Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 20:05:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514740.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_SRR5514740 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514740.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 20:05:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514740.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,206,159
Mapped reads	37,340,282 / 97.73%
Unmapped reads	865,877 / 2.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,257,316 / 3.29%
Read min/max/mean length	30 / 100 / 98.55
Duplicated reads (estimated)	22,630,071 / 59.23%
Duplication rate	34.99%
Clipped reads	5,979,282 / 15.65%

2.2. ACGT Content

Number/percentage of A's	935,856,985 / 26.19%
Number/percentage of C's	844,043,494 / 23.62%
Number/percentage of T's	946,500,793 / 26.49%
Number/percentage of G's	846,780,314 / 23.7%
Number/percentage of N's	152,573 / 0%
GC Percentage	47.32%

2.3. Coverage

Mean	1.1551

Standard Deviation	50.1186

2.4. Mapping Quality

Mean Mapping Quality	42.71

2.5. Mismatches and indels

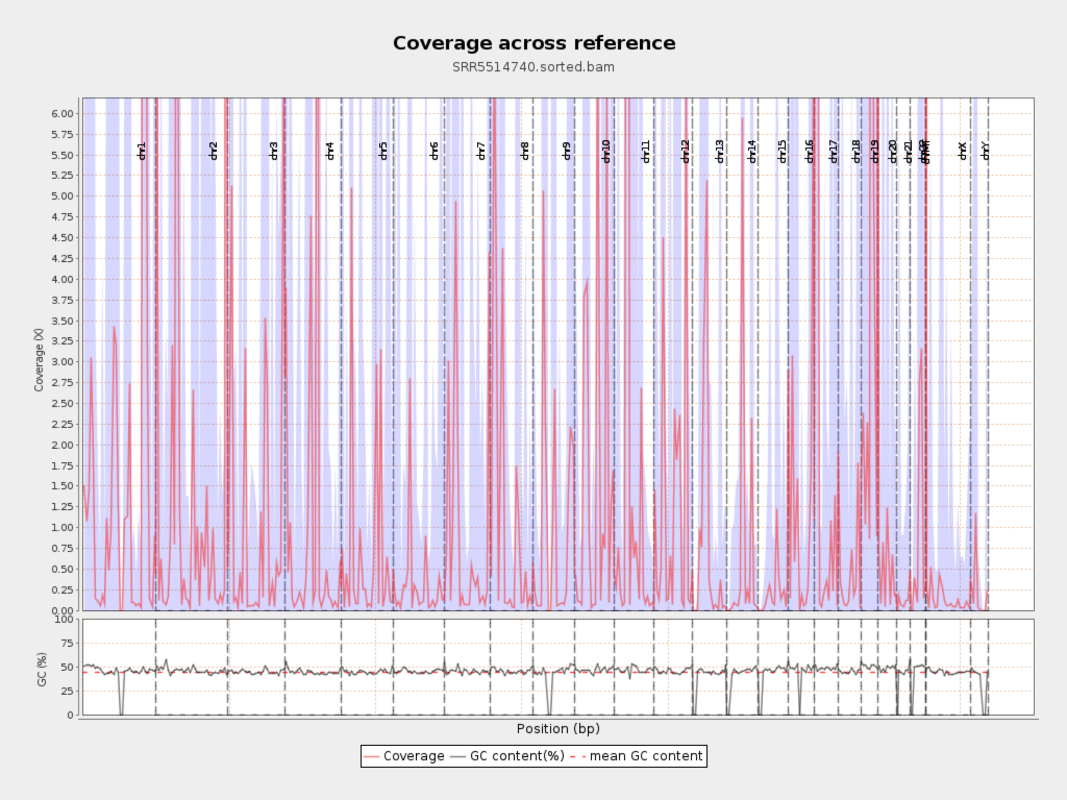
General error rate	0.89%
Mismatches	29,471,571
Insertions	1,258,075
Mapped reads with at least one insertion	3.26%
Deletions	1,083,999
Mapped reads with at least one deletion	2.77%
Homopolymer indels	40.25%

2.6. Chromosome stats

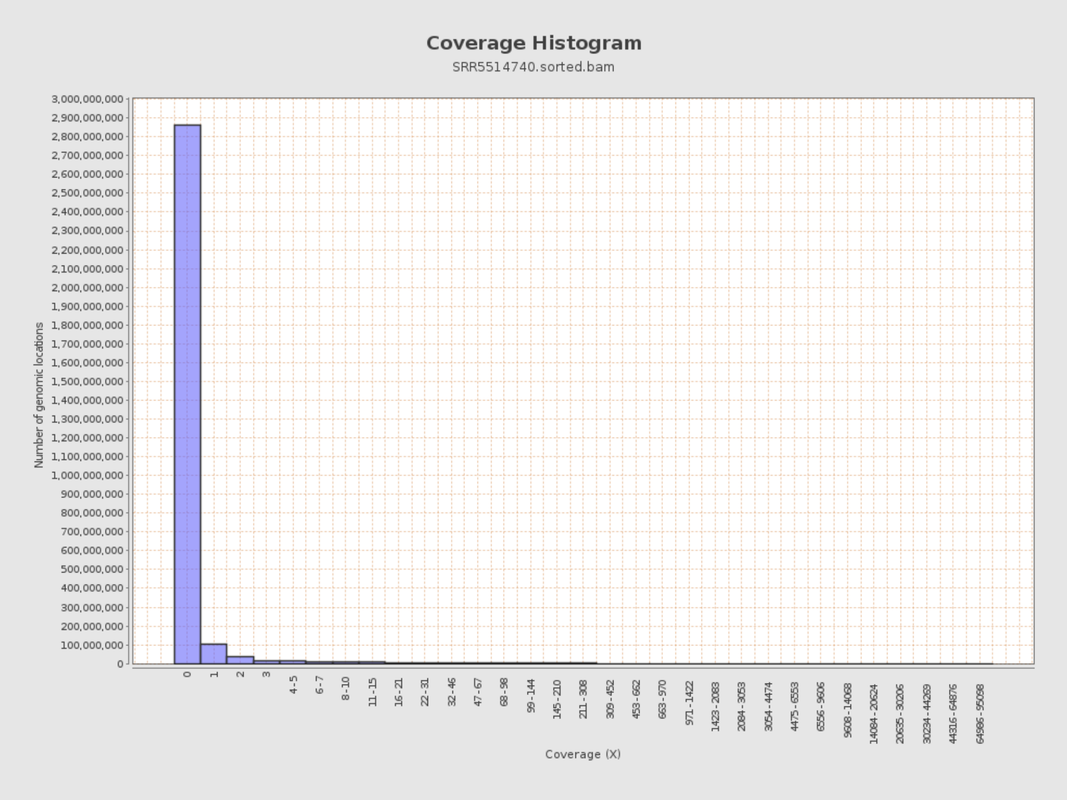
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	458685689	1.8403	17.7453
chr2	243199373	399932116	1.6445	150.1357
chr3	198022430	216472397	1.0932	15.1193
chr4	191154276	204257375	1.0685	14.2599
chr5	180915260	127043906	0.7022	13.4187
chr6	171115067	54124801	0.3163	6.9944
chr7	159138663	144391867	0.9073	58.7099

chr8	146364022	173697269	1.1867	25.3451
chr9	141213431	136574395	0.9671	23.8972
chr10	135534747	211089405	1.5575	24.9936
chr11	135006516	230997743	1.711	34.8032
chr12	133851895	166921018	1.2471	12.9151
chr13	115169878	87962270	0.7638	9.4867
chr14	107349540	72306265	0.6736	10.5227
chr15	102531392	22662542	0.221	3.0065
chr16	90354753	122652462	1.3575	42.799
chr17	81195210	269212227	3.3156	96.7287
chr18	78077248	36016900	0.4613	9.6
chr19	59128983	314924180	5.3261	45.5007
chr20	63025520	29007168	0.4602	6.221
chr21	48129895	6680096	0.1388	3.3295
chr22	51304566	51527780	1.0044	11.9844
chrMT	16571	5019409	302.9032	123.1292
chrX	155270560	19981151	0.1287	3.1173
chrY	59373566	13665133	0.2302	7.0237

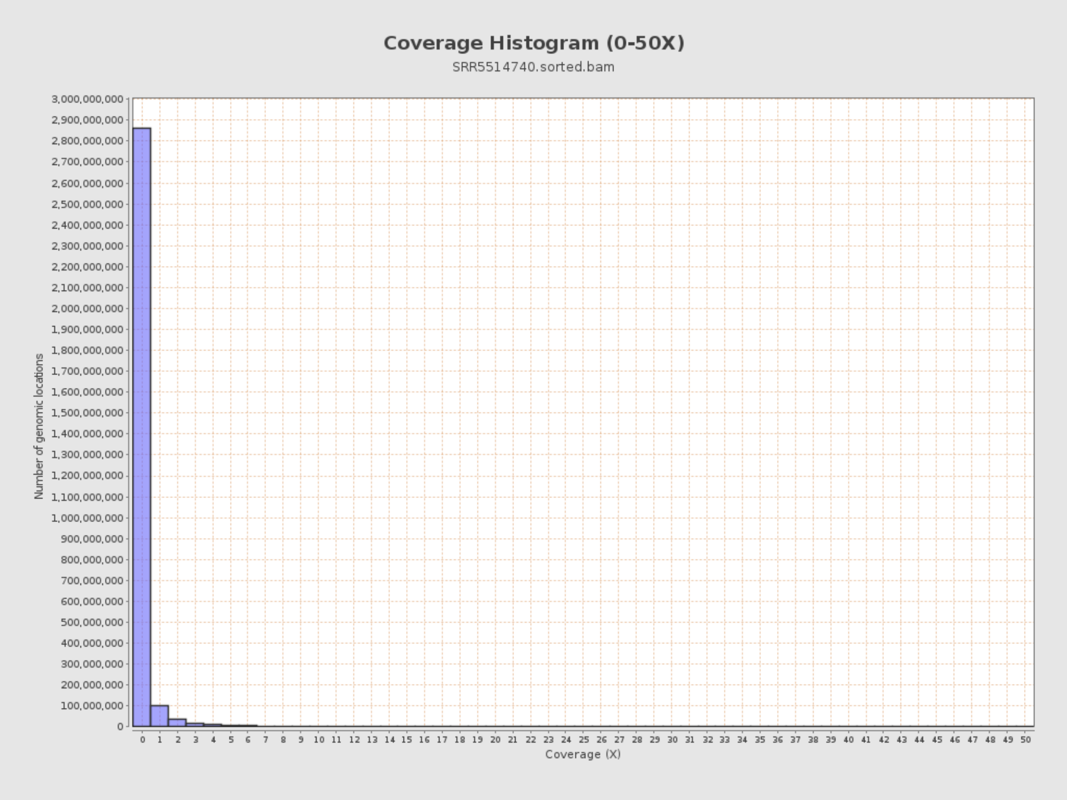
3. Results : Coverage across reference



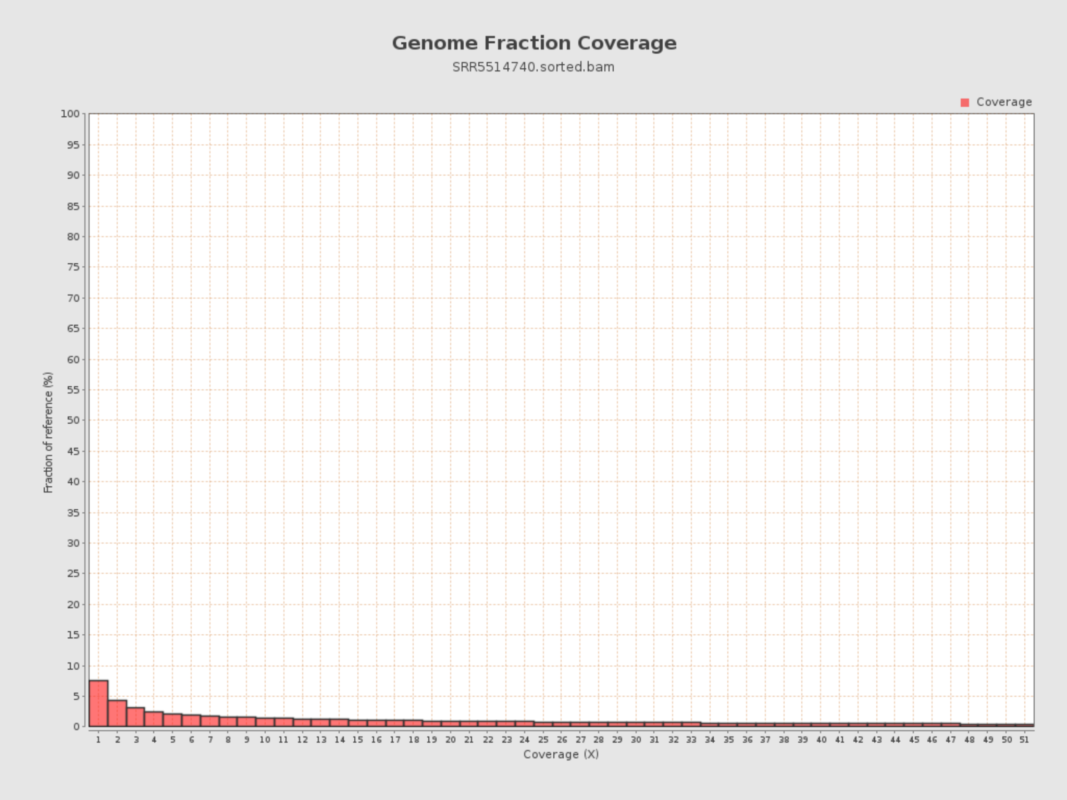
4. Results : Coverage Histogram



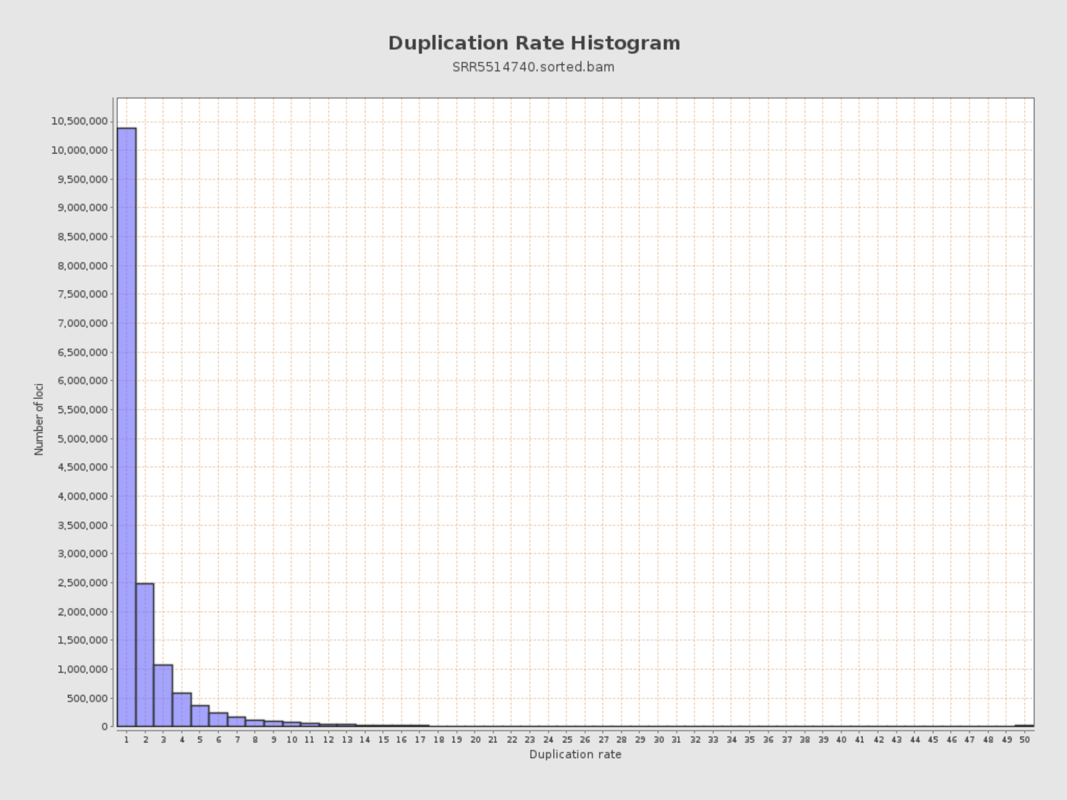
5. Results : Coverage Histogram (0-50X)



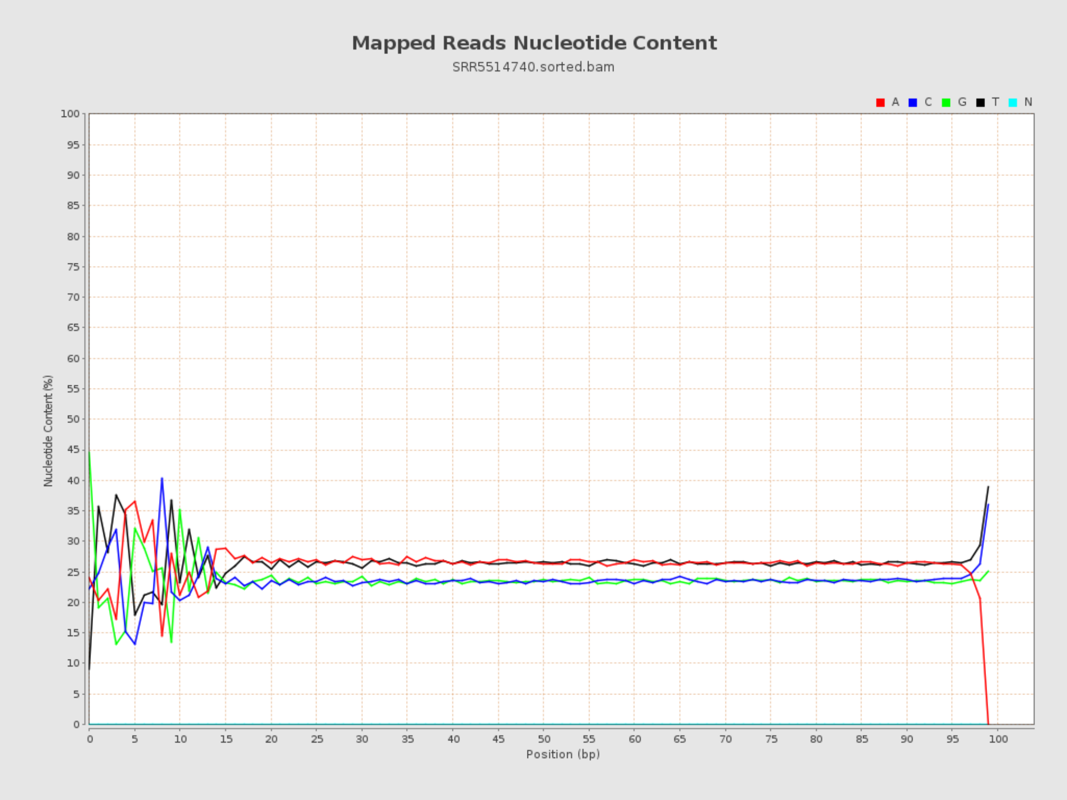
6. Results : Genome Fraction Coverage



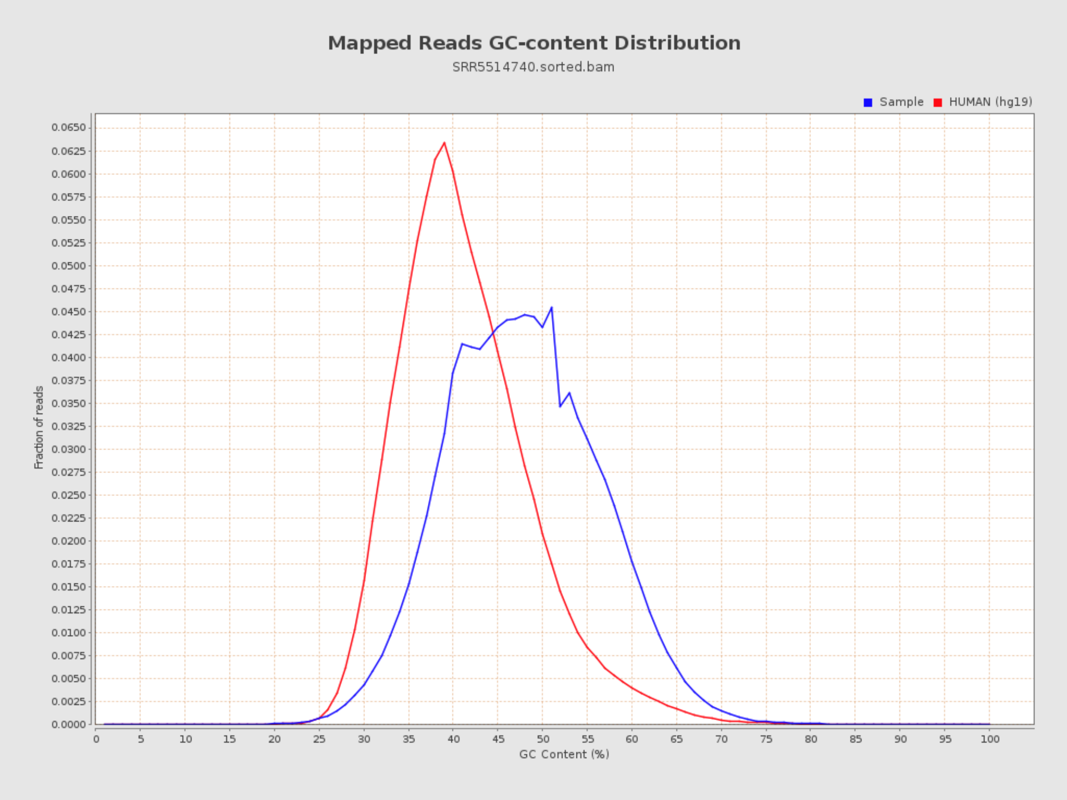
7. Results : Duplication Rate Histogram



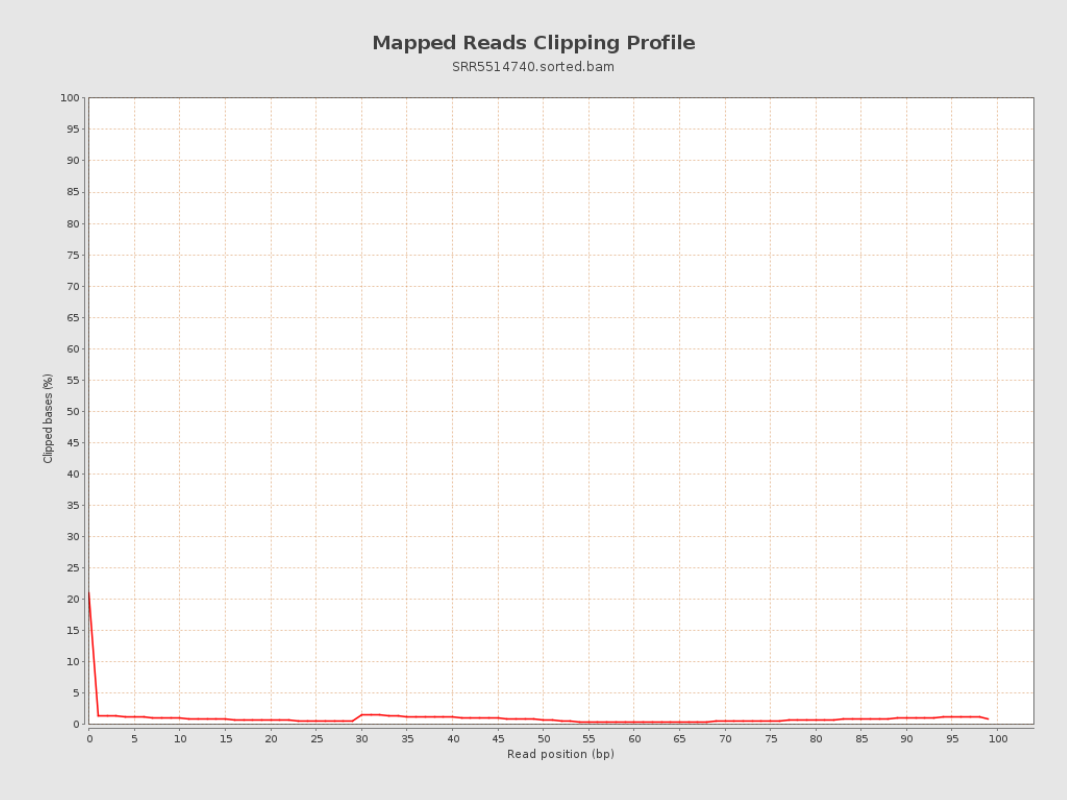
8. Results : Mapped Reads Nucleotide Content



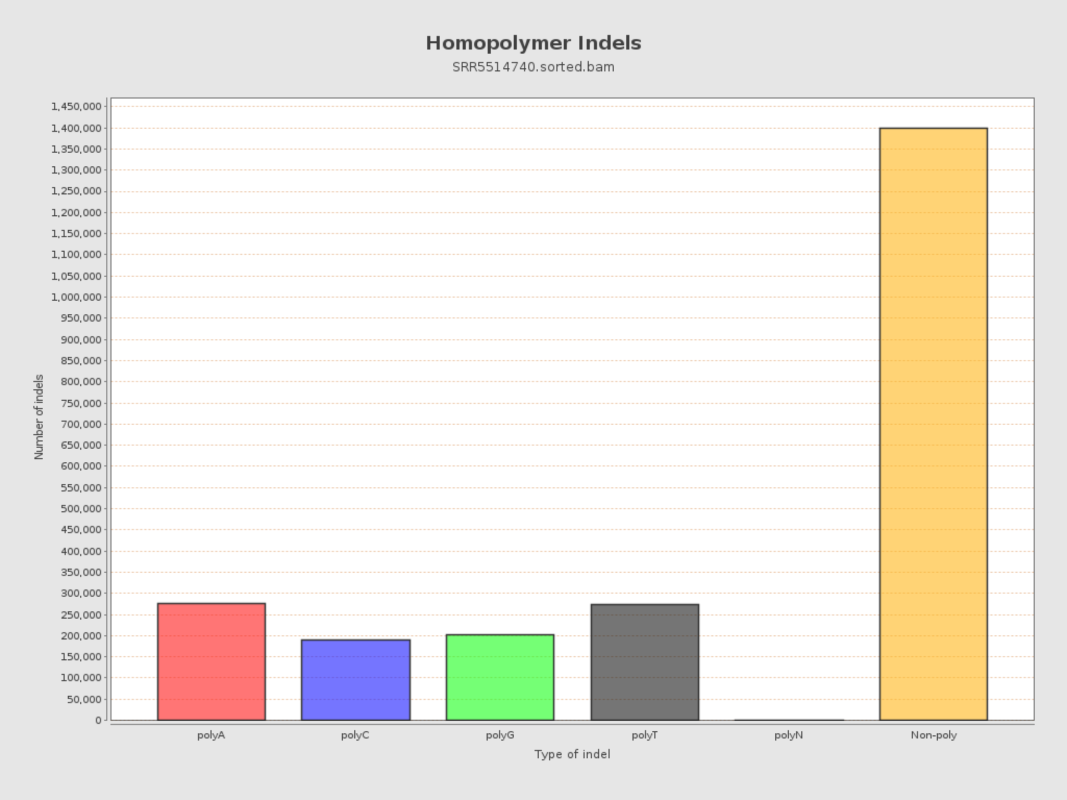
9. Results : Mapped Reads GC-content Distribution



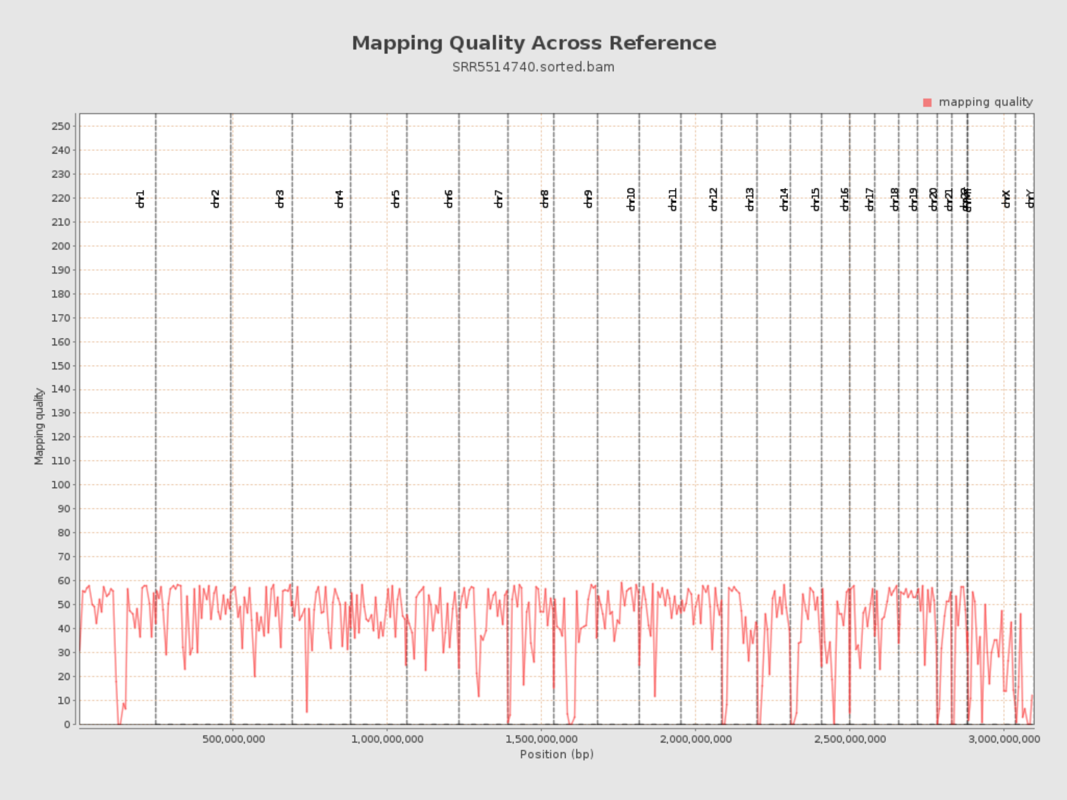
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram