Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 06:18:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514726.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_SRR5514726 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514726.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 06:18:29 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514726.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	71,669,416
Mapped reads	69,597,735 / 97.11%
Unmapped reads	2,071,681 / 2.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,004,682 / 2.8%
Read min/max/mean length	30 / 100 / 99.08
Duplicated reads (estimated)	51,199,111 / 71.44%
Duplication rate	49.07%
Clipped reads	12,014,559 / 16.76%

2.2. ACGT Content

Number/percentage of A's	1,710,757,135 / 25.95%
Number/percentage of C's	1,555,103,321 / 23.59%
Number/percentage of T's	1,728,232,136 / 26.22%
Number/percentage of G's	1,560,836,846 / 23.68%
Number/percentage of N's	36,377,057 / 0.55%
GC Percentage	47.27%

2.3. Coverage

Mean	2.1305

Standard Deviation	43.2893

2.4. Mapping Quality

Mean Mapping Quality	38.5

2.5. Mismatches and indels

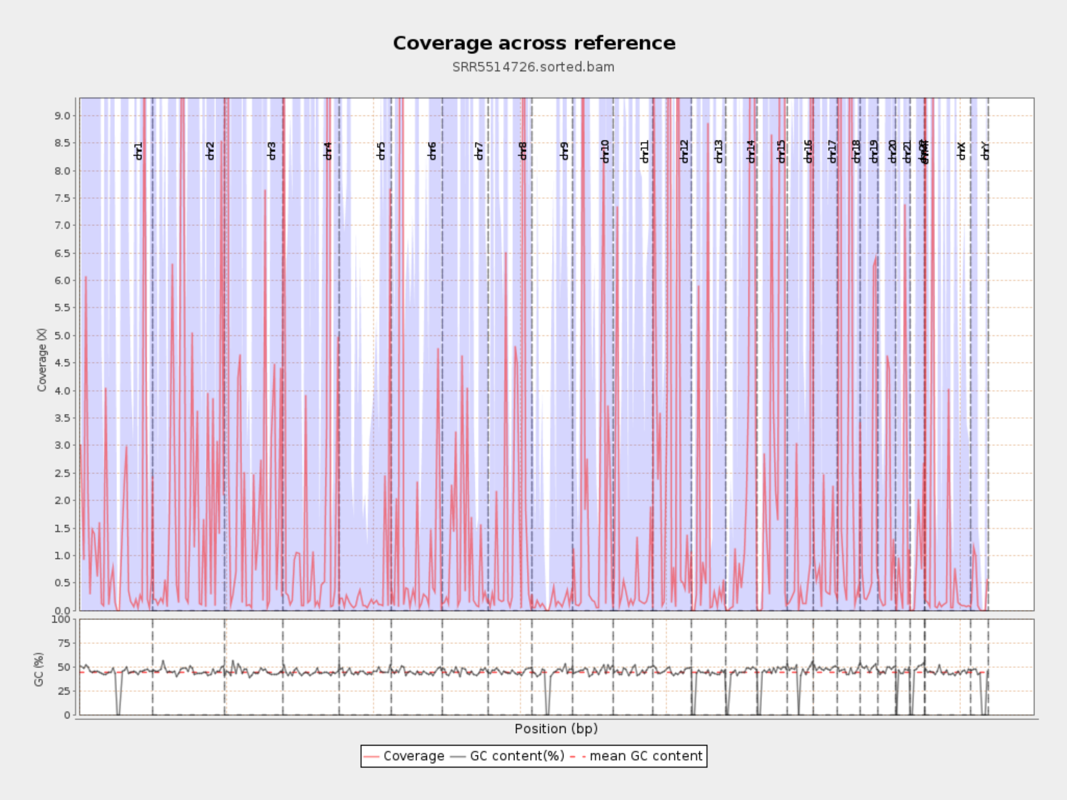
General error rate	0.96%
Mismatches	59,025,943
Insertions	2,326,384
Mapped reads with at least one insertion	3.2%
Deletions	1,839,819
Mapped reads with at least one deletion	2.56%
Homopolymer indels	43.84%

2.6. Chromosome stats

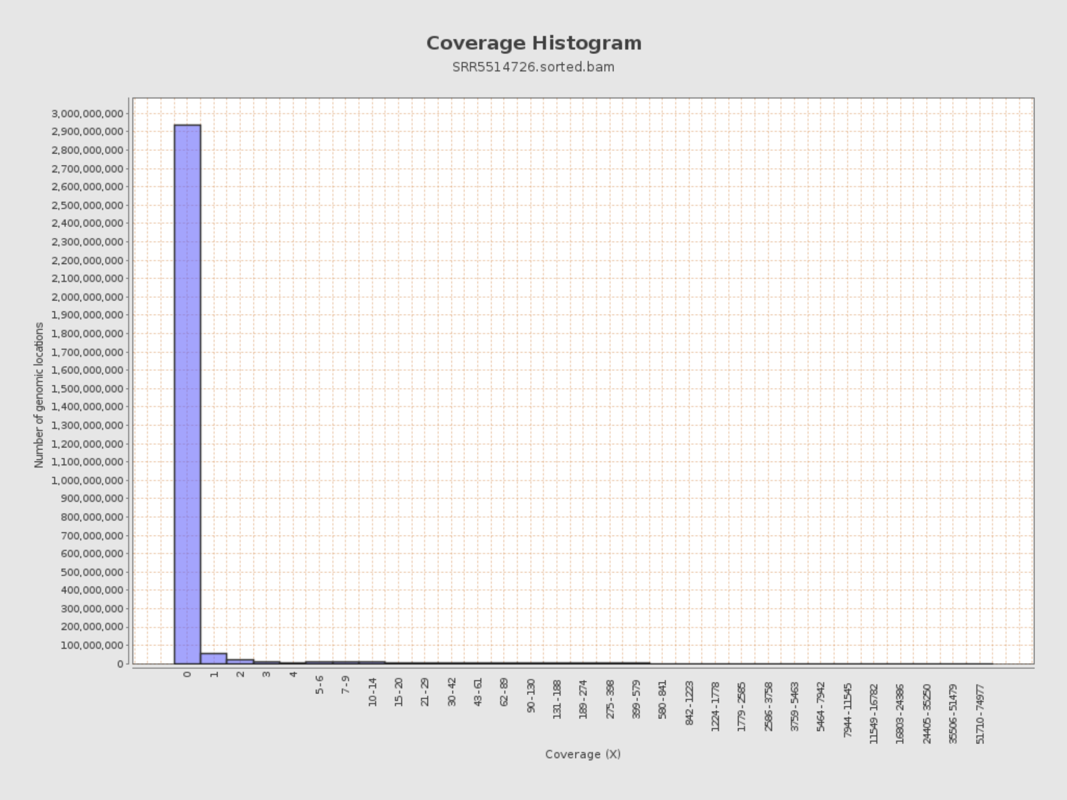
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	337655579	1.3547	25.5029
chr2	243199373	538024359	2.2123	69.223
chr3	198022430	692644876	3.4978	39.0774
chr4	191154276	409170128	2.1405	26.2263
chr5	180915260	102870503	0.5686	17.4074
chr6	171115067	342381107	2.0009	36.884
chr7	159138663	165110599	1.0375	28.0203

chr8	146364022	316893223	2.1651	30.209
chr9	141213431	20916963	0.1481	10.2179
chr10	135534747	294720646	2.1745	51.0021
chr11	135006516	108699546	0.8051	23.138
chr12	133851895	490749893	3.6664	37.6485
chr13	115169878	141076013	1.2249	26.1306
chr14	107349540	342886961	3.1941	33.7796
chr15	102531392	817169719	7.9699	79.717
chr16	90354753	321935964	3.563	81.3491
chr17	81195210	65597866	0.8079	13.2956
chr18	78077248	597284316	7.6499	97.9852
chr19	59128983	124438407	2.1045	79.7613
chr20	63025520	88400345	1.4026	25.7541
chr21	48129895	73958447	1.5366	21.3261
chr22	51304566	49226589	0.9595	16.9294
chrMT	16571	8310820	501.528	240.8347
chrX	155270560	122502683	0.789	22.368
chrY	59373566	22658373	0.3816	41.695

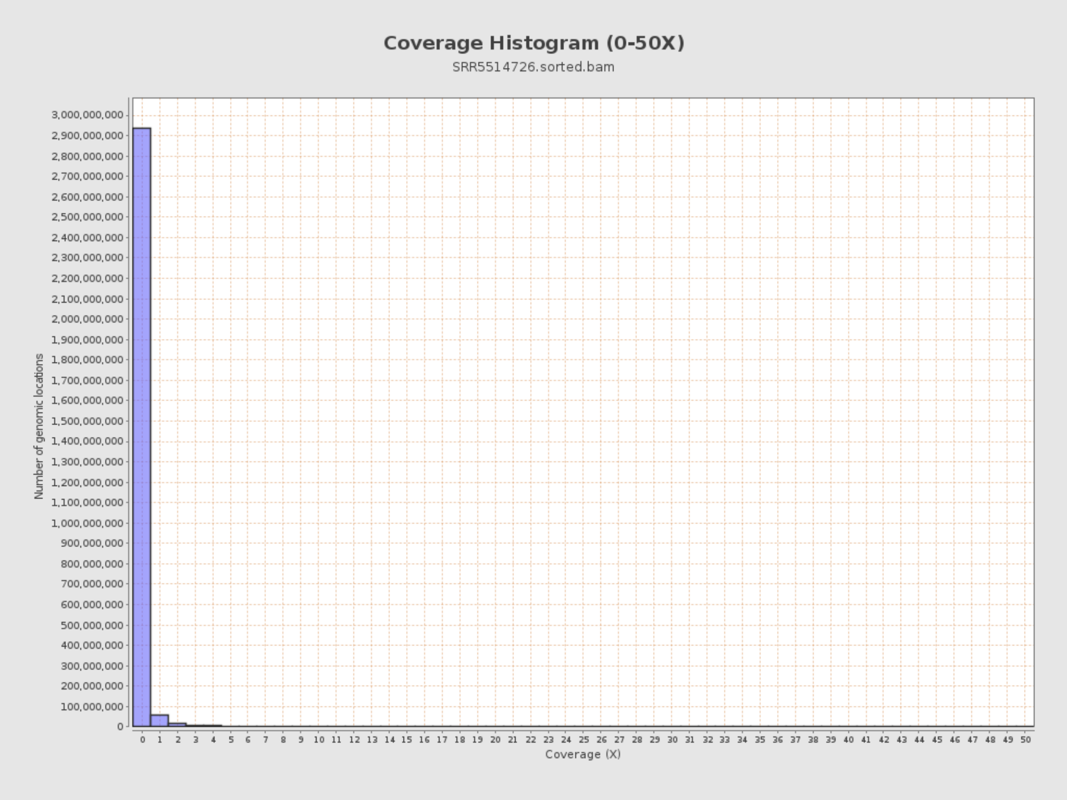
3. Results : Coverage across reference



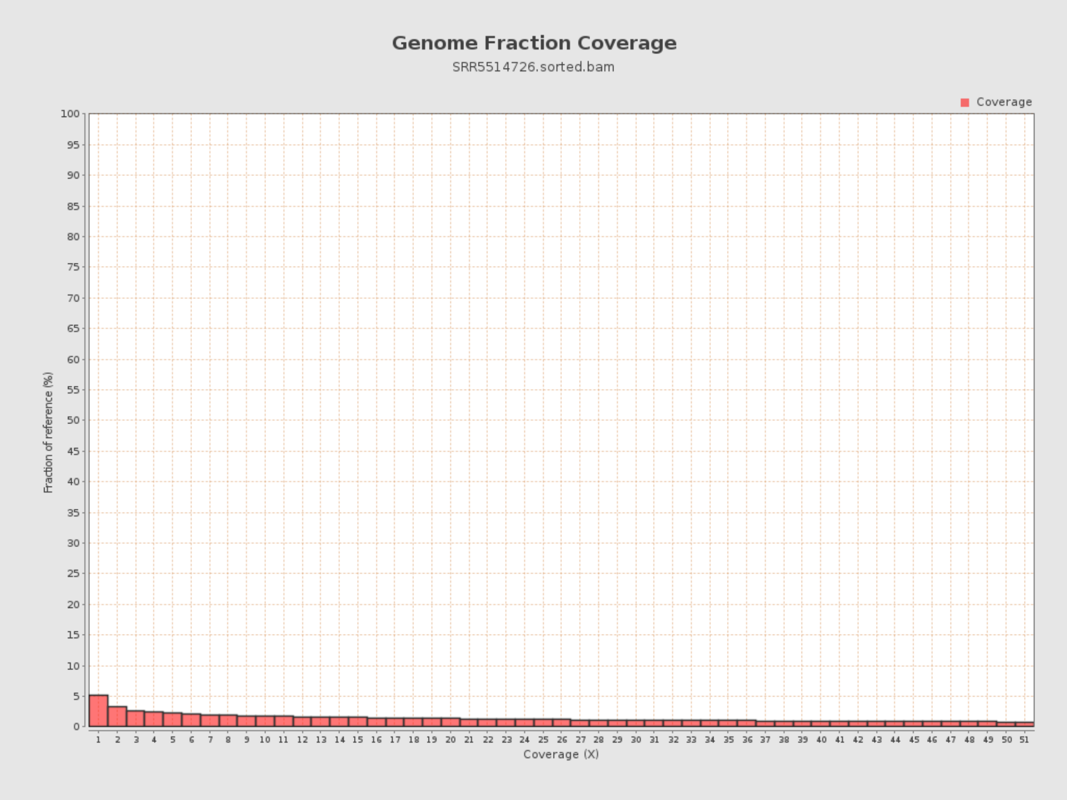
4. Results : Coverage Histogram



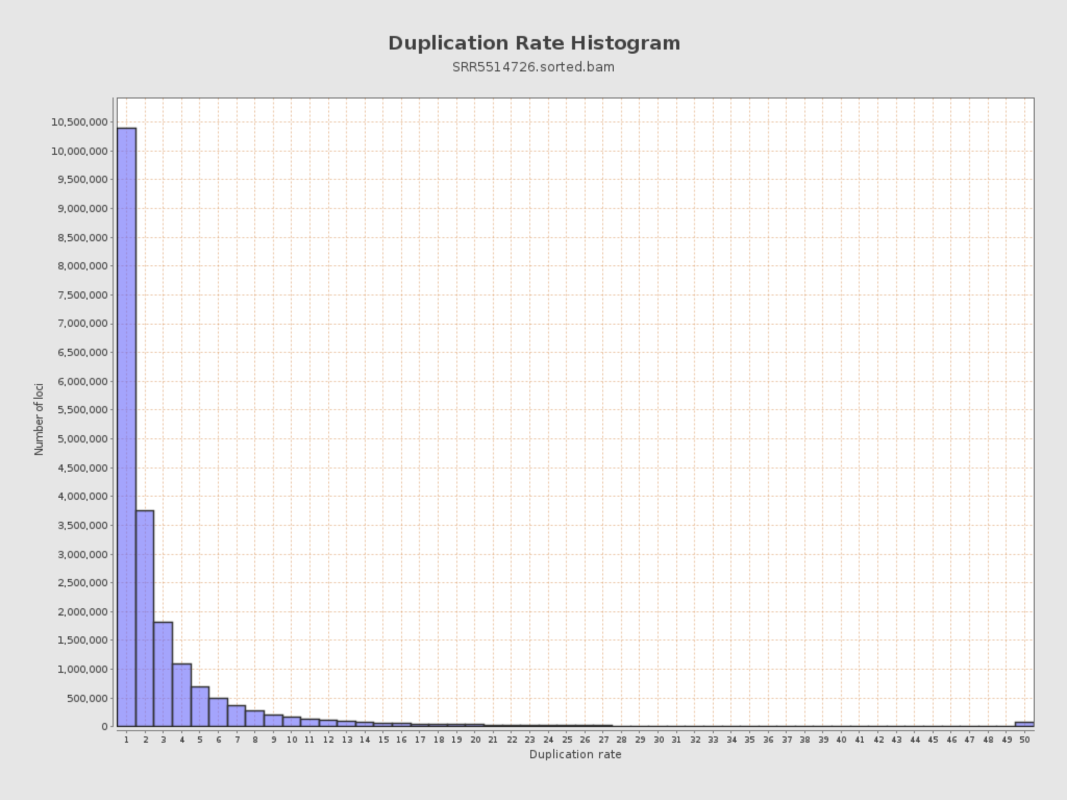
5. Results : Coverage Histogram (0-50X)



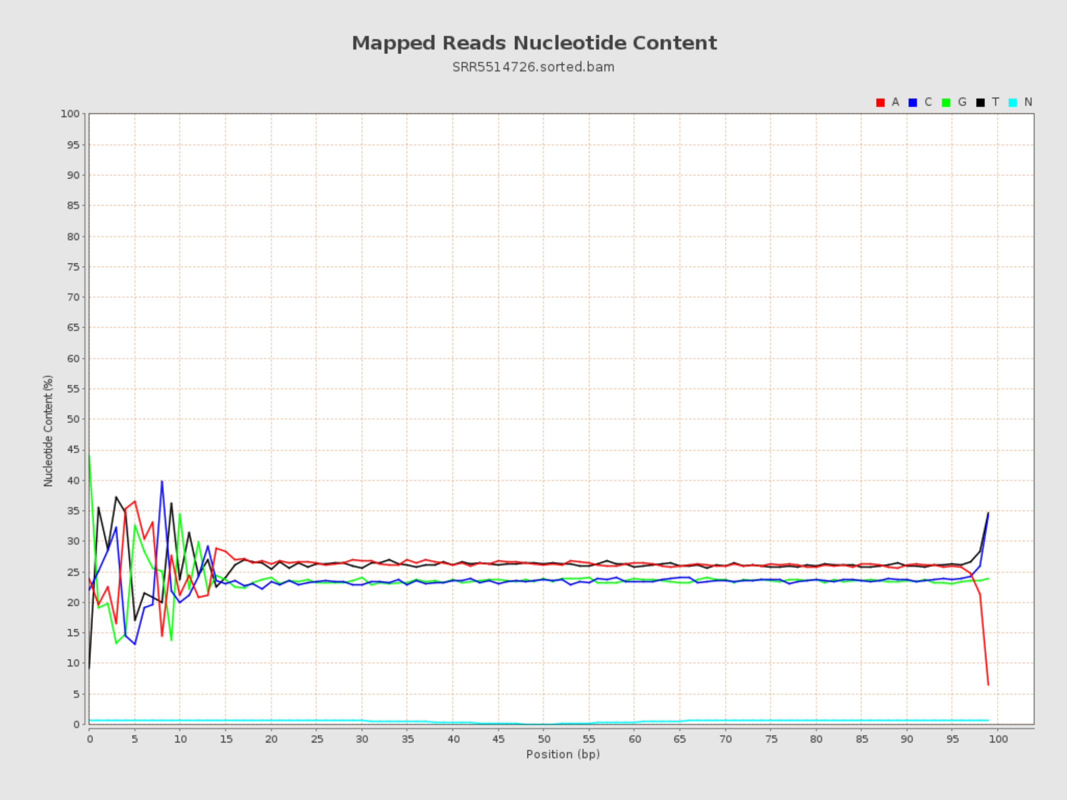
6. Results : Genome Fraction Coverage



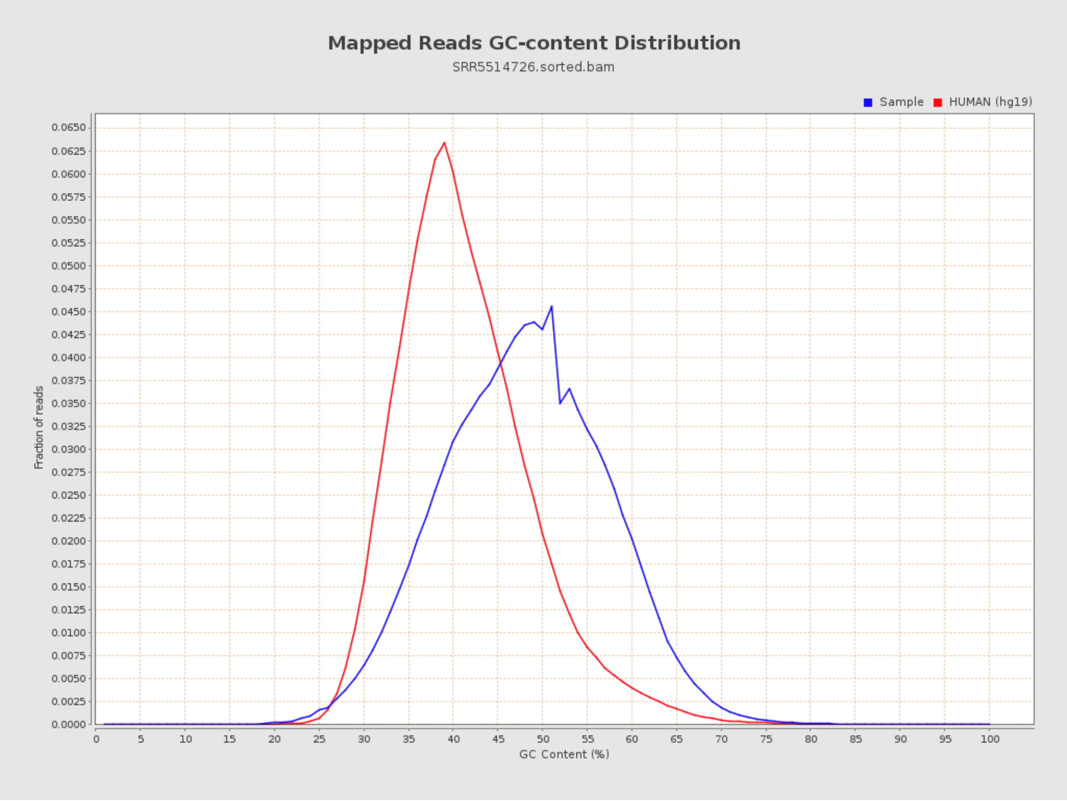
7. Results : Duplication Rate Histogram



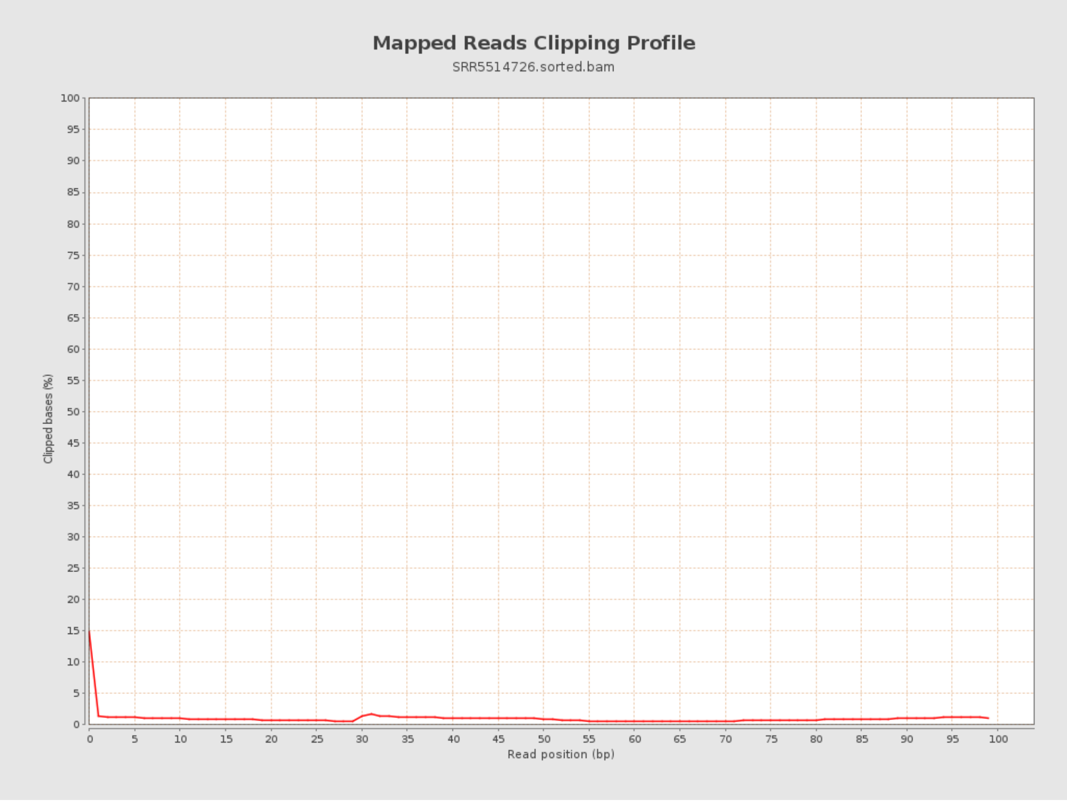
8. Results : Mapped Reads Nucleotide Content



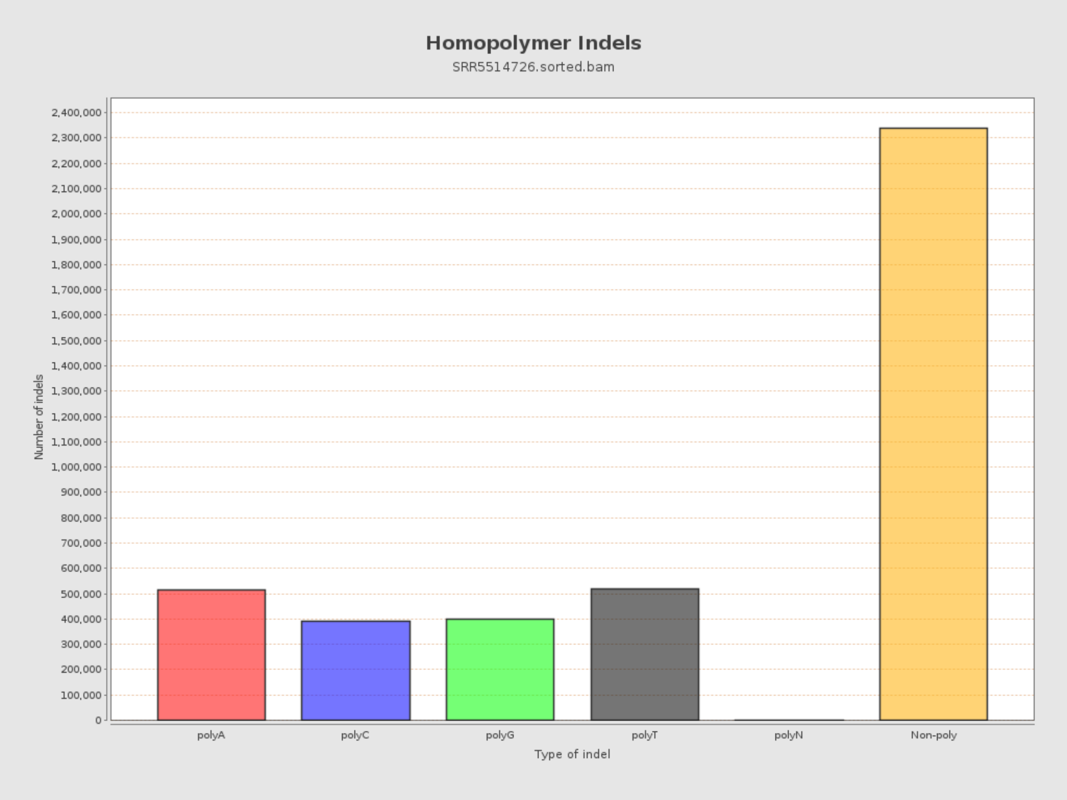
9. Results : Mapped Reads GC-content Distribution



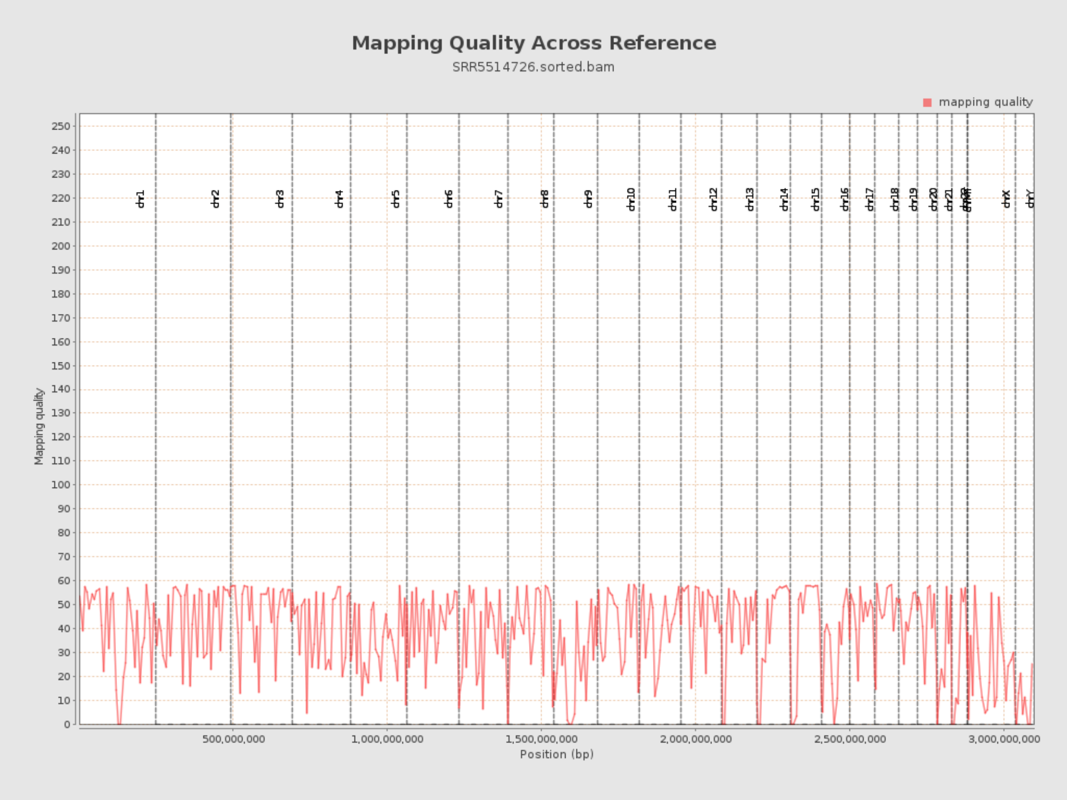
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram