Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 02:47:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514722.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_SRR5514722 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514722.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 02:47:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514722.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	167,397,893
Mapped reads	152,994,499 / 91.4%
Unmapped reads	14,403,394 / 8.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,685,630 / 6.38%
Read min/max/mean length	30 / 100 / 100.9
Duplicated reads (estimated)	148,674,811 / 88.82%
Duplication rate	49.92%
Clipped reads	56,344,910 / 33.66%

2.2. ACGT Content

Number/percentage of A's	3,649,136,405 / 26.5%
Number/percentage of C's	3,116,711,975 / 22.63%
Number/percentage of T's	3,679,462,735 / 26.72%
Number/percentage of G's	3,156,764,176 / 22.92%
Number/percentage of N's	168,053,481 / 1.22%
GC Percentage	45.56%

2.3. Coverage

Mean	4.4567

Standard Deviation	389.1126

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

General error rate	1.39%
Mismatches	165,364,243
Insertions	10,458,825
Mapped reads with at least one insertion	6.32%
Deletions	7,940,310
Mapped reads with at least one deletion	4.74%
Homopolymer indels	31.05%

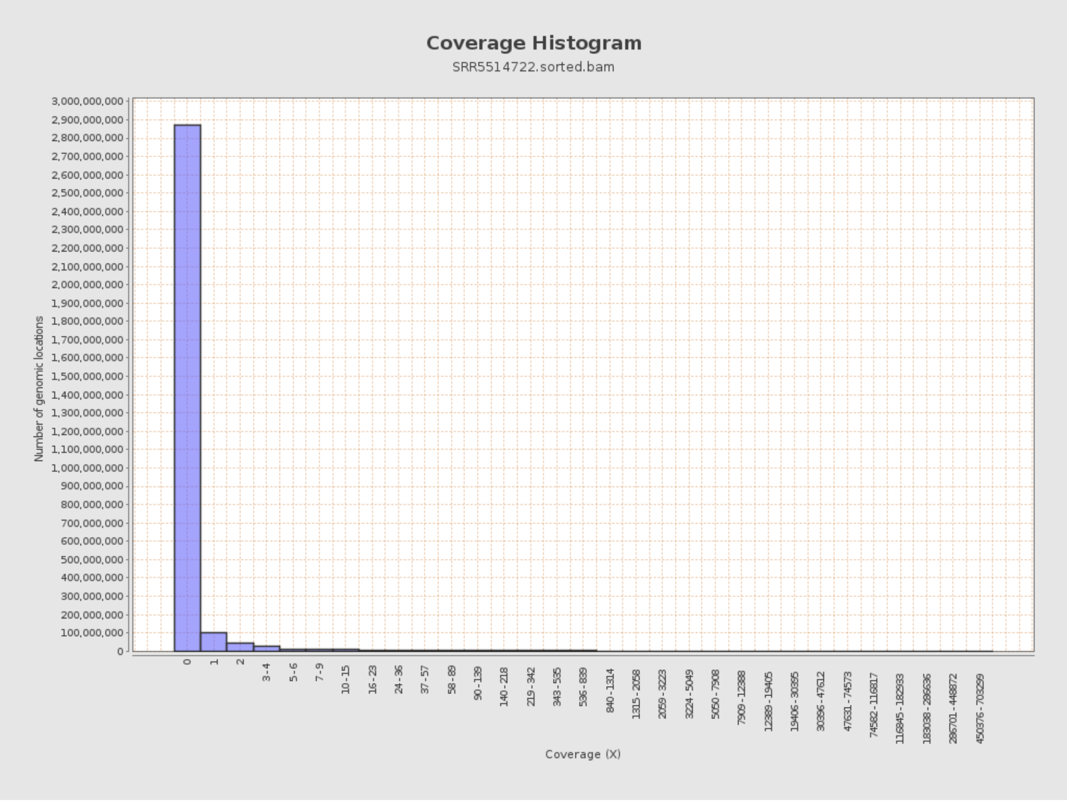
2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1023099449	4.1047	151.7519
chr2	243199373	1403939110	5.7728	733.7069
chr3	198022430	641801090	3.2411	103.4272
chr4	191154276	752718378	3.9378	247.9031
chr5	180915260	808257949	4.4676	302.5351
chr6	171115067	592170645	3.4607	212.6934
chr7	159138663	460259380	2.8922	140.041

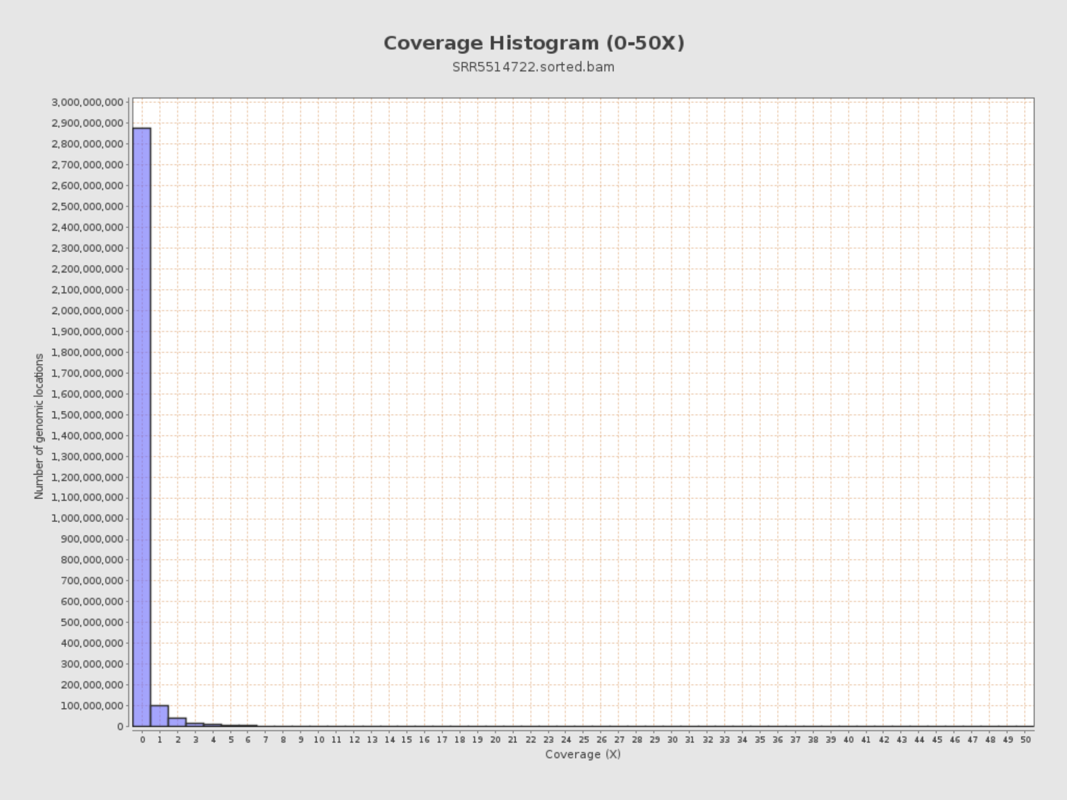
chr8	146364022	510813751	3.49	176.4503
chr9	141213431	731909885	5.183	251.7319
chr10	135534747	830168309	6.1251	373.094
chr11	135006516	728907436	5.3991	188.2377
chr12	133851895	566020165	4.2287	201.9142
chr13	115169878	768201723	6.6702	1,043.6394
chr14	107349540	450434121	4.196	252.2613
chr15	102531392	278980644	2.7209	105.3763
chr16	90354753	662094156	7.3277	502.6925
chr17	81195210	306042648	3.7692	148.3
chr18	78077248	311806567	3.9936	153.5905
chr19	59128983	457942490	7.7448	523.8511
chr20	63025520	223194318	3.5413	222.0516
chr21	48129895	345404592	7.1765	741.2324
chr22	51304566	290034093	5.6532	573.1018
chrMT	16571	3231196	194.991	267.725
chrX	155270560	397130199	2.5577	149.6451
chrY	59373566	252027973	4.2448	611.0837

3. Results : Coverage across reference

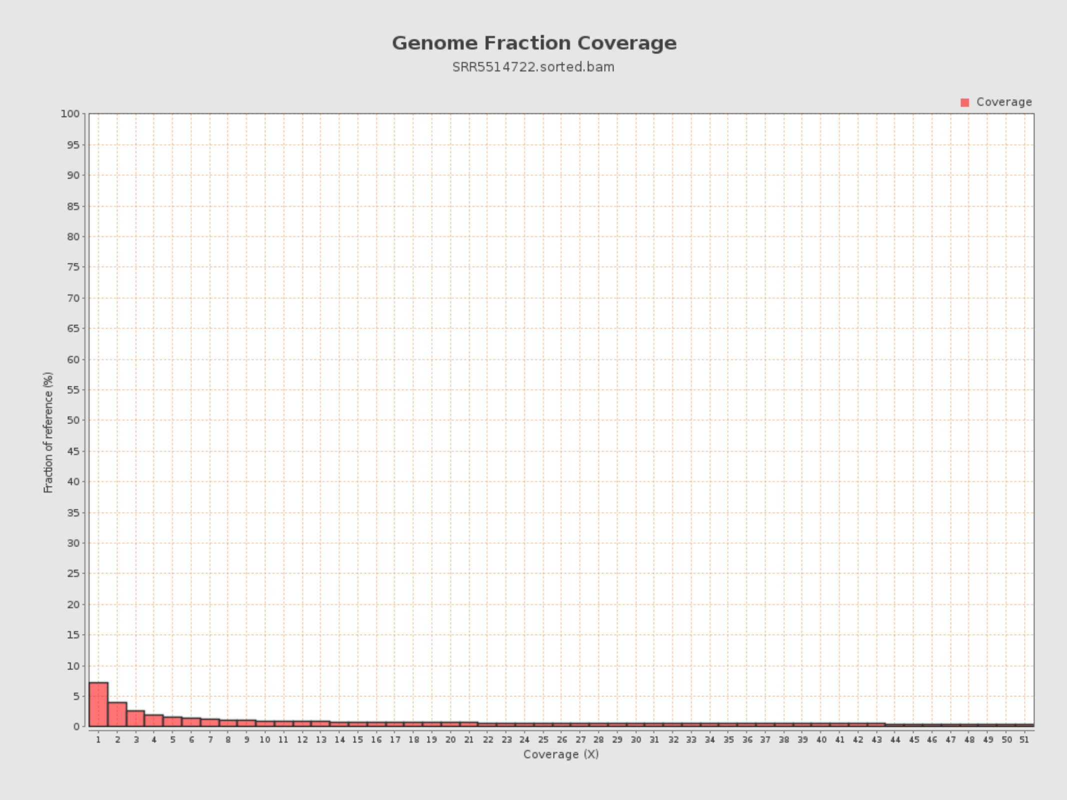
4. Results : Coverage Histogram



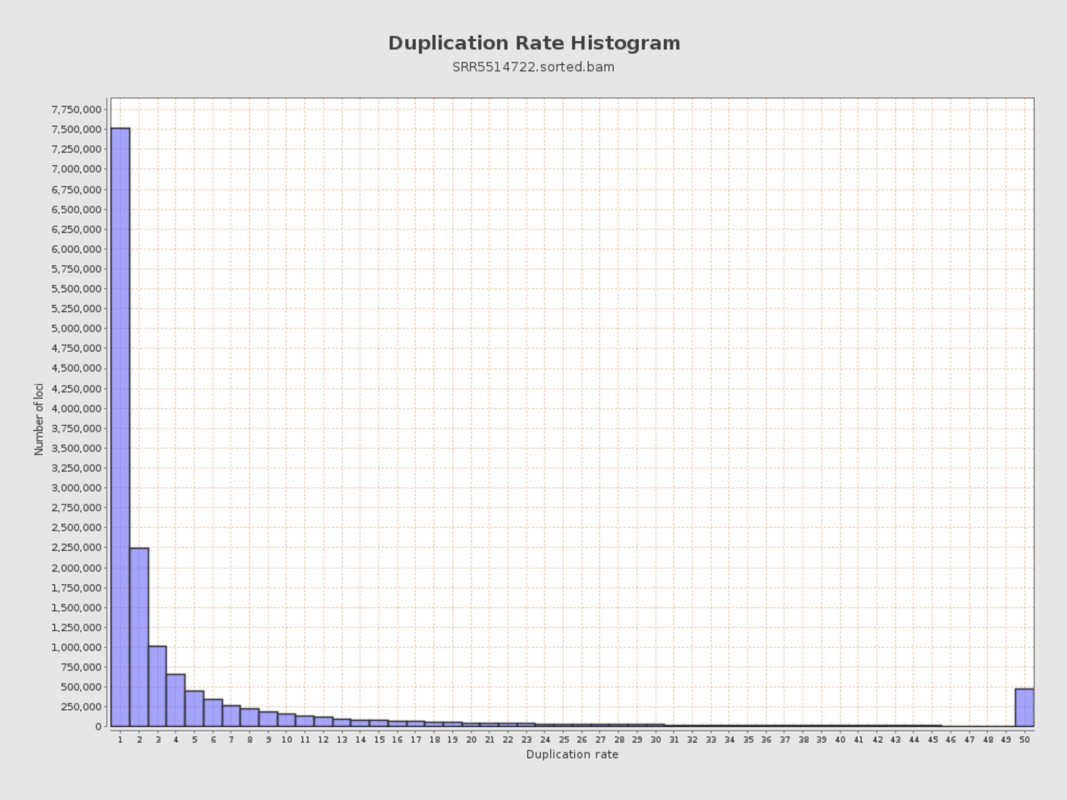
5. Results : Coverage Histogram (0-50X)



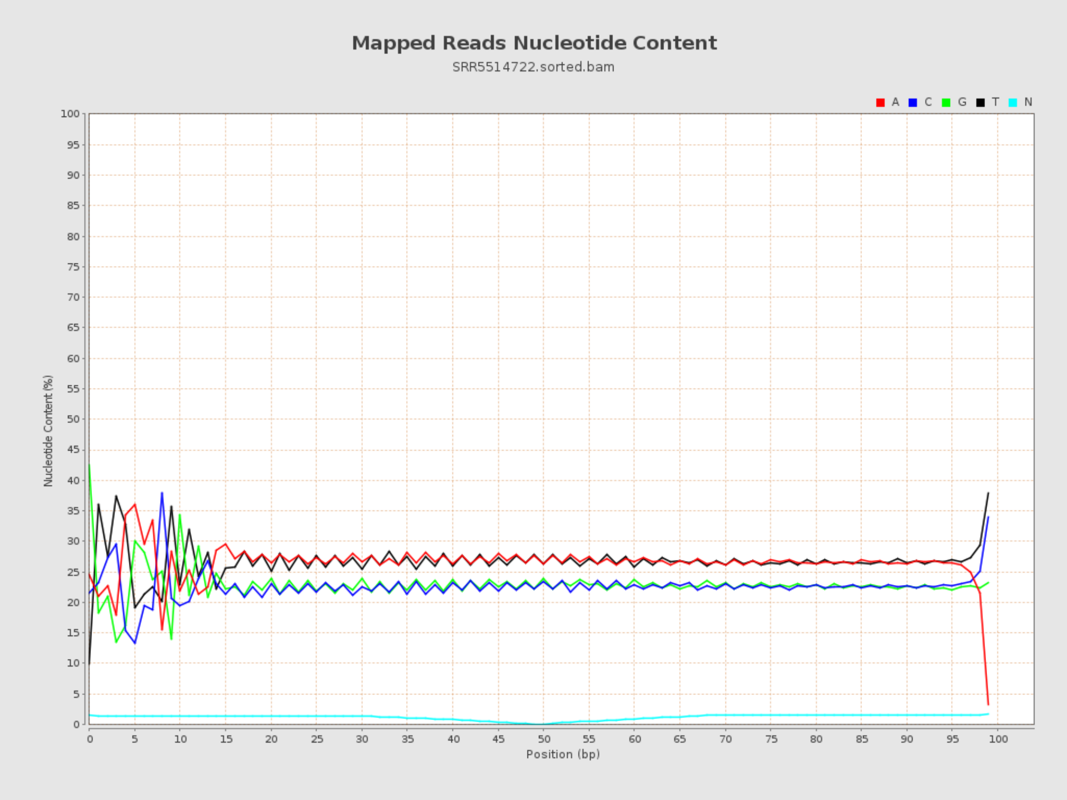
6. Results : Genome Fraction Coverage



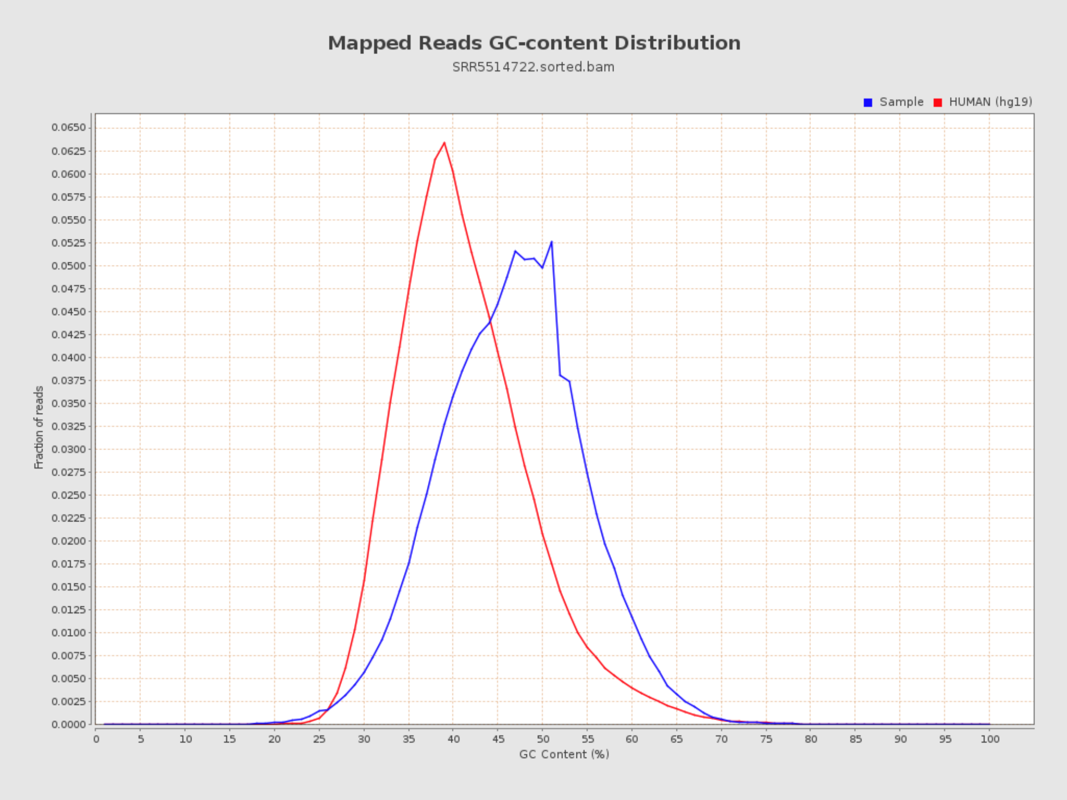
7. Results : Duplication Rate Histogram



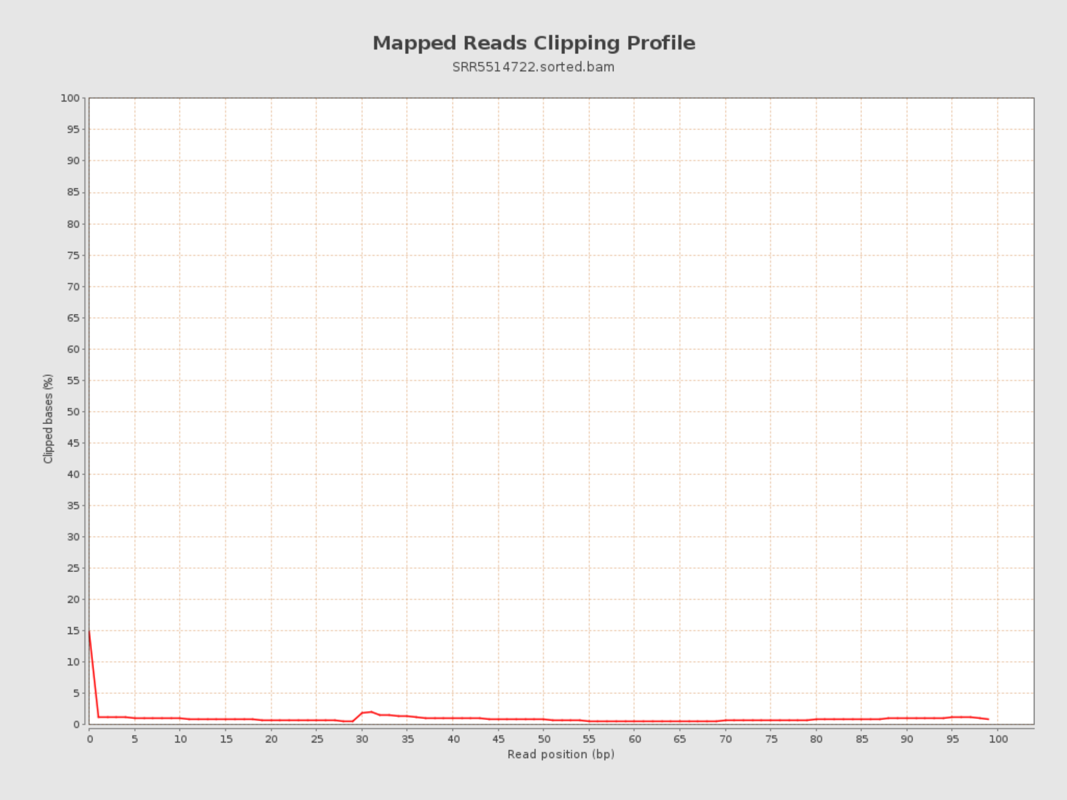
8. Results : Mapped Reads Nucleotide Content



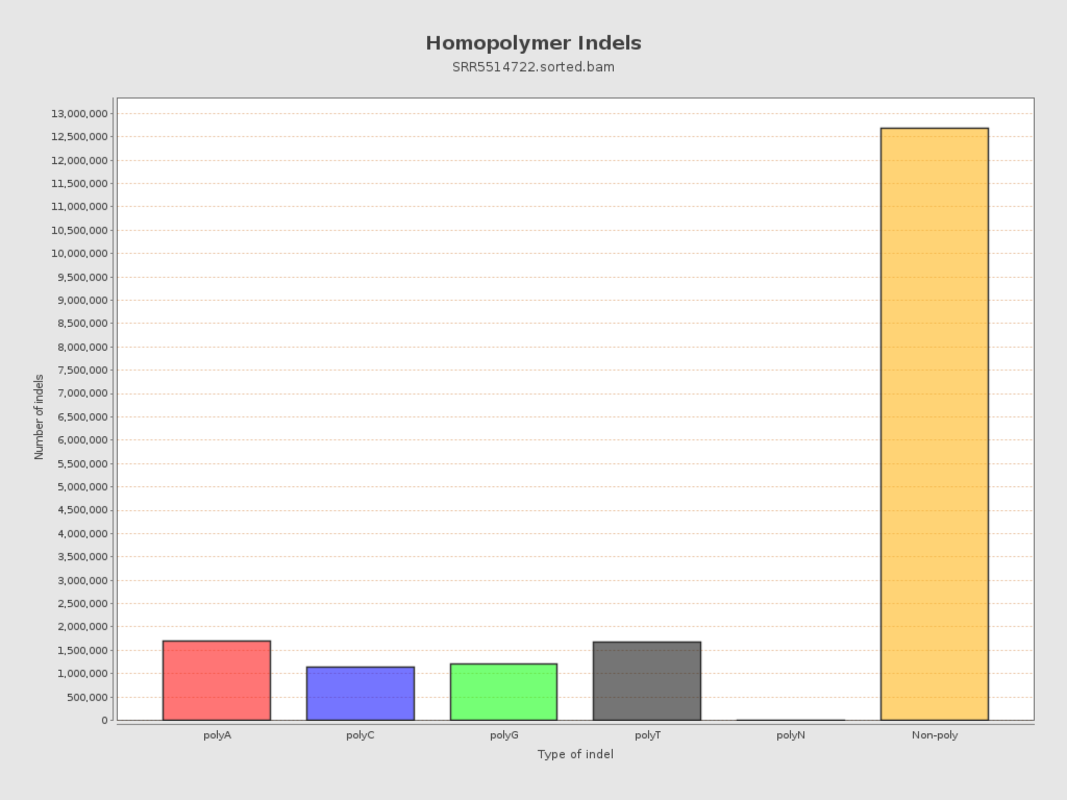
9. Results : Mapped Reads GC-content Distribution



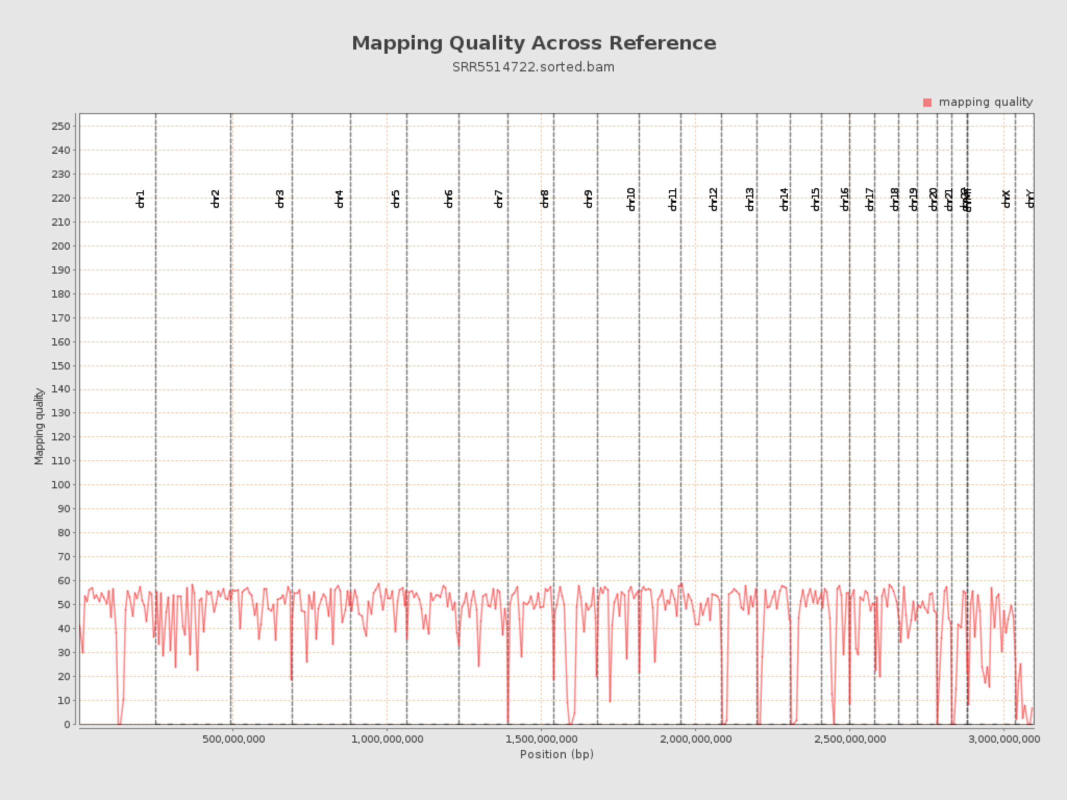
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram