3690855	0.036	0.2223
chr16	90354753	4250816	0.047	0.2767
chr17	81195210	3493251	0.043	0.2475
chr18	78077248	2976457	0.0381	0.4131
chr19	59128983	2795585	0.0473	0.3239
chr20	63025520	3019841	0.0479	0.2544
chr21	48129895	2078227	0.0432	0.2516
chr22	51304566	1454299	0.0283	0.1938
chrMT	16571	347910	20.9951	18.5367
chrX	155270560	6527138	0.042	0.2458
chrY	59373566	251061	0.0042	0.0871

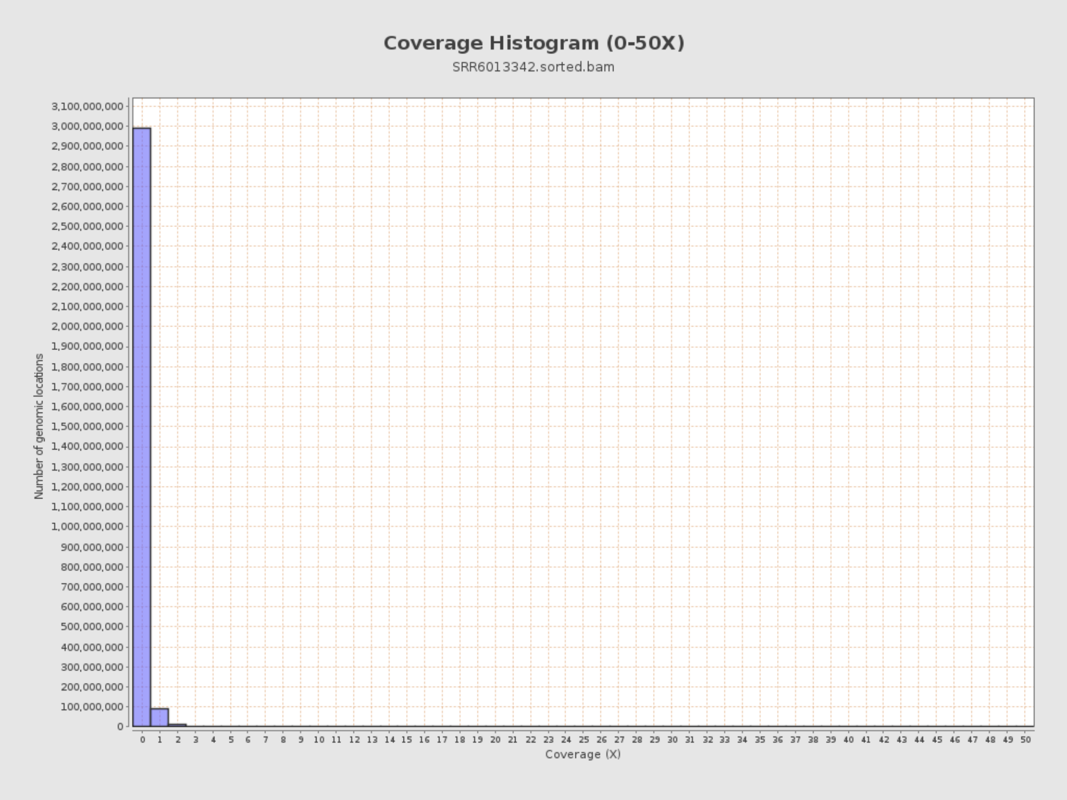
3. Results : Coverage across reference



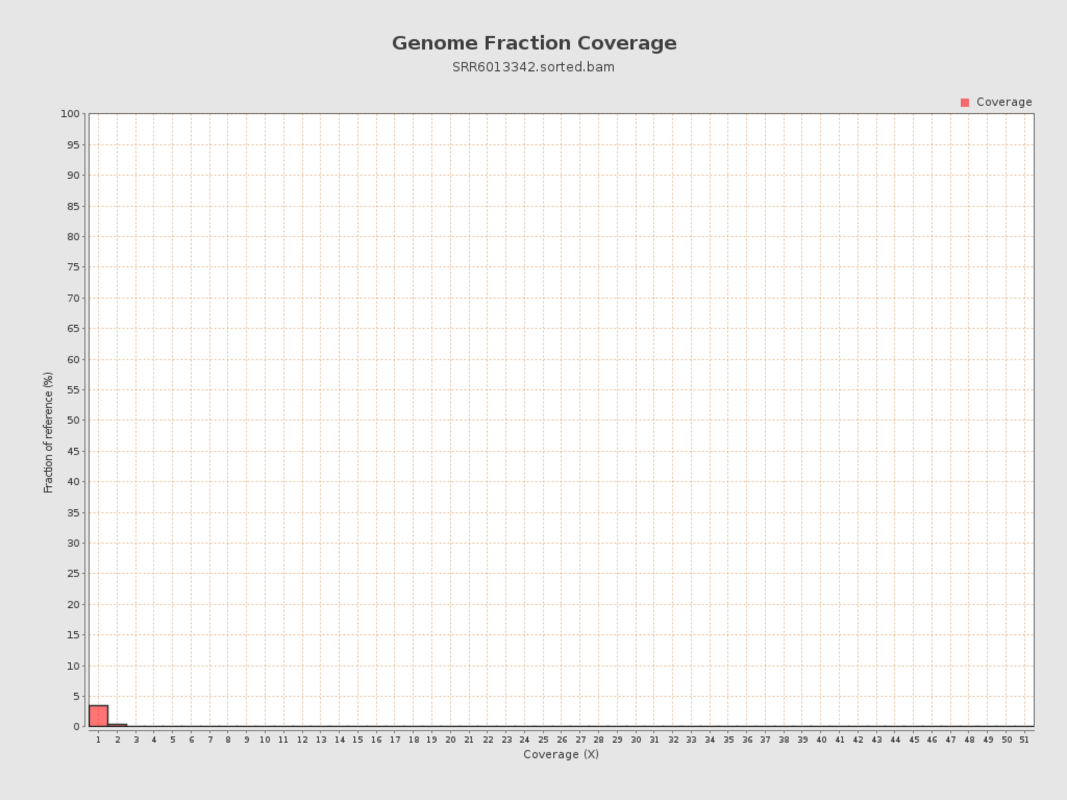
4. Results : Coverage Histogram



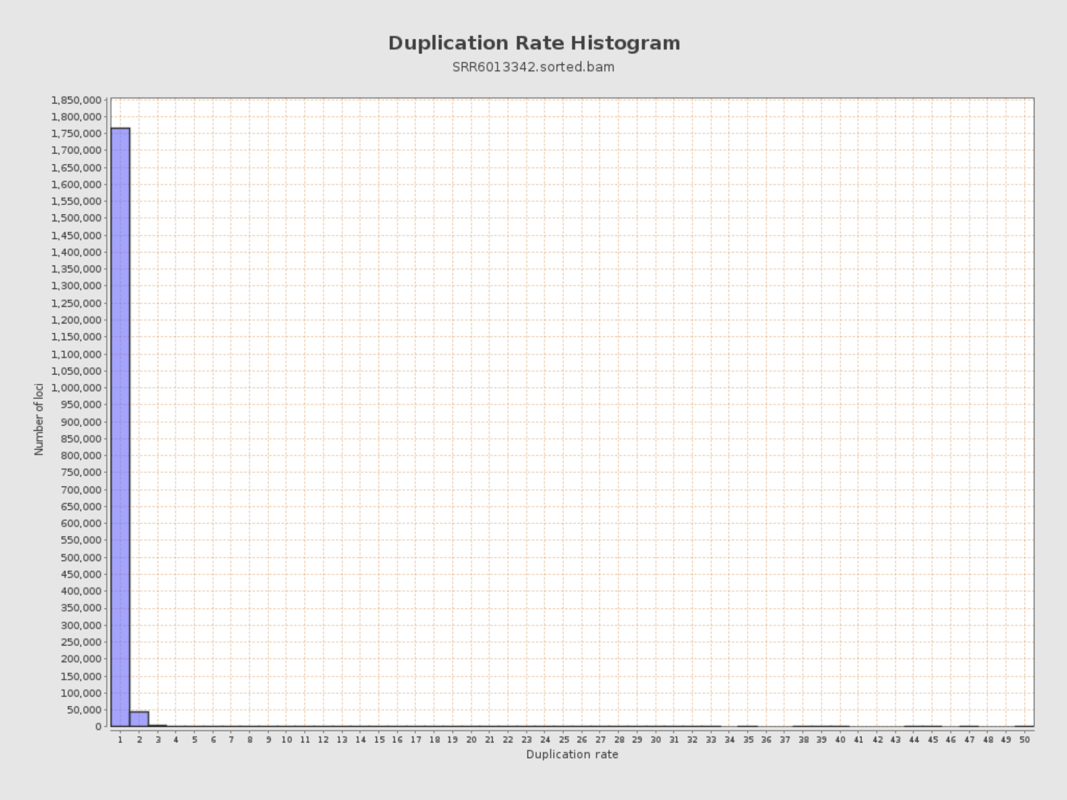
5. Results : Coverage Histogram (0-50X)



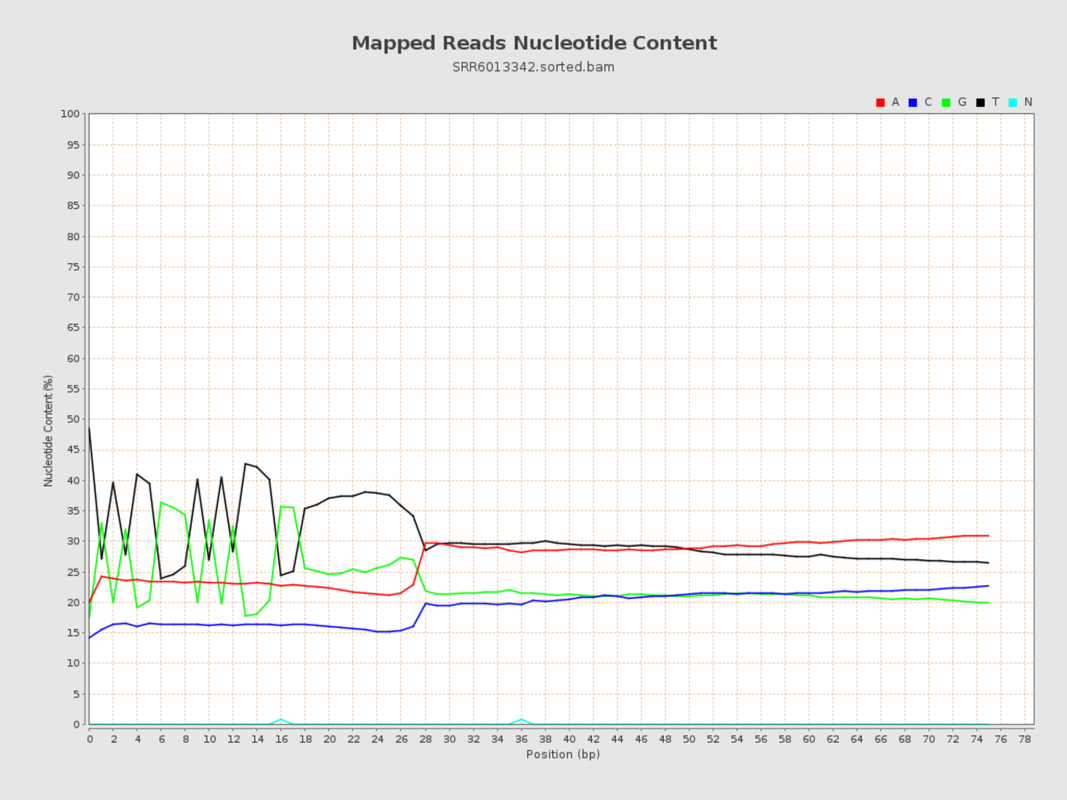
6. Results : Genome Fraction Coverage



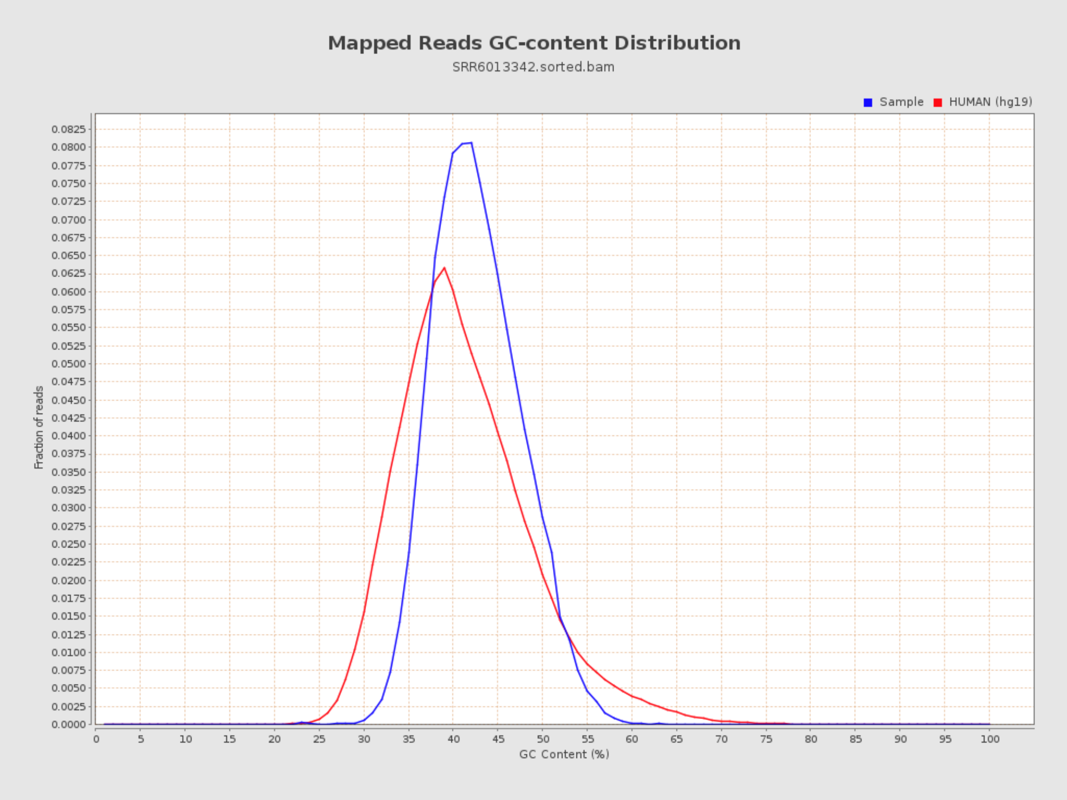
7. Results : Duplication Rate Histogram



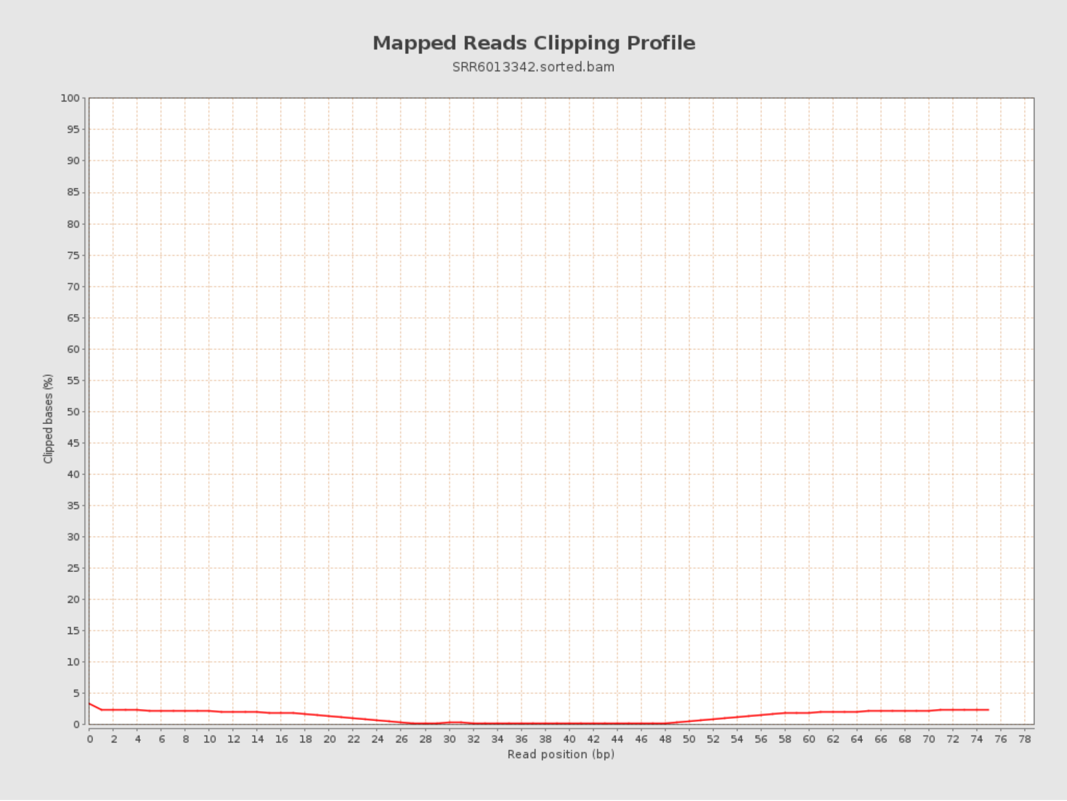
8. Results : Mapped Reads Nucleotide Content



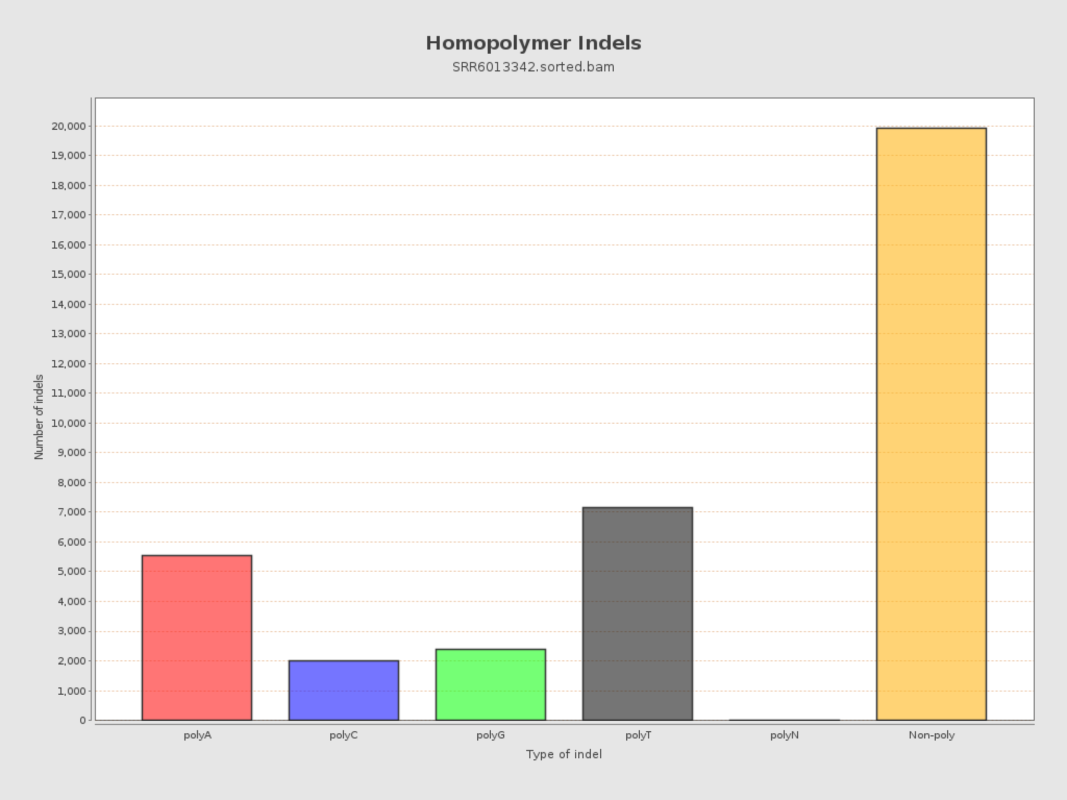
9. Results : Mapped Reads GC-content Distribution



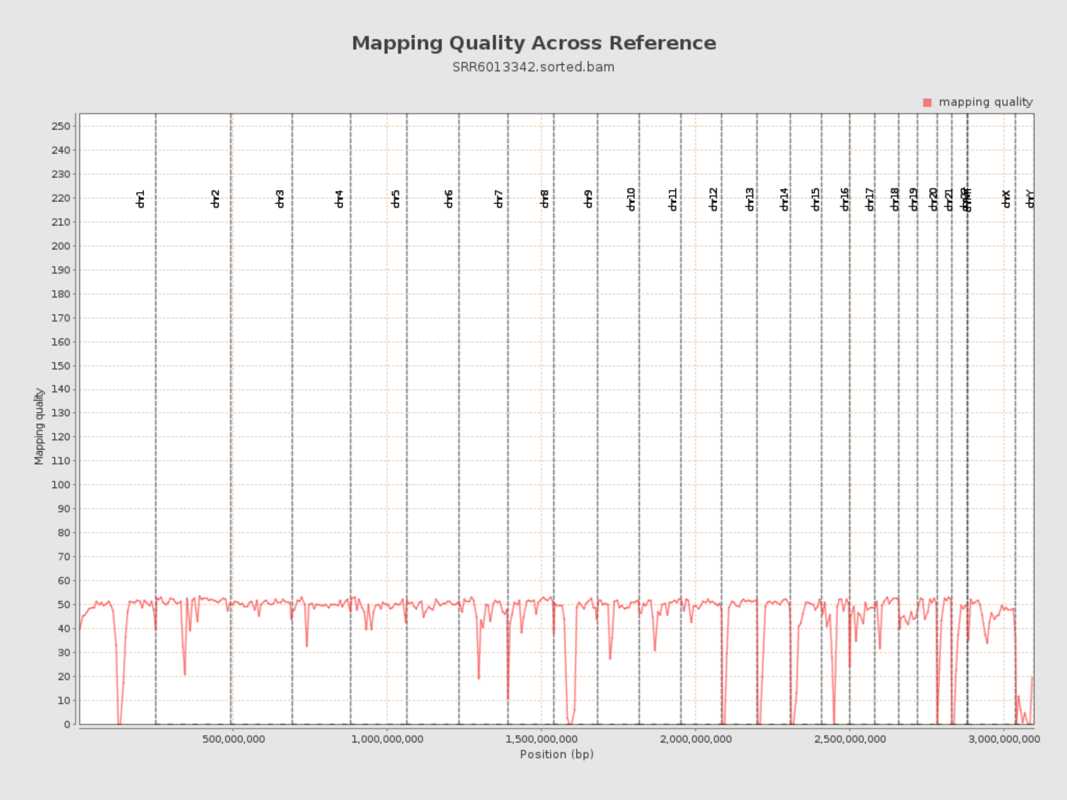
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram