Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:50:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004034.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_SRR6004034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004034.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:50:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,483,115
Mapped reads	2,273,318 / 91.55%
Unmapped reads	209,797 / 8.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,245 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	68,466 / 2.76%
Duplication rate	1.92%
Clipped reads	1,138,452 / 45.85%

2.2. ACGT Content

Number/percentage of A's	40,328,276 / 27.1%
Number/percentage of C's	29,046,419 / 19.52%
Number/percentage of T's	44,389,057 / 29.83%
Number/percentage of G's	35,042,030 / 23.55%
Number/percentage of N's	19,584 / 0.01%
GC Percentage	43.06%

2.3. Coverage

Mean	0.0481

Standard Deviation	0.4497

2.4. Mapping Quality

Mean Mapping Quality	42.21

2.5. Mismatches and indels

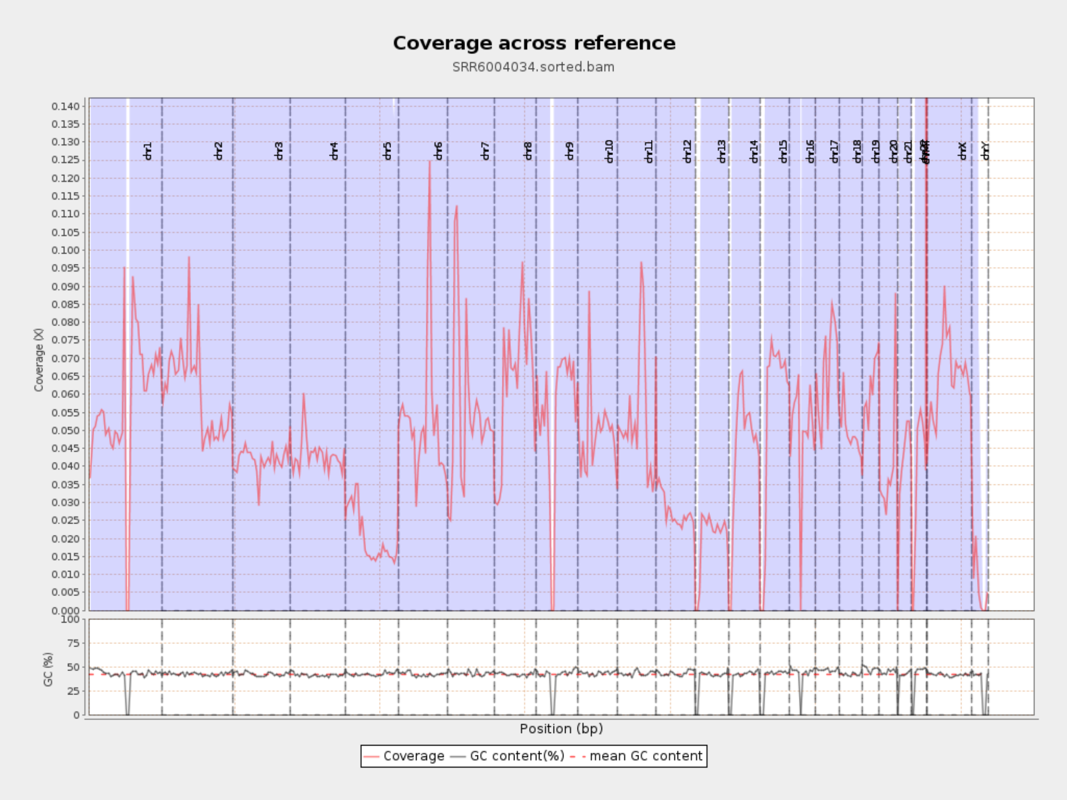
General error rate	0.84%
Mismatches	1,224,537
Insertions	12,005
Mapped reads with at least one insertion	0.52%
Deletions	39,912
Mapped reads with at least one deletion	1.73%
Homopolymer indels	44.66%

2.6. Chromosome stats

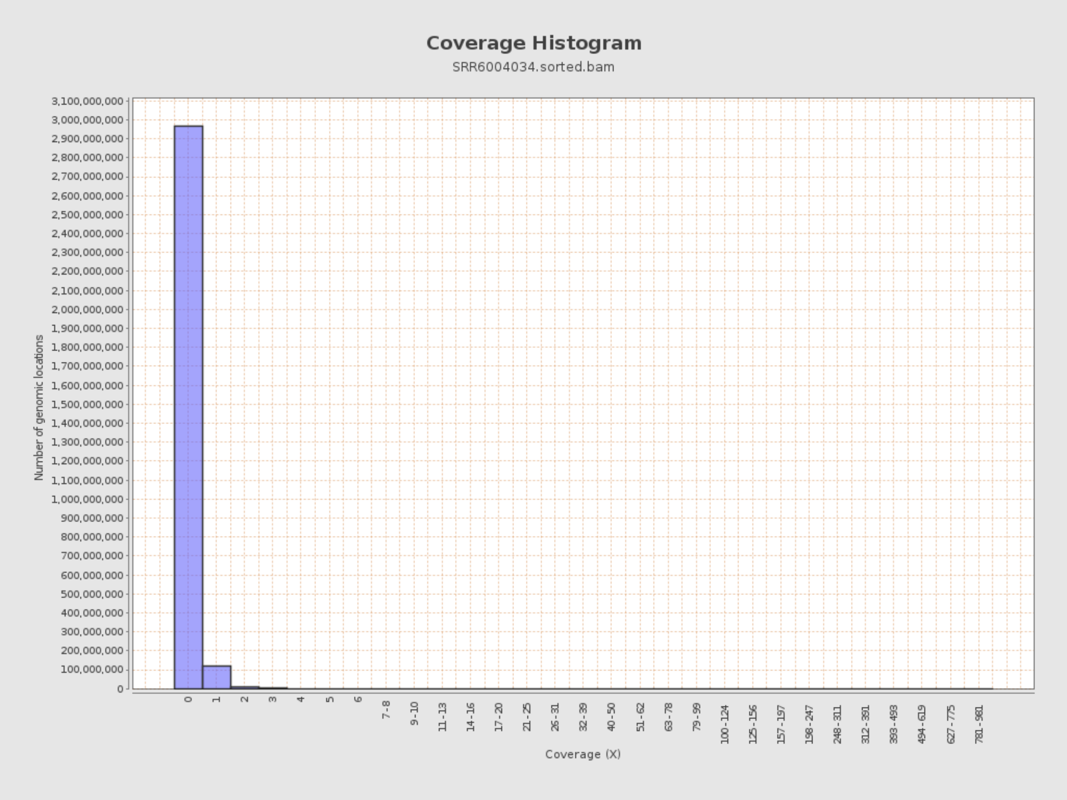
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14203360	0.057	0.8872
chr2	243199373	14812418	0.0609	0.5618
chr3	198022430	8269492	0.0418	0.2319
chr4	191154276	8232129	0.0431	0.2507
chr5	180915260	3672018	0.0203	0.1669
chr6	171115067	9142838	0.0534	0.2873
chr7	159138663	9063356	0.057	0.6279

chr8	146364022	9253974	0.0632	0.3652
chr9	141213431	7631327	0.054	0.4528
chr10	135534747	6670301	0.0492	0.4516
chr11	135006516	7253773	0.0537	0.3894
chr12	133851895	3667750	0.0274	0.1977
chr13	115169878	2285939	0.0198	0.1535
chr14	107349540	4804310	0.0448	0.3047
chr15	102531392	5638168	0.055	0.2644
chr16	90354753	4446777	0.0492	0.3166
chr17	81195210	5446060	0.0671	0.3182
chr18	78077248	3892789	0.0499	0.8793
chr19	59128983	3600462	0.0609	0.6
chr20	63025520	2617346	0.0415	0.2355
chr21	48129895	1925718	0.04	0.2658
chr22	51304566	1826619	0.0356	0.2061
chrMT	16571	16855	1.0171	1.2456
chrX	155270560	10087547	0.065	0.3302
chrY	59373566	430209	0.0072	0.1531

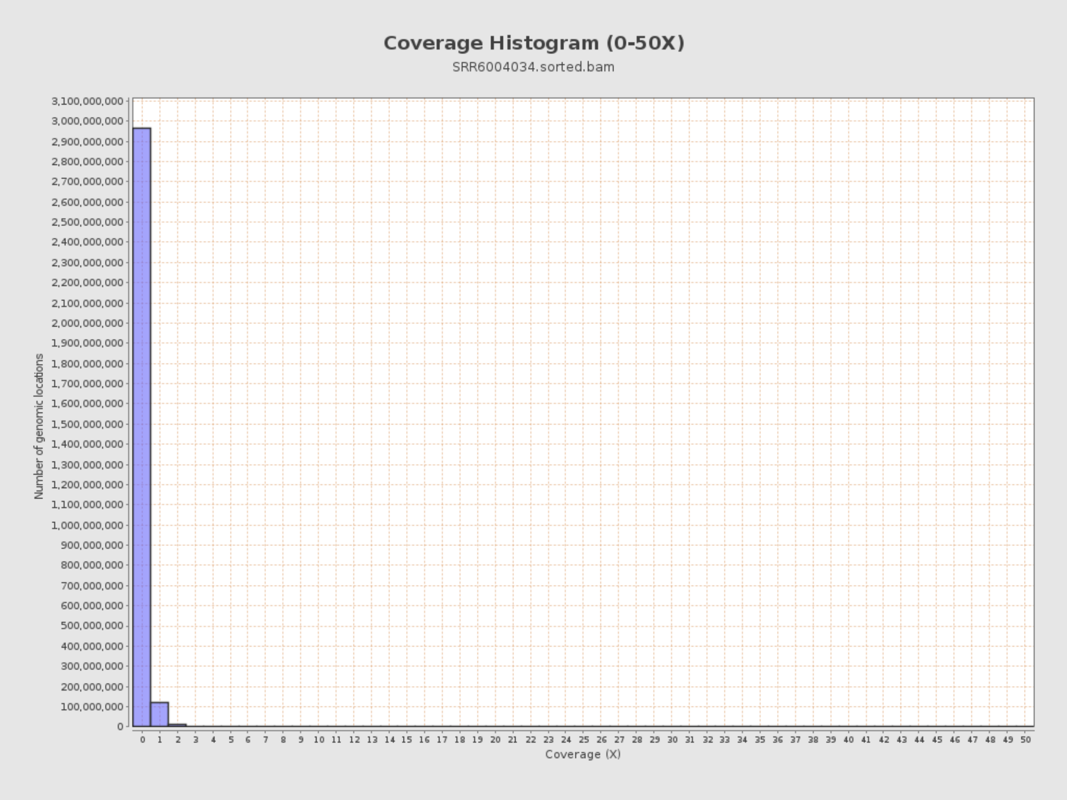
3. Results : Coverage across reference



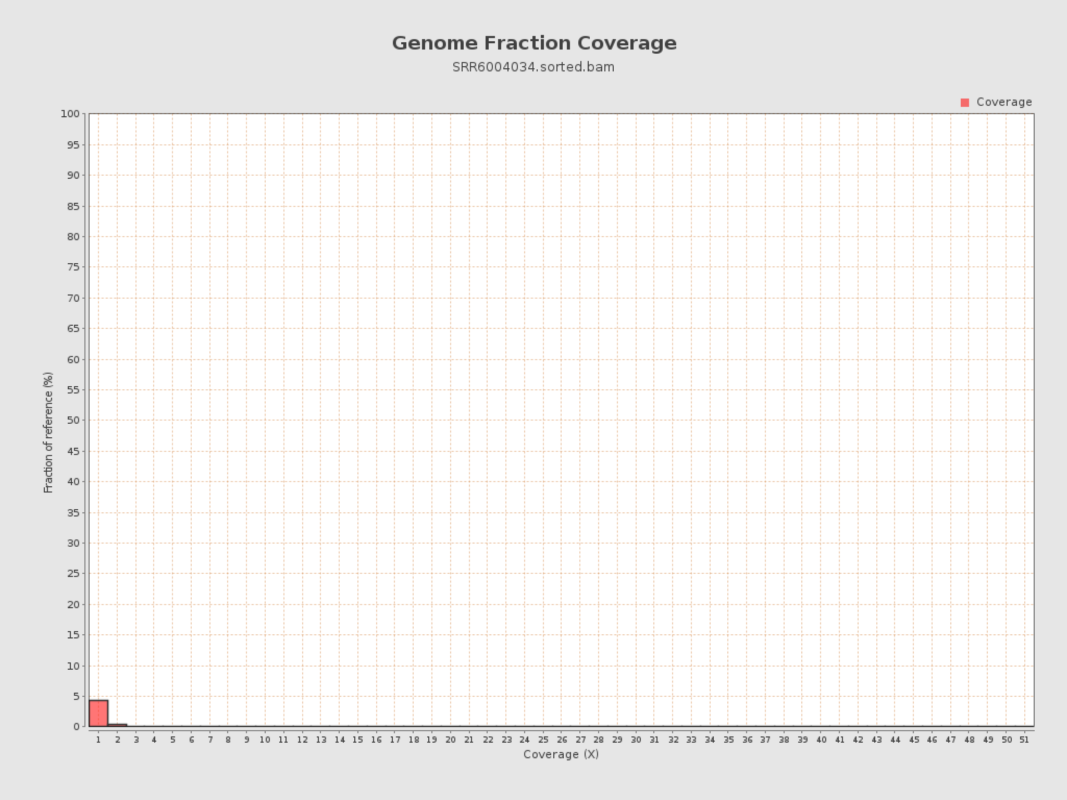
4. Results : Coverage Histogram



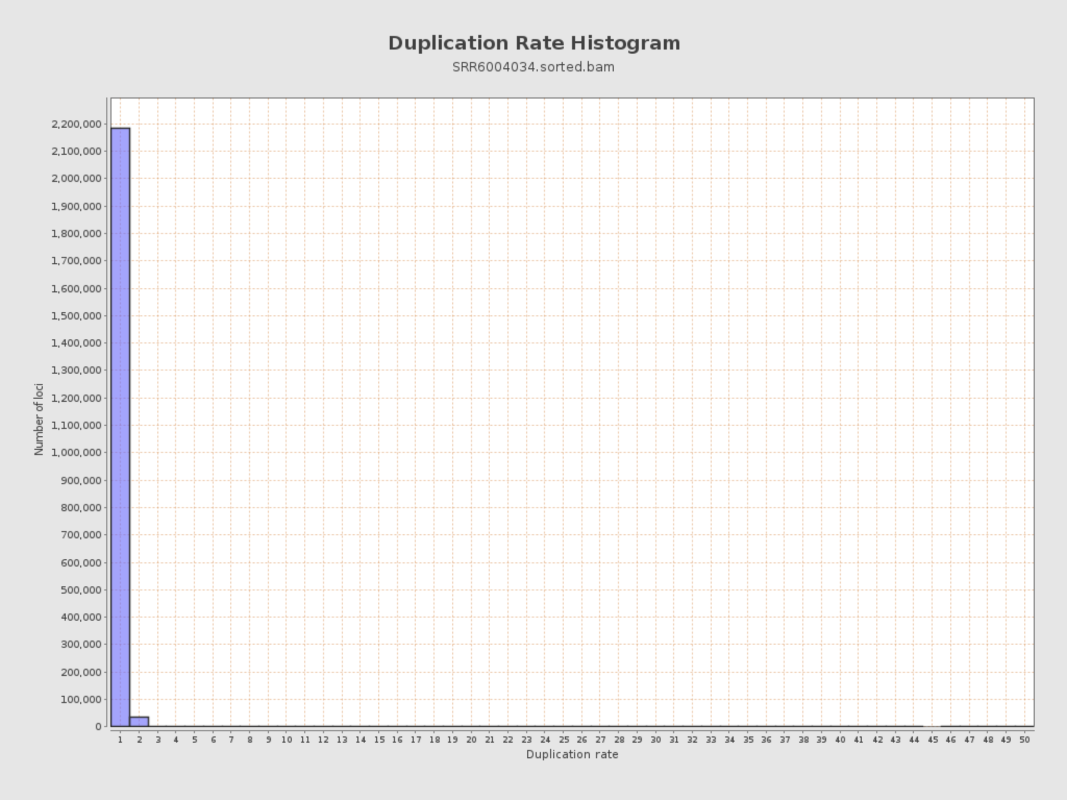
5. Results : Coverage Histogram (0-50X)



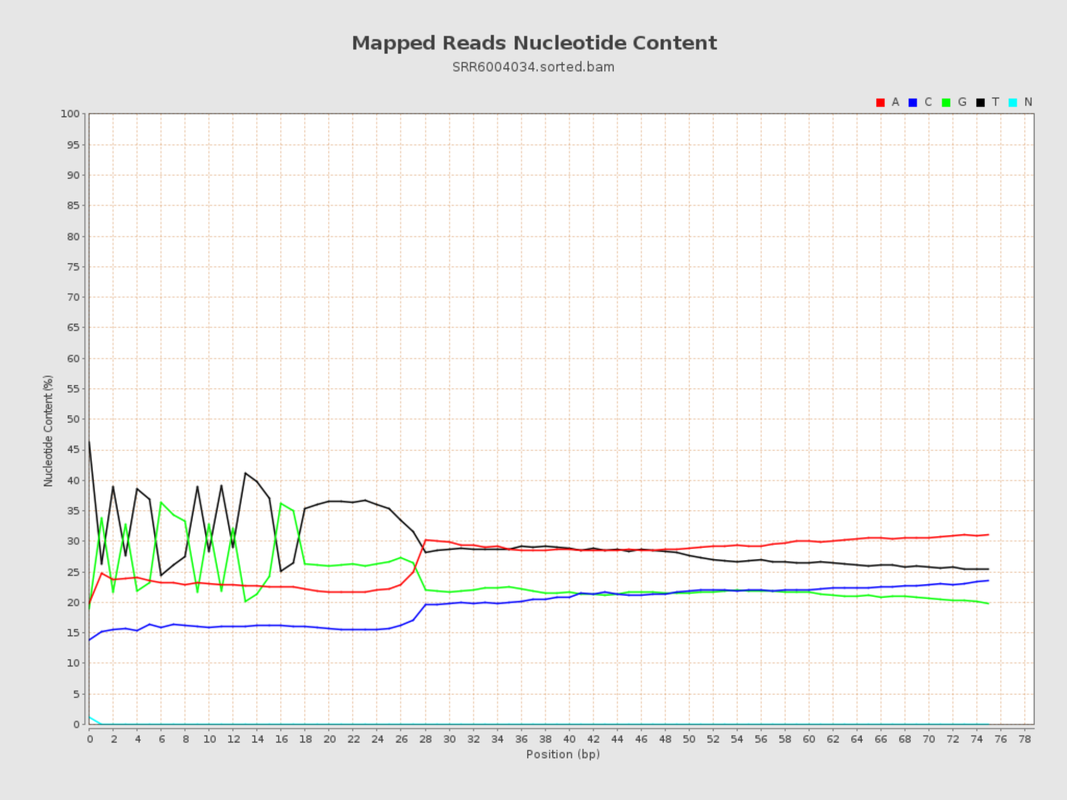
6. Results : Genome Fraction Coverage



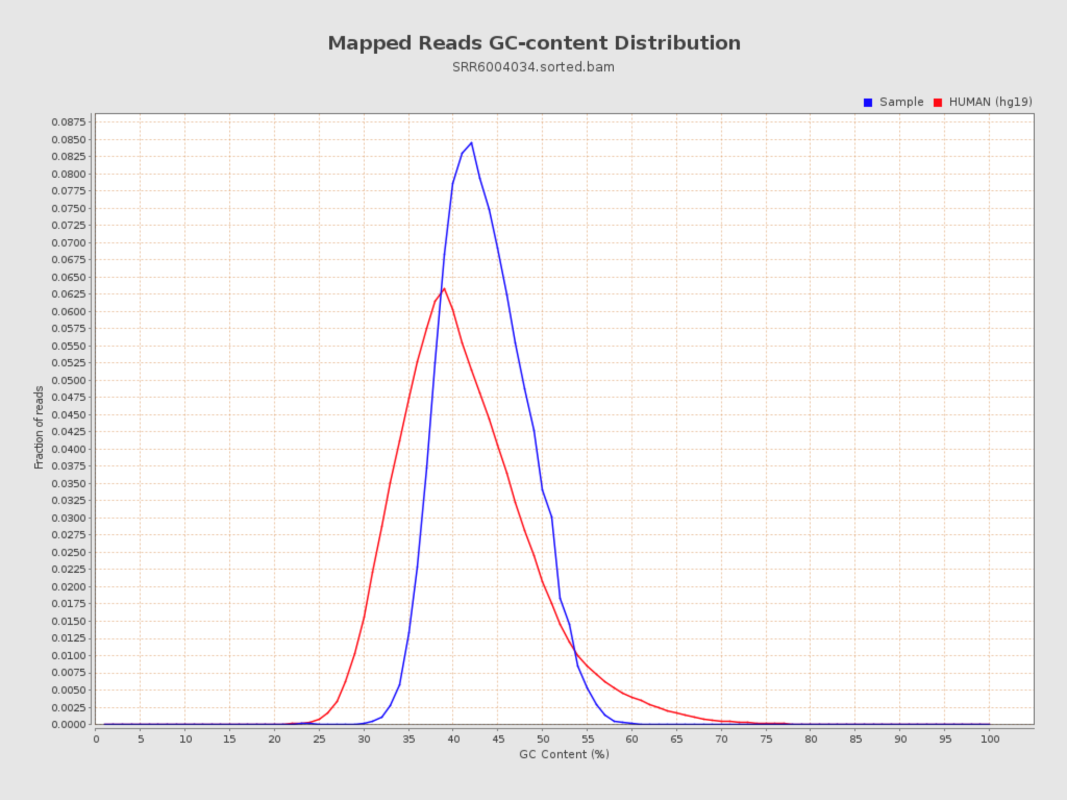
7. Results : Duplication Rate Histogram



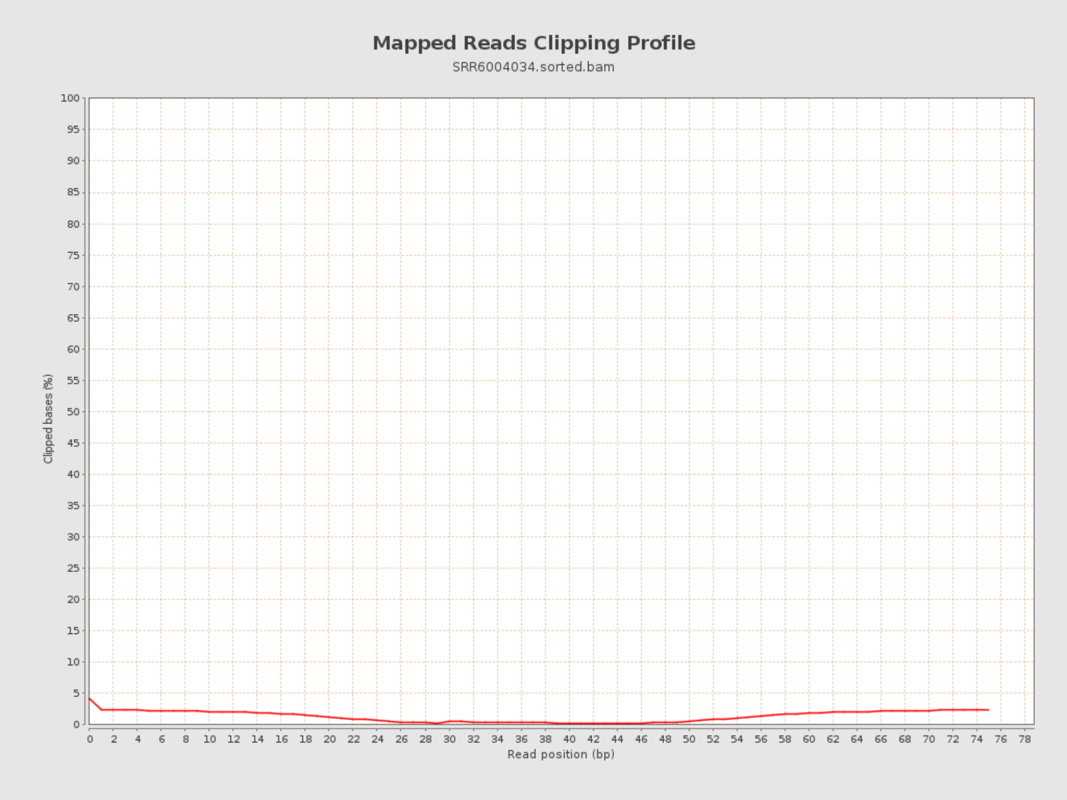
8. Results : Mapped Reads Nucleotide Content



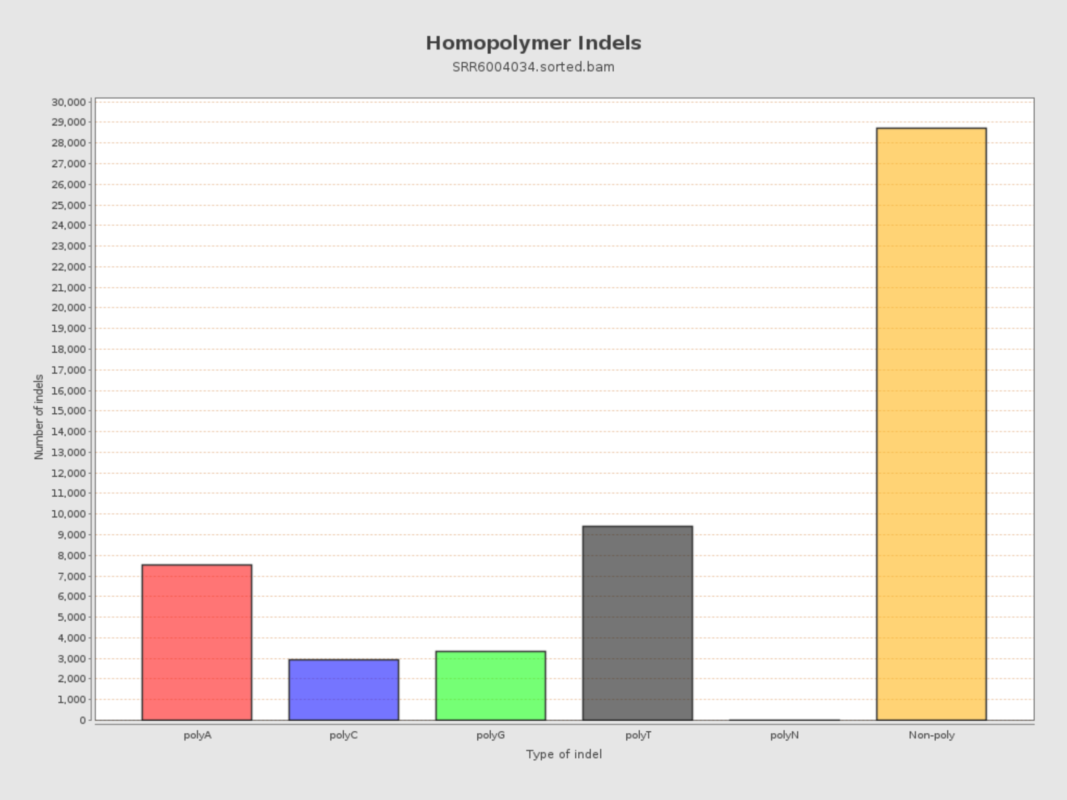
9. Results : Mapped Reads GC-content Distribution



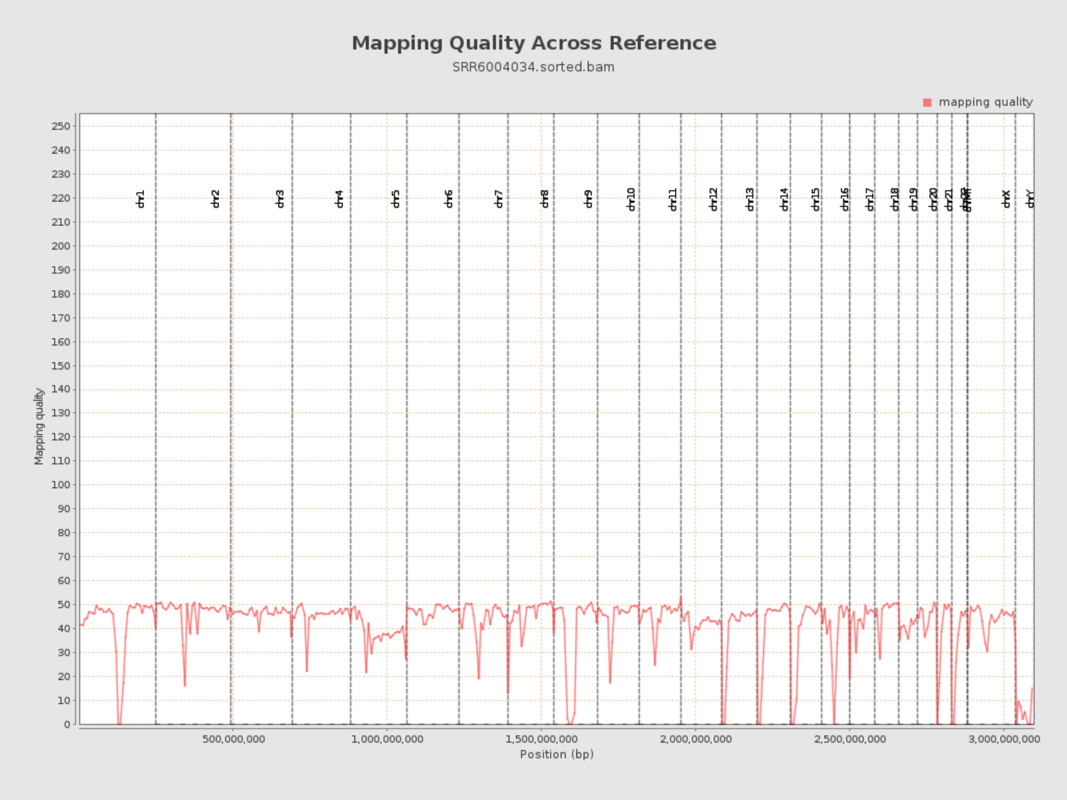
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram