Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/09 17:00:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514705.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_SRR5514705 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514705.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 09 17:00:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514705.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	102,816,684
Mapped reads	102,090,922 / 99.29%
Unmapped reads	725,762 / 0.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,596,038 / 4.47%
Read min/max/mean length	30 / 100 / 99.6
Duplicated reads (estimated)	63,760,786 / 62.01%
Duplication rate	43.33%
Clipped reads	18,547,302 / 18.04%

2.2. ACGT Content

Number/percentage of A's	2,884,216,055 / 29.39%
Number/percentage of C's	2,030,163,941 / 20.69%
Number/percentage of T's	2,833,505,900 / 28.88%
Number/percentage of G's	2,059,714,988 / 20.99%
Number/percentage of N's	4,687,933 / 0.05%
GC Percentage	41.68%

2.3. Coverage

Mean	3.1715

Standard Deviation	74.5857

2.4. Mapping Quality

Mean Mapping Quality	49.51

2.5. Mismatches and indels

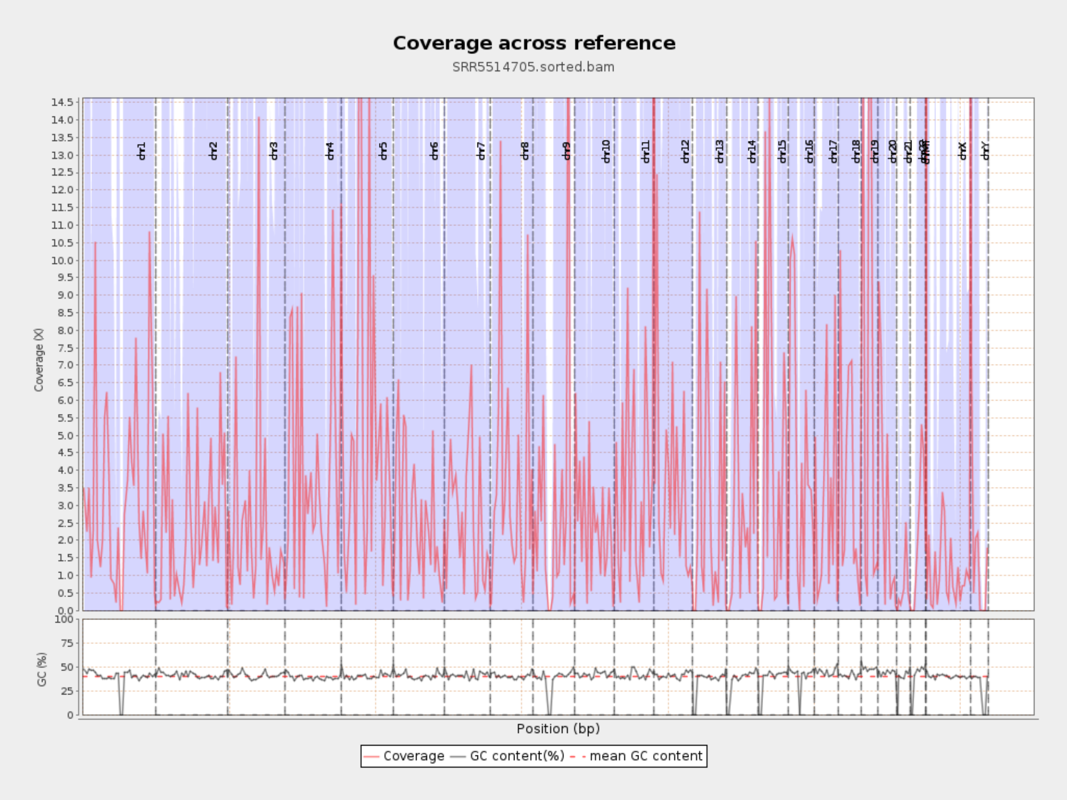
General error rate	0.62%
Mismatches	56,193,101
Insertions	2,986,762
Mapped reads with at least one insertion	2.84%
Deletions	2,965,312
Mapped reads with at least one deletion	2.82%
Homopolymer indels	45.75%

2.6. Chromosome stats

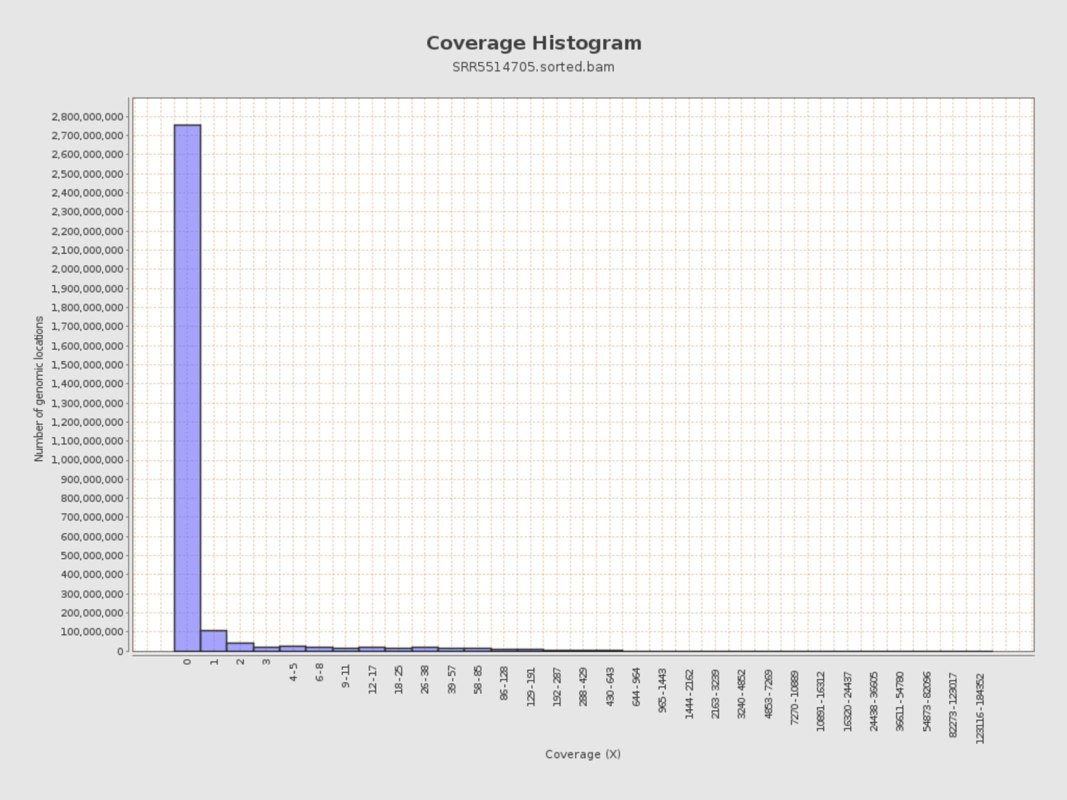
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	800724349	3.2125	41.234
chr2	243199373	591487608	2.4321	27.116
chr3	198022430	463235144	2.3393	25.1736
chr4	191154276	759534686	3.9734	29.512
chr5	180915260	877305165	4.8493	45.9332
chr6	171115067	430747104	2.5173	26.7057
chr7	159138663	419587738	2.6366	26.207

chr8	146364022	530567658	3.625	37.1558
chr9	141213431	426020806	3.0169	237.8657
chr10	135534747	350266524	2.5843	24.6506
chr11	135006516	495097699	3.6672	34.5974
chr12	133851895	474619896	3.5459	64.8522
chr13	115169878	371853169	3.2287	27.3685
chr14	107349540	358655916	3.341	116.2435
chr15	102531392	417665140	4.0735	65.5369
chr16	90354753	405138582	4.4839	52.6427
chr17	81195210	266495089	3.2822	37.825
chr18	78077248	283594459	3.6322	29.949
chr19	59128983	447893766	7.5749	262.6472
chr20	63025520	192686586	3.0573	29.5186
chr21	48129895	32520991	0.6757	10.3154
chr22	51304566	118697496	2.3136	33.6303
chrMT	16571	3708290	223.7819	104.2674
chrX	155270560	213031000	1.372	22.2199
chrY	59373566	87011289	1.4655	19.6676

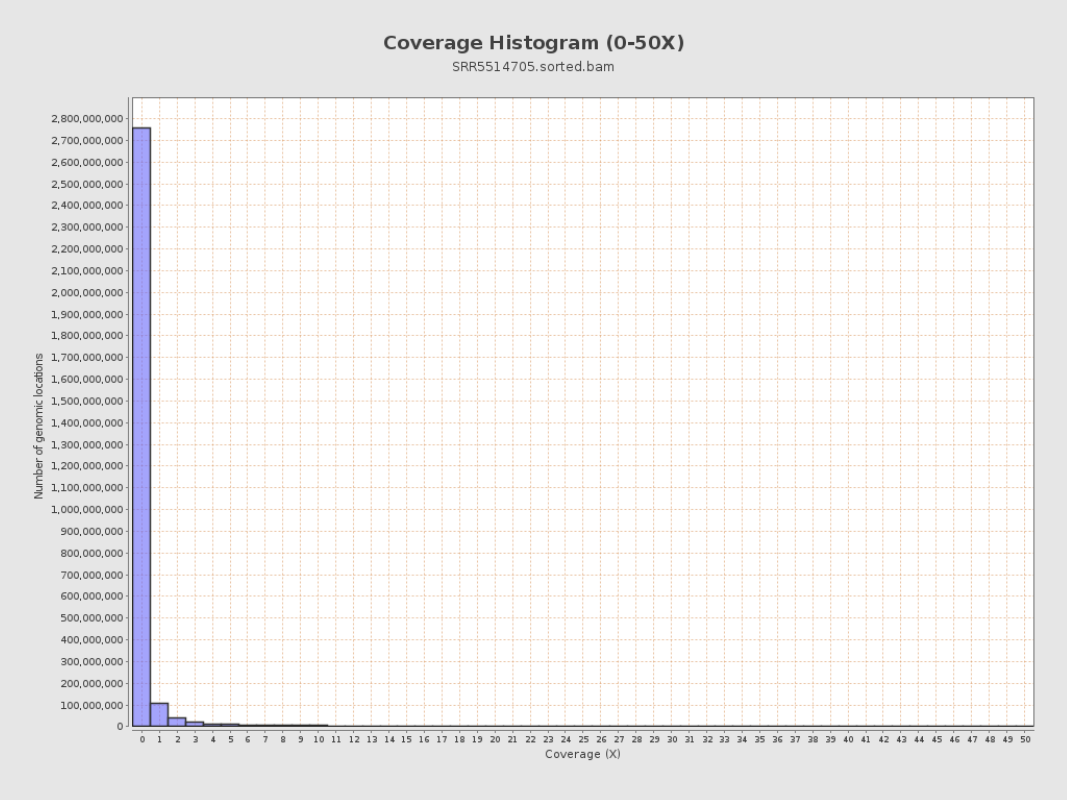
3. Results : Coverage across reference



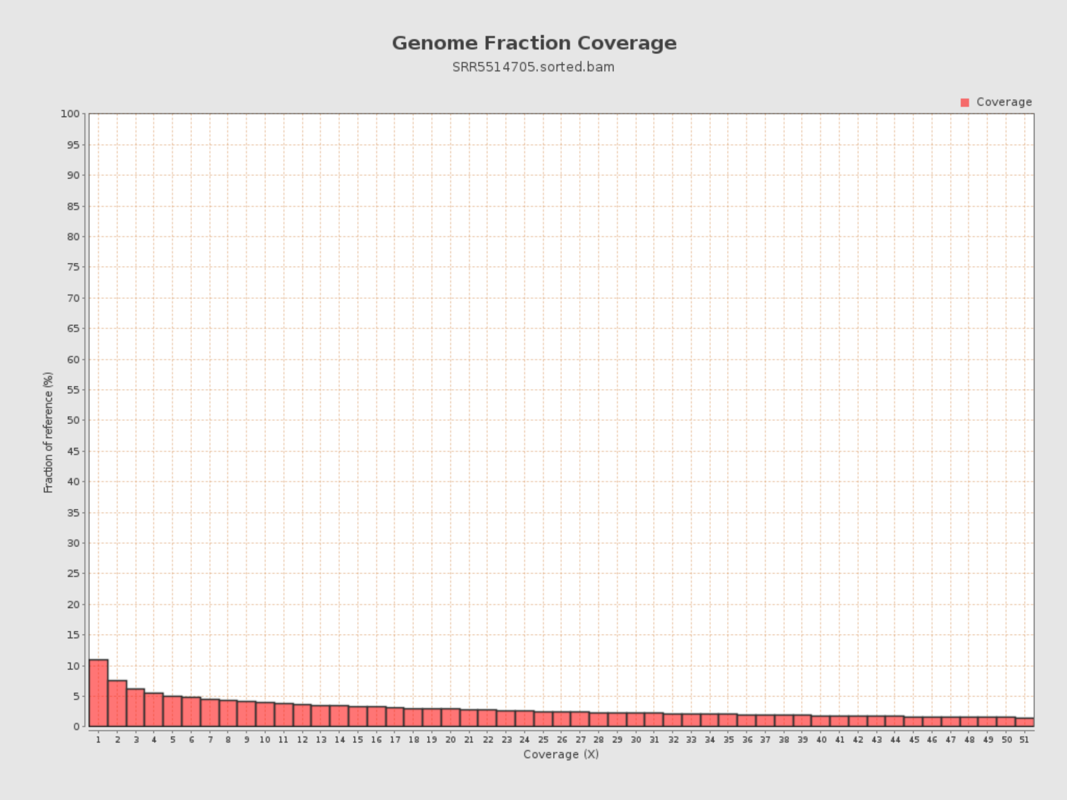
4. Results : Coverage Histogram



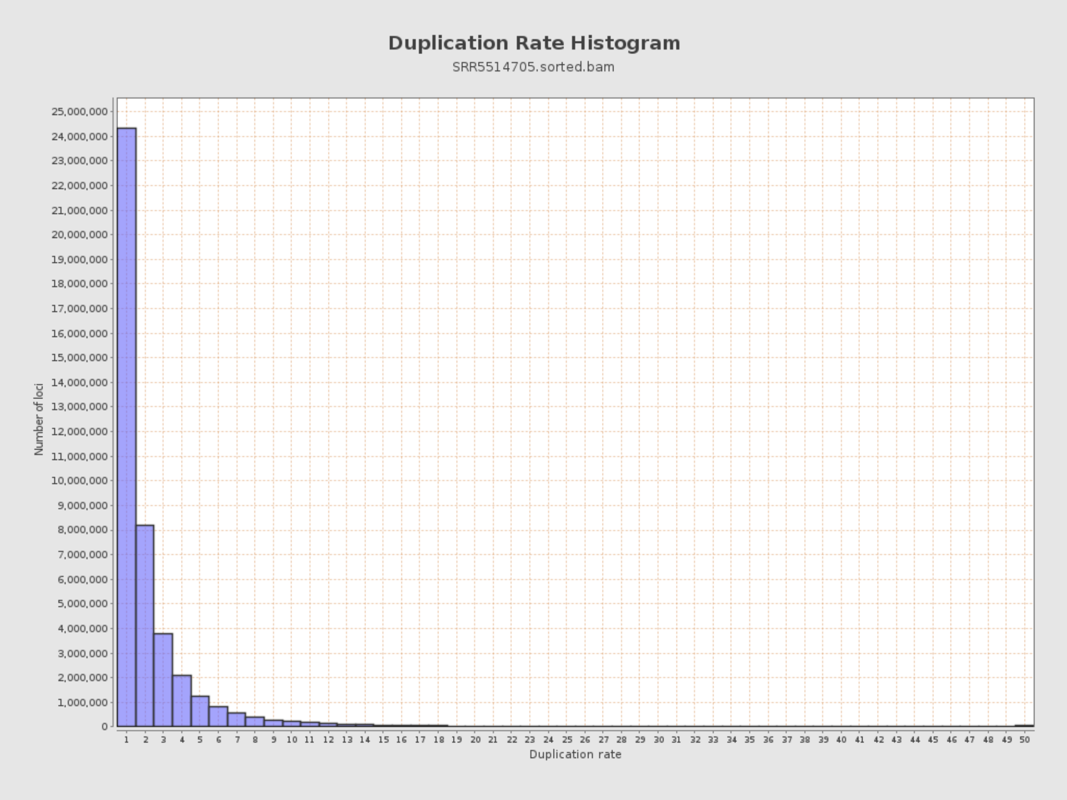
5. Results : Coverage Histogram (0-50X)



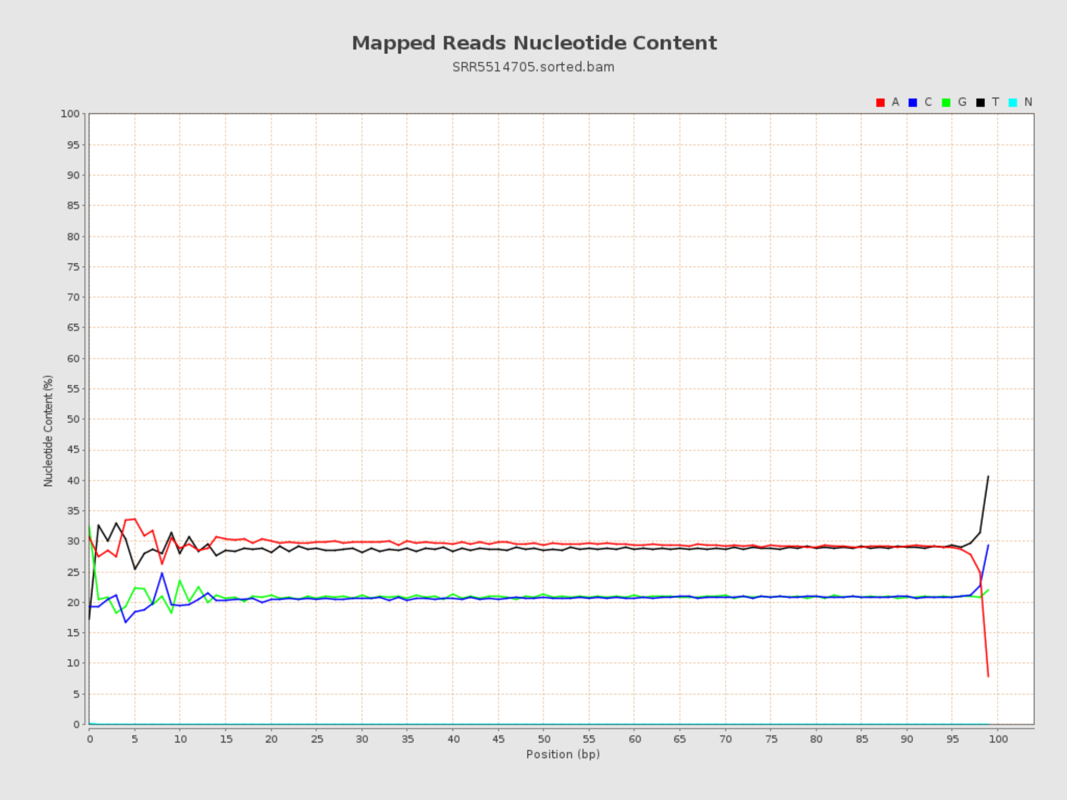
6. Results : Genome Fraction Coverage



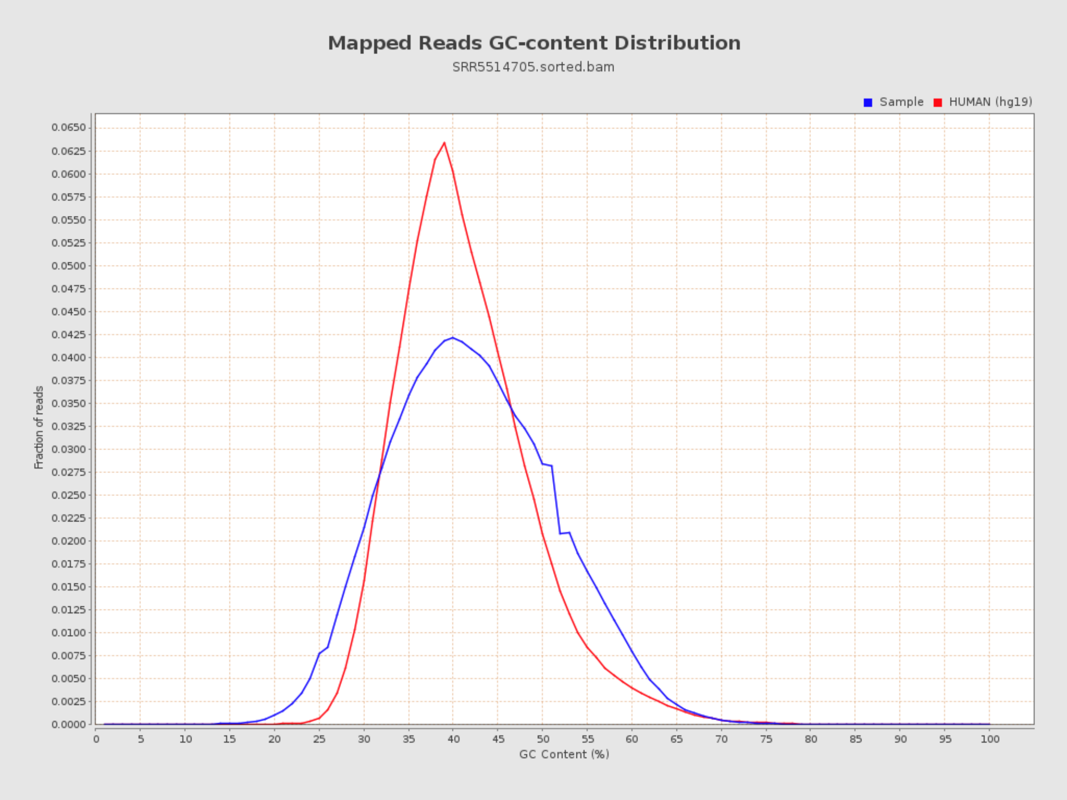
7. Results : Duplication Rate Histogram



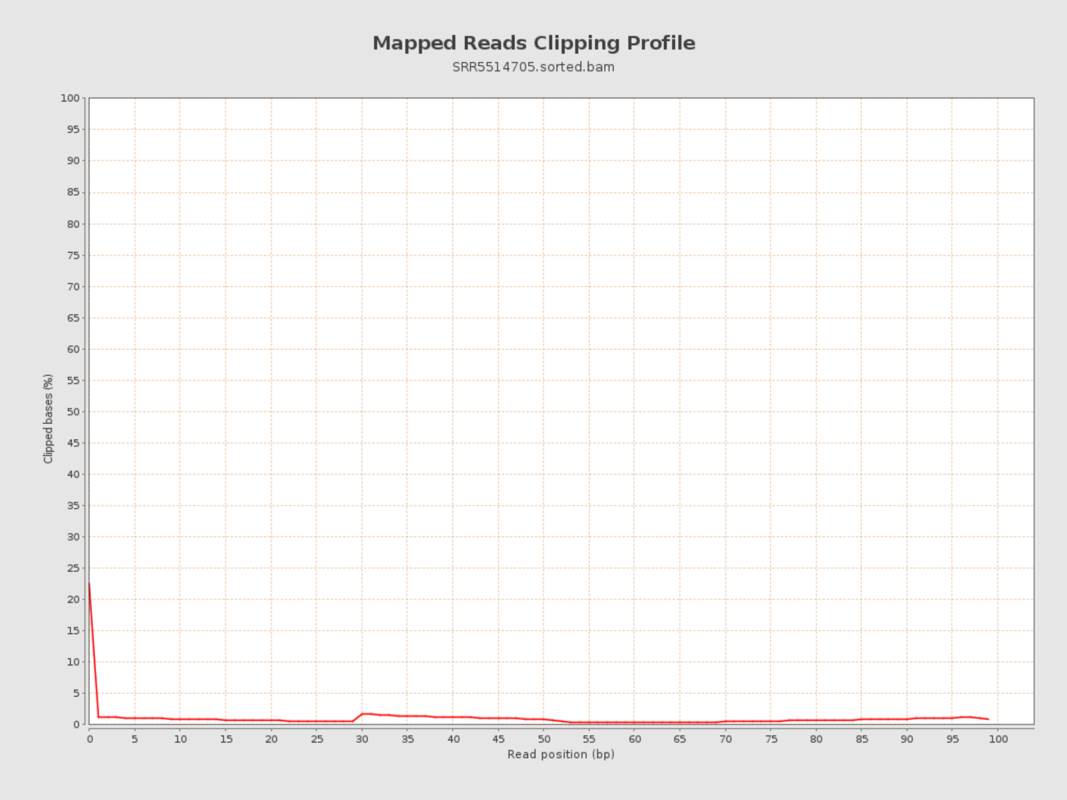
8. Results : Mapped Reads Nucleotide Content



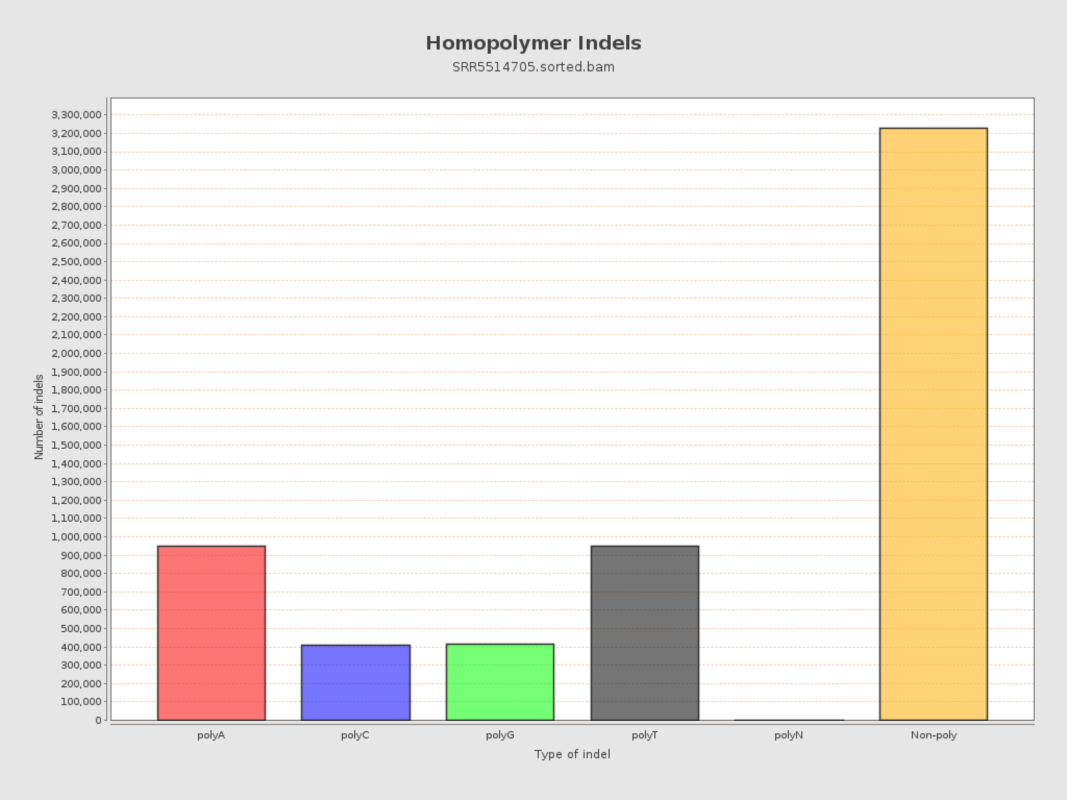
9. Results : Mapped Reads GC-content Distribution



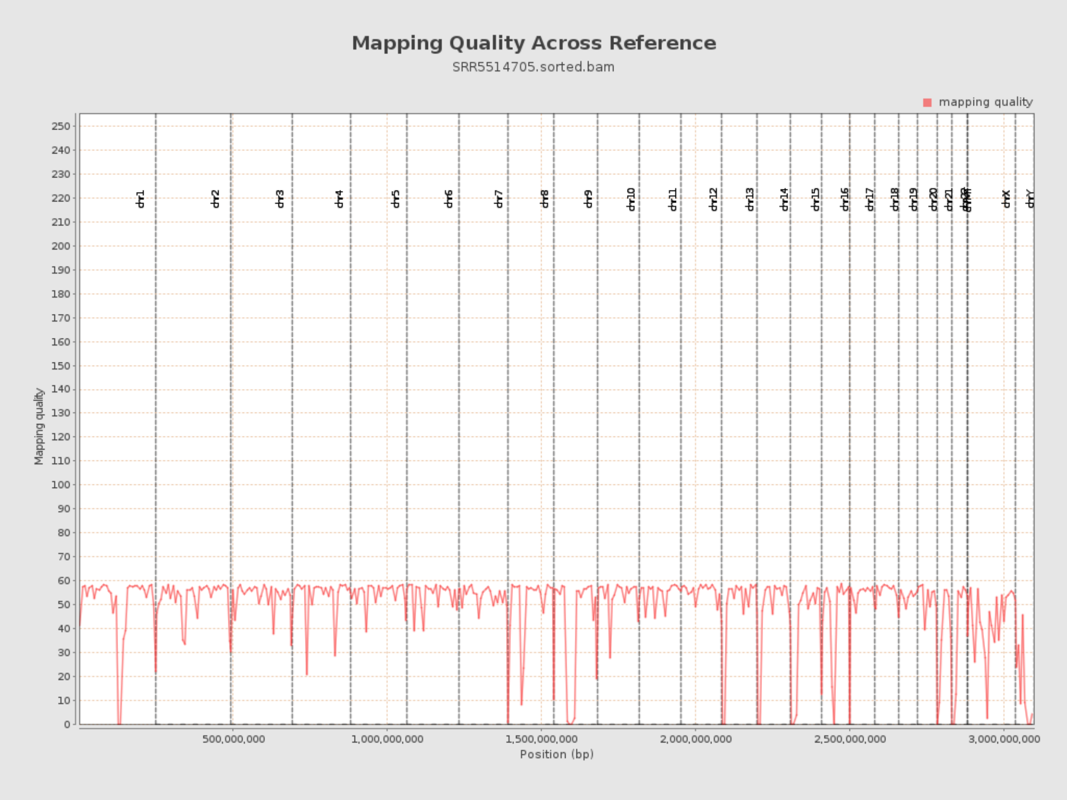
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram