Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 08:28:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514771.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_SRR5514771 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514771.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 08:28:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514771.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	47,136,964
Mapped reads	46,350,835 / 98.33%
Unmapped reads	786,129 / 1.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,535,052 / 7.5%
Read min/max/mean length	30 / 100 / 100.71
Duplicated reads (estimated)	39,423,560 / 83.64%
Duplication rate	49.23%
Clipped reads	14,659,205 / 31.1%

2.2. ACGT Content

Number/percentage of A's	1,257,385,025 / 28.91%
Number/percentage of C's	912,323,050 / 20.98%
Number/percentage of T's	1,246,110,226 / 28.65%
Number/percentage of G's	929,556,120 / 21.37%
Number/percentage of N's	3,652,927 / 0.08%
GC Percentage	42.35%

2.3. Coverage

Mean	1.4067

Standard Deviation	119.5932

2.4. Mapping Quality

Mean Mapping Quality	48.58

2.5. Mismatches and indels

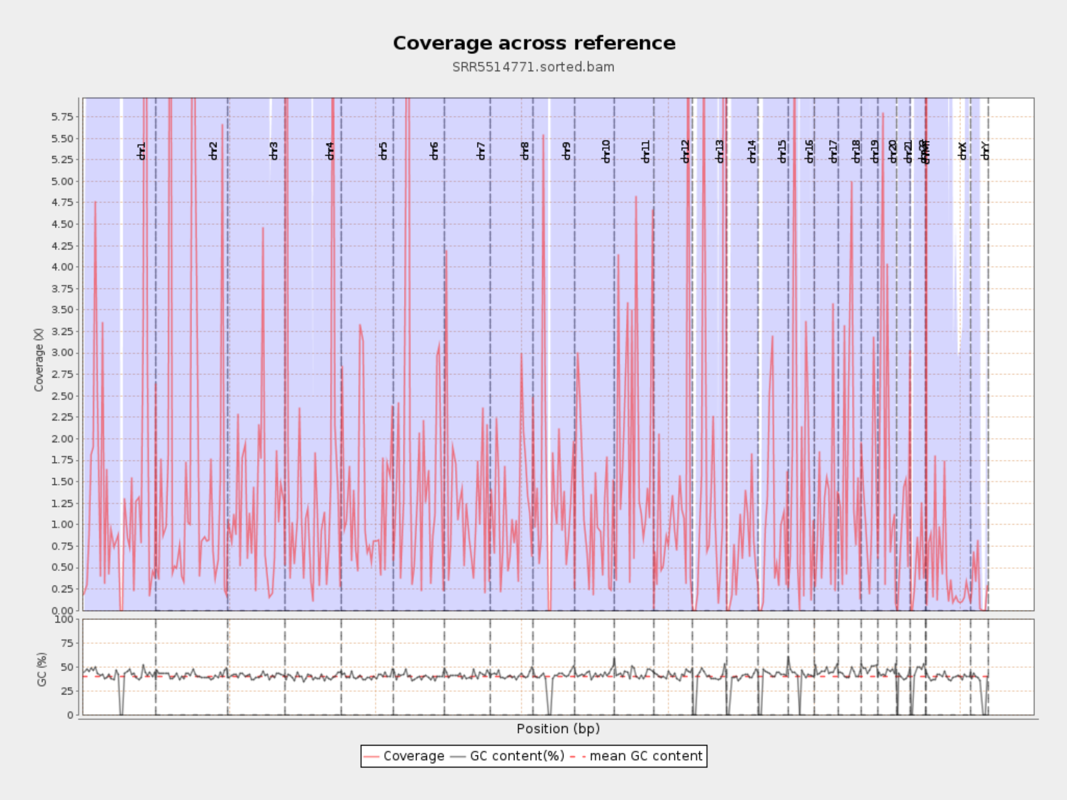
General error rate	0.85%
Mismatches	32,358,075
Insertions	2,599,083
Mapped reads with at least one insertion	5.1%
Deletions	2,314,315
Mapped reads with at least one deletion	4.41%
Homopolymer indels	34.47%

2.6. Chromosome stats

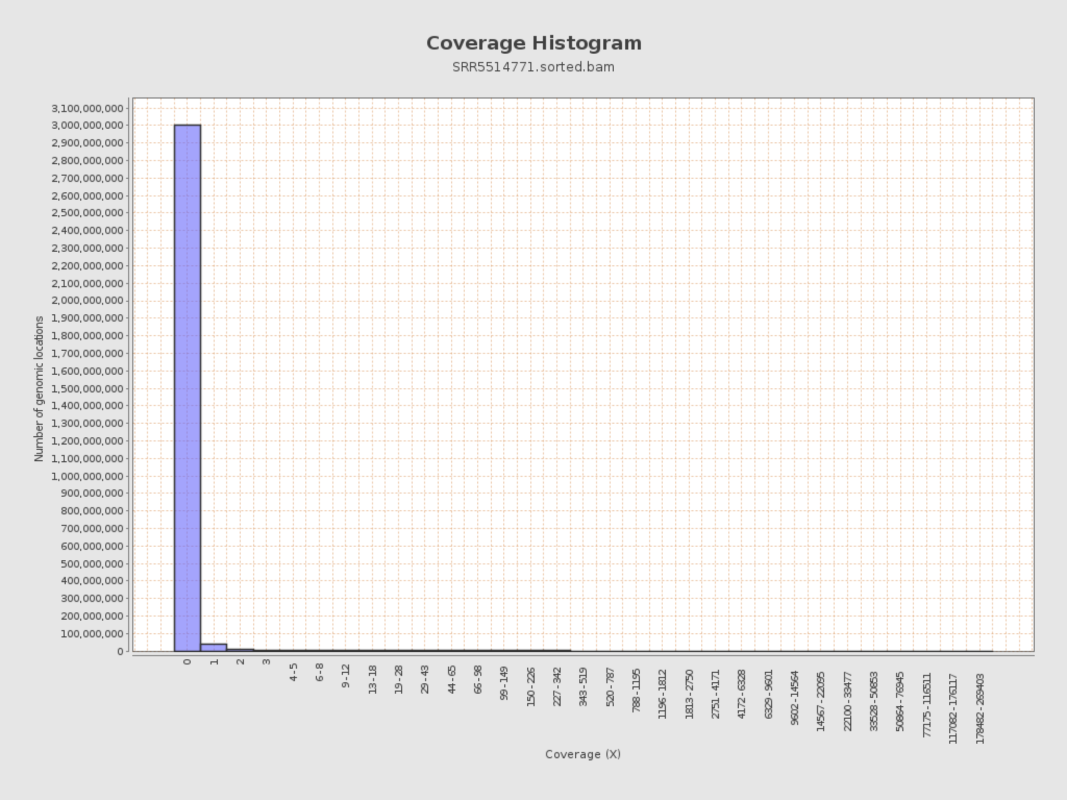
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	386196039	1.5494	48.2824
chr2	243199373	435821007	1.792	141.1115
chr3	198022430	239406864	1.209	53.632
chr4	191154276	338603354	1.7714	184.0378
chr5	180915260	233295789	1.2895	56.841
chr6	171115067	337627349	1.9731	62.1676
chr7	159138663	200291994	1.2586	58.0276

chr8	146364022	176004860	1.2025	82.5013
chr9	141213431	193555420	1.3707	107.3023
chr10	135534747	160843531	1.1867	40.8106
chr11	135006516	265165877	1.9641	65.8911
chr12	133851895	171631242	1.2822	34.2218
chr13	115169878	296457480	2.5741	455.8221
chr14	107349540	76018919	0.7081	23.3854
chr15	102531392	95661821	0.933	51.8896
chr16	90354753	148969138	1.6487	59.9105
chr17	81195210	95951354	1.1817	81.904
chr18	78077248	131948584	1.69	56.486
chr19	59128983	73782651	1.2478	62.427
chr20	63025520	133533449	2.1187	64.9455
chr21	48129895	49637264	1.0313	92.5846
chr22	51304566	25080136	0.4888	16.7954
chrMT	16571	1799002	108.5633	199.4278
chrX	155270560	69938021	0.4504	28.222
chrY	59373566	17614700	0.2967	9.5243

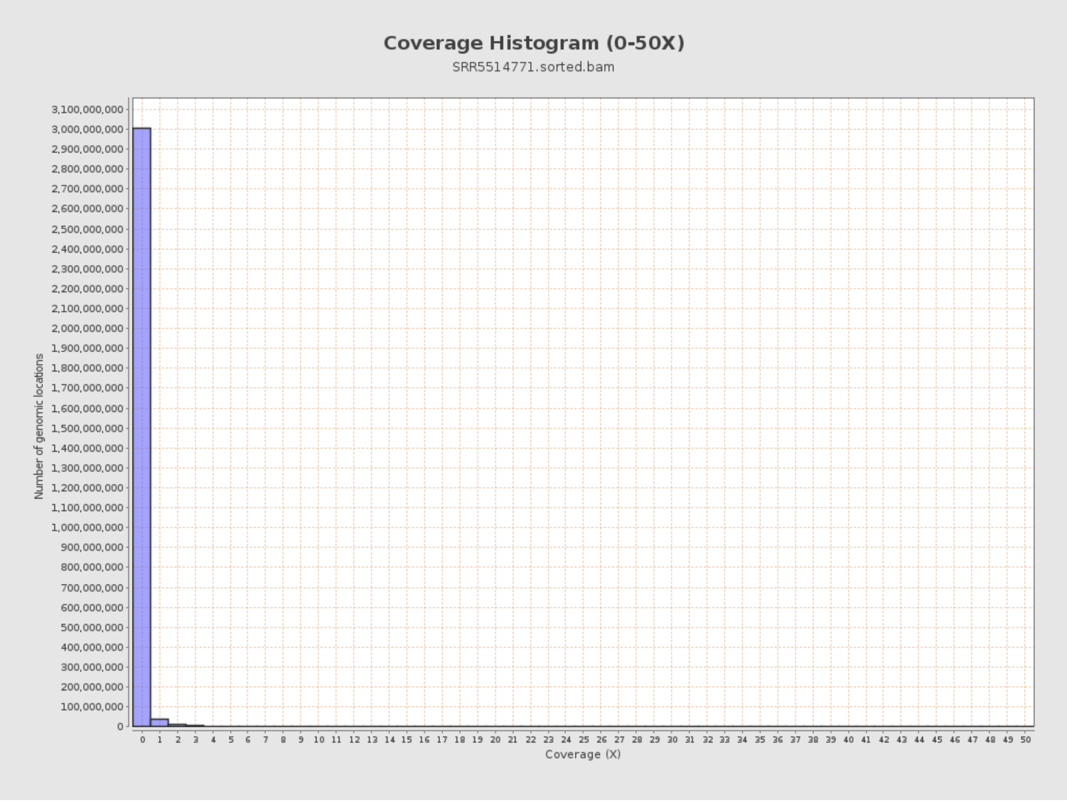
3. Results : Coverage across reference



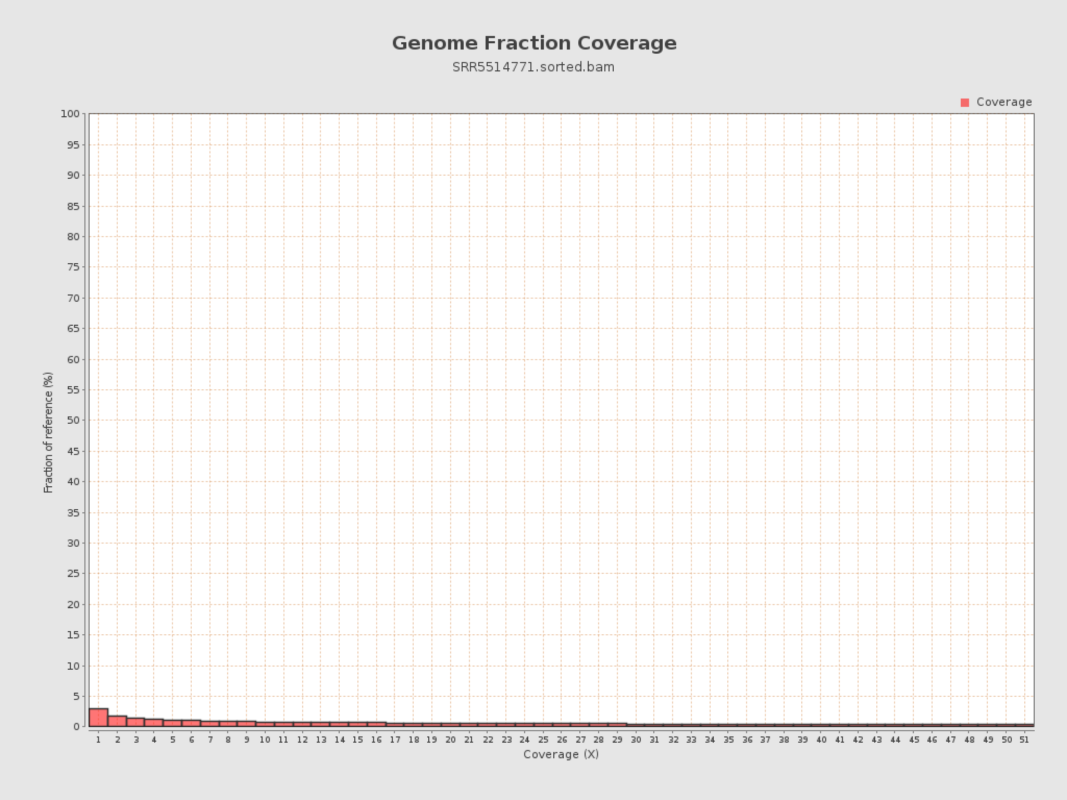
4. Results : Coverage Histogram



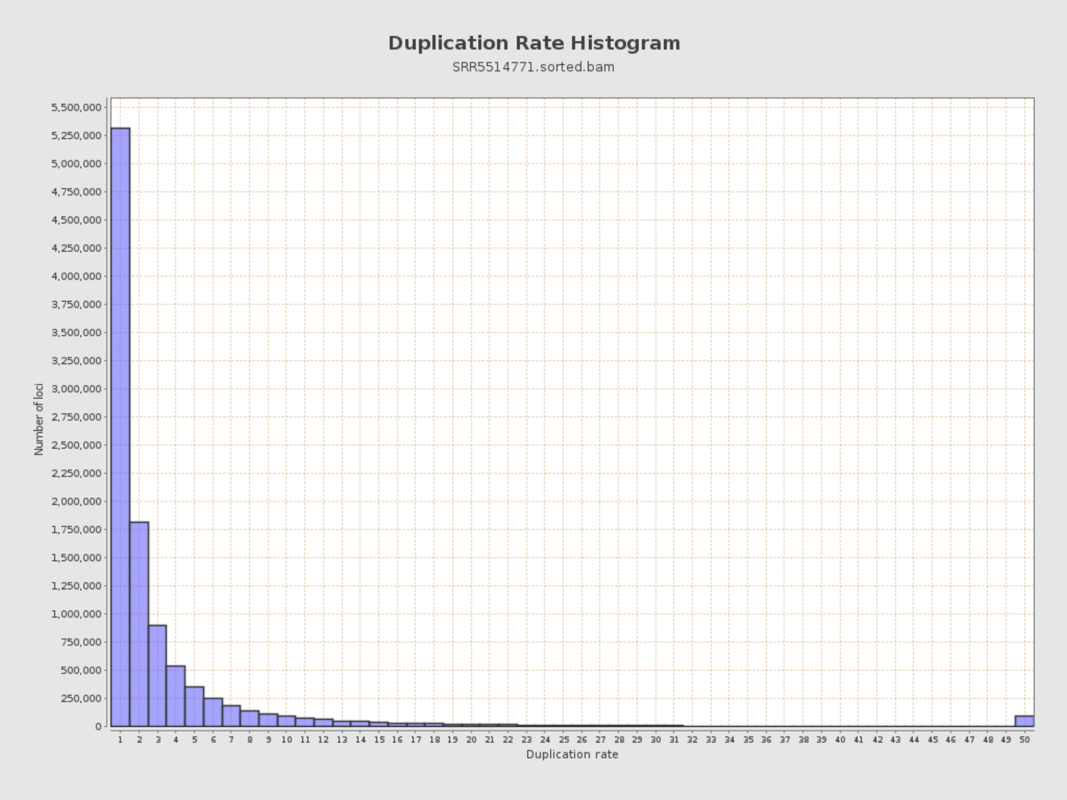
5. Results : Coverage Histogram (0-50X)



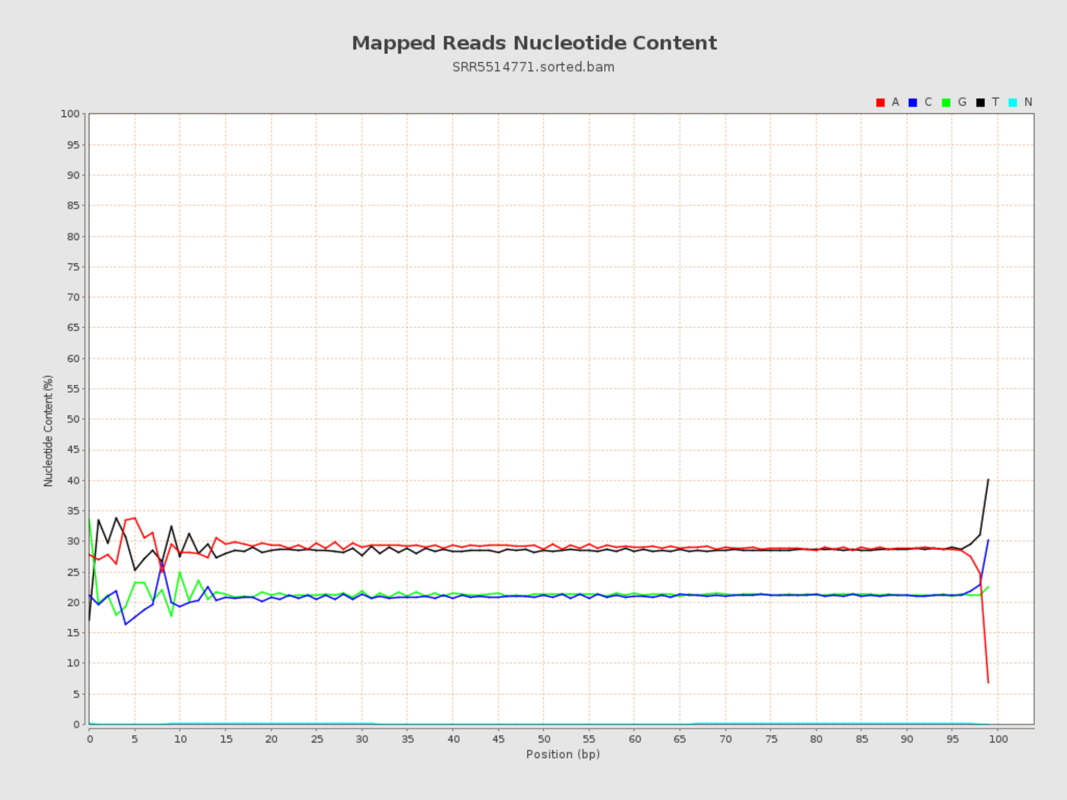
6. Results : Genome Fraction Coverage



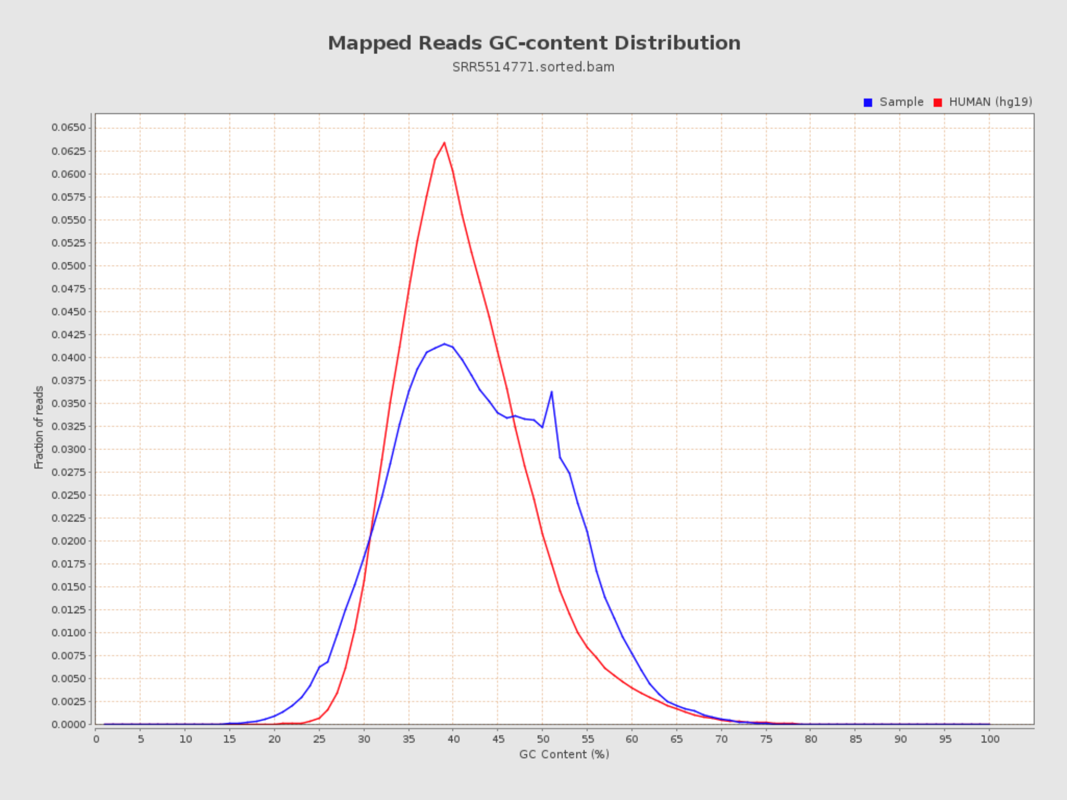
7. Results : Duplication Rate Histogram



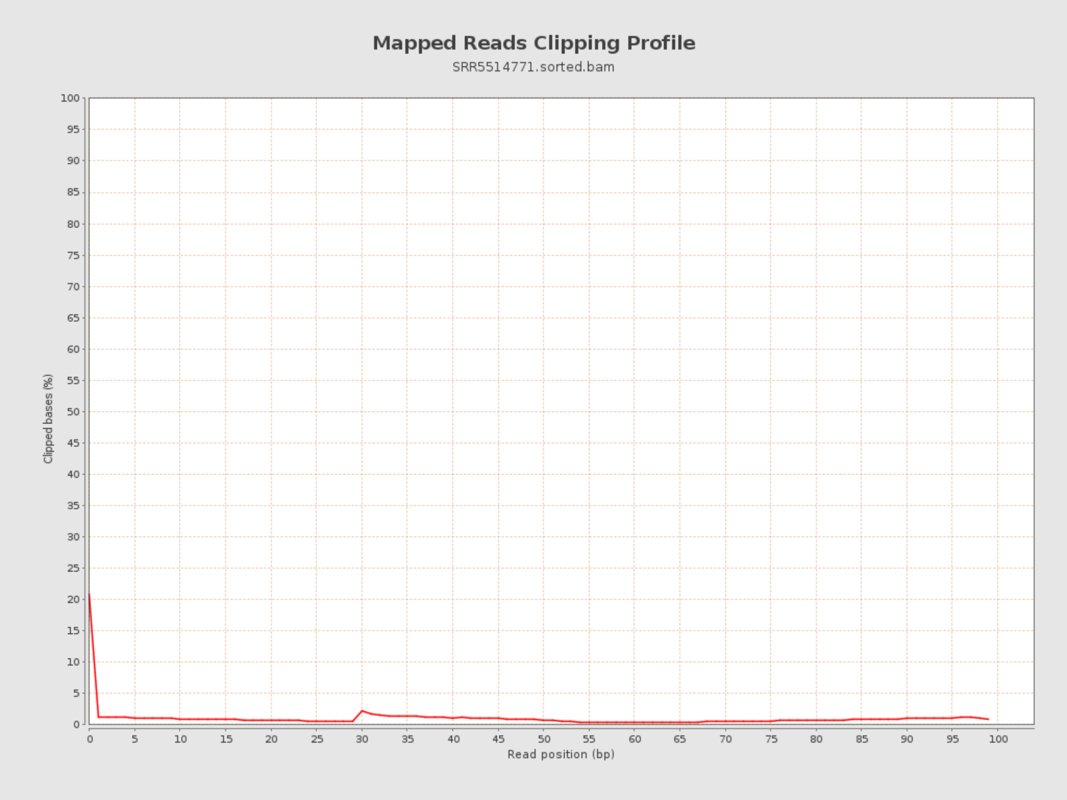
8. Results : Mapped Reads Nucleotide Content



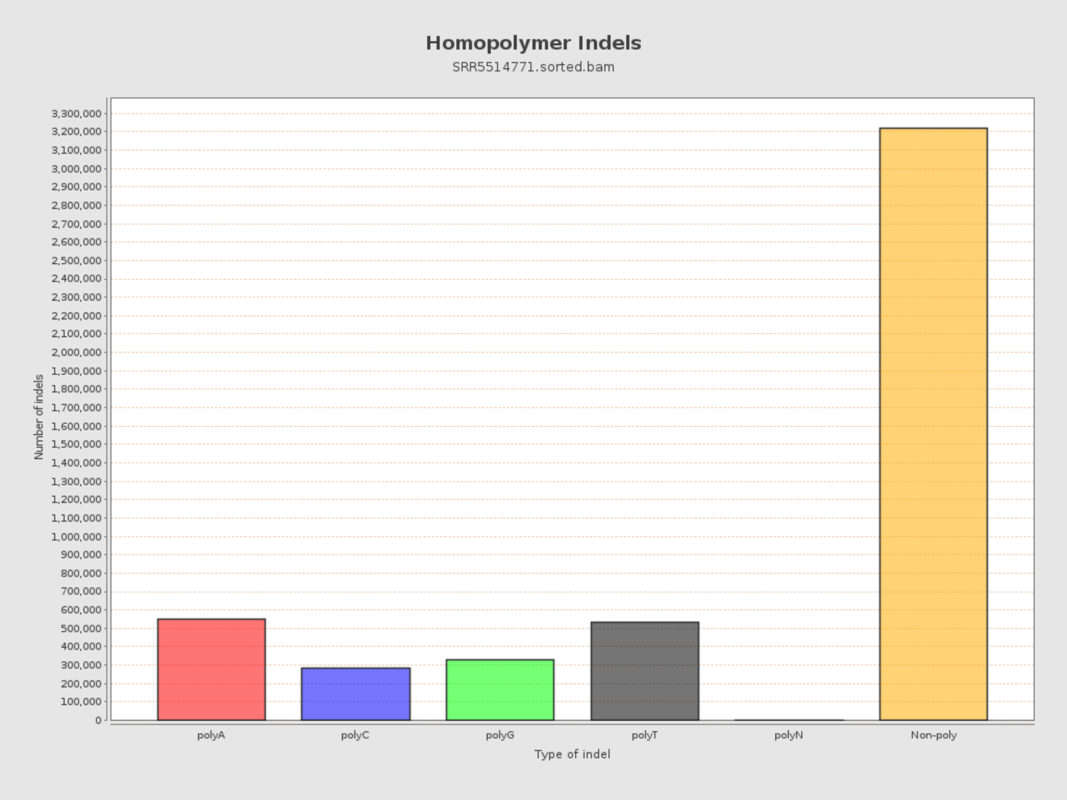
9. Results : Mapped Reads GC-content Distribution



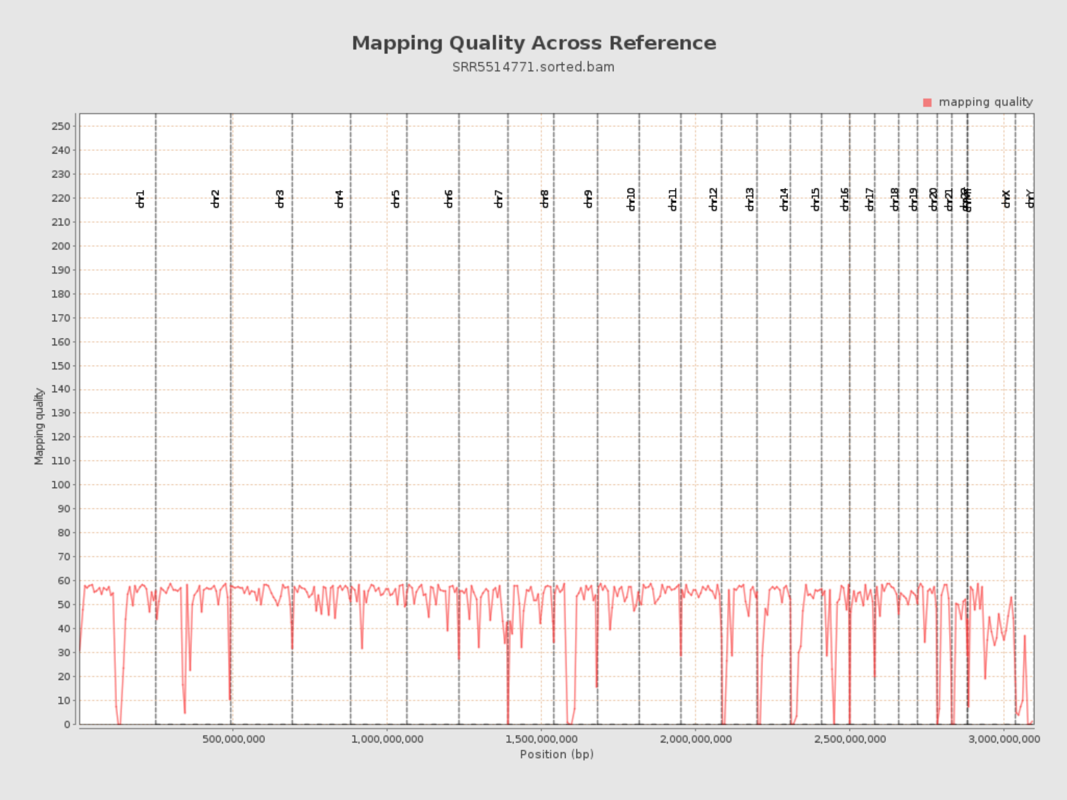
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram