Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 14:25:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514731.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_SRR5514731 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514731.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 14:25:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514731.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,344,547
Mapped reads	41,339,457 / 97.63%
Unmapped reads	1,005,090 / 2.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,176,919 / 2.78%
Read min/max/mean length	30 / 100 / 99.72
Duplicated reads (estimated)	25,574,329 / 60.4%
Duplication rate	34.71%
Clipped reads	7,319,124 / 17.28%

2.2. ACGT Content

Number/percentage of A's	1,001,746,051 / 25.41%
Number/percentage of C's	951,288,963 / 24.13%
Number/percentage of T's	1,013,233,325 / 25.71%
Number/percentage of G's	952,346,203 / 24.16%
Number/percentage of N's	23,090,442 / 0.59%
GC Percentage	48.29%

2.3. Coverage

Mean	1.274

Standard Deviation	30.5365

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

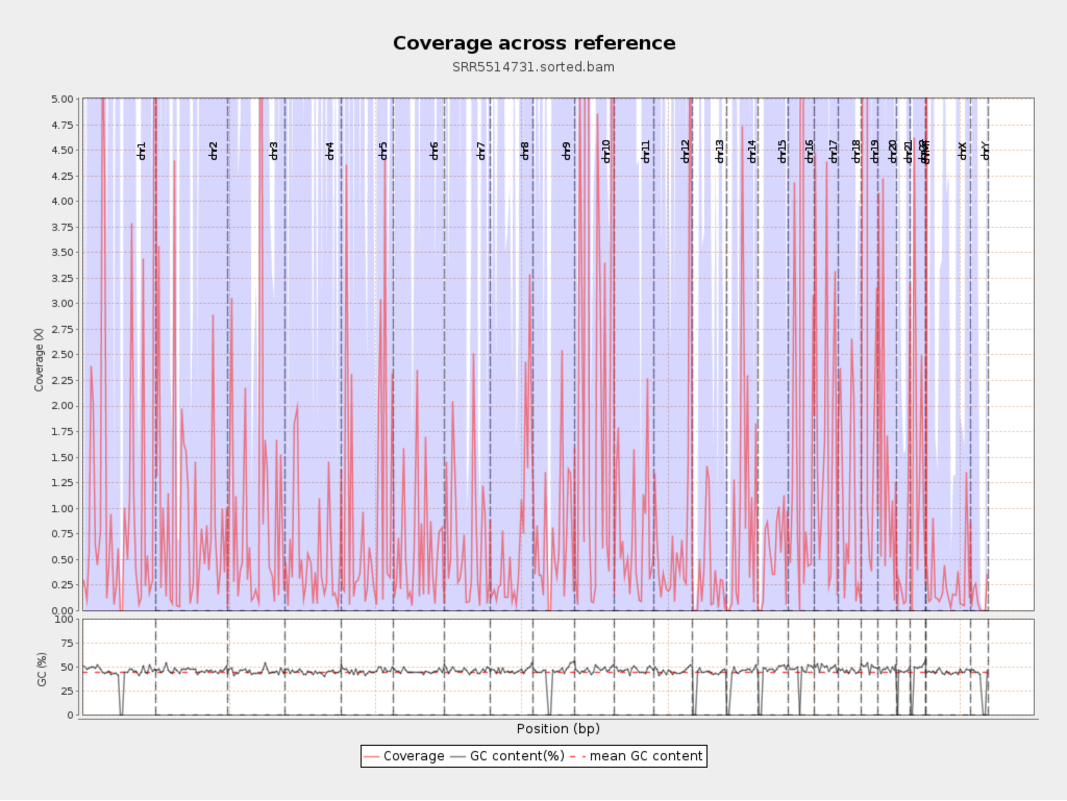
General error rate	1%
Mismatches	37,179,376
Insertions	1,423,636
Mapped reads with at least one insertion	3.32%
Deletions	1,106,987
Mapped reads with at least one deletion	2.6%
Homopolymer indels	45.24%

2.6. Chromosome stats

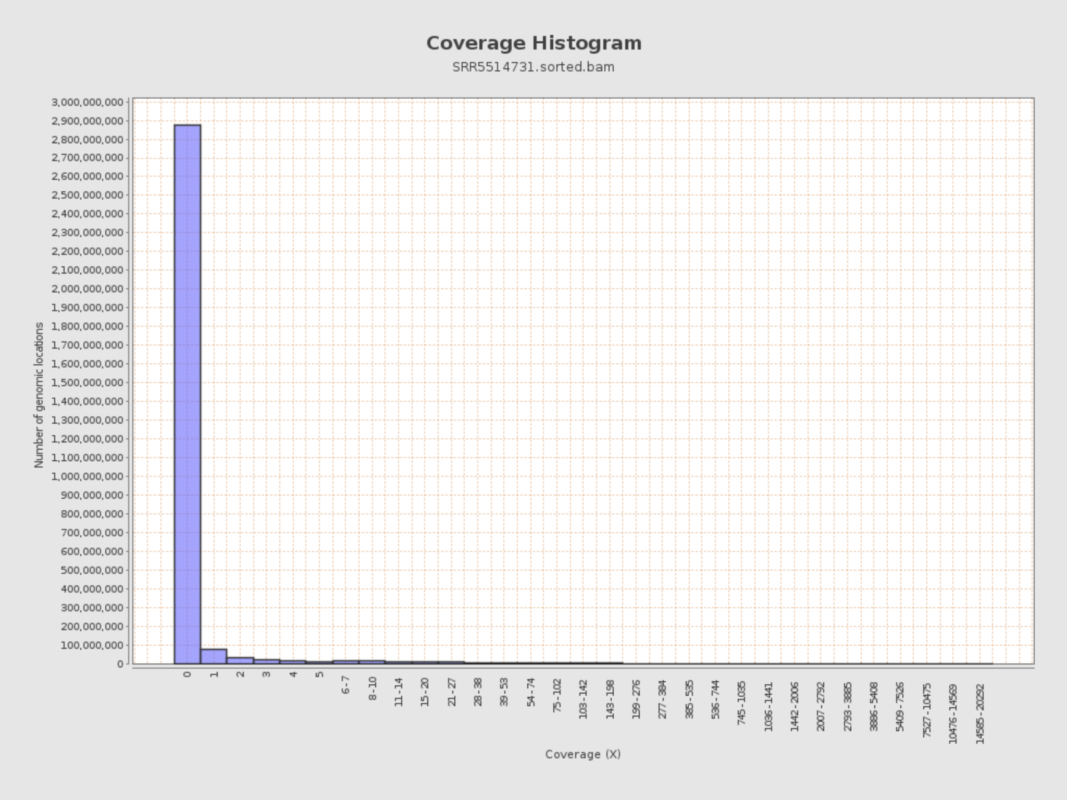
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	325687034	1.3067	16.2642
chr2	243199373	230808339	0.949	17.9155
chr3	198022430	212288192	1.072	23.241
chr4	191154276	99192954	0.5189	8.7945
chr5	180915260	186128686	1.0288	42.3789
chr6	171115067	101410657	0.5926	22.359
chr7	159138663	109949412	0.6909	9.7442

chr8	146364022	104786084	0.7159	9.1016
chr9	141213431	94121231	0.6665	13.1118
chr10	135534747	388698857	2.8679	46.541
chr11	135006516	103202237	0.7644	15.2825
chr12	133851895	115231471	0.8609	37.0914
chr13	115169878	37871750	0.3288	9.2683
chr14	107349540	107524060	1.0016	14.6735
chr15	102531392	55067346	0.5371	9.8887
chr16	90354753	245526055	2.7174	56.4263
chr17	81195210	149510407	1.8414	33.7292
chr18	78077248	84933463	1.0878	11.3337
chr19	59128983	941696522	15.9261	139.0238
chr20	63025520	93552298	1.4844	14.247
chr21	48129895	29789662	0.6189	19.792
chr22	51304566	75220369	1.4662	17.3264
chrMT	16571	2887987	174.2796	89.7682
chrX	155270560	41542985	0.2676	7.3144
chrY	59373566	7288065	0.1227	7.843

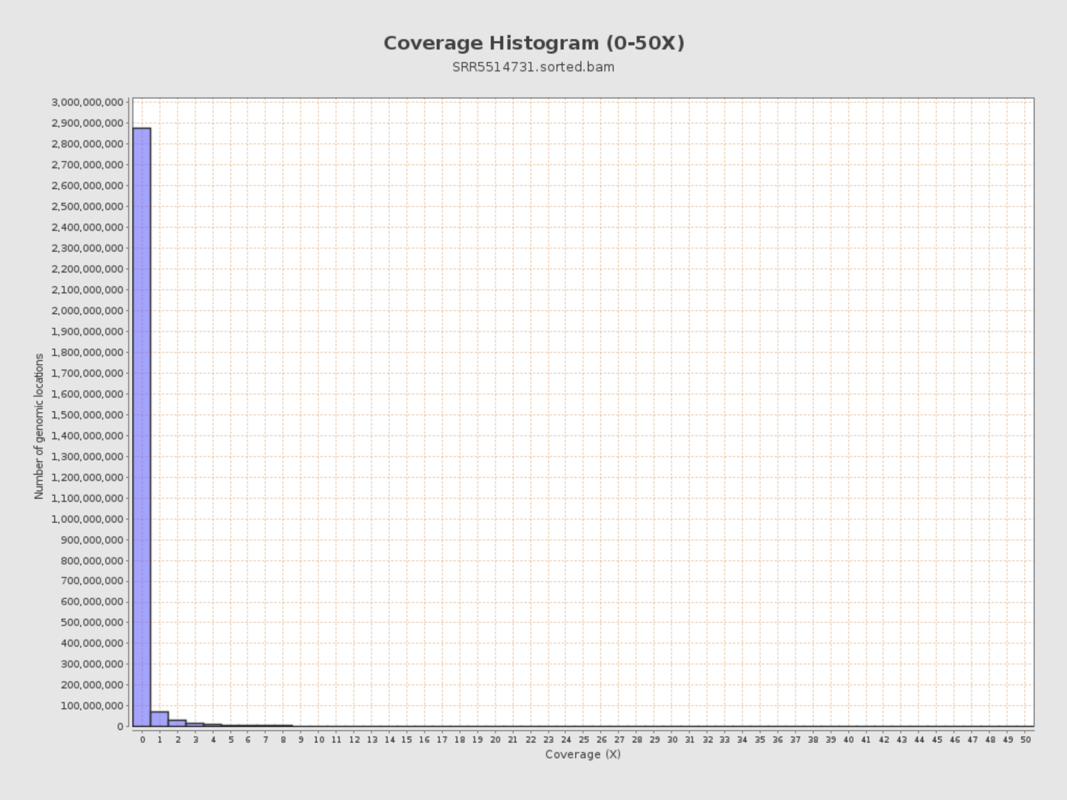
3. Results : Coverage across reference



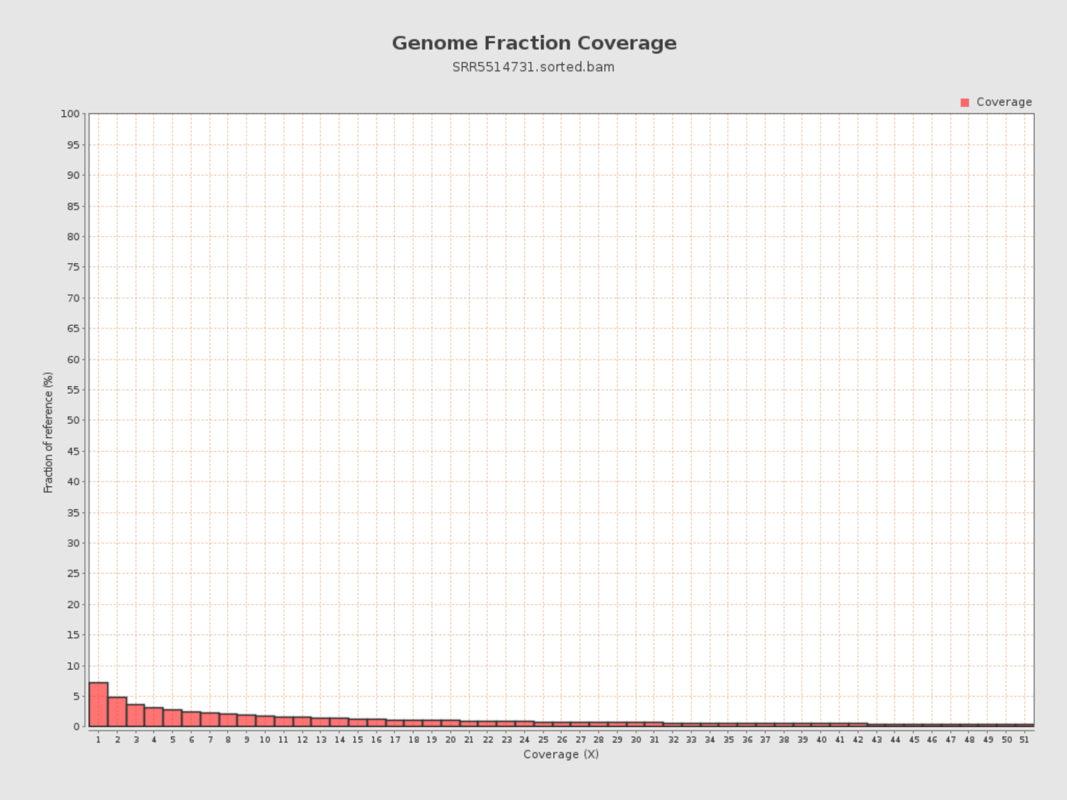
4. Results : Coverage Histogram



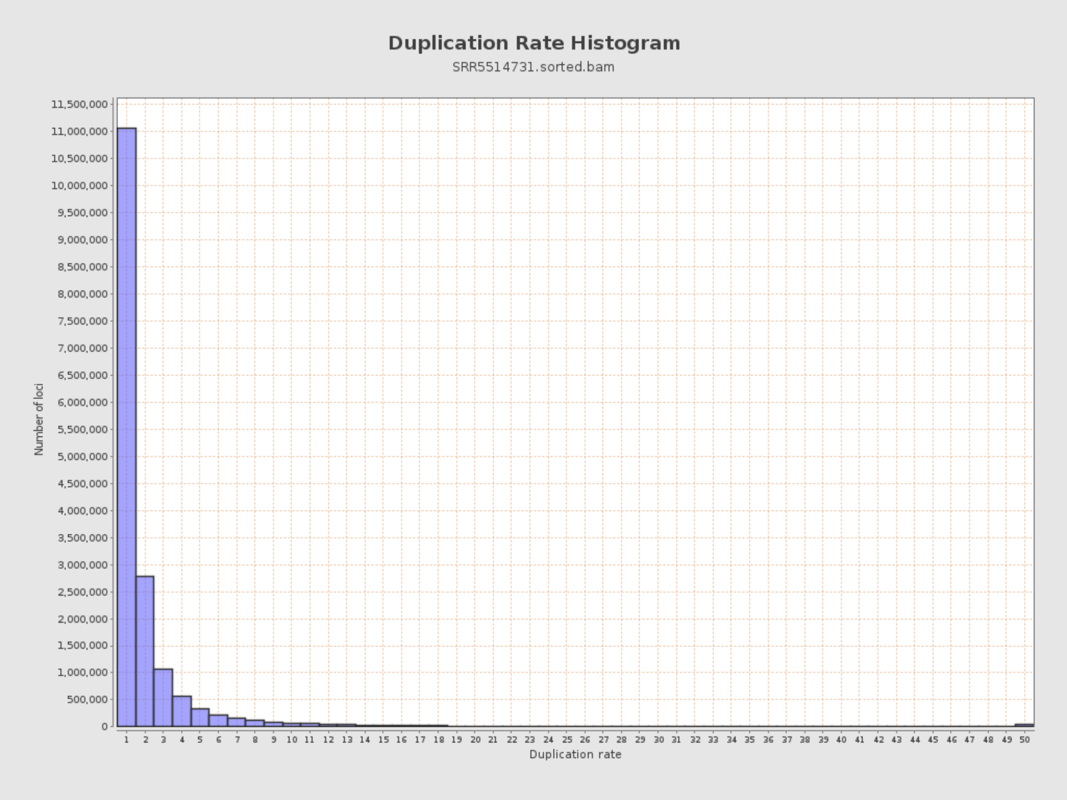
5. Results : Coverage Histogram (0-50X)



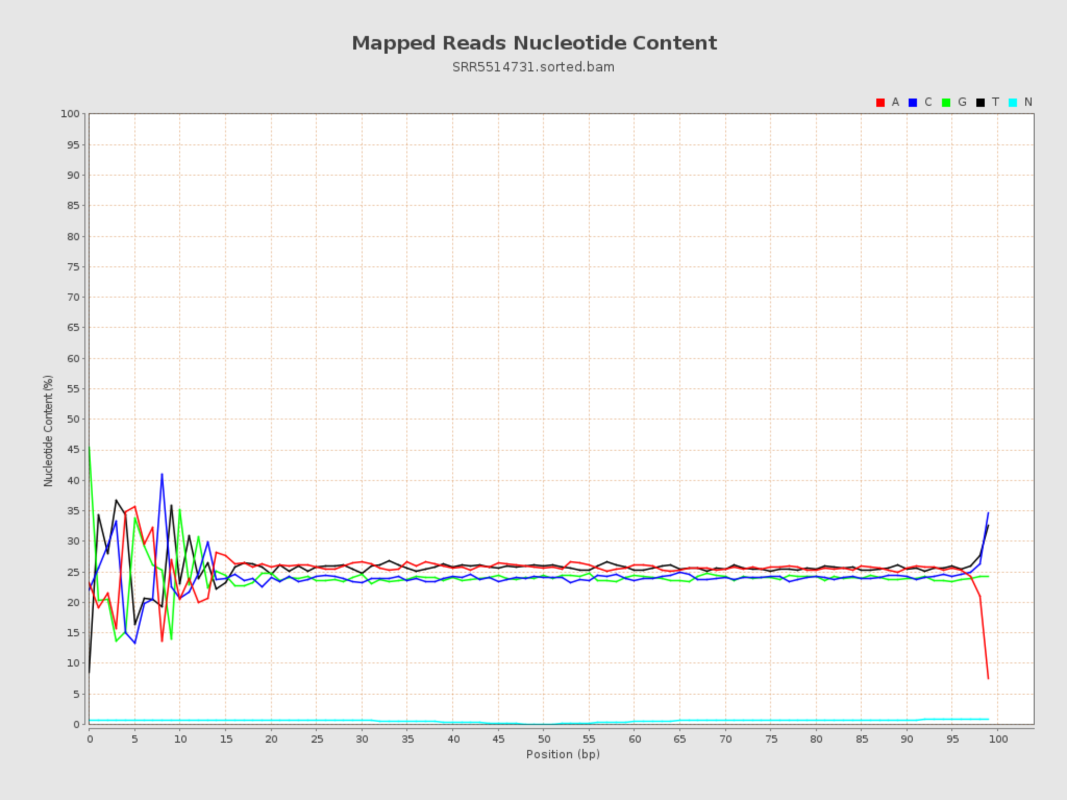
6. Results : Genome Fraction Coverage



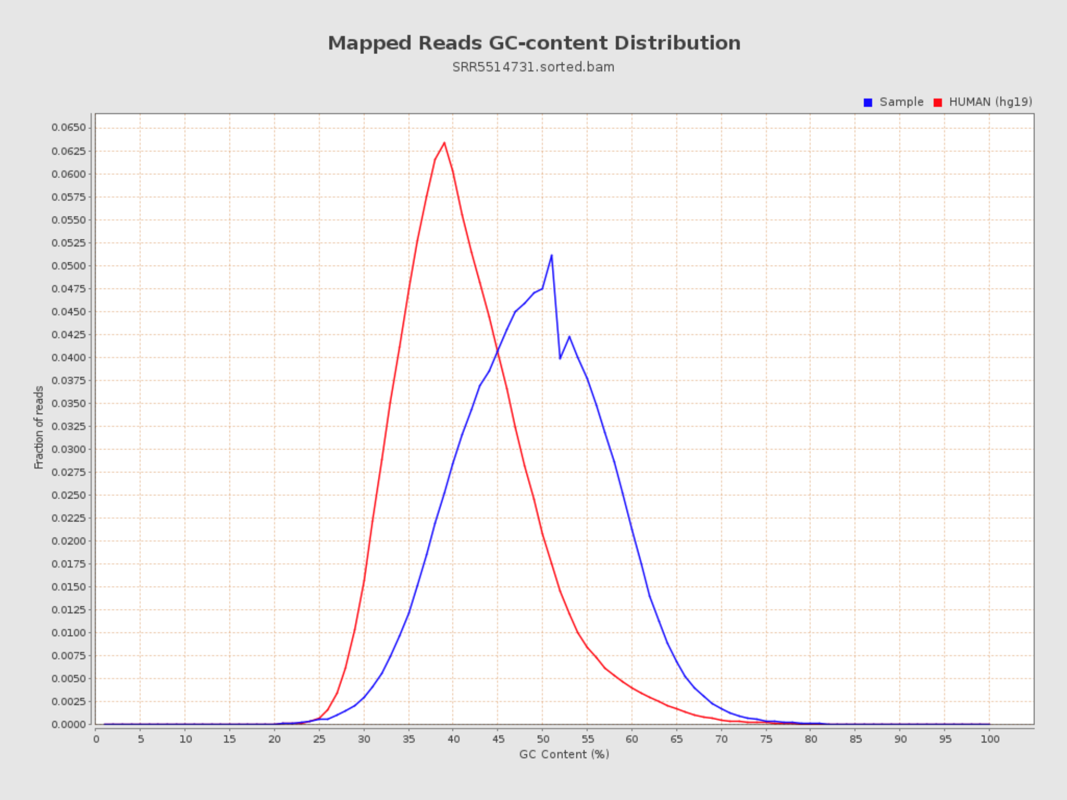
7. Results : Duplication Rate Histogram



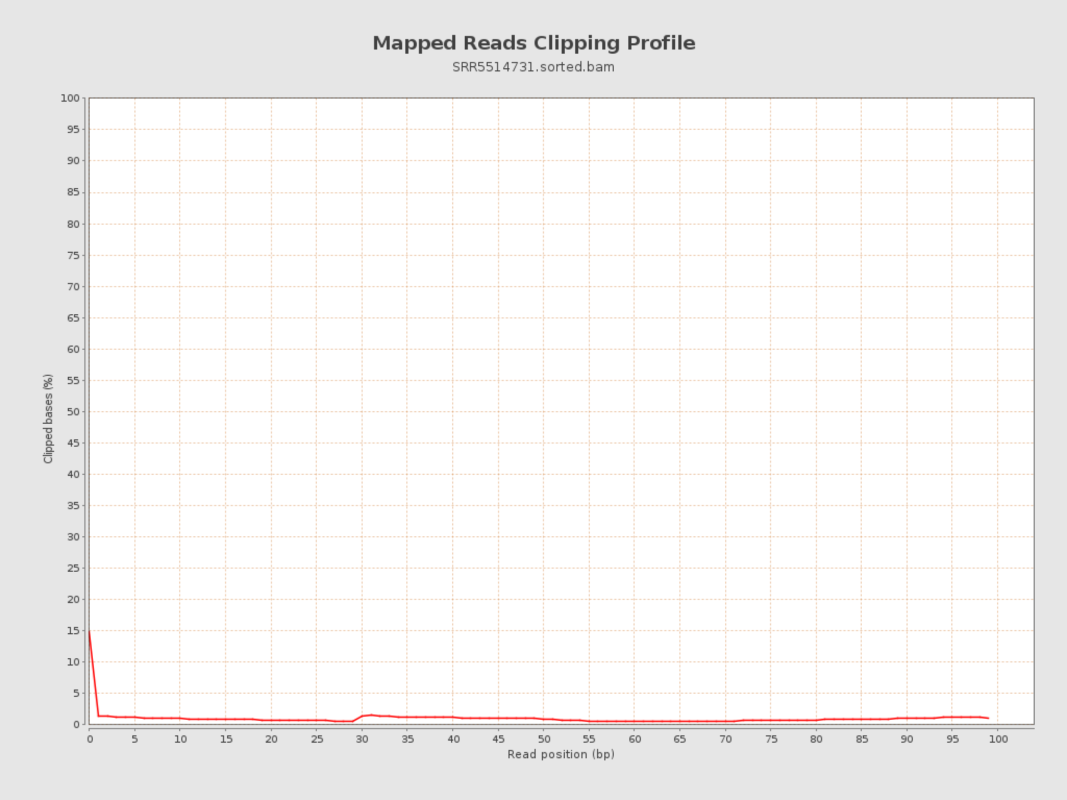
8. Results : Mapped Reads Nucleotide Content



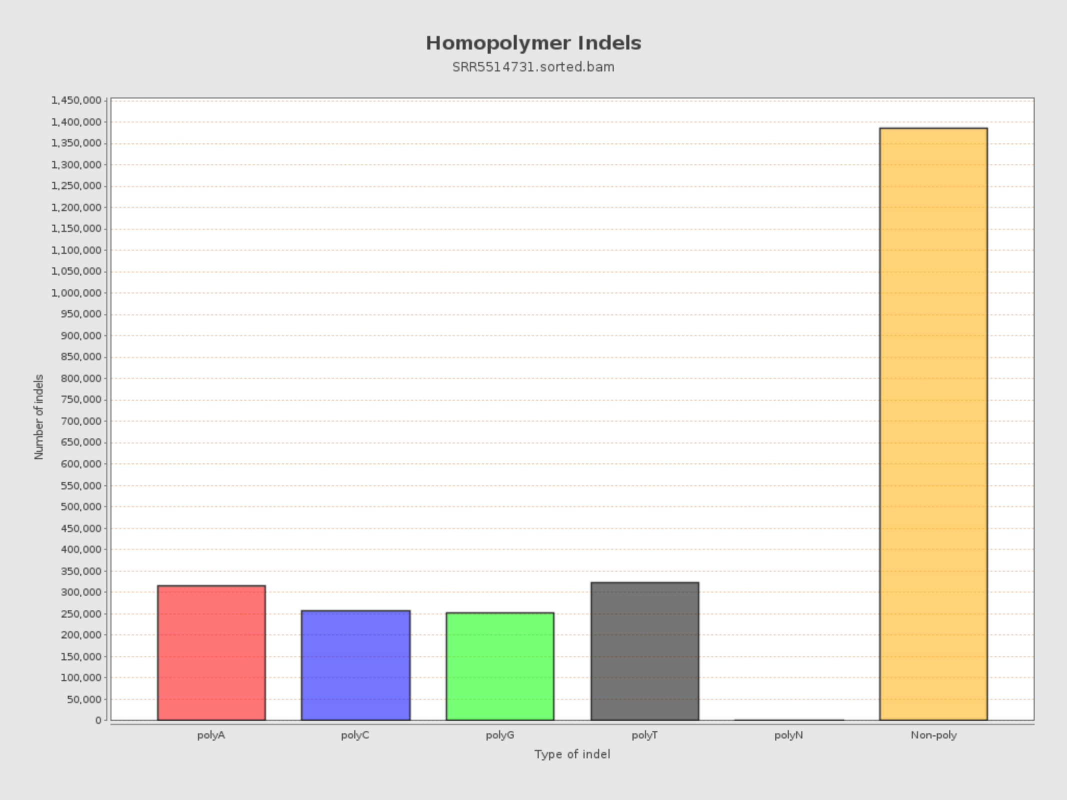
9. Results : Mapped Reads GC-content Distribution



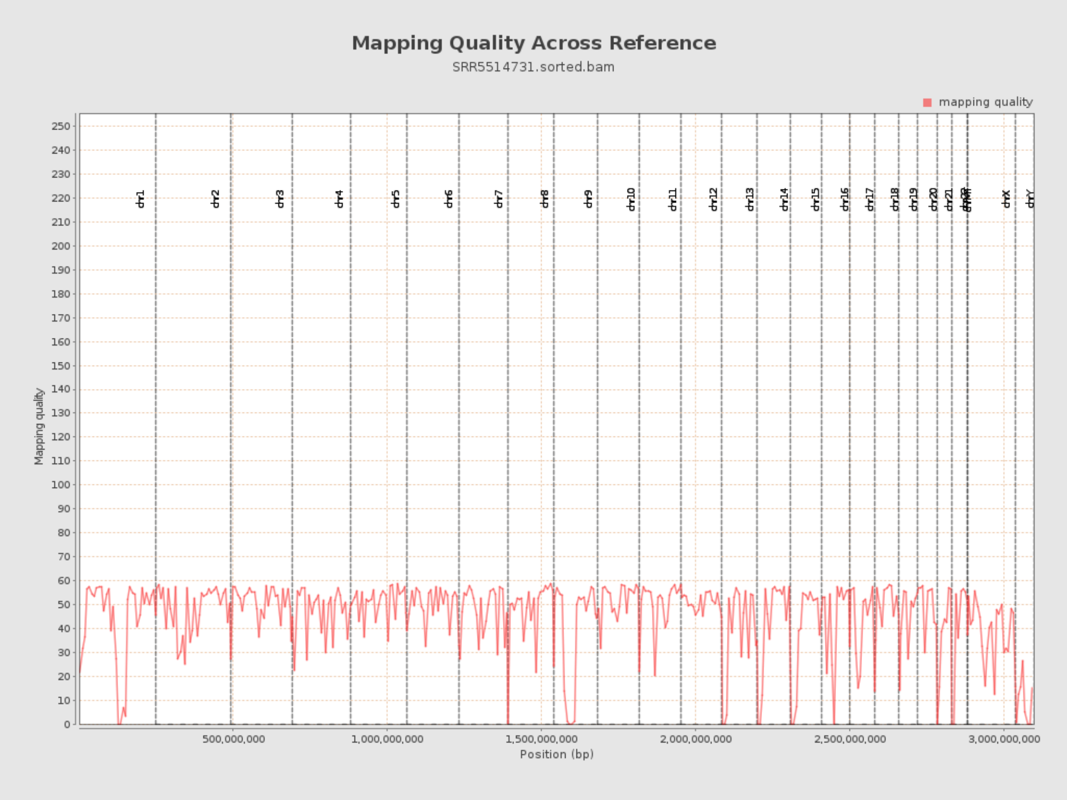
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram