Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 03:31:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514711.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_SRR5514711 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514711.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 03:30:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514711.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	95,060,582
Mapped reads	94,216,975 / 99.11%
Unmapped reads	843,607 / 0.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,085,172 / 5.35%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	61,130,897 / 64.31%
Duplication rate	40.52%
Clipped reads	22,175,930 / 23.33%

2.2. ACGT Content

Number/percentage of A's	2,548,668,676 / 28.42%
Number/percentage of C's	1,930,456,026 / 21.53%
Number/percentage of T's	2,525,180,439 / 28.16%
Number/percentage of G's	1,956,519,868 / 21.82%
Number/percentage of N's	7,055,752 / 0.08%
GC Percentage	43.34%

2.3. Coverage

Mean	2.9004

Standard Deviation	253.5699

2.4. Mapping Quality

Mean Mapping Quality	48.64

2.5. Mismatches and indels

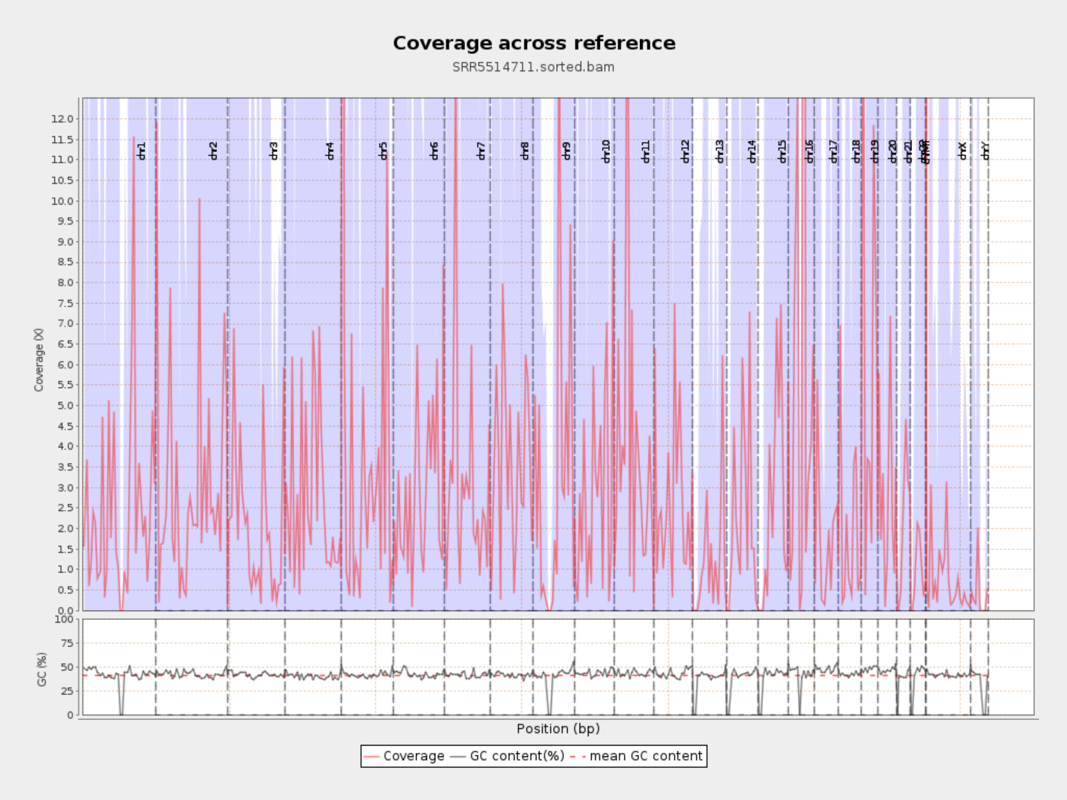
General error rate	0.86%
Mismatches	71,177,957
Insertions	3,281,279
Mapped reads with at least one insertion	3.37%
Deletions	3,721,847
Mapped reads with at least one deletion	3.76%
Homopolymer indels	36.09%

2.6. Chromosome stats

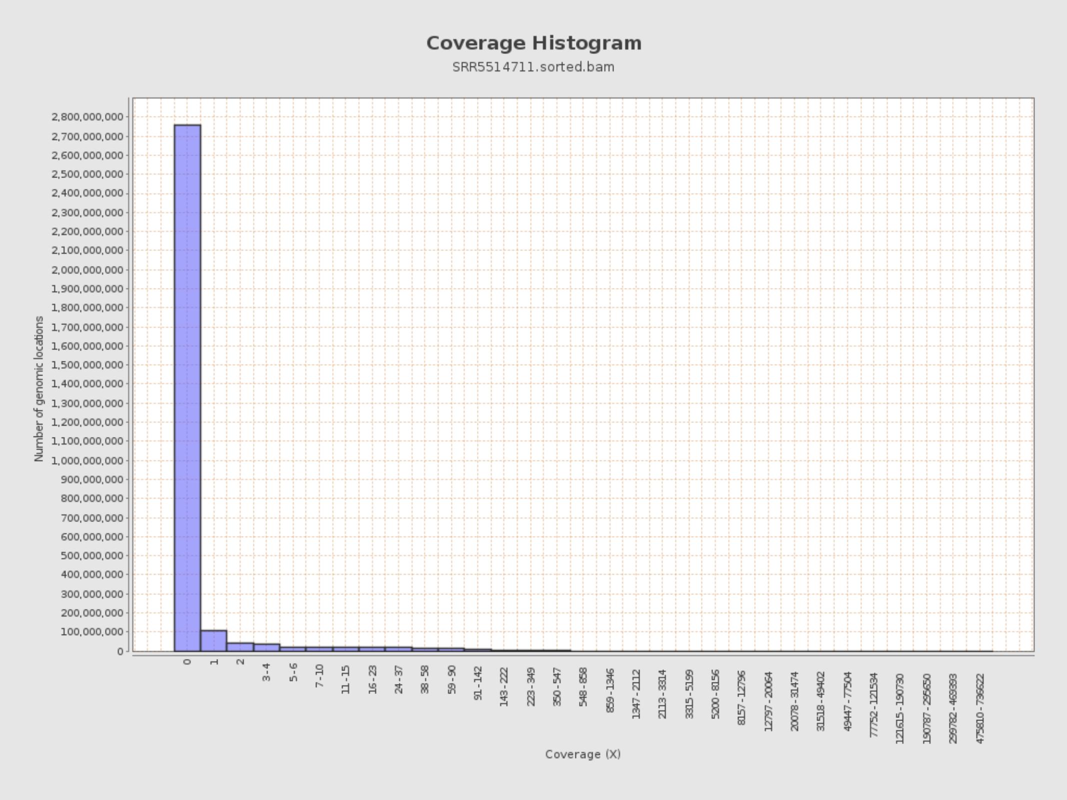
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	619415019	2.4851	25.6034
chr2	243199373	753188678	3.097	84.3855
chr3	198022430	416889860	2.1053	22.2226
chr4	191154276	536277958	2.8055	24.1839
chr5	180915260	1012451323	5.5963	930.0115
chr6	171115067	486686652	2.8442	24.7627
chr7	159138663	489201653	3.0741	48.5577

chr8	146364022	531910387	3.6342	43.1433
chr9	141213431	432405513	3.0621	103.257
chr10	135534747	382990375	2.8258	30.68
chr11	135006516	531357163	3.9358	56.0092
chr12	133851895	363441330	2.7152	36.1194
chr13	115169878	142955995	1.2413	17.2424
chr14	107349540	244795186	2.2804	24.4802
chr15	102531392	258285162	2.5191	23.945
chr16	90354753	658260072	7.2853	533.3839
chr17	81195210	144042872	1.774	20.8406
chr18	78077248	155857354	1.9962	30.5693
chr19	59128983	351532158	5.9452	432.1834
chr20	63025520	171079194	2.7144	54.4695
chr21	48129895	101747395	2.114	61.8064
chr22	51304566	47657119	0.9289	15.6184
chrMT	16571	3747445	226.1448	133.0482
chrX	155270560	117265000	0.7552	20.979
chrY	59373566	25249154	0.4253	9.6755

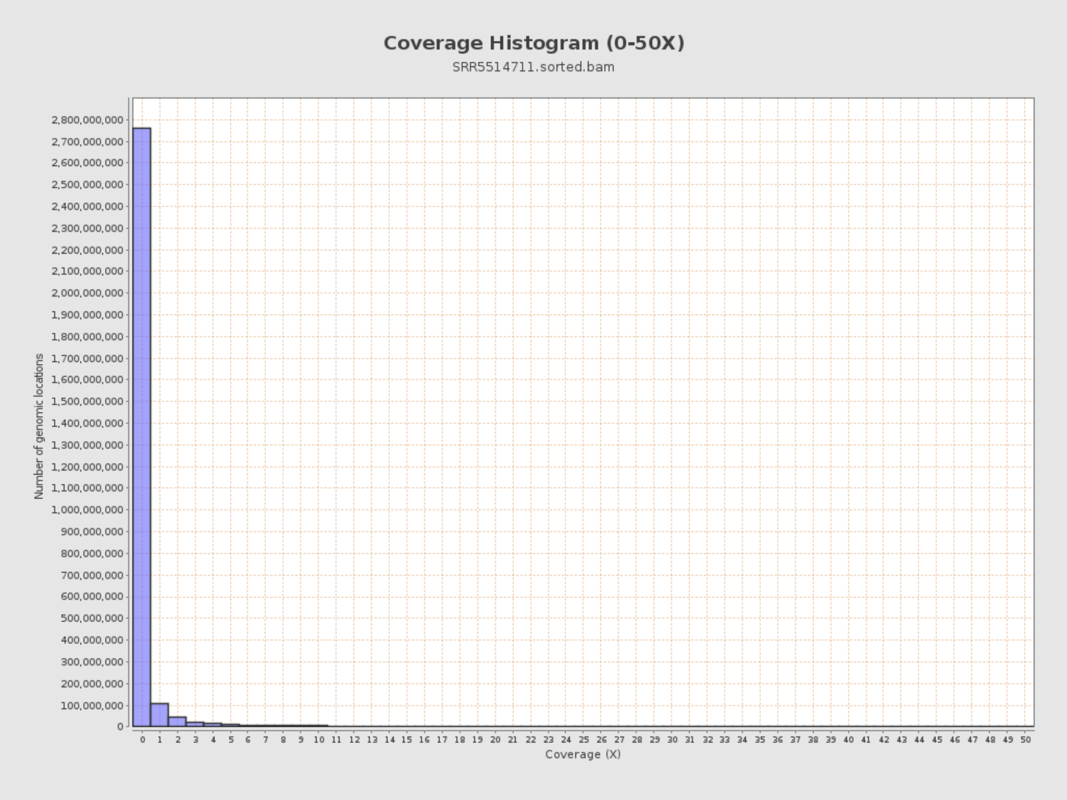
3. Results : Coverage across reference



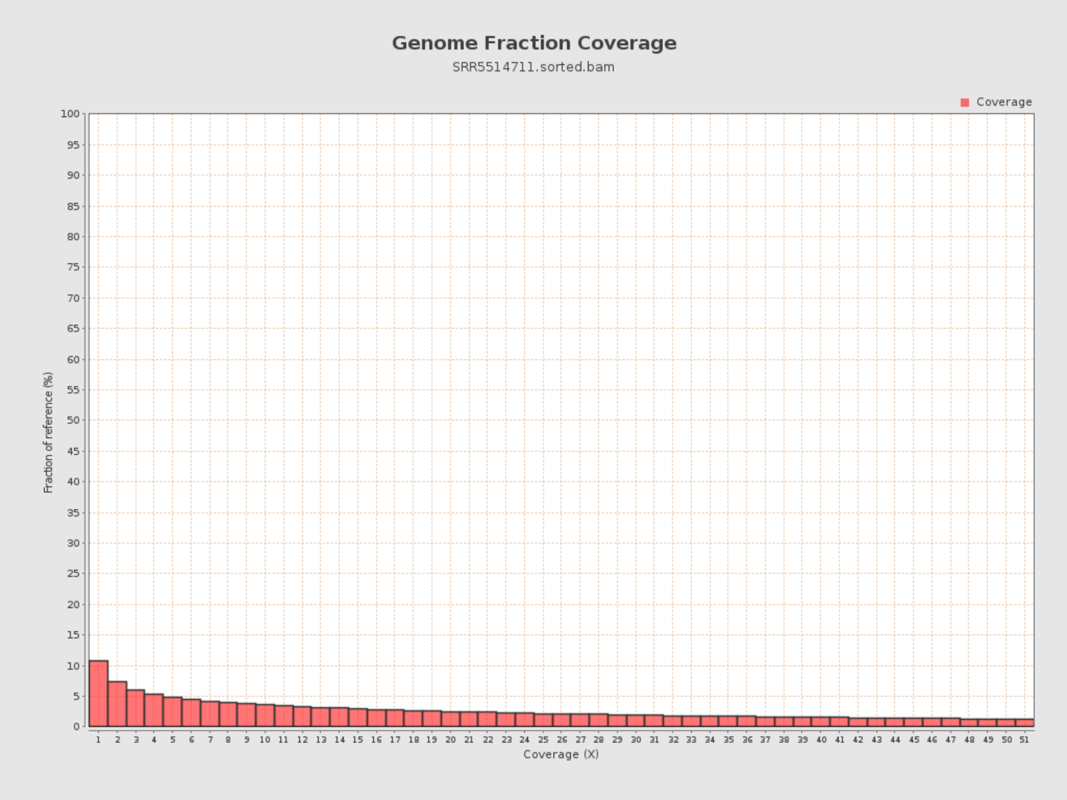
4. Results : Coverage Histogram



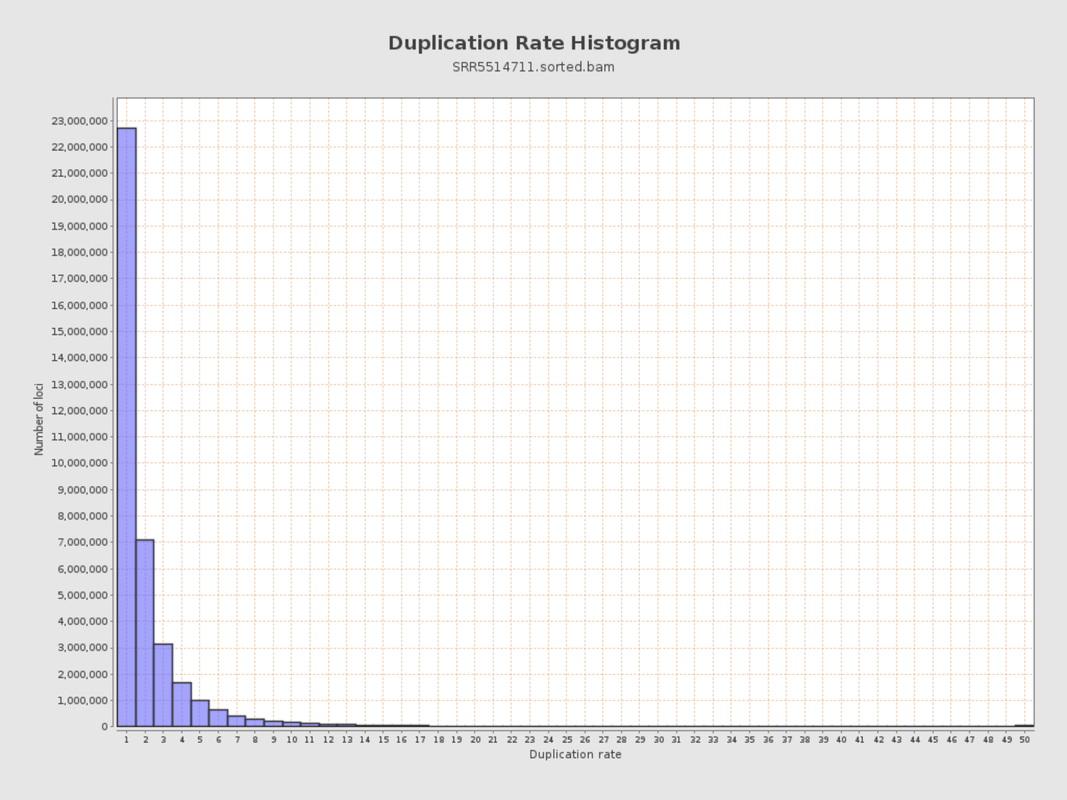
5. Results : Coverage Histogram (0-50X)



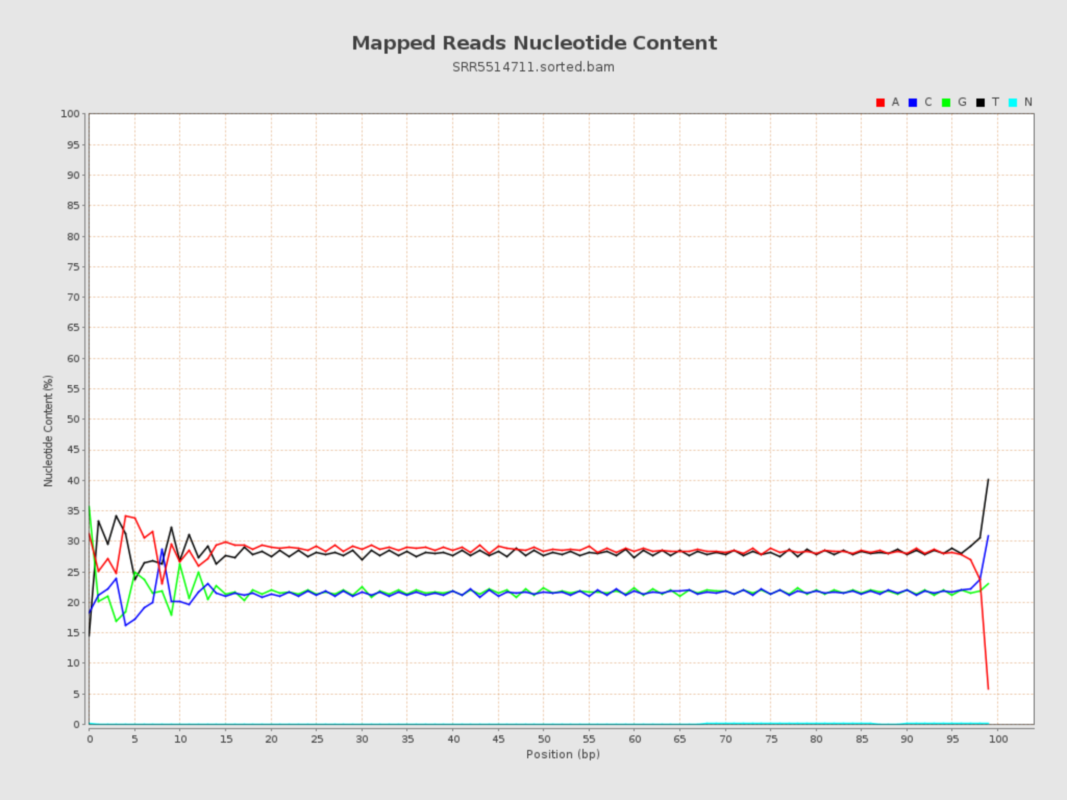
6. Results : Genome Fraction Coverage



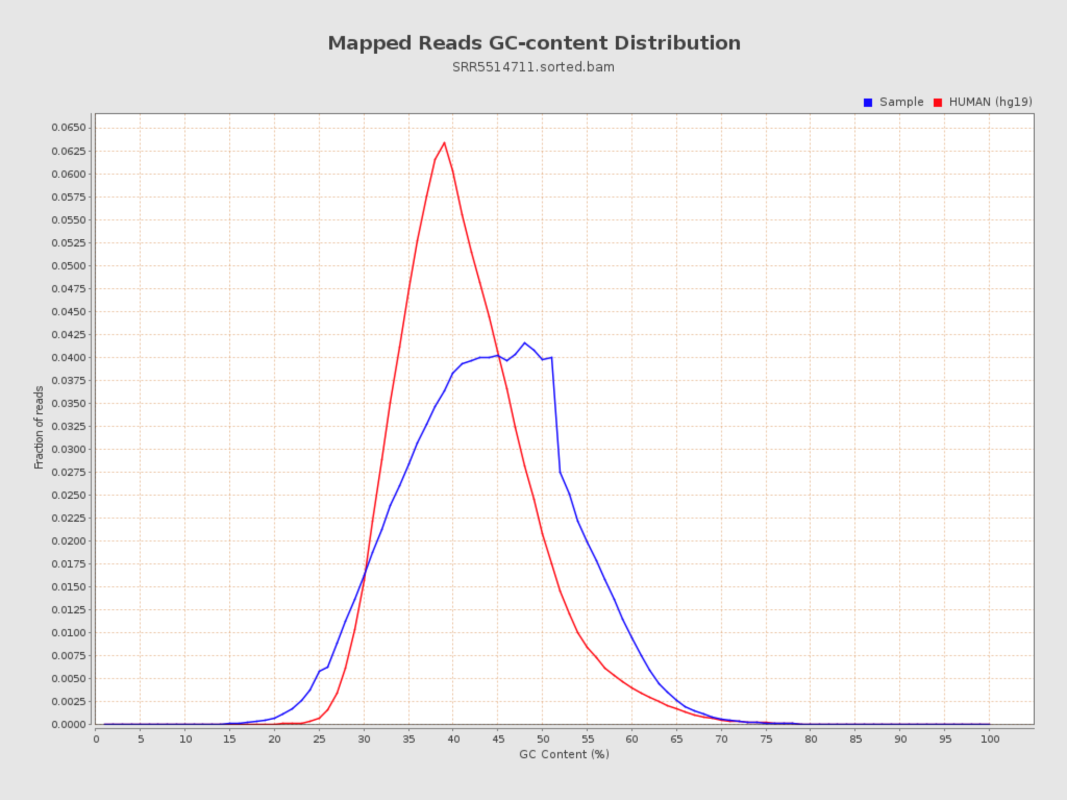
7. Results : Duplication Rate Histogram



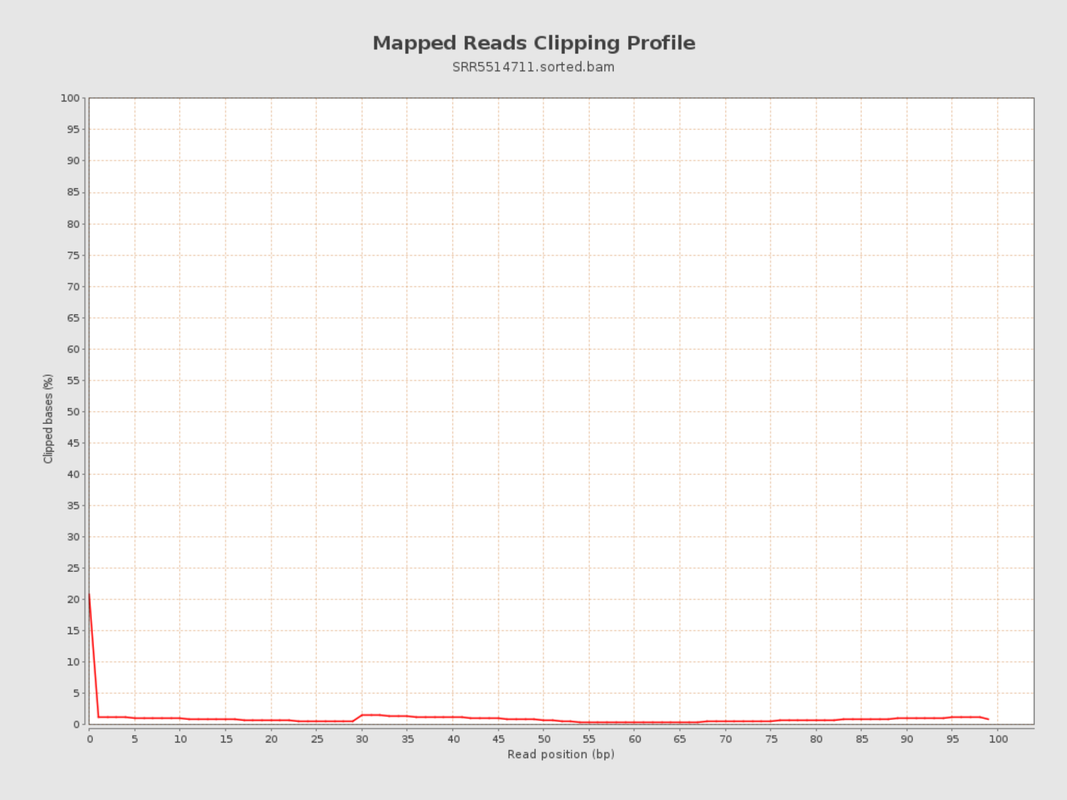
8. Results : Mapped Reads Nucleotide Content



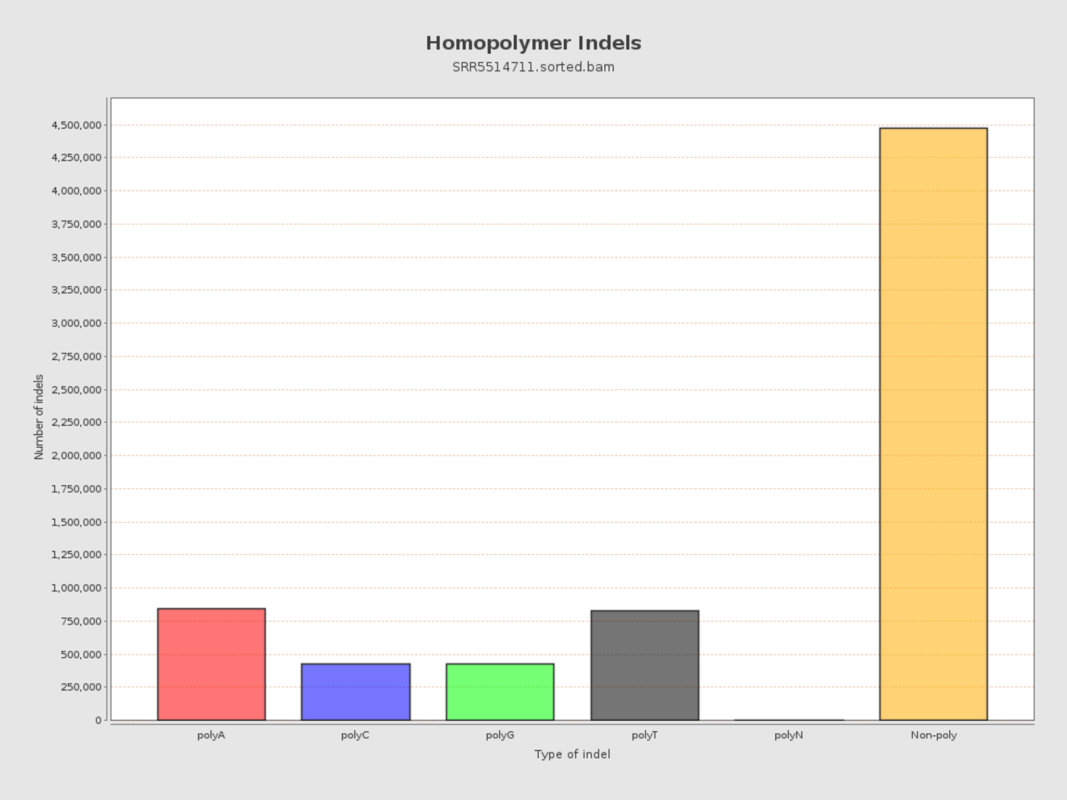
9. Results : Mapped Reads GC-content Distribution



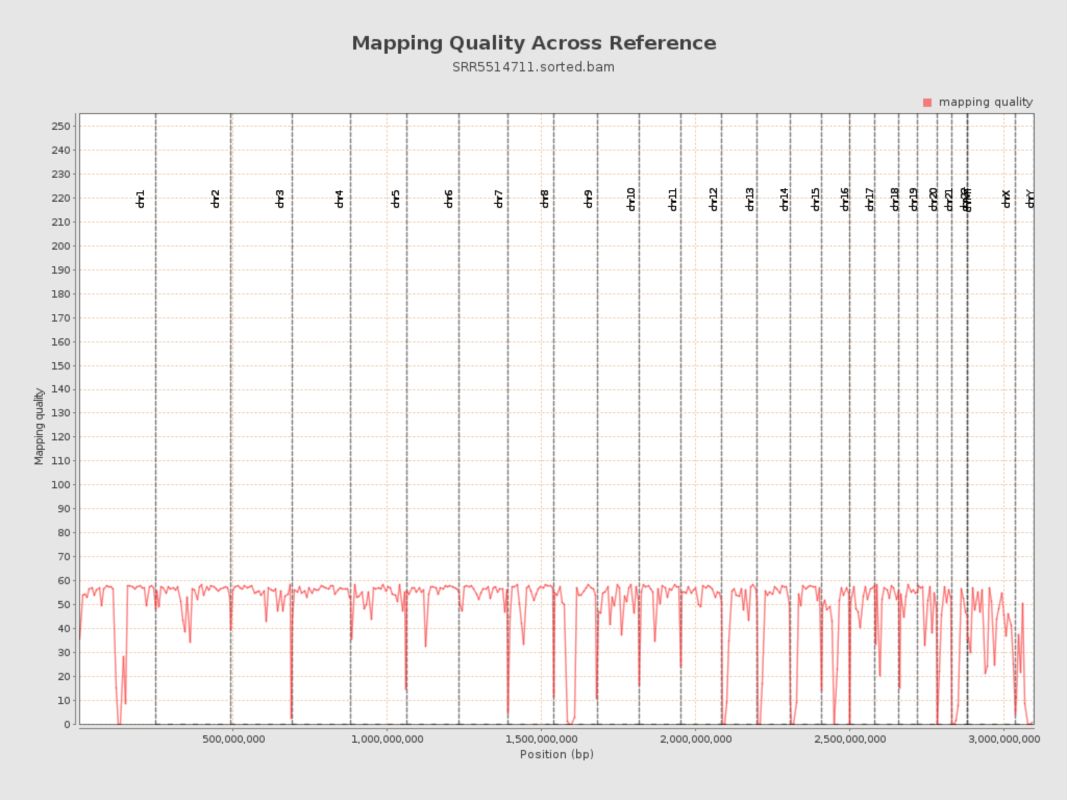
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram