Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:33:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084784.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_SRR3084784 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084784.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:33:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084784.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,617,170
Mapped reads	1,460,869 / 90.33%
Unmapped reads	156,301 / 9.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,117 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	53,831 / 3.33%
Duplication rate	2.88%
Clipped reads	616,611 / 38.13%

2.2. ACGT Content

Number/percentage of A's	27,147,555 / 27.64%
Number/percentage of C's	18,173,694 / 18.5%
Number/percentage of T's	31,151,581 / 31.72%
Number/percentage of G's	21,700,182 / 22.1%
Number/percentage of N's	38,160 / 0.04%
GC Percentage	40.6%

2.3. Coverage

Mean	0.0317

Standard Deviation	0.2895

2.4. Mapping Quality

Mean Mapping Quality	46.82

2.5. Mismatches and indels

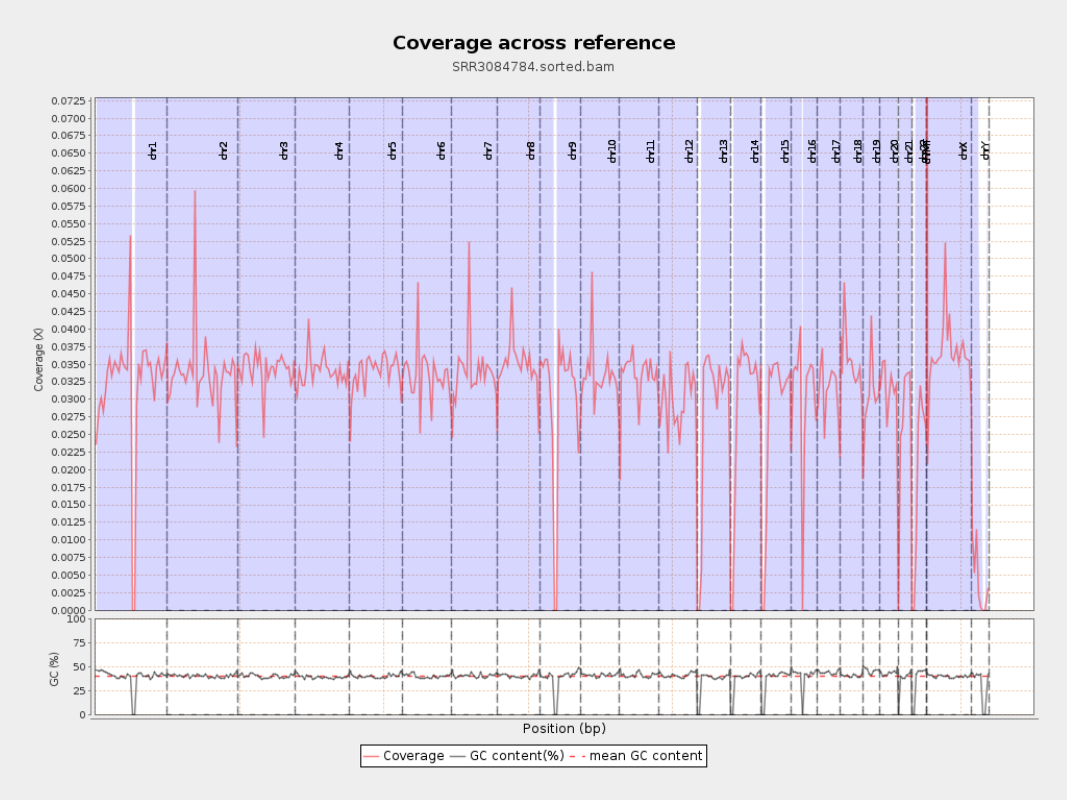
General error rate	0.9%
Mismatches	867,945
Insertions	7,594
Mapped reads with at least one insertion	0.52%
Deletions	26,411
Mapped reads with at least one deletion	1.79%
Homopolymer indels	46.87%

2.6. Chromosome stats

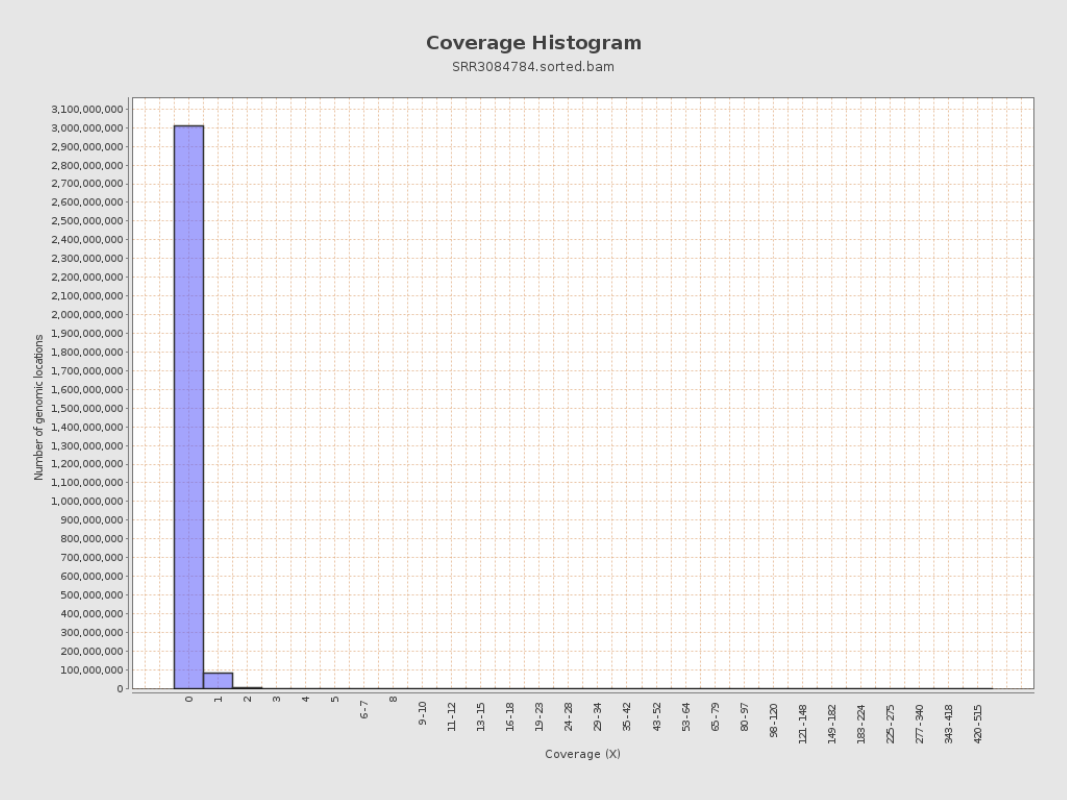
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7964926	0.032	0.4777
chr2	243199373	8189958	0.0337	0.3604
chr3	198022430	6797356	0.0343	0.2006
chr4	191154276	6518299	0.0341	0.2081
chr5	180915260	6175651	0.0341	0.2011
chr6	171115067	5723315	0.0334	0.2434
chr7	159138663	5415848	0.034	0.3454

chr8	146364022	5144641	0.0351	0.3254
chr9	141213431	4200002	0.0297	0.2785
chr10	135534747	4524265	0.0334	0.2705
chr11	135006516	4527971	0.0335	0.2649
chr12	133851895	3997902	0.0299	0.1911
chr13	115169878	3196373	0.0278	0.1811
chr14	107349540	3094158	0.0288	0.1965
chr15	102531392	2767506	0.027	0.1842
chr16	90354753	2688833	0.0298	0.2069
chr17	81195210	2534842	0.0312	0.2217
chr18	78077248	2759358	0.0353	0.5765
chr19	59128983	1832392	0.031	0.3618
chr20	63025520	1972861	0.0313	0.2045
chr21	48129895	1295598	0.0269	0.1858
chr22	51304566	1003232	0.0196	0.1499
chrMT	16571	6098	0.368	0.6315
chrX	155270560	5693262	0.0367	0.2352
chrY	59373566	229601	0.0039	0.0922

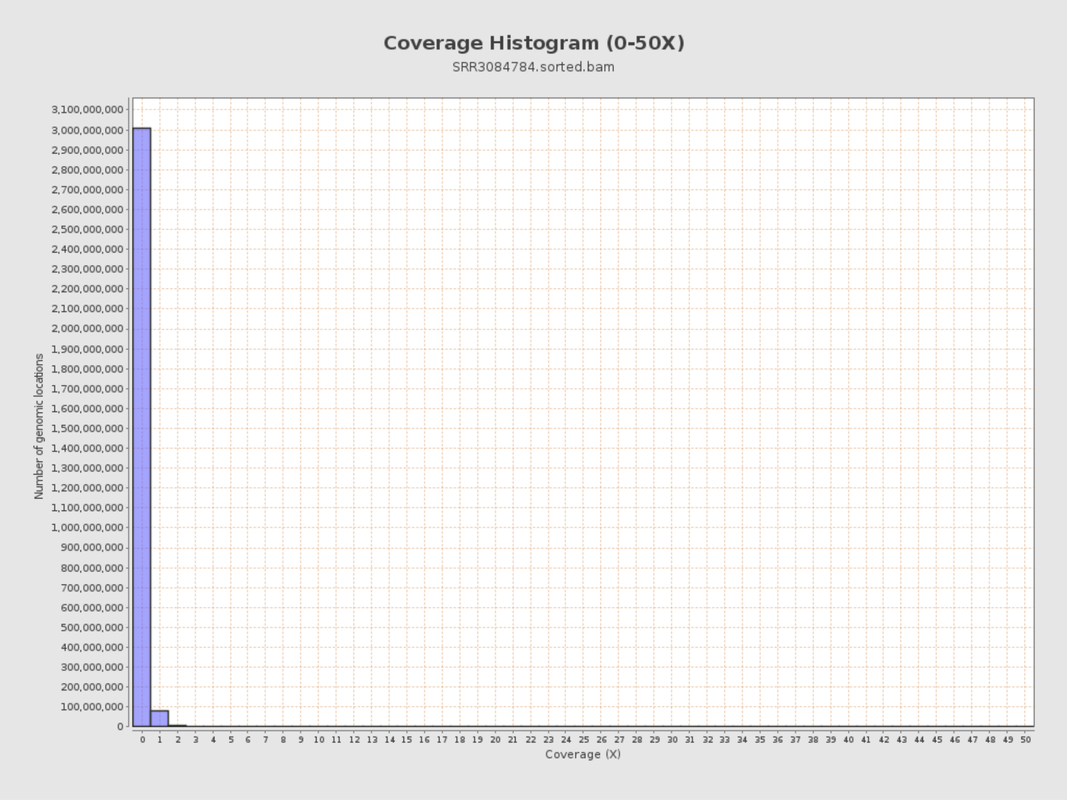
3. Results : Coverage across reference



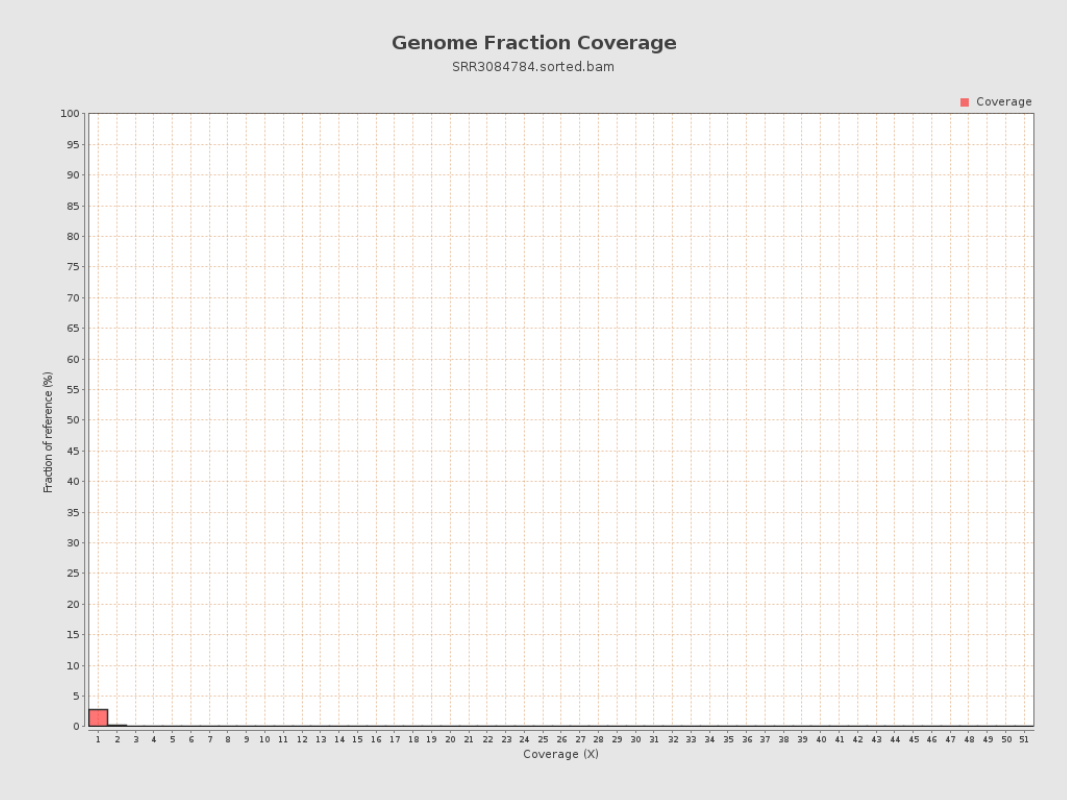
4. Results : Coverage Histogram



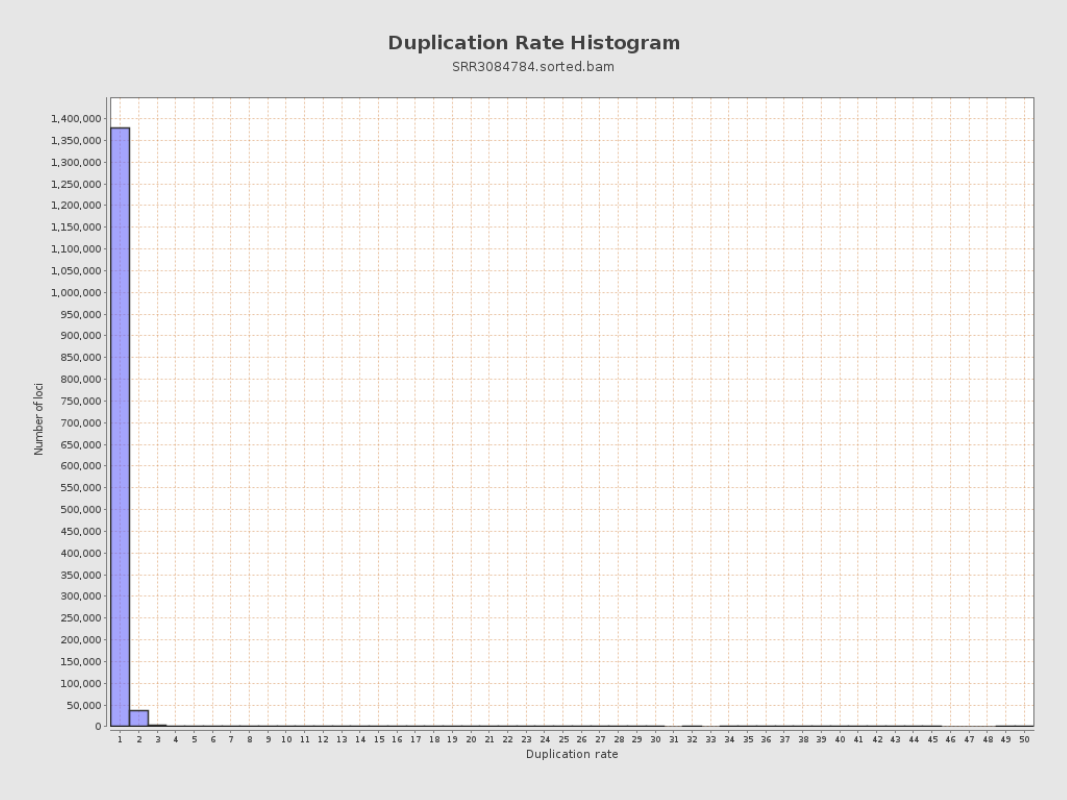
5. Results : Coverage Histogram (0-50X)



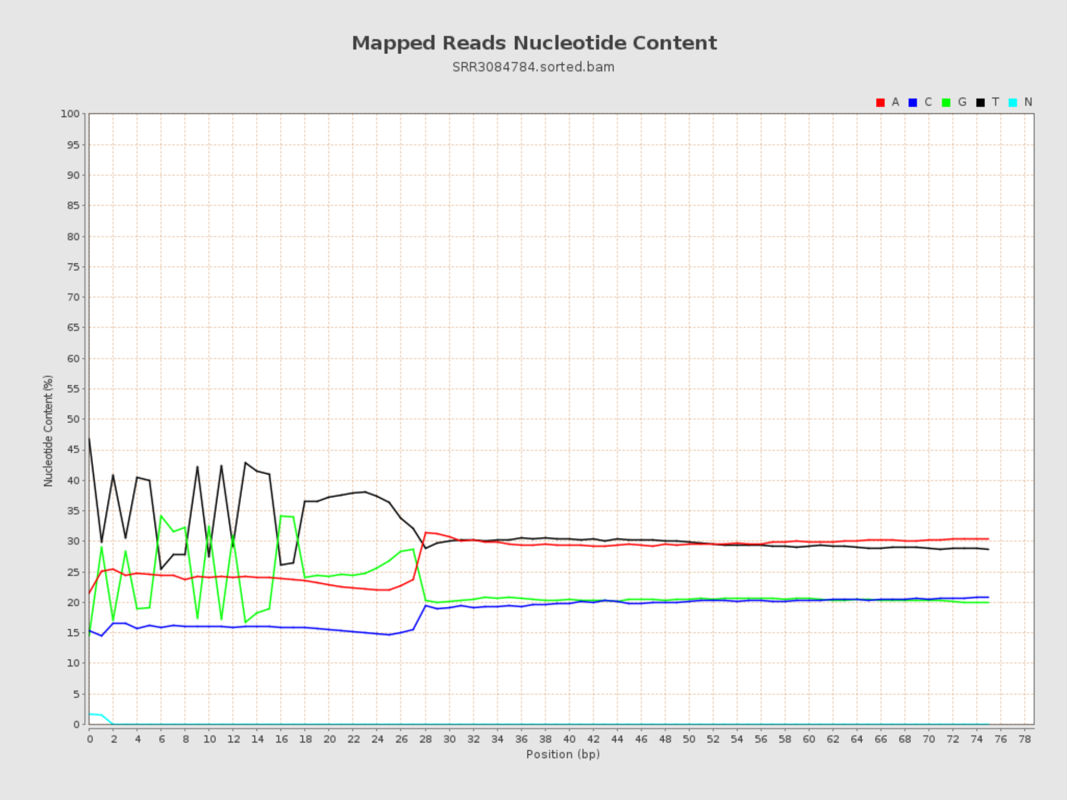
6. Results : Genome Fraction Coverage



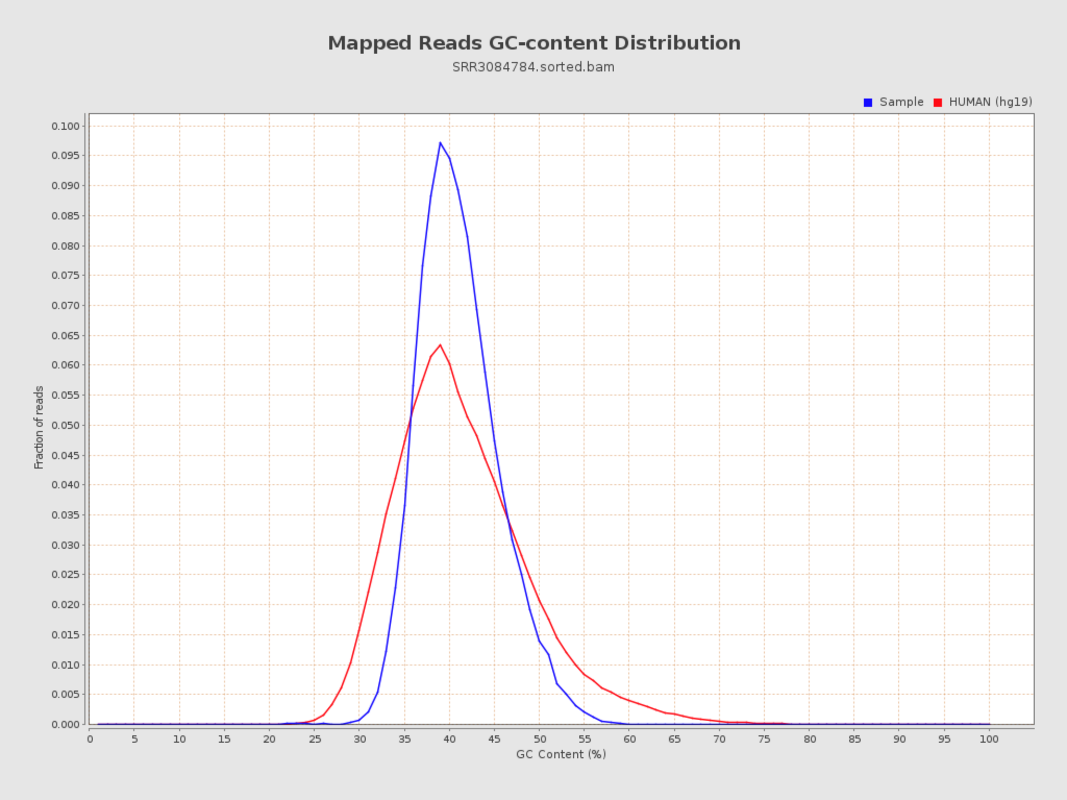
7. Results : Duplication Rate Histogram



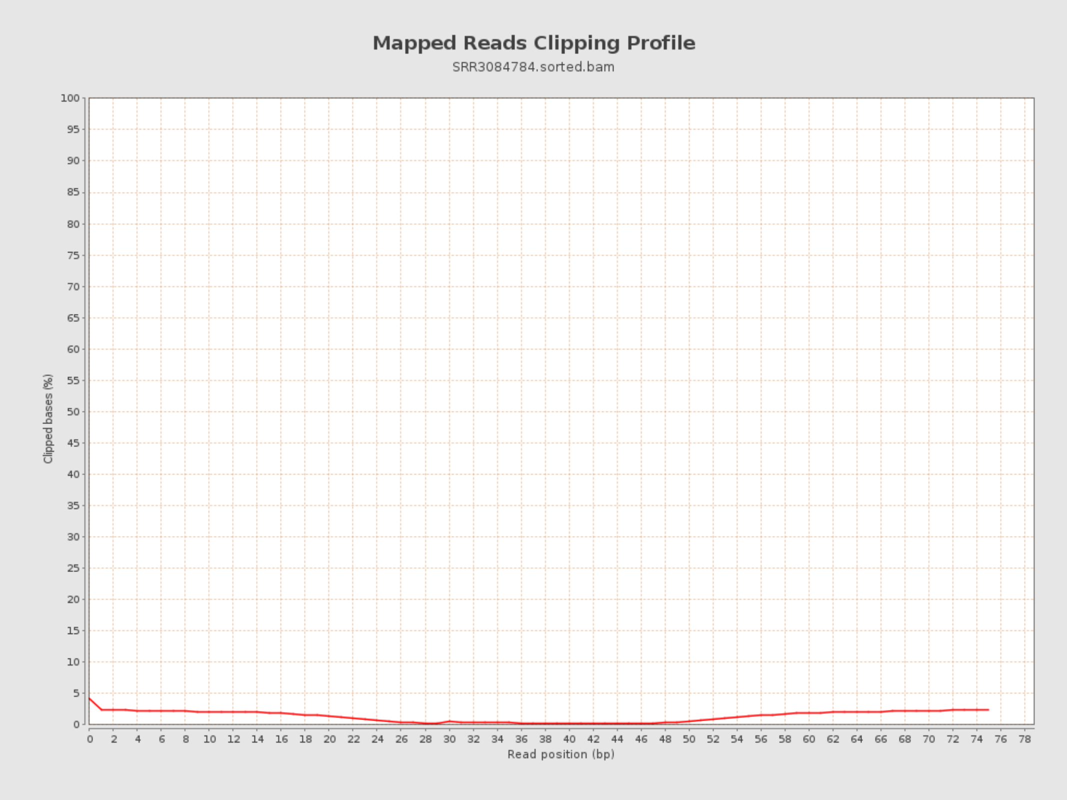
8. Results : Mapped Reads Nucleotide Content



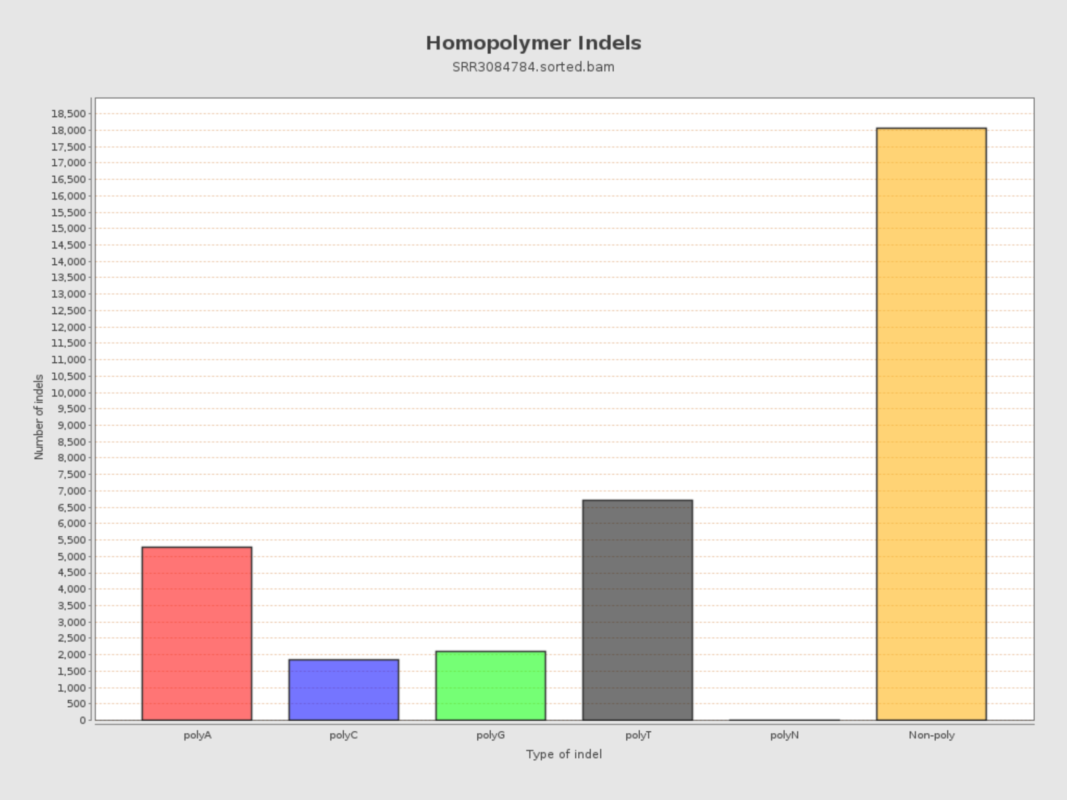
9. Results : Mapped Reads GC-content Distribution



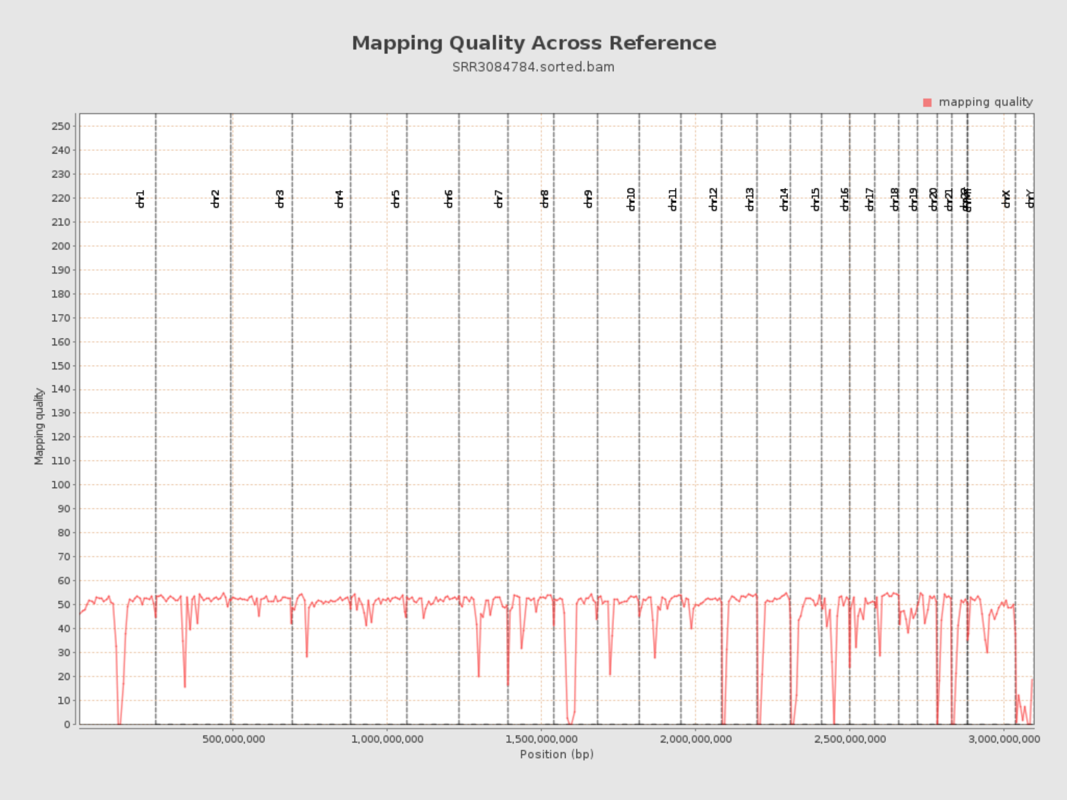
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram