Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 11:06:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514723.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_SRR5514723 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514723.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 11:06:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514723.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	72,535,785
Mapped reads	72,000,368 / 99.26%
Unmapped reads	535,417 / 0.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,055,737 / 6.97%
Read min/max/mean length	30 / 100 / 100.65
Duplicated reads (estimated)	70,002,285 / 96.51%
Duplication rate	49.28%
Clipped reads	19,582,345 / 27%

2.2. ACGT Content

Number/percentage of A's	1,973,276,334 / 28.7%
Number/percentage of C's	1,454,106,867 / 21.15%
Number/percentage of T's	1,960,962,033 / 28.52%
Number/percentage of G's	1,482,889,218 / 21.57%
Number/percentage of N's	3,888,393 / 0.06%
GC Percentage	42.72%

2.3. Coverage

Mean	2.2221

Standard Deviation	187.3391

2.4. Mapping Quality

Mean Mapping Quality	46.57

2.5. Mismatches and indels

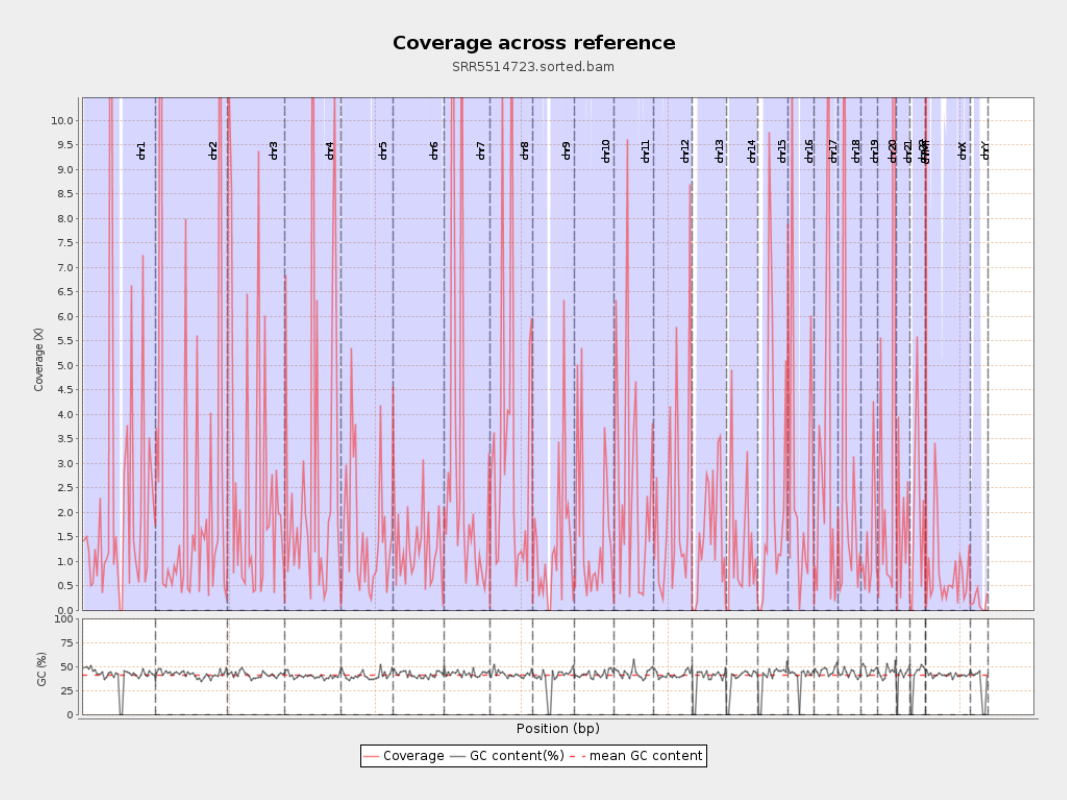
General error rate	0.77%
Mismatches	48,095,928
Insertions	2,927,166
Mapped reads with at least one insertion	3.97%
Deletions	1,934,088
Mapped reads with at least one deletion	2.62%
Homopolymer indels	47.07%

2.6. Chromosome stats

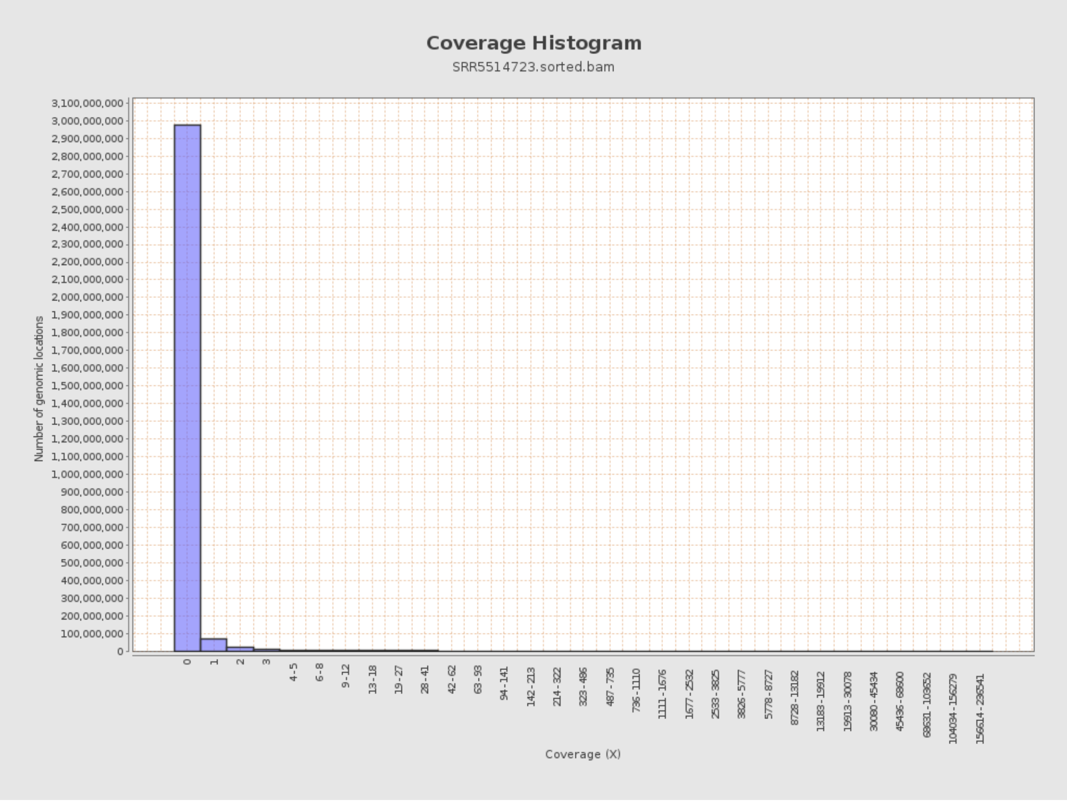
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	537852625	2.1579	229.8006
chr2	243199373	654755941	2.6923	342.4558
chr3	198022430	523508365	2.6437	163.2035
chr4	191154276	565155366	2.9565	205.1704
chr5	180915260	298119061	1.6478	89.4864
chr6	171115067	214506622	1.2536	66.7985
chr7	159138663	472530737	2.9693	136.2007

chr8	146364022	508024765	3.471	256.0459
chr9	141213431	190063406	1.3459	66.4633
chr10	135534747	221131117	1.6315	100.3604
chr11	135006516	343127314	2.5416	167.5095
chr12	133851895	271009811	2.0247	114.0614
chr13	115169878	182189101	1.5819	78.261
chr14	107349540	139451348	1.299	80.9304
chr15	102531392	241184628	2.3523	156.2898
chr16	90354753	258134265	2.8569	191.4335
chr17	81195210	260463979	3.2079	259.9221
chr18	78077248	222597007	2.851	249.503
chr19	59128983	74493319	1.2598	52.6068
chr20	63025520	383804142	6.0897	443.2494
chr21	48129895	79376150	1.6492	83.3309
chr22	51304566	101519149	1.9788	93.6347
chrMT	16571	871010	52.5623	89.2864
chrX	155270560	123975474	0.7984	53.8652
chrY	59373566	11087745	0.1867	12.256

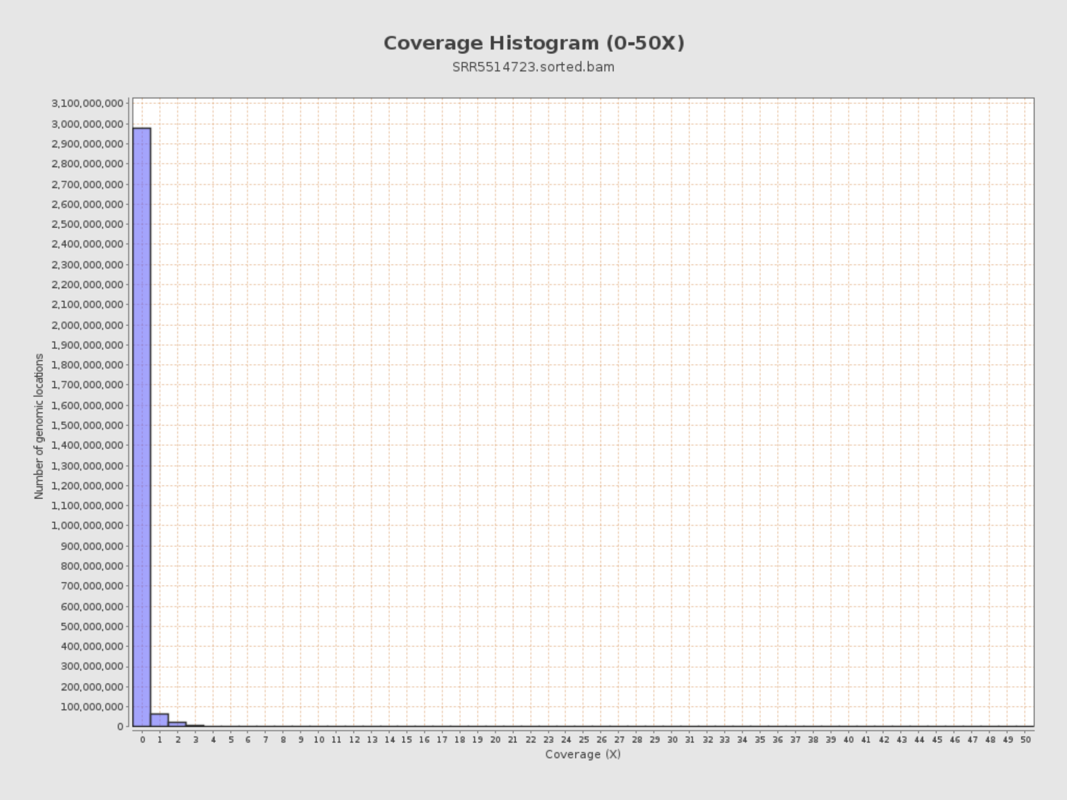
3. Results : Coverage across reference



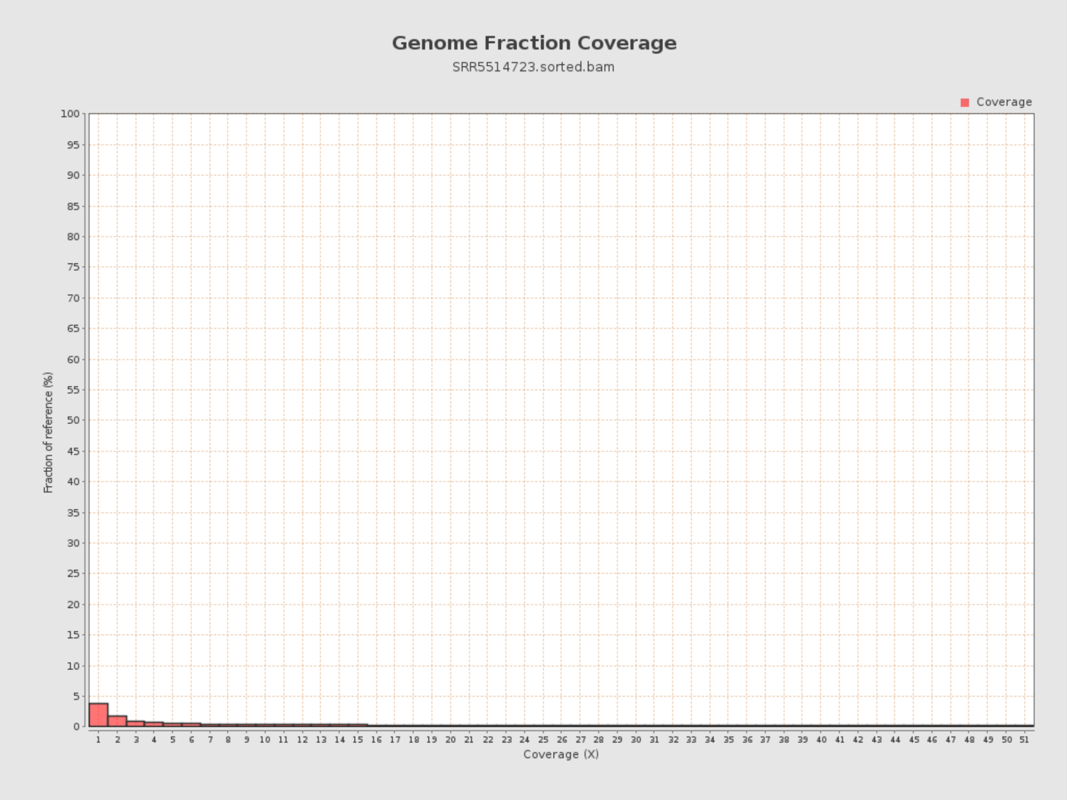
4. Results : Coverage Histogram



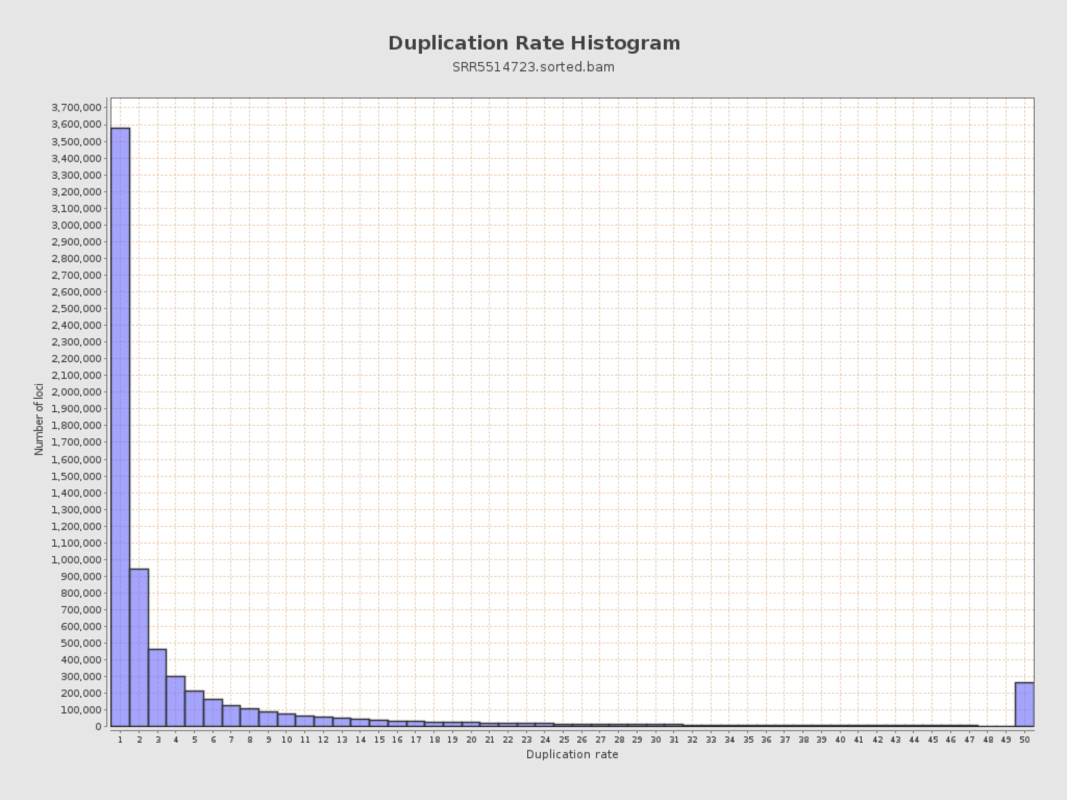
5. Results : Coverage Histogram (0-50X)



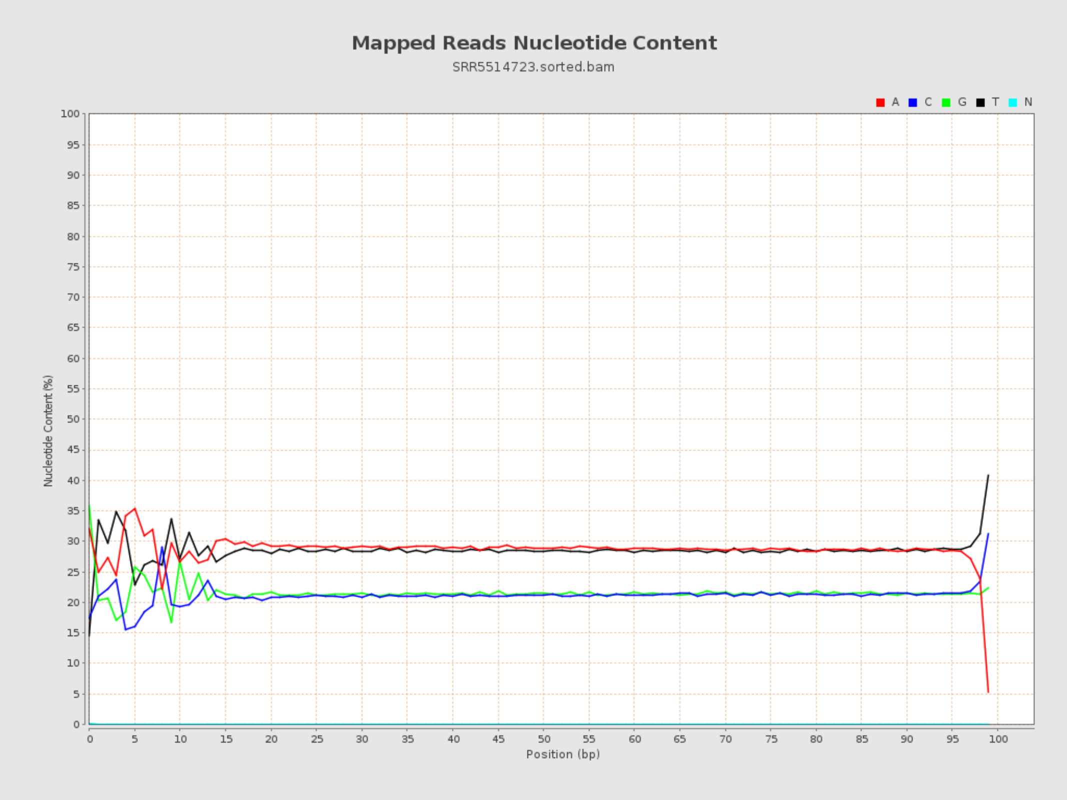
6. Results : Genome Fraction Coverage



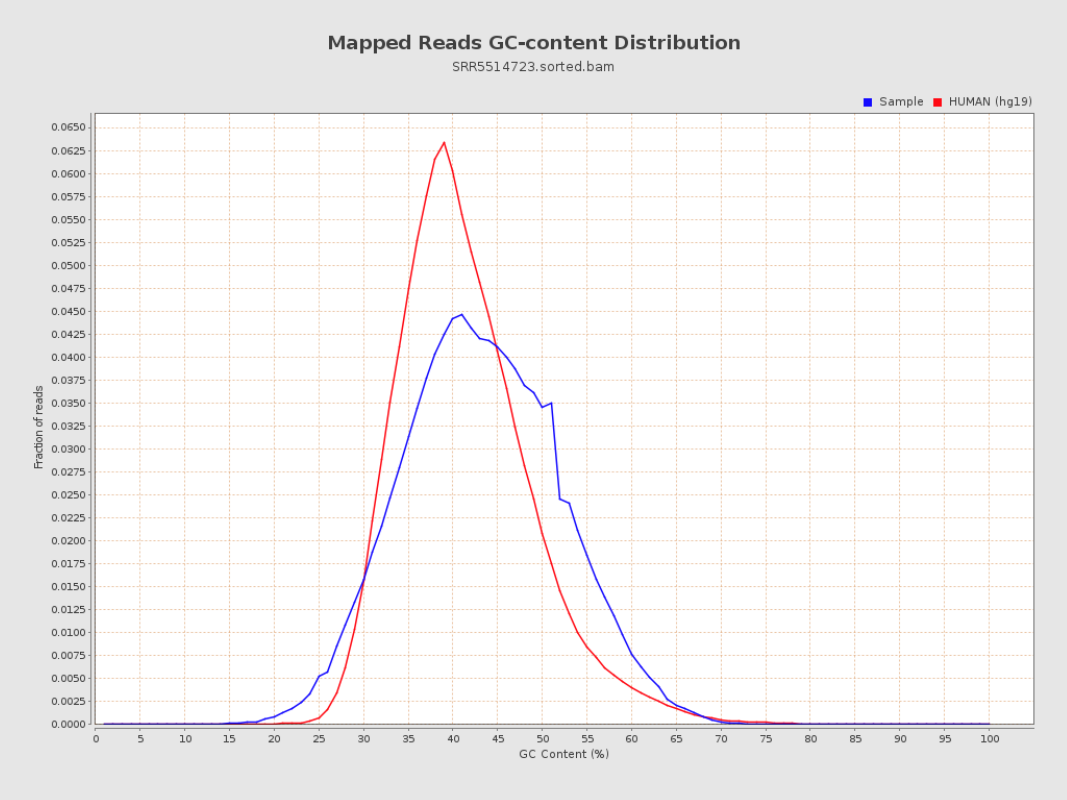
7. Results : Duplication Rate Histogram



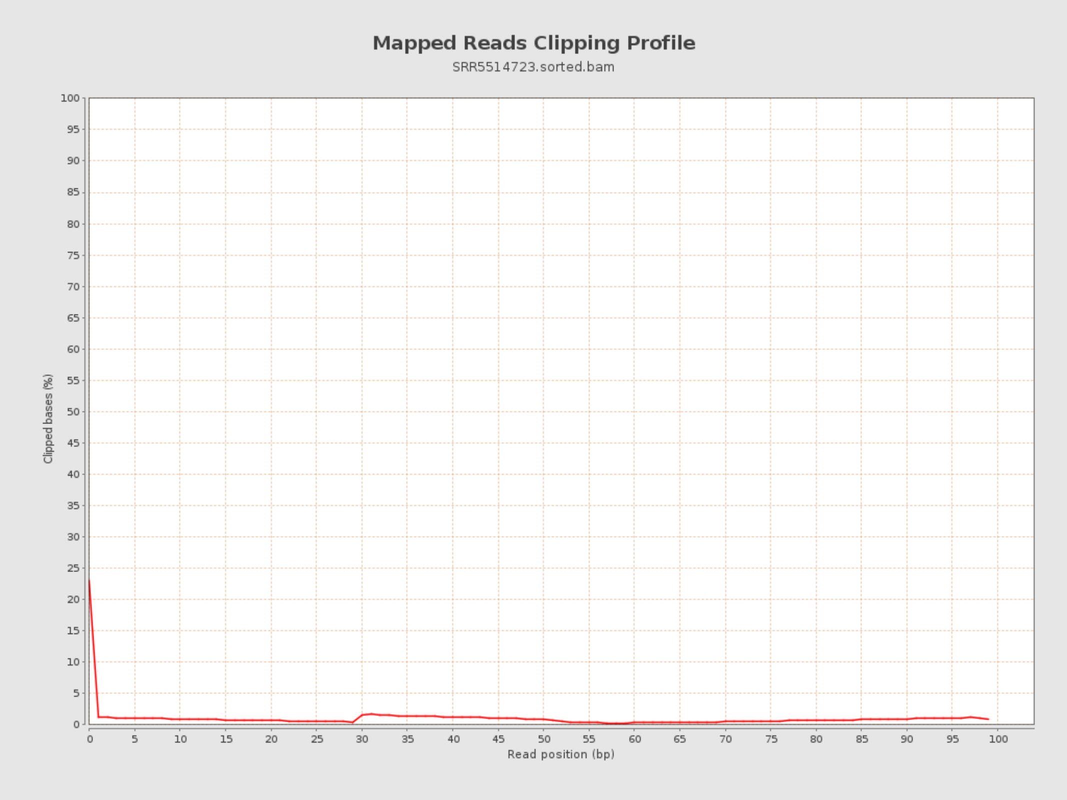
8. Results : Mapped Reads Nucleotide Content



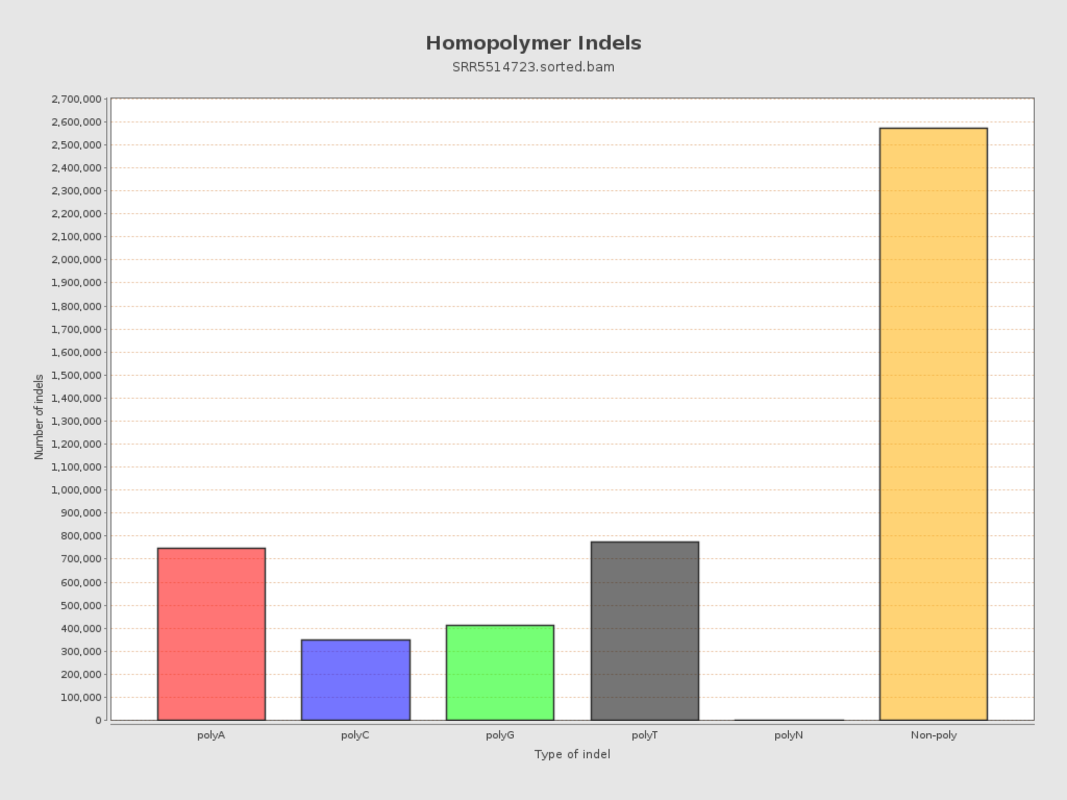
9. Results : Mapped Reads GC-content Distribution



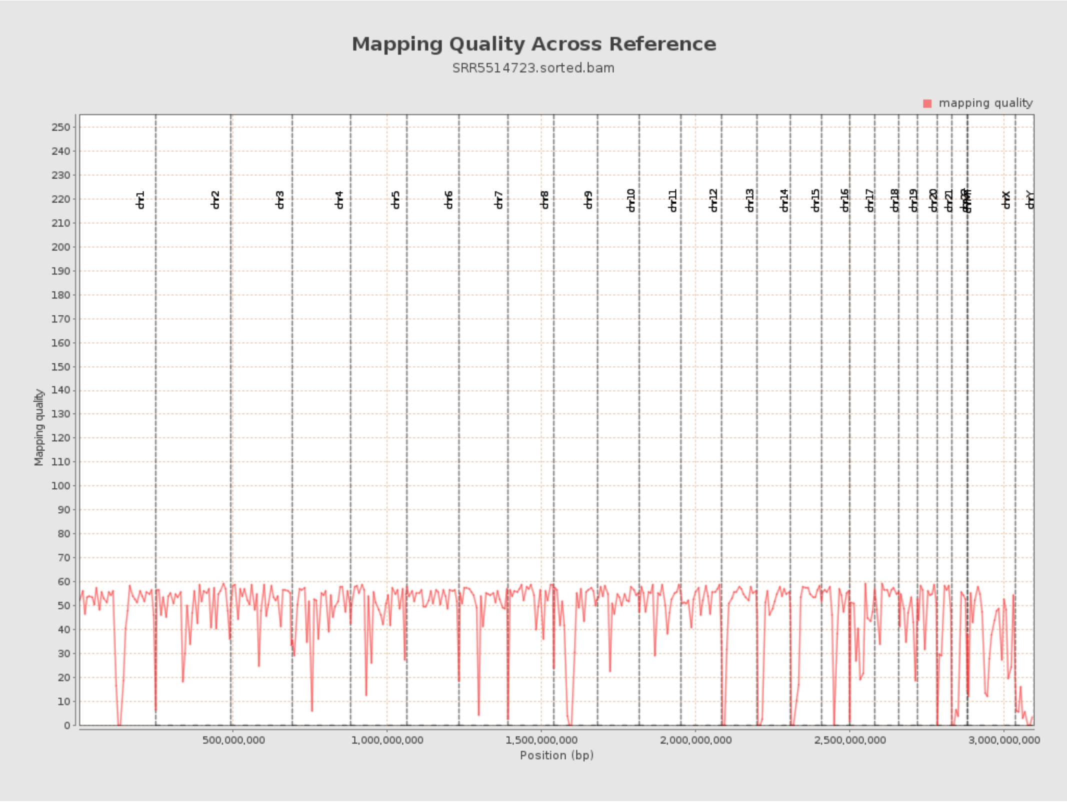
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram