Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 19:04:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536746.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_SRR536746 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536746.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 19:04:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536746.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,227,472
Mapped reads	15,622,250 / 81.25%
Unmapped reads	3,605,222 / 18.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	343 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	111,139 / 0.58%
Duplication rate	0.67%
Clipped reads	270,659 / 1.41%

2.2. ACGT Content

Number/percentage of A's	245,163,471 / 31.48%
Number/percentage of C's	143,798,281 / 18.46%
Number/percentage of T's	243,635,655 / 31.28%
Number/percentage of G's	146,181,709 / 18.77%
Number/percentage of N's	16,701 / 0%
GC Percentage	37.23%

2.3. Coverage

Mean	0.2516

Standard Deviation	0.6736

2.4. Mapping Quality

Mean Mapping Quality	47.52

2.5. Mismatches and indels

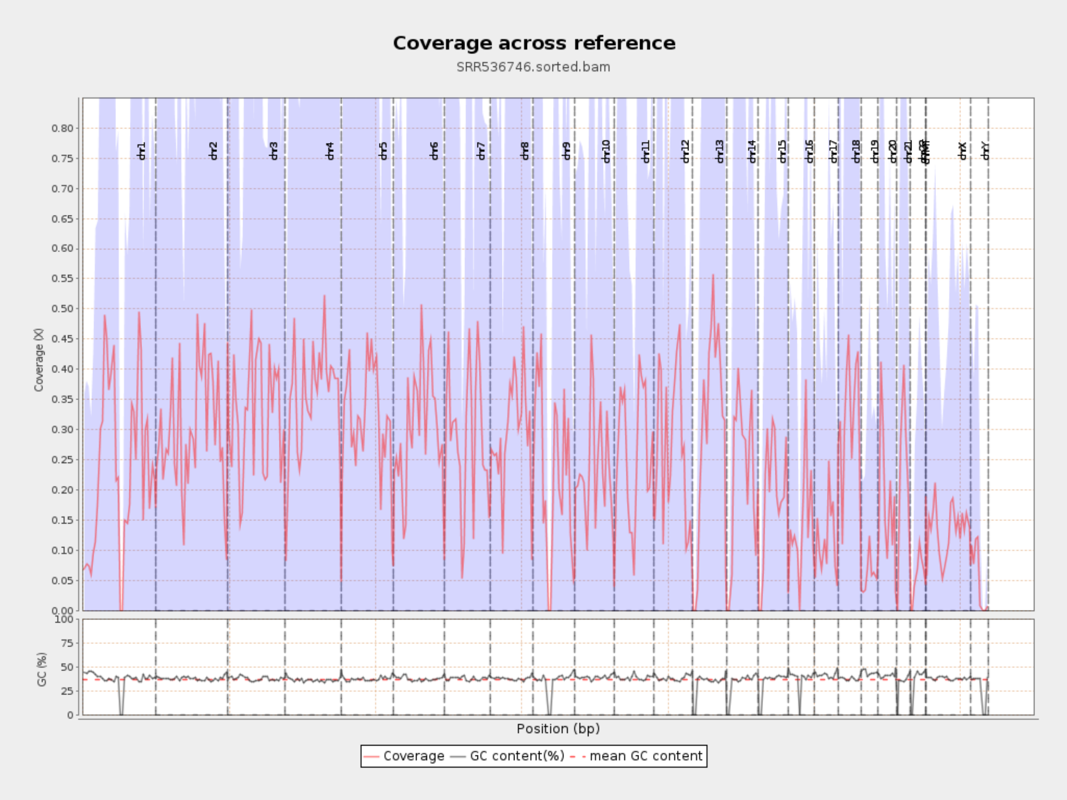
General error rate	0.36%
Mismatches	2,712,767
Insertions	52,932
Mapped reads with at least one insertion	0.34%
Deletions	40,645
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.28%

2.6. Chromosome stats

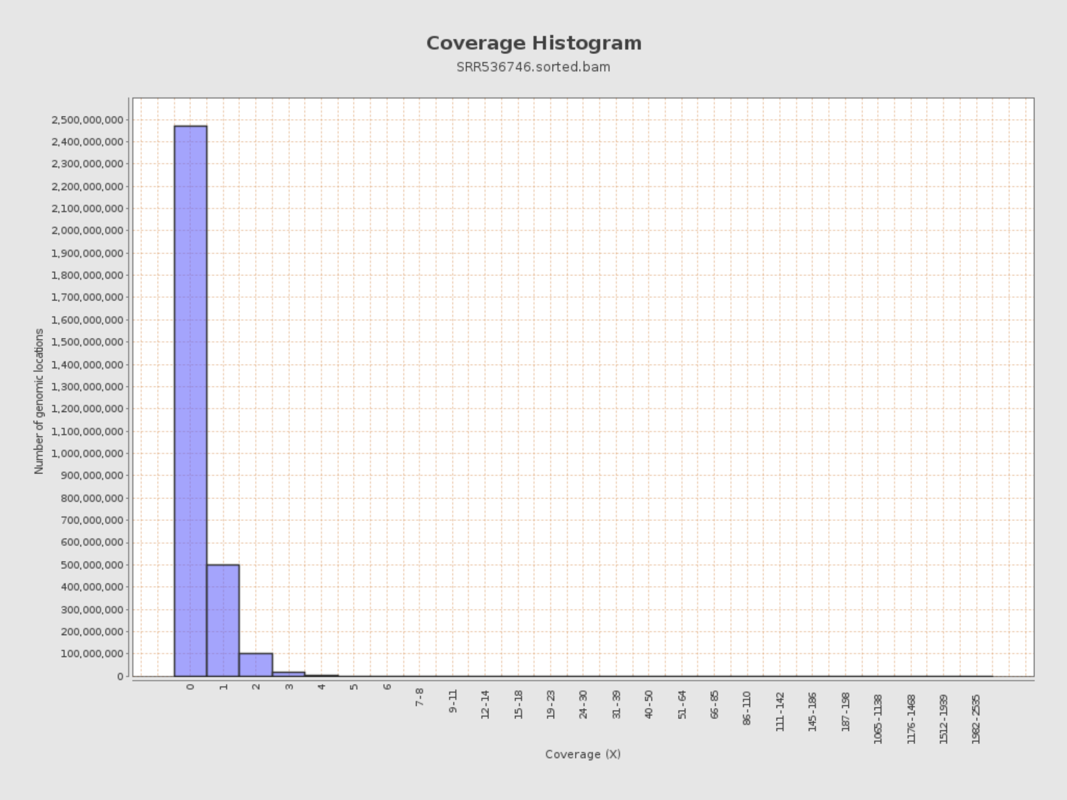
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	58838742	0.2361	0.5483
chr2	243199373	73211617	0.301	1.467
chr3	198022430	64848530	0.3275	0.6273
chr4	191154276	67977139	0.3556	0.6564
chr5	180915260	56851600	0.3142	0.6107
chr6	171115067	52908297	0.3092	0.6083
chr7	159138663	45008220	0.2828	0.5925

chr8	146364022	43592872	0.2978	0.597
chr9	141213431	32758294	0.232	0.542
chr10	135534747	32298723	0.2383	0.5304
chr11	135006516	35304140	0.2615	0.5662
chr12	133851895	35775316	0.2673	0.5732
chr13	115169878	35386156	0.3073	0.618
chr14	107349540	24325121	0.2266	0.5324
chr15	102531392	19262532	0.1879	0.4813
chr16	90354753	12845801	0.1422	0.4162
chr17	81195210	9647486	0.1188	0.3791
chr18	78077248	25213703	0.3229	0.6575
chr19	59128983	3622765	0.0613	0.2645
chr20	63025520	12145401	0.1927	0.4913
chr21	48129895	10320700	0.2144	0.5313
chr22	51304566	2998333	0.0584	0.26
chrMT	16571	3136	0.1892	0.4754
chrX	155270560	20568658	0.1325	0.3813
chrY	59373566	3150377	0.0531	0.2511

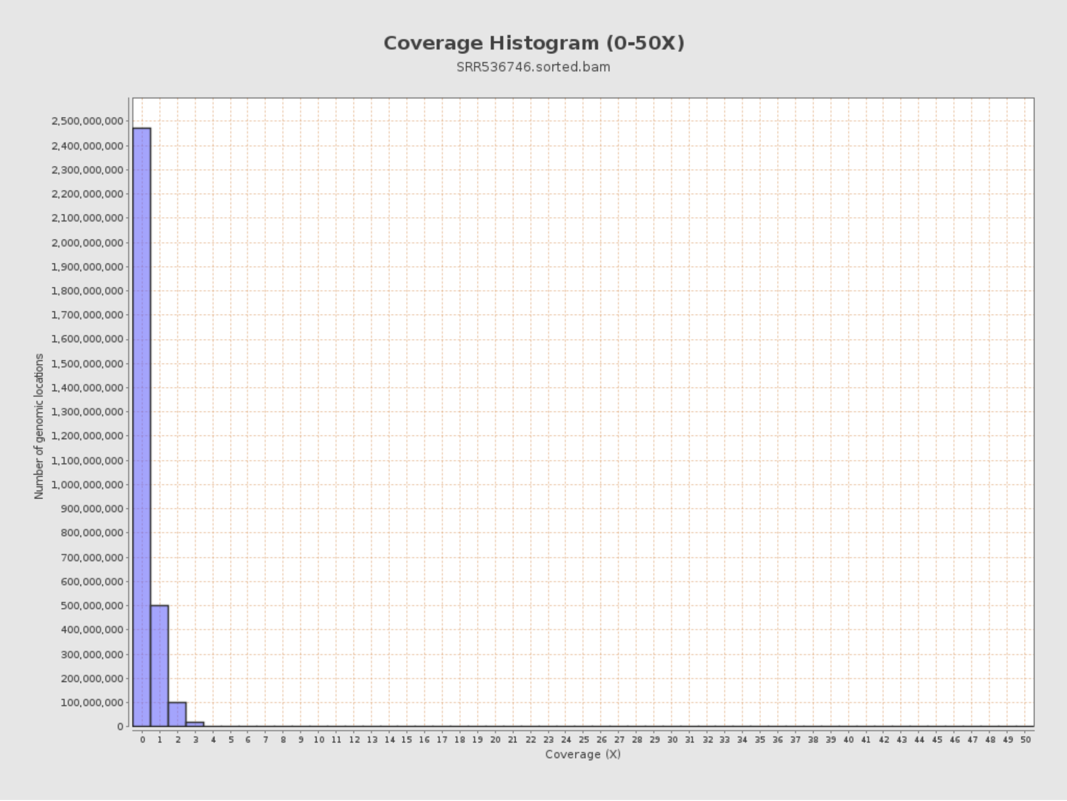
3. Results : Coverage across reference



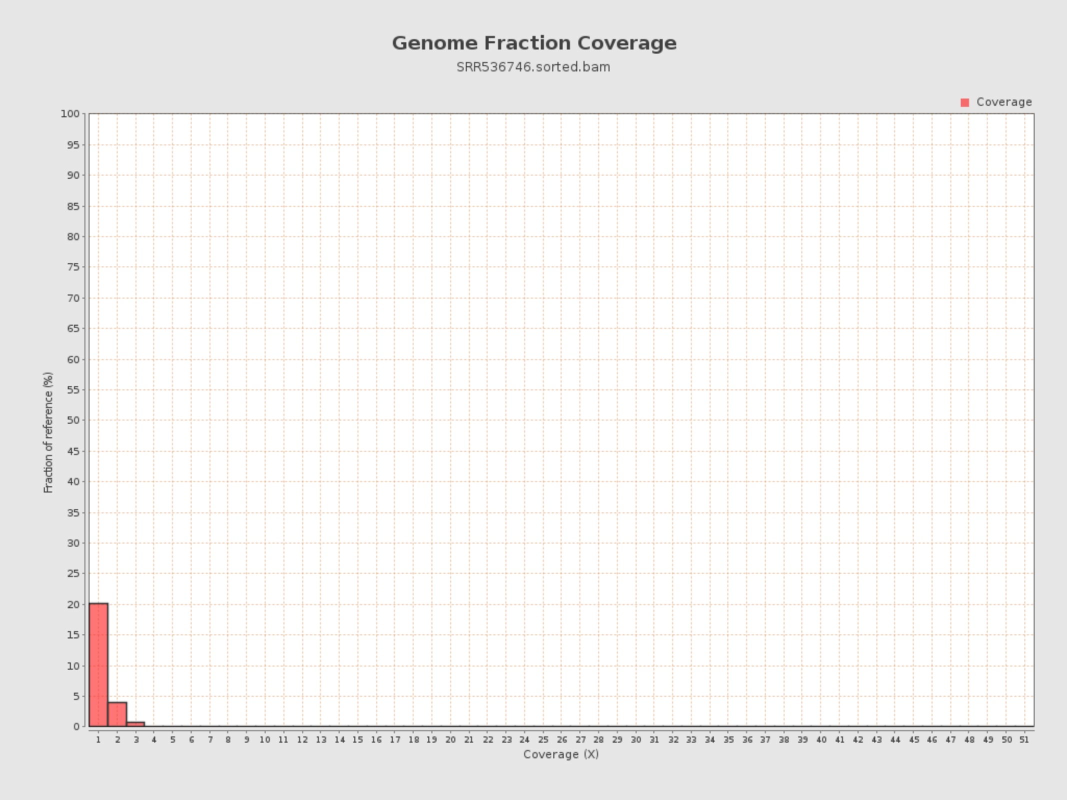
4. Results : Coverage Histogram



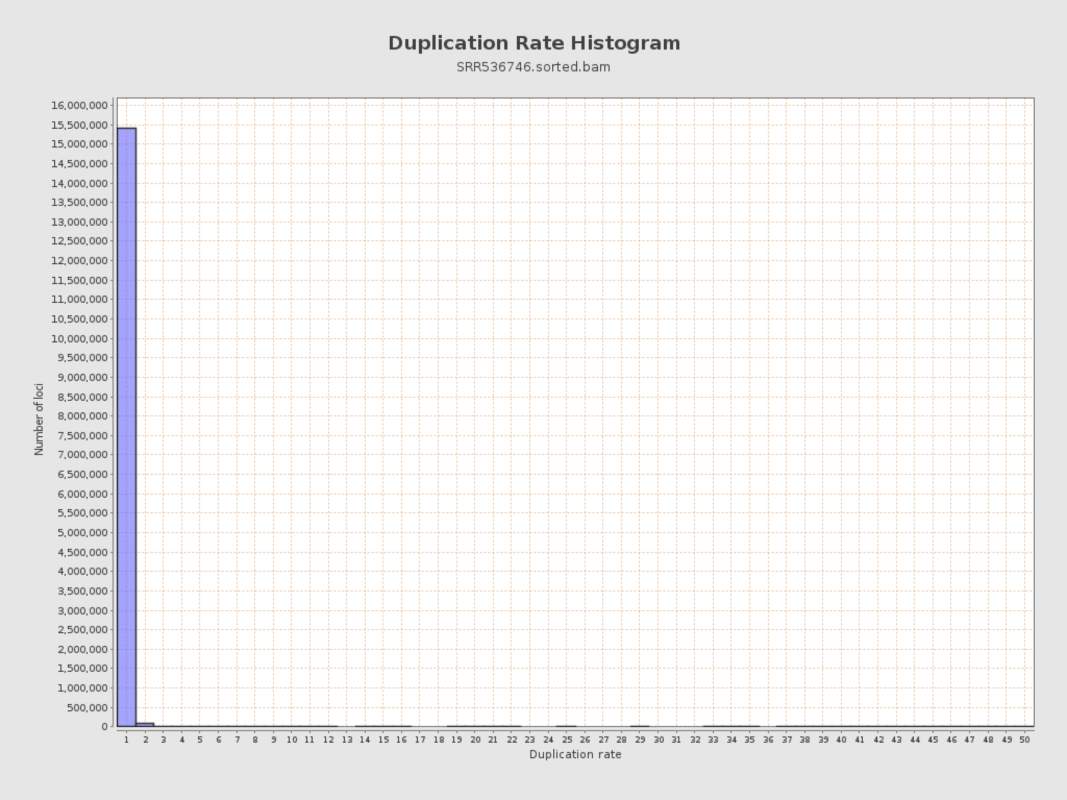
5. Results : Coverage Histogram (0-50X)



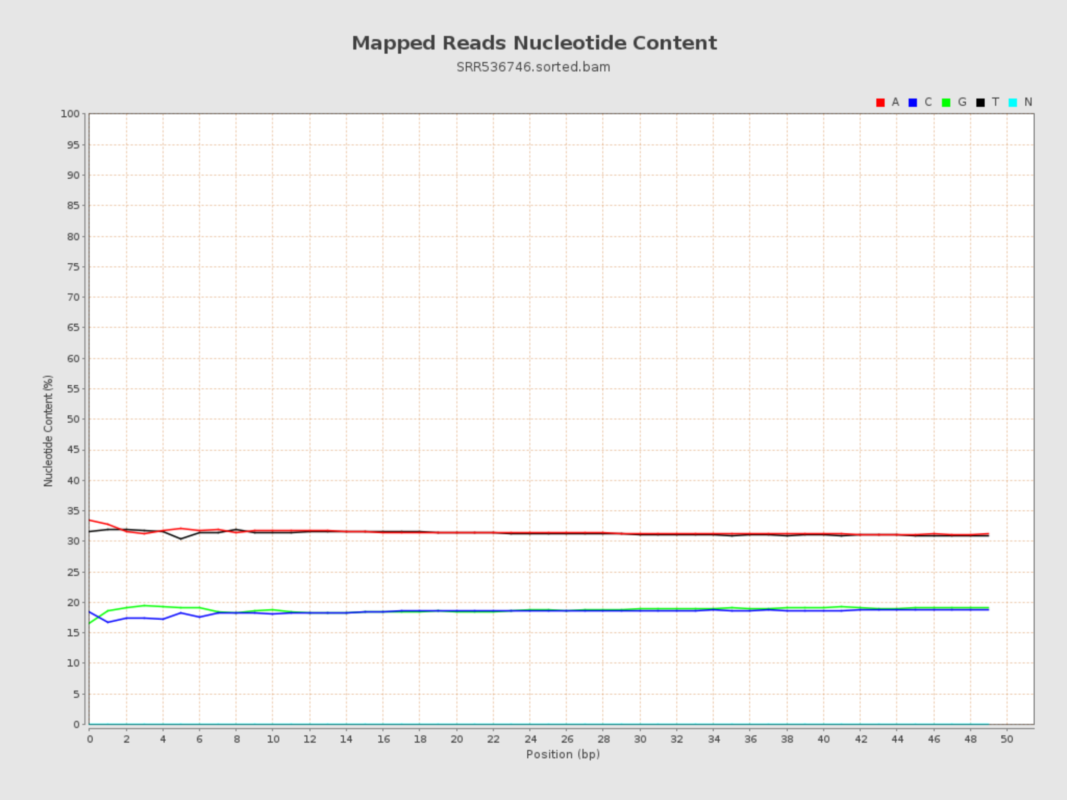
6. Results : Genome Fraction Coverage



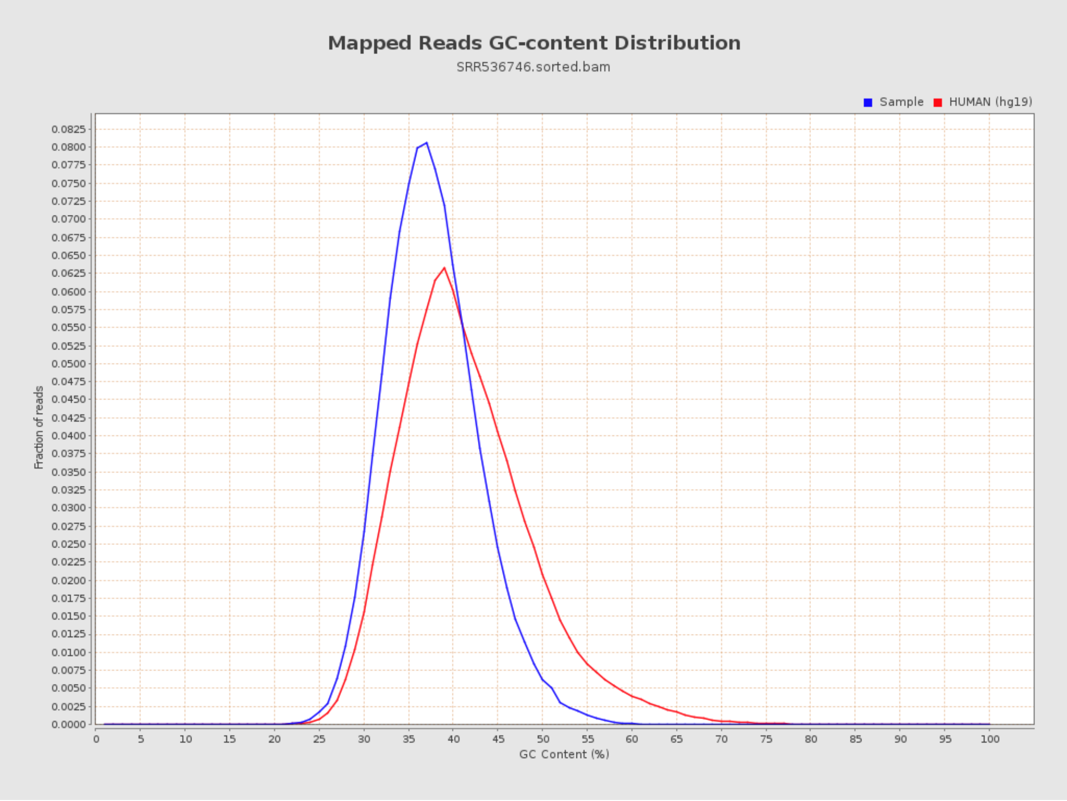
7. Results : Duplication Rate Histogram



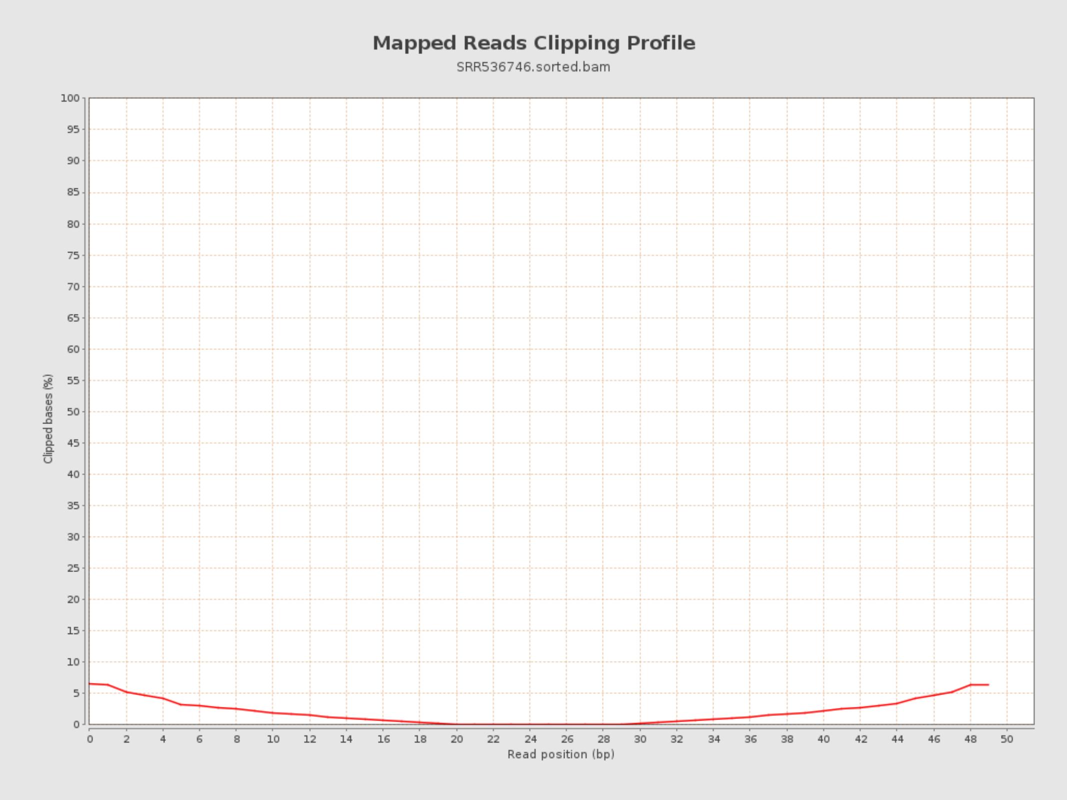
8. Results : Mapped Reads Nucleotide Content



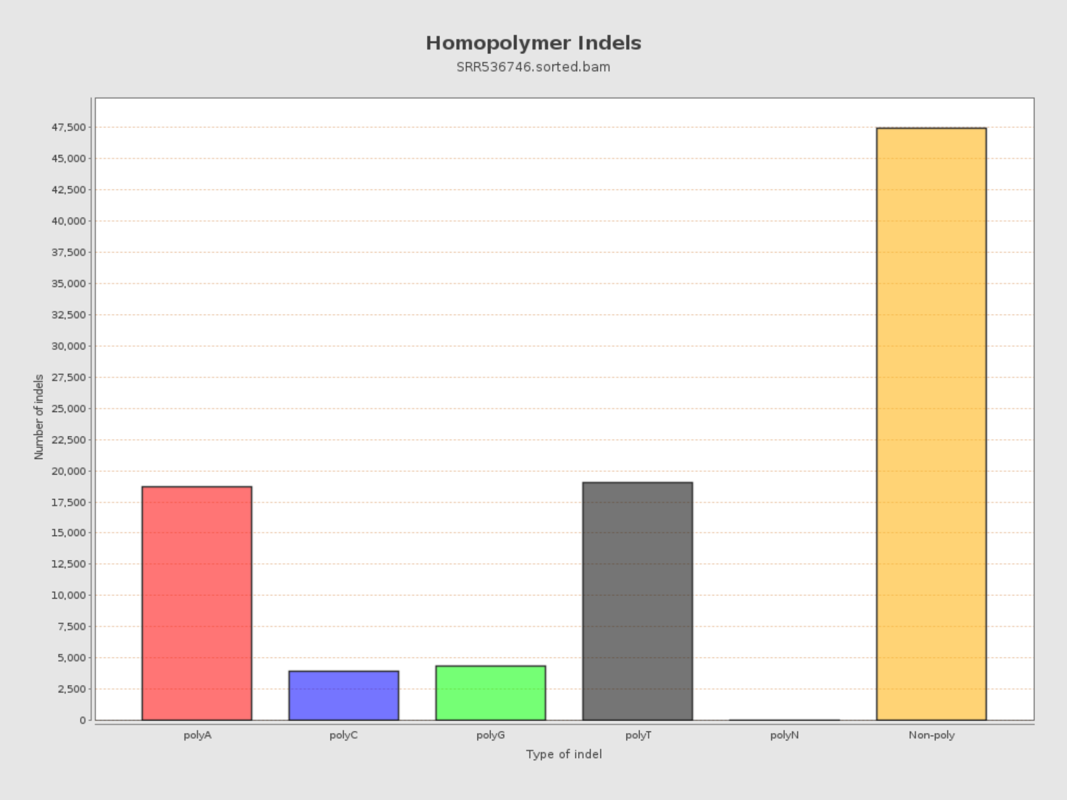
9. Results : Mapped Reads GC-content Distribution



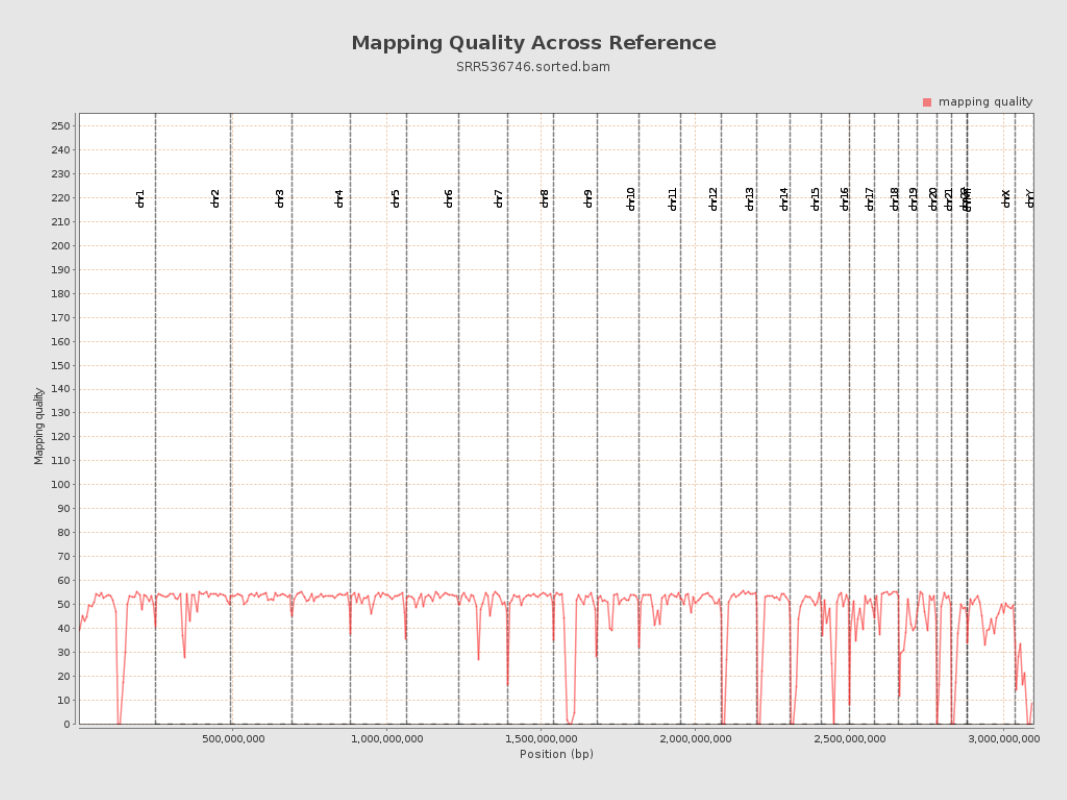
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram