Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 12:38:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536748.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_SRR536748 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536748.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 12:38:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536748.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,409,789
Mapped reads	14,140,490 / 81.22%
Unmapped reads	3,269,299 / 18.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	337 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	87,817 / 0.5%
Duplication rate	0.61%
Clipped reads	249,571 / 1.43%

2.2. ACGT Content

Number/percentage of A's	222,229,280 / 31.52%
Number/percentage of C's	129,701,496 / 18.4%
Number/percentage of T's	220,027,414 / 31.21%
Number/percentage of G's	132,972,487 / 18.86%
Number/percentage of N's	14,921 / 0%
GC Percentage	37.26%

2.3. Coverage

Mean	0.2277

Standard Deviation	0.5287

2.4. Mapping Quality

Mean Mapping Quality	47.32

2.5. Mismatches and indels

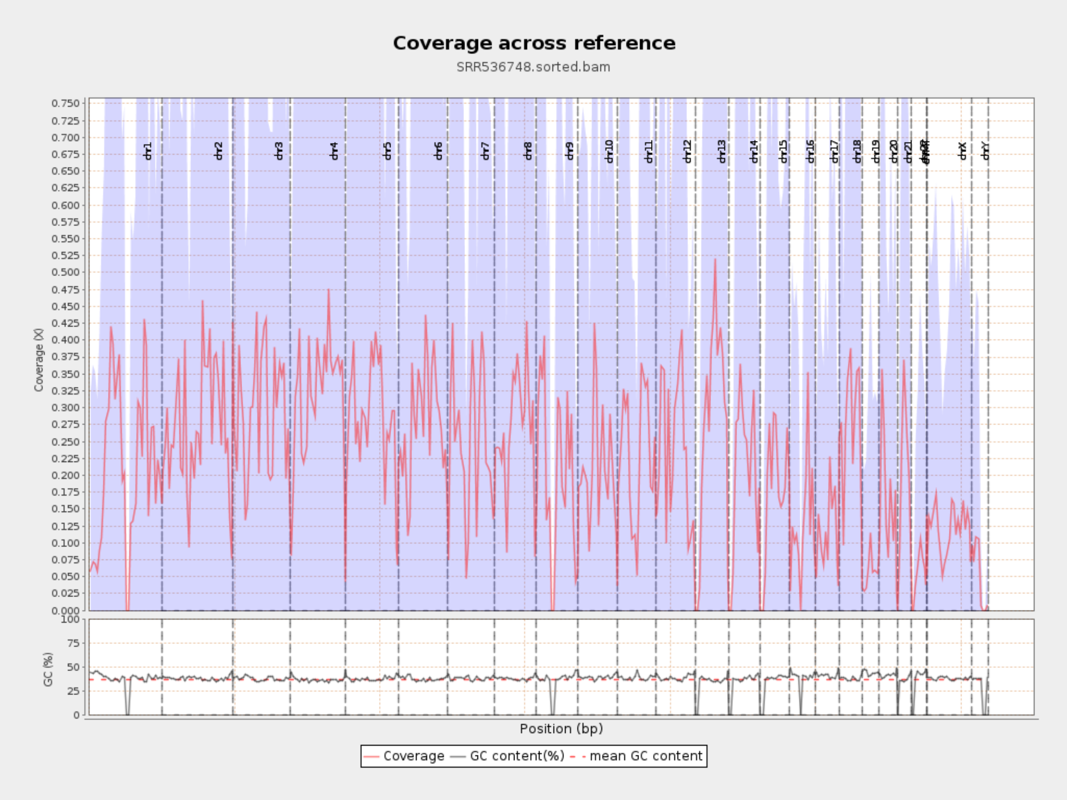
General error rate	0.36%
Mismatches	2,500,215
Insertions	46,488
Mapped reads with at least one insertion	0.33%
Deletions	36,756
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.91%

2.6. Chromosome stats

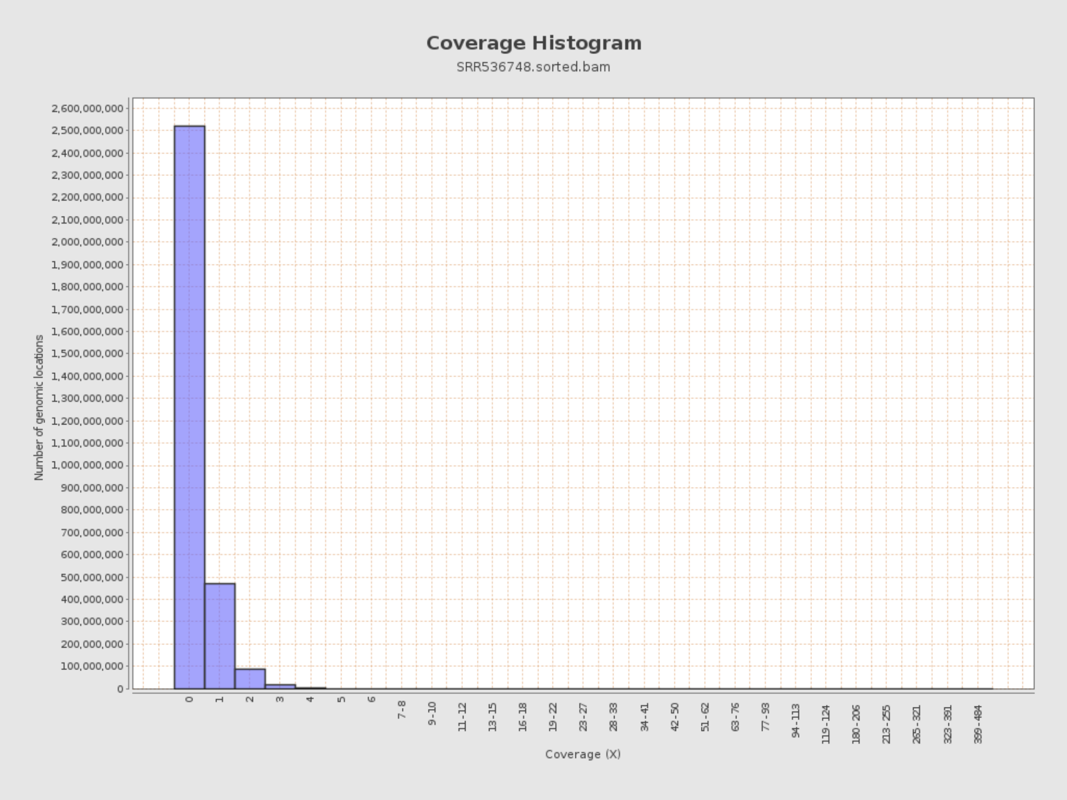
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	52851046	0.212	0.5104
chr2	243199373	66300173	0.2726	0.5659
chr3	198022430	58927804	0.2976	0.5919
chr4	191154276	62032452	0.3245	0.6154
chr5	180915260	52147991	0.2882	0.5803
chr6	171115067	47418545	0.2771	0.6257
chr7	159138663	40379059	0.2537	0.5521

chr8	146364022	40082678	0.2739	0.5667
chr9	141213431	29671606	0.2101	0.5084
chr10	135534747	29420002	0.2171	0.5022
chr11	135006516	31366786	0.2323	0.5268
chr12	133851895	31593782	0.236	0.5317
chr13	115169878	32649542	0.2835	0.5882
chr14	107349540	21903720	0.204	0.4984
chr15	102531392	17849191	0.1741	0.4725
chr16	90354753	11658250	0.129	0.3931
chr17	81195210	9211140	0.1134	0.3702
chr18	78077248	21839953	0.2797	0.5796
chr19	59128983	3435729	0.0581	0.2562
chr20	63025520	10874179	0.1725	0.4565
chr21	48129895	9327867	0.1938	0.4994
chr22	51304566	2753034	0.0537	0.2474
chrMT	16571	2336	0.141	0.3803
chrX	155270560	18492358	0.1191	0.3589
chrY	59373566	2817265	0.0474	0.2349

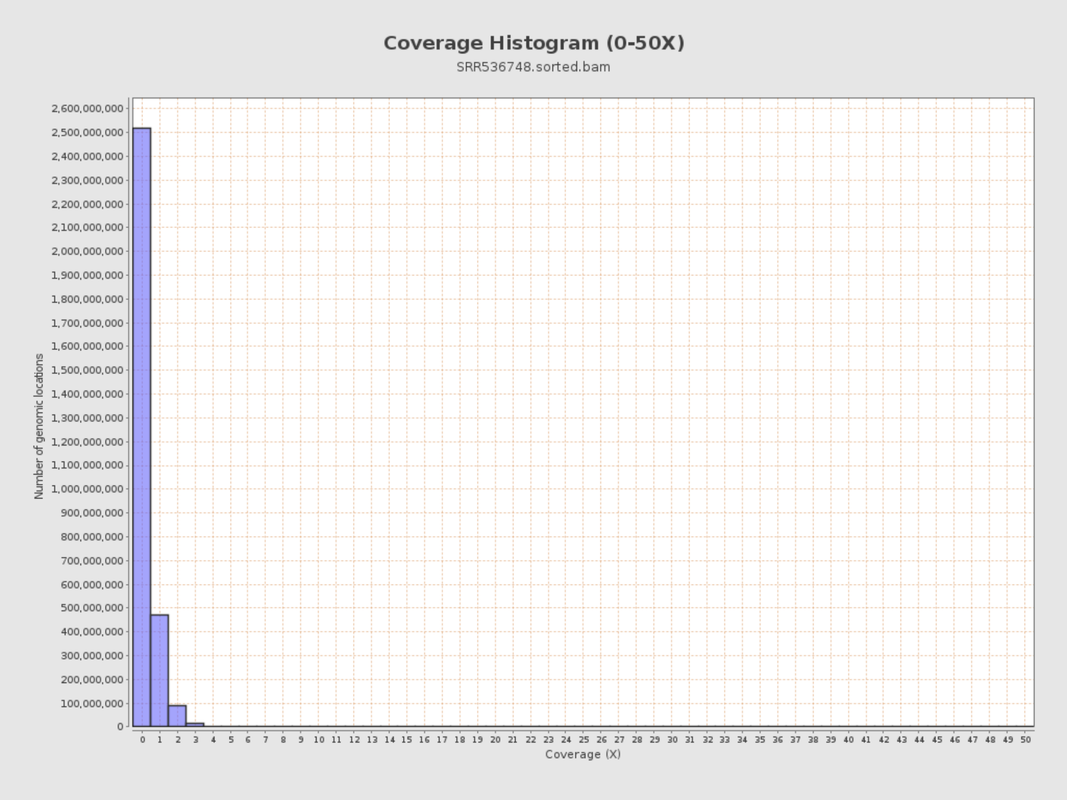
3. Results : Coverage across reference



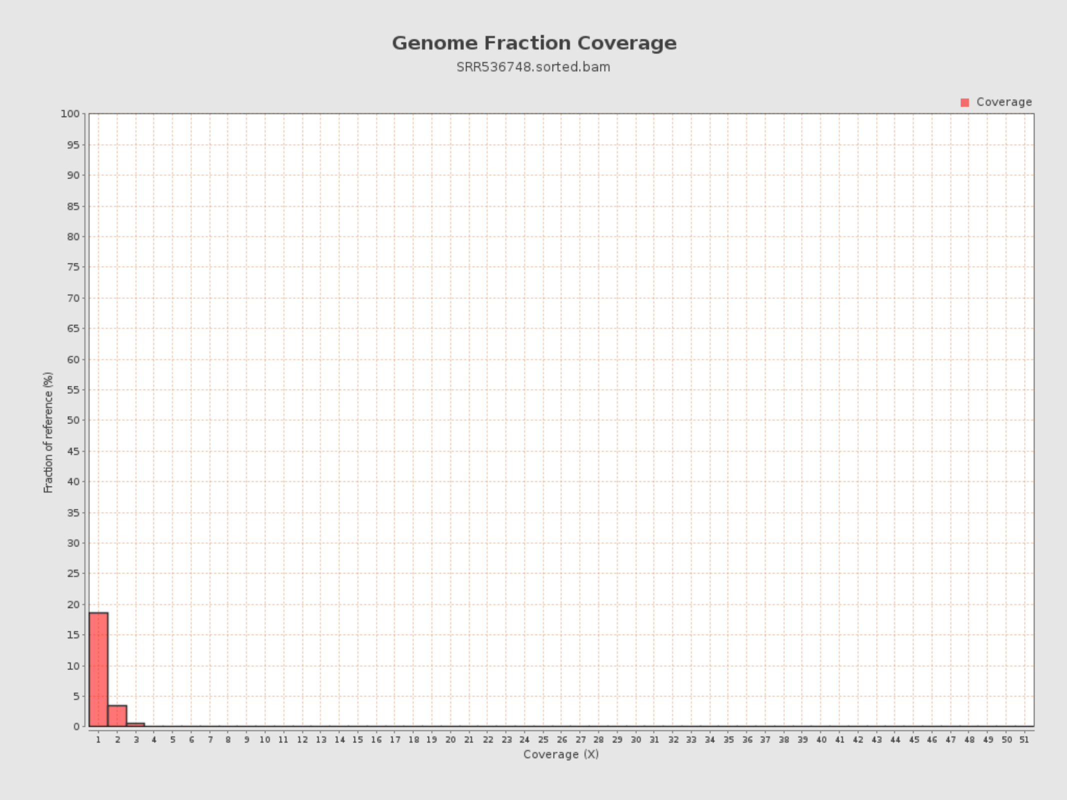
4. Results : Coverage Histogram



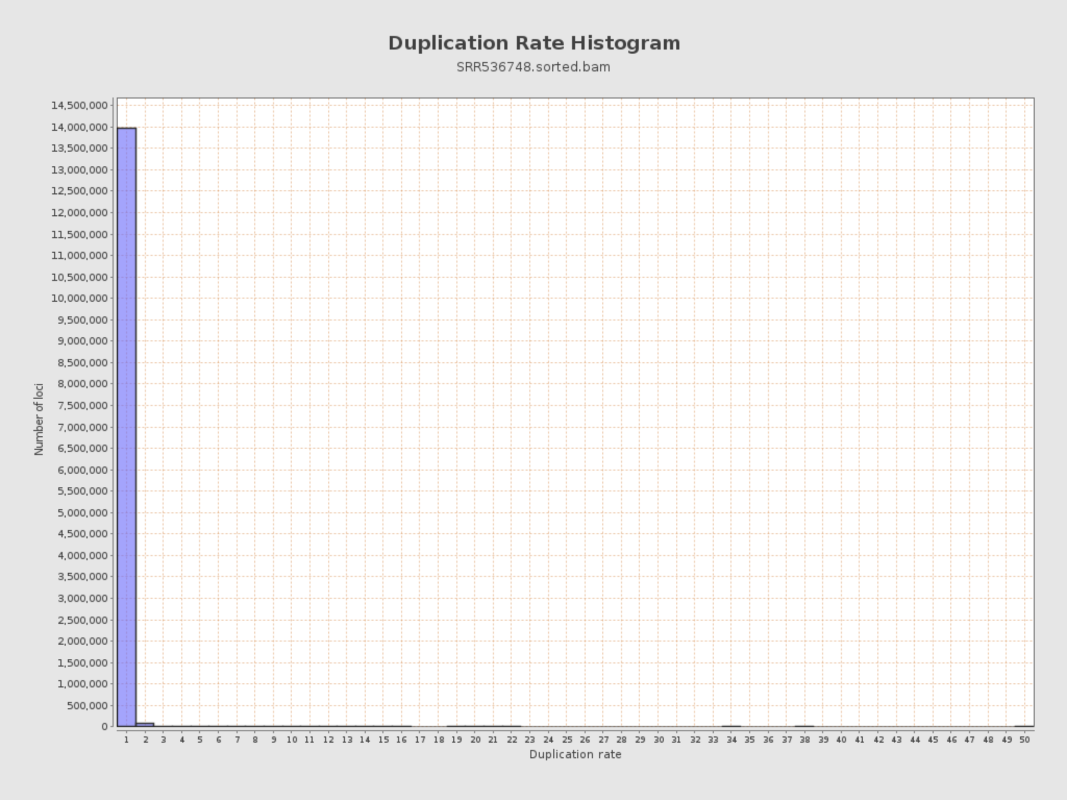
5. Results : Coverage Histogram (0-50X)



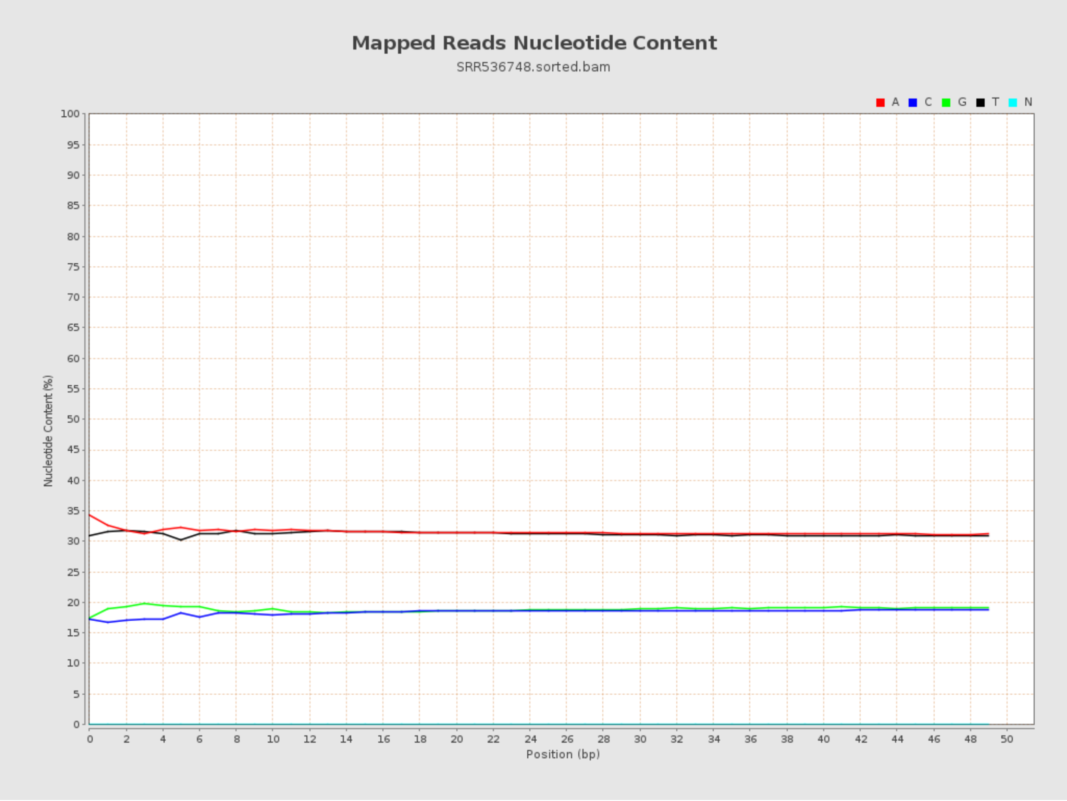
6. Results : Genome Fraction Coverage



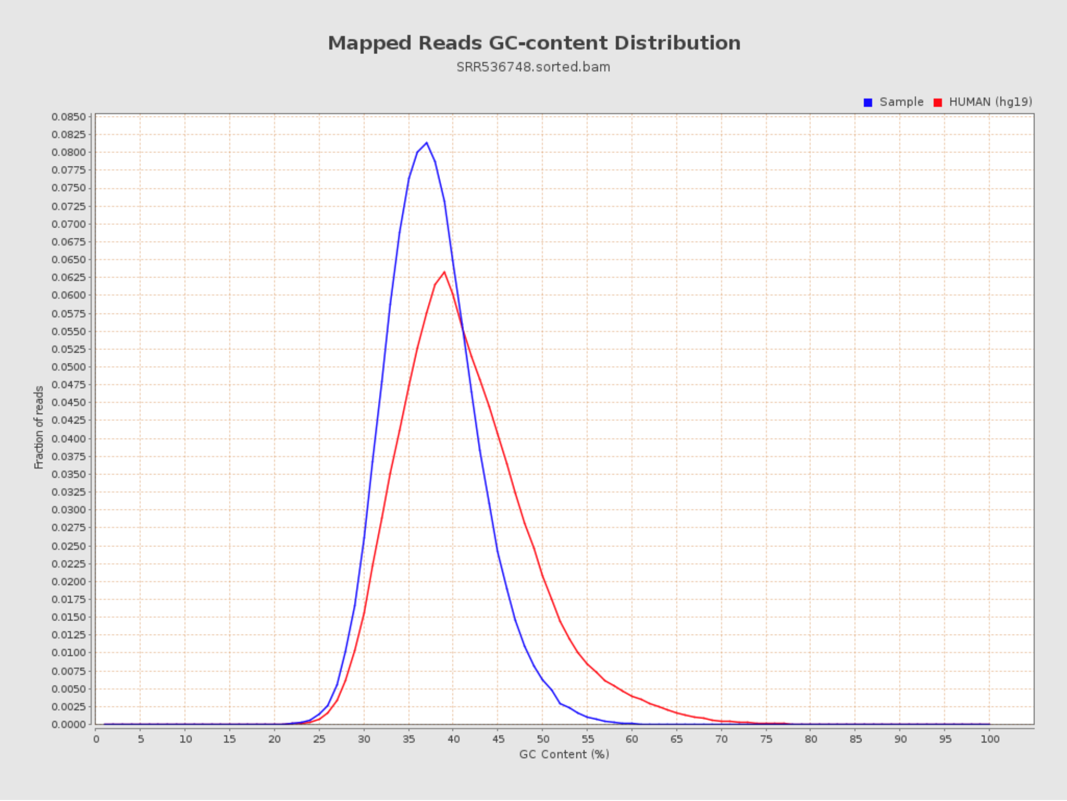
7. Results : Duplication Rate Histogram



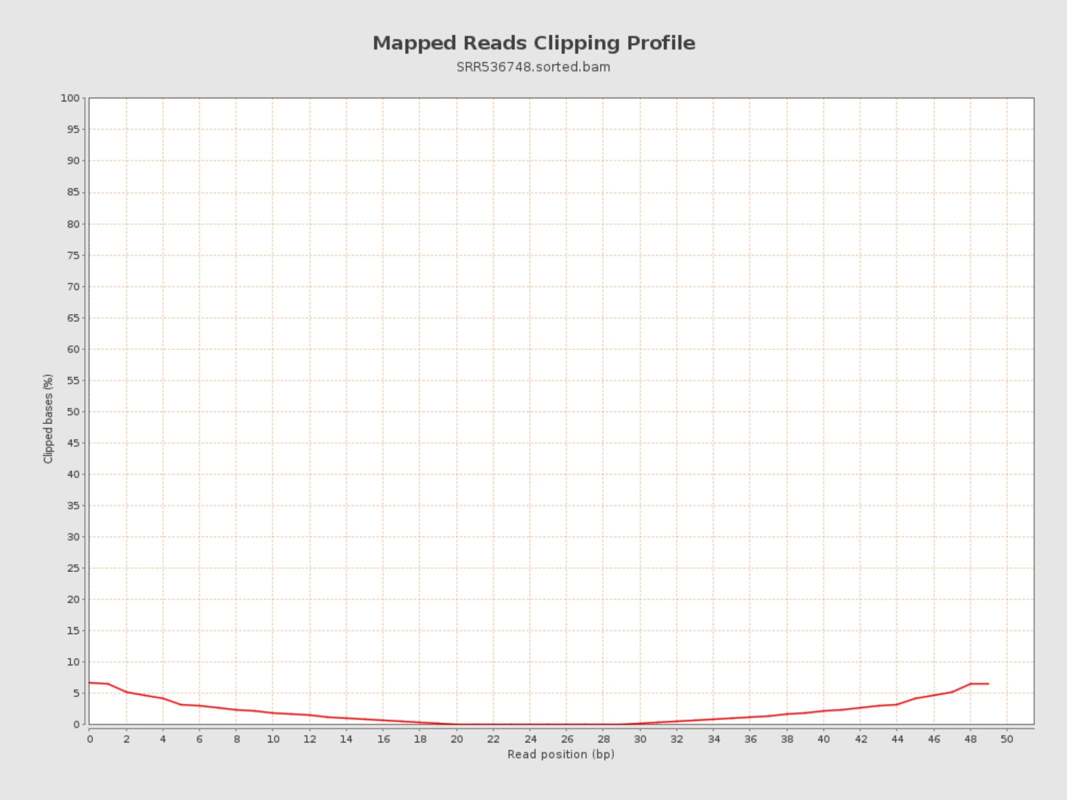
8. Results : Mapped Reads Nucleotide Content



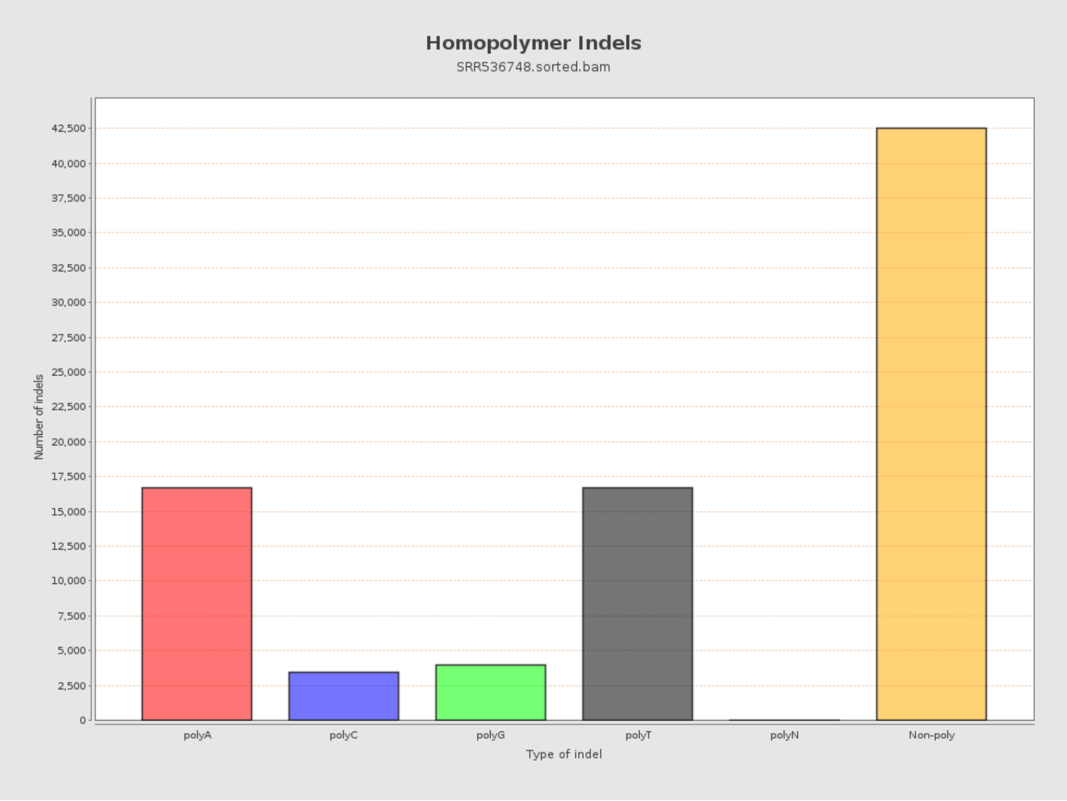
9. Results : Mapped Reads GC-content Distribution



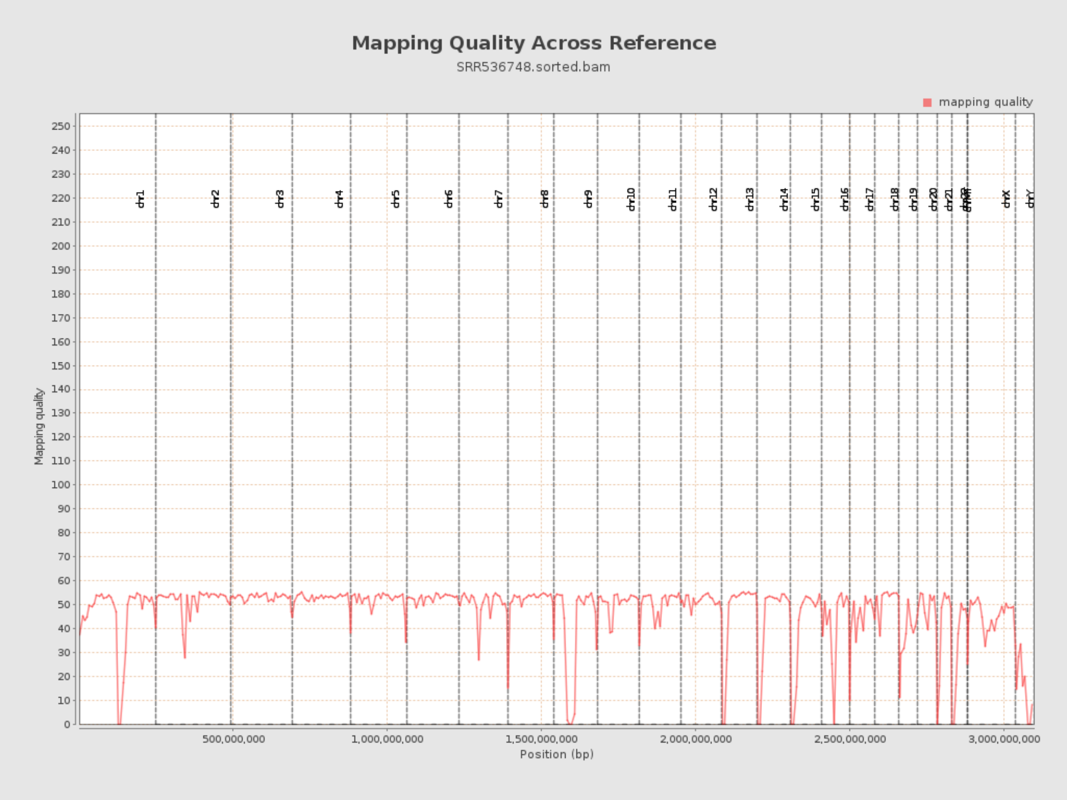
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram