Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 21:39:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514743.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_SRR5514743 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514743.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 21:39:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514743.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,634,186
Mapped reads	1,553,248 / 42.74%
Unmapped reads	2,080,938 / 57.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	272,020 / 7.49%
Read min/max/mean length	30 / 100 / 101.86
Duplicated reads (estimated)	835,875 / 23%
Duplication rate	28.63%
Clipped reads	942,117 / 25.92%

2.2. ACGT Content

Number/percentage of A's	45,074,469 / 31.18%
Number/percentage of C's	26,727,292 / 18.49%
Number/percentage of T's	44,428,861 / 30.74%
Number/percentage of G's	28,301,613 / 19.58%
Number/percentage of N's	9,400 / 0.01%
GC Percentage	38.07%

2.3. Coverage

Mean	0.0467

Standard Deviation	3.1184

2.4. Mapping Quality

Mean Mapping Quality	38.65

2.5. Mismatches and indels

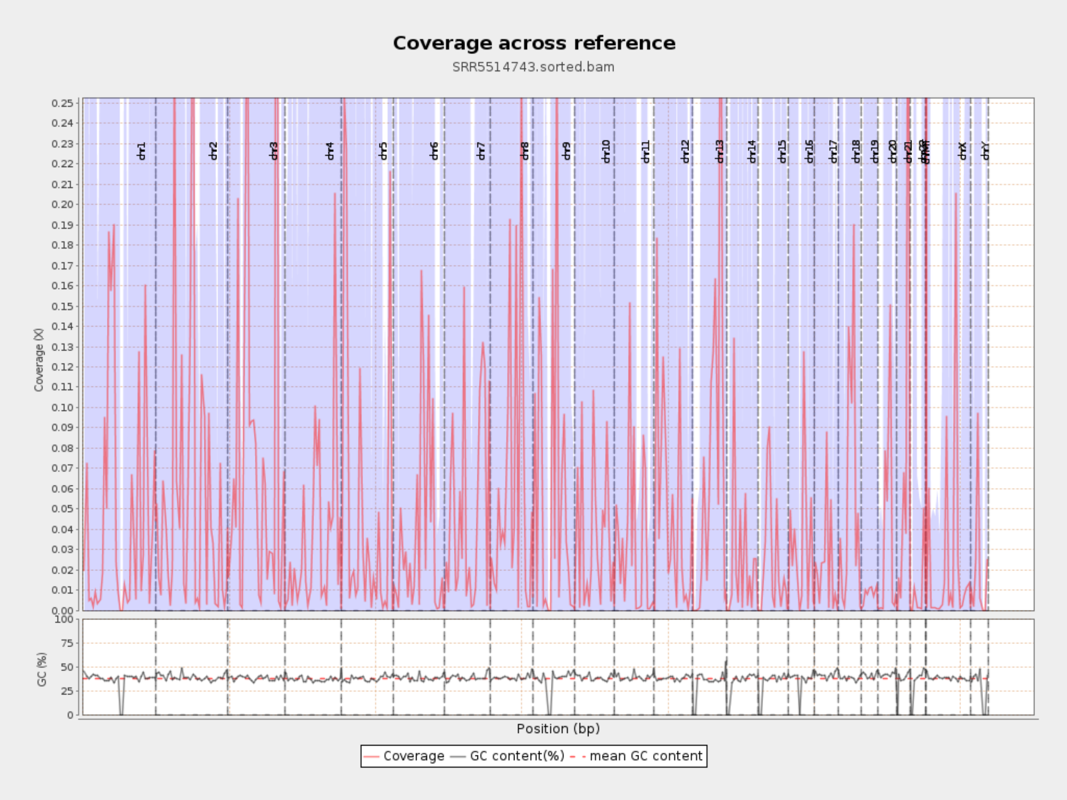
General error rate	0.72%
Mismatches	887,883
Insertions	91,403
Mapped reads with at least one insertion	5.64%
Deletions	38,233
Mapped reads with at least one deletion	2.3%
Homopolymer indels	49.06%

2.6. Chromosome stats

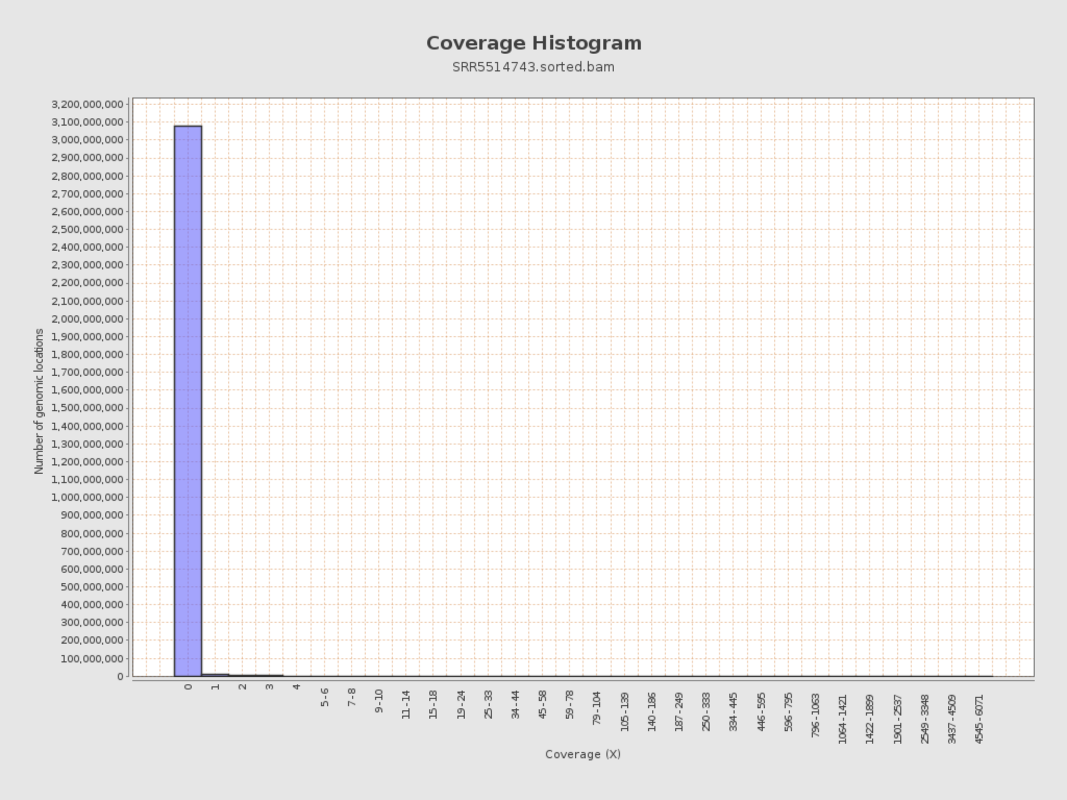
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11776227	0.0472	2.1063
chr2	243199373	13841443	0.0569	3.8966
chr3	198022430	16648867	0.0841	4.5016
chr4	191154276	7109428	0.0372	1.8834
chr5	180915260	8424401	0.0466	1.9096
chr6	171115067	6651561	0.0389	2.1192
chr7	159138663	8050385	0.0506	3.9513

chr8	146364022	9131893	0.0624	2.2933
chr9	141213431	8714004	0.0617	4.2367
chr10	135534747	5204683	0.0384	1.8337
chr11	135006516	4812124	0.0356	1.9188
chr12	133851895	6316327	0.0472	1.6317
chr13	115169878	8896941	0.0773	2.6992
chr14	107349540	2677099	0.0249	1.1383
chr15	102531392	2523697	0.0246	1.4568
chr16	90354753	2985089	0.033	2.983
chr17	81195210	1903352	0.0234	1.8657
chr18	78077248	4397501	0.0563	2.5366
chr19	59128983	494180	0.0084	0.4195
chr20	63025520	2292757	0.0364	2.5823
chr21	48129895	3906823	0.0812	12.4504
chr22	51304566	518252	0.0101	1.3165
chrMT	16571	2620017	158.1086	202.2497
chrX	155270560	3521976	0.0227	1.0333
chrY	59373566	1245905	0.021	1.0407

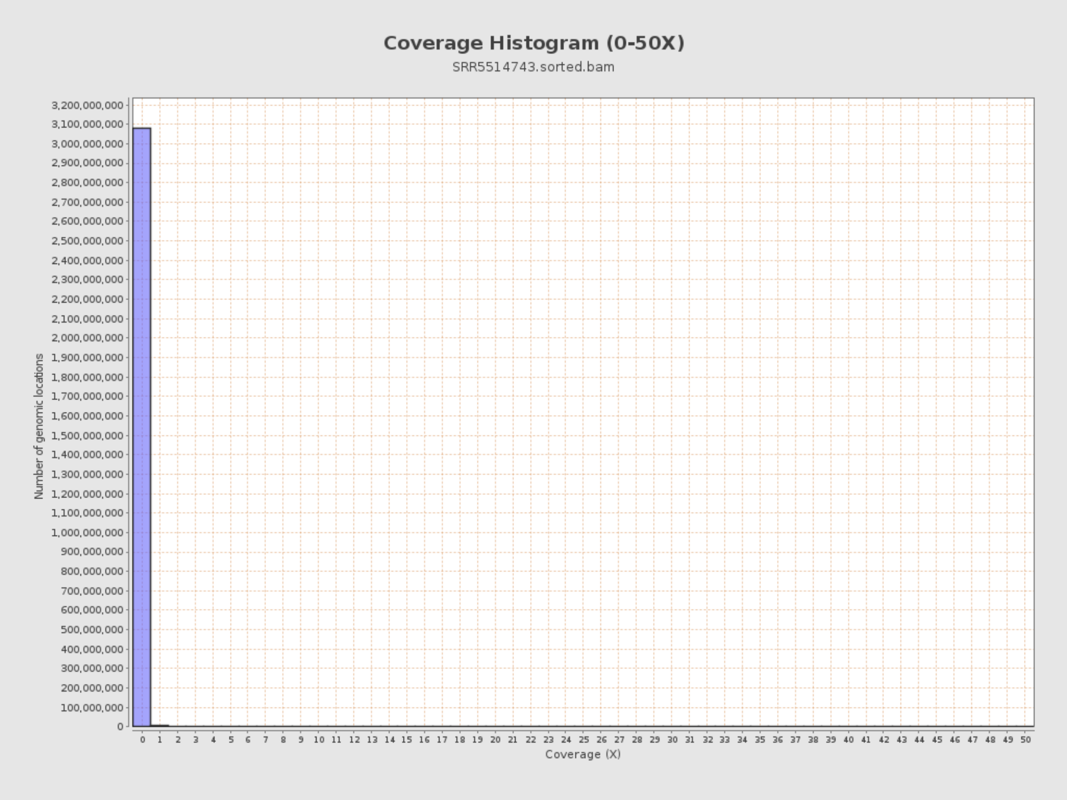
3. Results : Coverage across reference



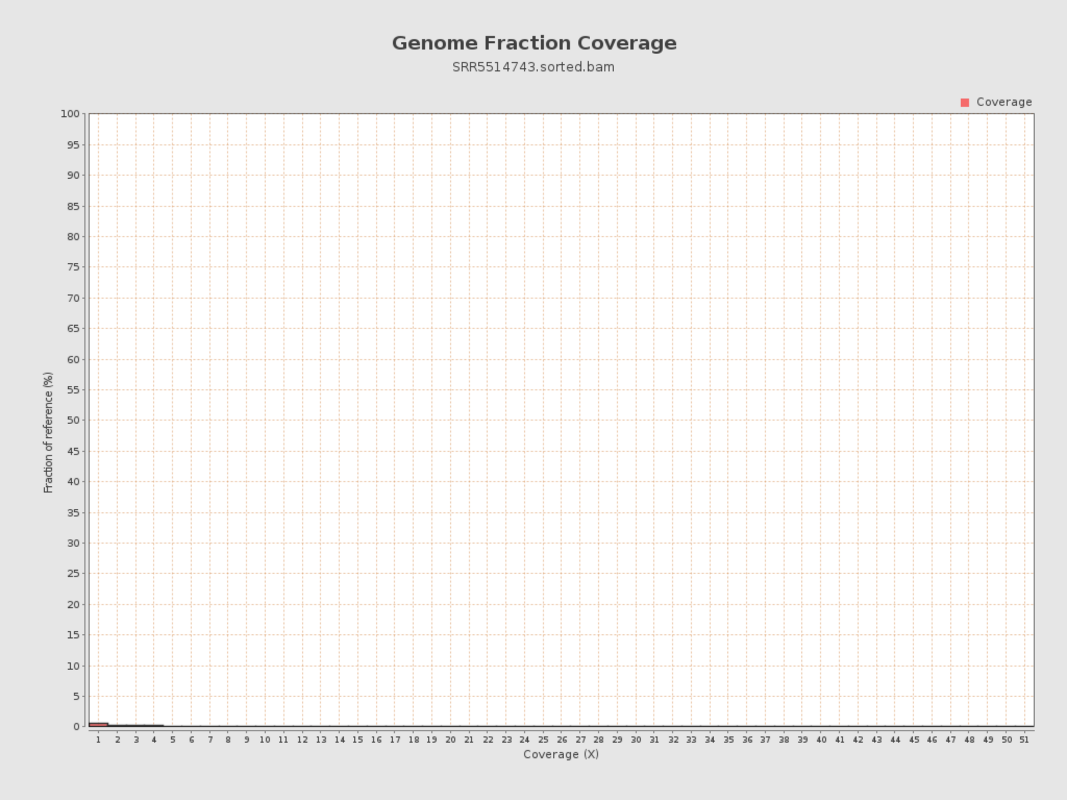
4. Results : Coverage Histogram



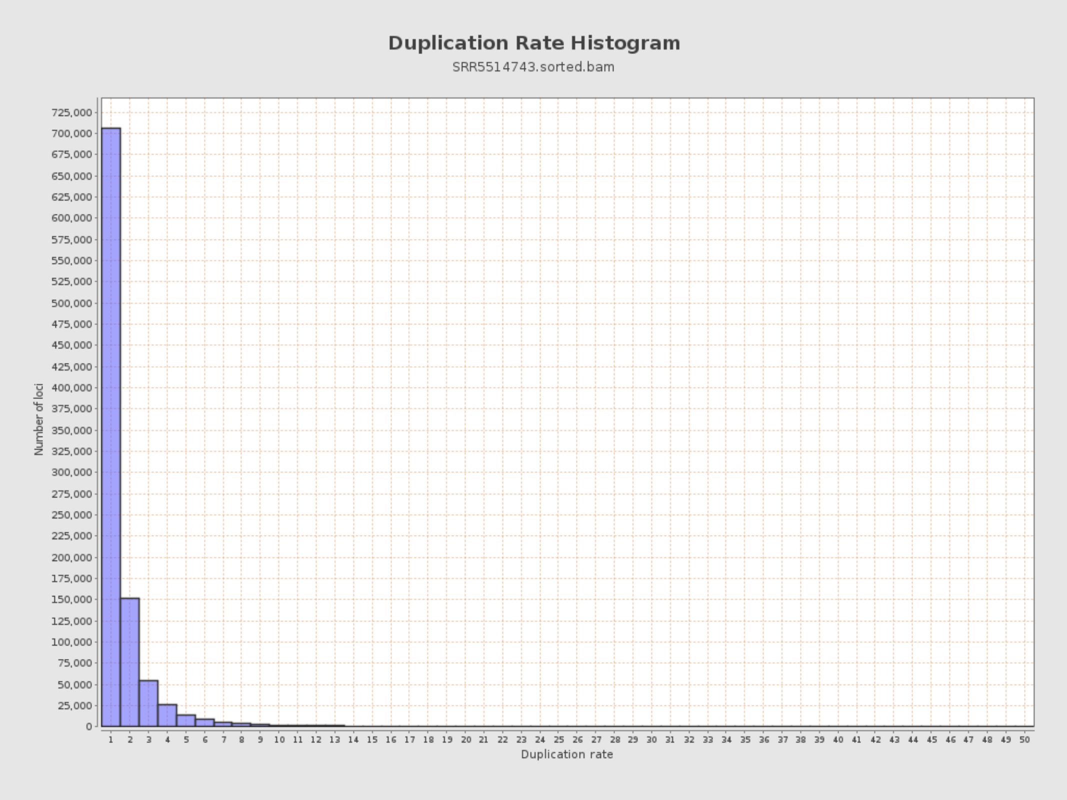
5. Results : Coverage Histogram (0-50X)



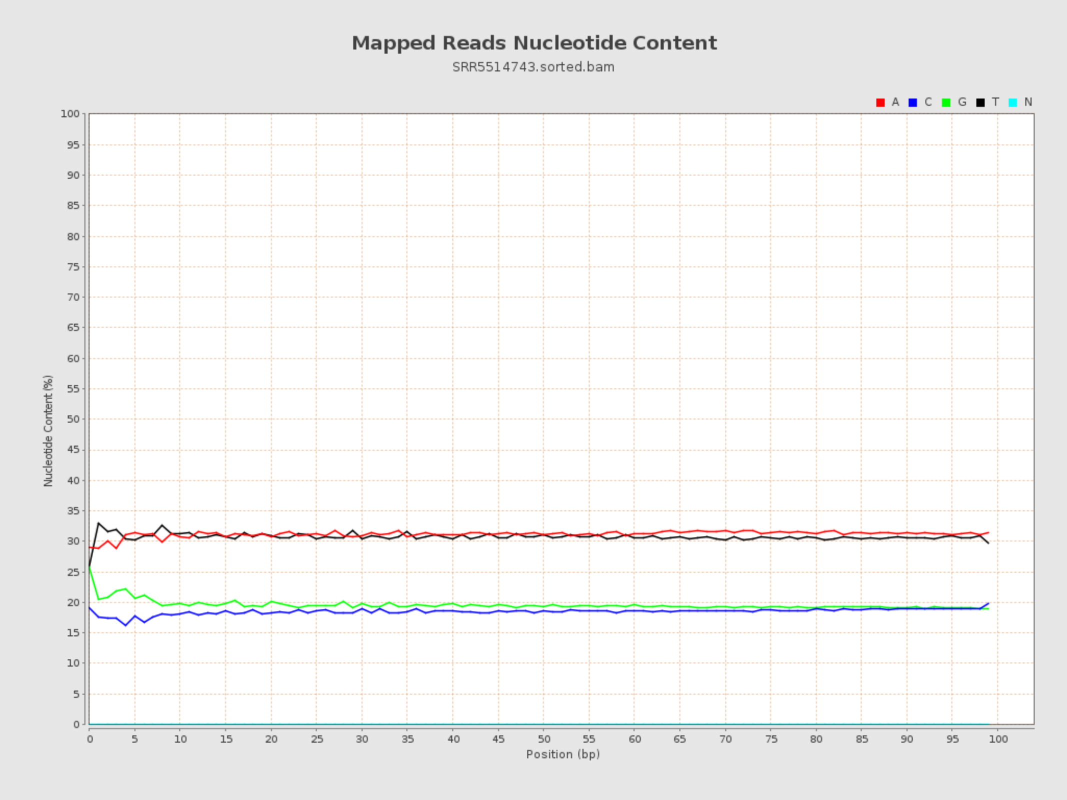
6. Results : Genome Fraction Coverage



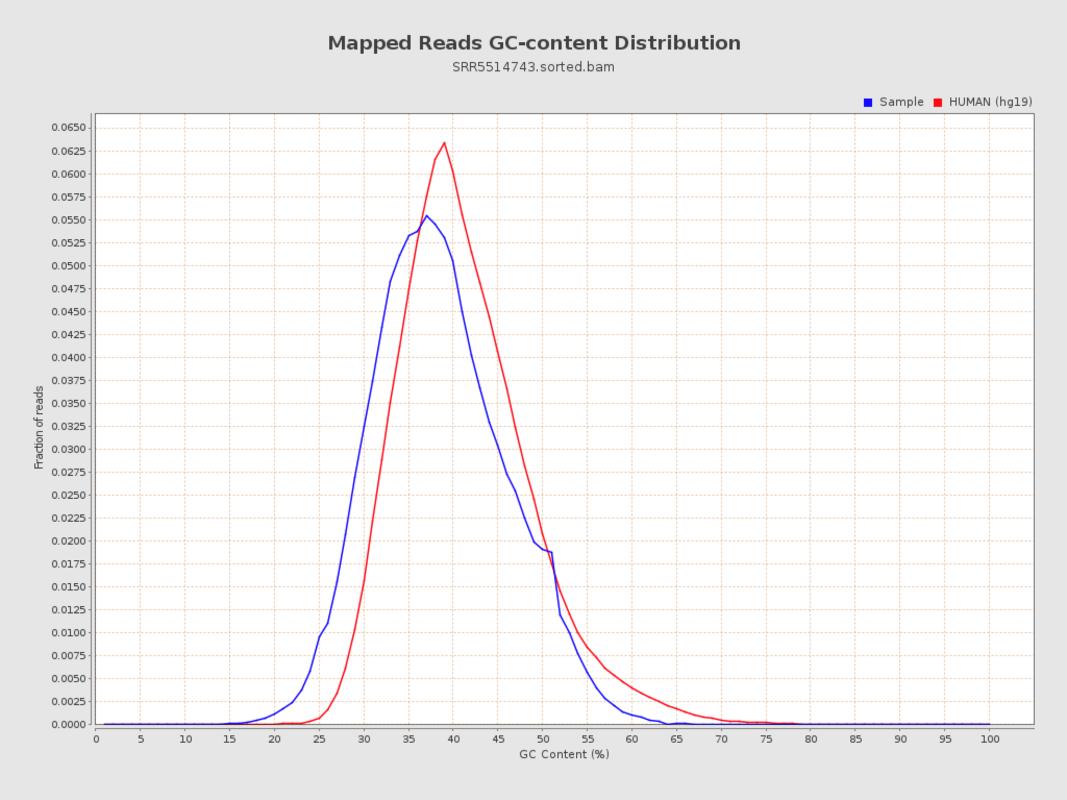
7. Results : Duplication Rate Histogram



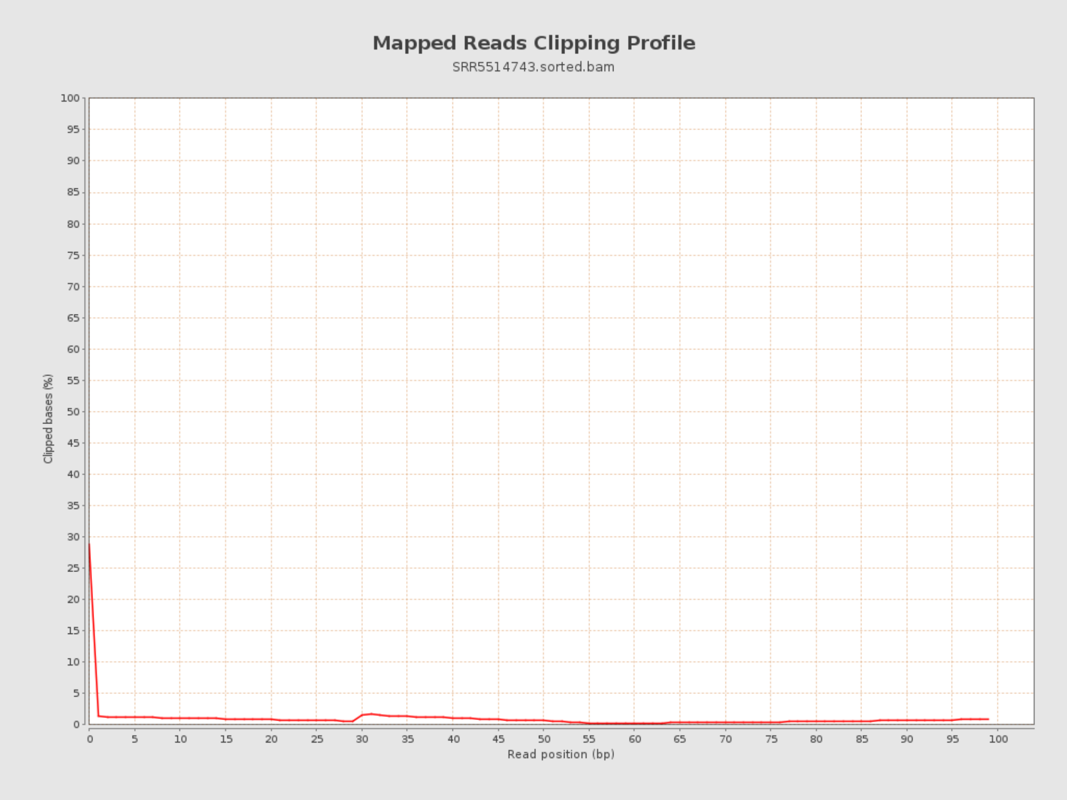
8. Results : Mapped Reads Nucleotide Content



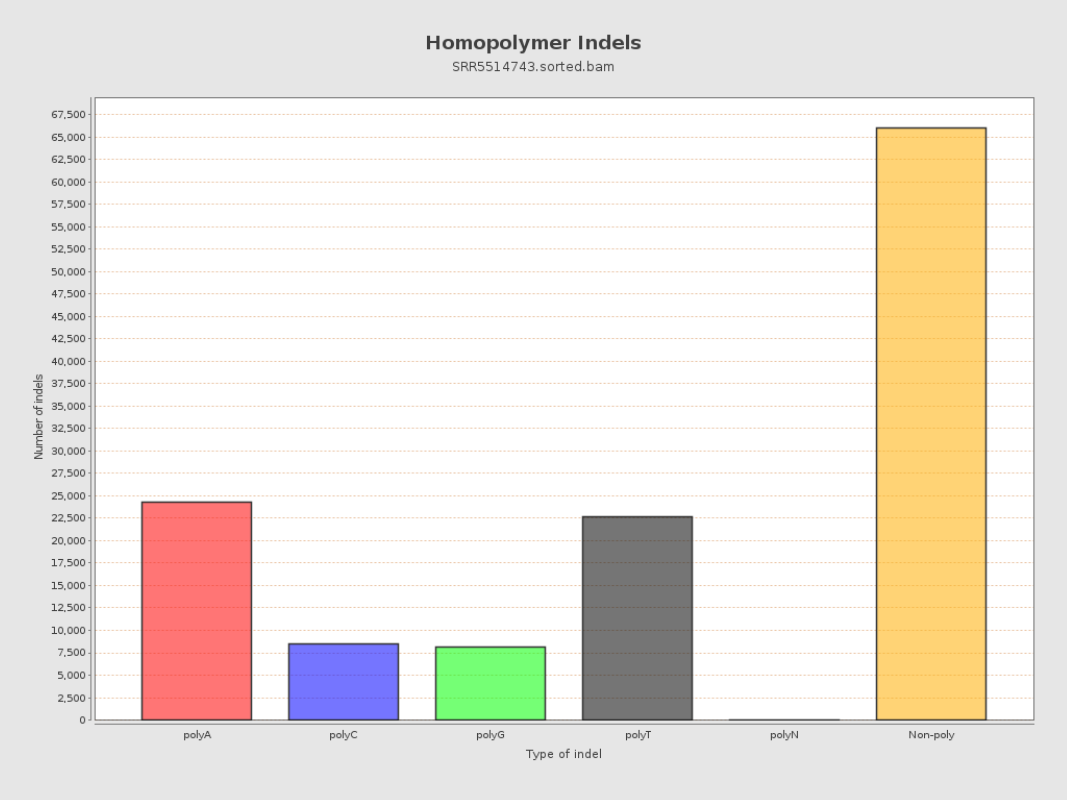
9. Results : Mapped Reads GC-content Distribution



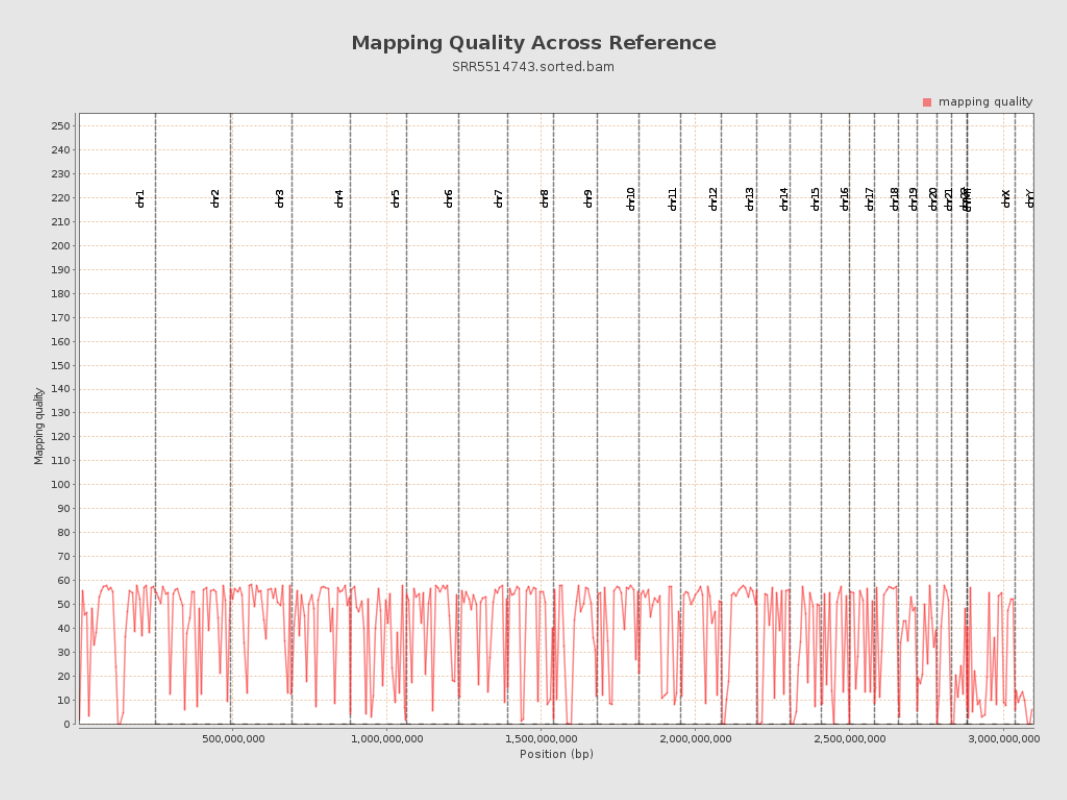
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram