Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 16:17:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514734.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_SRR5514734 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514734.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 16:17:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514734.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	62,771,213
Mapped reads	62,255,685 / 99.18%
Unmapped reads	515,528 / 0.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,291,290 / 6.84%
Read min/max/mean length	30 / 100 / 100.51
Duplicated reads (estimated)	59,855,984 / 95.36%
Duplication rate	52.28%
Clipped reads	16,942,484 / 26.99%

2.2. ACGT Content

Number/percentage of A's	1,704,266,652 / 28.78%
Number/percentage of C's	1,246,447,741 / 21.05%
Number/percentage of T's	1,698,549,540 / 28.68%
Number/percentage of G's	1,264,563,796 / 21.35%
Number/percentage of N's	8,250,955 / 0.14%
GC Percentage	42.4%

2.3. Coverage

Mean	1.9147

Standard Deviation	166.8923

2.4. Mapping Quality

Mean Mapping Quality	47.68

2.5. Mismatches and indels

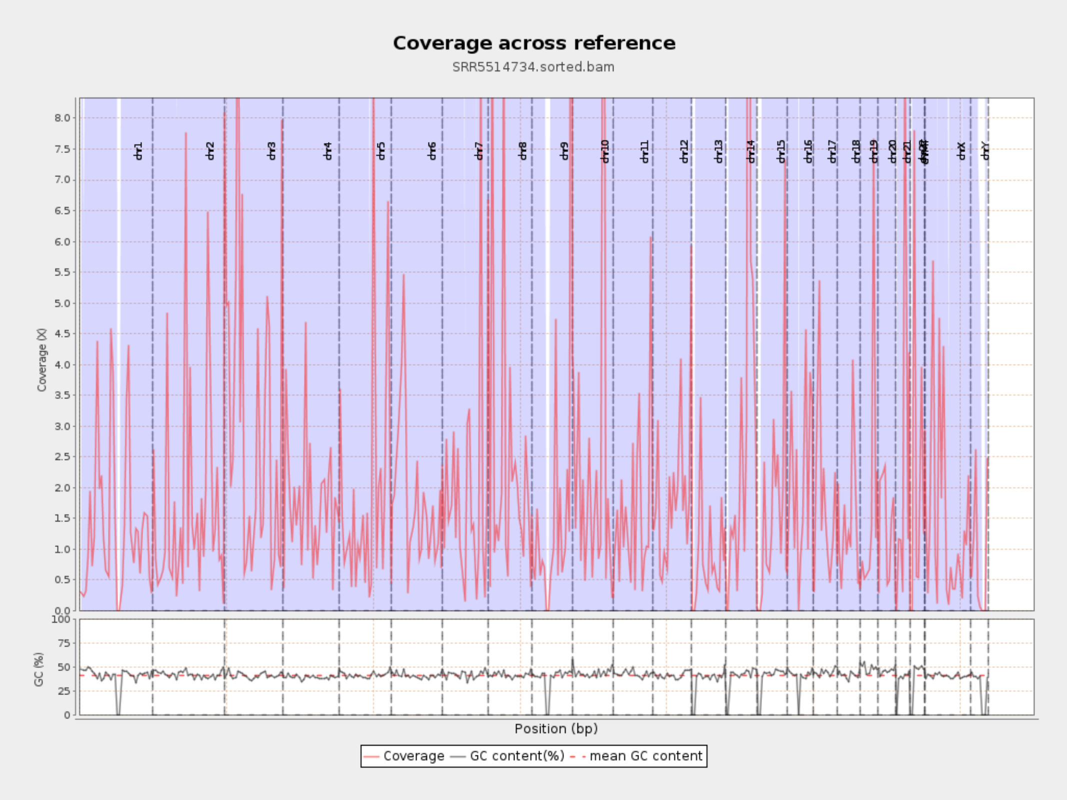
General error rate	0.86%
Mismatches	44,896,908
Insertions	3,125,179
Mapped reads with at least one insertion	4.8%
Deletions	2,230,663
Mapped reads with at least one deletion	3.36%
Homopolymer indels	41.1%

2.6. Chromosome stats

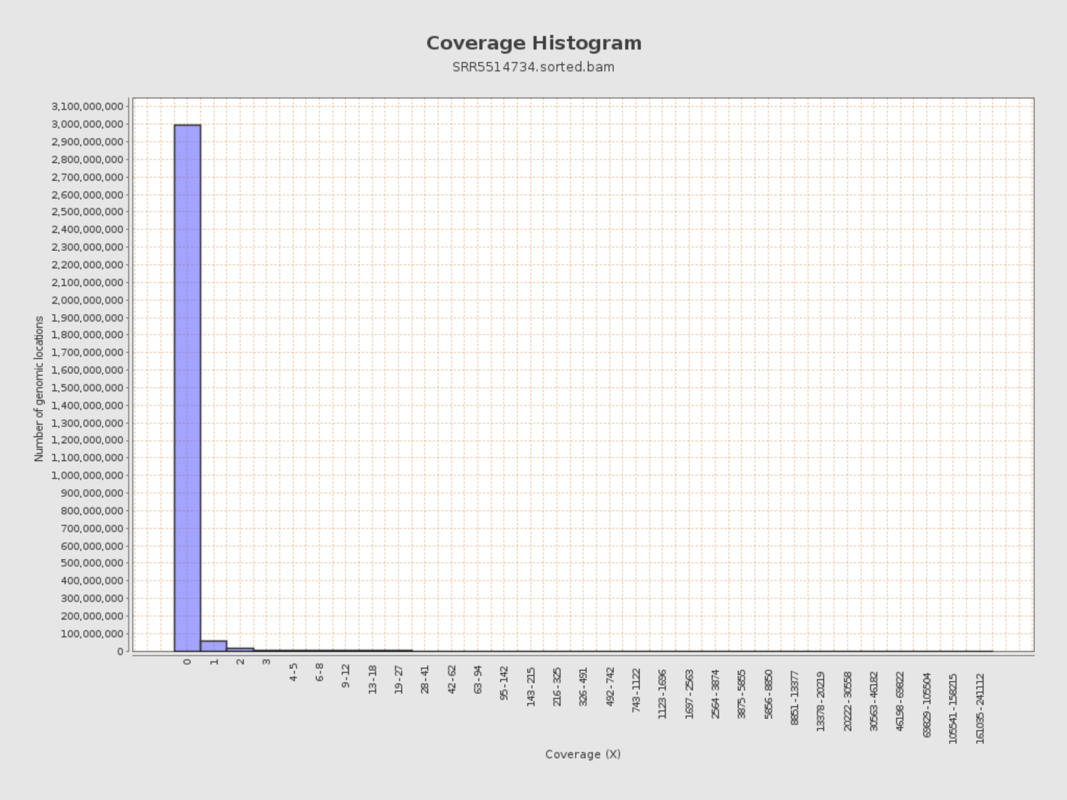
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	360727148	1.4472	73.8211
chr2	243199373	414105560	1.7027	92.0304
chr3	198022430	608653962	3.0737	192.2934
chr4	191154276	339585665	1.7765	78.023
chr5	180915260	330109405	1.8247	131.9243
chr6	171115067	321304243	1.8777	82.6304
chr7	159138663	303920945	1.9098	172.4575

chr8	146364022	359122517	2.4536	229.7284
chr9	141213431	314495557	2.2271	432.6224
chr10	135534747	320385325	2.3639	225.0076
chr11	135006516	215253511	1.5944	89.0992
chr12	133851895	240241272	1.7948	82.1679
chr13	115169878	101673516	0.8828	42.3538
chr14	107349540	367536848	3.4237	319.2936
chr15	102531392	181379736	1.769	101.3821
chr16	90354753	190014735	2.103	122.6931
chr17	81195210	142793504	1.7586	119.6404
chr18	78077248	112035112	1.4349	68.414
chr19	59128983	104643240	1.7697	189.0188
chr20	63025520	86923240	1.3792	71.8654
chr21	48129895	121649844	2.5275	155.4659
chr22	51304566	112492151	2.1926	217.2742
chrMT	16571	48659	2.9364	3.2292
chrX	155270560	224433790	1.4454	84.6584
chrY	59373566	53680979	0.9041	28.8257

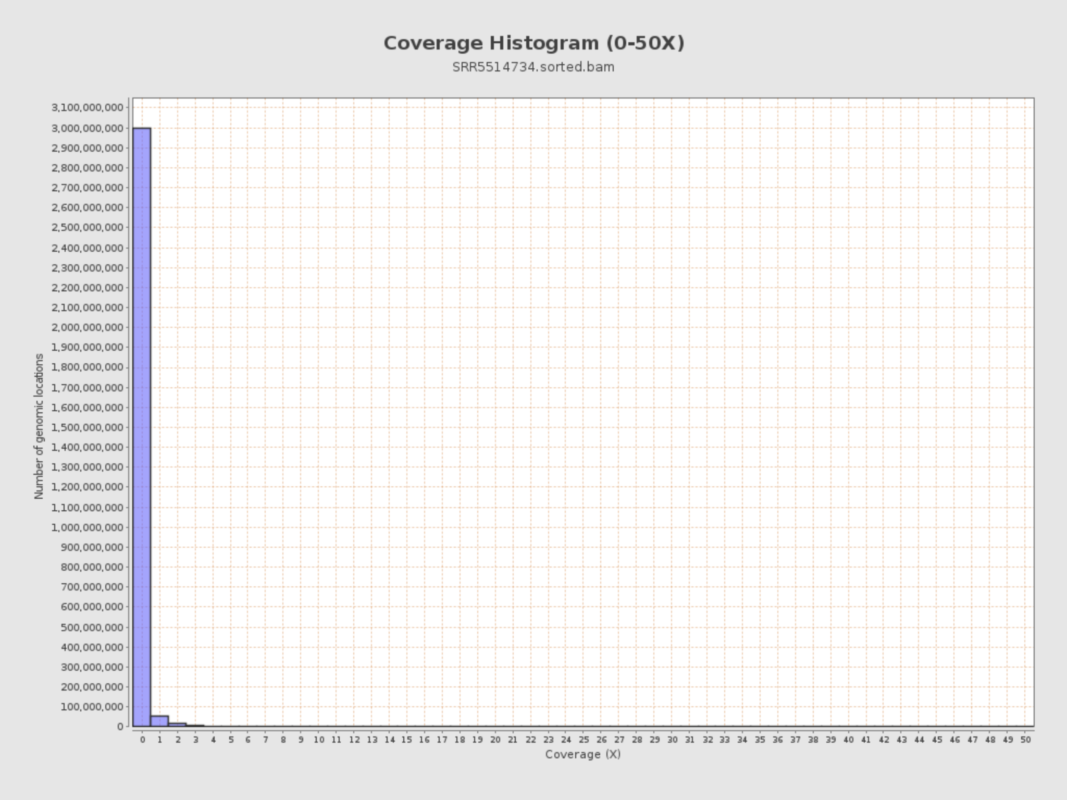
3. Results : Coverage across reference



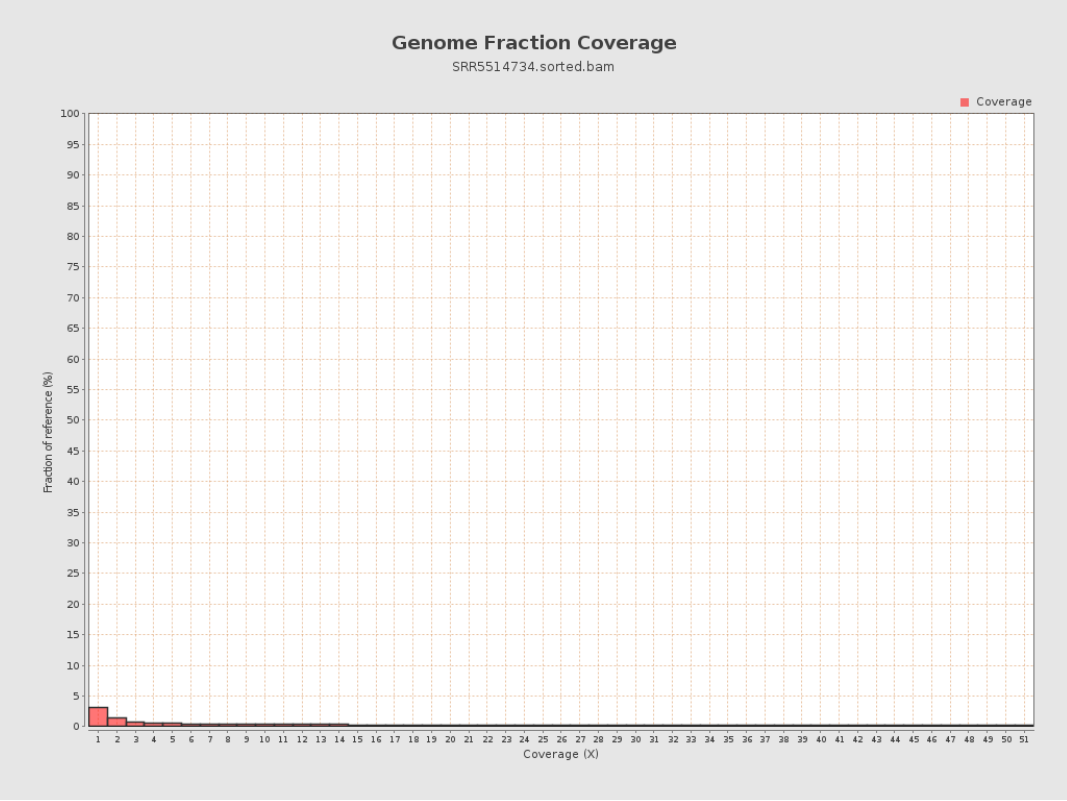
4. Results : Coverage Histogram



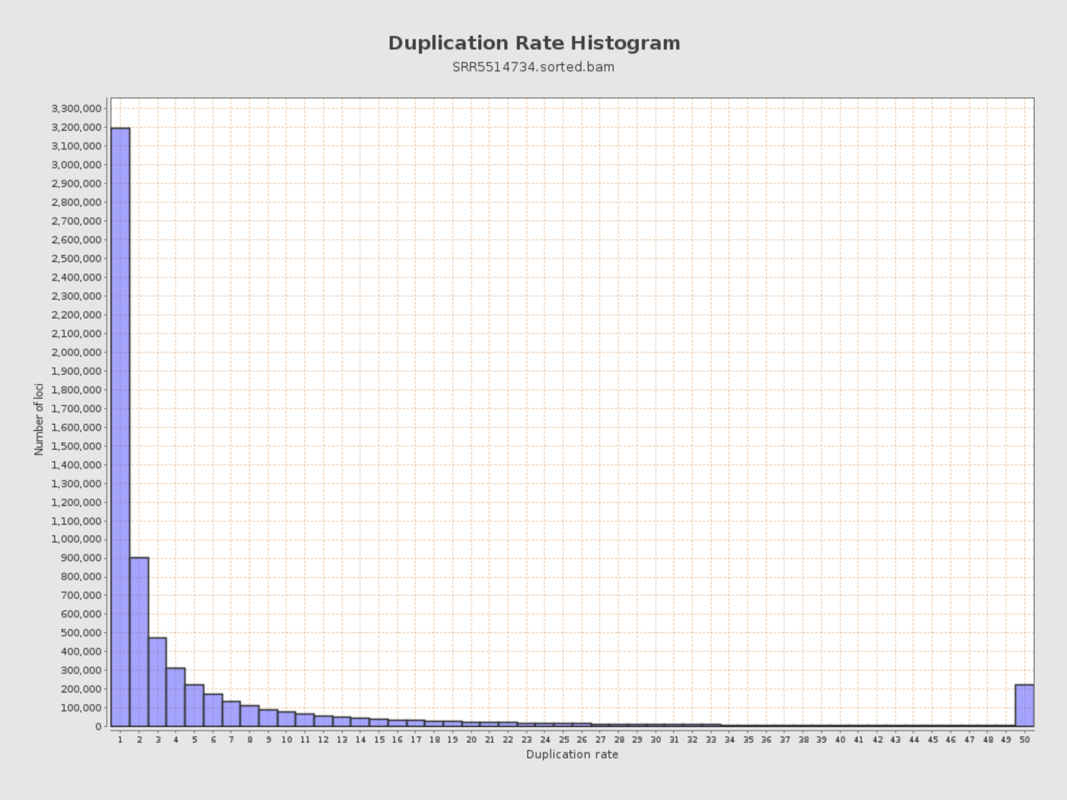
5. Results : Coverage Histogram (0-50X)



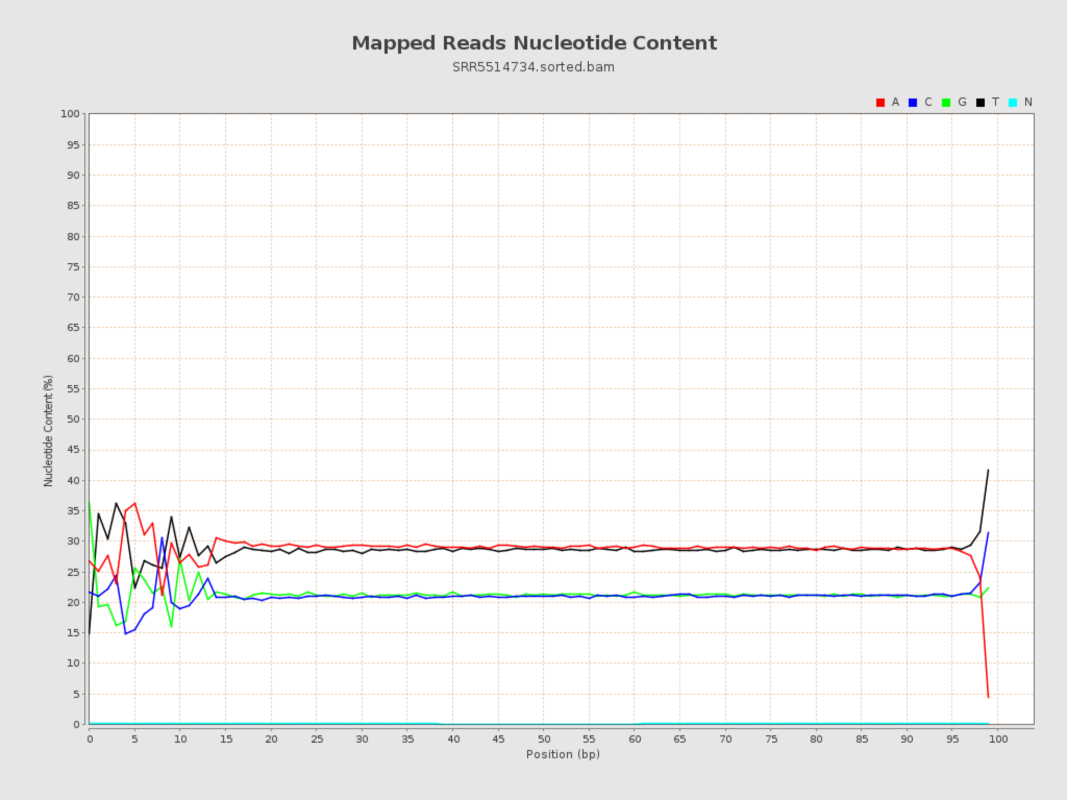
6. Results : Genome Fraction Coverage



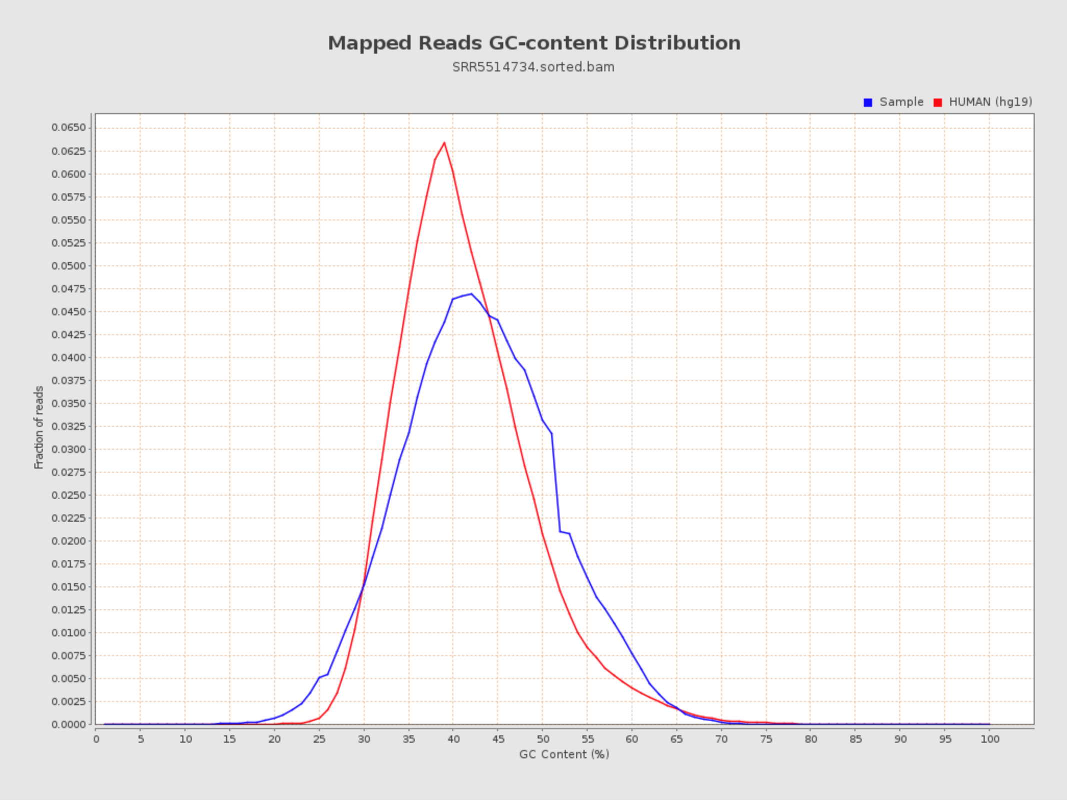
7. Results : Duplication Rate Histogram



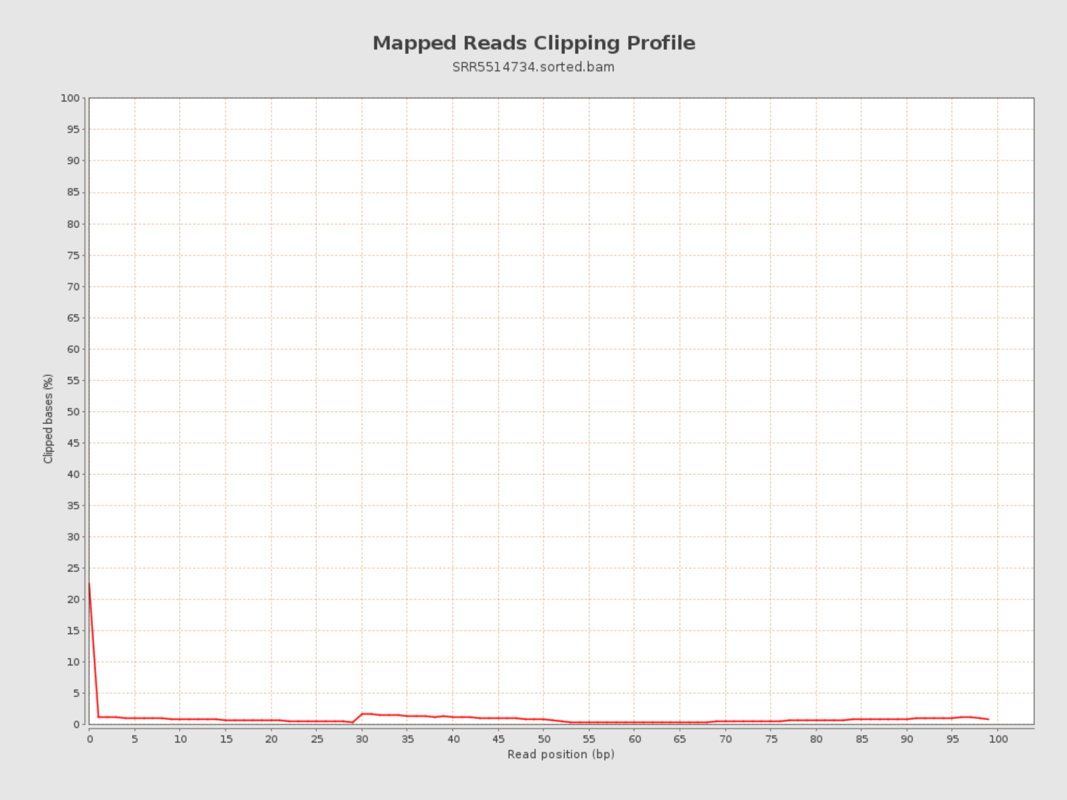
8. Results : Mapped Reads Nucleotide Content



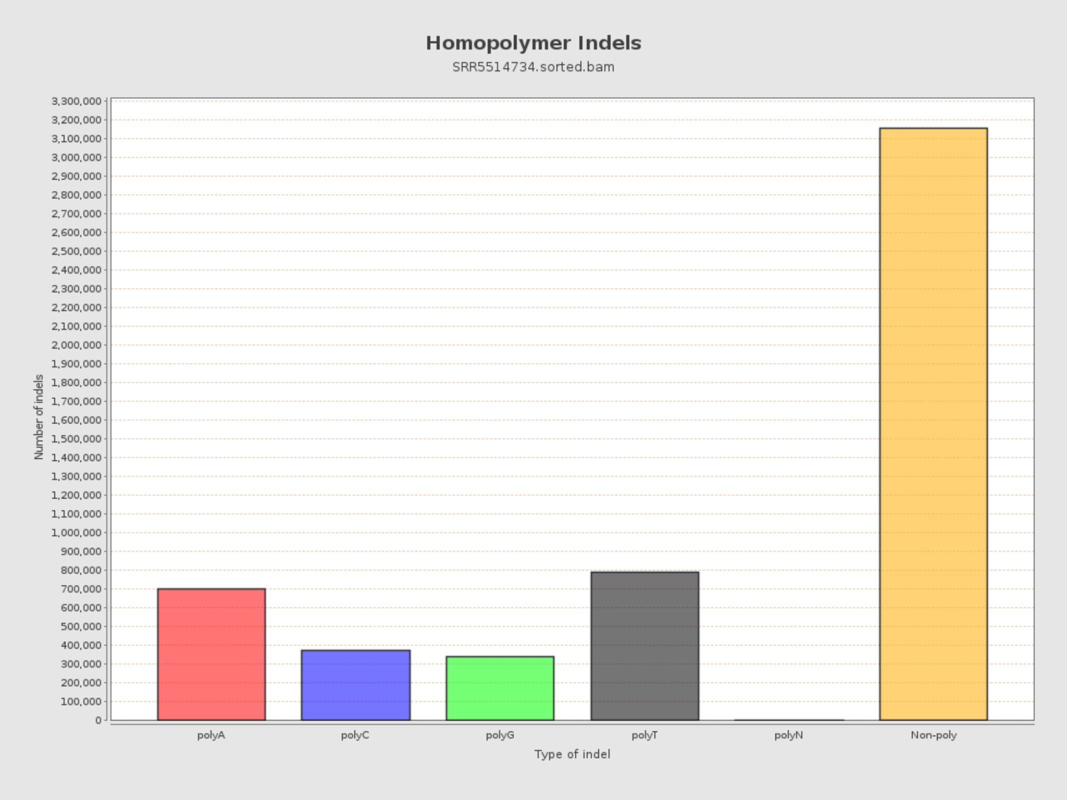
9. Results : Mapped Reads GC-content Distribution



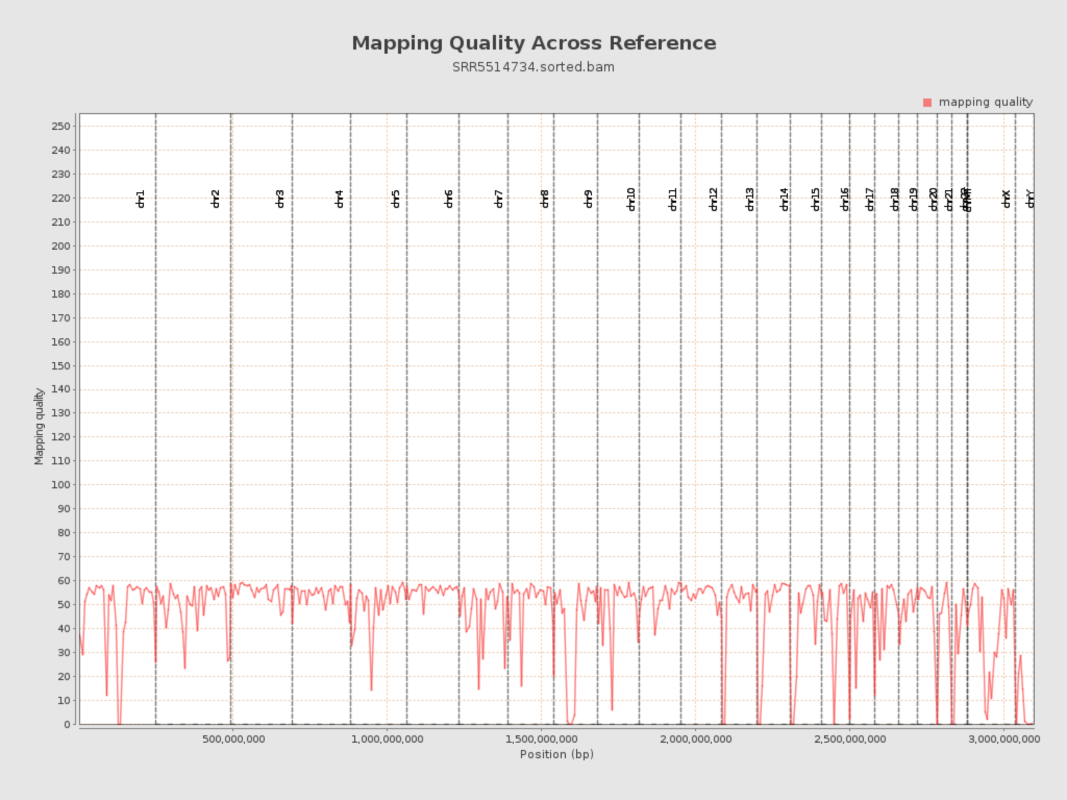
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram