Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:59:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124801.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_SRR3124801 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124801.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:59:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124801.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	202,938
Mapped reads	196,011 / 96.59%
Unmapped reads	6,927 / 3.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,139 / 3.52%
Read min/max/mean length	30 / 151 / 152.61
Duplicated reads (estimated)	66,673 / 32.85%
Duplication rate	1.42%
Clipped reads	152,068 / 74.93%

2.2. ACGT Content

Number/percentage of A's	7,488,349 / 28.85%
Number/percentage of C's	5,150,550 / 19.84%
Number/percentage of T's	7,115,042 / 27.41%
Number/percentage of G's	6,202,959 / 23.9%
Number/percentage of N's	0 / 0%
GC Percentage	43.74%

2.3. Coverage

Mean	0.0084

Standard Deviation	5.8525

2.4. Mapping Quality

Mean Mapping Quality	50.65

2.5. Mismatches and indels

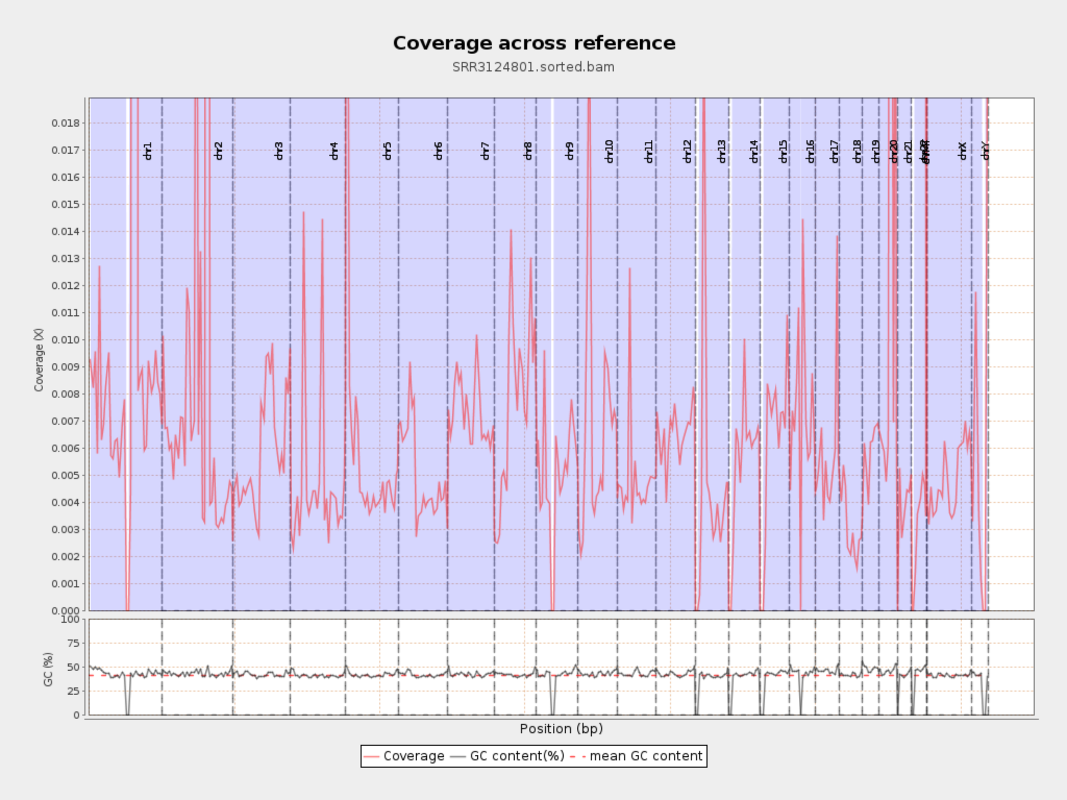
General error rate	1.29%
Mismatches	322,029
Insertions	4,770
Mapped reads with at least one insertion	2.26%
Deletions	8,140
Mapped reads with at least one deletion	3.96%
Homopolymer indels	43.95%

2.6. Chromosome stats

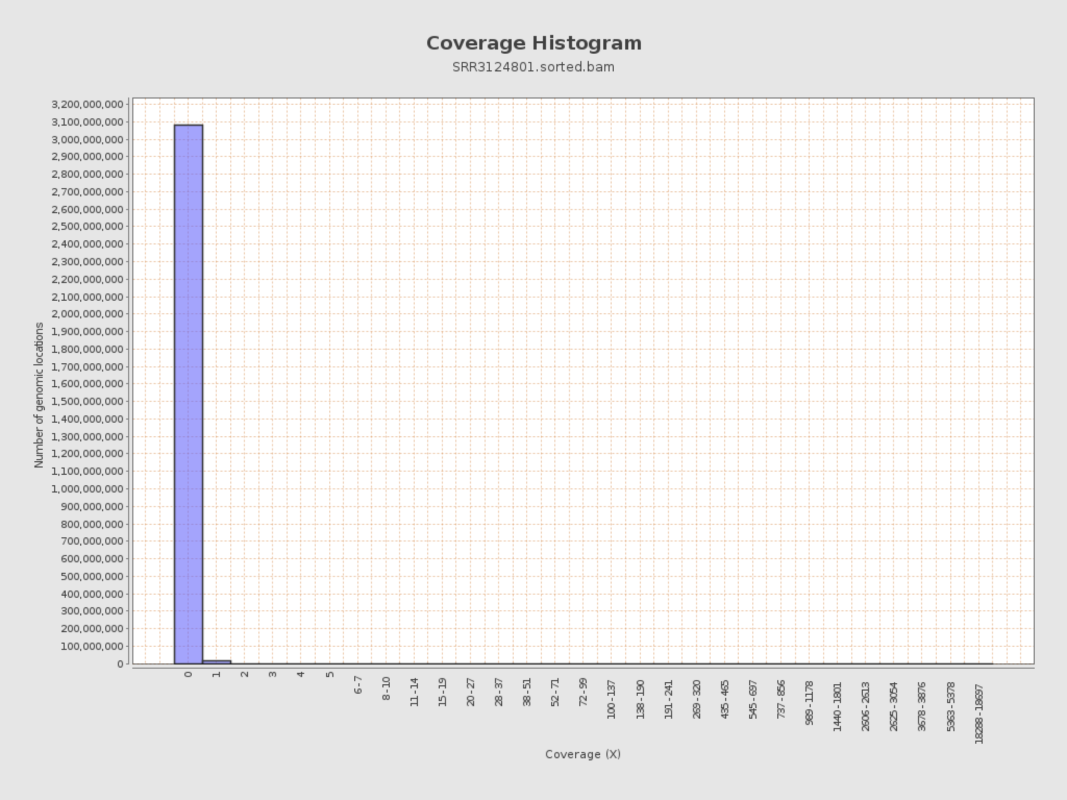
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7837780	0.0314	20.068
chr2	243199373	2716294	0.0112	4.1585
chr3	198022430	1162609	0.0059	0.1084
chr4	191154276	886201	0.0046	0.3674
chr5	180915260	1146132	0.0063	1.5369
chr6	171115067	869582	0.0051	0.0753
chr7	159138663	1173303	0.0074	0.1373

chr8	146364022	1142235	0.0078	0.133
chr9	141213431	713093	0.005	0.2764
chr10	135534747	926704	0.0068	0.254
chr11	135006516	653558	0.0048	0.4561
chr12	133851895	872504	0.0065	0.1017
chr13	115169878	512410	0.0044	1.0524
chr14	107349540	583859	0.0054	0.1704
chr15	102531392	640427	0.0062	0.2411
chr16	90354753	654865	0.0072	0.1662
chr17	81195210	471774	0.0058	0.6671
chr18	78077248	243408	0.0031	0.0708
chr19	59128983	344910	0.0058	0.0868
chr20	63025520	977721	0.0155	3.4689
chr21	48129895	180300	0.0037	0.0805
chr22	51304566	152996	0.003	0.0613
chrMT	16571	18385	1.1095	1.0975
chrX	155270560	753898	0.0049	0.0922
chrY	59373566	339710	0.0057	0.1672

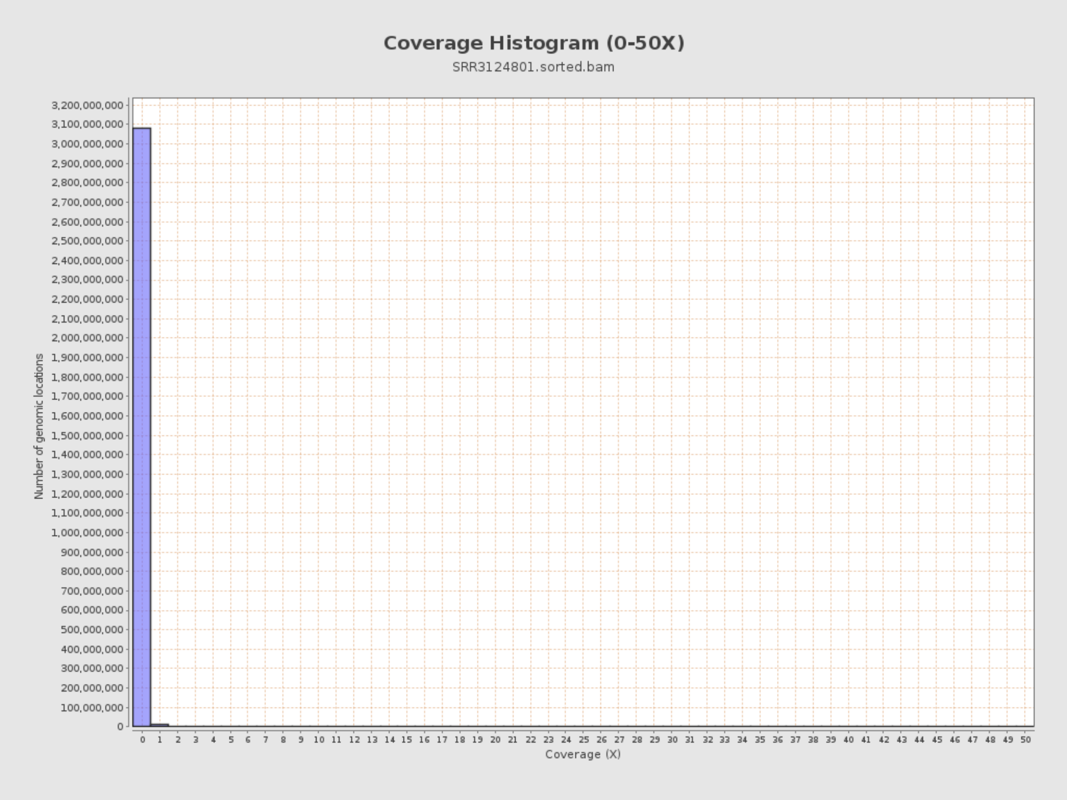
3. Results : Coverage across reference



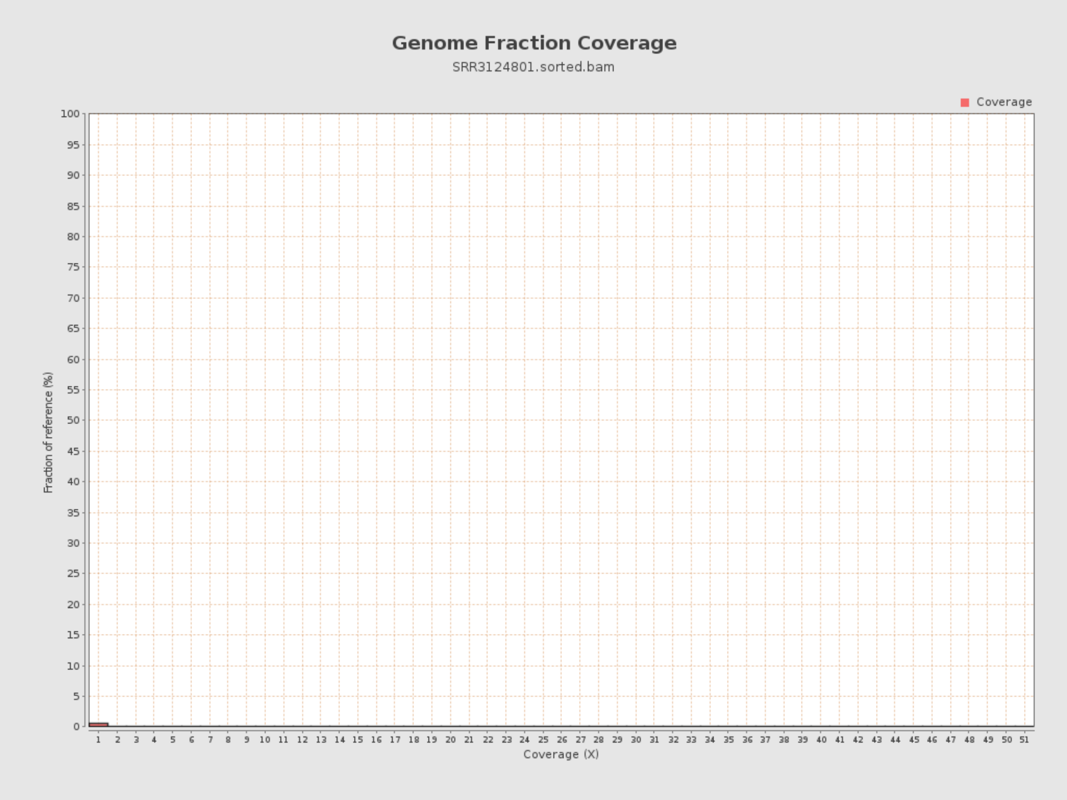
4. Results : Coverage Histogram



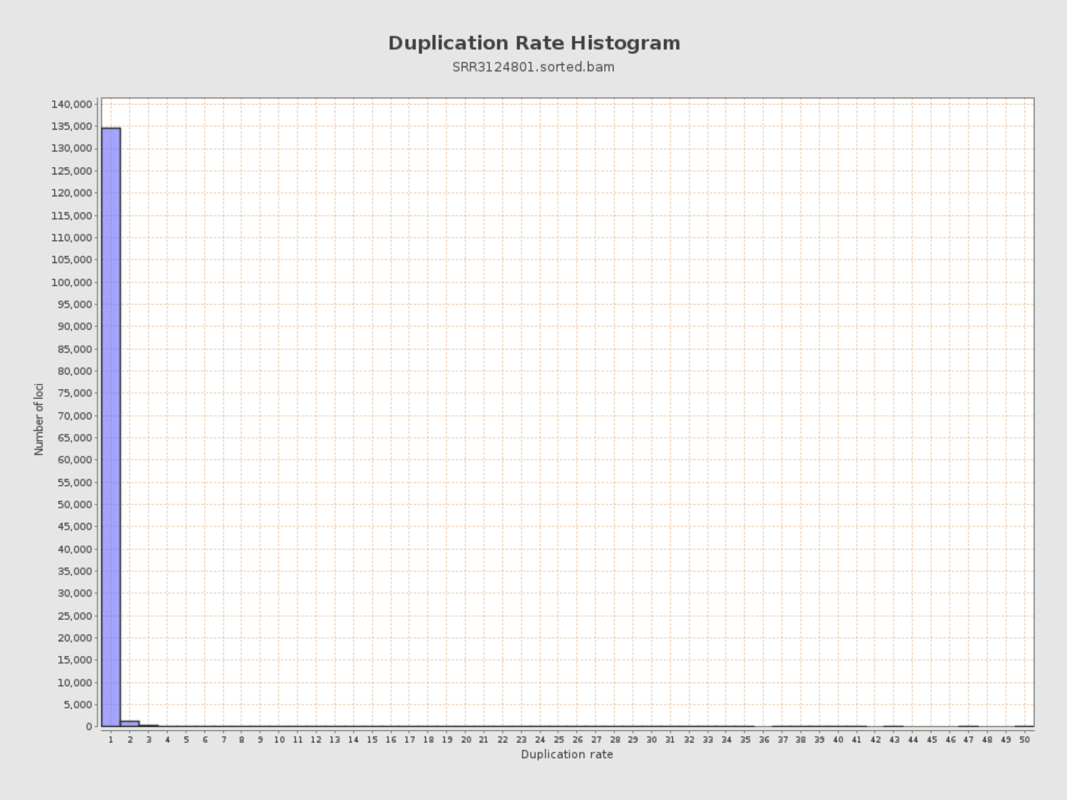
5. Results : Coverage Histogram (0-50X)



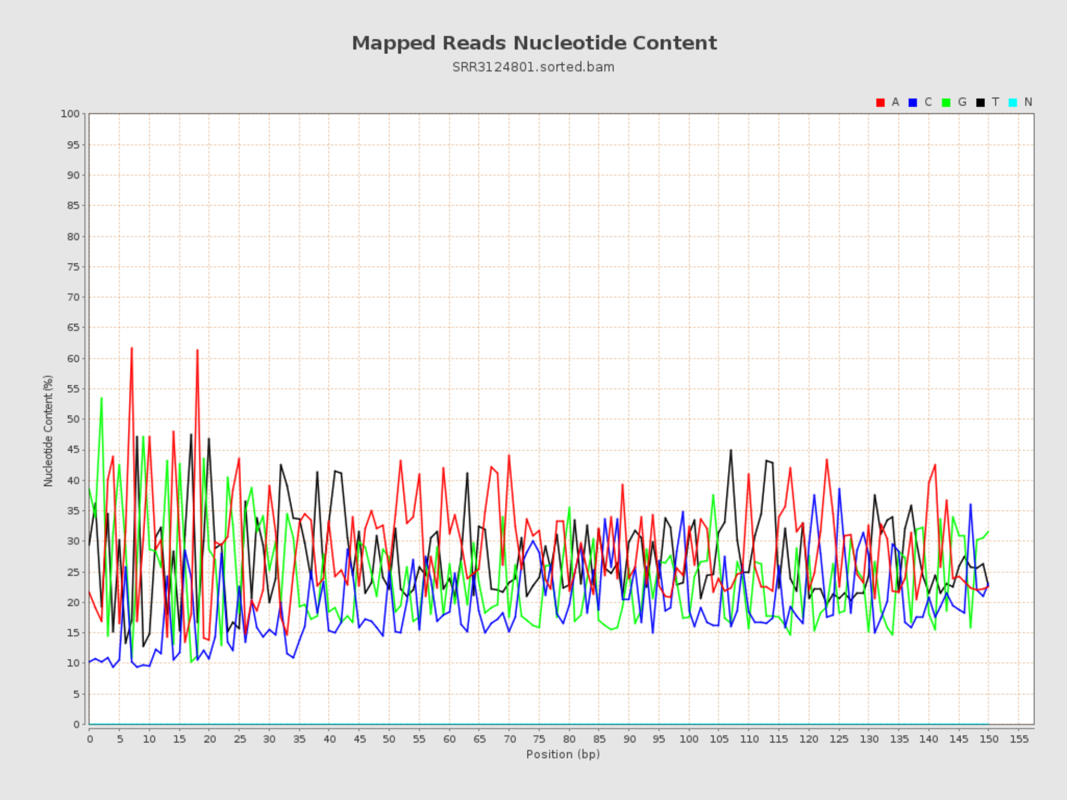
6. Results : Genome Fraction Coverage



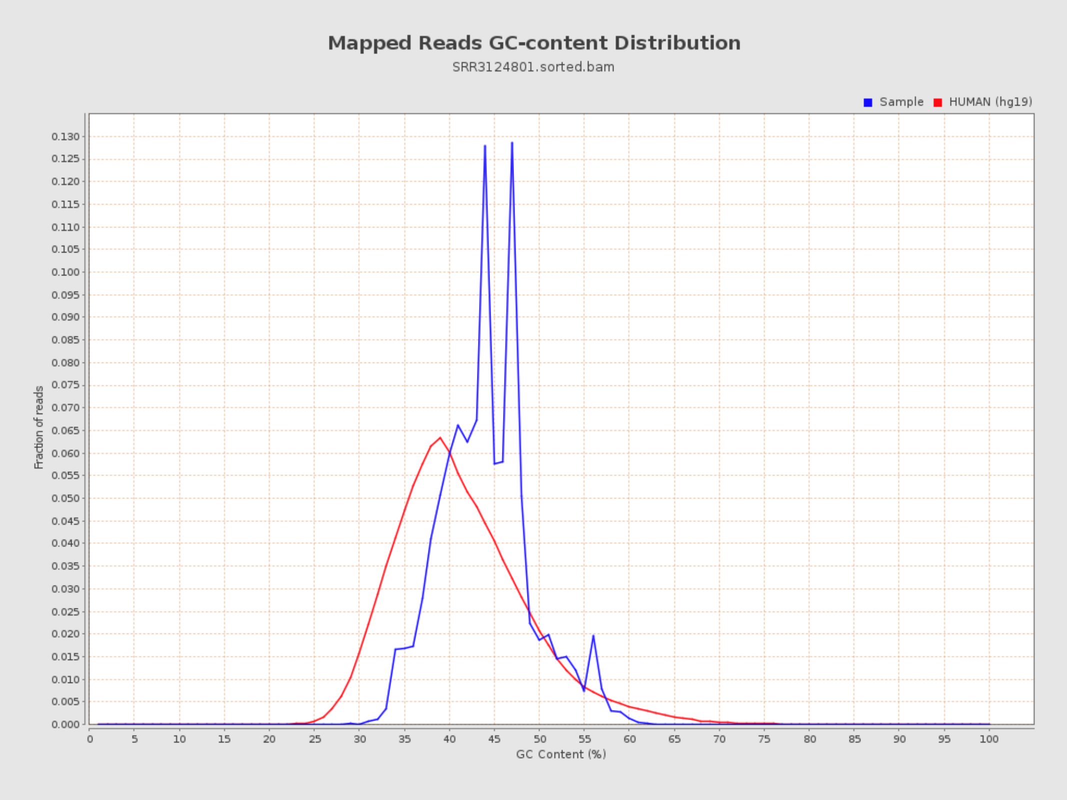
7. Results : Duplication Rate Histogram



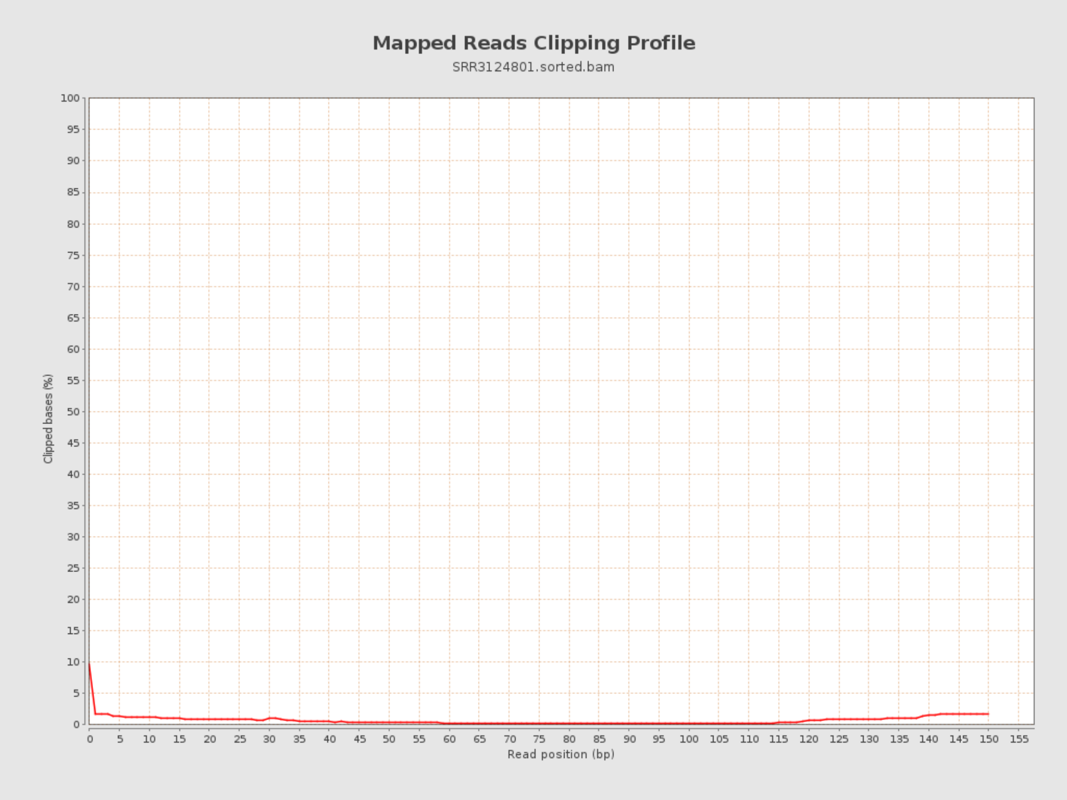
8. Results : Mapped Reads Nucleotide Content



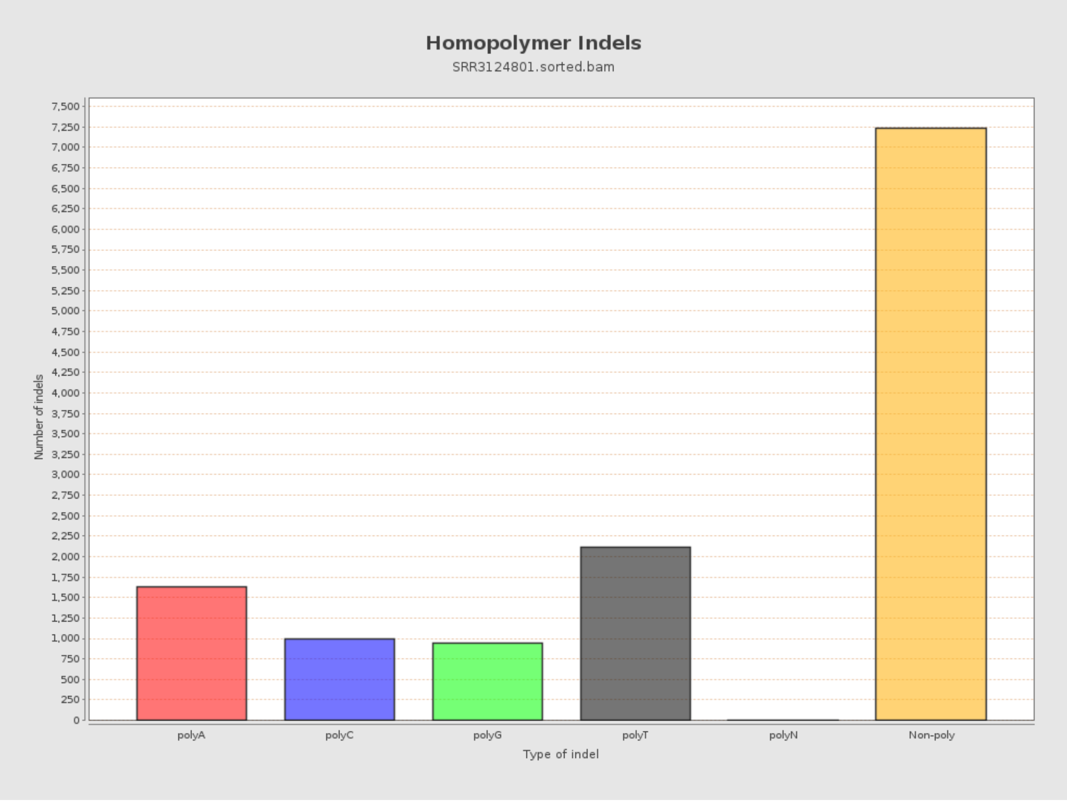
9. Results : Mapped Reads GC-content Distribution



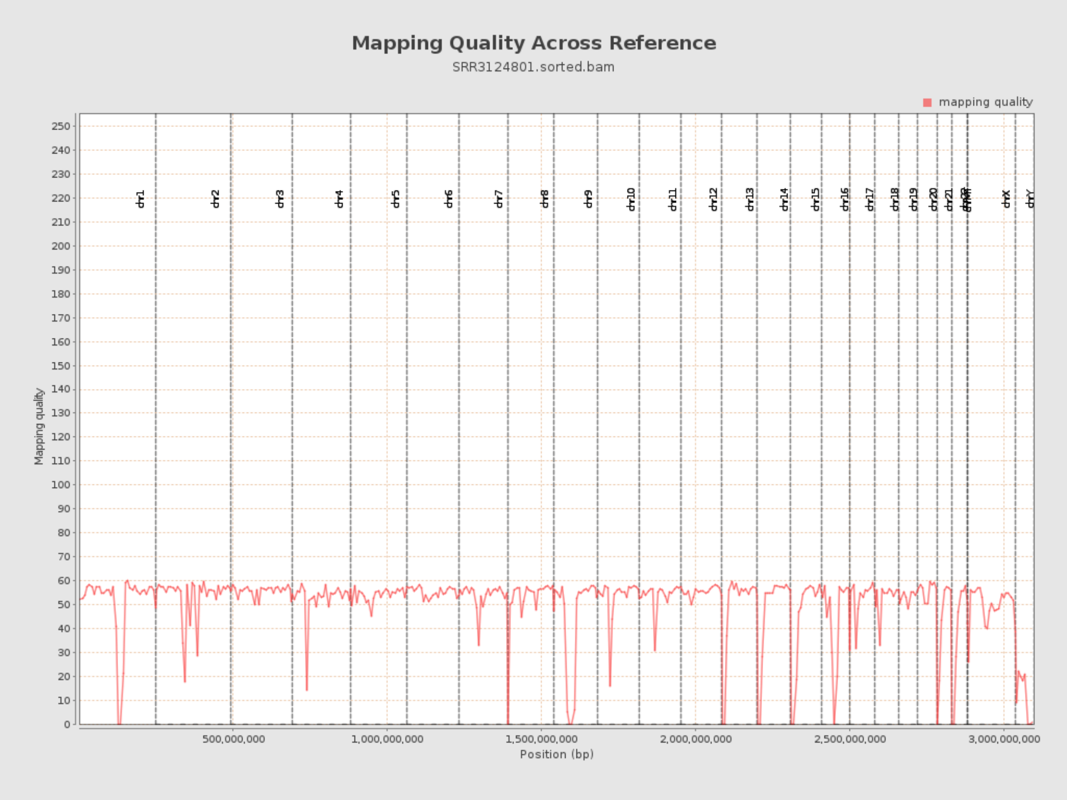
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram