Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 22:37:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514745.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_SRR5514745 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514745.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 22:37:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514745.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	117,615,784
Mapped reads	116,756,541 / 99.27%
Unmapped reads	859,243 / 0.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,142,707 / 8.62%
Read min/max/mean length	30 / 100 / 101.24
Duplicated reads (estimated)	118,602,141 / 100.84%
Duplication rate	51.63%
Clipped reads	38,144,181 / 32.43%

2.2. ACGT Content

Number/percentage of A's	3,115,596,797 / 28.14%
Number/percentage of C's	2,394,462,526 / 21.63%
Number/percentage of T's	3,132,391,014 / 28.29%
Number/percentage of G's	2,425,610,116 / 21.91%
Number/percentage of N's	3,589,175 / 0.03%
GC Percentage	43.54%

2.3. Coverage

Mean	3.5809

Standard Deviation	672.4837

2.4. Mapping Quality

Mean Mapping Quality	48.67

2.5. Mismatches and indels

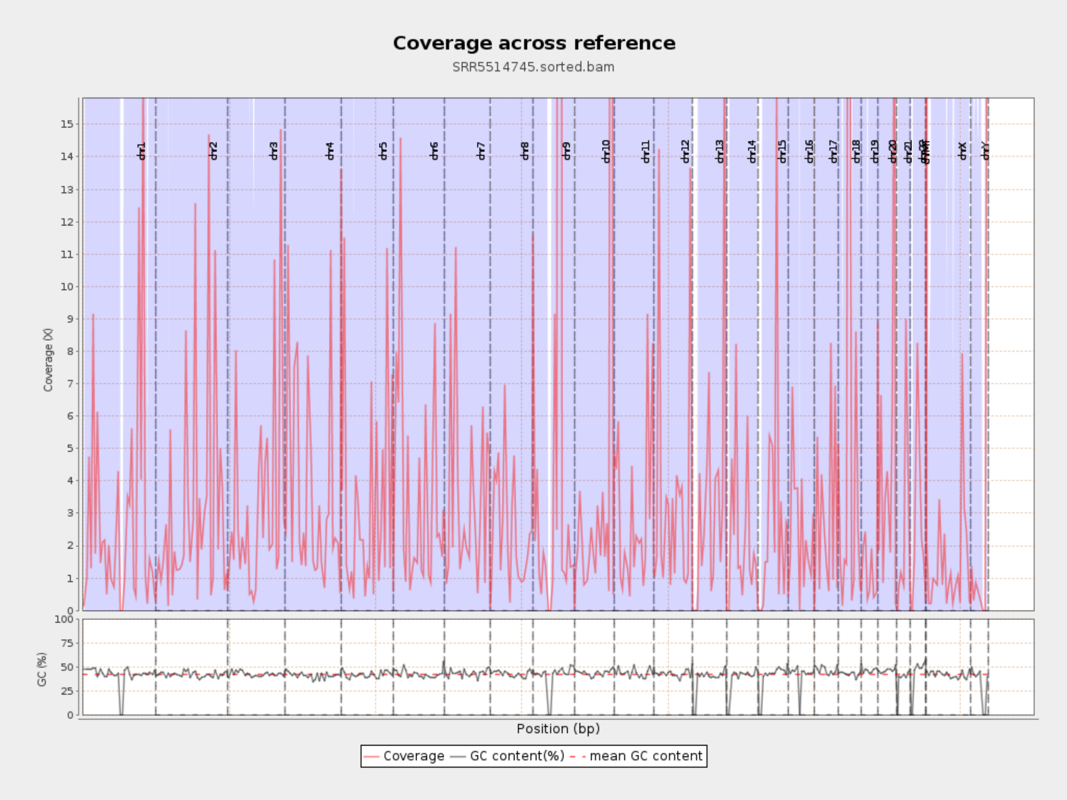
General error rate	0.91%
Mismatches	89,553,387
Insertions	5,933,839
Mapped reads with at least one insertion	4.9%
Deletions	5,214,654
Mapped reads with at least one deletion	4.24%
Homopolymer indels	35.21%

2.6. Chromosome stats

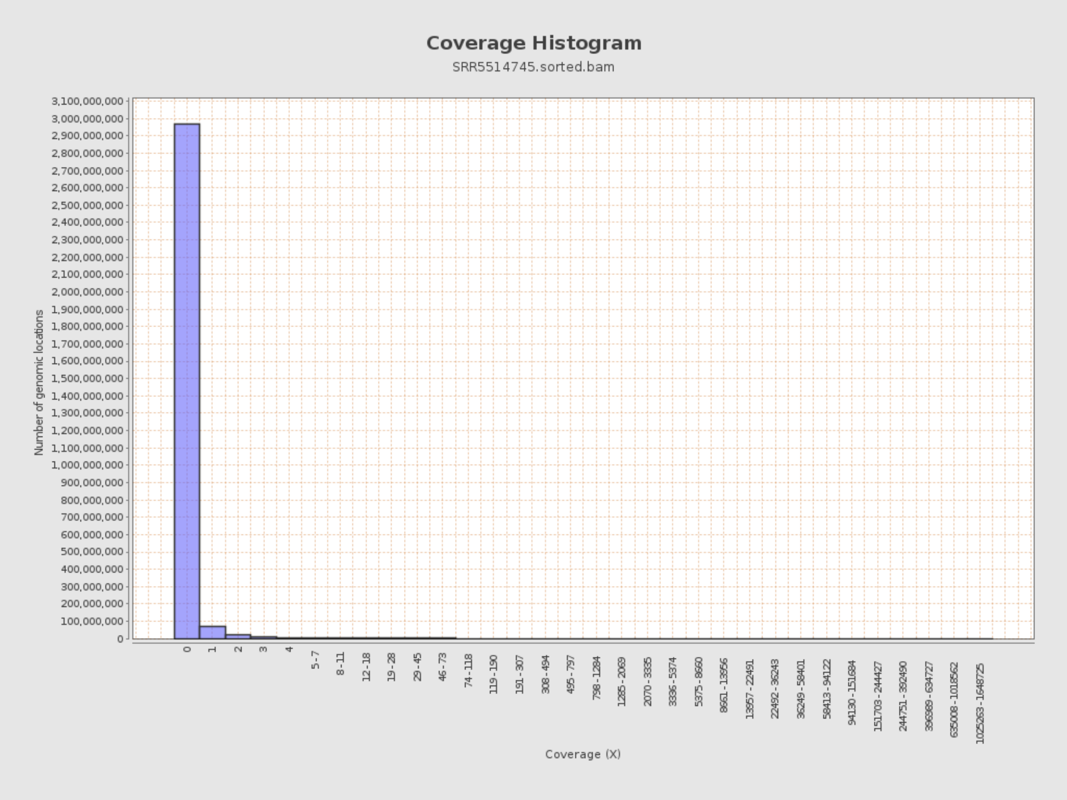
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	726237662	2.9137	314.4728
chr2	243199373	785881018	3.2314	203.3205
chr3	198022430	653087658	3.298	180.7914
chr4	191154276	693050550	3.6256	238.7929
chr5	180915260	600822238	3.321	175.612
chr6	171115067	630549250	3.6849	296.3734
chr7	159138663	551036794	3.4626	224.4504

chr8	146364022	363833276	2.4858	119.5963
chr9	141213431	1519735704	10.762	2,903.6502
chr10	135534747	645008269	4.759	561.6682
chr11	135006516	404468714	2.9959	163.1236
chr12	133851895	465123265	3.4749	216.5303
chr13	115169878	420296994	3.6494	519.7394
chr14	107349540	249621393	2.3253	136.6521
chr15	102531392	306778527	2.992	222.0676
chr16	90354753	224010322	2.4792	98.7227
chr17	81195210	247860886	3.0527	186.8099
chr18	78077248	445750862	5.7091	284.9007
chr19	59128983	84206335	1.4241	69.9531
chr20	63025520	364077490	5.7767	532.6963
chr21	48129895	126993644	2.6386	213.8634
chr22	51304566	144295033	2.8125	125.9774
chrMT	16571	2287104	138.0185	301.1327
chrX	155270560	229074657	1.4753	134.9797
chrY	59373566	201422559	3.3925	169.6321

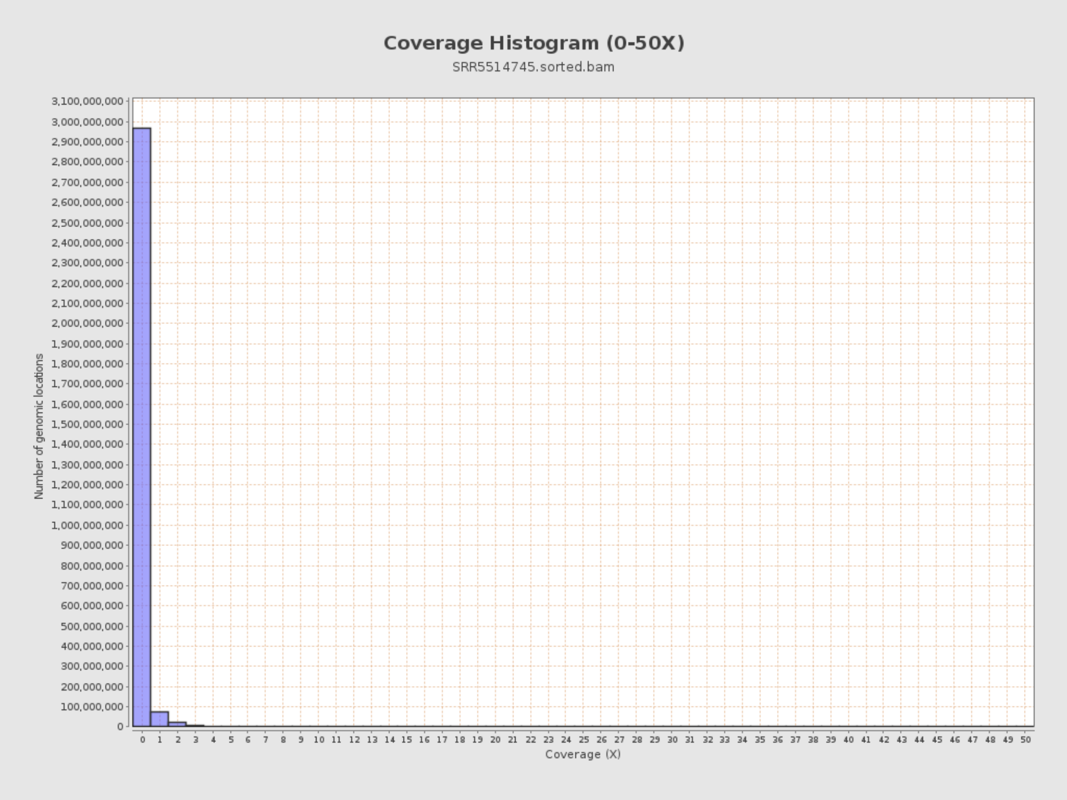
3. Results : Coverage across reference



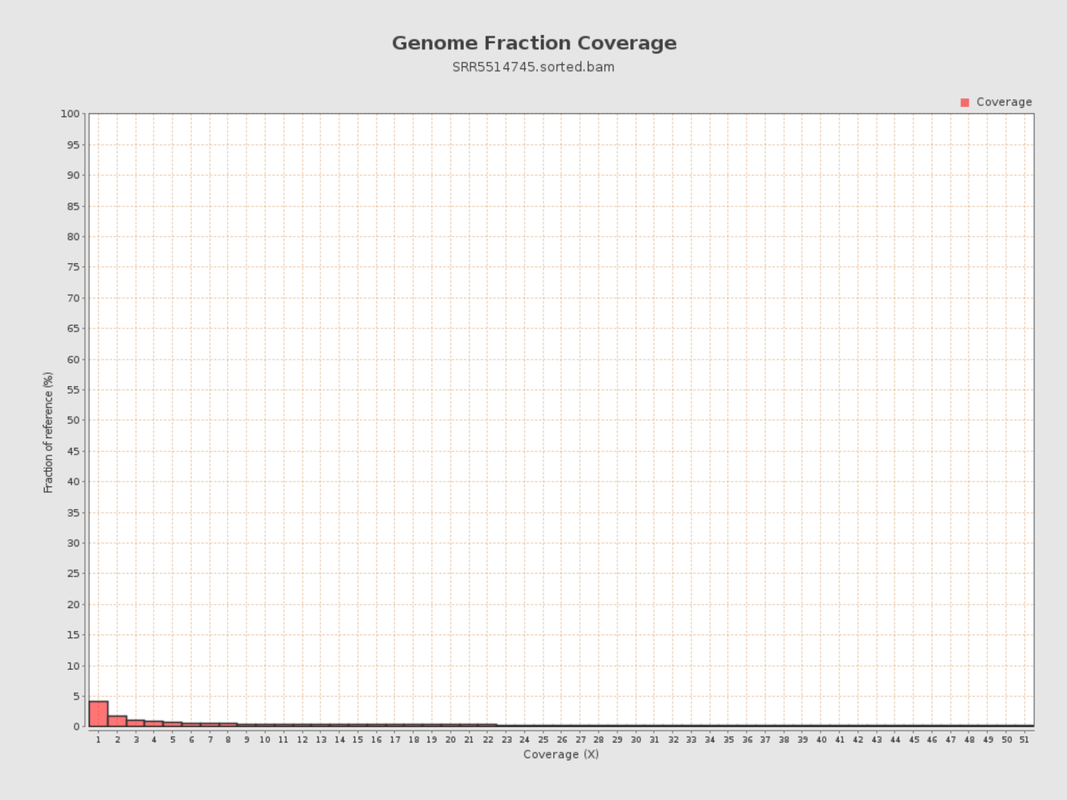
4. Results : Coverage Histogram



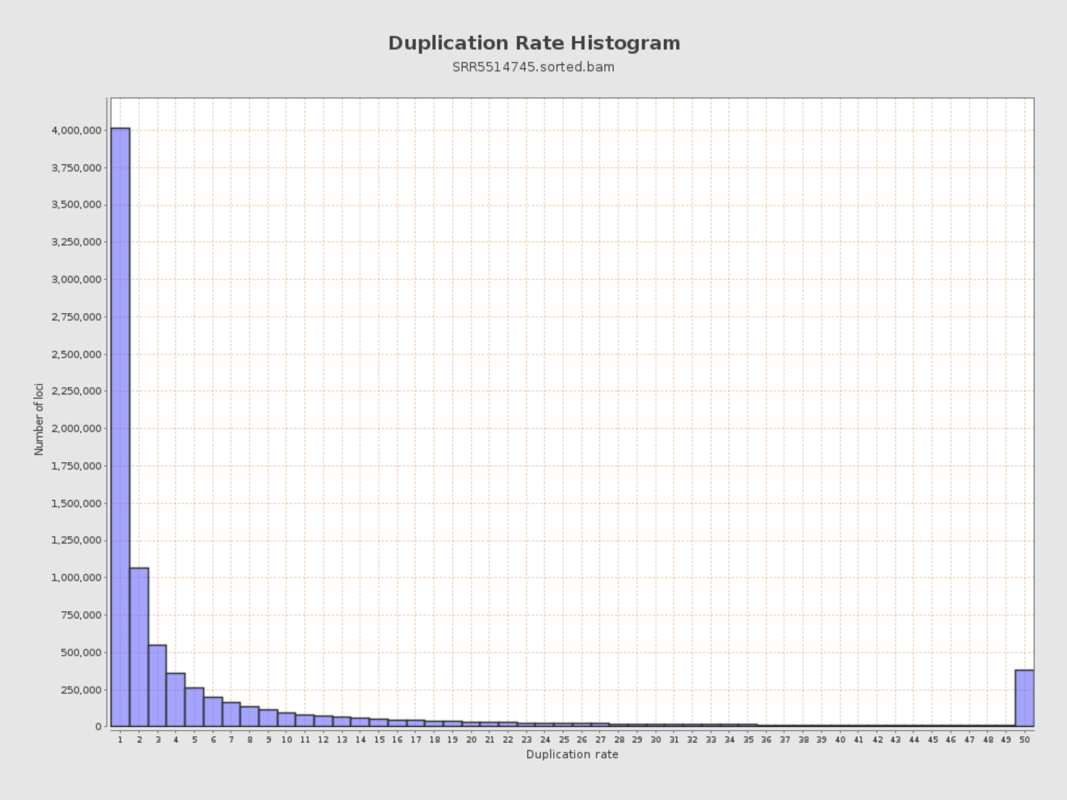
5. Results : Coverage Histogram (0-50X)



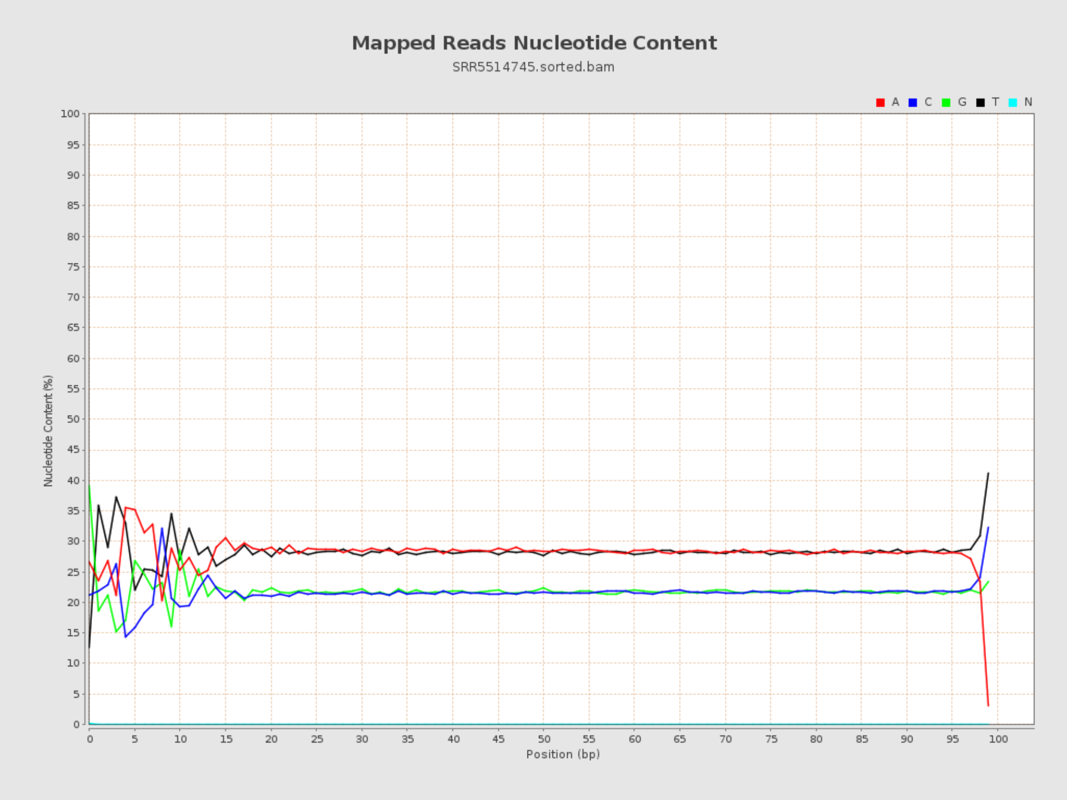
6. Results : Genome Fraction Coverage



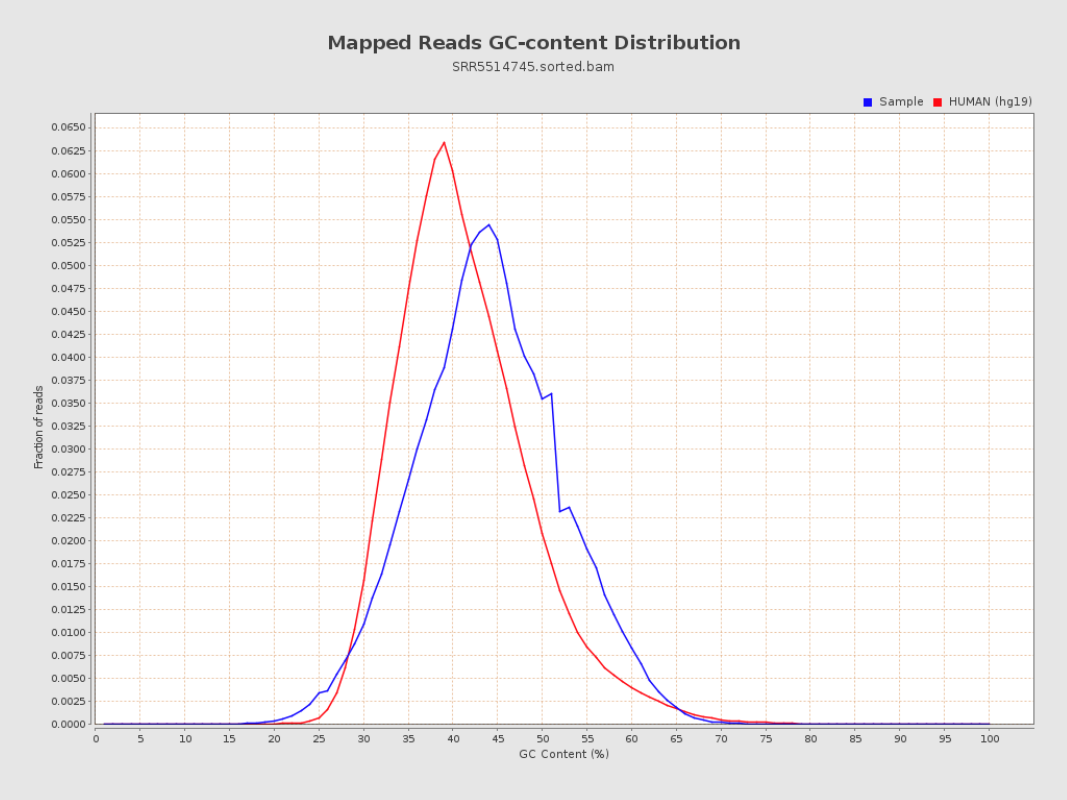
7. Results : Duplication Rate Histogram



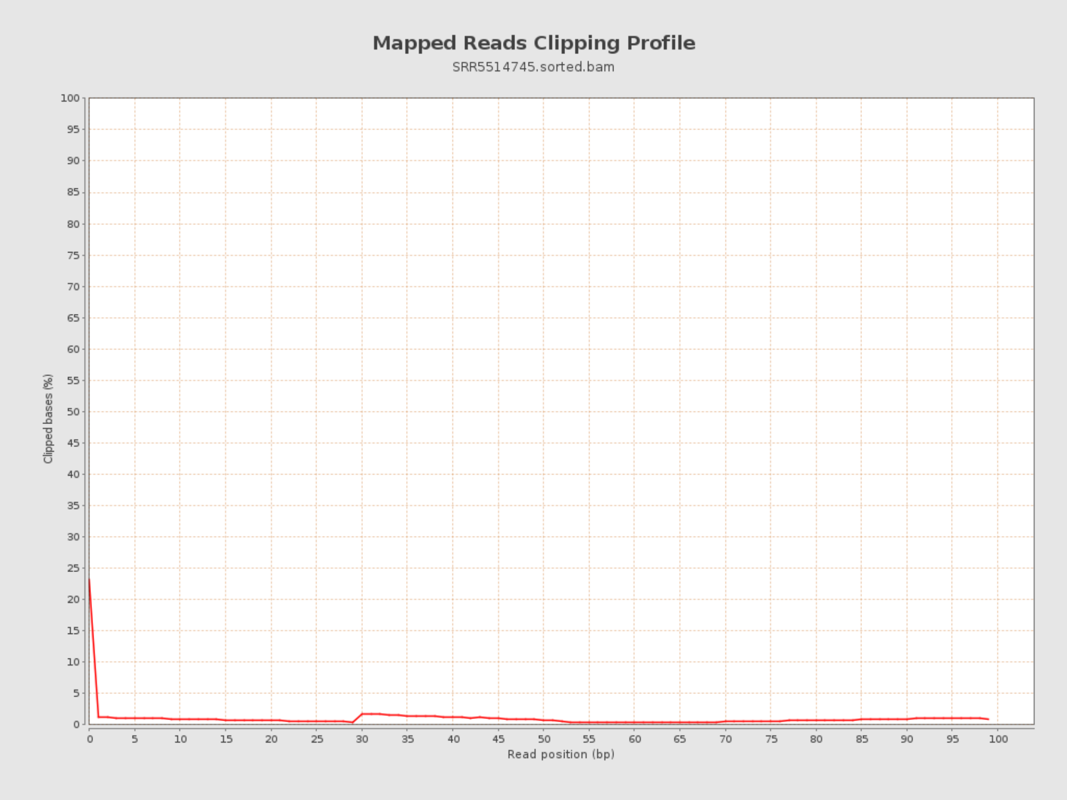
8. Results : Mapped Reads Nucleotide Content



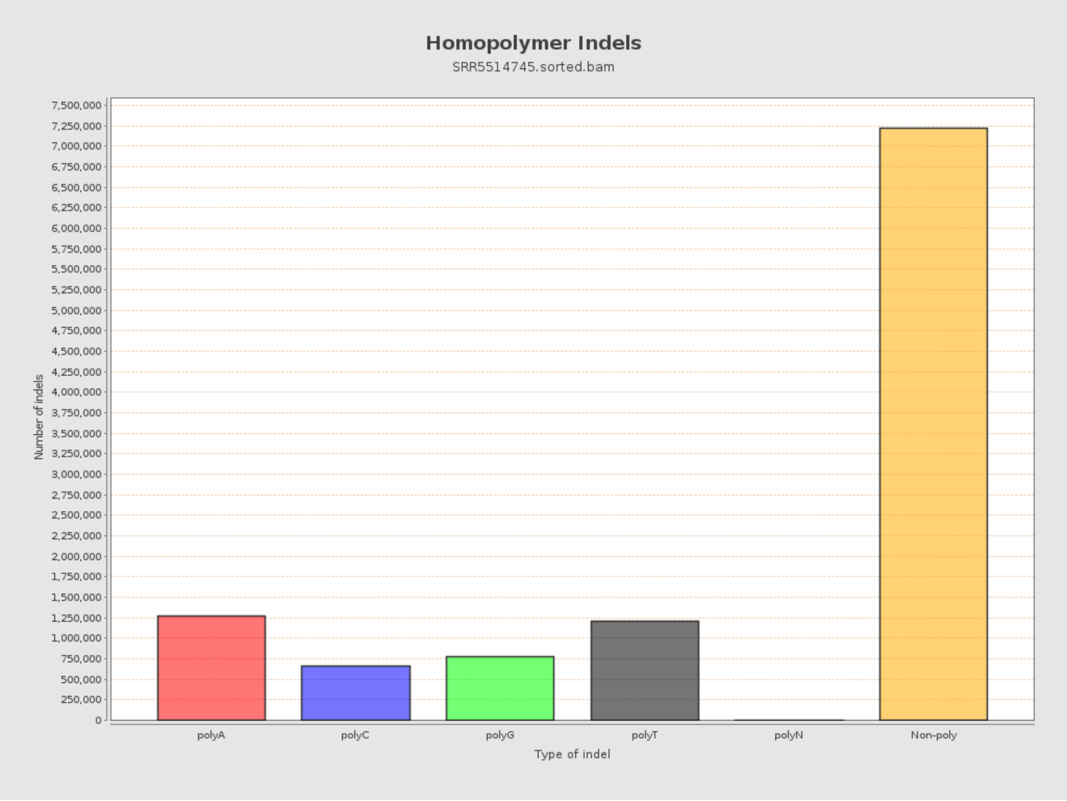
9. Results : Mapped Reads GC-content Distribution



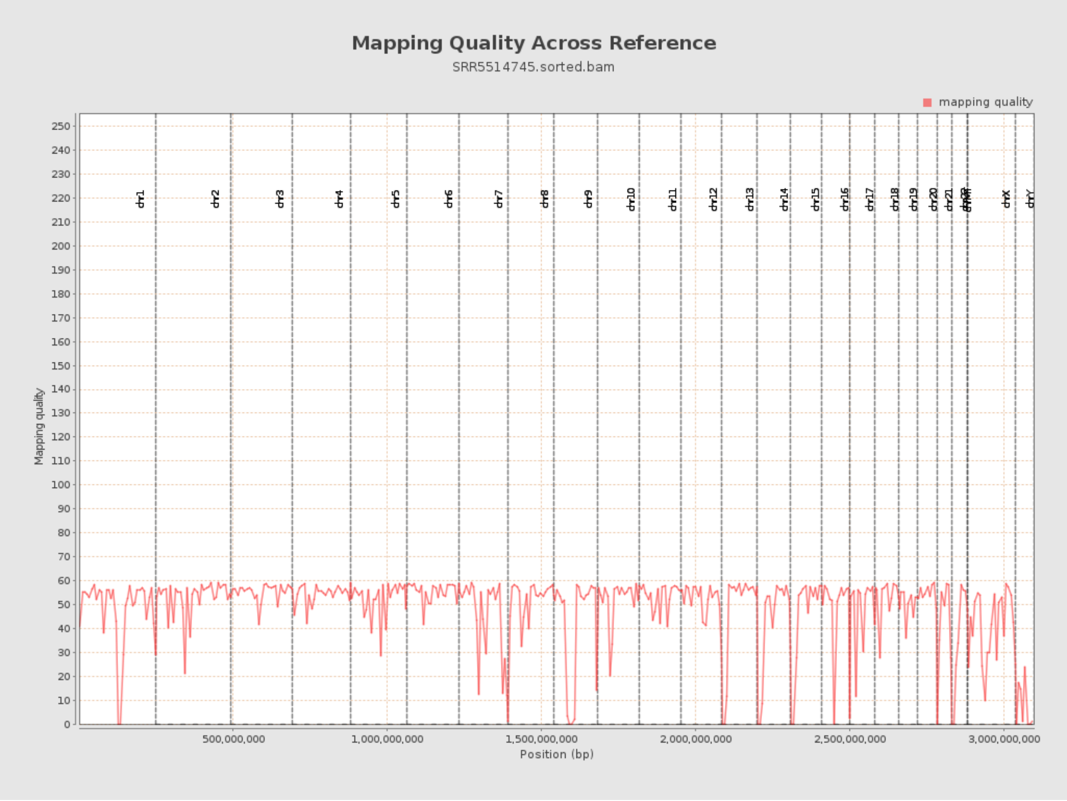
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram