Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:51:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549074.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_SRR1549074 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549074.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:51:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,039,987
Mapped reads	8,828,549 / 87.93%
Unmapped reads	1,211,438 / 12.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	329,676 / 3.28%
Duplication rate	2.68%
Clipped reads	389,317 / 3.88%

2.2. ACGT Content

Number/percentage of A's	101,915,774 / 29.05%
Number/percentage of C's	74,084,488 / 21.12%
Number/percentage of T's	103,126,157 / 29.4%
Number/percentage of G's	71,616,950 / 20.41%
Number/percentage of N's	83,905 / 0.02%
GC Percentage	41.53%

2.3. Coverage

Mean	0.1133
Standard Deviation	0.852

2.4. Mapping Quality

Mean Mapping Quality	44.25

2.5. Mismatches and indels

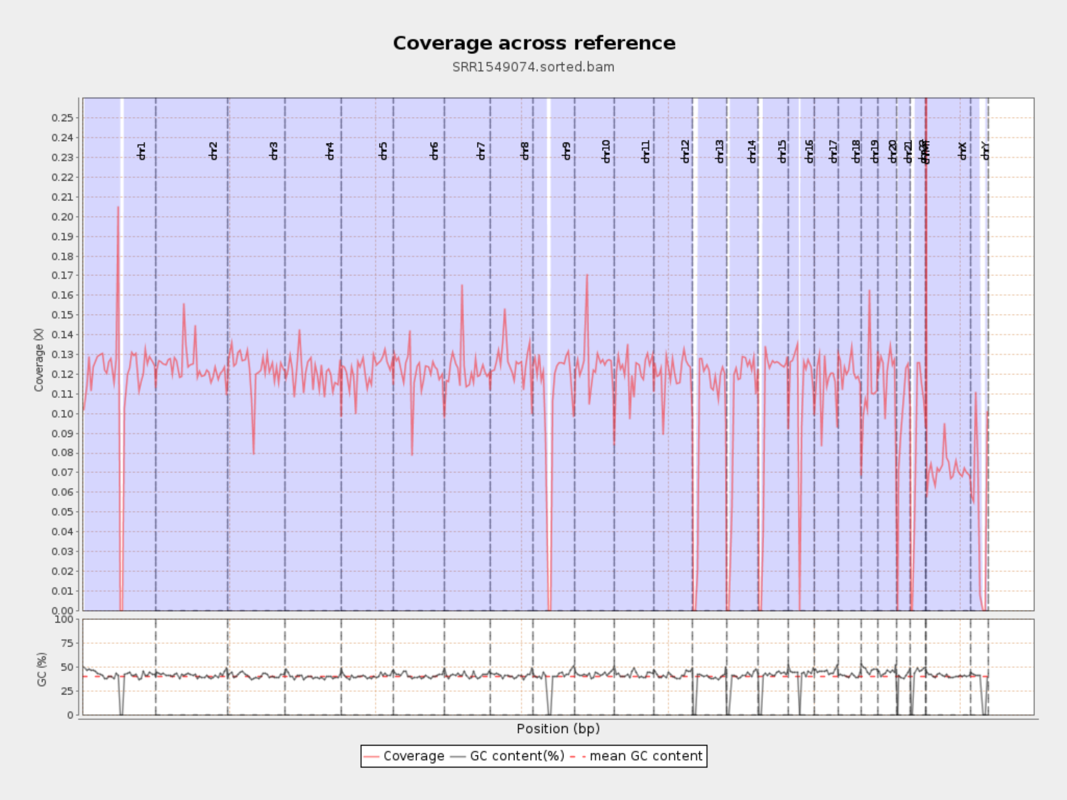
General error rate	0.39%
Mismatches	1,359,646
Insertions	7,580
Mapped reads with at least one insertion	0.09%
Deletions	26,512
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.16%

2.6. Chromosome stats

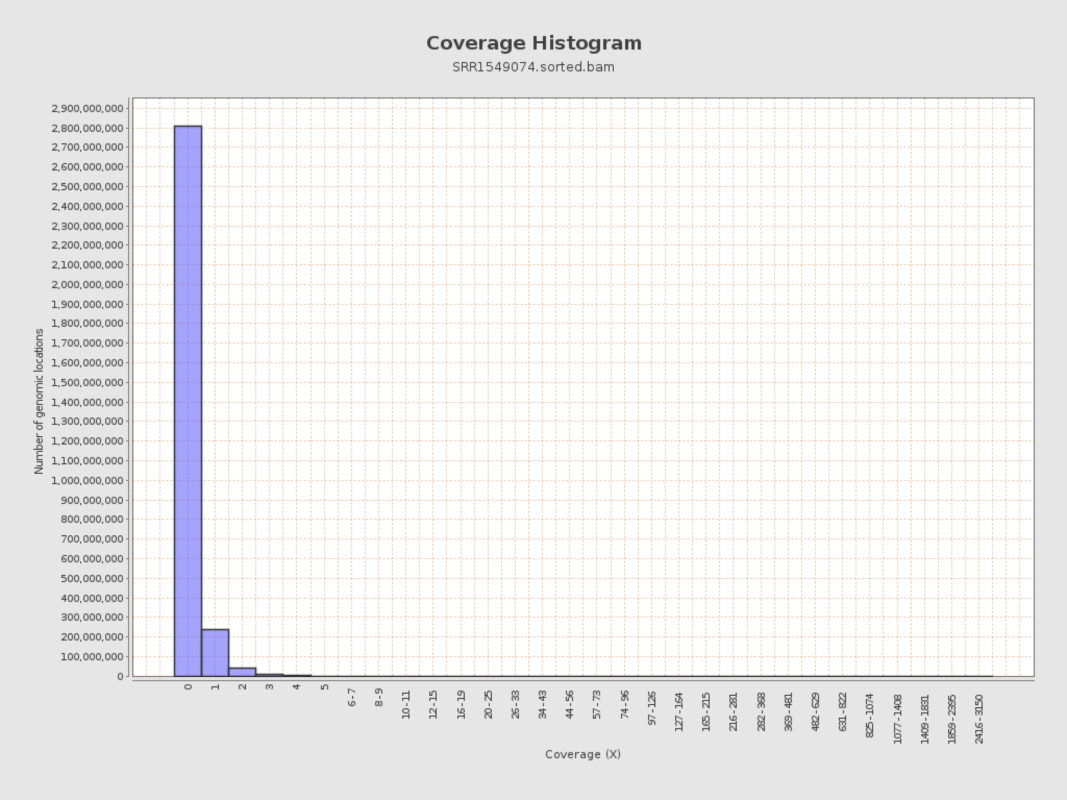
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29303807	0.1176	1.9883
chr2	243199373	30227487	0.1243	0.5868
chr3	198022430	24257633	0.1225	0.4112
chr4	191154276	23052611	0.1206	0.4355
chr5	180915260	22073961	0.122	0.4178
chr6	171115067	20719839	0.1211	0.507
chr7	159138663	19449123	0.1222	0.8494
chr8	146364022	18389909	0.1256	1.6058

chr9	141213431	15032974	0.1065	0.5652
chr10	135534747	16986453	0.1253	0.6616
chr11	135006516	16384357	0.1214	0.5806
chr12	133851895	16152992	0.1207	0.4248
chr13	115169878	11486241	0.0997	0.3613
chr14	107349540	10944040	0.1019	0.4258
chr15	102531392	10457358	0.102	0.3681
chr16	90354753	9952381	0.1101	0.4368
chr17	81195210	9363122	0.1153	0.4506
chr18	78077248	9500445	0.1217	1.0788
chr19	59128983	6687942	0.1131	1.4672
chr20	63025520	7634235	0.1211	0.4217
chr21	48129895	4524287	0.094	0.4169
chr22	51304566	4151760	0.0809	0.3597
chrMT	16571	10756	0.6491	1.1338
chrX	155270560	11098560	0.0715	0.3874
chrY	59373566	3018804	0.0508	0.52

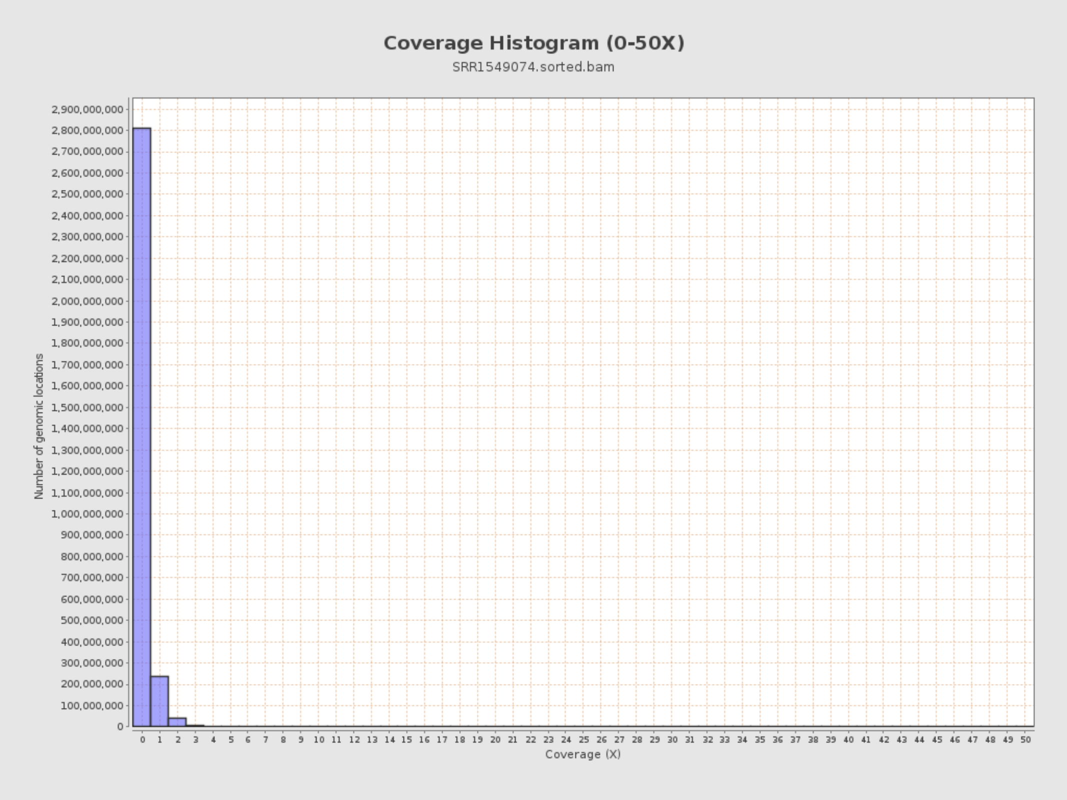
3. Results : Coverage across reference



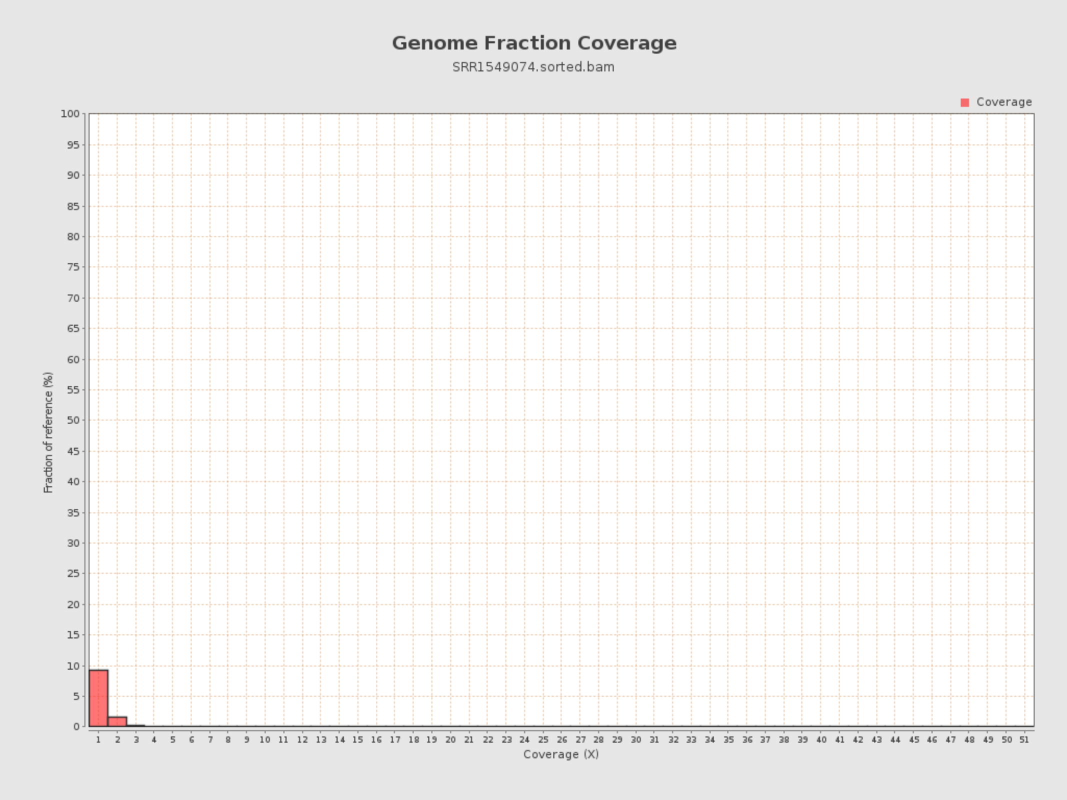
4. Results : Coverage Histogram



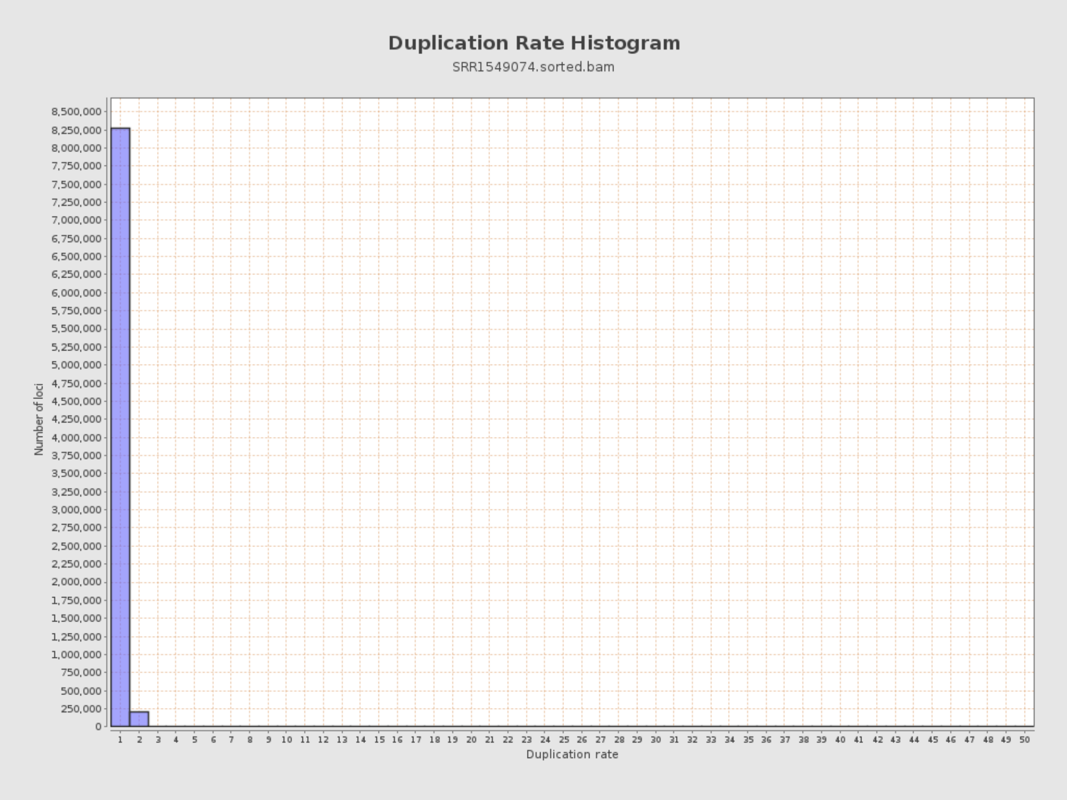
5. Results : Coverage Histogram (0-50X)



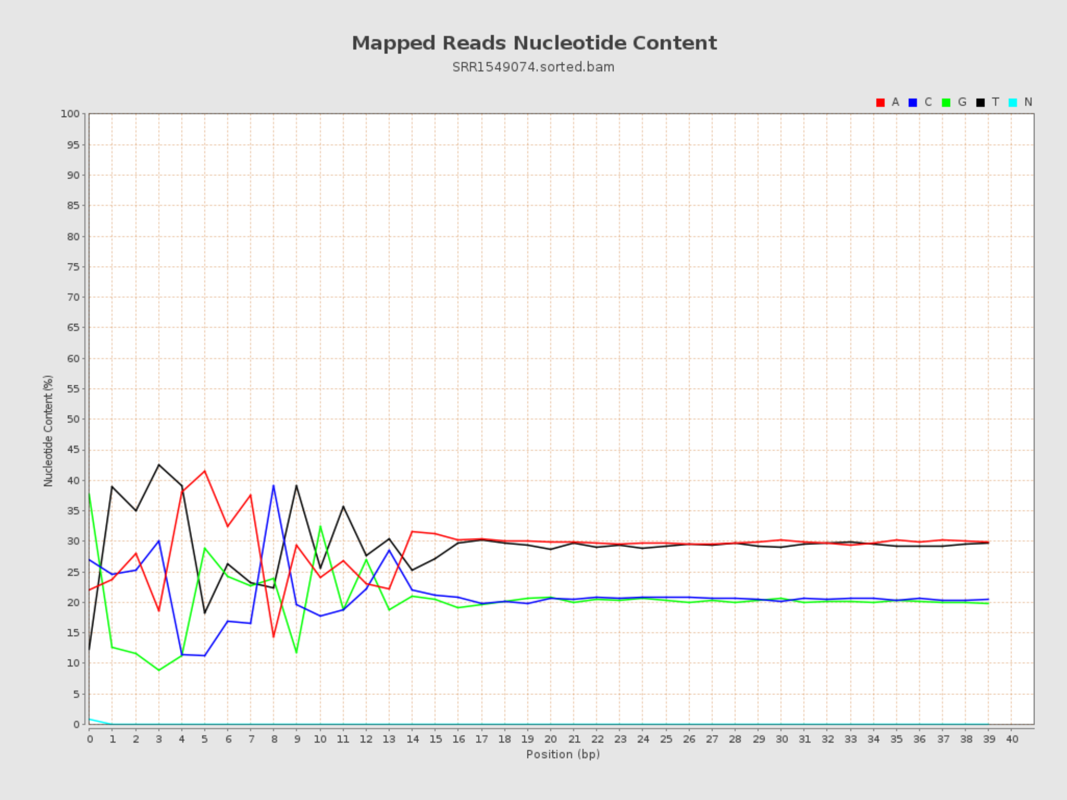
6. Results : Genome Fraction Coverage



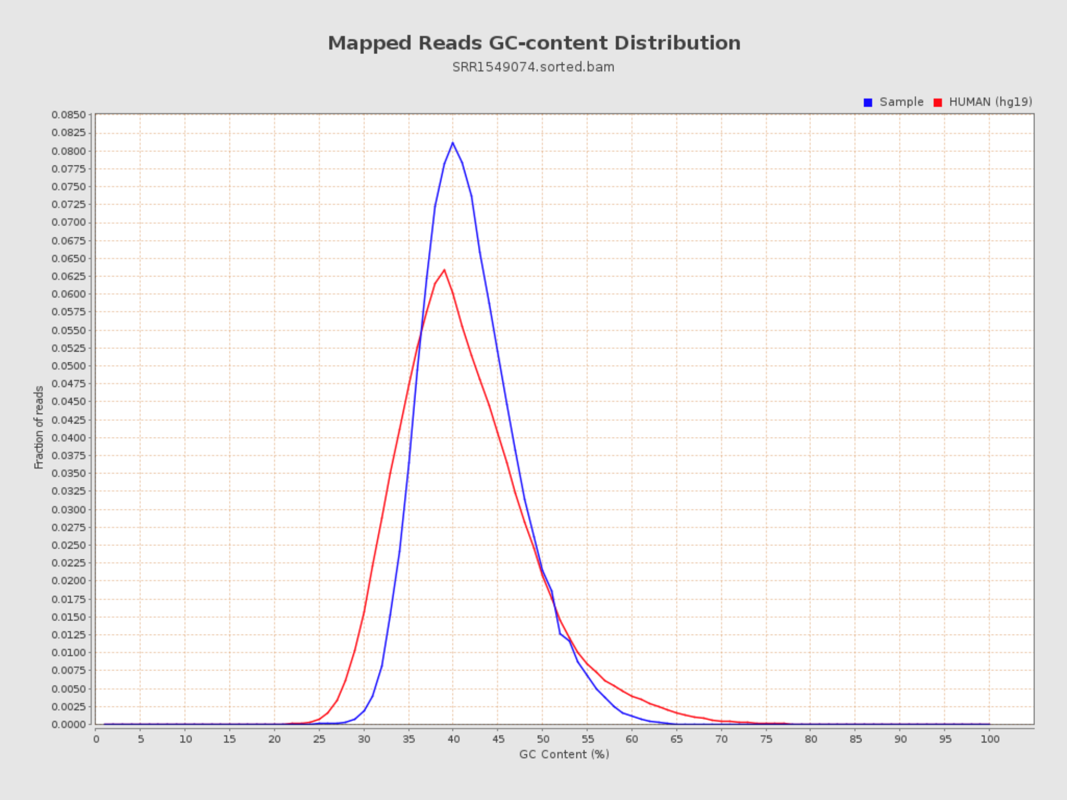
7. Results : Duplication Rate Histogram



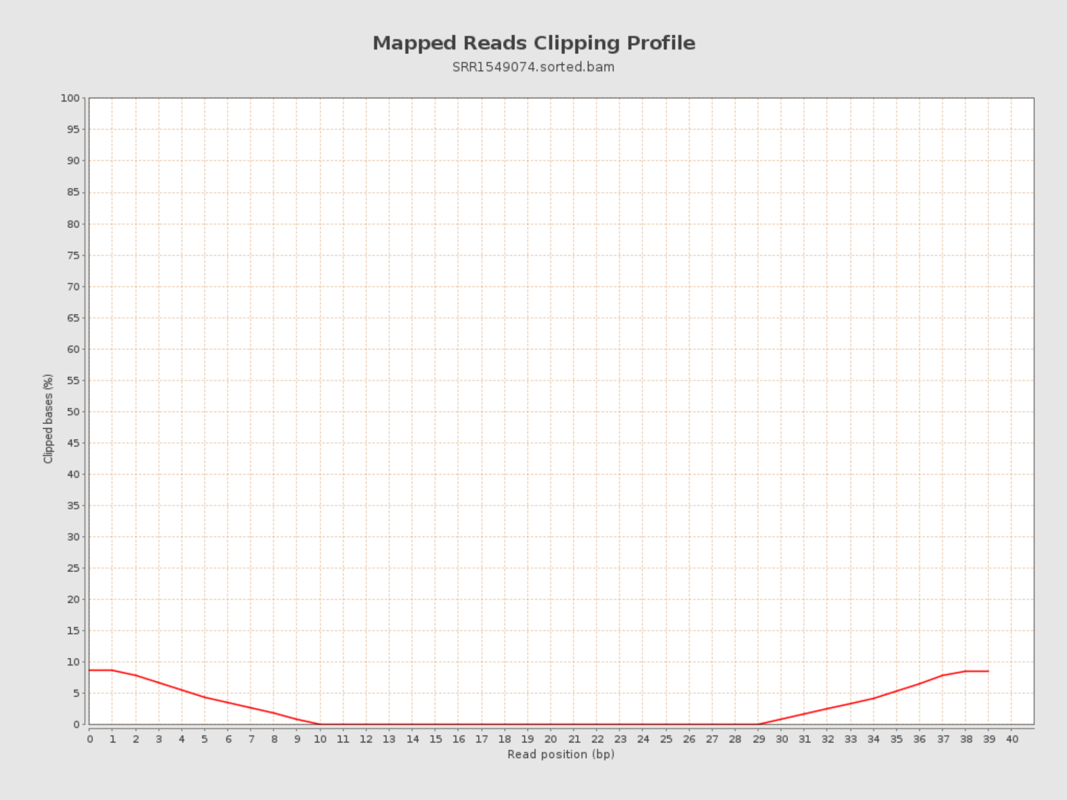
8. Results : Mapped Reads Nucleotide Content



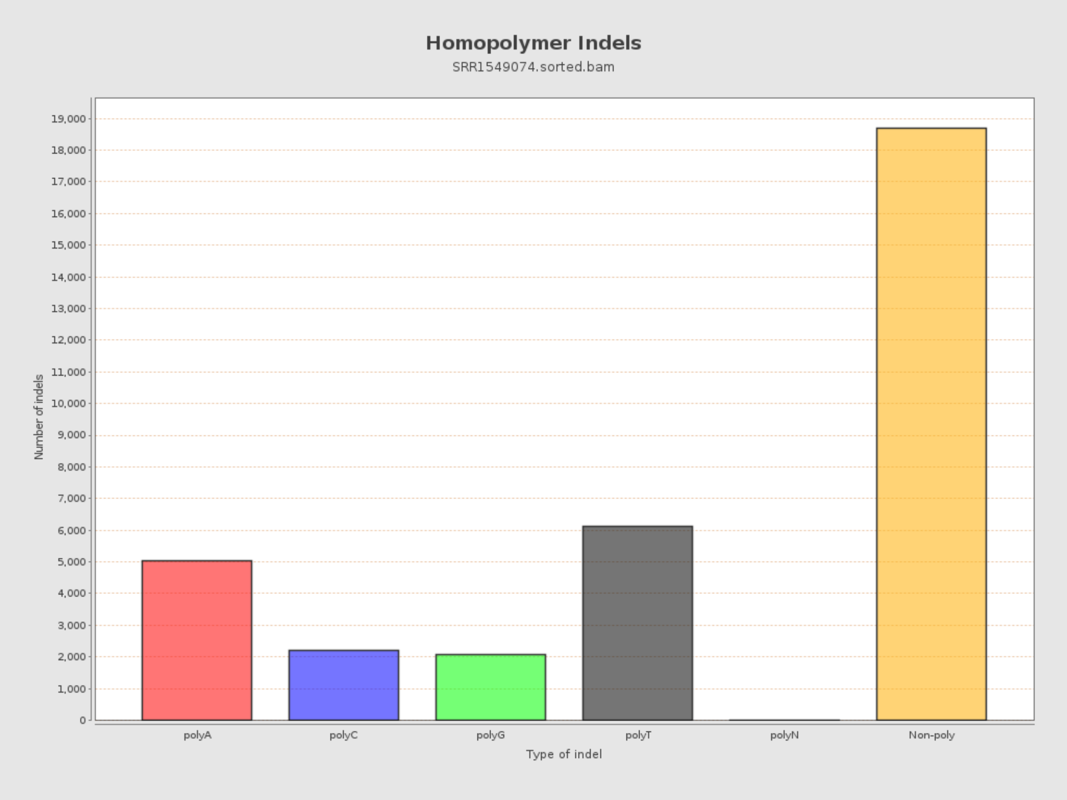
9. Results : Mapped Reads GC-content Distribution



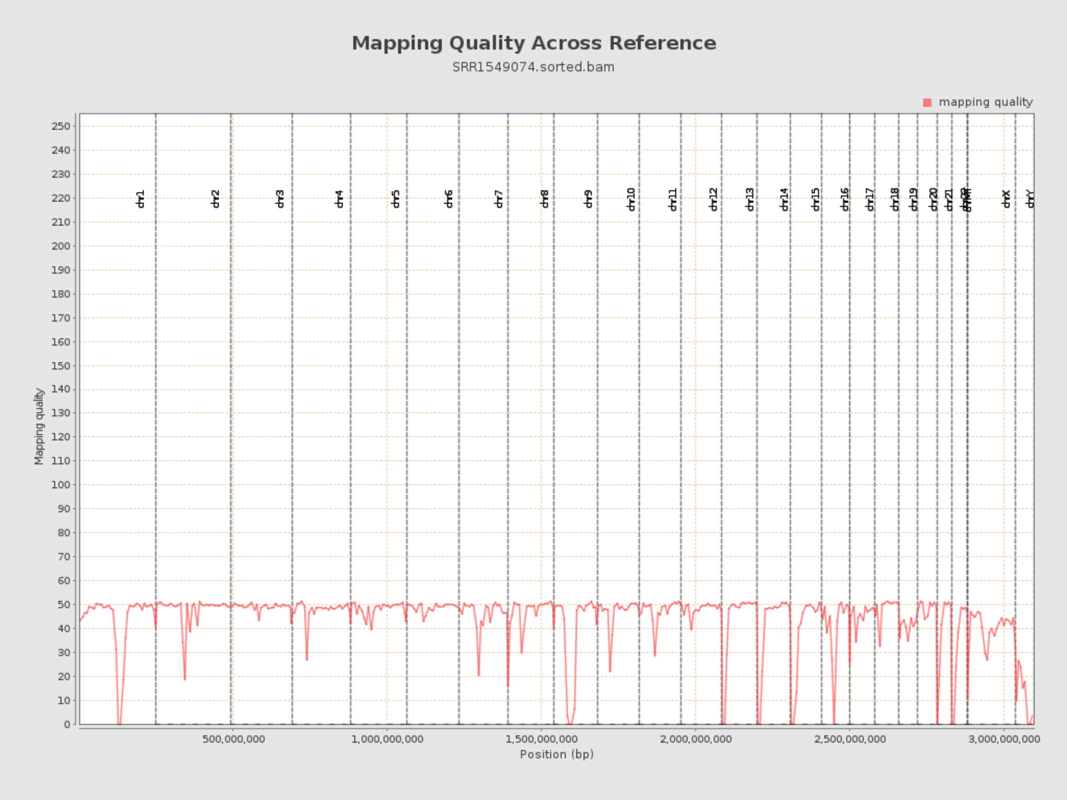
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram