Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/09 18:18:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514708.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_SRR5514708 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514708.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 09 18:18:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514708.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	78,349,227
Mapped reads	77,501,993 / 98.92%
Unmapped reads	847,234 / 1.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,261,553 / 5.44%
Read min/max/mean length	30 / 100 / 99.95
Duplicated reads (estimated)	41,447,624 / 52.9%
Duplication rate	32.94%
Clipped reads	19,116,545 / 24.4%

2.2. ACGT Content

Number/percentage of A's	2,145,581,650 / 29.3%
Number/percentage of C's	1,508,110,034 / 20.59%
Number/percentage of T's	2,123,335,508 / 29%
Number/percentage of G's	1,531,534,653 / 20.91%
Number/percentage of N's	14,443,631 / 0.2%
GC Percentage	41.51%

2.3. Coverage

Mean	2.3685

Standard Deviation	164.8076

2.4. Mapping Quality

Mean Mapping Quality	48.54

2.5. Mismatches and indels

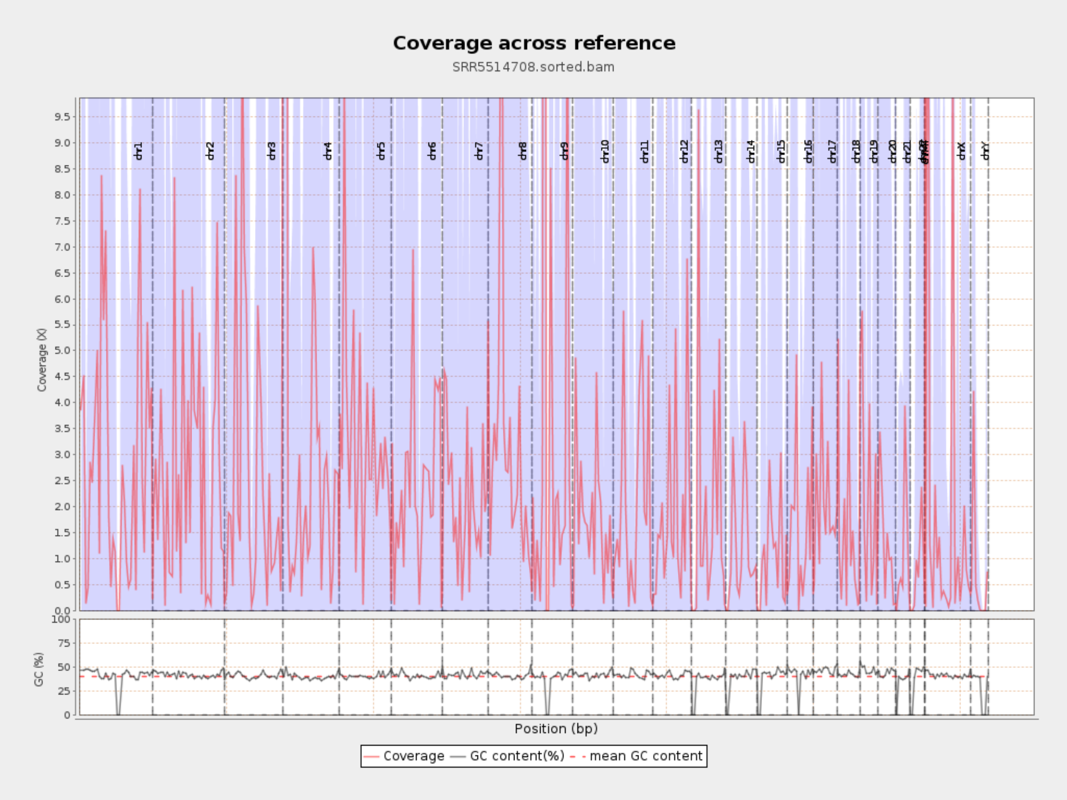
General error rate	0.79%
Mismatches	51,485,818
Insertions	3,199,151
Mapped reads with at least one insertion	3.93%
Deletions	3,606,086
Mapped reads with at least one deletion	4.36%
Homopolymer indels	35.62%

2.6. Chromosome stats

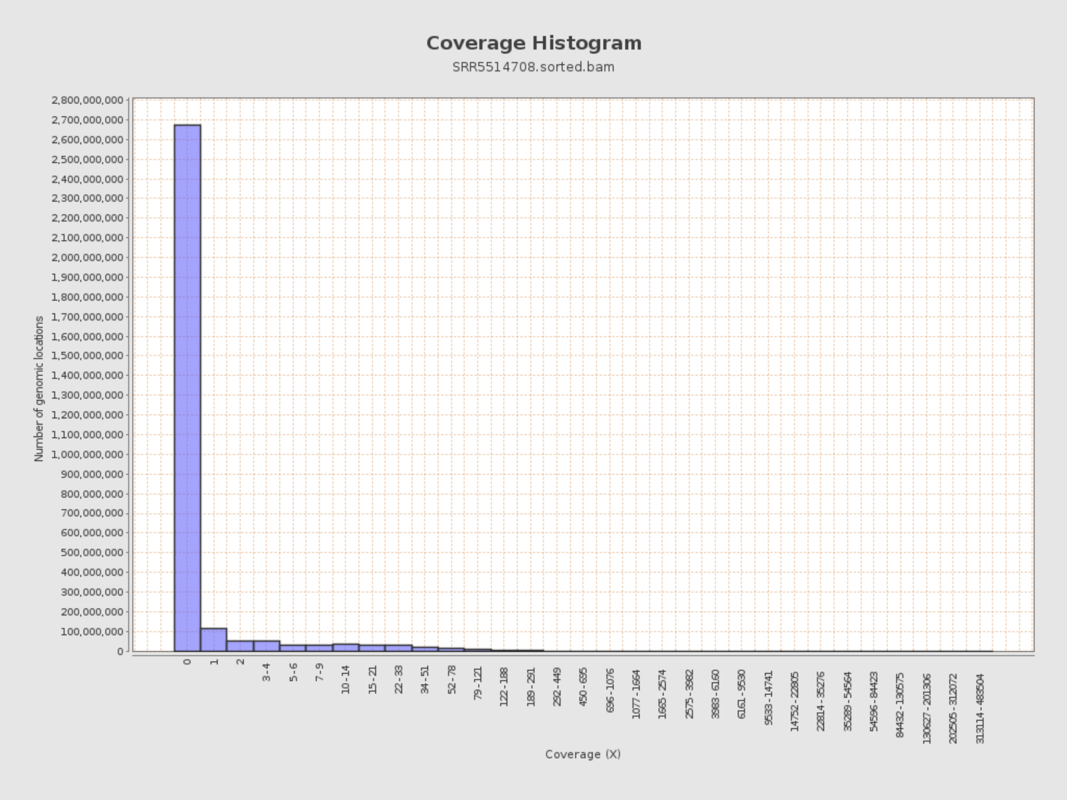
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	705418821	2.8302	93.5072
chr2	243199373	666821844	2.7419	22.1265
chr3	198022430	502998472	2.5401	16.1937
chr4	191154276	738778620	3.8648	407.1838
chr5	180915260	584090330	3.2285	19.07
chr6	171115067	417176312	2.438	35.1228
chr7	159138663	337578619	2.1213	34.8241

chr8	146364022	461972468	3.1563	402.5198
chr9	141213431	578636894	4.0976	377.2649
chr10	135534747	247173760	1.8237	15.0738
chr11	135006516	279186904	2.068	13.2301
chr12	133851895	258180572	1.9289	48.3827
chr13	115169878	220647229	1.9158	24.4055
chr14	107349540	131399425	1.224	10.1532
chr15	102531392	107830274	1.0517	8.4368
chr16	90354753	151613899	1.678	12.0008
chr17	81195210	168001234	2.0691	16.2803
chr18	78077248	104940451	1.3441	54.0122
chr19	59128983	135797685	2.2966	63.3337
chr20	63025520	86178673	1.3674	15.9969
chr21	48129895	52336998	1.0874	8.8437
chr22	51304566	39136379	0.7628	22.4625
chrMT	16571	2792494	168.5169	82.6682
chrX	155270560	307299115	1.9791	174.9411
chrY	59373566	46028662	0.7752	6.991

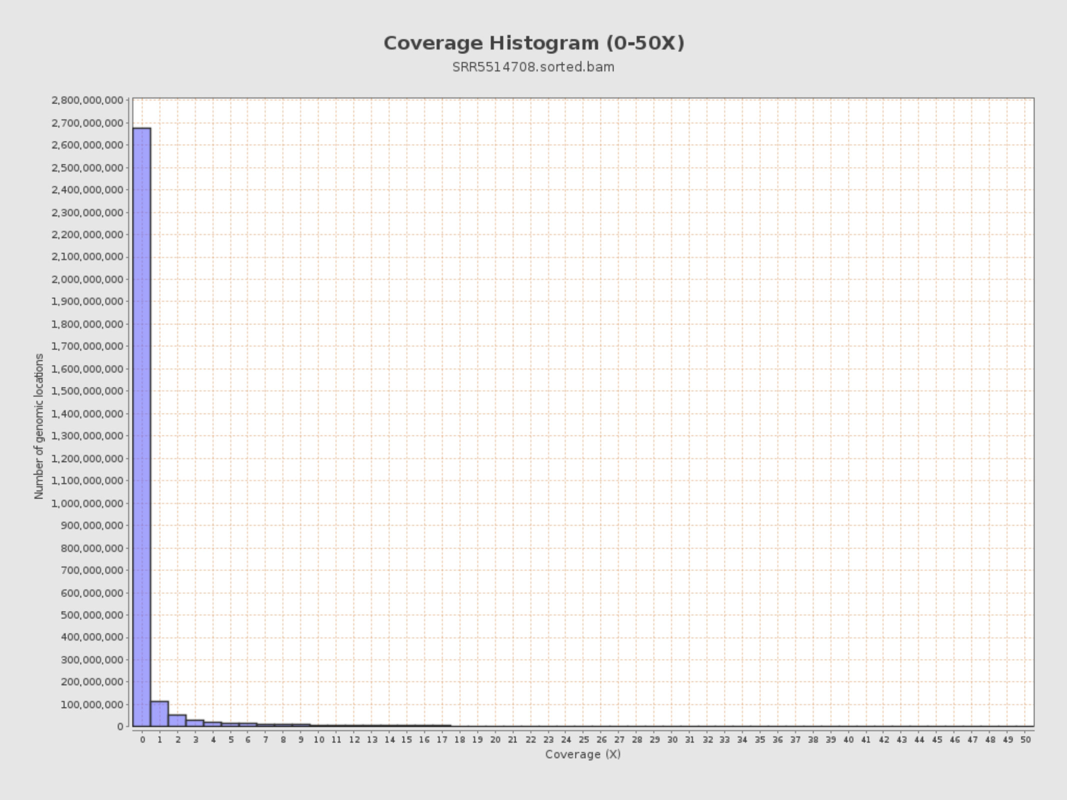
3. Results : Coverage across reference



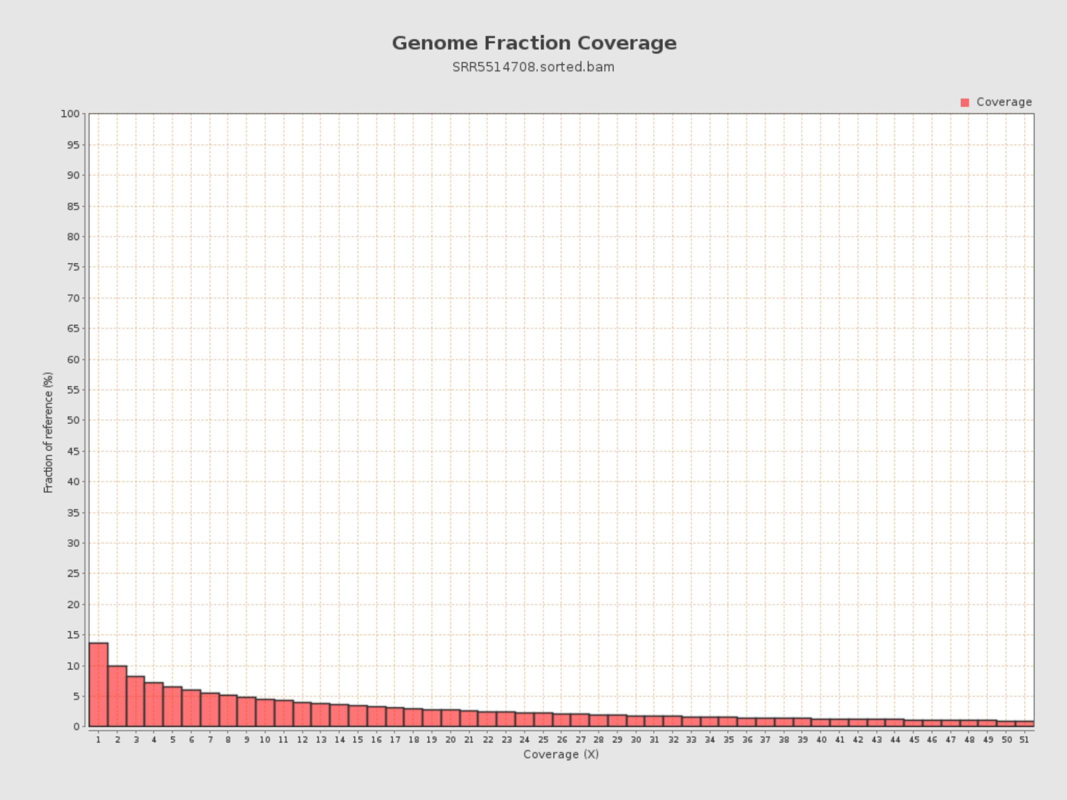
4. Results : Coverage Histogram



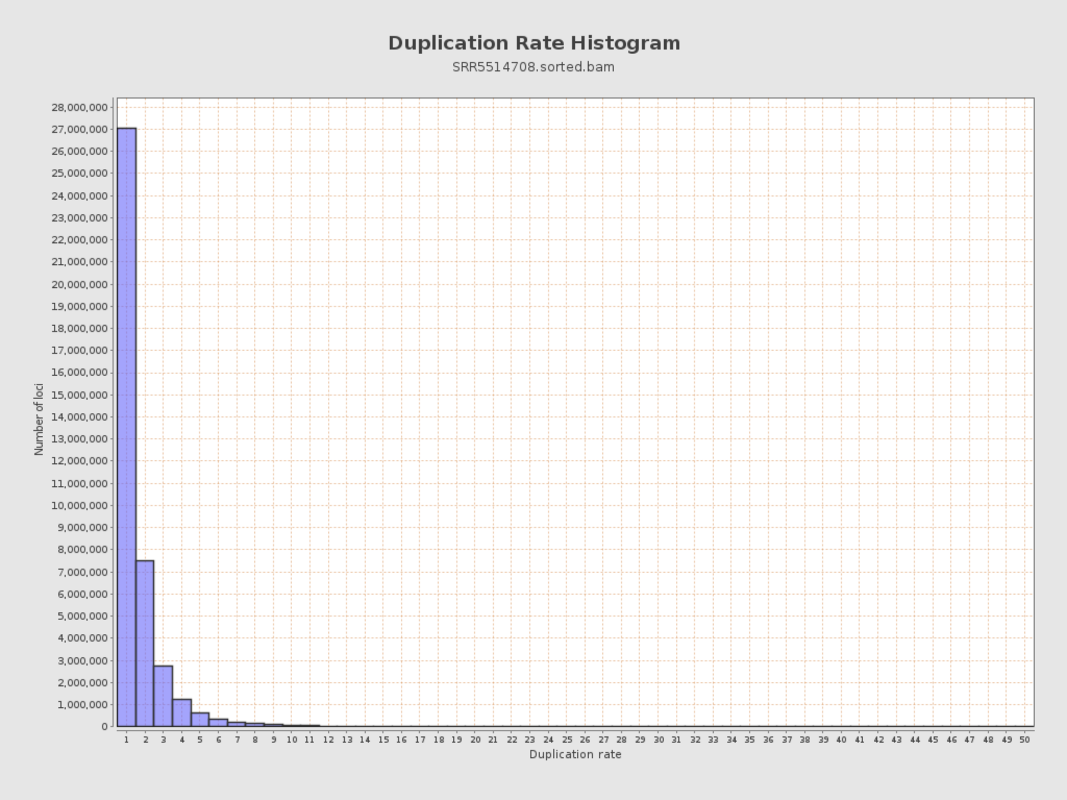
5. Results : Coverage Histogram (0-50X)



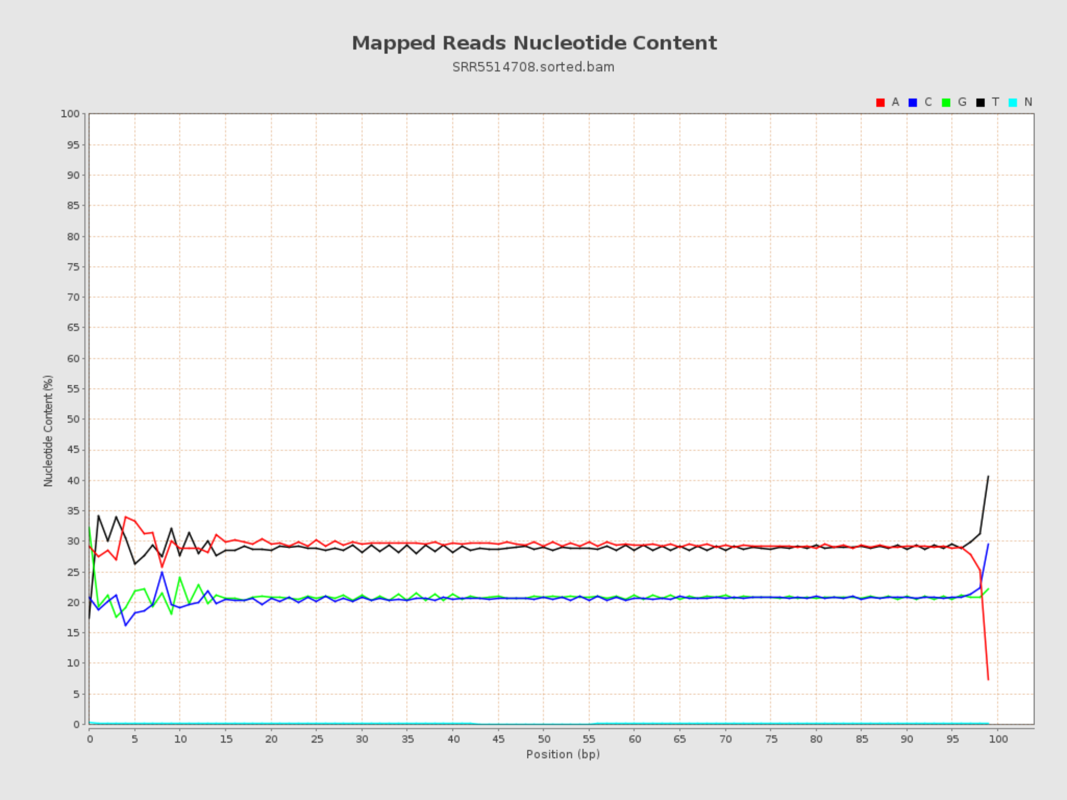
6. Results : Genome Fraction Coverage



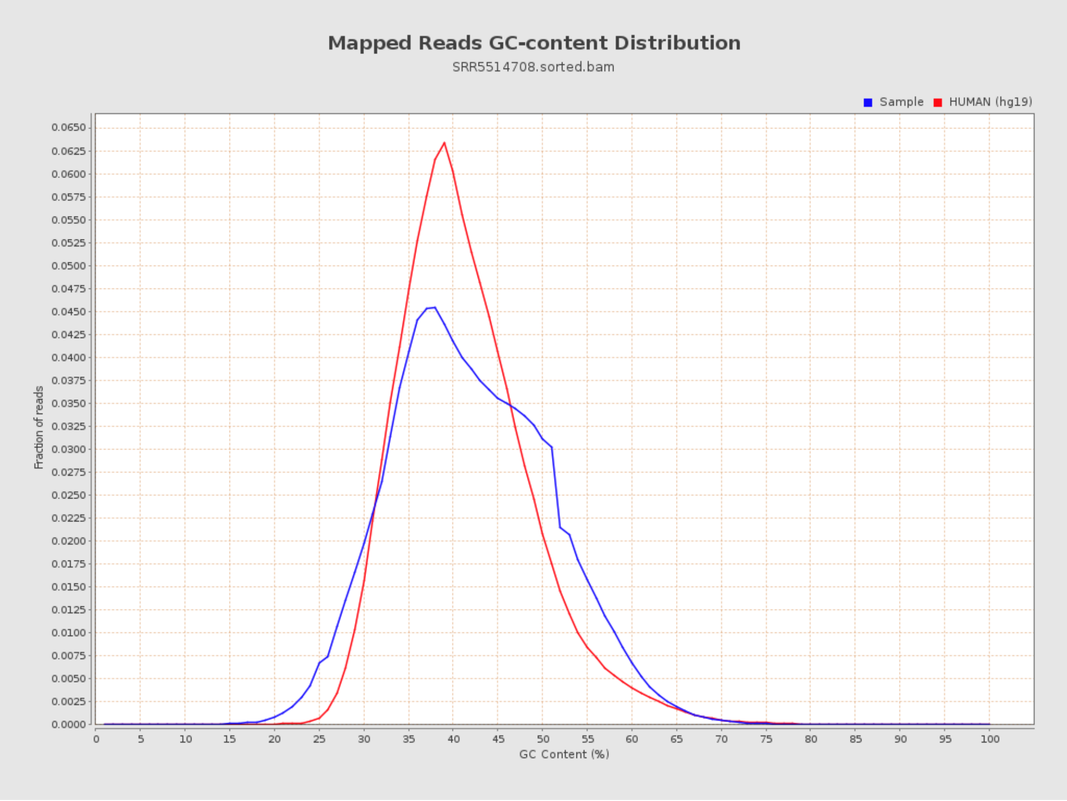
7. Results : Duplication Rate Histogram



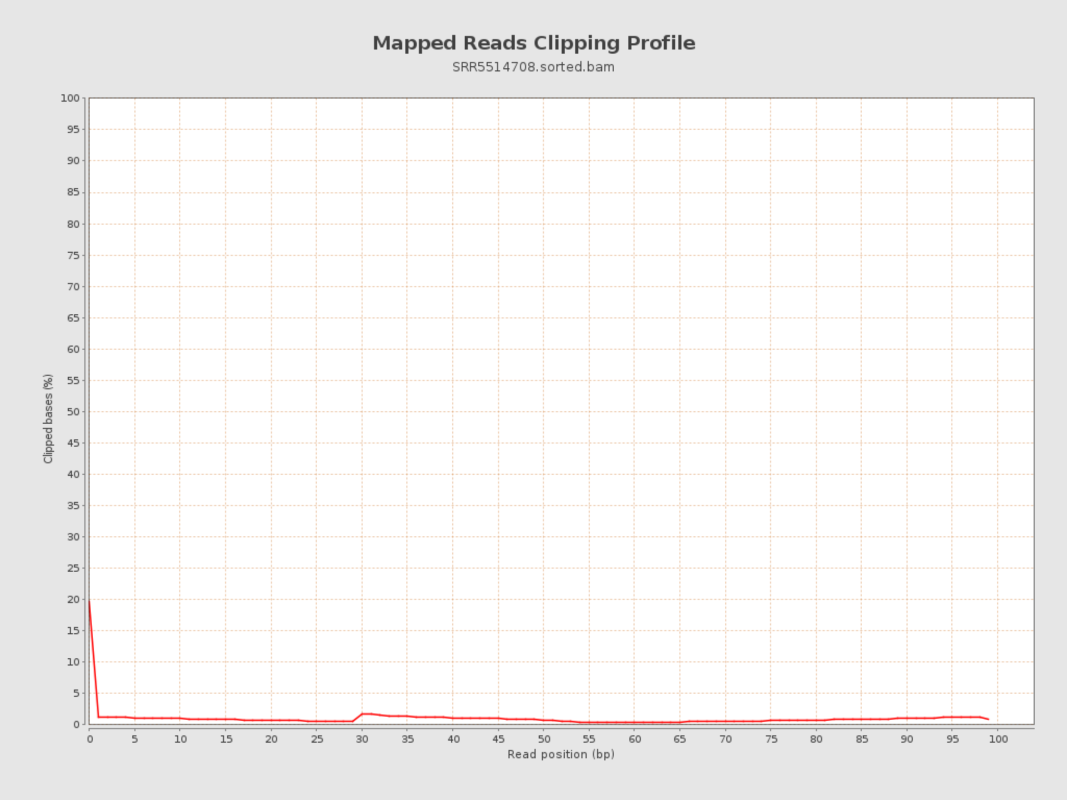
8. Results : Mapped Reads Nucleotide Content



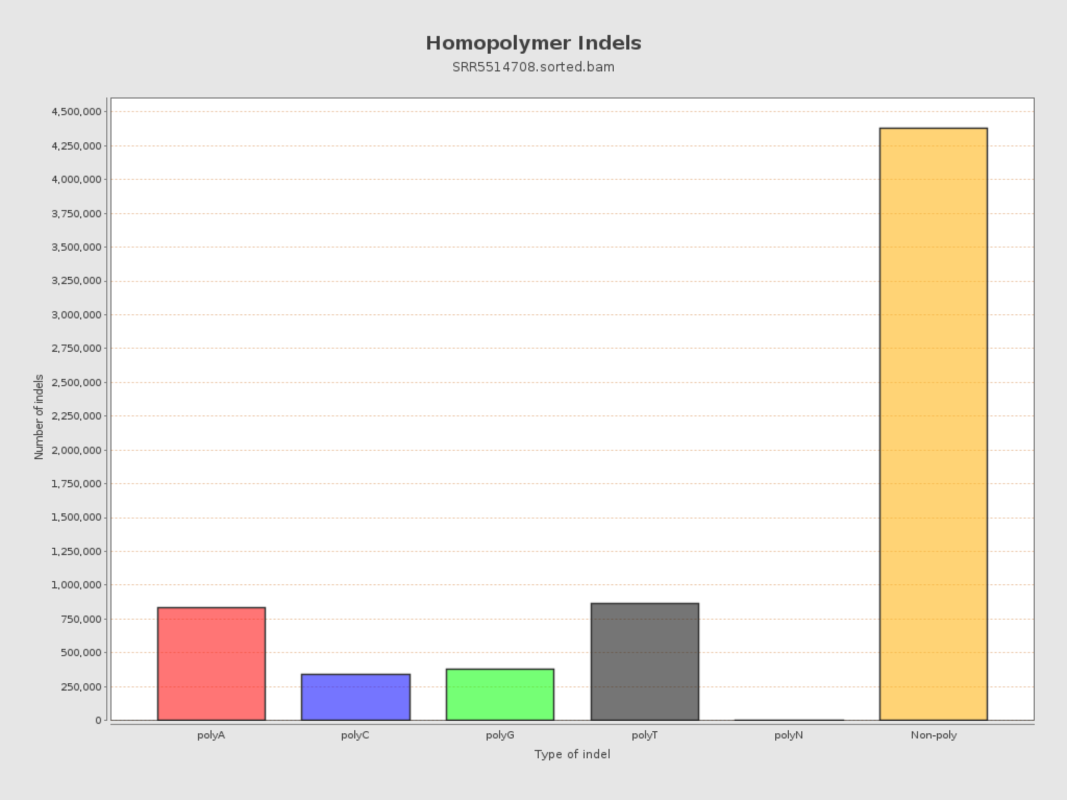
9. Results : Mapped Reads GC-content Distribution



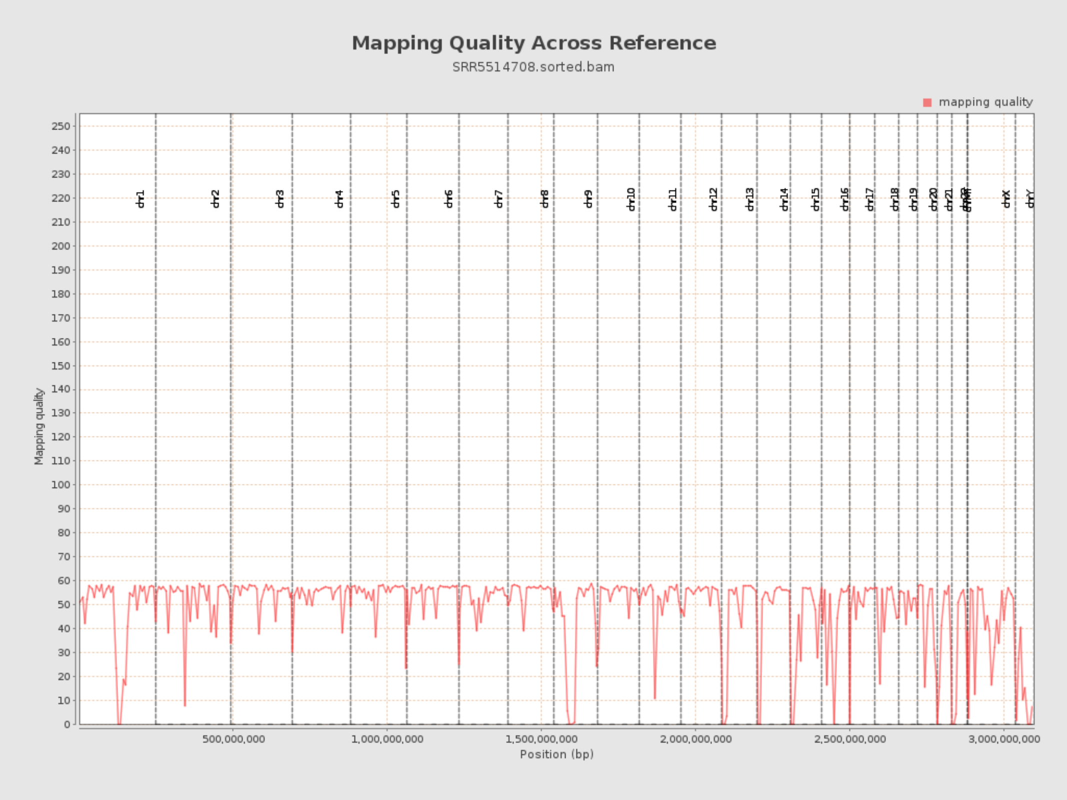
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram