Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 18:23:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536744.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_SRR536744 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536744.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 18:23:24 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536744.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,131,201
Mapped reads	17,959,377 / 81.15%
Unmapped reads	4,171,824 / 18.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	382 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	195,449 / 0.88%
Duplication rate	0.88%
Clipped reads	315,509 / 1.43%

2.2. ACGT Content

Number/percentage of A's	281,752,125 / 31.47%
Number/percentage of C's	165,405,782 / 18.48%
Number/percentage of T's	280,308,551 / 31.31%
Number/percentage of G's	167,716,939 / 18.74%
Number/percentage of N's	19,159 / 0%
GC Percentage	37.21%

2.3. Coverage

Mean	0.2892

Standard Deviation	2.2944

2.4. Mapping Quality

Mean Mapping Quality	47.53

2.5. Mismatches and indels

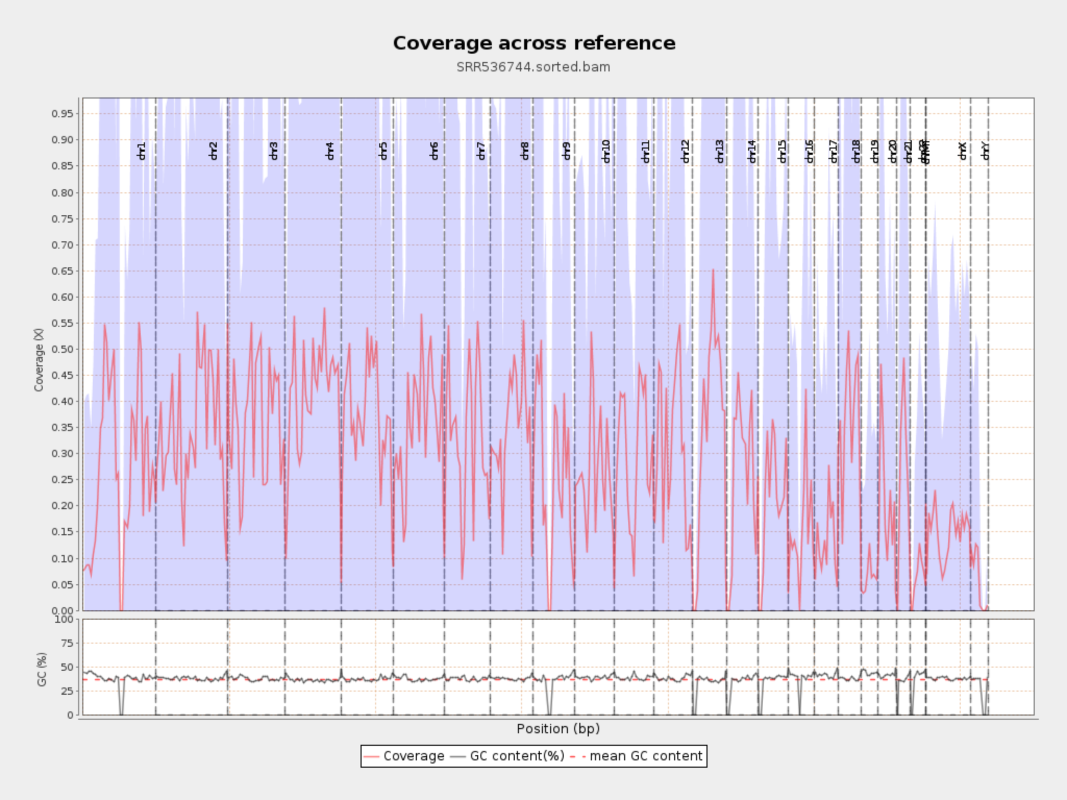
General error rate	0.35%
Mismatches	3,060,302
Insertions	62,332
Mapped reads with at least one insertion	0.35%
Deletions	46,500
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.24%

2.6. Chromosome stats

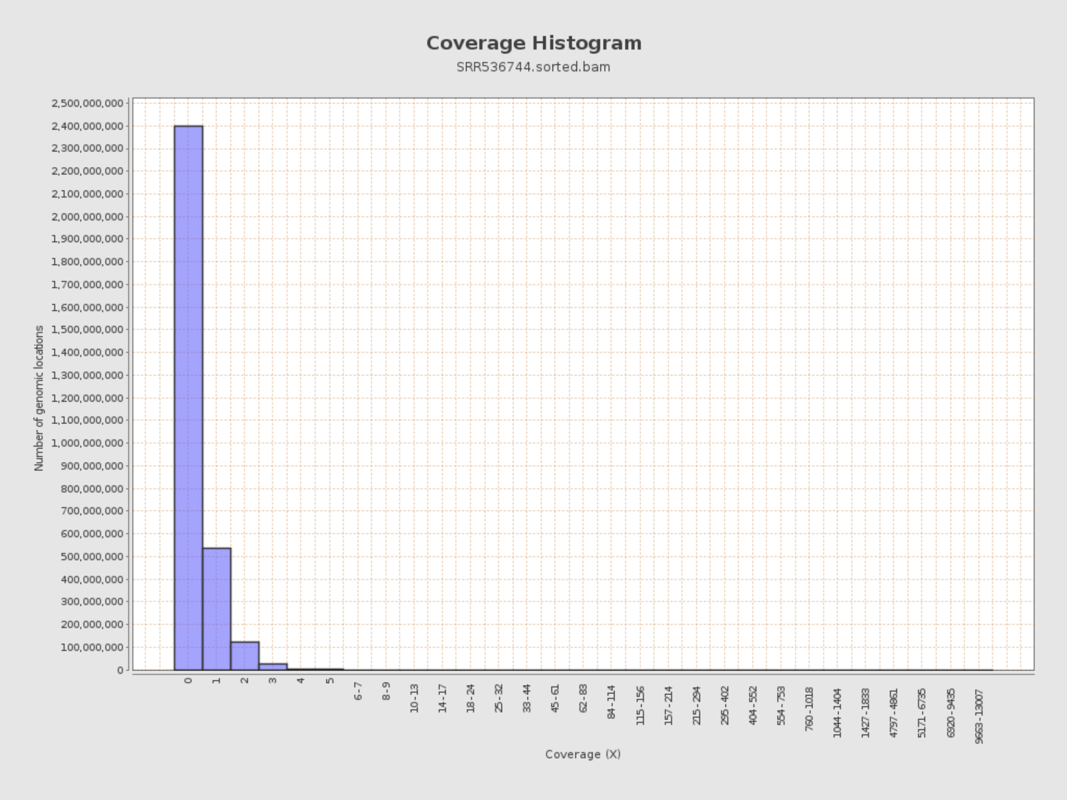
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	67084944	0.2691	0.6685
chr2	243199373	83982788	0.3453	0.6801
chr3	198022430	73519977	0.3713	0.6863
chr4	191154276	79406732	0.4154	0.9665
chr5	180915260	66926008	0.3699	0.6744
chr6	171115067	62064855	0.3627	9.3346
chr7	159138663	51697462	0.3249	0.6459

chr8	146364022	51544739	0.3522	0.6584
chr9	141213431	37143012	0.263	1.1793
chr10	135534747	36761393	0.2712	0.6712
chr11	135006516	40495767	0.3	0.6164
chr12	133851895	40661087	0.3038	0.6184
chr13	115169878	41182226	0.3576	0.6784
chr14	107349540	27904451	0.2599	0.5804
chr15	102531392	21741923	0.2121	0.5191
chr16	90354753	13923049	0.1541	0.4369
chr17	81195210	10898081	0.1342	0.4107
chr18	78077248	29043903	0.372	0.9637
chr19	59128983	3881802	0.0656	0.2746
chr20	63025520	13603823	0.2158	0.5259
chr21	48129895	12015320	0.2496	0.5854
chr22	51304566	3328399	0.0649	0.2758
chrMT	16571	3382	0.2041	0.4816
chrX	155270560	23143367	0.1491	0.4066
chrY	59373566	3321838	0.0559	0.2589

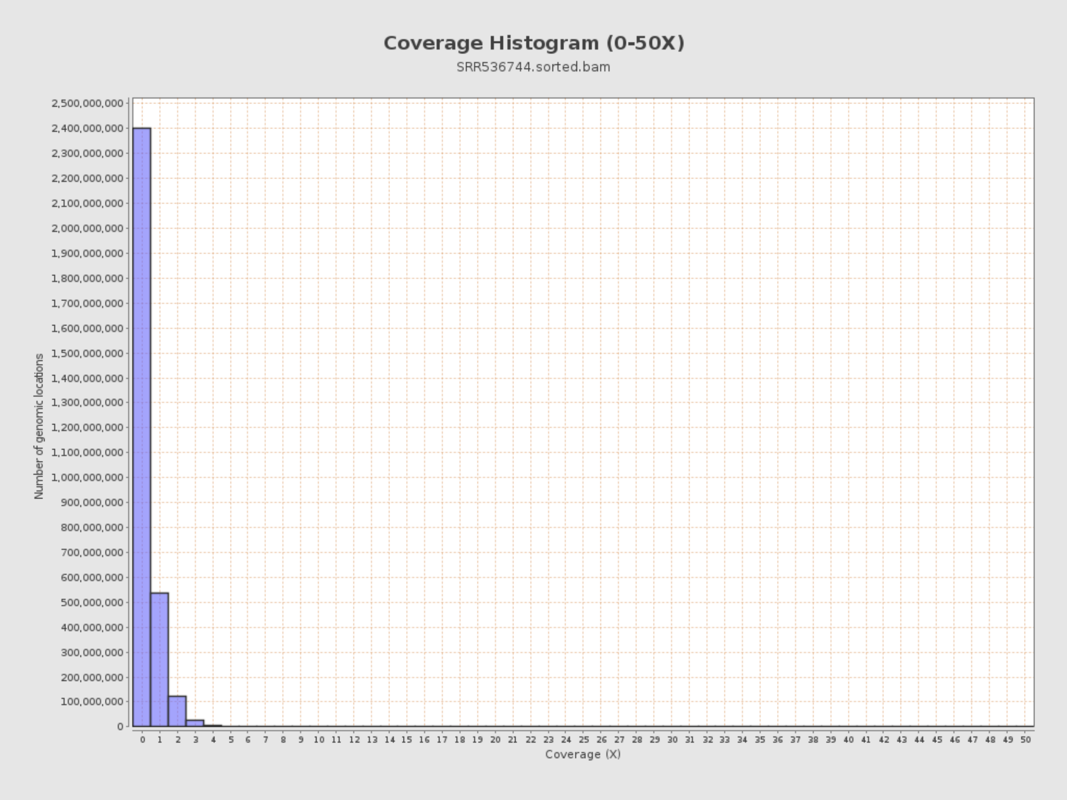
3. Results : Coverage across reference



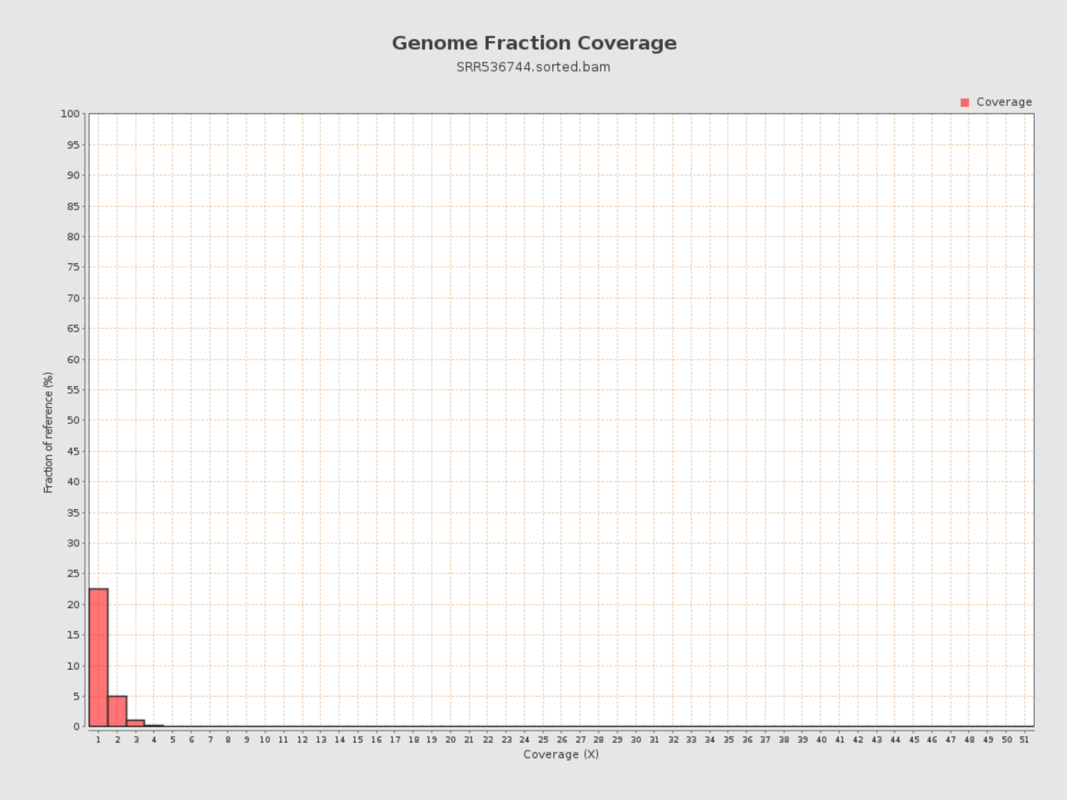
4. Results : Coverage Histogram



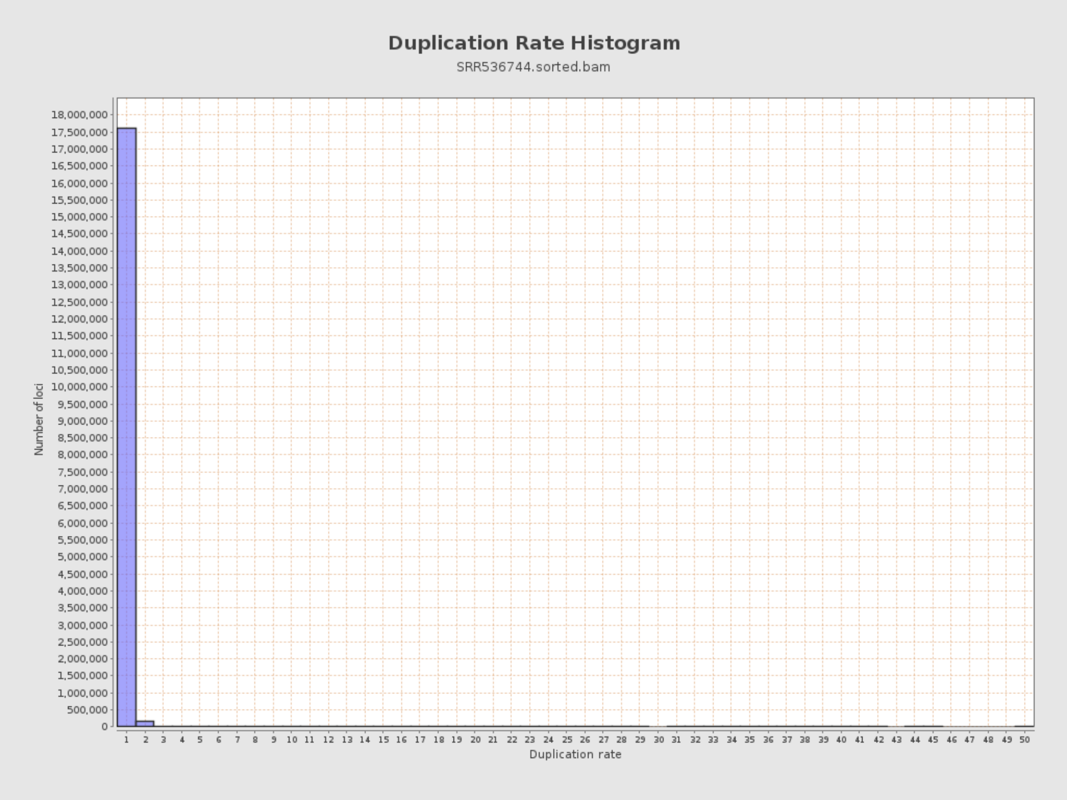
5. Results : Coverage Histogram (0-50X)



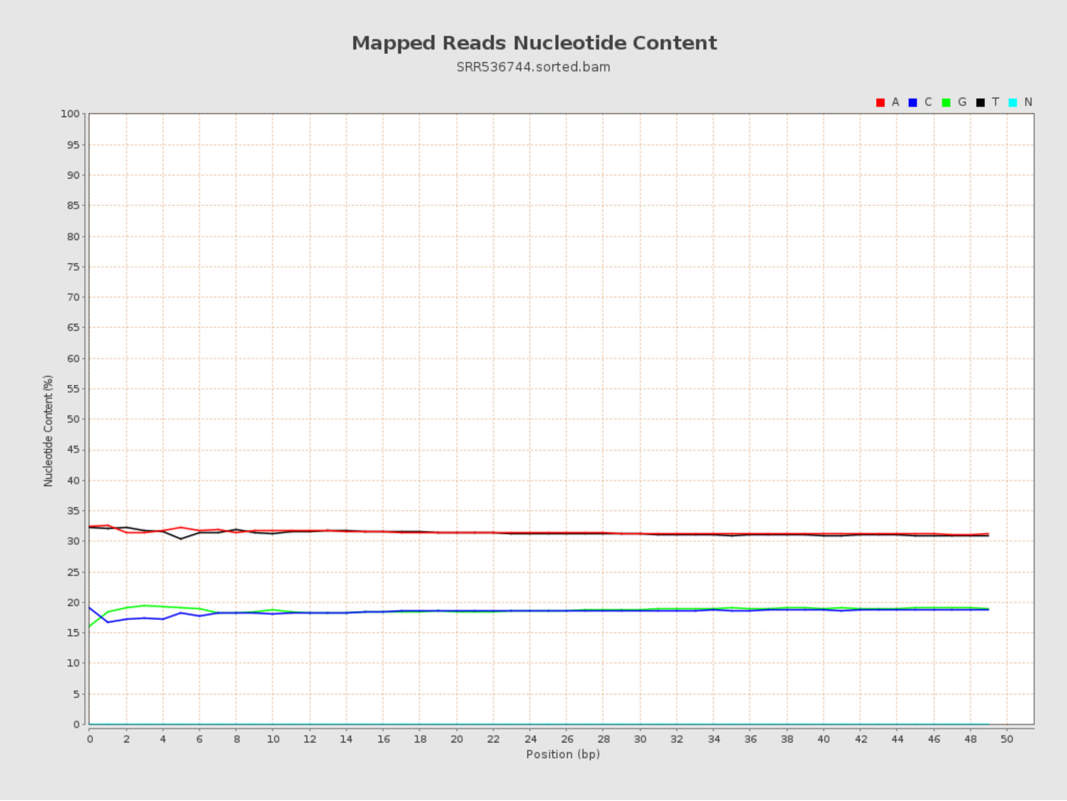
6. Results : Genome Fraction Coverage



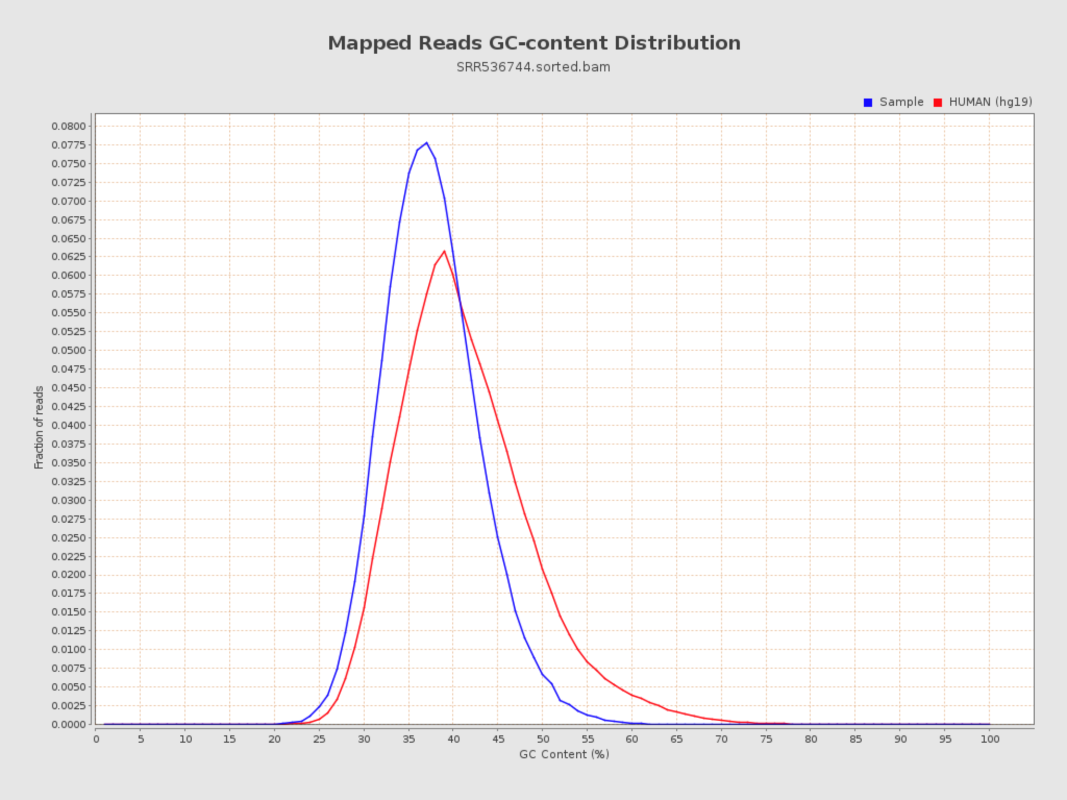
7. Results : Duplication Rate Histogram



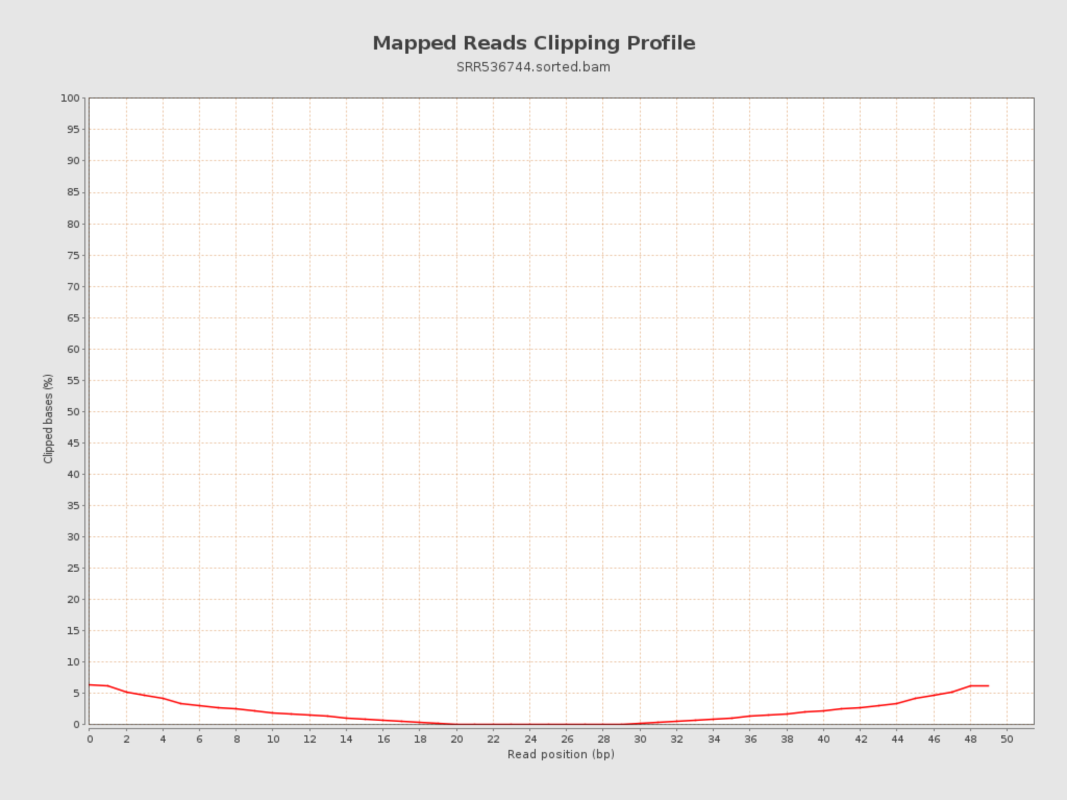
8. Results : Mapped Reads Nucleotide Content



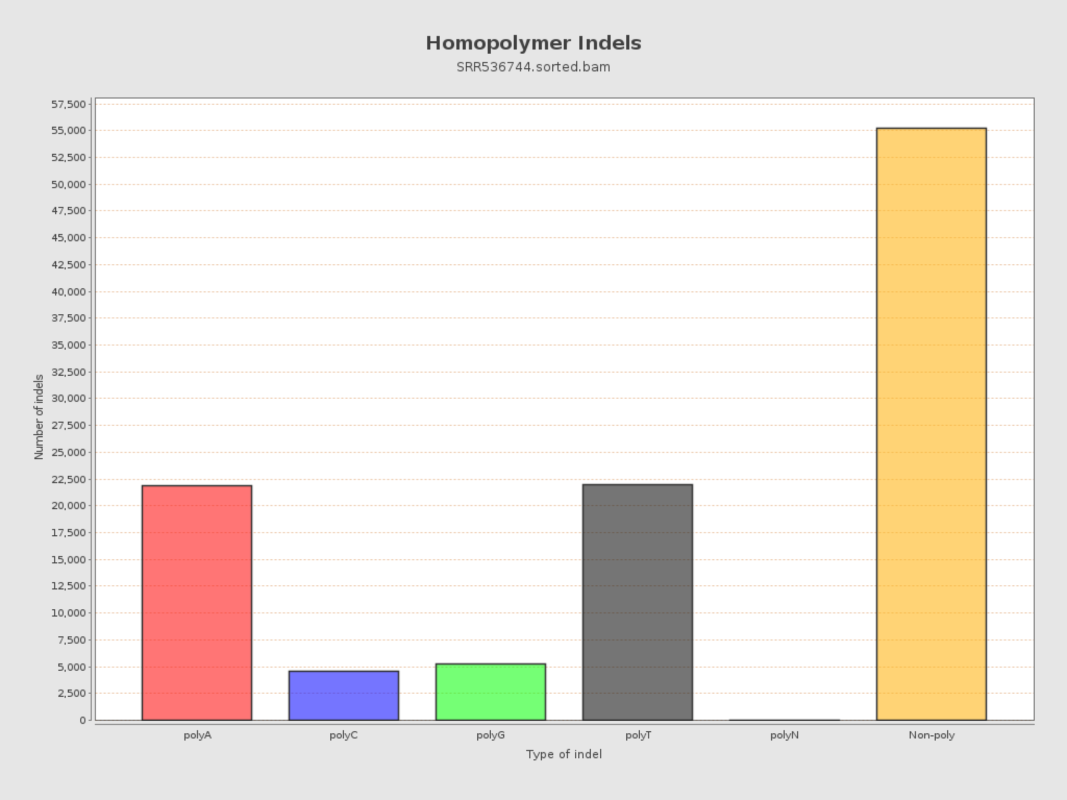
9. Results : Mapped Reads GC-content Distribution



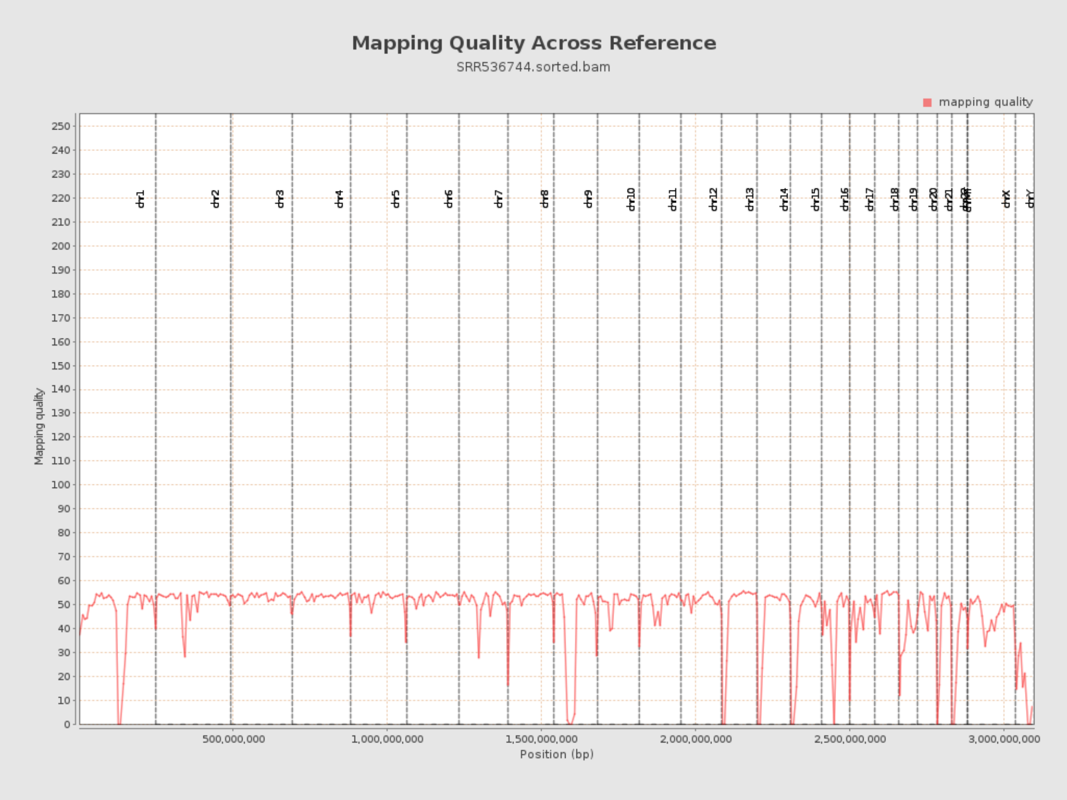
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram