Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 21:30:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514766.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_SRR5514766 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514766.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 21:30:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514766.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,934,265
Mapped reads	4,748,172 / 36.71%
Unmapped reads	8,186,093 / 63.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	925,292 / 7.15%
Read min/max/mean length	30 / 100 / 101.63
Duplicated reads (estimated)	2,884,243 / 22.3%
Duplication rate	24.74%
Clipped reads	3,233,754 / 25%

2.2. ACGT Content

Number/percentage of A's	133,029,773 / 30.74%
Number/percentage of C's	81,863,964 / 18.92%
Number/percentage of T's	131,707,384 / 30.44%
Number/percentage of G's	86,105,453 / 19.9%
Number/percentage of N's	28,076 / 0.01%
GC Percentage	38.82%

2.3. Coverage

Mean	0.14

Standard Deviation	18.0509

2.4. Mapping Quality

Mean Mapping Quality	43.08

2.5. Mismatches and indels

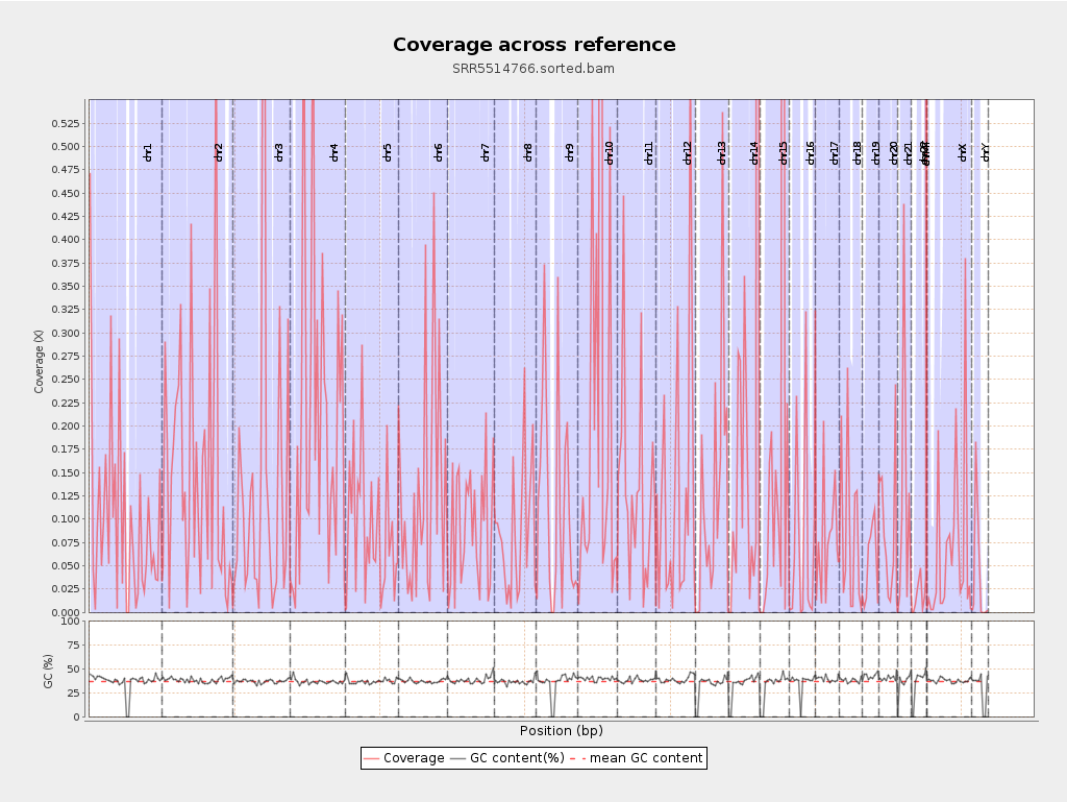
General error rate	0.87%
Mismatches	3,146,338
Insertions	314,148
Mapped reads with at least one insertion	6.25%
Deletions	188,714
Mapped reads with at least one deletion	3.62%
Homopolymer indels	34.97%

2.6. Chromosome stats

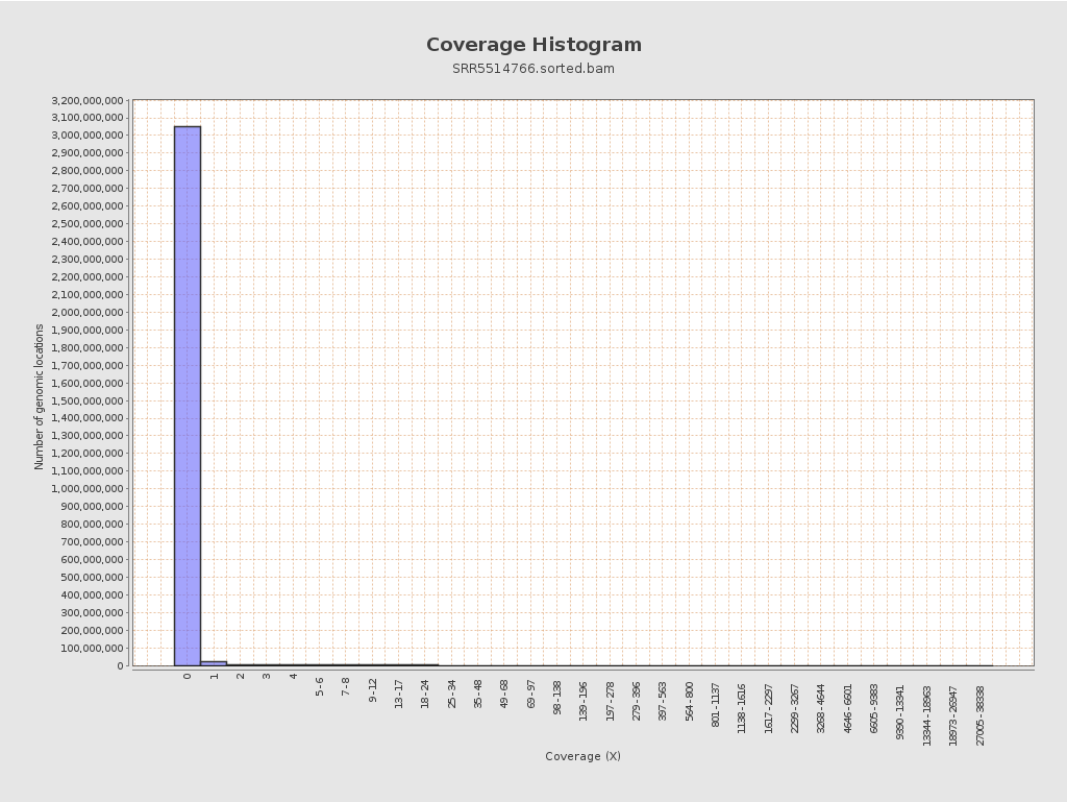
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24409404	0.0979	5.0851
chr2	243199373	36679973	0.1508	6.0611
chr3	198022430	26273510	0.1327	2.9652
chr4	191154276	39898995	0.2087	4.014
chr5	180915260	16266172	0.0899	2.3941
chr6	171115067	22202179	0.1297	2.7431
chr7	159138663	15239651	0.0958	4.6468

chr8	146364022	12975639	0.0887	1.8486
chr9	141213431	17248157	0.1221	3.4931
chr10	135534747	39358666	0.2904	54.6839
chr11	135006516	17931607	0.1328	2.6283
chr12	133851895	15945620	0.1191	9.5565
chr13	115169878	14935349	0.1297	3.5016
chr14	107349540	47811516	0.4454	54.4016
chr15	102531392	23630144	0.2305	45.0105
chr16	90354753	6713490	0.0743	2.2187
chr17	81195210	6265292	0.0772	2.4008
chr18	78077248	6626814	0.0849	2.0925
chr19	59128983	3414143	0.0577	1.6881
chr20	63025520	5589079	0.0887	2.1225
chr21	48129895	5498076	0.1142	3.9807
chr22	51304566	869337	0.0169	0.9492
chrMT	16571	14845721	895.8856	1,060.7986
chrX	155270560	10645674	0.0686	1.9598
chrY	59373566	2081553	0.0351	1.546

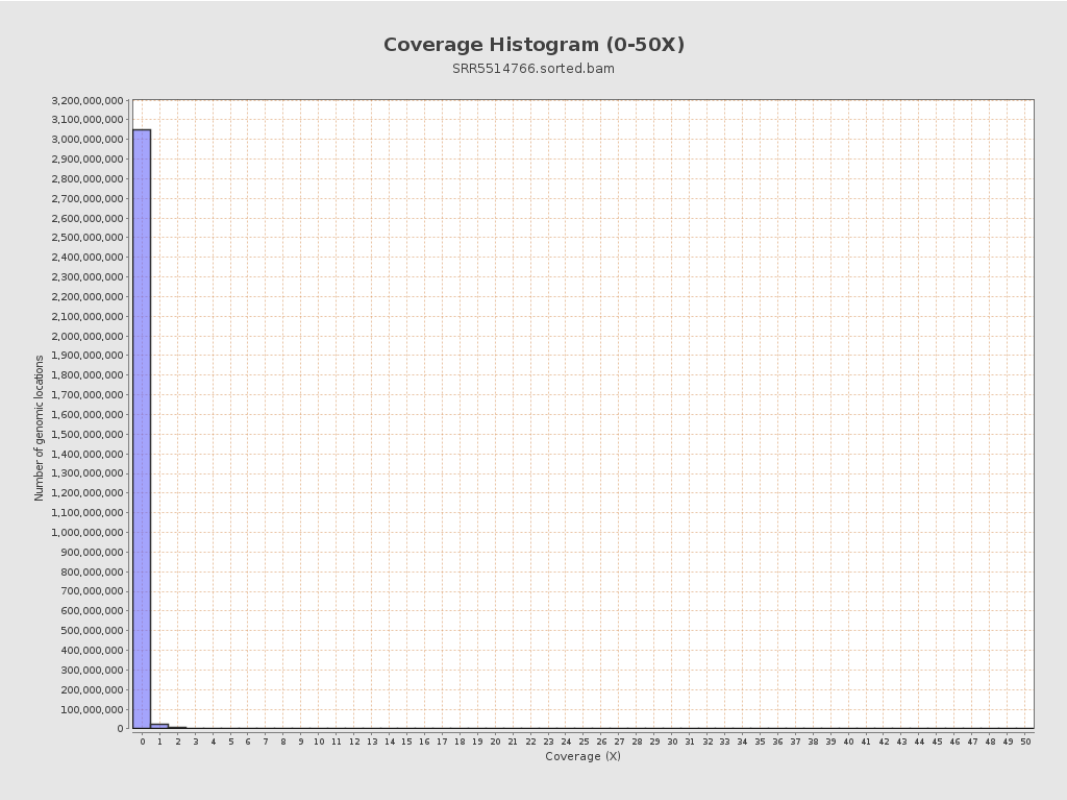
3. Results : Coverage across reference



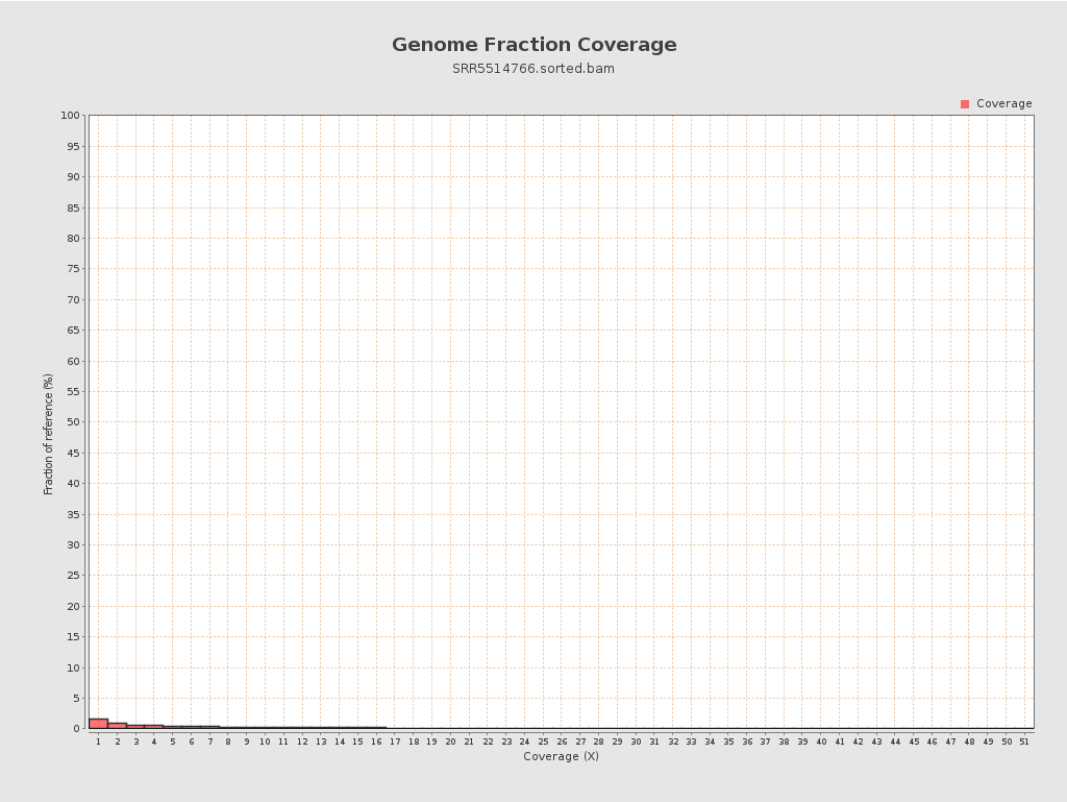
4. Results : Coverage Histogram



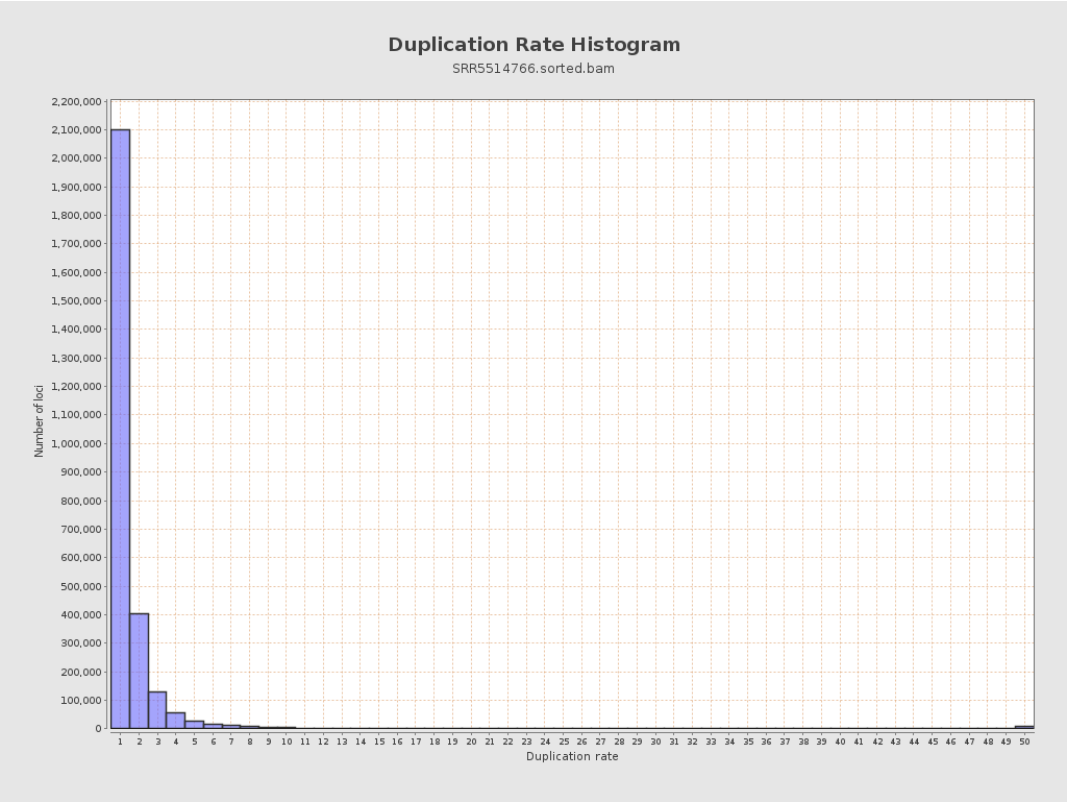
5. Results : Coverage Histogram (0-50X)



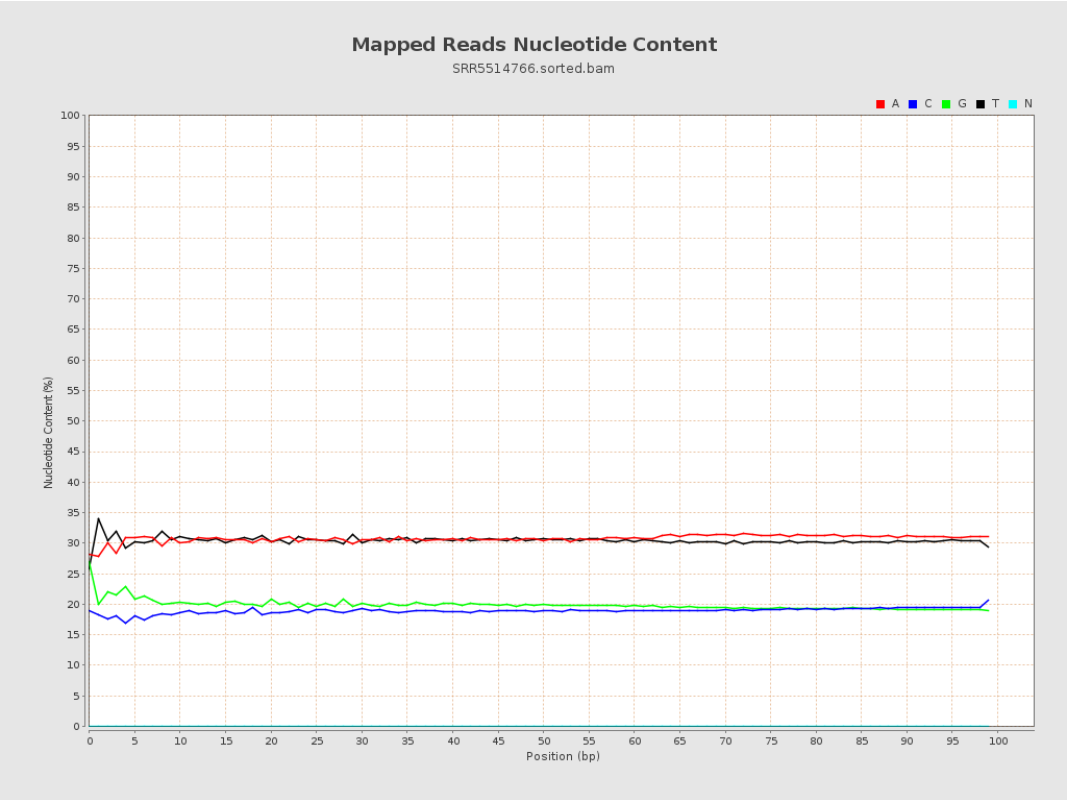
6. Results : Genome Fraction Coverage



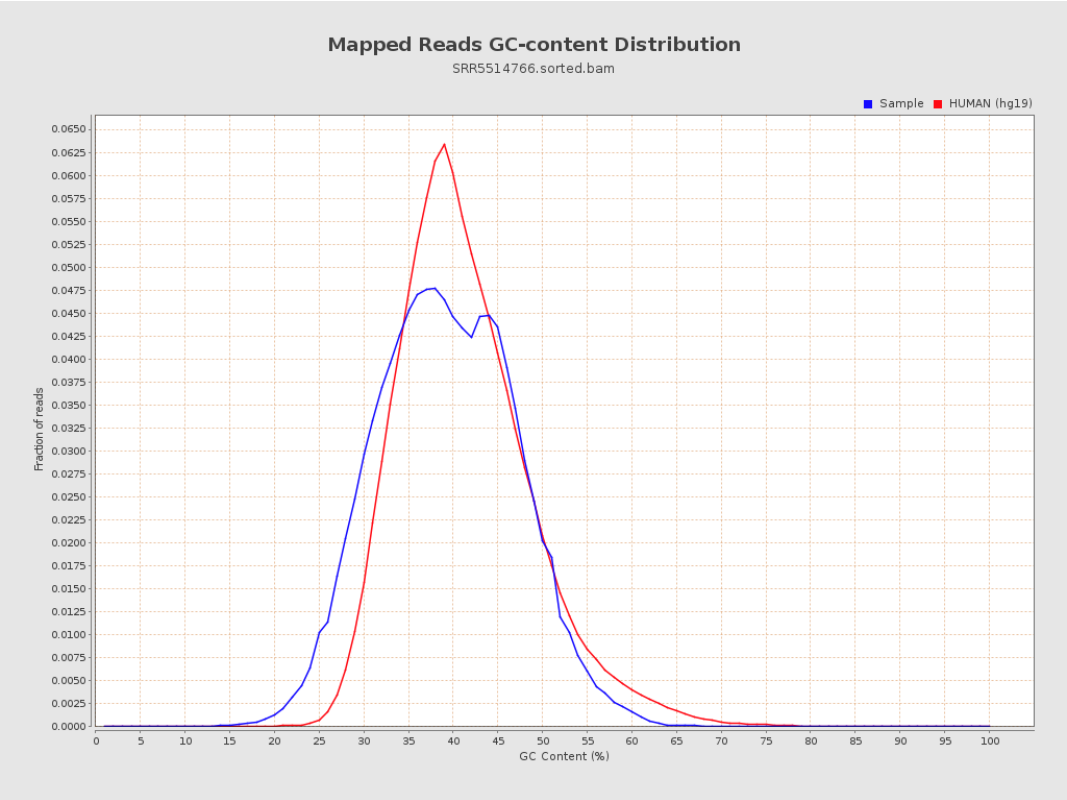
7. Results : Duplication Rate Histogram



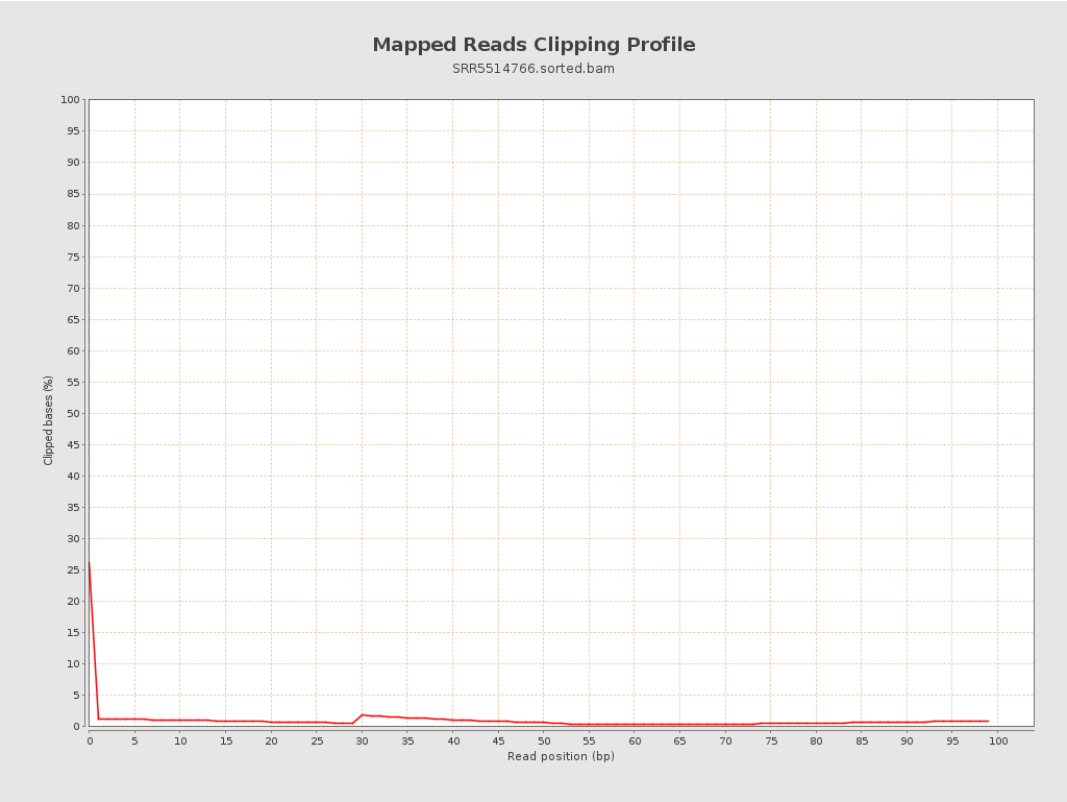
8. Results : Mapped Reads Nucleotide Content



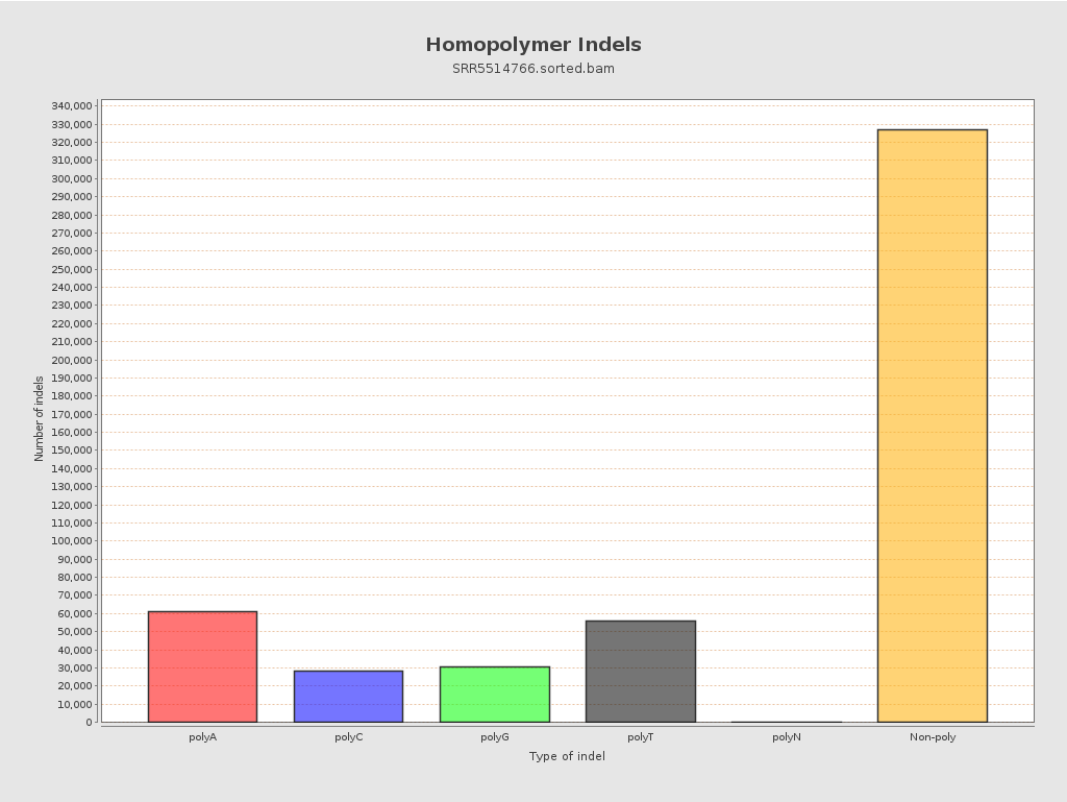
9. Results : Mapped Reads GC-content Distribution



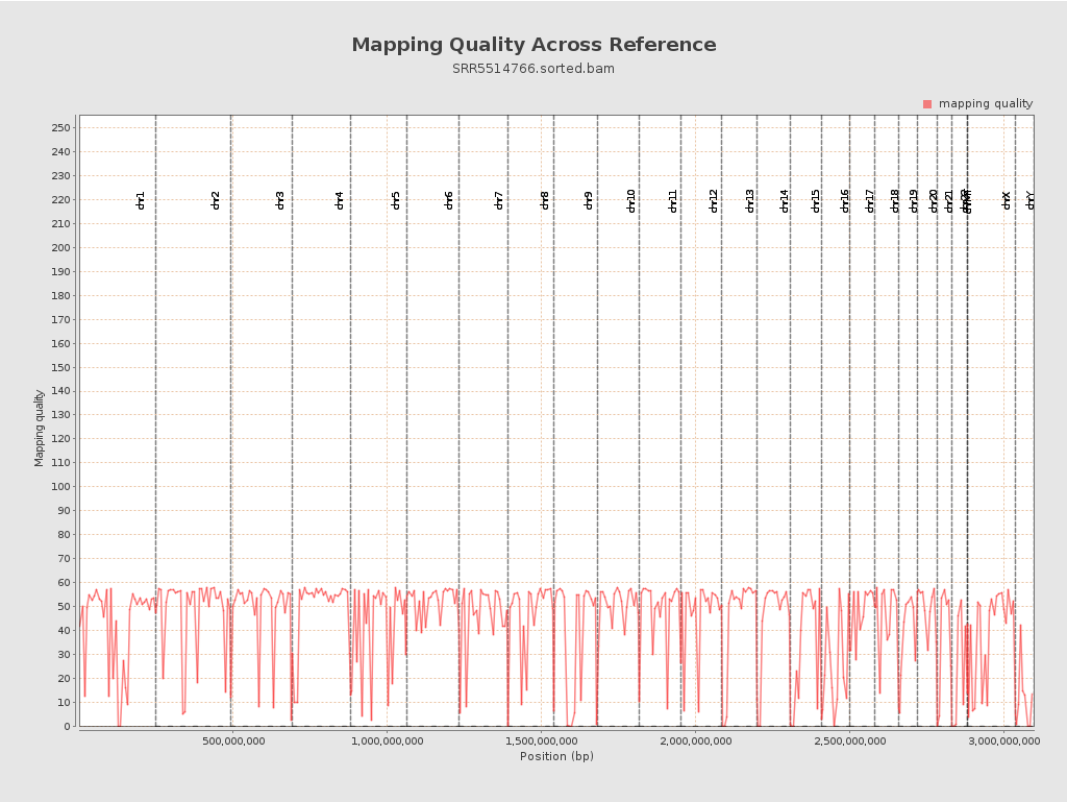
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram