Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 08:34:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514730.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_SRR5514730 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514730.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 08:34:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514730.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	49,841,482
Mapped reads	48,350,943 / 97.01%
Unmapped reads	1,490,539 / 2.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,320,457 / 2.65%
Read min/max/mean length	30 / 100 / 98.58
Duplicated reads (estimated)	28,693,329 / 57.57%
Duplication rate	38.86%
Clipped reads	8,287,330 / 16.63%

2.2. ACGT Content

Number/percentage of A's	1,189,416,421 / 26.1%
Number/percentage of C's	1,070,532,624 / 23.49%
Number/percentage of T's	1,201,052,323 / 26.35%
Number/percentage of G's	1,071,376,813 / 23.51%
Number/percentage of N's	25,259,484 / 0.55%
GC Percentage	47%

2.3. Coverage

Mean	1.4731

Standard Deviation	59.392

2.4. Mapping Quality

Mean Mapping Quality	41.75

2.5. Mismatches and indels

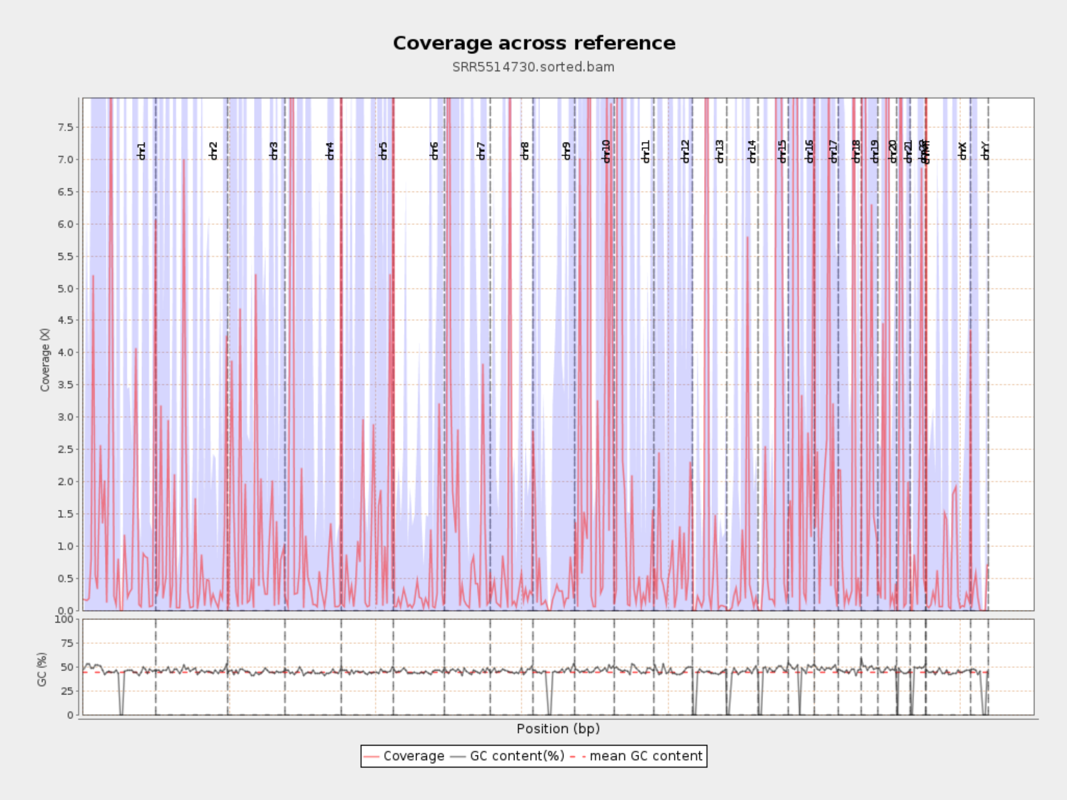
General error rate	0.96%
Mismatches	40,992,233
Insertions	1,600,543
Mapped reads with at least one insertion	3.14%
Deletions	1,227,624
Mapped reads with at least one deletion	2.46%
Homopolymer indels	43.14%

2.6. Chromosome stats

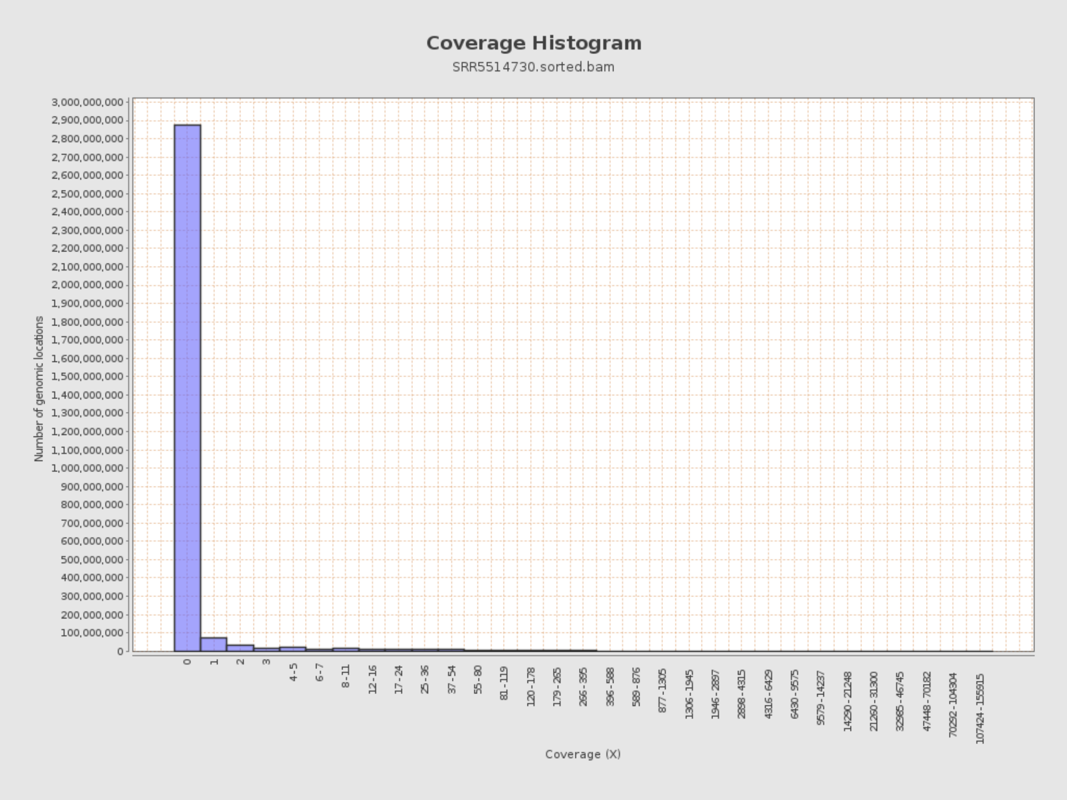
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	329860193	1.3234	14.406
chr2	243199373	230990627	0.9498	25.6924
chr3	198022430	220840896	1.1152	21.701
chr4	191154276	241413057	1.2629	15.7963
chr5	180915260	209445521	1.1577	16.2536
chr6	171115067	57464300	0.3358	8.7663
chr7	159138663	257858772	1.6203	20.6914

chr8	146364022	106220029	0.7257	9.2874
chr9	141213431	50093176	0.3547	20.5074
chr10	135534747	416202238	3.0708	268.5007
chr11	135006516	447925716	3.3178	36.4688
chr12	133851895	102663299	0.767	11.3564
chr13	115169878	136224350	1.1828	14.0471
chr14	107349540	69880866	0.651	8.7957
chr15	102531392	291166176	2.8398	21.0307
chr16	90354753	319305223	3.5339	30.1182
chr17	81195210	173305783	2.1344	23.6177
chr18	78077248	127832191	1.6373	16.346
chr19	59128983	312853248	5.291	30.4414
chr20	63025520	167271544	2.654	23.879
chr21	48129895	112353776	2.3344	30.2947
chr22	51304566	81960220	1.5975	18.2447
chrMT	16571	2526755	152.4805	94.5292
chrX	155270560	79895672	0.5146	6.5912
chrY	59373566	14638568	0.2466	13.288

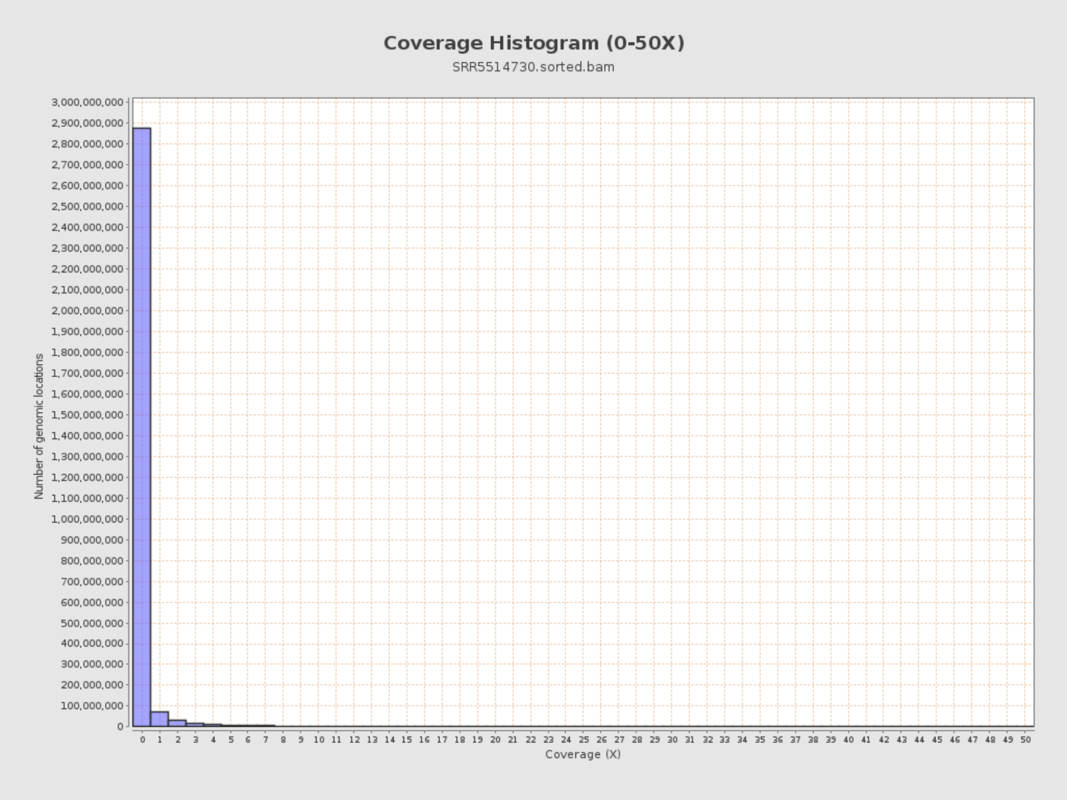
3. Results : Coverage across reference



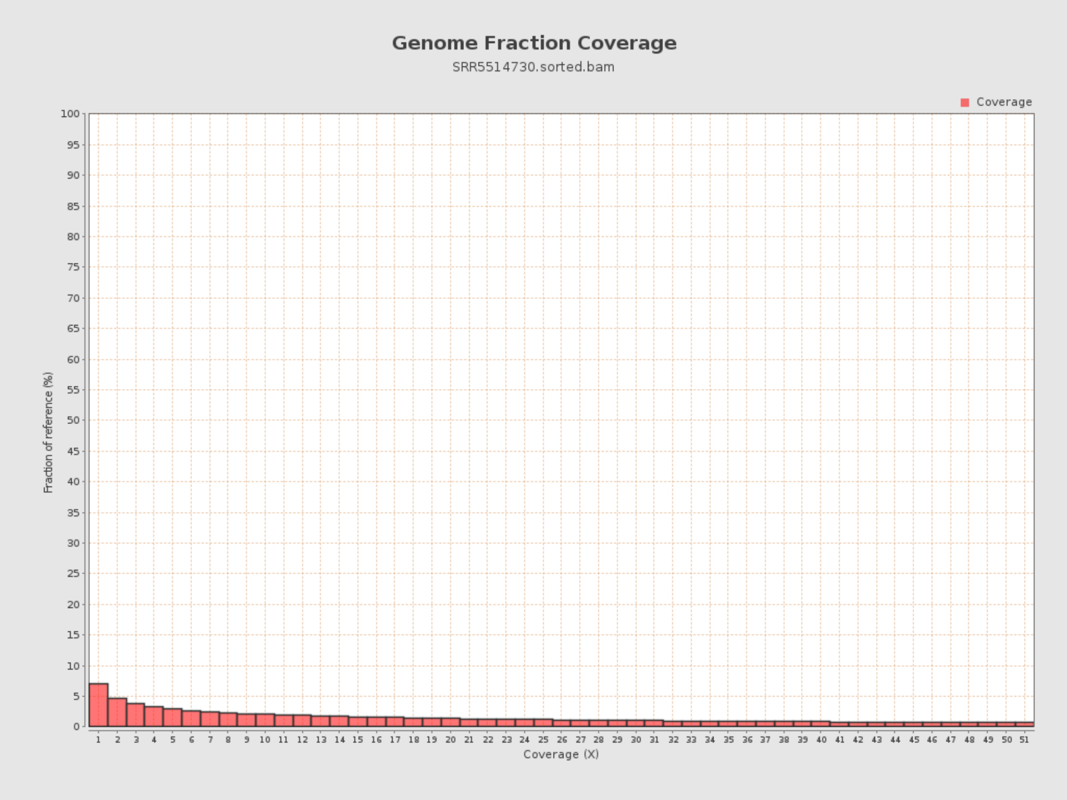
4. Results : Coverage Histogram



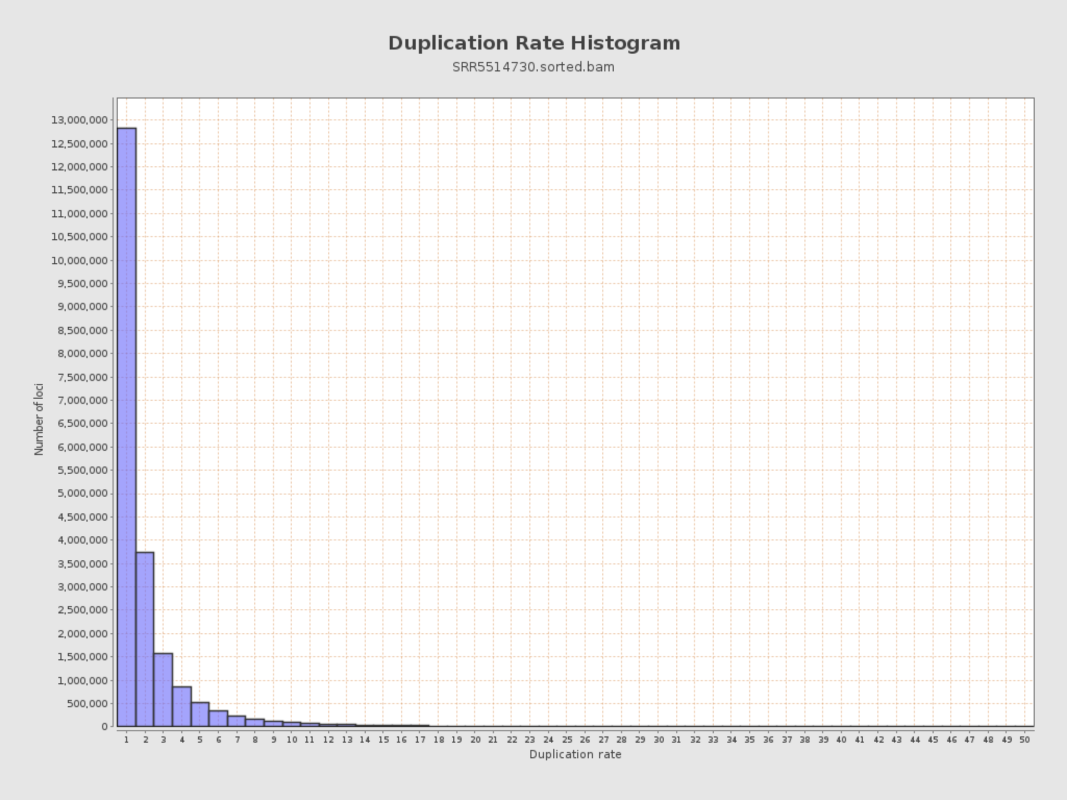
5. Results : Coverage Histogram (0-50X)



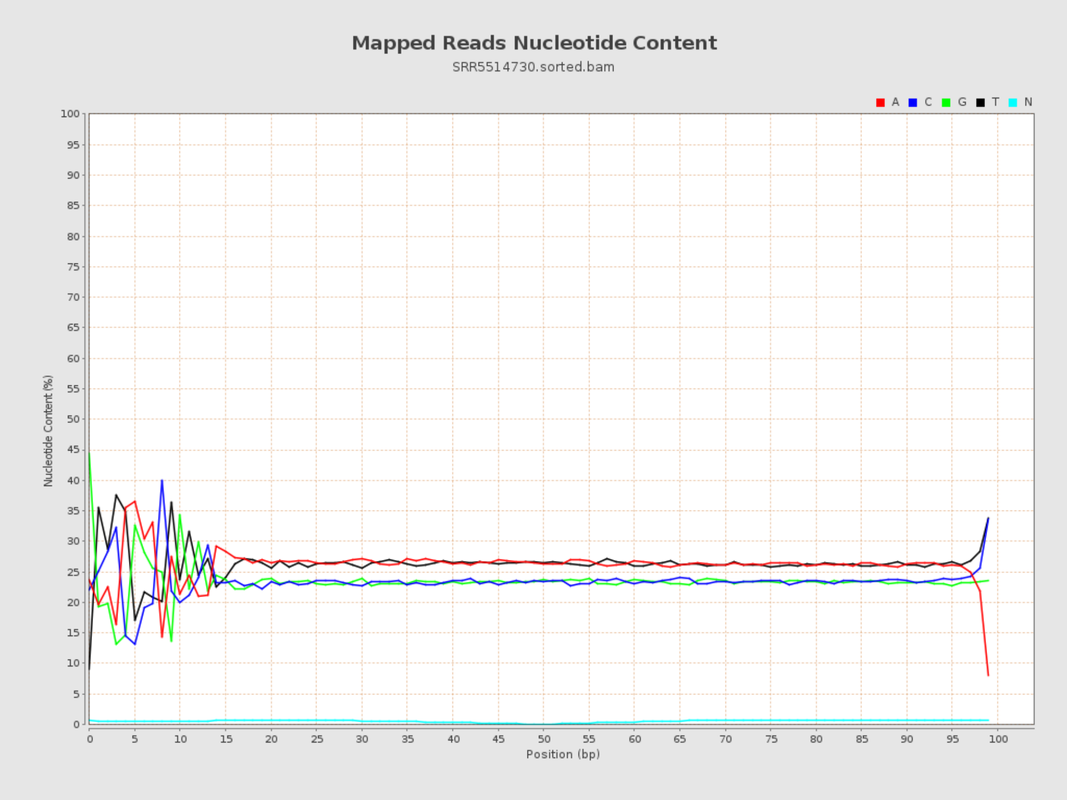
6. Results : Genome Fraction Coverage



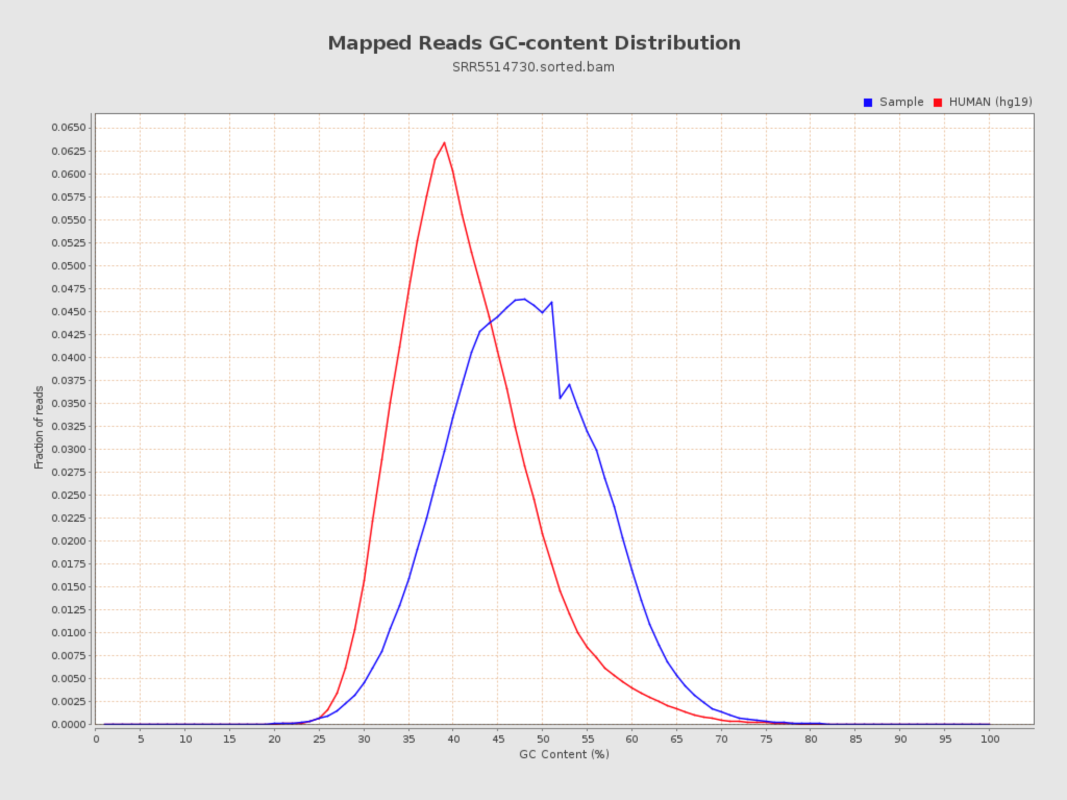
7. Results : Duplication Rate Histogram



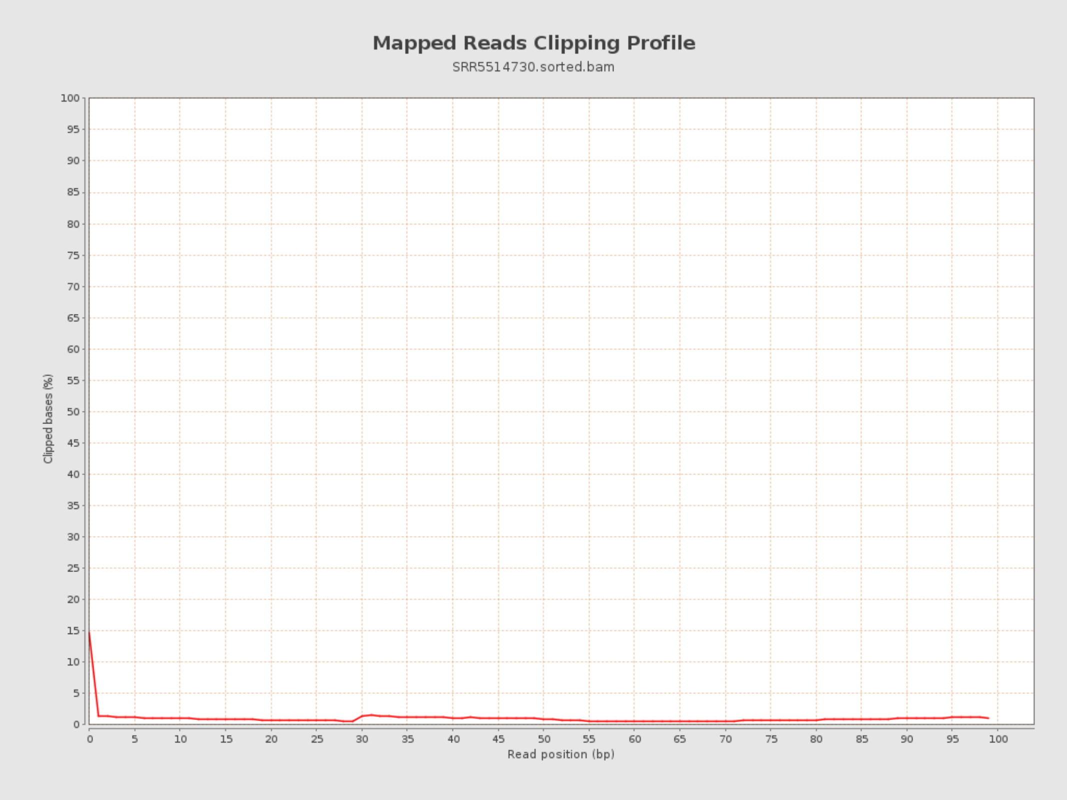
8. Results : Mapped Reads Nucleotide Content



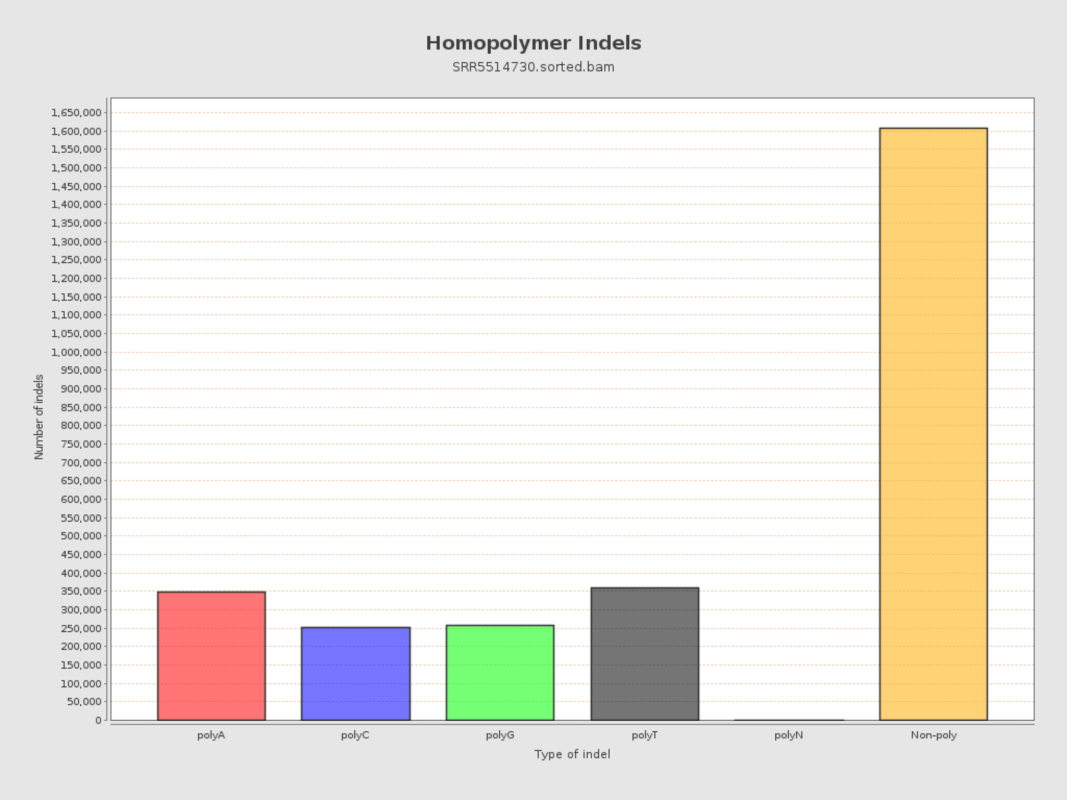
9. Results : Mapped Reads GC-content Distribution



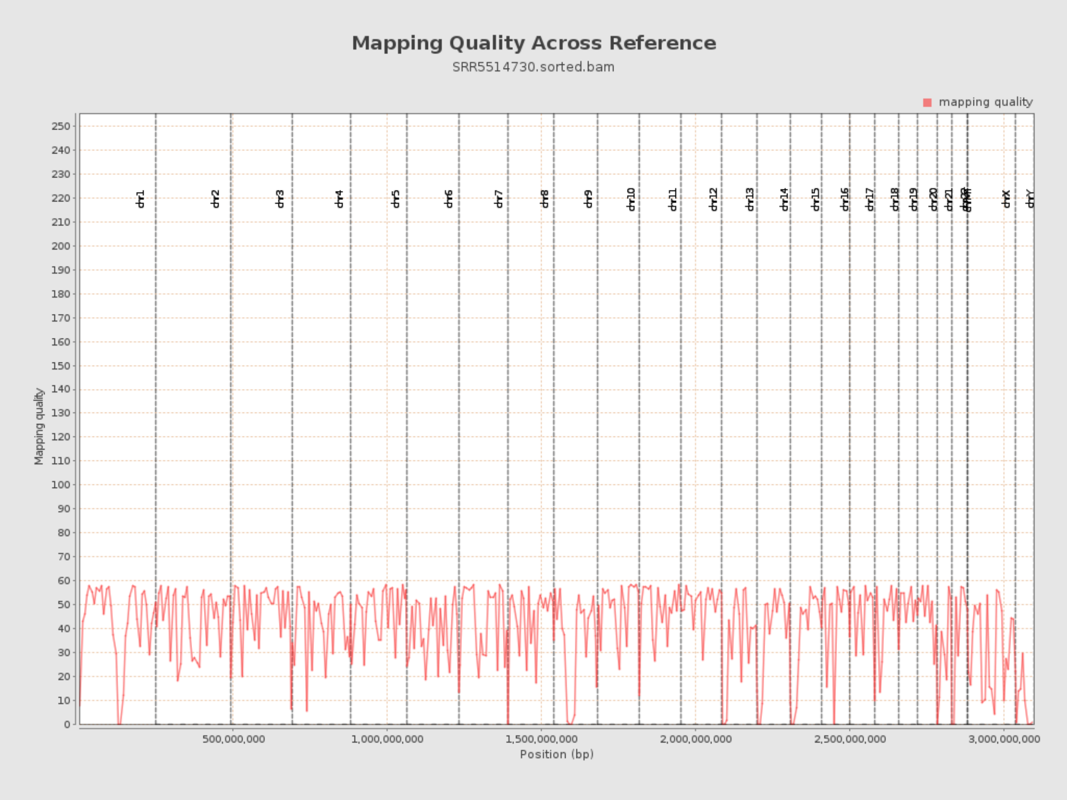
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram