Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 21:18:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514765.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_SRR5514765 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514765.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 21:18:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514765.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,353,952
Mapped reads	7,440,920 / 38.45%
Unmapped reads	11,913,032 / 61.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,200,415 / 6.2%
Read min/max/mean length	30 / 100 / 101.46
Duplicated reads (estimated)	4,032,853 / 20.84%
Duplication rate	28.86%
Clipped reads	4,424,136 / 22.86%

2.2. ACGT Content

Number/percentage of A's	213,110,659 / 31.37%
Number/percentage of C's	125,697,413 / 18.5%
Number/percentage of T's	209,382,597 / 30.82%
Number/percentage of G's	131,091,099 / 19.3%
Number/percentage of N's	45,035 / 0.01%
GC Percentage	37.8%

2.3. Coverage

Mean	0.2196

Standard Deviation	12.4985

2.4. Mapping Quality

Mean Mapping Quality	44.28

2.5. Mismatches and indels

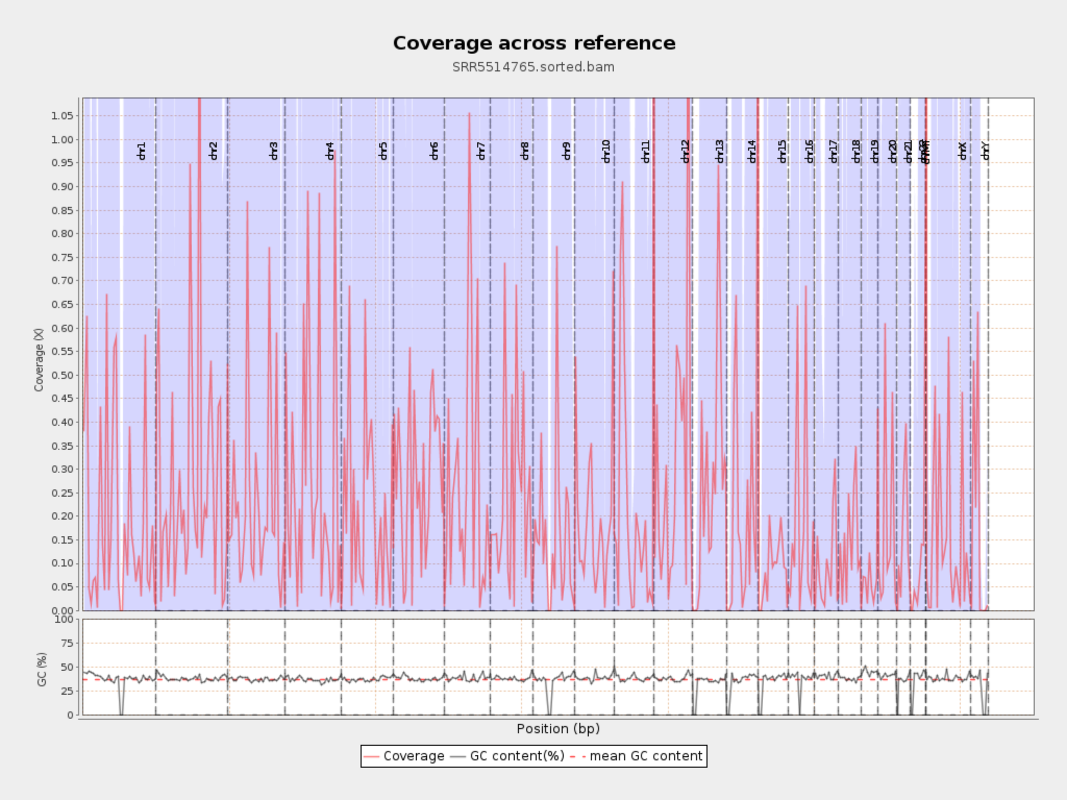
General error rate	0.67%
Mismatches	3,895,716
Insertions	381,097
Mapped reads with at least one insertion	4.91%
Deletions	183,657
Mapped reads with at least one deletion	2.31%
Homopolymer indels	48.01%

2.6. Chromosome stats

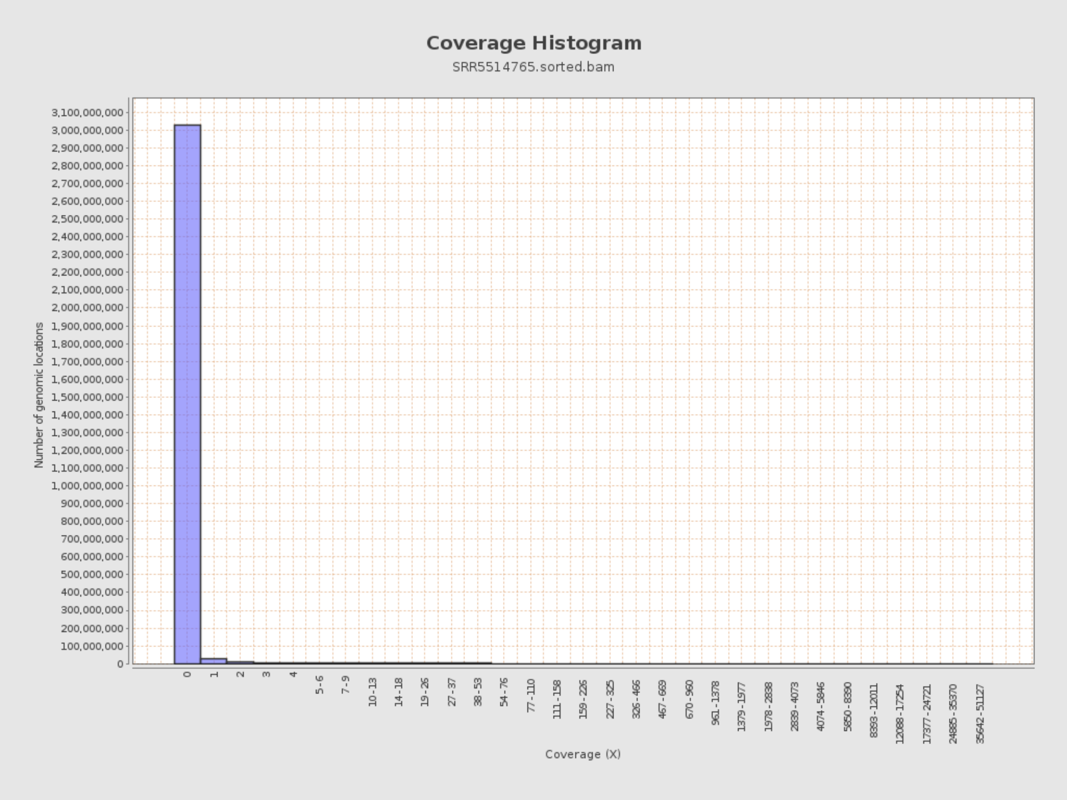
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	47342432	0.1899	5.1777
chr2	243199373	69935058	0.2876	26.0618
chr3	198022430	46147288	0.233	4.7804
chr4	191154276	53348941	0.2791	5.7752
chr5	180915260	39738693	0.2197	4.6045
chr6	171115067	49792807	0.291	22.1611
chr7	159138663	42602860	0.2677	7.4186

chr8	146364022	35615364	0.2433	9.2999
chr9	141213431	23210424	0.1644	3.9034
chr10	135534747	25959707	0.1915	9.0349
chr11	135006516	28185747	0.2088	4.23
chr12	133851895	42757669	0.3194	21.4779
chr13	115169878	31608827	0.2745	4.6054
chr14	107349540	21168684	0.1972	3.3467
chr15	102531392	8950217	0.0873	2.2824
chr16	90354753	16749883	0.1854	12.8391
chr17	81195210	8150073	0.1004	4.2003
chr18	78077248	11317211	0.1449	2.9435
chr19	59128983	4098517	0.0693	2.3597
chr20	63025520	11612025	0.1842	8.3125
chr21	48129895	7412183	0.154	2.9704
chr22	51304566	5045632	0.0983	22.2811
chrMT	16571	14381819	867.8908	820.1202
chrX	155270560	23866557	0.1537	14.4785
chrY	59373566	10865545	0.183	10.2319

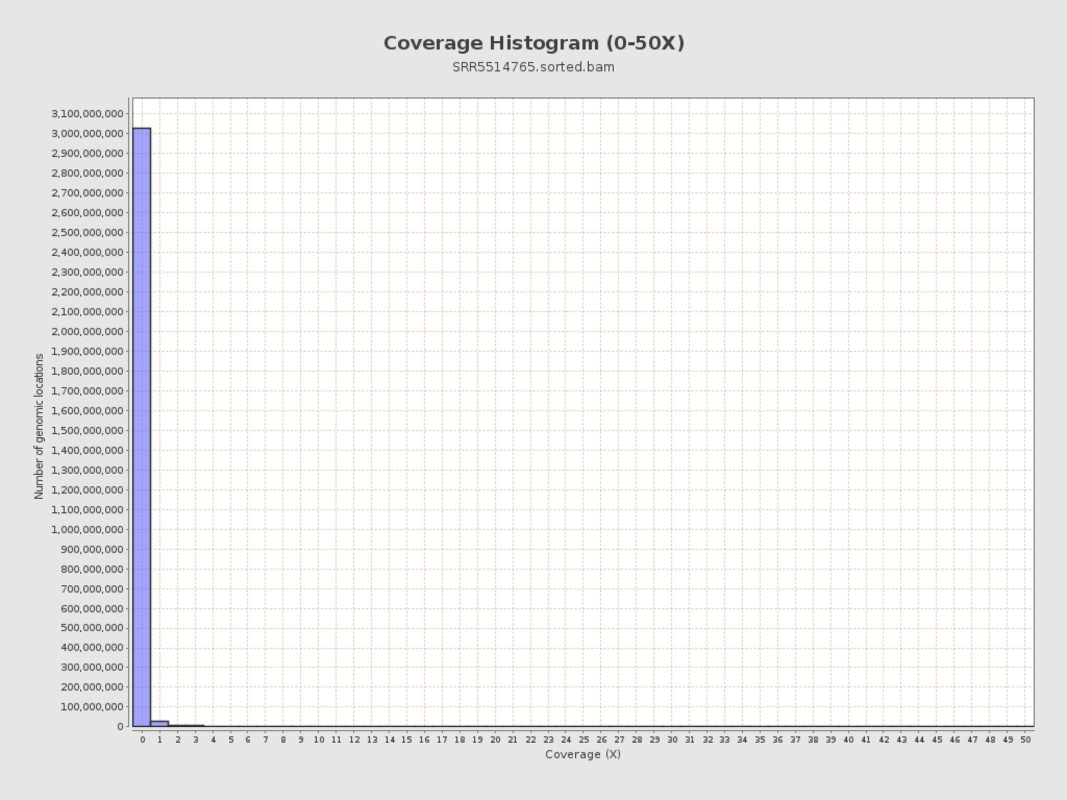
3. Results : Coverage across reference



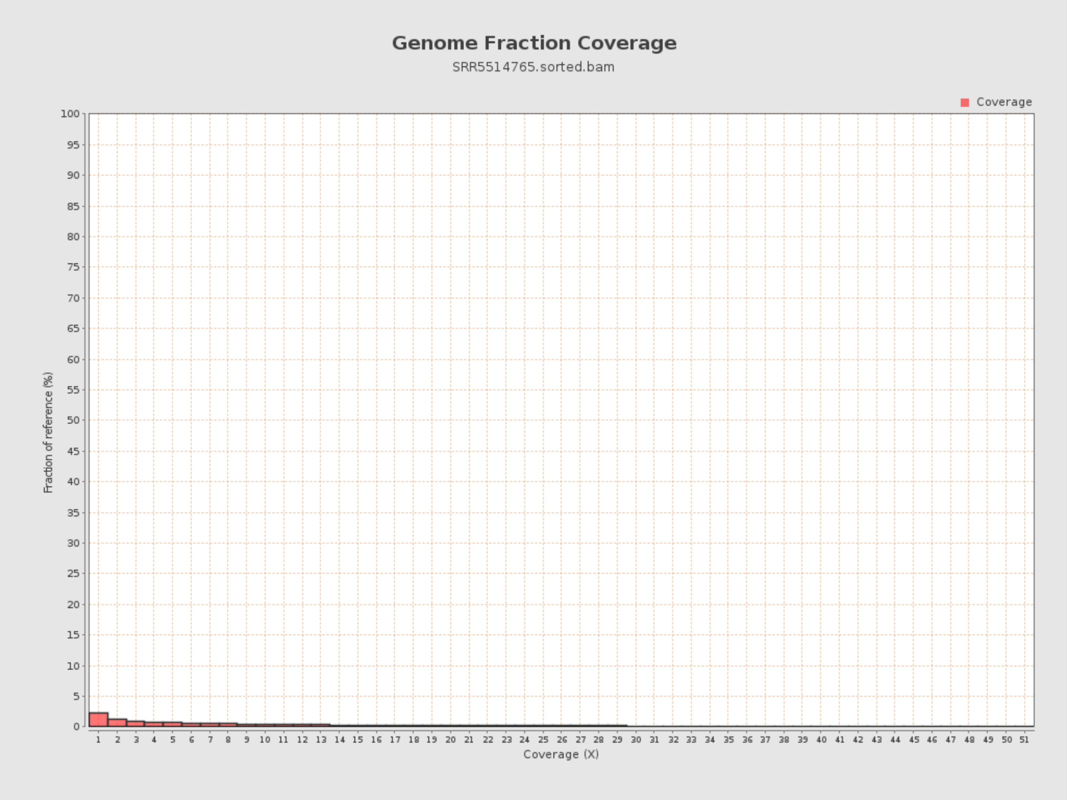
4. Results : Coverage Histogram



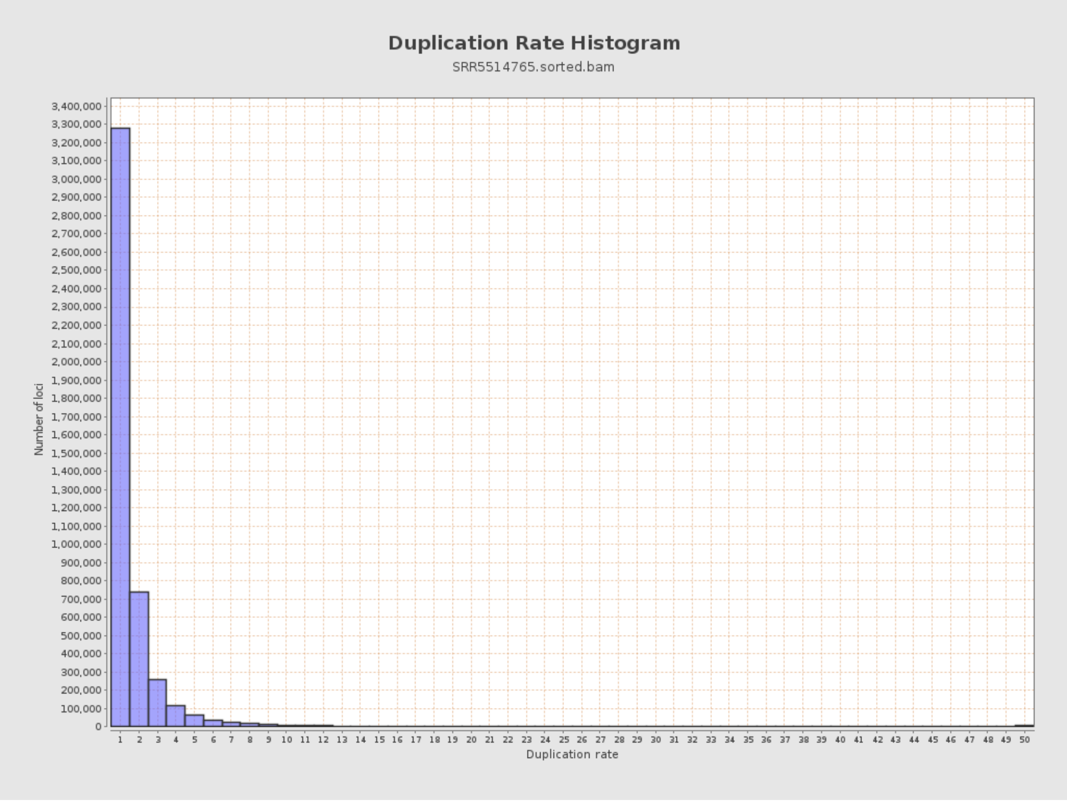
5. Results : Coverage Histogram (0-50X)



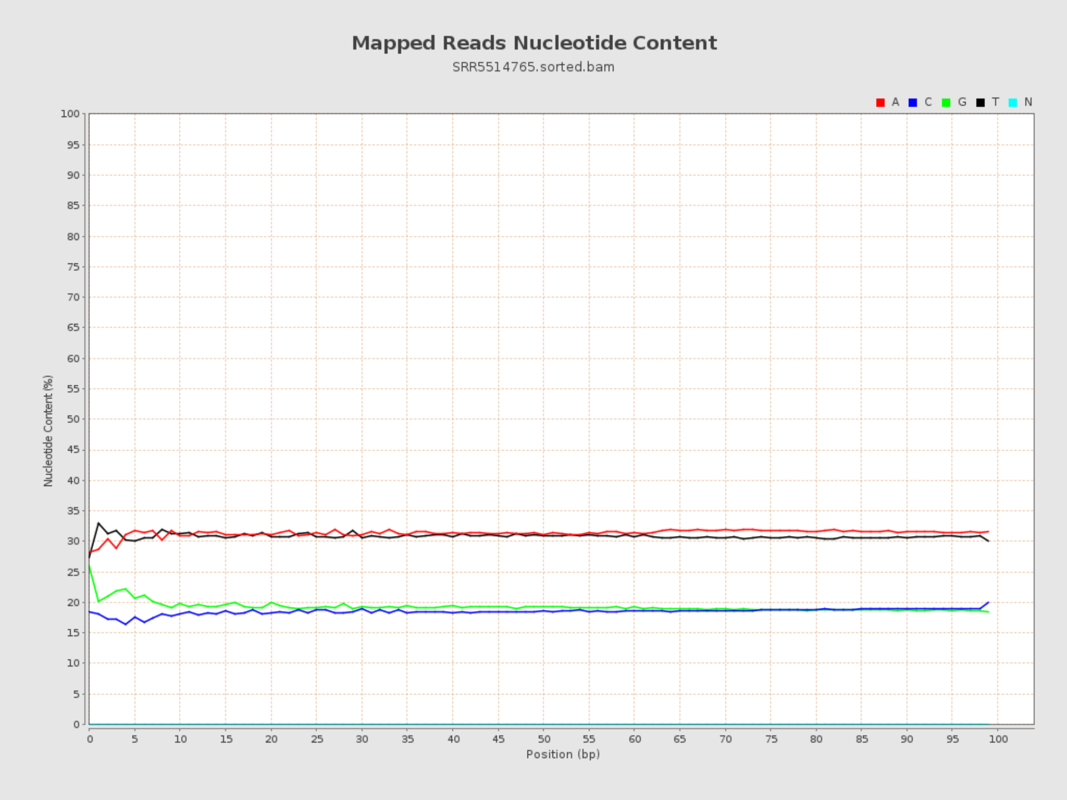
6. Results : Genome Fraction Coverage



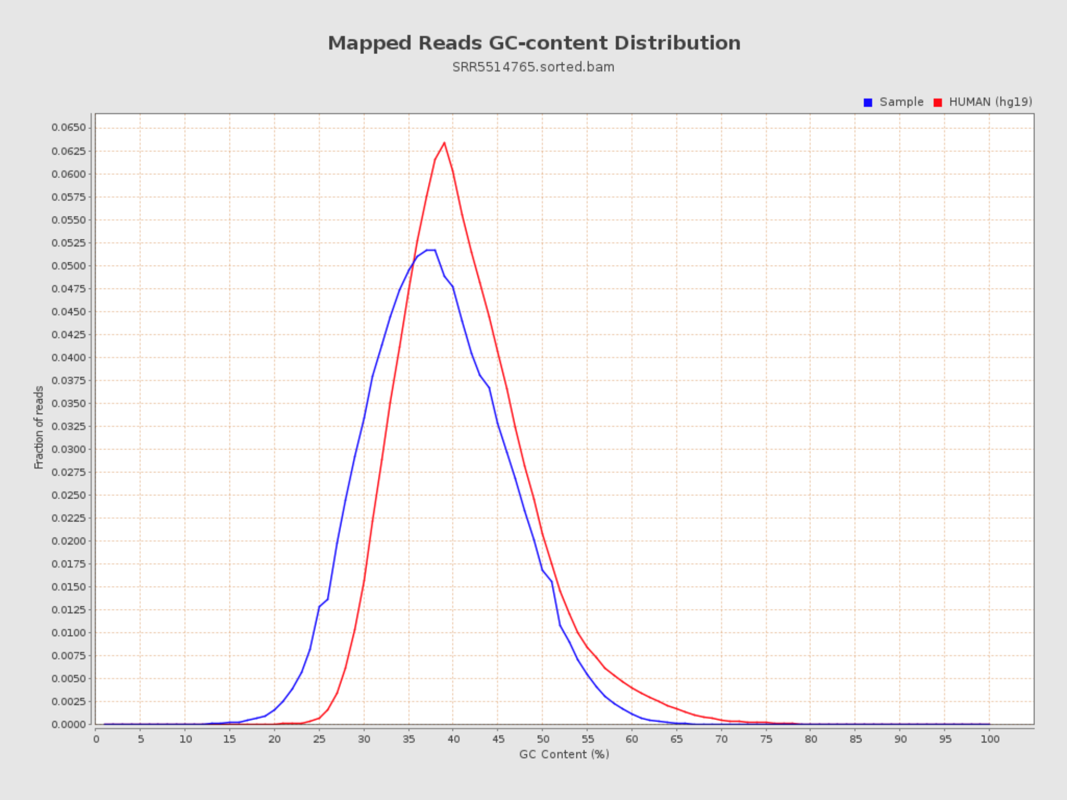
7. Results : Duplication Rate Histogram



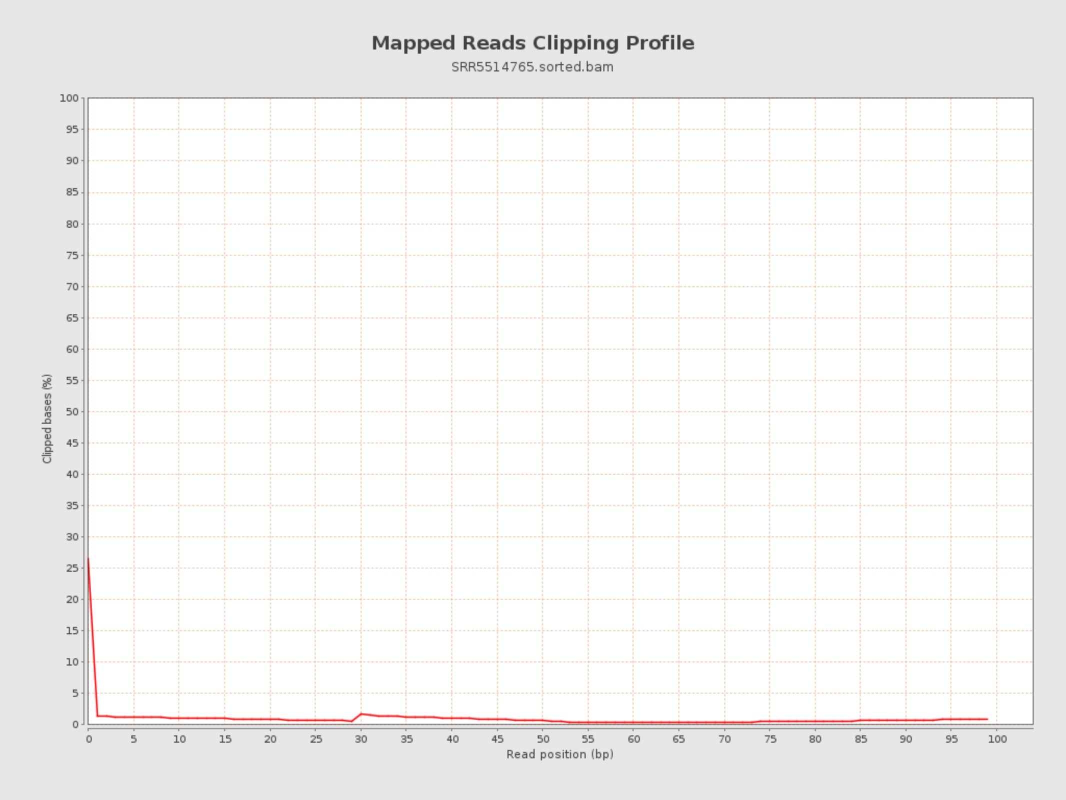
8. Results : Mapped Reads Nucleotide Content



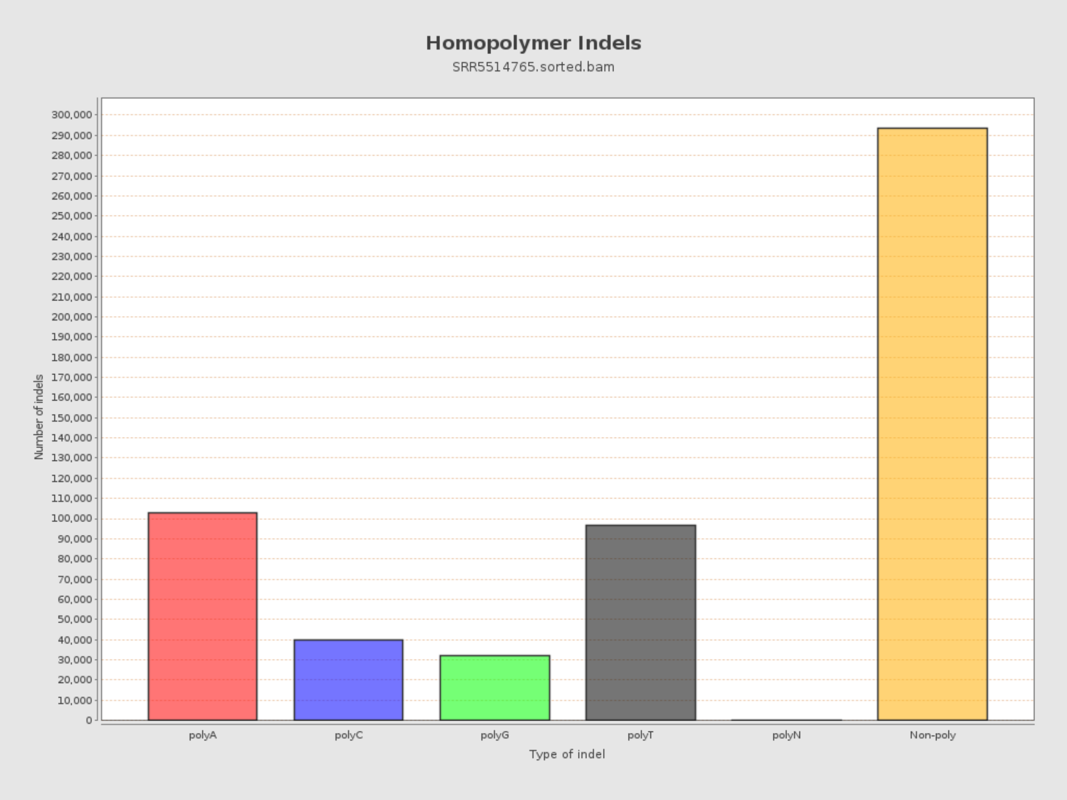
9. Results : Mapped Reads GC-content Distribution



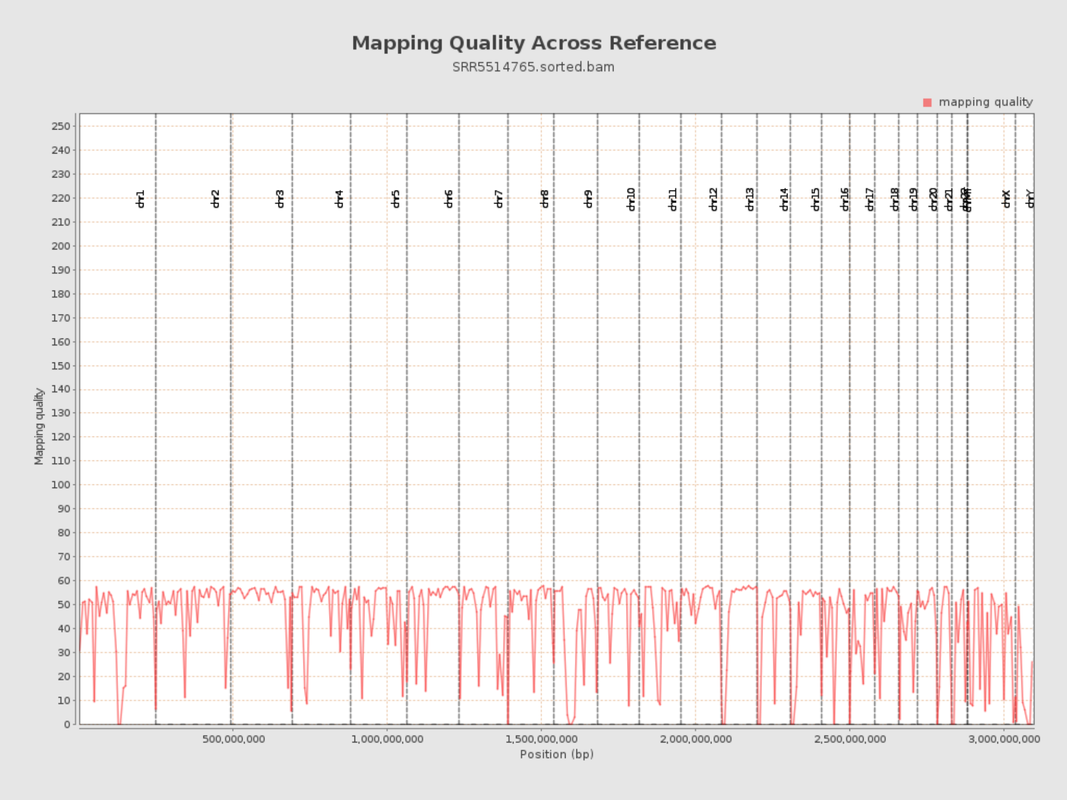
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram