Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:11:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004142.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_SRR6004142 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004142.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:11:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004142.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,779,050
Mapped reads	1,366,424 / 76.81%
Unmapped reads	412,626 / 23.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,174 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	191,102 / 10.74%
Duplication rate	10.82%
Clipped reads	781,245 / 43.91%

2.2. ACGT Content

Number/percentage of A's	22,984,051 / 26.4%
Number/percentage of C's	16,616,511 / 19.09%
Number/percentage of T's	27,083,177 / 31.11%
Number/percentage of G's	20,367,111 / 23.39%
Number/percentage of N's	11,957 / 0.01%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0281

Standard Deviation	0.3306

2.4. Mapping Quality

Mean Mapping Quality	44.33

2.5. Mismatches and indels

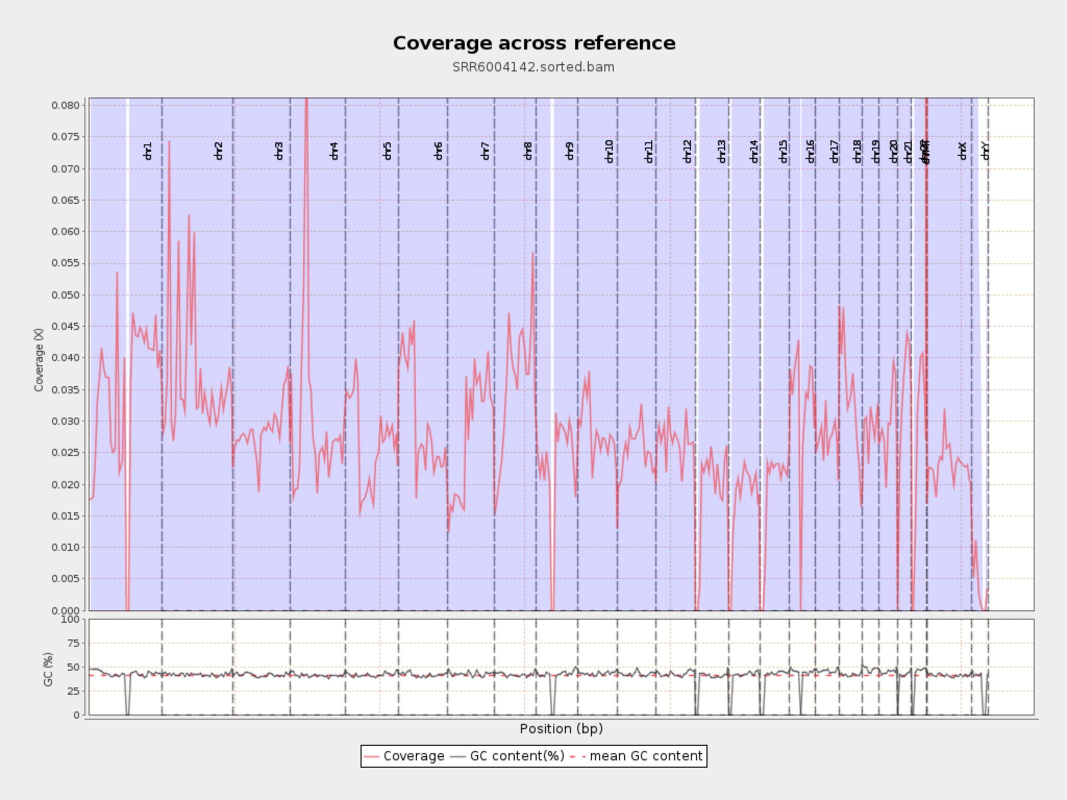
General error rate	0.99%
Mismatches	851,838
Insertions	6,970
Mapped reads with at least one insertion	0.5%
Deletions	26,351
Mapped reads with at least one deletion	1.91%
Homopolymer indels	47.51%

2.6. Chromosome stats

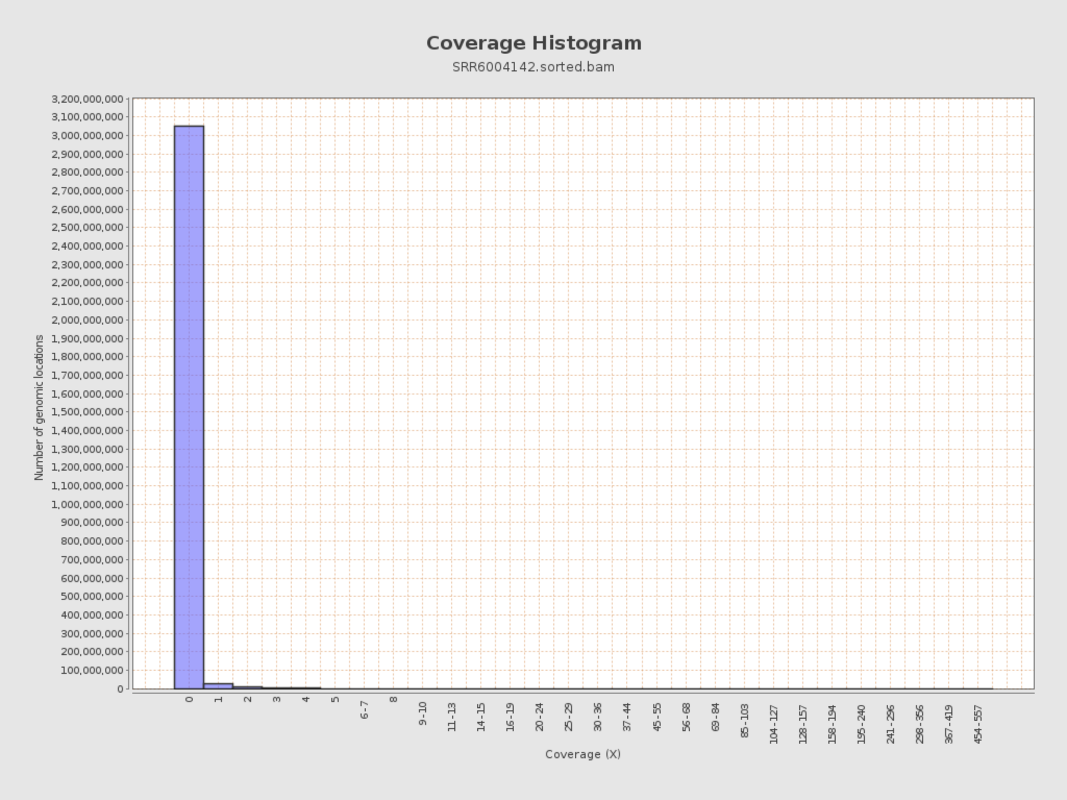
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8544853	0.0343	0.3898
chr2	243199373	9061608	0.0373	0.4487
chr3	198022430	5677847	0.0287	0.2786
chr4	191154276	5750878	0.0301	0.2864
chr5	180915260	4821055	0.0266	0.2697
chr6	171115067	5225869	0.0305	0.3176
chr7	159138663	4475897	0.0281	0.3342

chr8	146364022	5241458	0.0358	0.4441
chr9	141213431	3201247	0.0227	0.2962
chr10	135534747	3874776	0.0286	0.2982
chr11	135006516	3406882	0.0252	0.315
chr12	133851895	3587642	0.0268	0.2732
chr13	115169878	2121348	0.0184	0.2203
chr14	107349540	1841370	0.0172	0.2347
chr15	102531392	1878856	0.0183	0.2217
chr16	90354753	2951340	0.0327	0.3067
chr17	81195210	2201041	0.0271	0.2817
chr18	78077248	2673565	0.0342	0.5114
chr19	59128983	1705336	0.0288	0.3511
chr20	63025520	1875500	0.0298	0.294
chr21	48129895	1555124	0.0323	0.3055
chr22	51304566	1279737	0.0249	0.2629
chrMT	16571	343388	20.7222	15.8812
chrX	155270560	3582838	0.0231	0.2655
chrY	59373566	226631	0.0038	0.0982

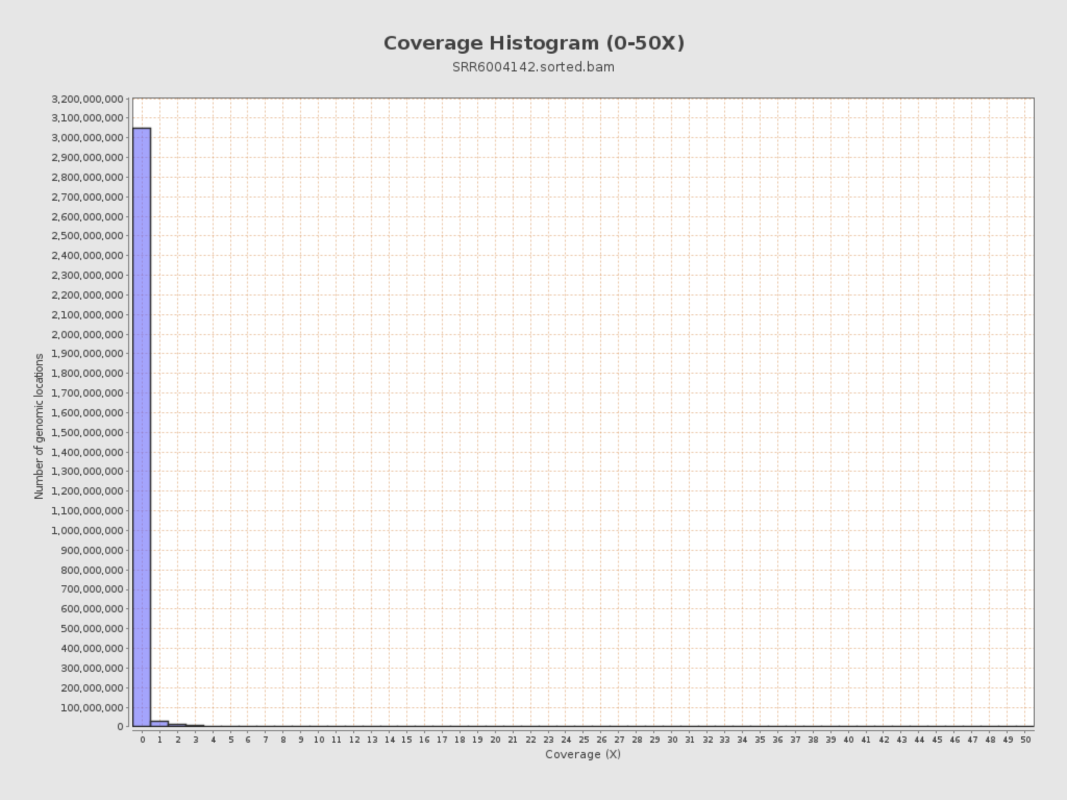
3. Results : Coverage across reference



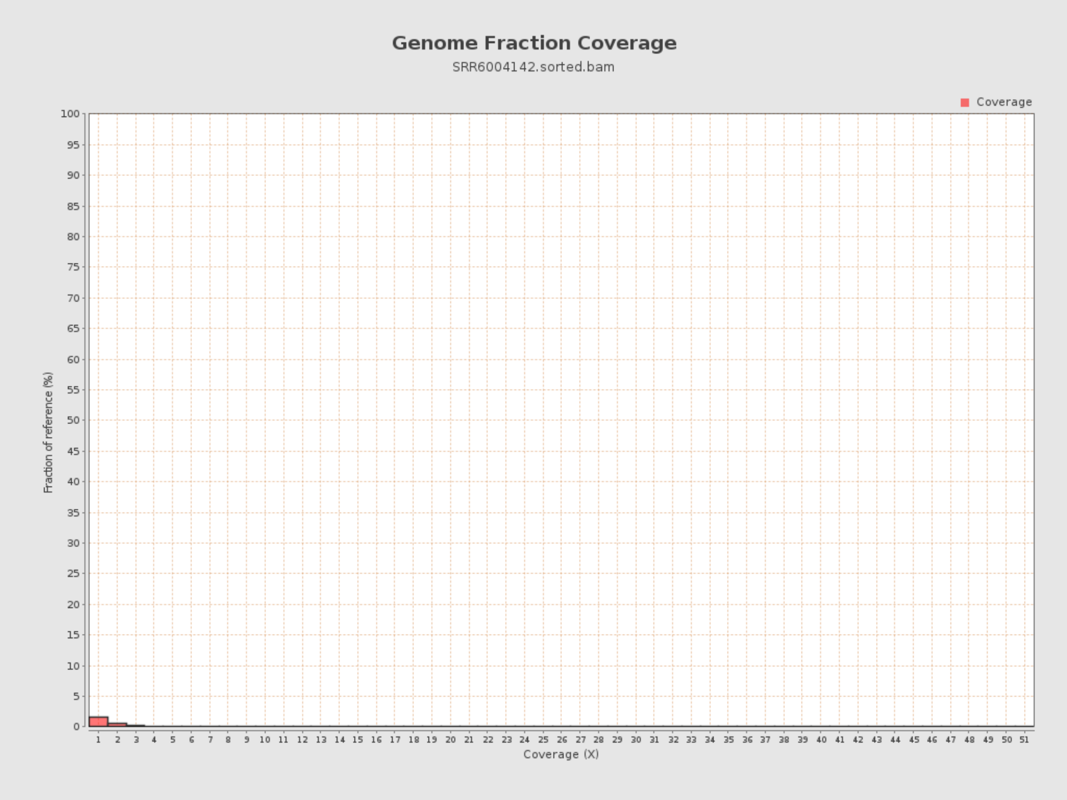
4. Results : Coverage Histogram



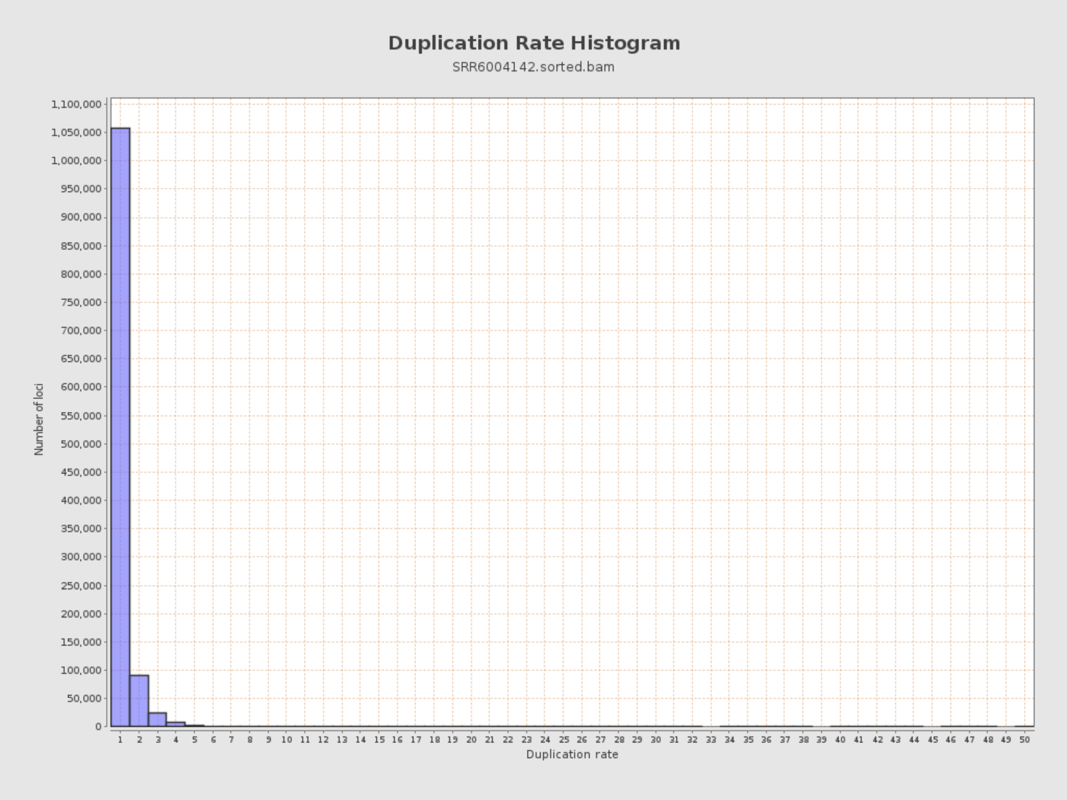
5. Results : Coverage Histogram (0-50X)



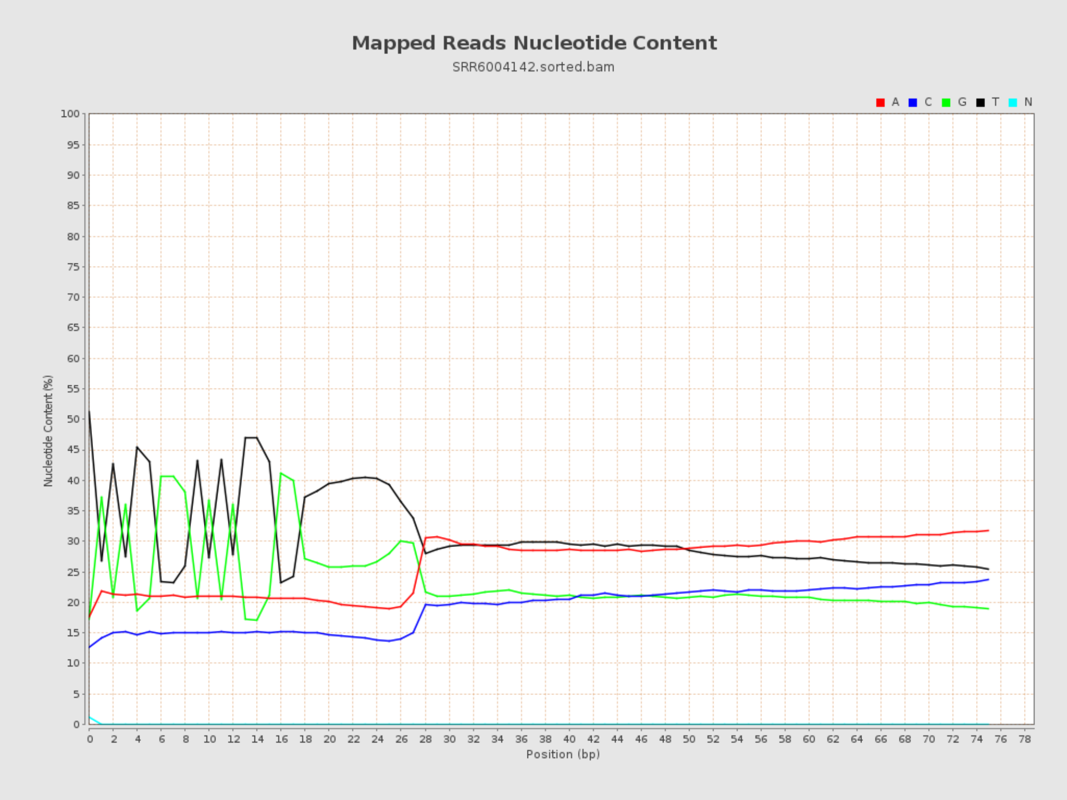
6. Results : Genome Fraction Coverage



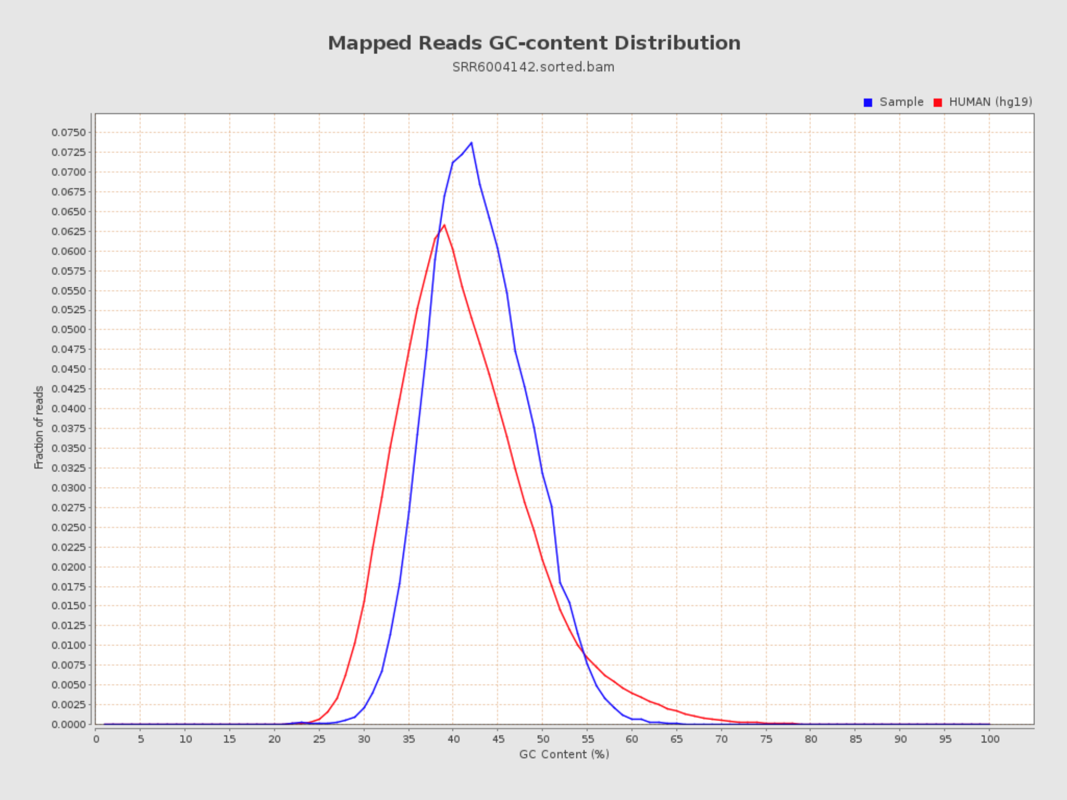
7. Results : Duplication Rate Histogram



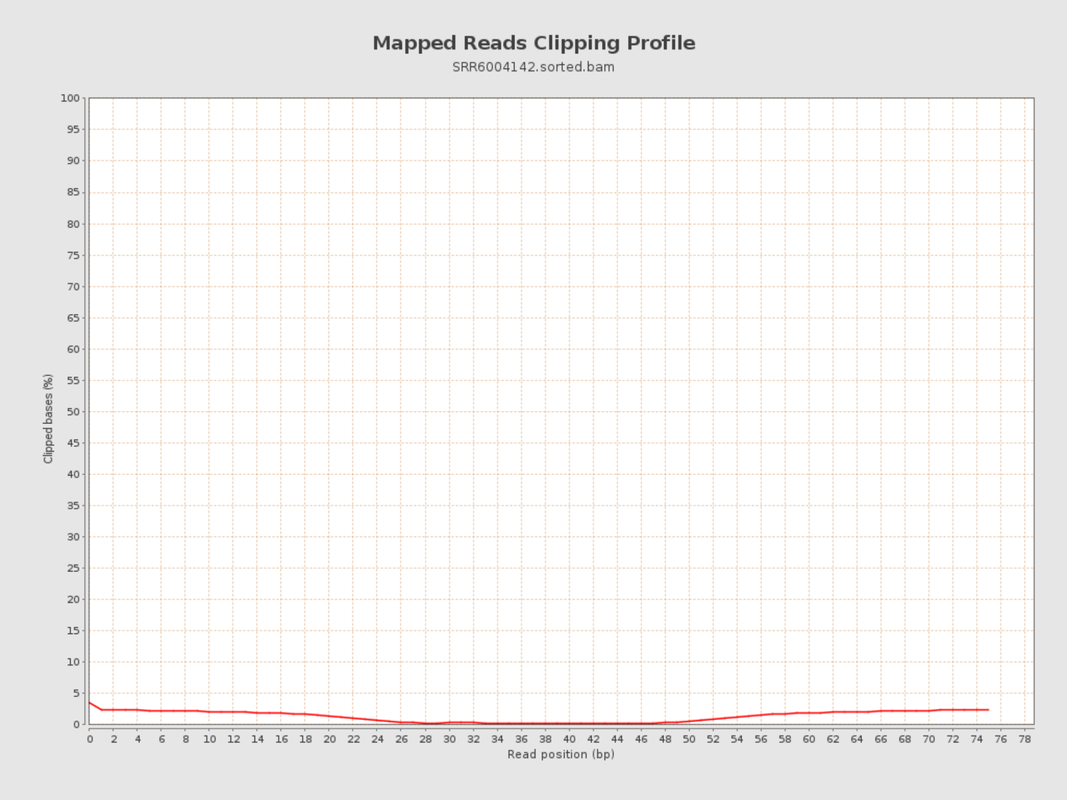
8. Results : Mapped Reads Nucleotide Content



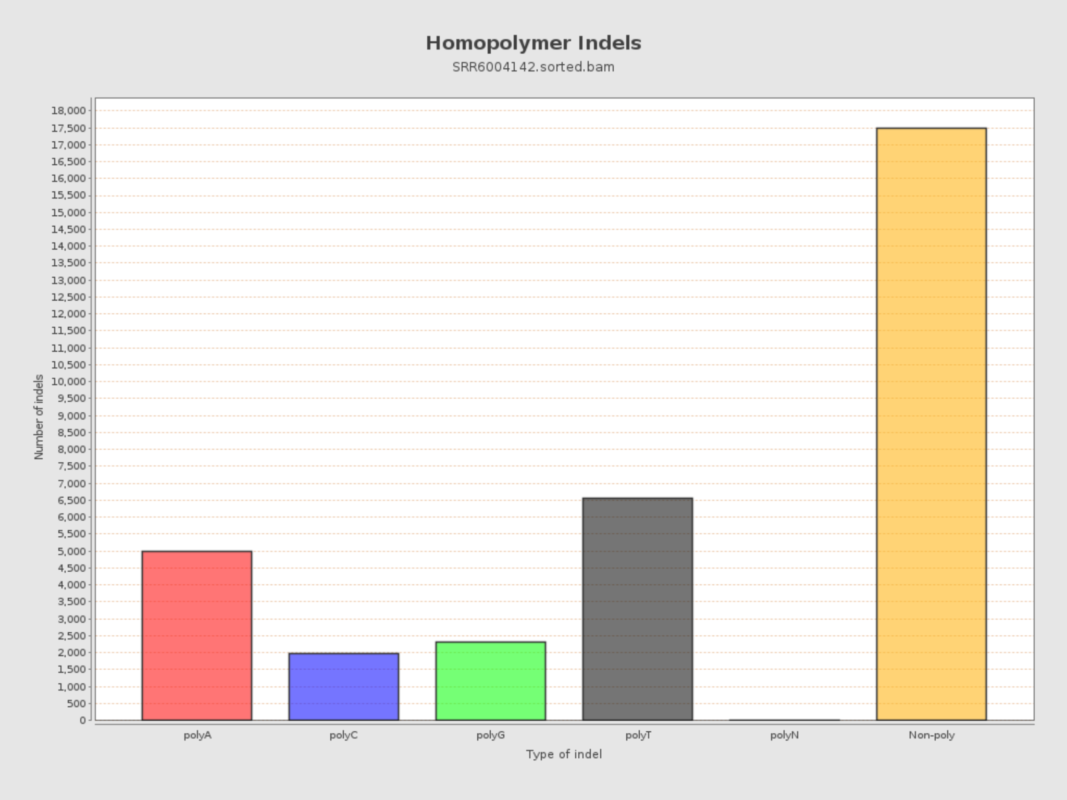
9. Results : Mapped Reads GC-content Distribution



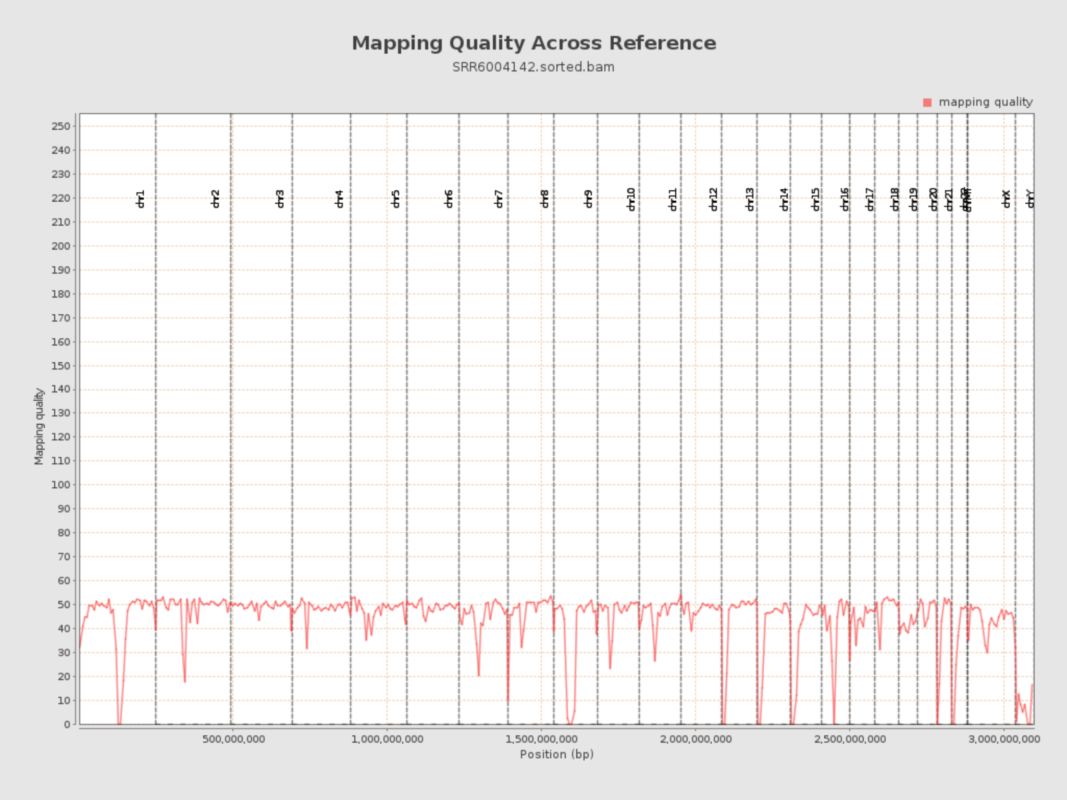
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram