Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:41:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013348.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_SRR6013348 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013348.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:41:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013348.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,666,920
Mapped reads	1,053,324 / 63.19%
Unmapped reads	613,596 / 36.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,358 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	278,084 / 16.68%
Duplication rate	16.29%
Clipped reads	692,212 / 41.53%

2.2. ACGT Content

Number/percentage of A's	17,546,221 / 27.06%
Number/percentage of C's	11,781,436 / 18.17%
Number/percentage of T's	20,745,694 / 32%
Number/percentage of G's	14,755,940 / 22.76%
Number/percentage of N's	6,758 / 0.01%
GC Percentage	40.93%

2.3. Coverage

Mean	0.021

Standard Deviation	0.3609

2.4. Mapping Quality

Mean Mapping Quality	43.33

2.5. Mismatches and indels

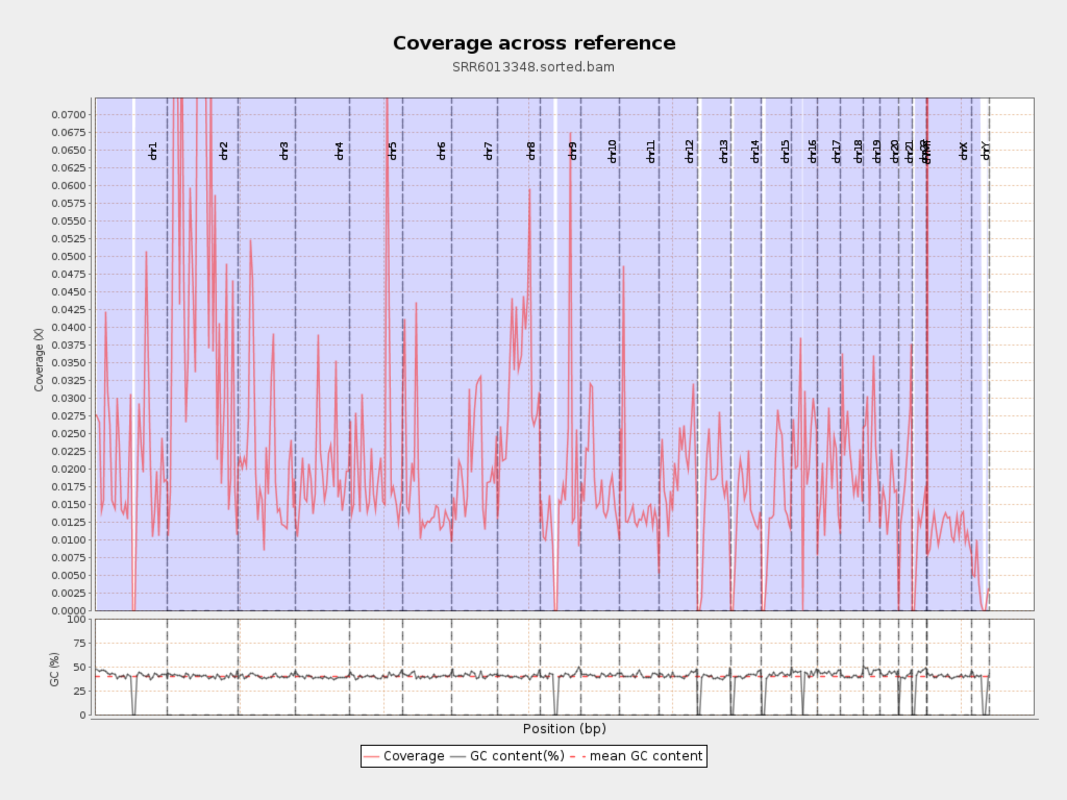
General error rate	0.91%
Mismatches	580,535
Insertions	4,446
Mapped reads with at least one insertion	0.42%
Deletions	24,871
Mapped reads with at least one deletion	2.33%
Homopolymer indels	43.83%

2.6. Chromosome stats

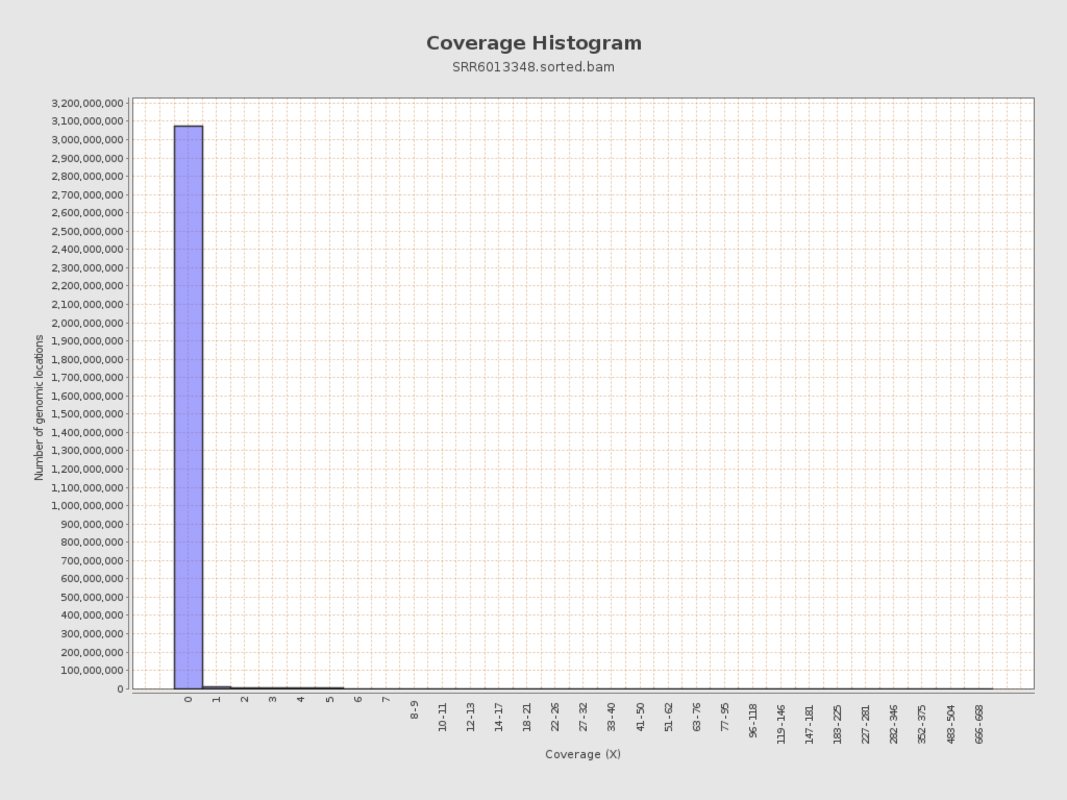
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5152730	0.0207	0.4287
chr2	243199373	11474483	0.0472	0.5881
chr3	198022430	4239723	0.0214	0.3396
chr4	191154276	3653958	0.0191	0.3189
chr5	180915260	3832619	0.0212	0.3353
chr6	171115067	2909273	0.017	0.3213
chr7	159138663	3282237	0.0206	0.3603

chr8	146364022	4908099	0.0335	0.4456
chr9	141213431	2283542	0.0162	0.2994
chr10	135534747	2464250	0.0182	0.319
chr11	135006516	2119380	0.0157	0.2832
chr12	133851895	2740310	0.0205	0.3311
chr13	115169878	1797361	0.0156	0.2934
chr14	107349540	1442134	0.0134	0.2652
chr15	102531392	1461414	0.0143	0.2822
chr16	90354753	2085008	0.0231	0.3449
chr17	81195210	1467459	0.0181	0.3043
chr18	78077248	1711135	0.0219	0.4373
chr19	59128983	1411857	0.0239	0.3967
chr20	63025520	989777	0.0157	0.2937
chr21	48129895	921583	0.0191	0.3248
chr22	51304566	509777	0.0099	0.2213
chrMT	16571	47357	2.8578	6.0866
chrX	155270560	1771384	0.0114	0.2322
chrY	59373566	201695	0.0034	0.1098

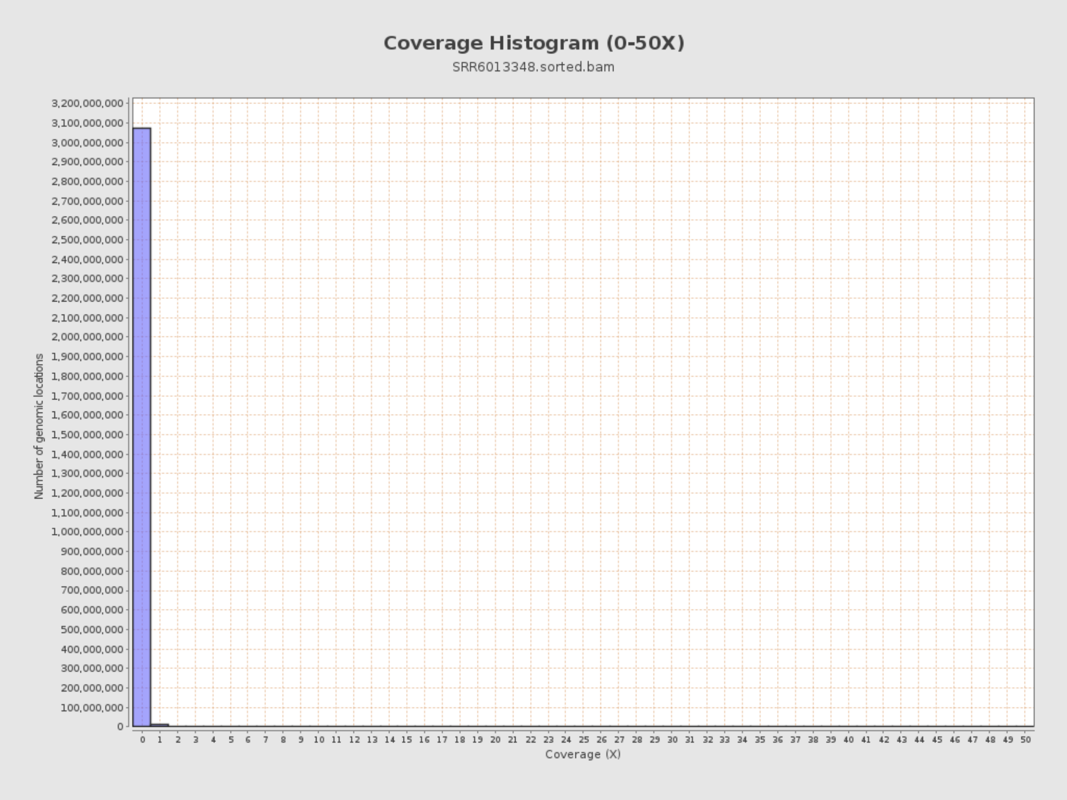
3. Results : Coverage across reference



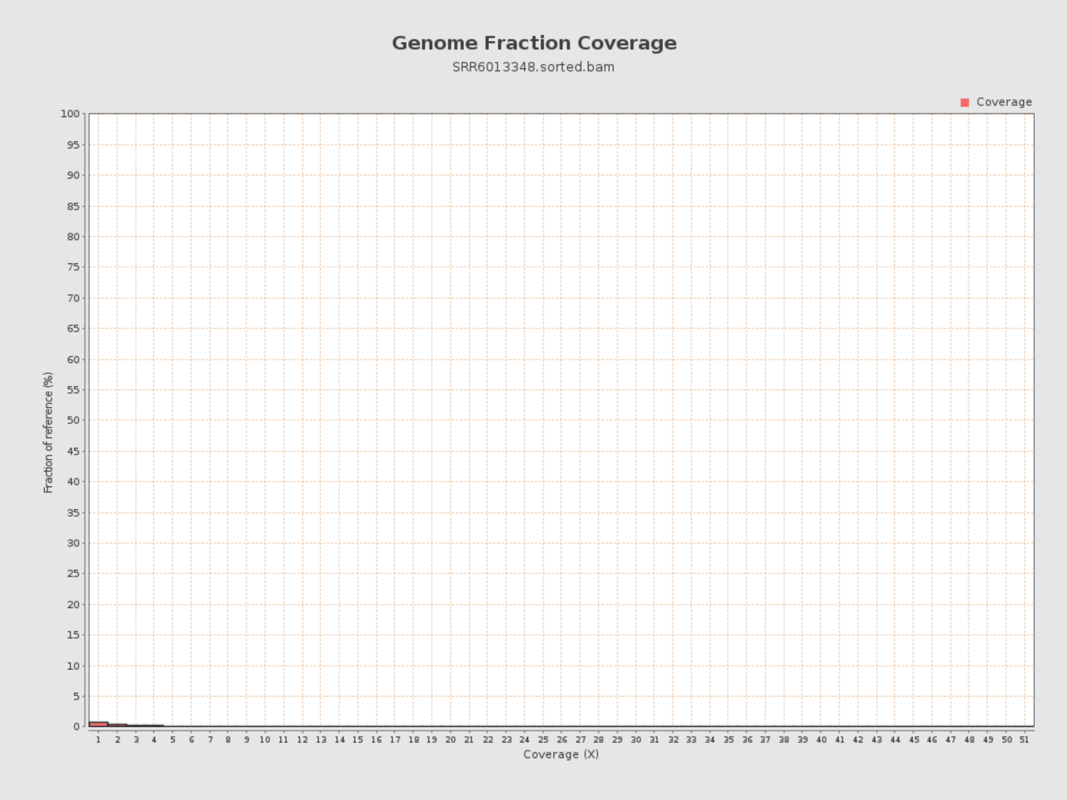
4. Results : Coverage Histogram



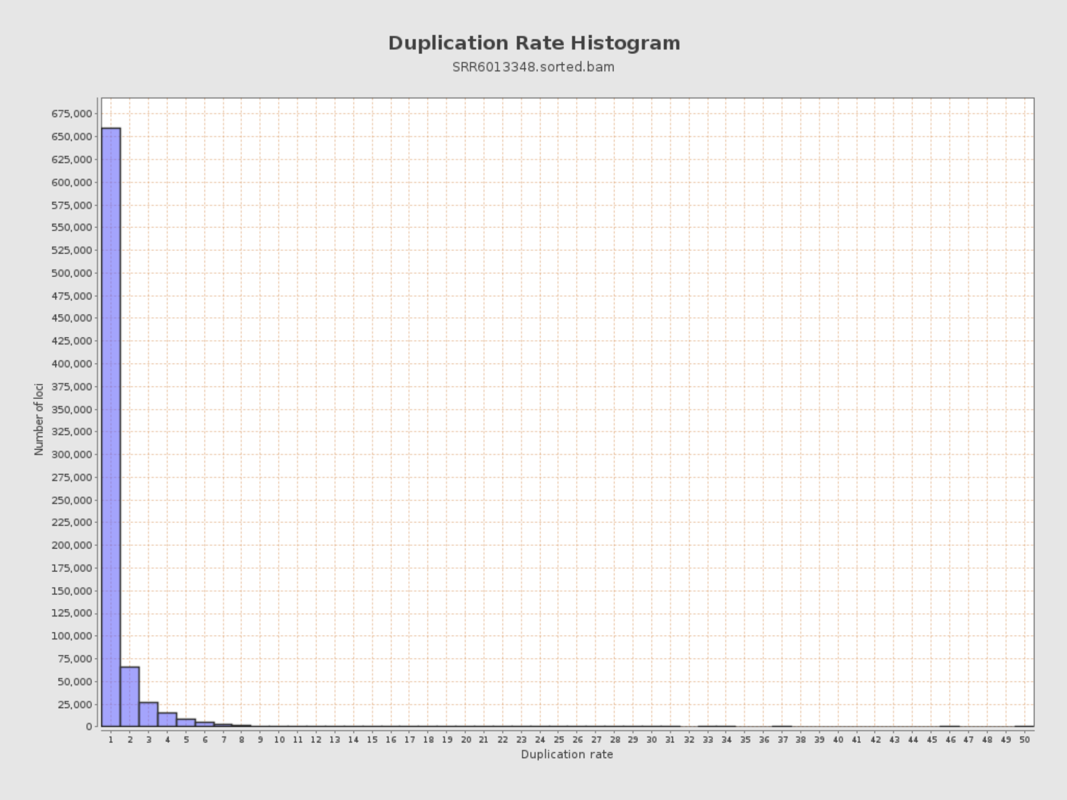
5. Results : Coverage Histogram (0-50X)



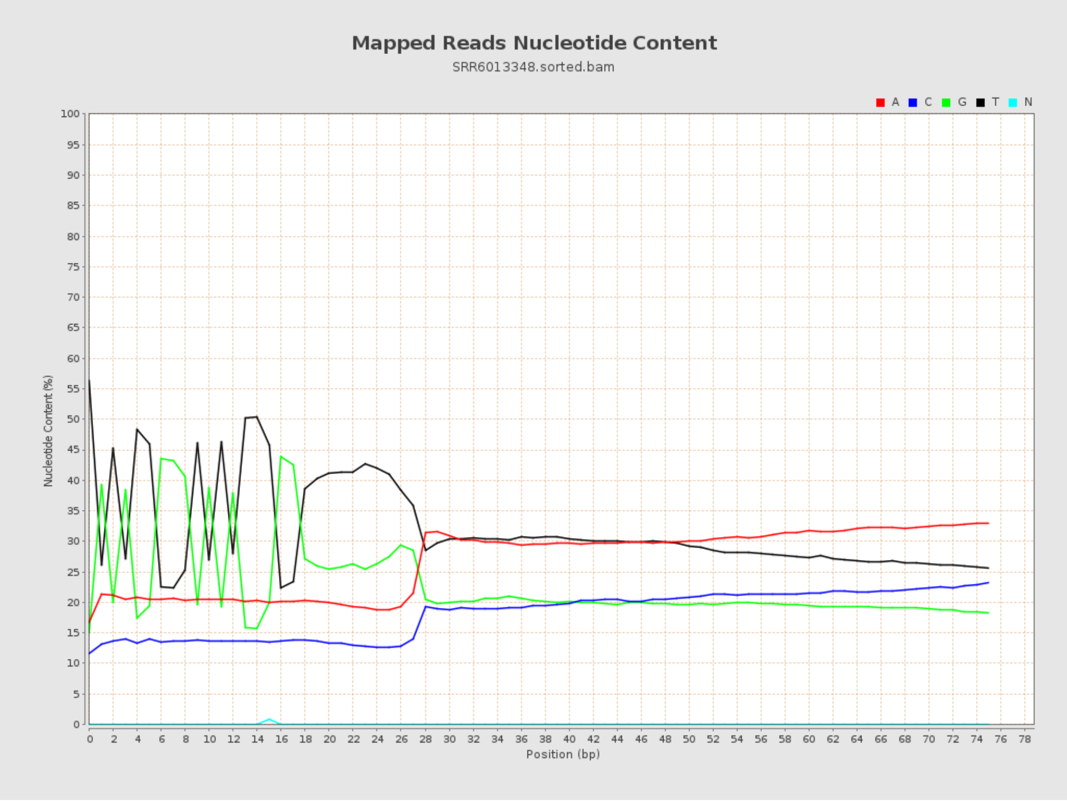
6. Results : Genome Fraction Coverage



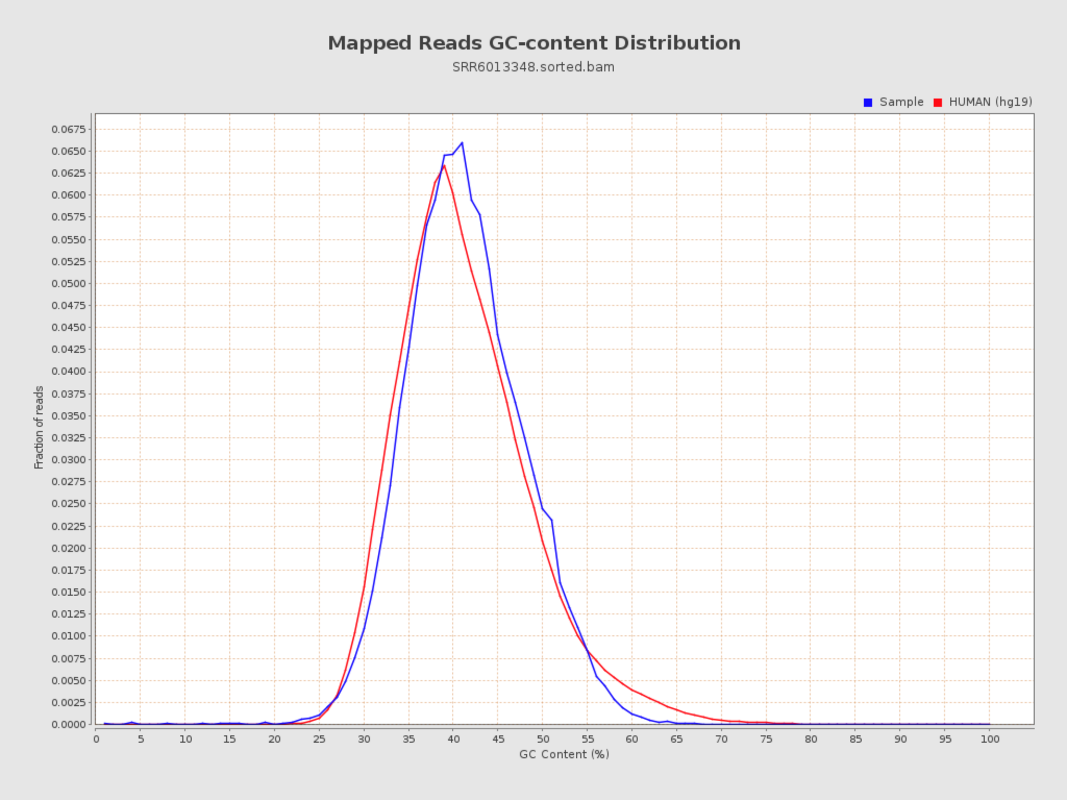
7. Results : Duplication Rate Histogram



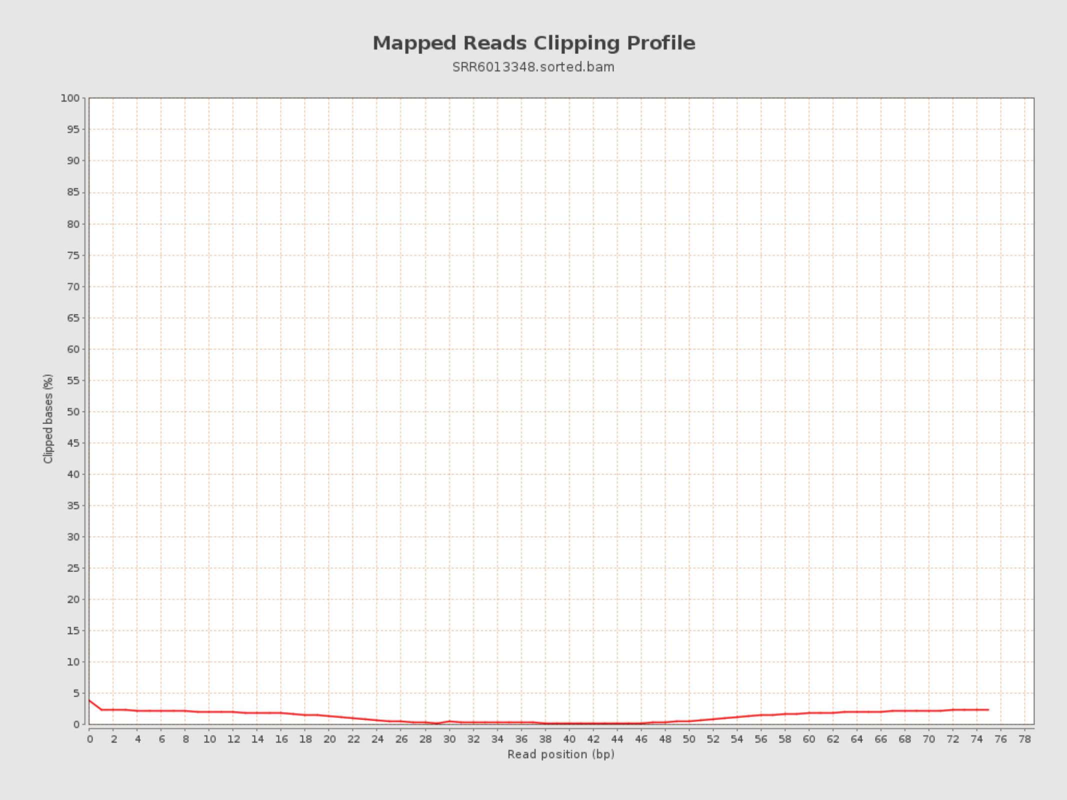
8. Results : Mapped Reads Nucleotide Content



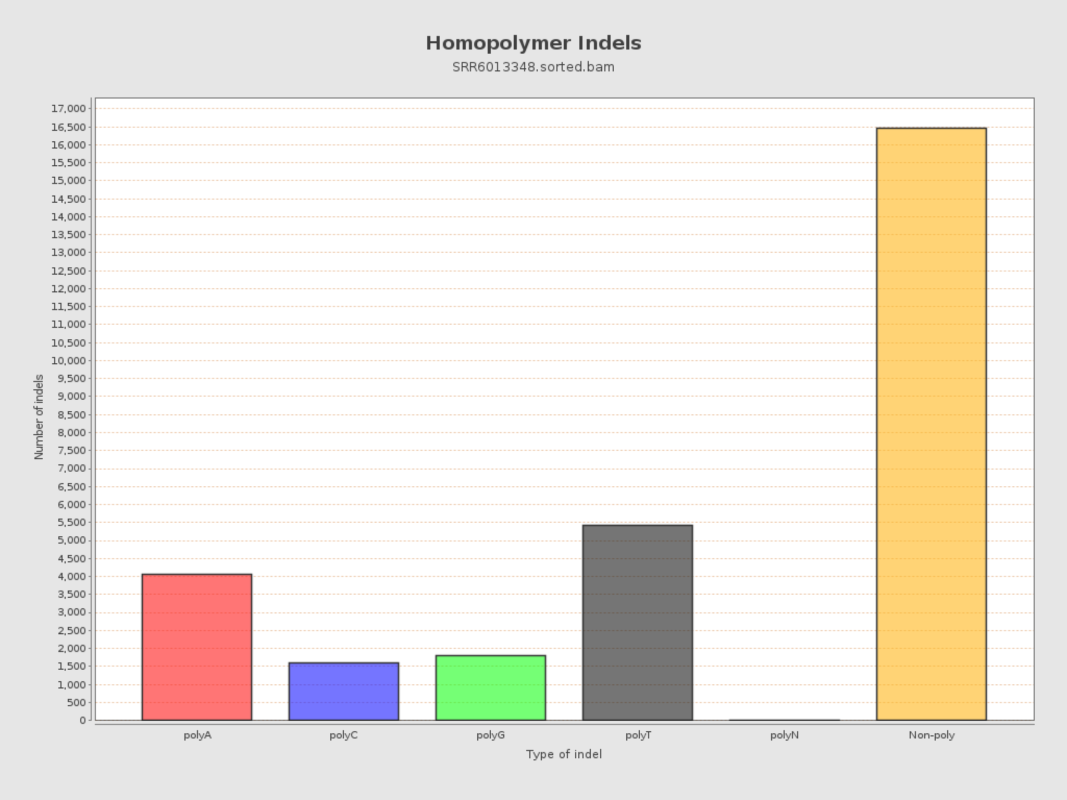
9. Results : Mapped Reads GC-content Distribution



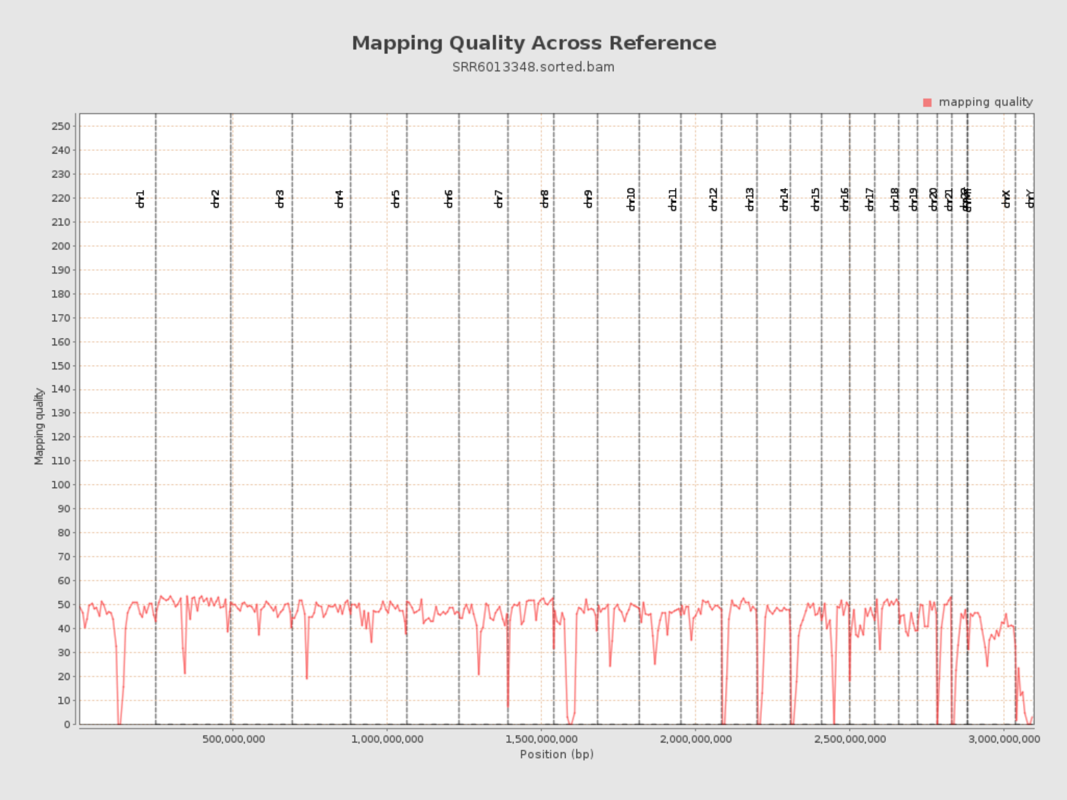
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram