Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 14:26:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514739.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_SRR5514739 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514739.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 14:26:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514739.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	53,261,248
Mapped reads	50,409,660 / 94.65%
Unmapped reads	2,851,588 / 5.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,577,910 / 2.96%
Read min/max/mean length	30 / 100 / 98.97
Duplicated reads (estimated)	33,142,740 / 62.23%
Duplication rate	42.48%
Clipped reads	9,452,991 / 17.75%

2.2. ACGT Content

Number/percentage of A's	1,253,853,740 / 26.42%
Number/percentage of C's	1,098,019,705 / 23.14%
Number/percentage of T's	1,265,309,237 / 26.66%
Number/percentage of G's	1,100,388,703 / 23.19%
Number/percentage of N's	28,048,355 / 0.59%
GC Percentage	46.33%

2.3. Coverage

Mean	1.5341

Standard Deviation	34.7347

2.4. Mapping Quality

Mean Mapping Quality	38.15

2.5. Mismatches and indels

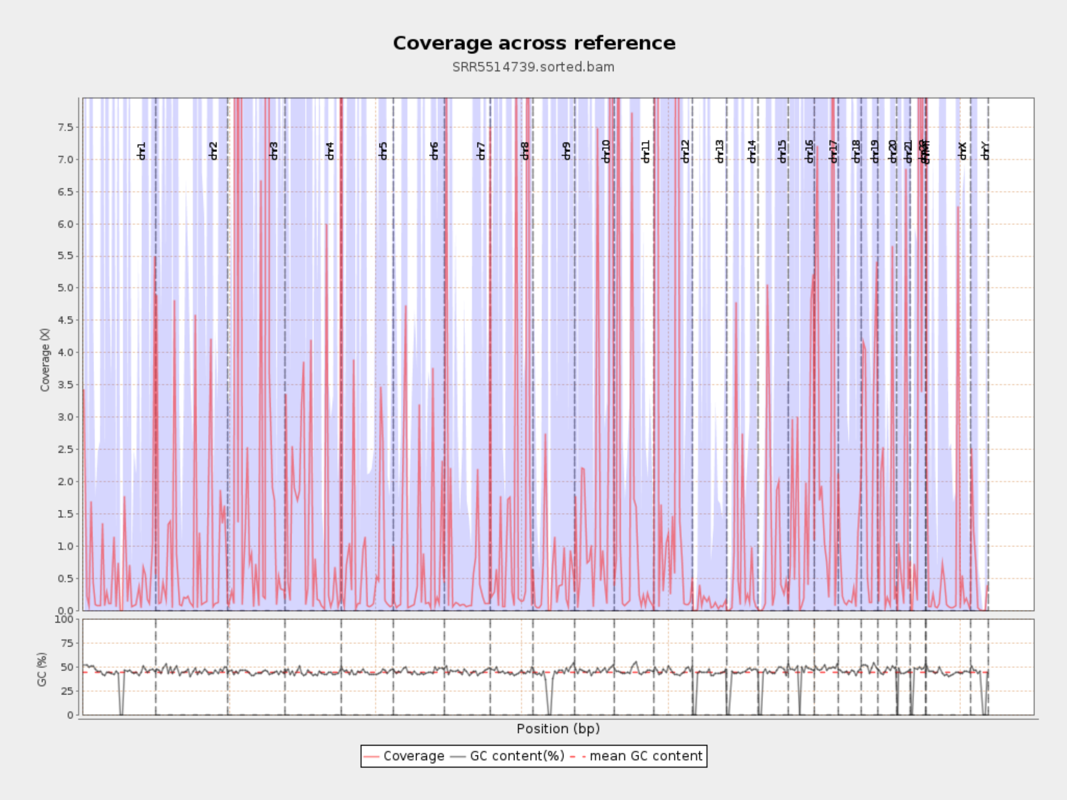
General error rate	1%
Mismatches	44,185,692
Insertions	1,803,448
Mapped reads with at least one insertion	3.42%
Deletions	1,434,018
Mapped reads with at least one deletion	2.74%
Homopolymer indels	42.37%

2.6. Chromosome stats

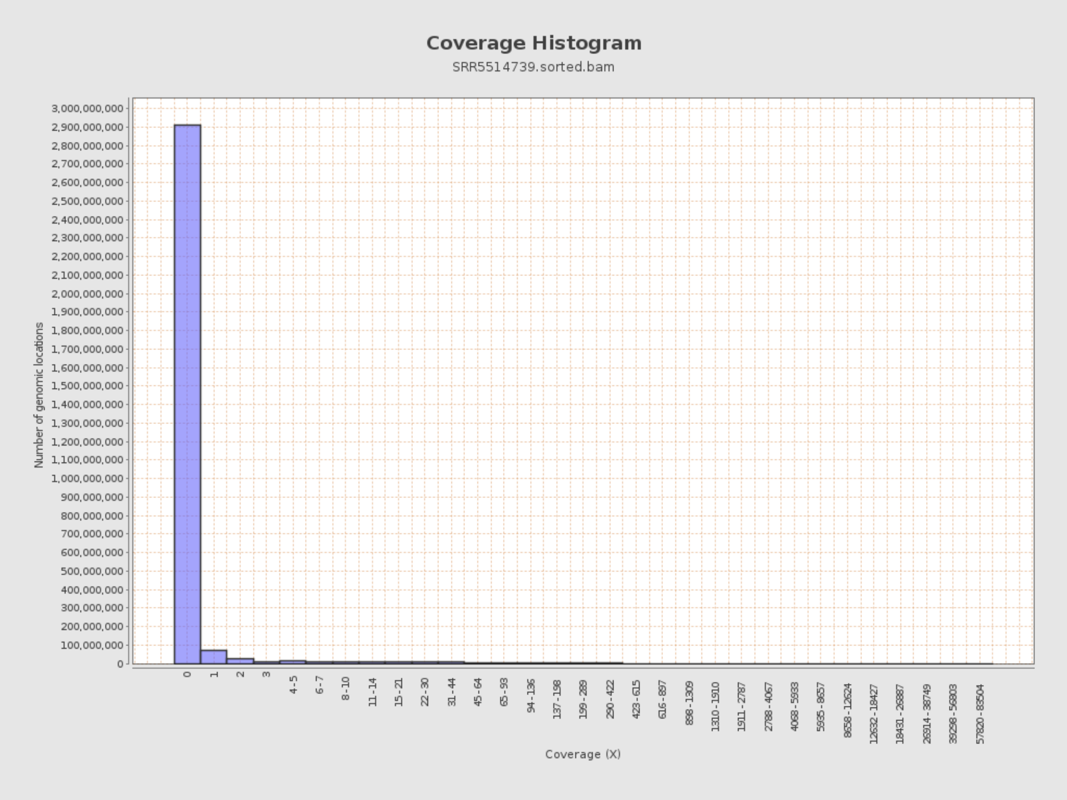
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	165438861	0.6637	13.347
chr2	243199373	250995123	1.0321	62.4284
chr3	198022430	1042576512	5.2649	49.0426
chr4	191154276	244616782	1.2797	19.226
chr5	180915260	151226475	0.8359	15.2974
chr6	171115067	152670612	0.8922	16.3489
chr7	159138663	126178246	0.7929	12.2571

chr8	146364022	252786979	1.7271	26.1904
chr9	141213431	72223933	0.5115	34.5921
chr10	135534747	314421599	2.3199	44.9179
chr11	135006516	198378368	1.4694	21.4362
chr12	133851895	430634139	3.2172	25.8691
chr13	115169878	12543549	0.1089	6.4348
chr14	107349540	83233152	0.7753	14.1169
chr15	102531392	108172830	1.055	17.1686
chr16	90354753	154371151	1.7085	48.9803
chr17	81195210	250137156	3.0807	41.1152
chr18	78077248	41360858	0.5297	32.7063
chr19	59128983	145488157	2.4605	27.088
chr20	63025520	85806477	1.3615	23.3658
chr21	48129895	73005198	1.5168	38.5036
chr22	51304566	270382929	5.2702	107.0857
chrMT	16571	5097645	307.6245	149.6803
chrX	155270560	85405728	0.55	14.314
chrY	59373566	31908705	0.5374	44.7249

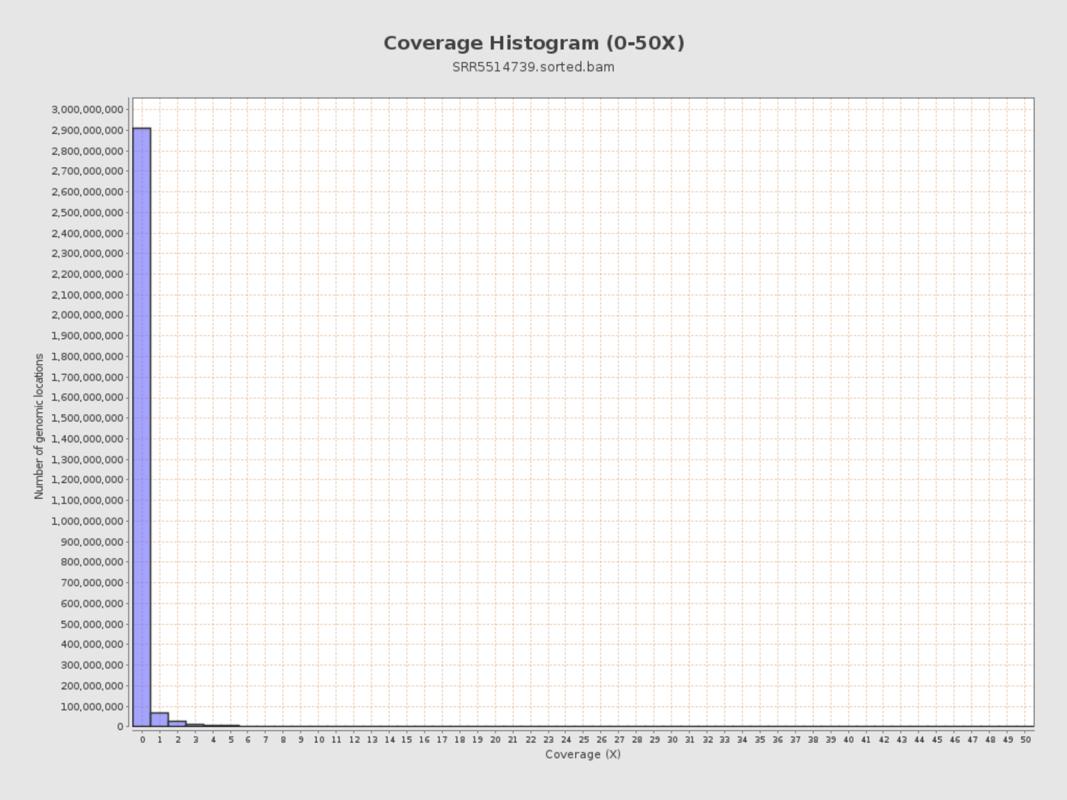
3. Results : Coverage across reference



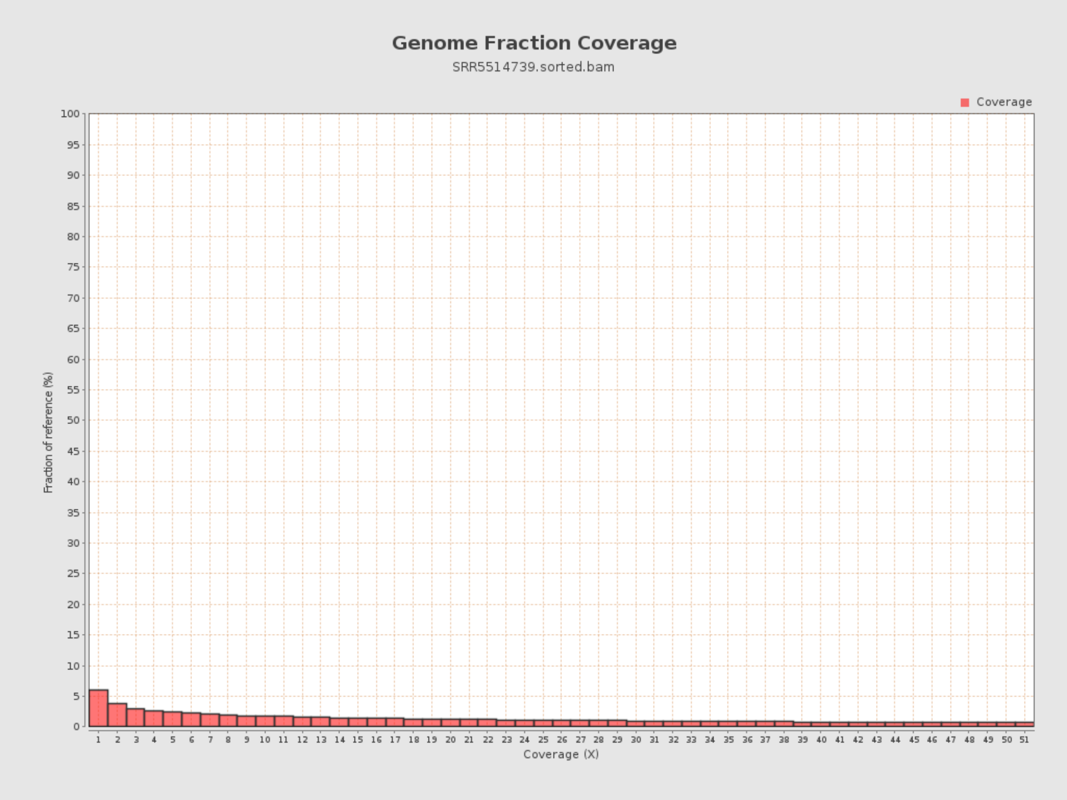
4. Results : Coverage Histogram



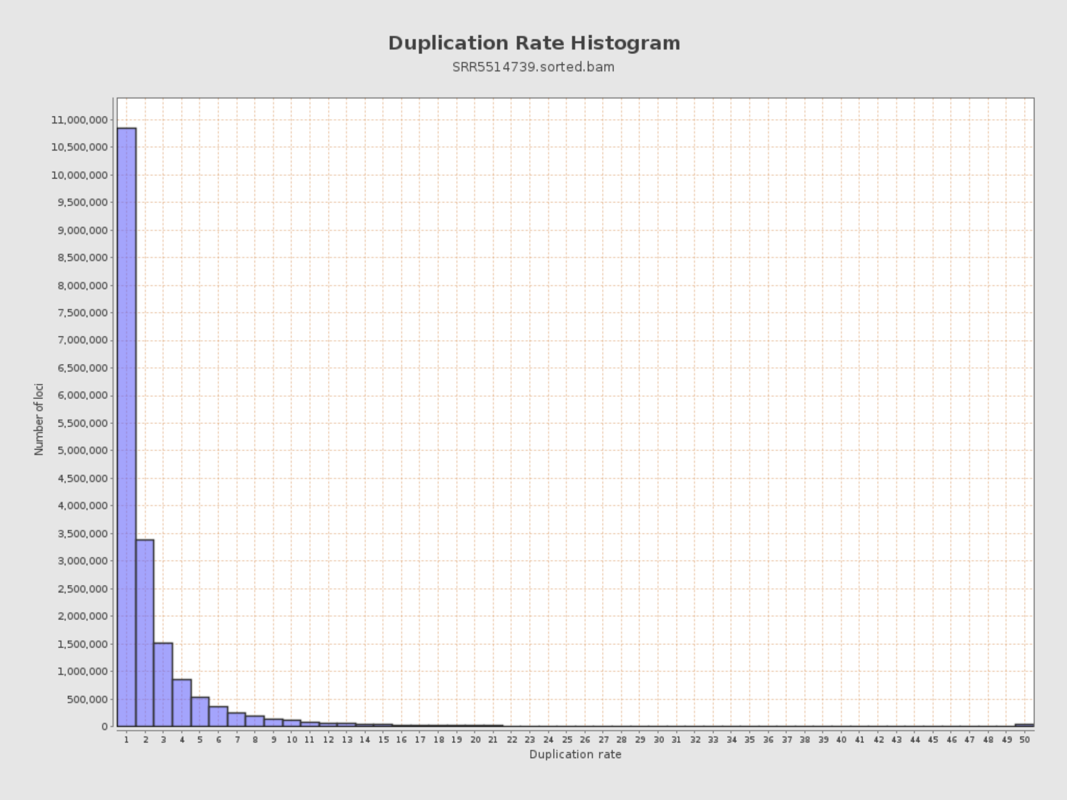
5. Results : Coverage Histogram (0-50X)



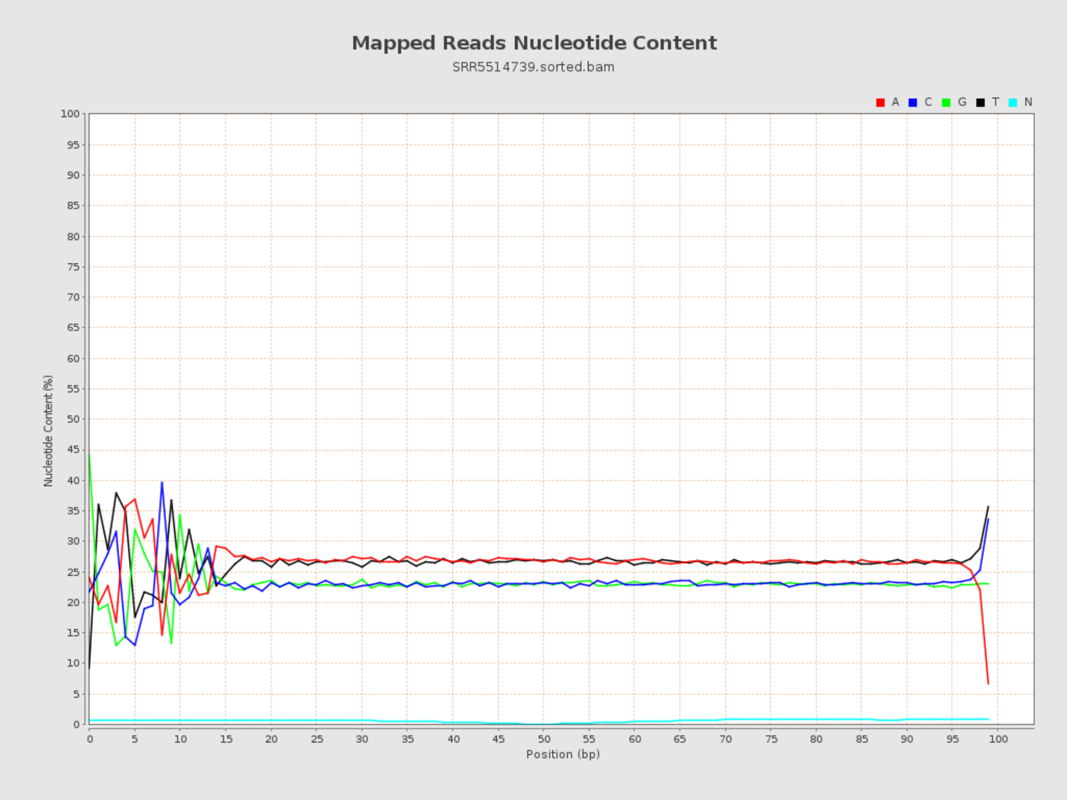
6. Results : Genome Fraction Coverage



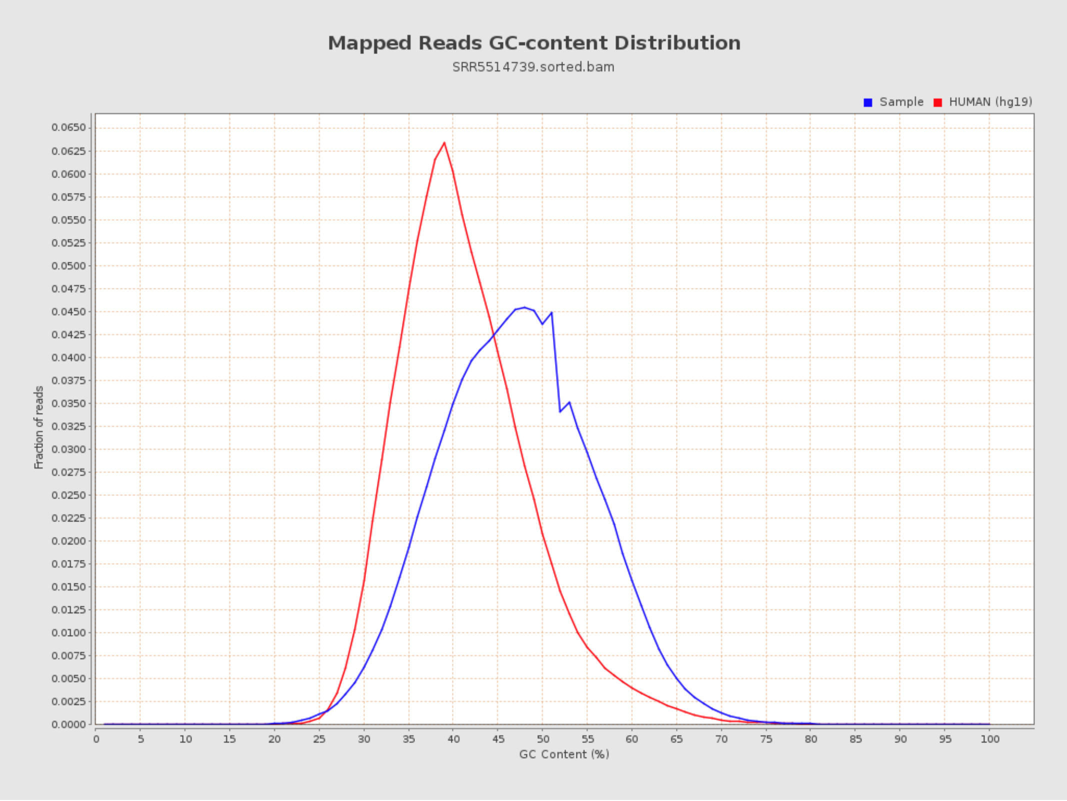
7. Results : Duplication Rate Histogram



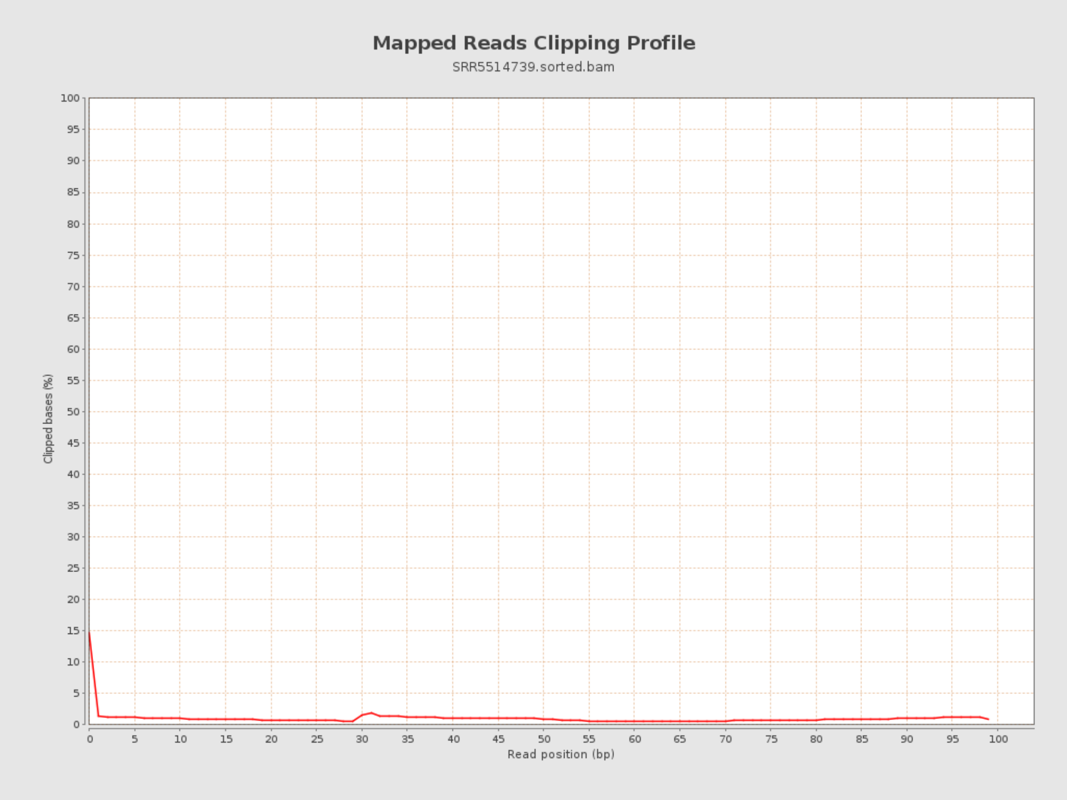
8. Results : Mapped Reads Nucleotide Content



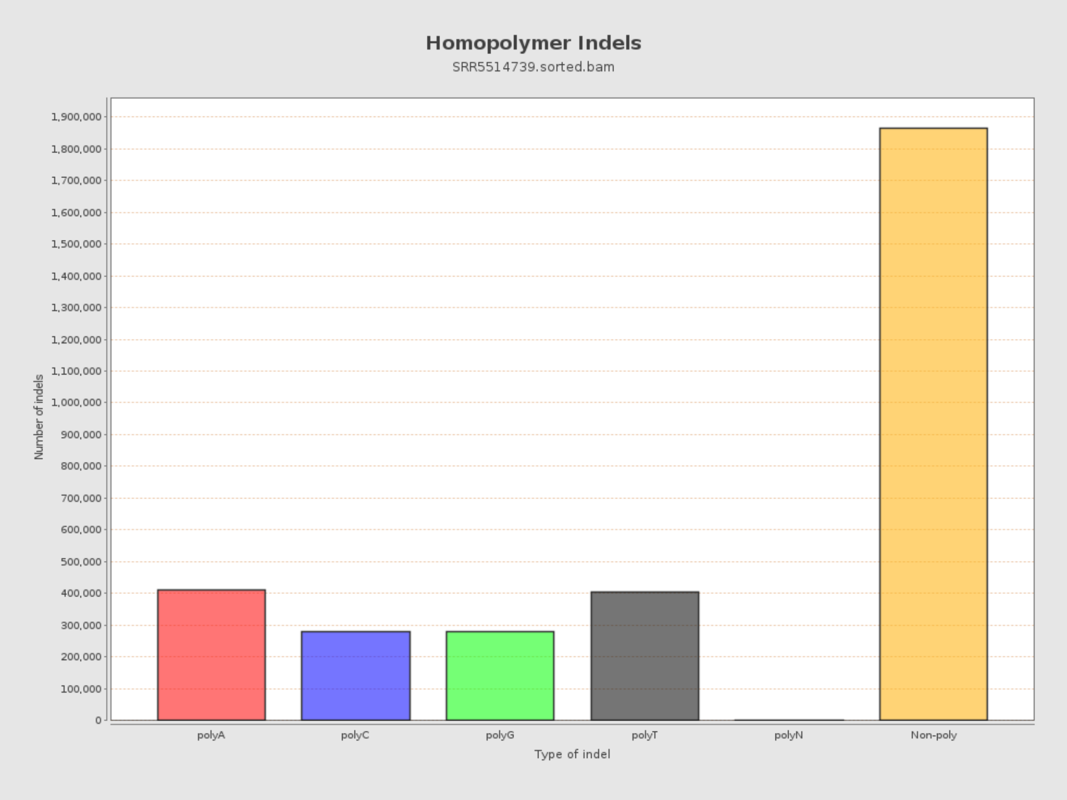
9. Results : Mapped Reads GC-content Distribution



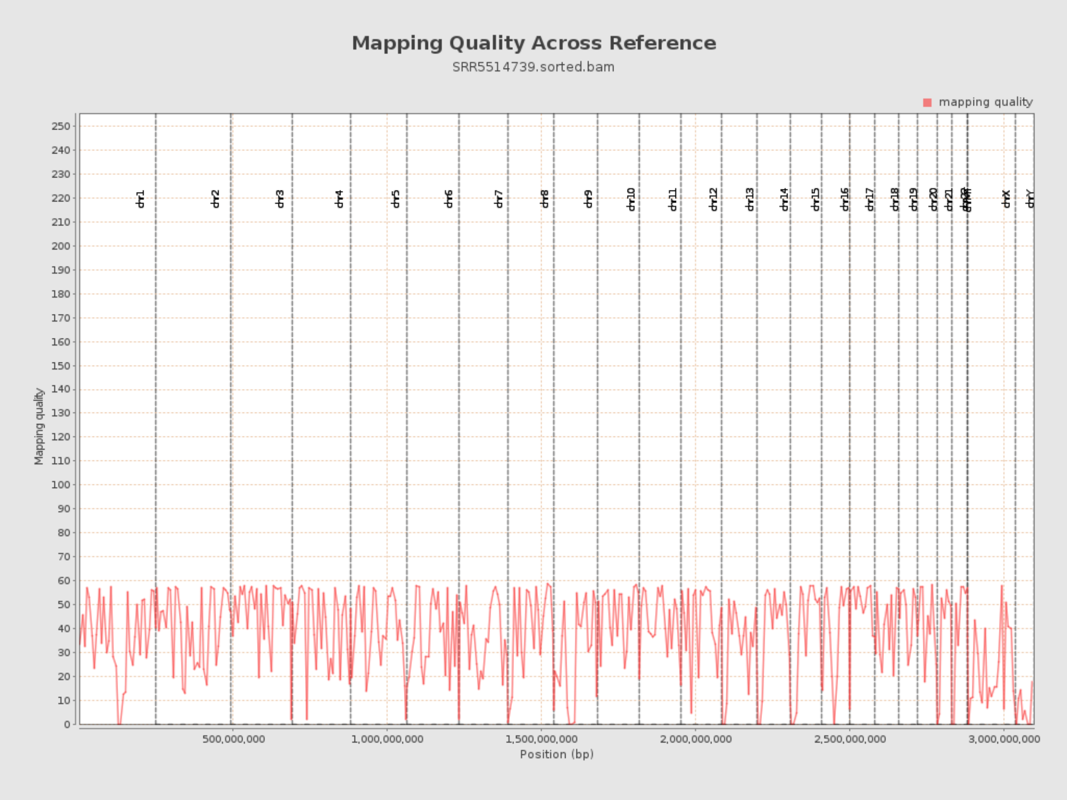
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram