Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 20:23:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514760.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_SRR5514760 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514760.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 20:23:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514760.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	76,565,125
Mapped reads	71,864,445 / 93.86%
Unmapped reads	4,700,680 / 6.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,055,261 / 15.75%
Read min/max/mean length	30 / 100 / 105.52
Duplicated reads (estimated)	65,014,176 / 84.91%
Duplication rate	49.31%
Clipped reads	40,521,552 / 52.92%

2.2. ACGT Content

Number/percentage of A's	2,056,033,238 / 30.5%
Number/percentage of C's	1,288,052,520 / 19.11%
Number/percentage of T's	2,046,925,102 / 30.37%
Number/percentage of G's	1,349,384,521 / 20.02%
Number/percentage of N's	458,116 / 0.01%
GC Percentage	39.13%

2.3. Coverage

Mean	2.1795

Standard Deviation	231.9177

2.4. Mapping Quality

Mean Mapping Quality	42.81

2.5. Mismatches and indels

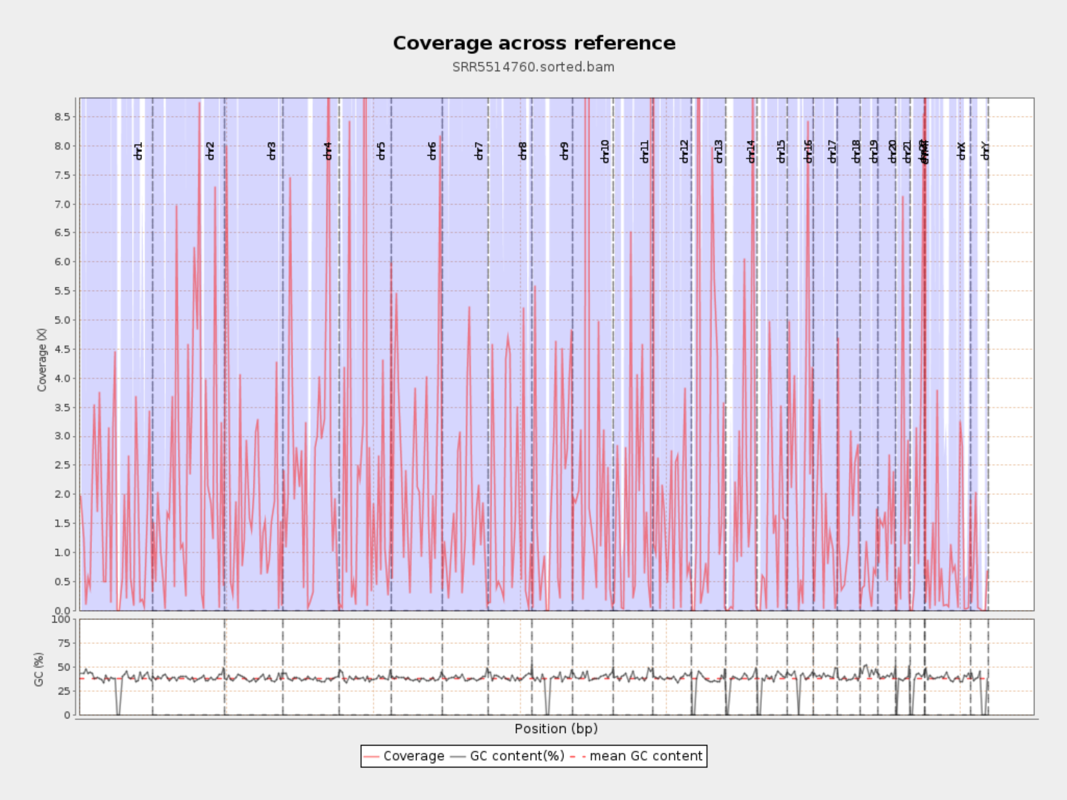
General error rate	0.7%
Mismatches	38,250,330
Insertions	5,118,014
Mapped reads with at least one insertion	6.78%
Deletions	2,076,954
Mapped reads with at least one deletion	2.67%
Homopolymer indels	46.31%

2.6. Chromosome stats

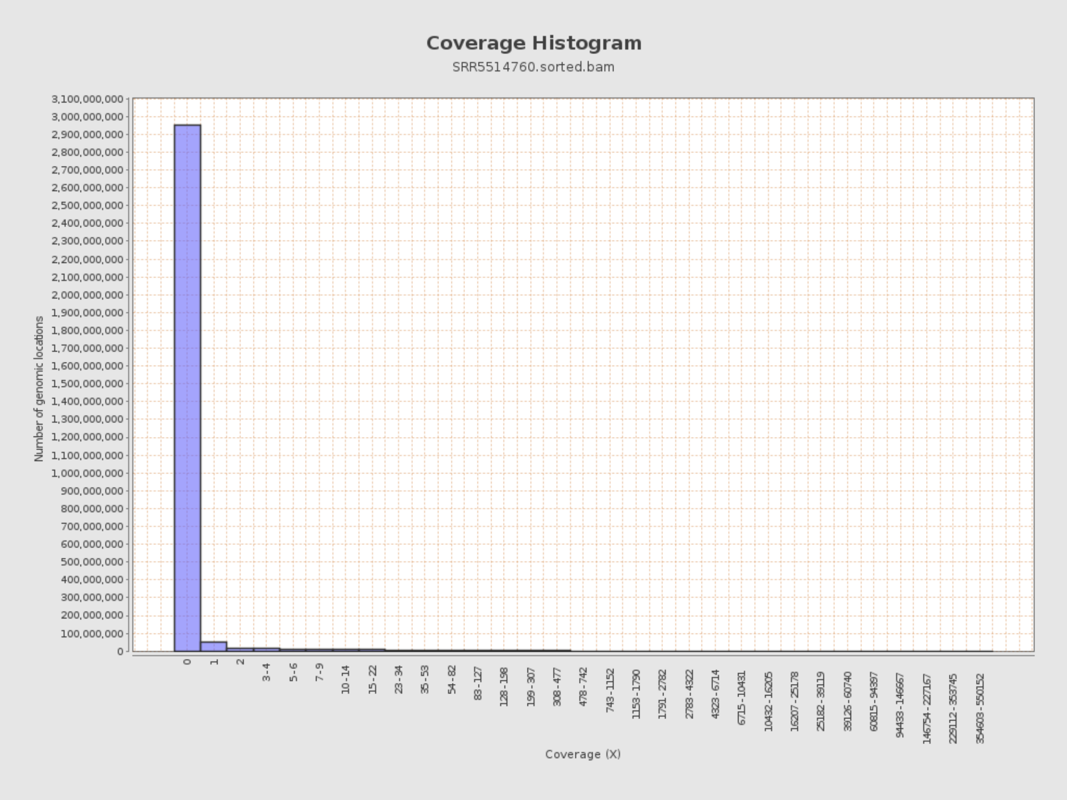
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	372289679	1.4936	36.1023
chr2	243199373	603350417	2.4809	44.0229
chr3	198022430	390326298	1.9711	35.9646
chr4	191154276	526765490	2.7557	47.1477
chr5	180915260	430949556	2.3821	45.9632
chr6	171115067	441684002	2.5812	53.5889
chr7	159138663	261651277	1.6442	29.3925

chr8	146364022	280838985	1.9188	38.5253
chr9	141213431	288955233	2.0462	66.7017
chr10	135534747	730403685	5.3891	1,043.8187
chr11	135006516	334443462	2.4772	203.7374
chr12	133851895	203741416	1.5221	32.7924
chr13	115169878	339529496	2.9481	141.8308
chr14	107349540	216366183	2.0155	97.8131
chr15	102531392	149429236	1.4574	34.2938
chr16	90354753	256255936	2.8361	84.9723
chr17	81195210	99627343	1.227	34.1731
chr18	78077248	129112606	1.6537	36.7036
chr19	59128983	32894469	0.5563	27.2333
chr20	63025520	93709828	1.4869	29.9242
chr21	48129895	95352491	1.9811	35.2444
chr22	51304566	135112696	2.6335	172.675
chrMT	16571	173887087	10,493.4577	10,470.7296
chrX	155270560	131906463	0.8495	23.7974
chrY	59373566	28612121	0.4819	14.6867

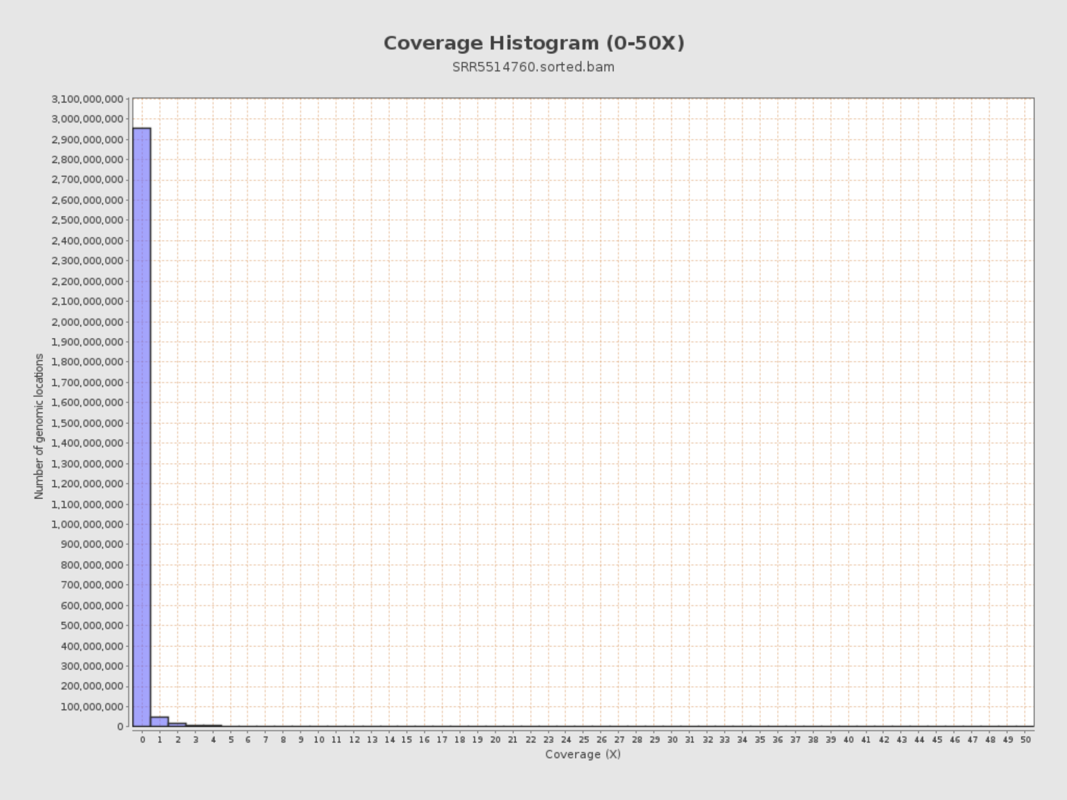
3. Results : Coverage across reference



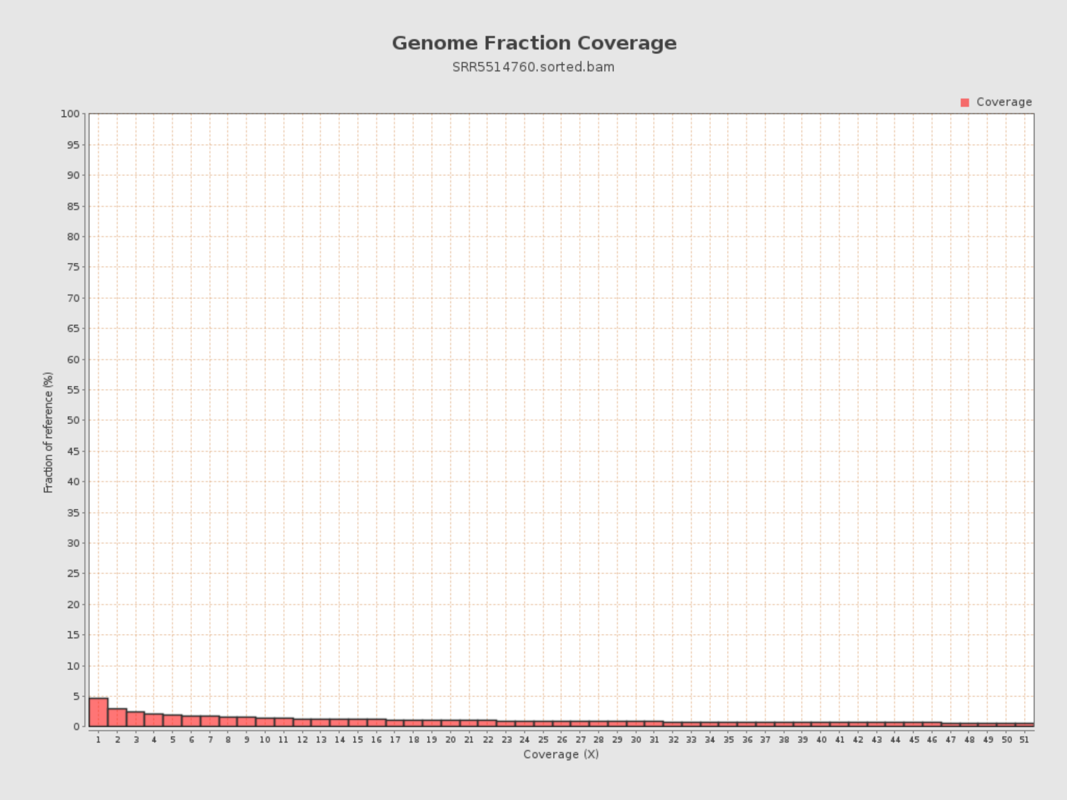
4. Results : Coverage Histogram



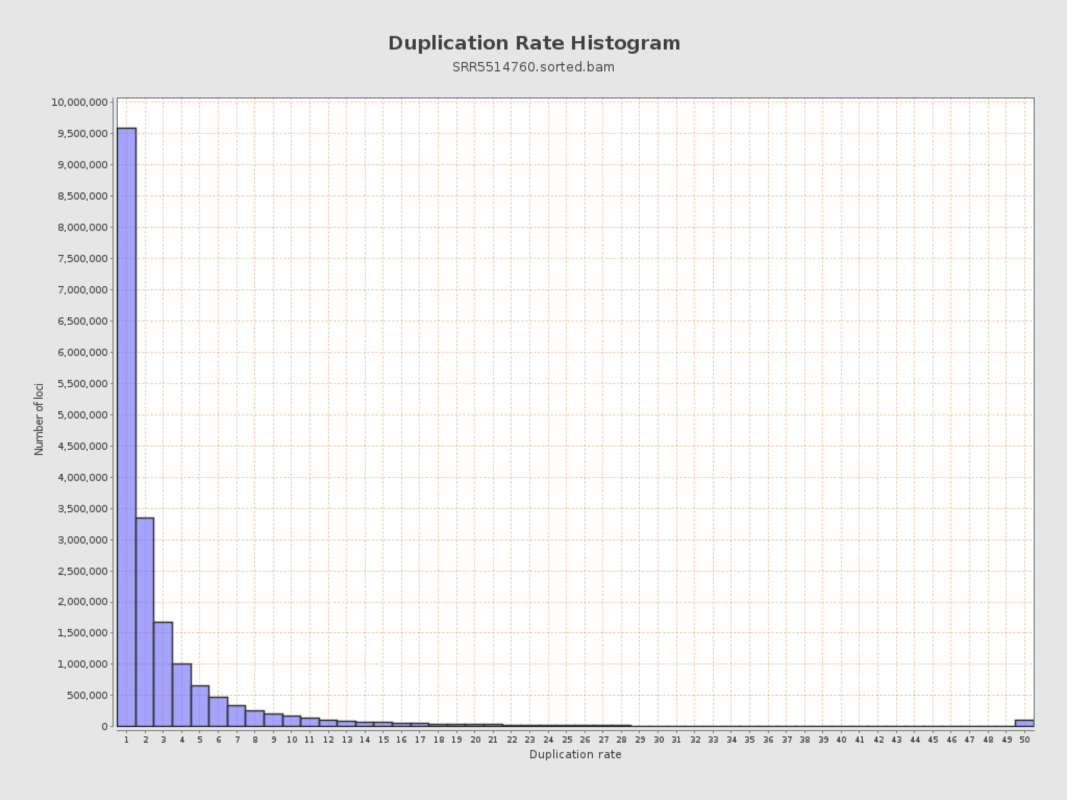
5. Results : Coverage Histogram (0-50X)



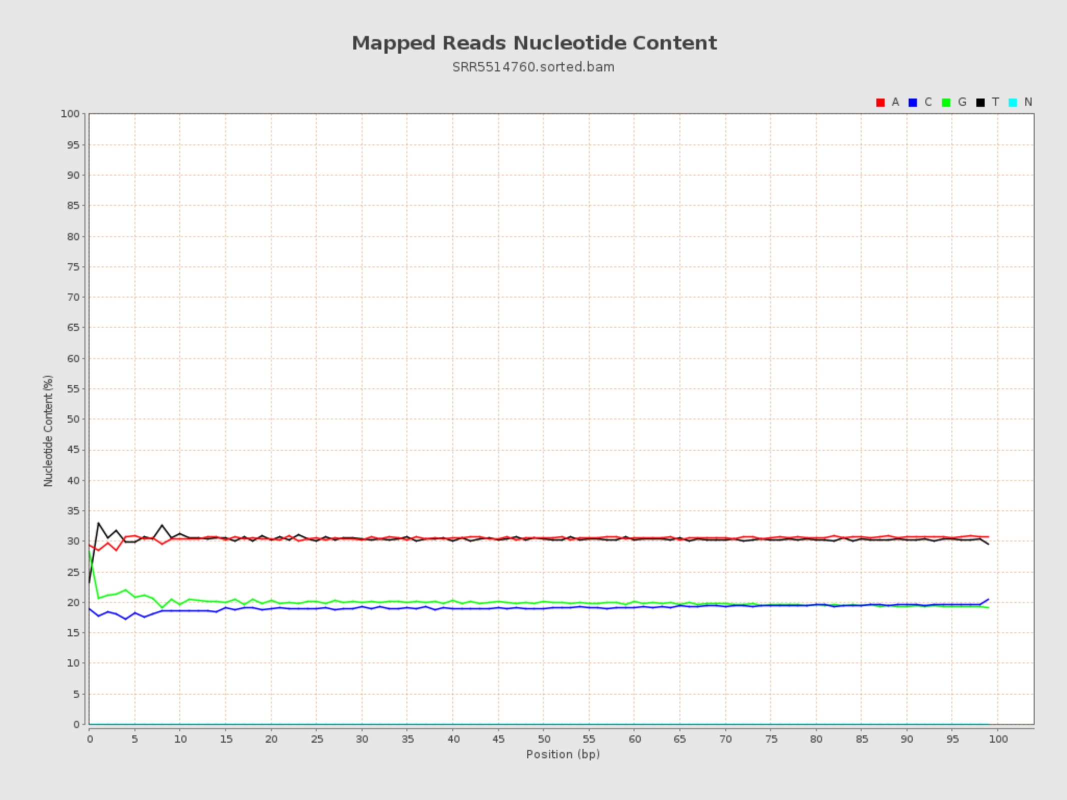
6. Results : Genome Fraction Coverage



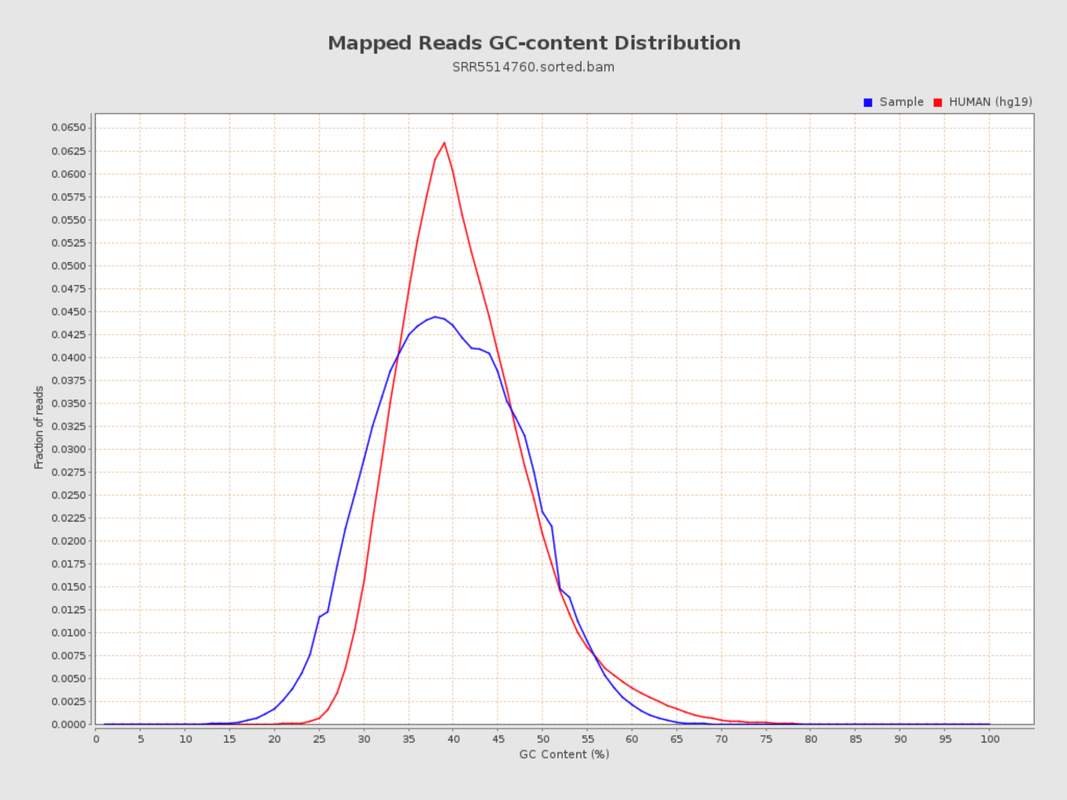
7. Results : Duplication Rate Histogram



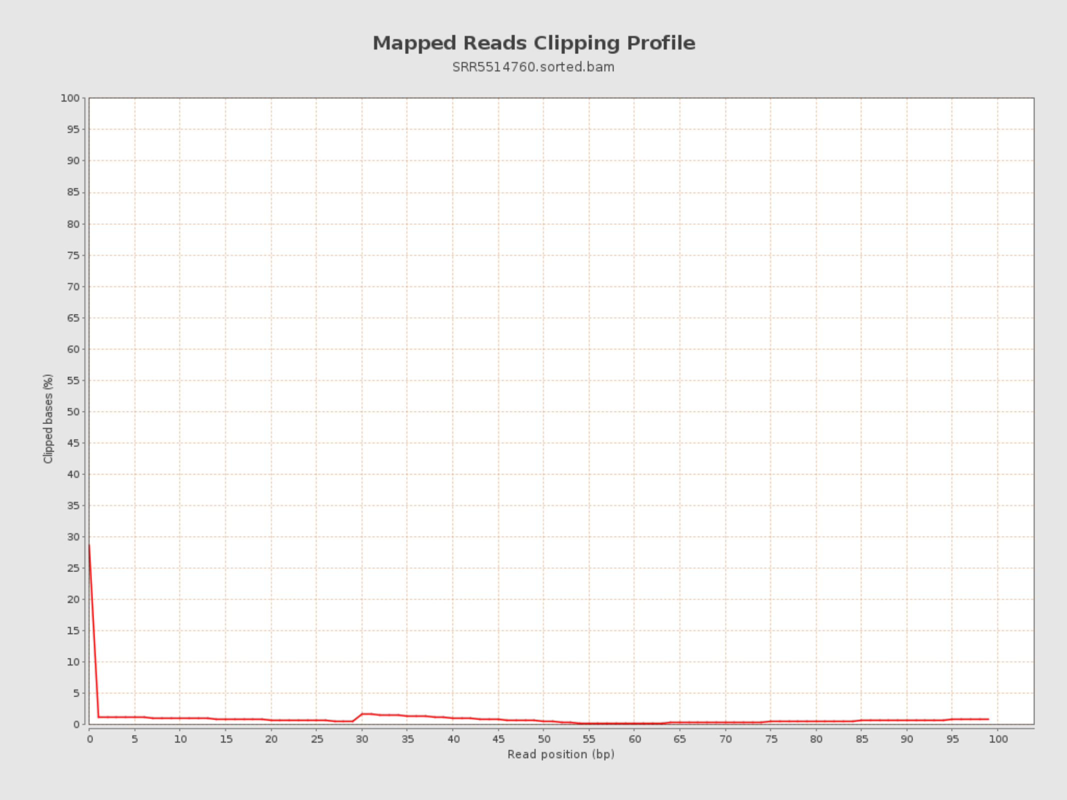
8. Results : Mapped Reads Nucleotide Content



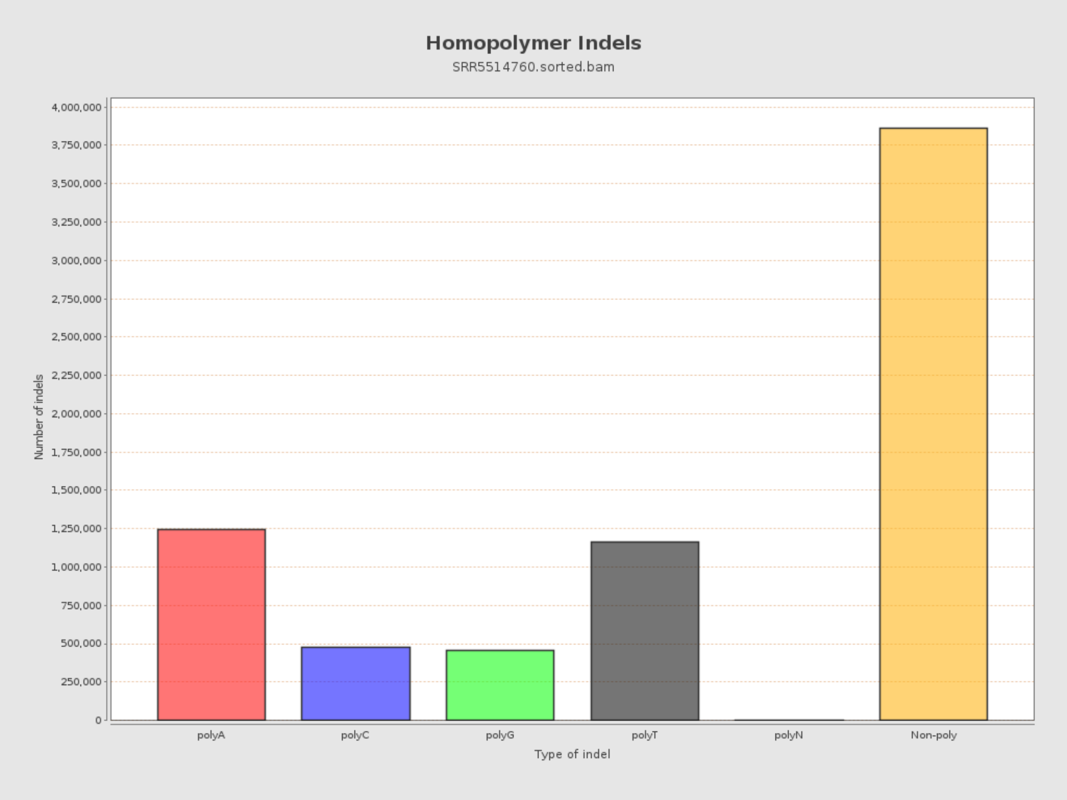
9. Results : Mapped Reads GC-content Distribution



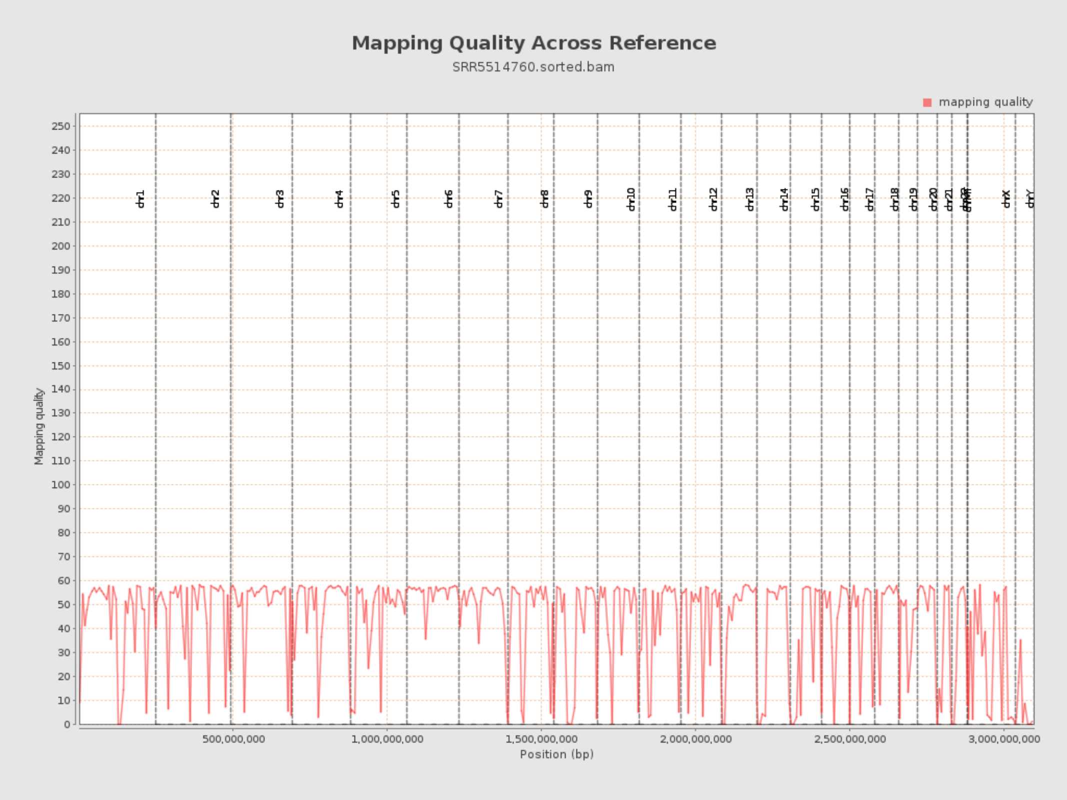
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram