Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 17:43:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536742.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_SRR536742 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536742.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 17:43:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536742.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,958,304
Mapped reads	15,416,657 / 81.32%
Unmapped reads	3,541,647 / 18.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	393 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	111,292 / 0.59%
Duplication rate	0.68%
Clipped reads	270,739 / 1.43%

2.2. ACGT Content

Number/percentage of A's	242,000,349 / 31.49%
Number/percentage of C's	141,653,266 / 18.43%
Number/percentage of T's	241,123,697 / 31.38%
Number/percentage of G's	143,690,617 / 18.7%
Number/percentage of N's	16,268 / 0%
GC Percentage	37.13%

2.3. Coverage

Mean	0.2483

Standard Deviation	0.7271

2.4. Mapping Quality

Mean Mapping Quality	47.39

2.5. Mismatches and indels

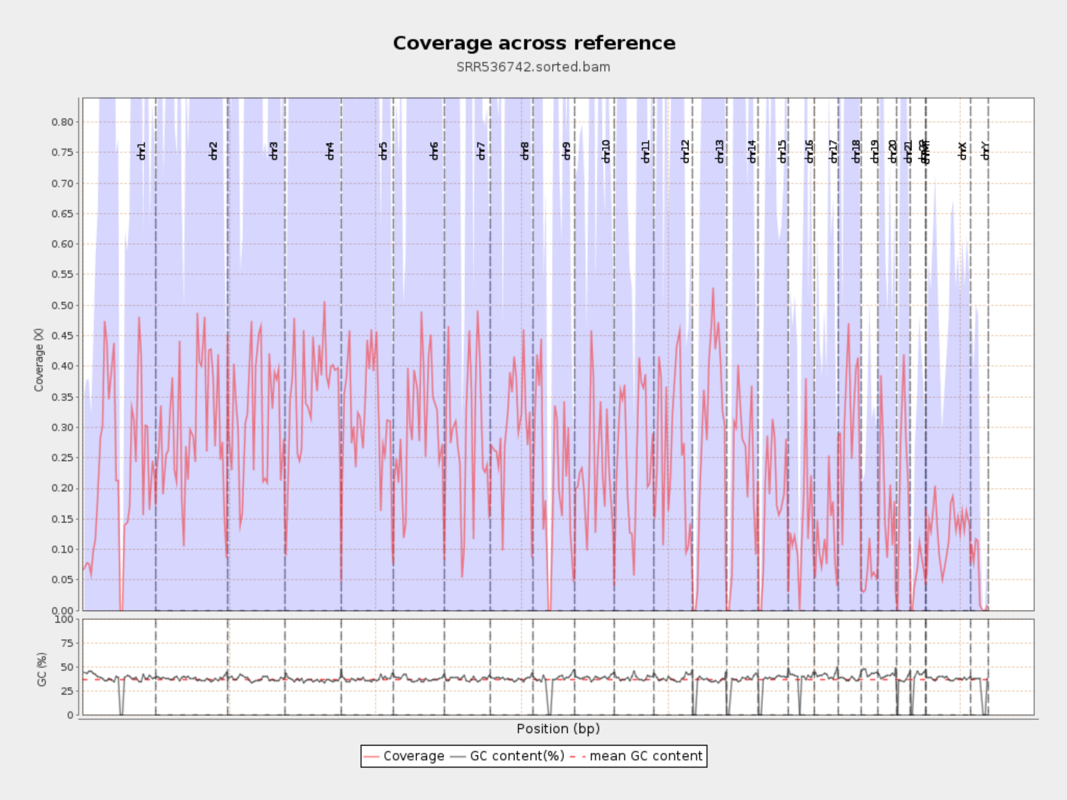
General error rate	0.35%
Mismatches	2,654,453
Insertions	53,645
Mapped reads with at least one insertion	0.35%
Deletions	39,761
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.01%

2.6. Chromosome stats

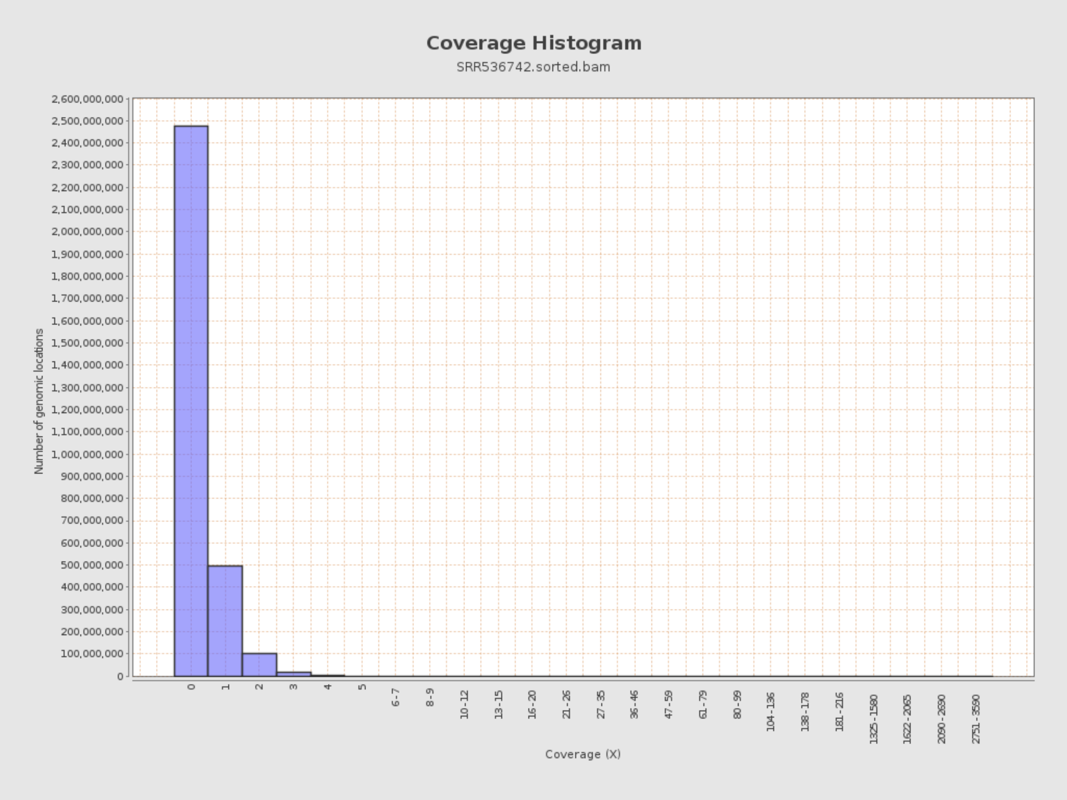
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	57521952	0.2308	0.5372
chr2	243199373	72558529	0.2983	0.5977
chr3	198022430	63223394	0.3193	0.6158
chr4	191154276	67967822	0.3556	0.6487
chr5	180915260	57016842	0.3152	0.612
chr6	171115067	52629319	0.3076	2.0968
chr7	159138663	44839591	0.2818	0.589

chr8	146364022	43615657	0.298	0.5961
chr9	141213431	31676615	0.2243	0.5303
chr10	135534747	31815769	0.2347	0.5257
chr11	135006516	35117991	0.2601	0.563
chr12	133851895	34884761	0.2606	0.5746
chr13	115169878	34712310	0.3014	0.6099
chr14	107349540	23900592	0.2226	0.5256
chr15	102531392	18530230	0.1807	0.4698
chr16	90354753	12298015	0.1361	0.4052
chr17	81195210	9626581	0.1186	0.3803
chr18	78077248	24760903	0.3171	0.6142
chr19	59128983	3507985	0.0593	0.2596
chr20	63025520	11550361	0.1833	0.4749
chr21	48129895	10328622	0.2146	0.5293
chr22	51304566	2995822	0.0584	0.2597
chrMT	16571	2777	0.1676	0.4208
chrX	155270560	20375182	0.1312	0.3783
chrY	59373566	3093782	0.0521	0.249

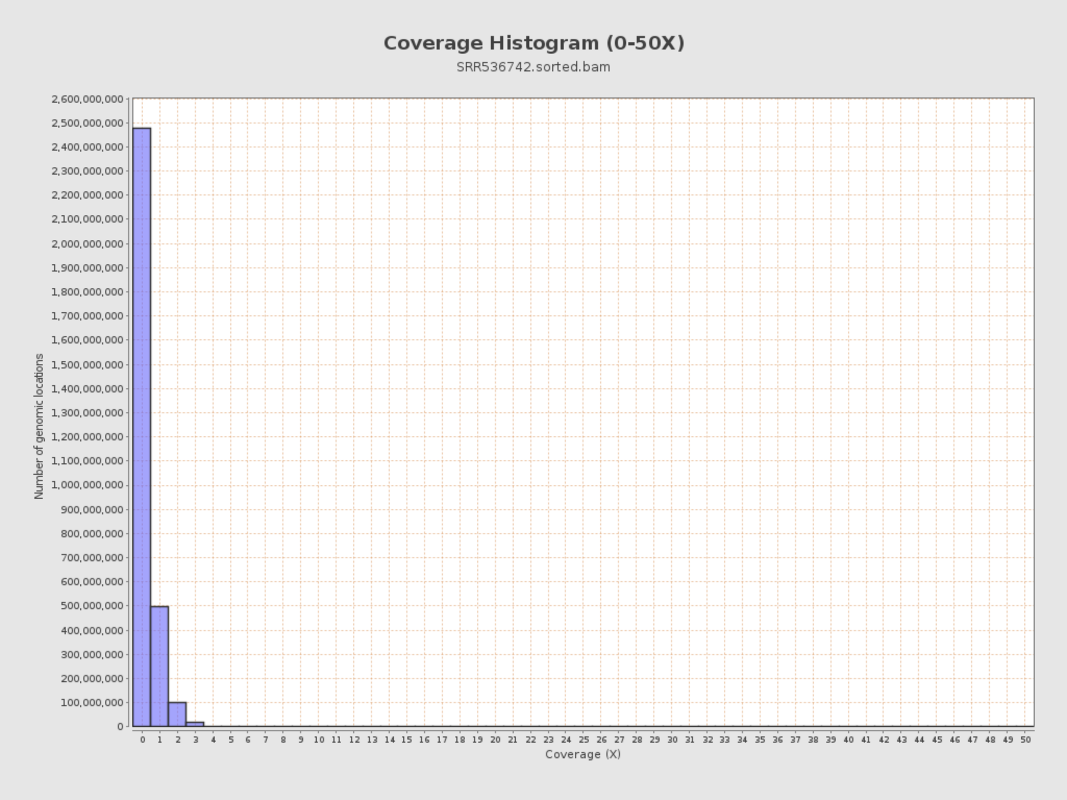
3. Results : Coverage across reference



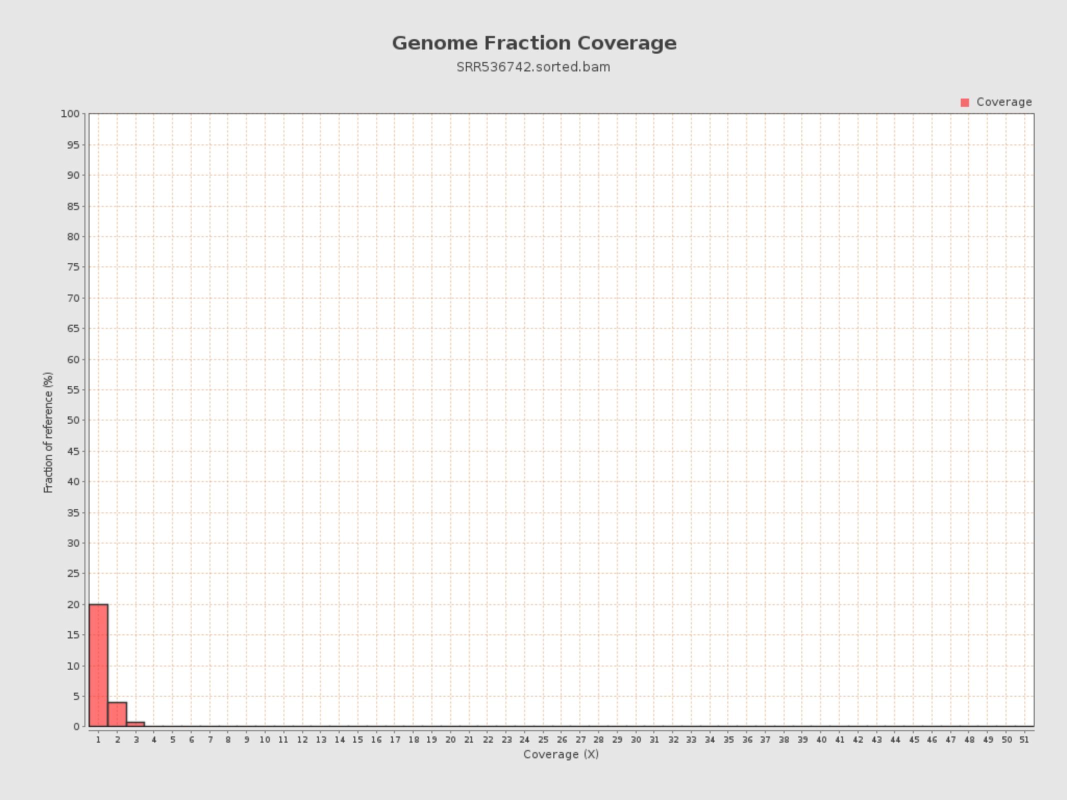
4. Results : Coverage Histogram



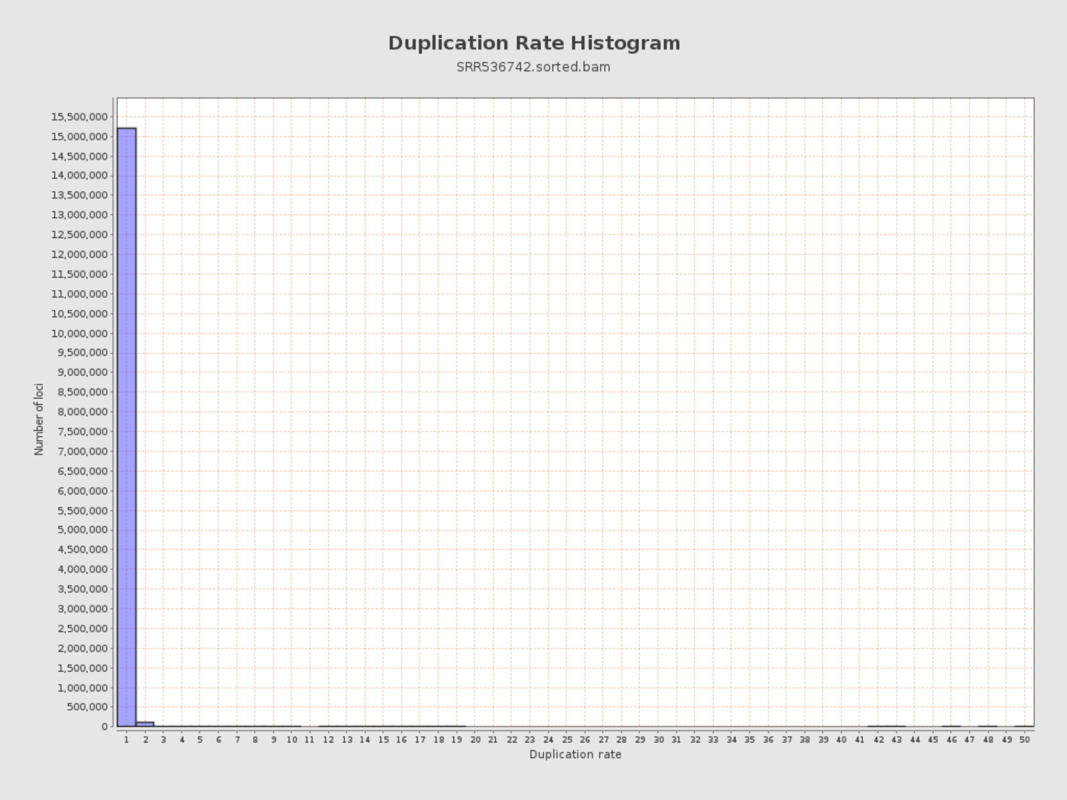
5. Results : Coverage Histogram (0-50X)



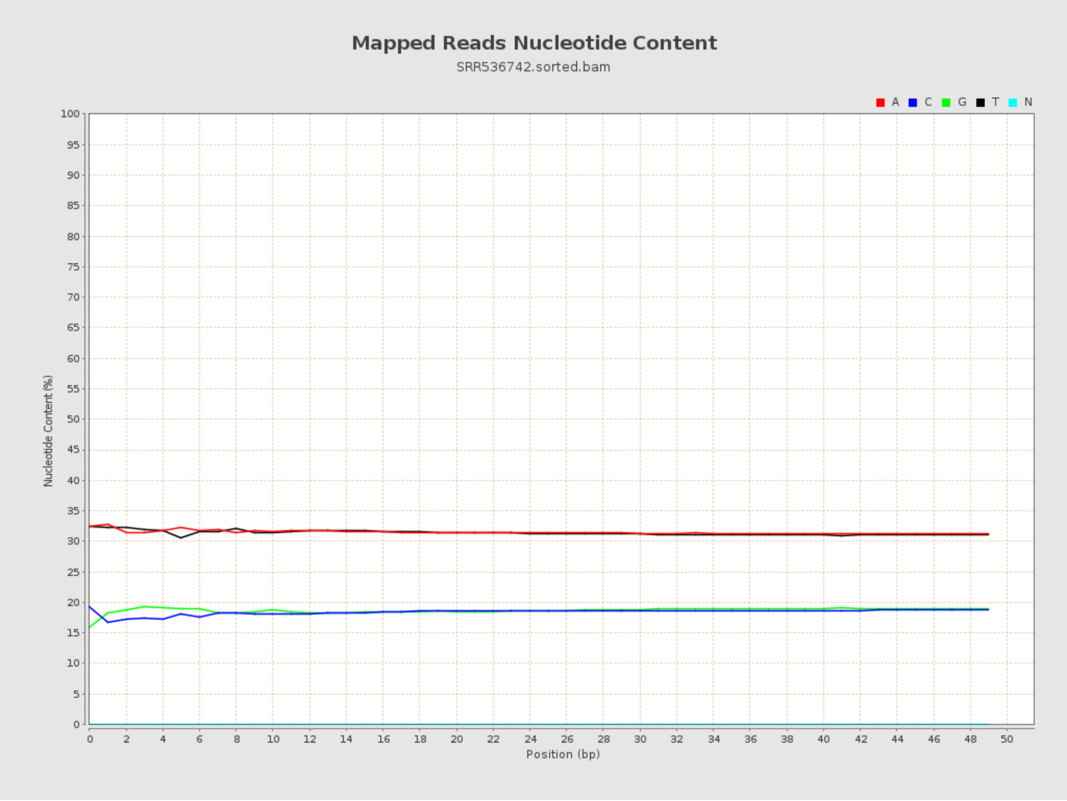
6. Results : Genome Fraction Coverage



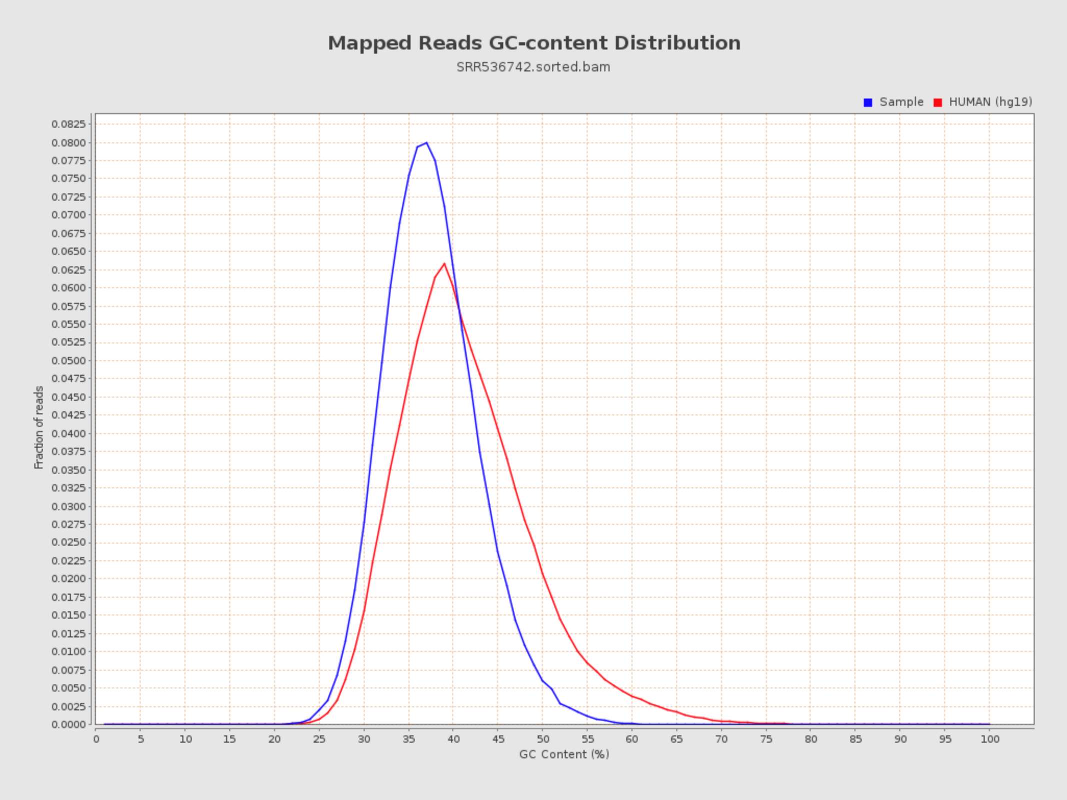
7. Results : Duplication Rate Histogram



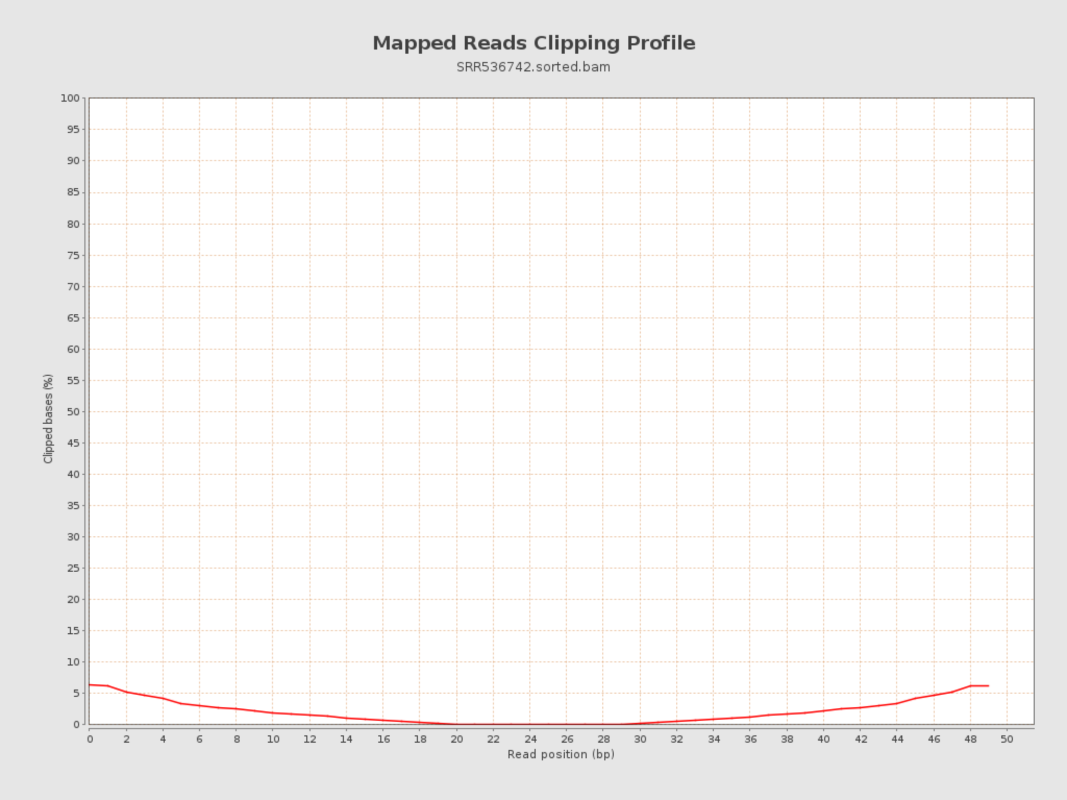
8. Results : Mapped Reads Nucleotide Content



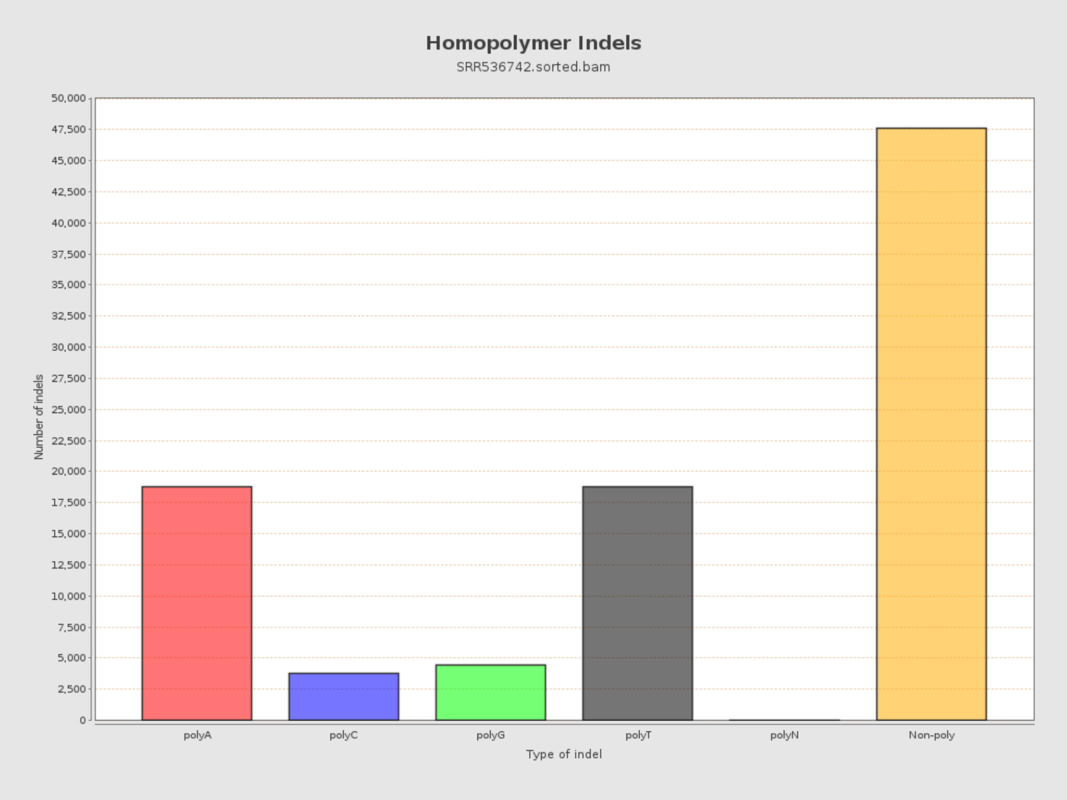
9. Results : Mapped Reads GC-content Distribution



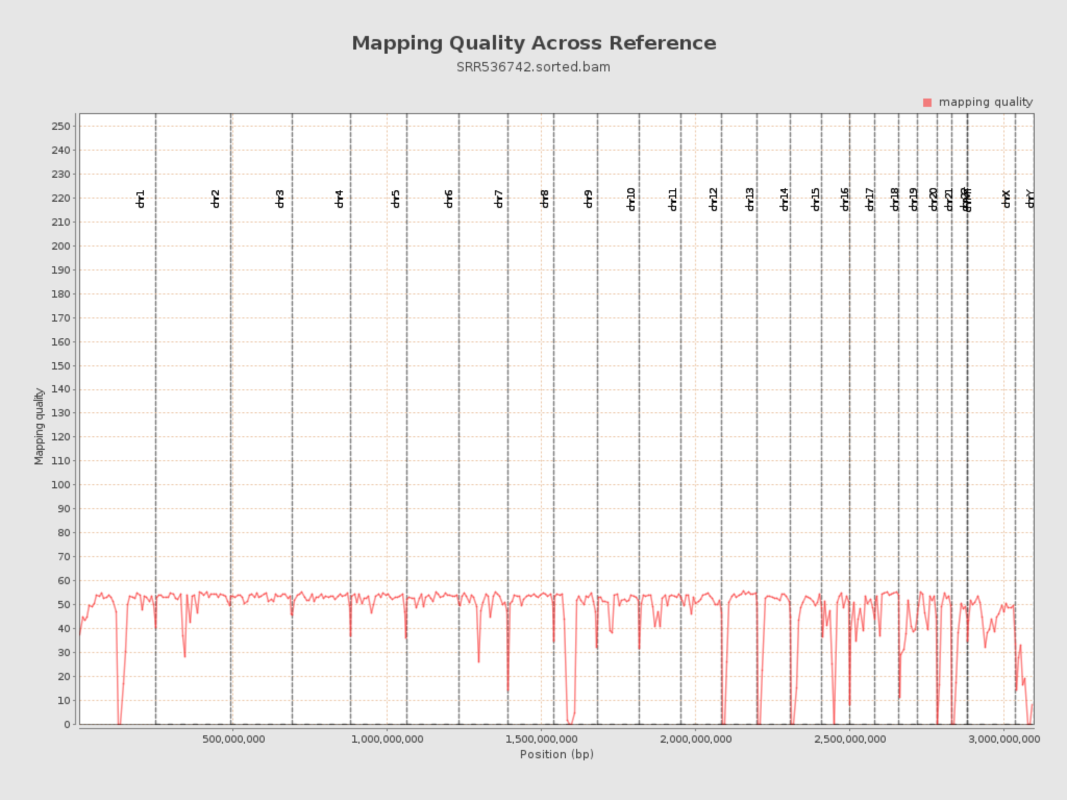
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram