Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 18:32:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514756.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_SRR5514756 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514756.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 18:32:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514756.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,632,023
Mapped reads	58,278,797 / 97.73%
Unmapped reads	1,353,226 / 2.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,114,580 / 8.58%
Read min/max/mean length	30 / 100 / 101.1
Duplicated reads (estimated)	56,140,077 / 94.14%
Duplication rate	50.74%
Clipped reads	22,395,325 / 37.56%

2.2. ACGT Content

Number/percentage of A's	1,543,516,799 / 28.62%
Number/percentage of C's	1,133,268,523 / 21.01%
Number/percentage of T's	1,551,855,879 / 28.77%
Number/percentage of G's	1,160,432,796 / 21.52%
Number/percentage of N's	4,041,178 / 0.07%
GC Percentage	42.53%

2.3. Coverage

Mean	1.7454

Standard Deviation	433.0035

2.4. Mapping Quality

Mean Mapping Quality	48.98

2.5. Mismatches and indels

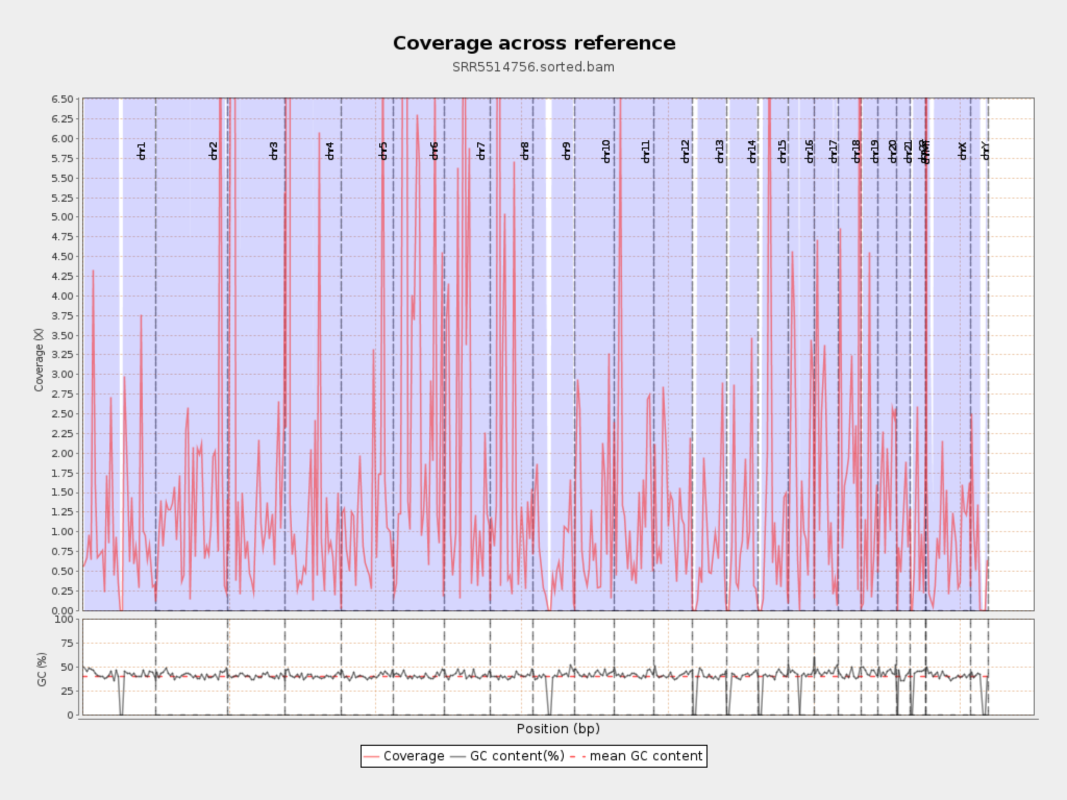
General error rate	1.08%
Mismatches	51,758,900
Insertions	3,299,615
Mapped reads with at least one insertion	5.23%
Deletions	3,512,458
Mapped reads with at least one deletion	5.43%
Homopolymer indels	27.84%

2.6. Chromosome stats

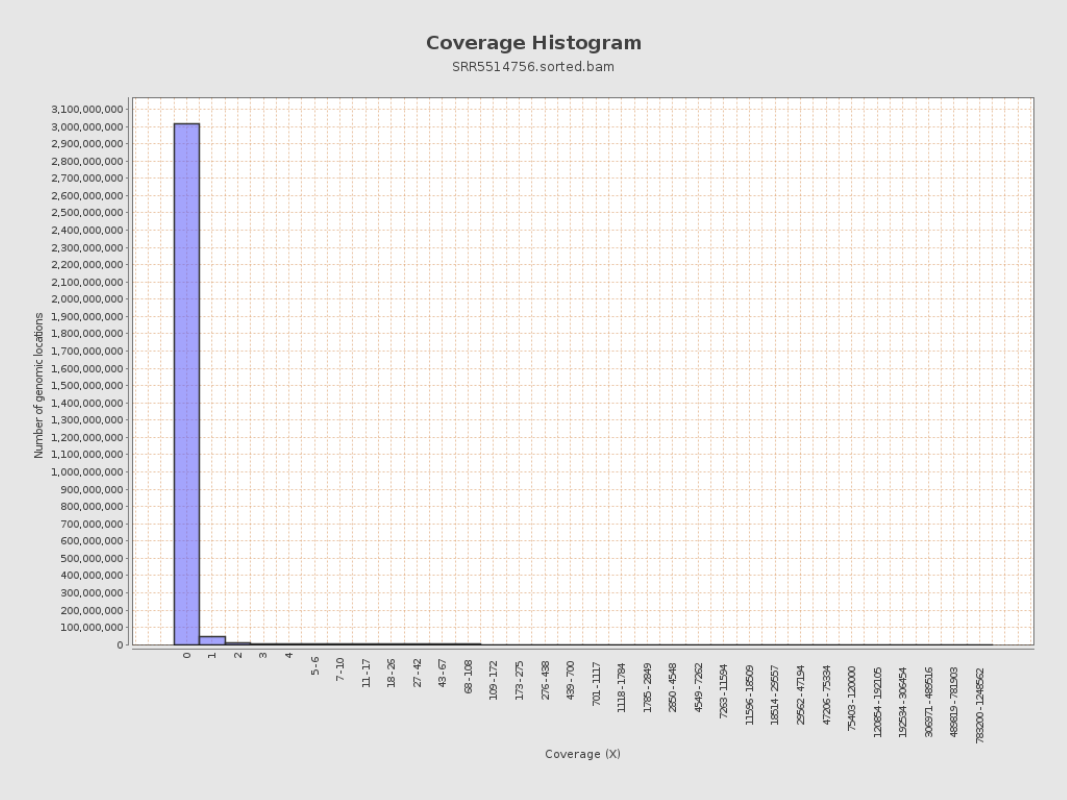
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	266666590	1.0699	61.8175
chr2	243199373	358475060	1.474	126.318
chr3	198022430	418695757	2.1144	155.6667
chr4	191154276	895256297	4.6834	1,597.5154
chr5	180915260	246198086	1.3608	70.0851
chr6	171115067	573352110	3.3507	481.0451
chr7	159138663	380314460	2.3898	139.7266

chr8	146364022	339151483	2.3172	465.0117
chr9	141213431	95046456	0.6731	32.2486
chr10	135534747	165417750	1.2205	53.7851
chr11	135006516	206946777	1.5329	58.2564
chr12	133851895	164530103	1.2292	59.0063
chr13	115169878	97365888	0.8454	45.4774
chr14	107349540	106198838	0.9893	50.8438
chr15	102531392	135341846	1.32	67.5377
chr16	90354753	166628564	1.8442	120.4124
chr17	81195210	142031920	1.7493	70.2996
chr18	78077248	204426917	2.6183	166.0528
chr19	59128983	66897838	1.1314	82.4857
chr20	63025520	111778124	1.7735	72.8677
chr21	48129895	47528882	0.9875	46.155
chr22	51304566	39621185	0.7723	46.4747
chrMT	16571	1114660	67.2657	181.9485
chrX	155270560	133822794	0.8619	45.8492
chrY	59373566	40448574	0.6813	44.4696

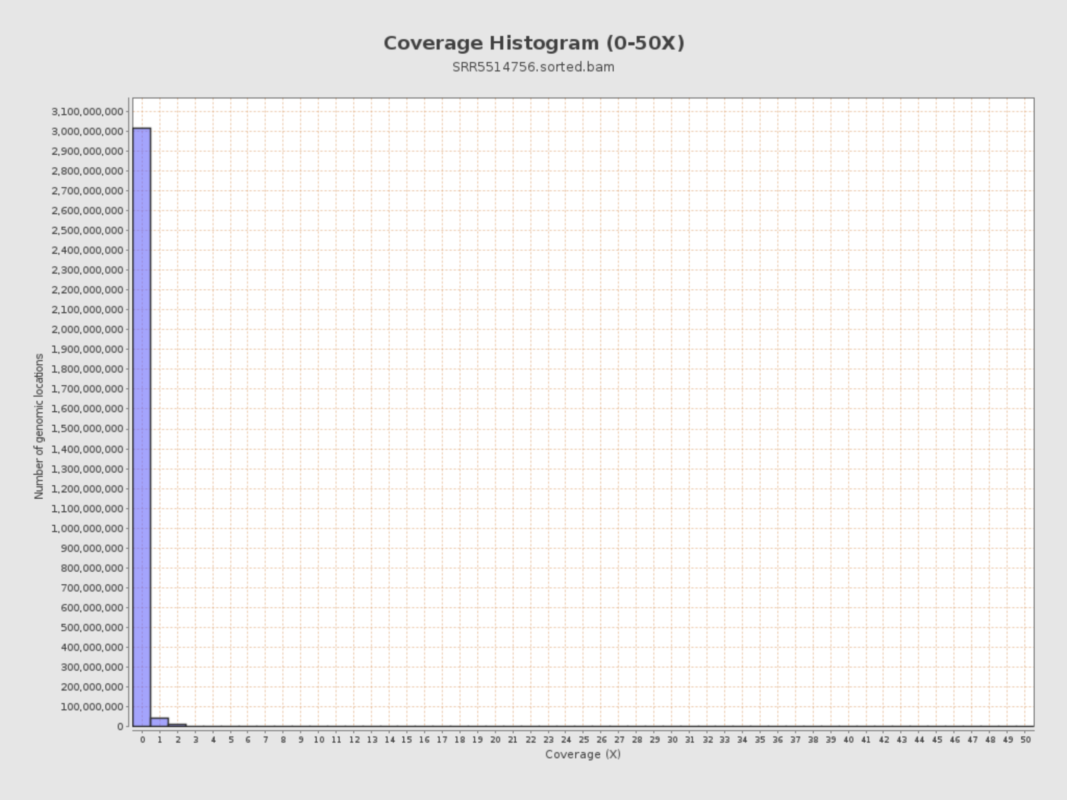
3. Results : Coverage across reference



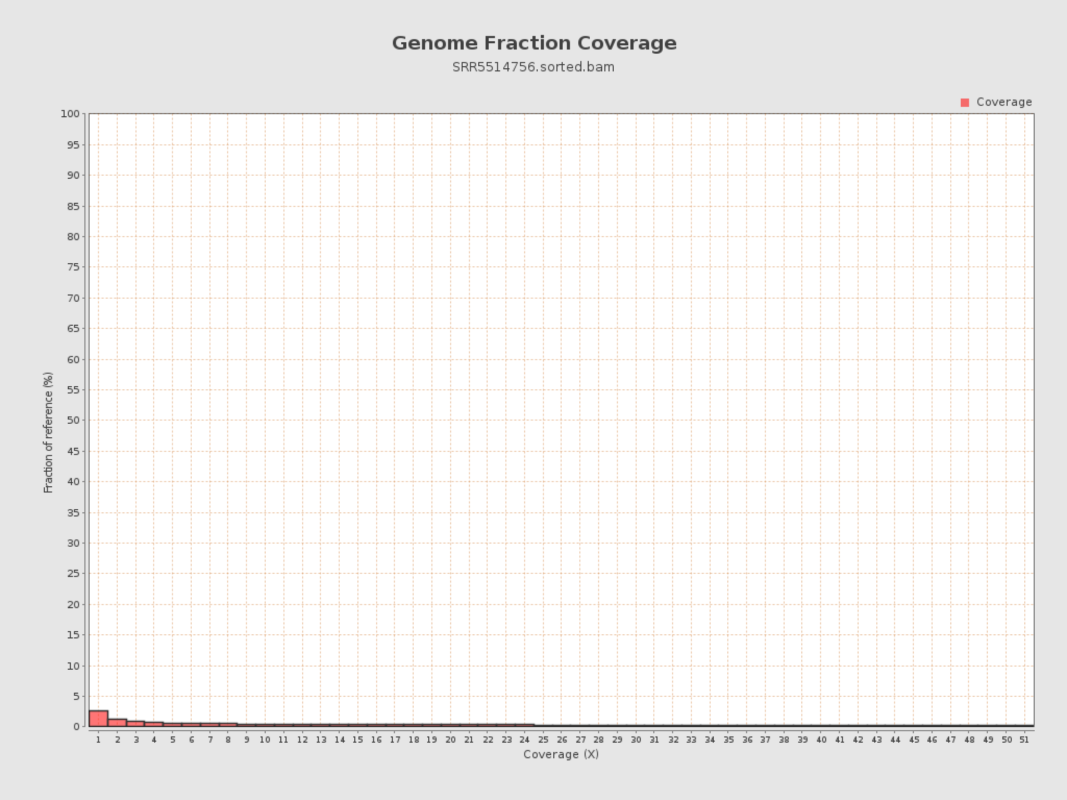
4. Results : Coverage Histogram



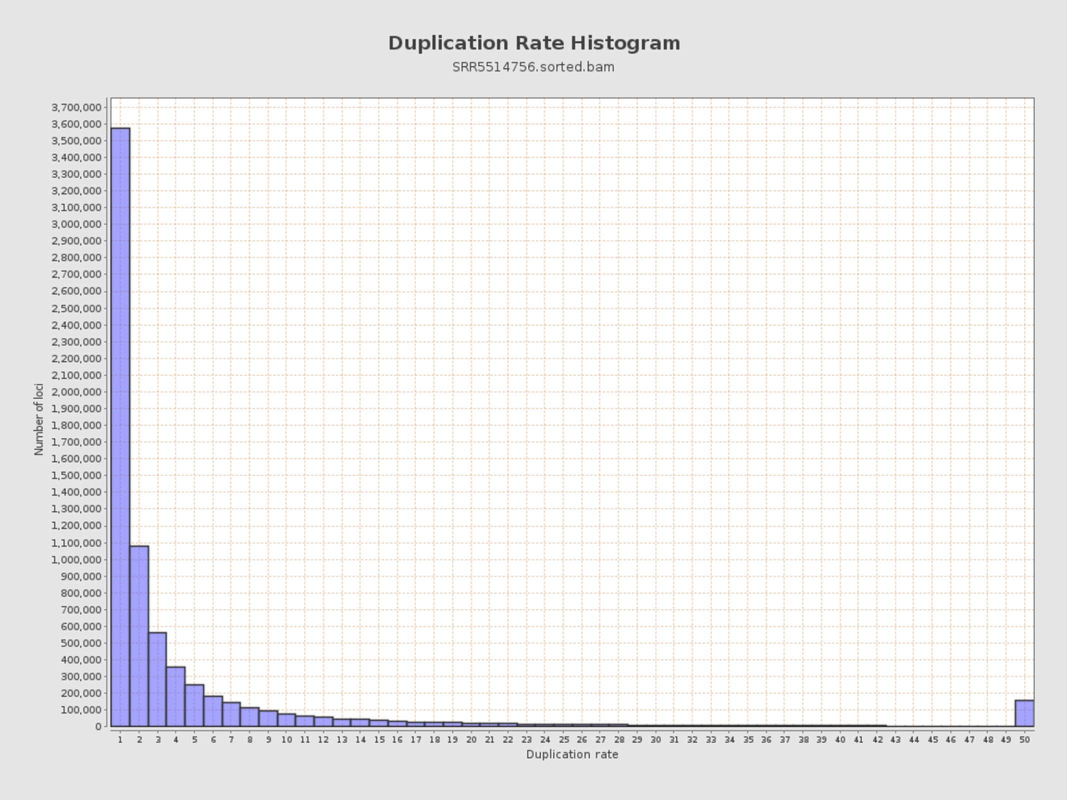
5. Results : Coverage Histogram (0-50X)



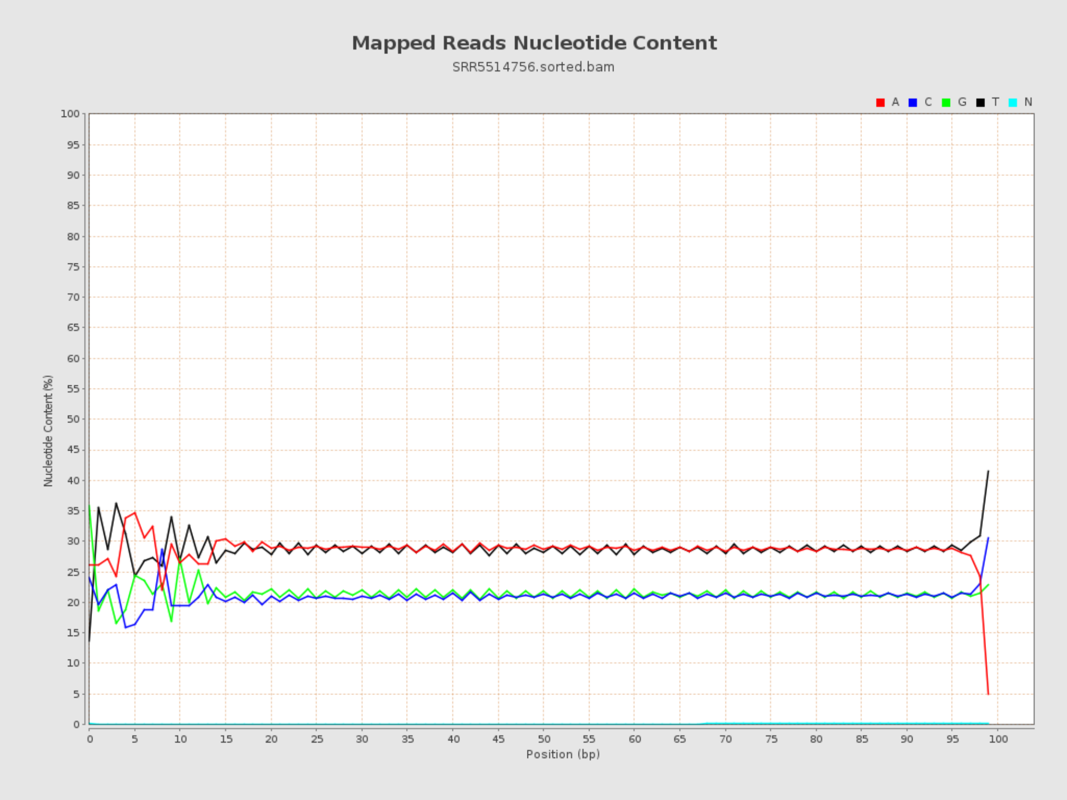
6. Results : Genome Fraction Coverage



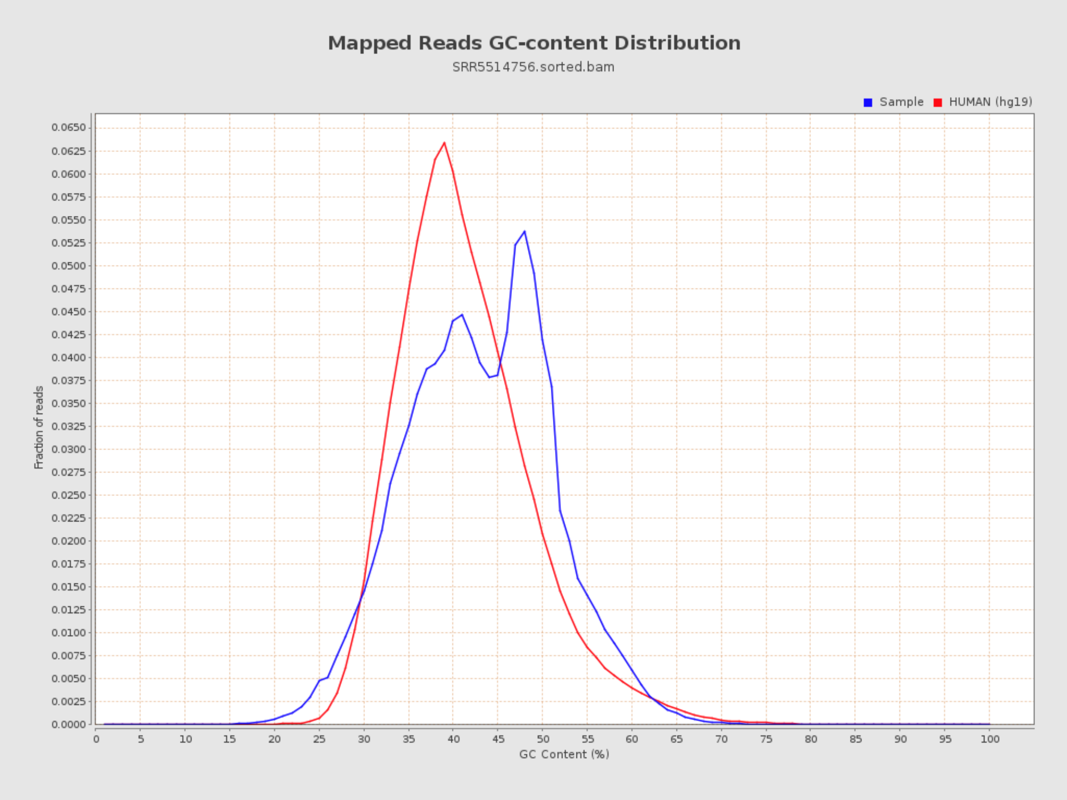
7. Results : Duplication Rate Histogram



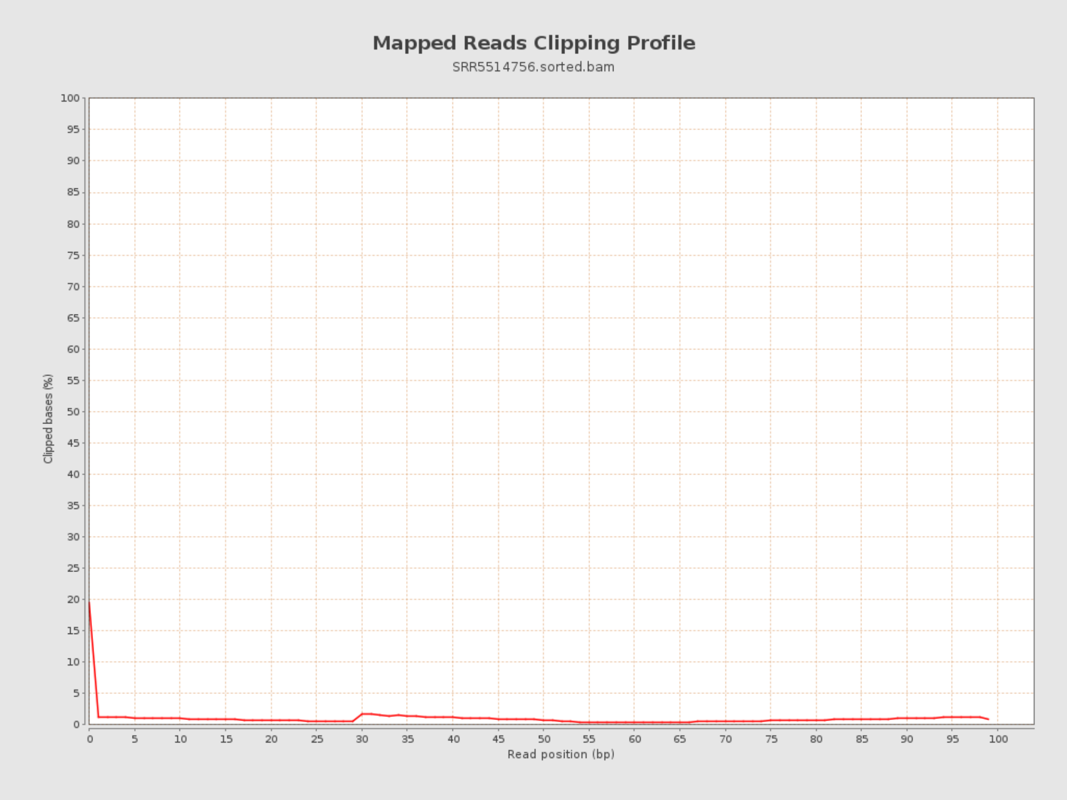
8. Results : Mapped Reads Nucleotide Content



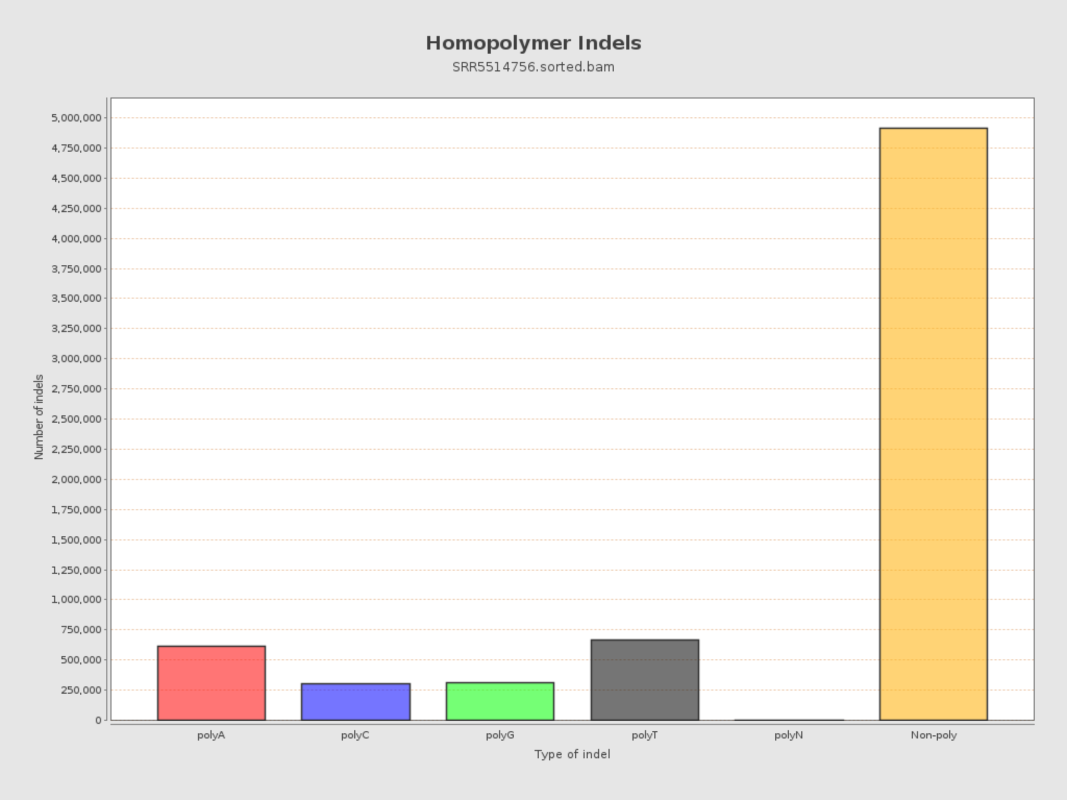
9. Results : Mapped Reads GC-content Distribution



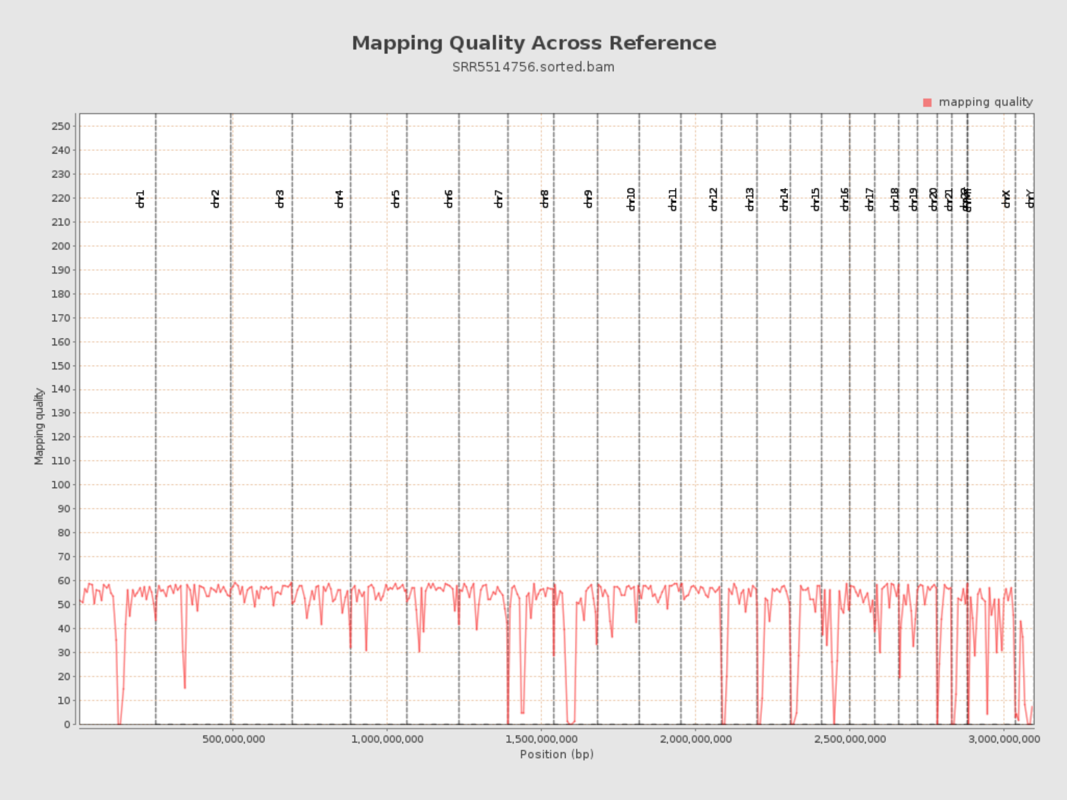
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram