Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 22:32:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536756.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_SRR536756 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536756.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 22:32:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536756.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,543,897
Mapped reads	19,814,361 / 96.45%
Unmapped reads	729,536 / 3.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	448 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	165,426 / 0.81%
Duplication rate	0.83%
Clipped reads	317,548 / 1.55%

2.2. ACGT Content

Number/percentage of A's	309,918,615 / 31.37%
Number/percentage of C's	182,954,879 / 18.52%
Number/percentage of T's	309,192,333 / 31.29%
Number/percentage of G's	185,565,313 / 18.78%
Number/percentage of N's	417,944 / 0.04%
GC Percentage	37.3%

2.3. Coverage

Mean	0.3192

Standard Deviation	0.6245

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Mismatches and indels

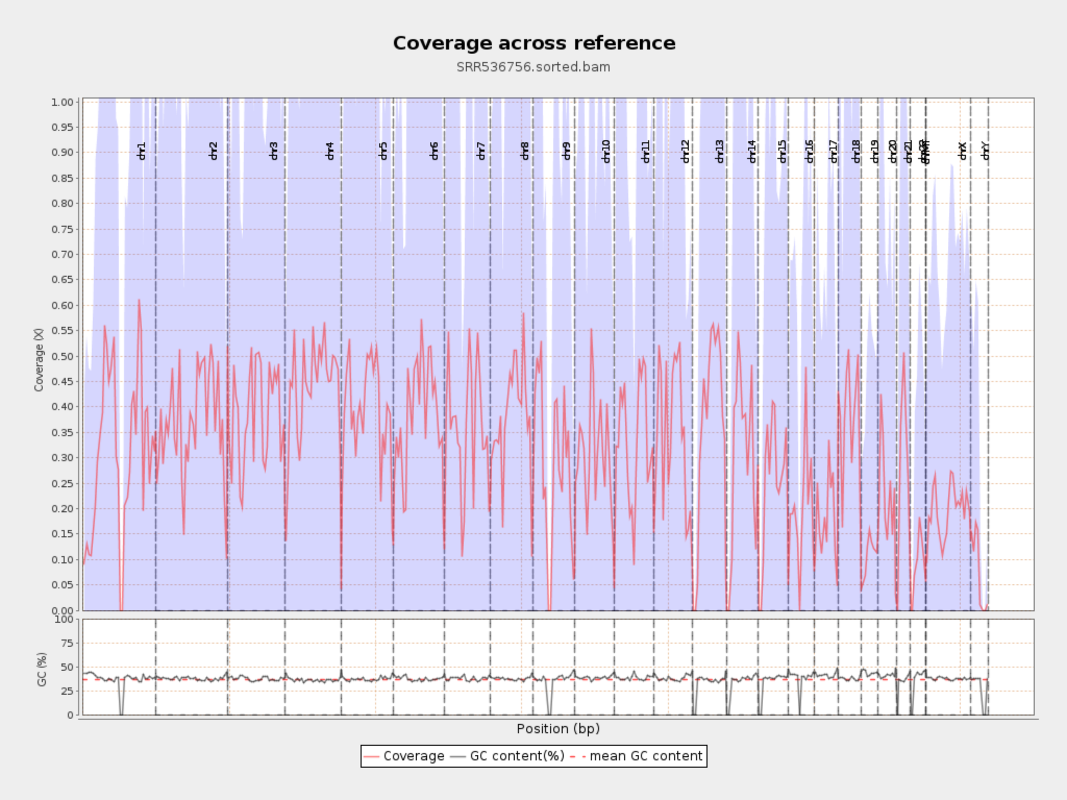
General error rate	0.36%
Mismatches	3,472,447
Insertions	55,333
Mapped reads with at least one insertion	0.28%
Deletions	51,701
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.35%

2.6. Chromosome stats

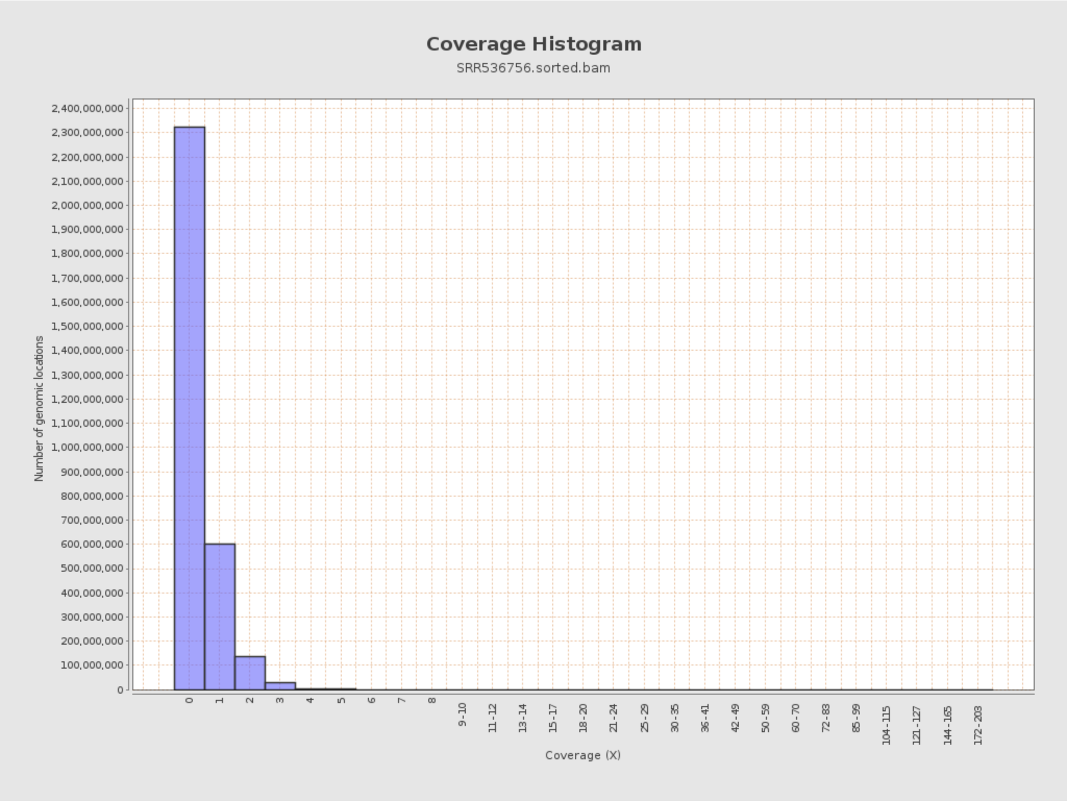
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	77178085	0.3096	0.6257
chr2	243199373	89899284	0.3697	0.6595
chr3	198022430	76781241	0.3877	0.6723
chr4	191154276	83942720	0.4391	0.7138
chr5	180915260	70261204	0.3884	0.6721
chr6	171115067	66883434	0.3909	0.6776
chr7	159138663	56462291	0.3548	0.6554

chr8	146364022	55946239	0.3822	0.6704
chr9	141213431	40989966	0.2903	0.6004
chr10	135534747	42478501	0.3134	0.6086
chr11	135006516	44567030	0.3301	0.6357
chr12	133851895	46133407	0.3447	0.6463
chr13	115169878	42255644	0.3669	0.6721
chr14	107349540	32410760	0.3019	0.6172
chr15	102531392	25647373	0.2501	0.5595
chr16	90354753	17788253	0.1969	0.4918
chr17	81195210	14899407	0.1835	0.477
chr18	78077248	29740622	0.3809	0.6708
chr19	59128983	6449733	0.1091	0.3567
chr20	63025520	14609840	0.2318	0.5338
chr21	48129895	13102204	0.2722	0.6025
chr22	51304566	4806265	0.0937	0.3378
chrMT	16571	1819	0.1098	0.3463
chrX	155270560	30463548	0.1962	0.4645
chrY	59373566	4435915	0.0747	0.3036

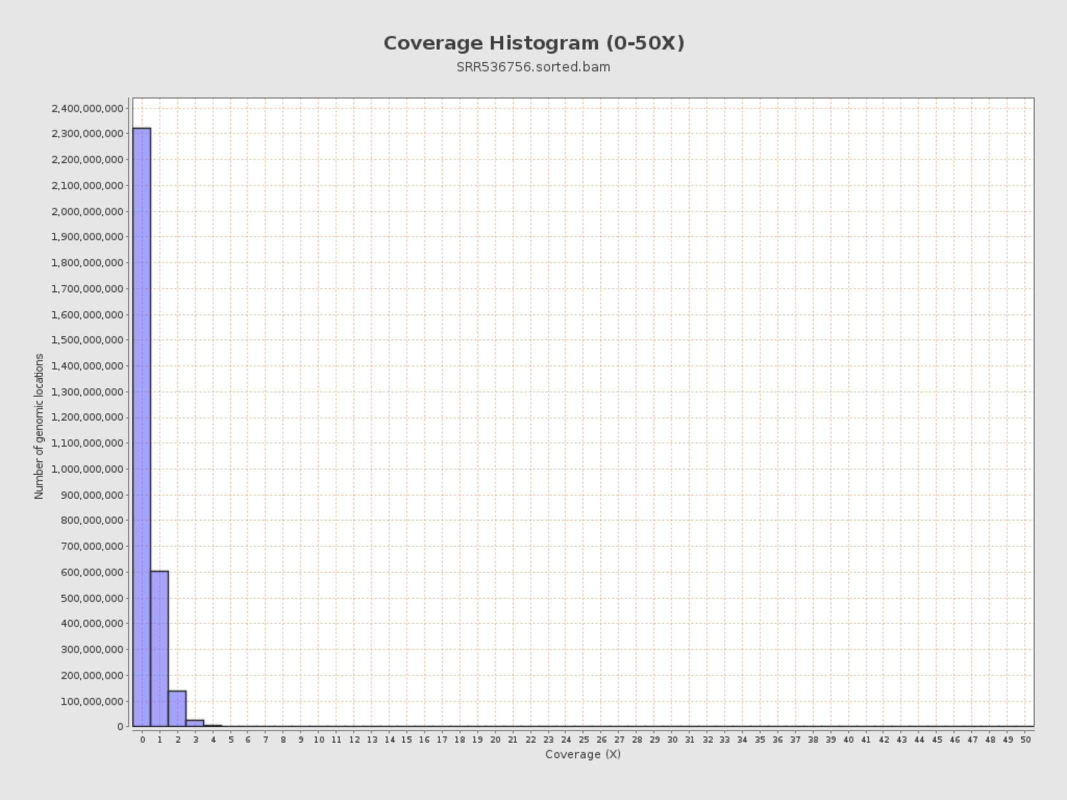
3. Results : Coverage across reference



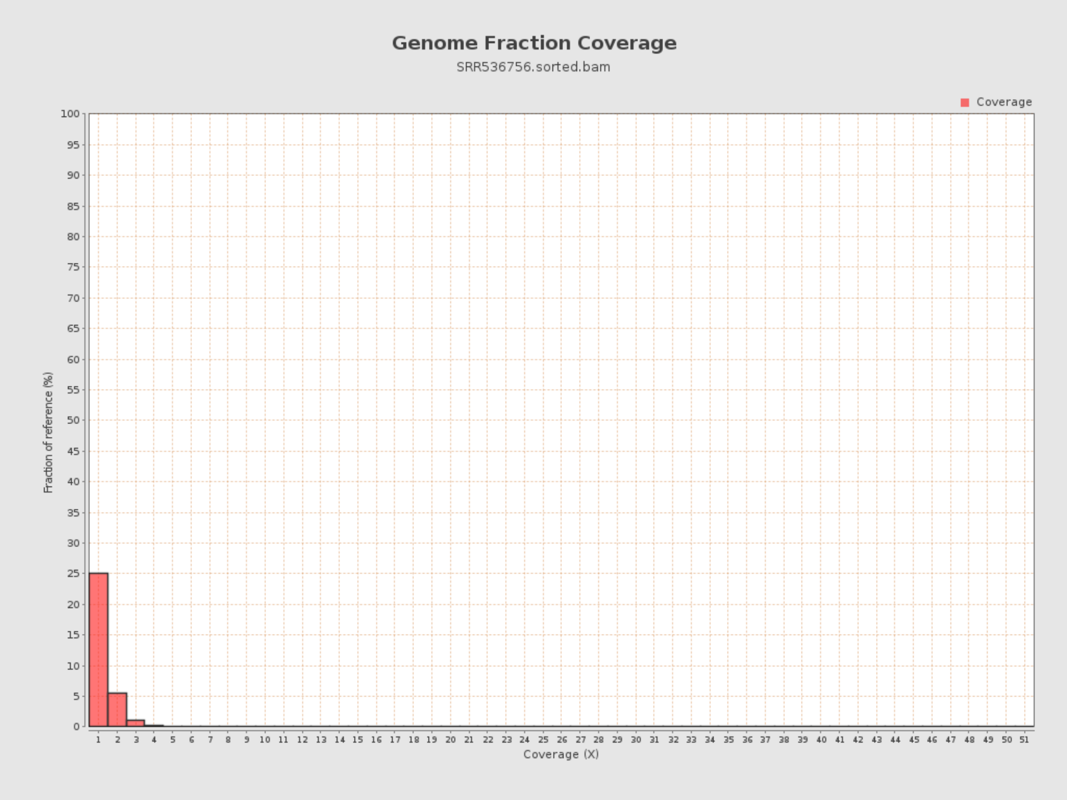
4. Results : Coverage Histogram



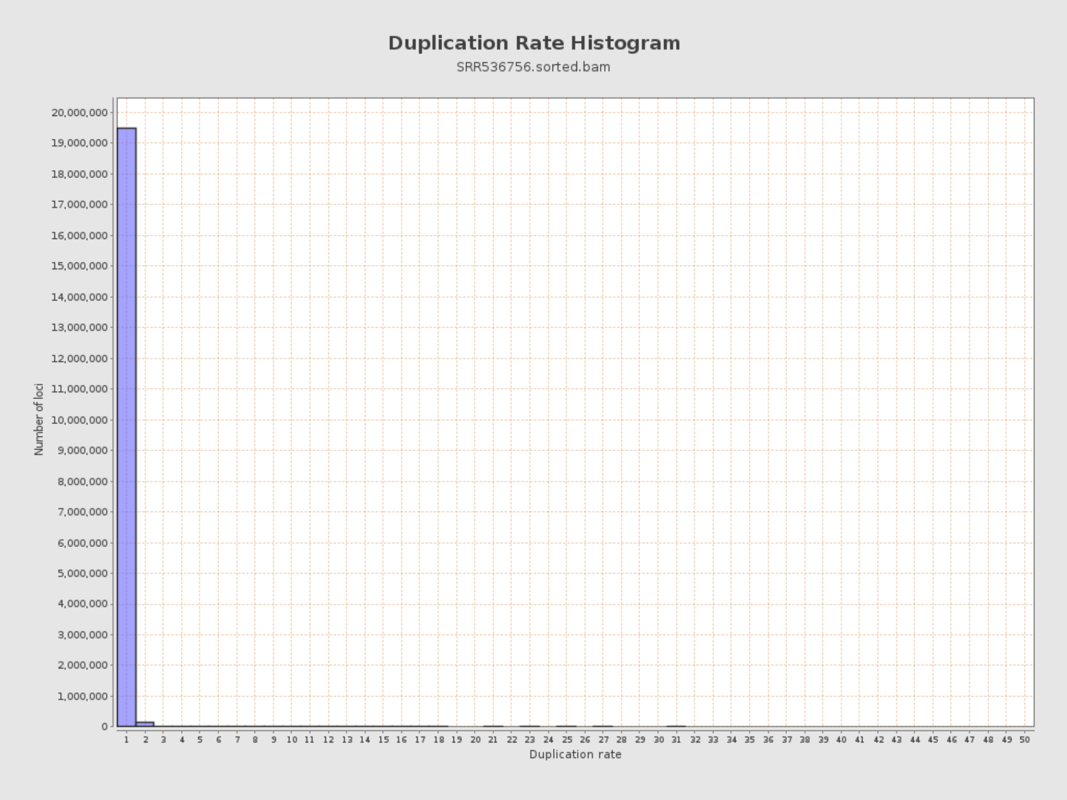
5. Results : Coverage Histogram (0-50X)



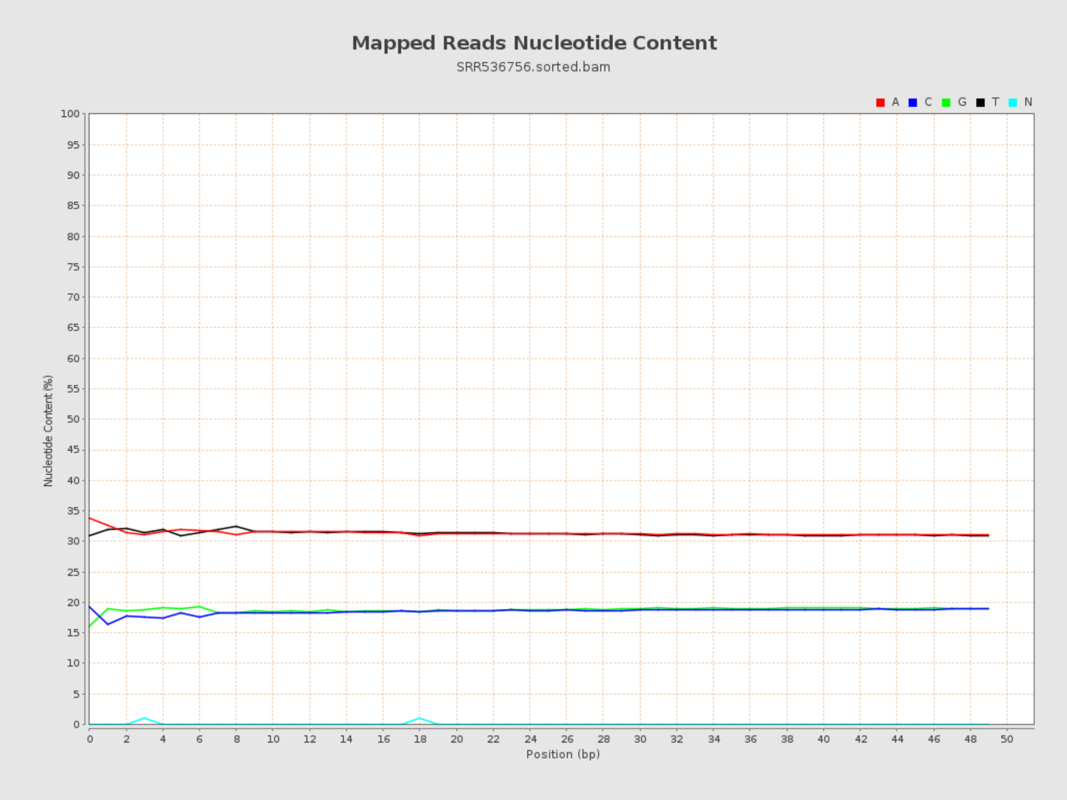
6. Results : Genome Fraction Coverage



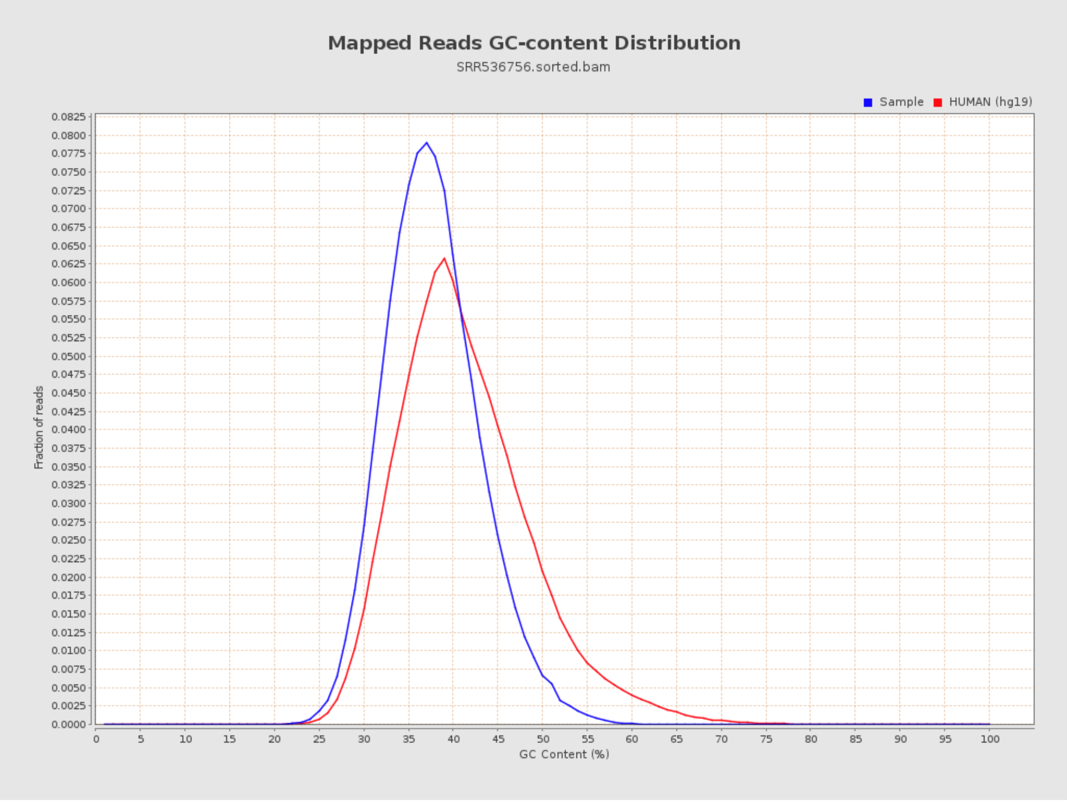
7. Results : Duplication Rate Histogram



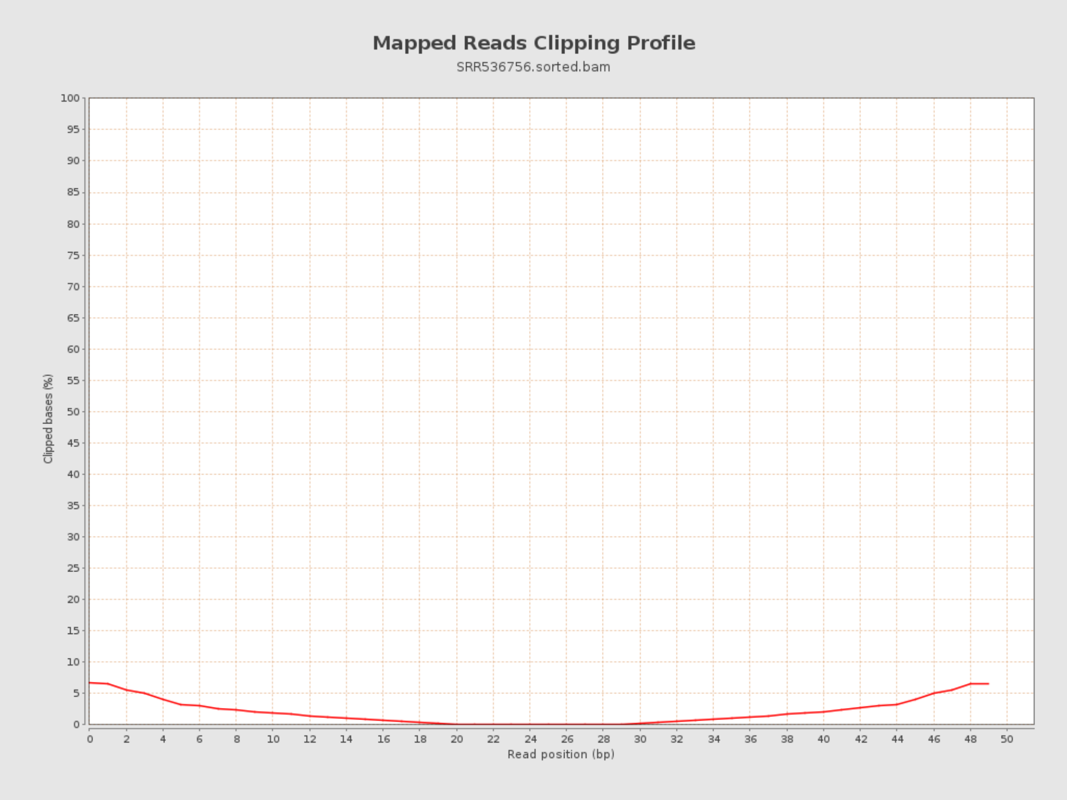
8. Results : Mapped Reads Nucleotide Content



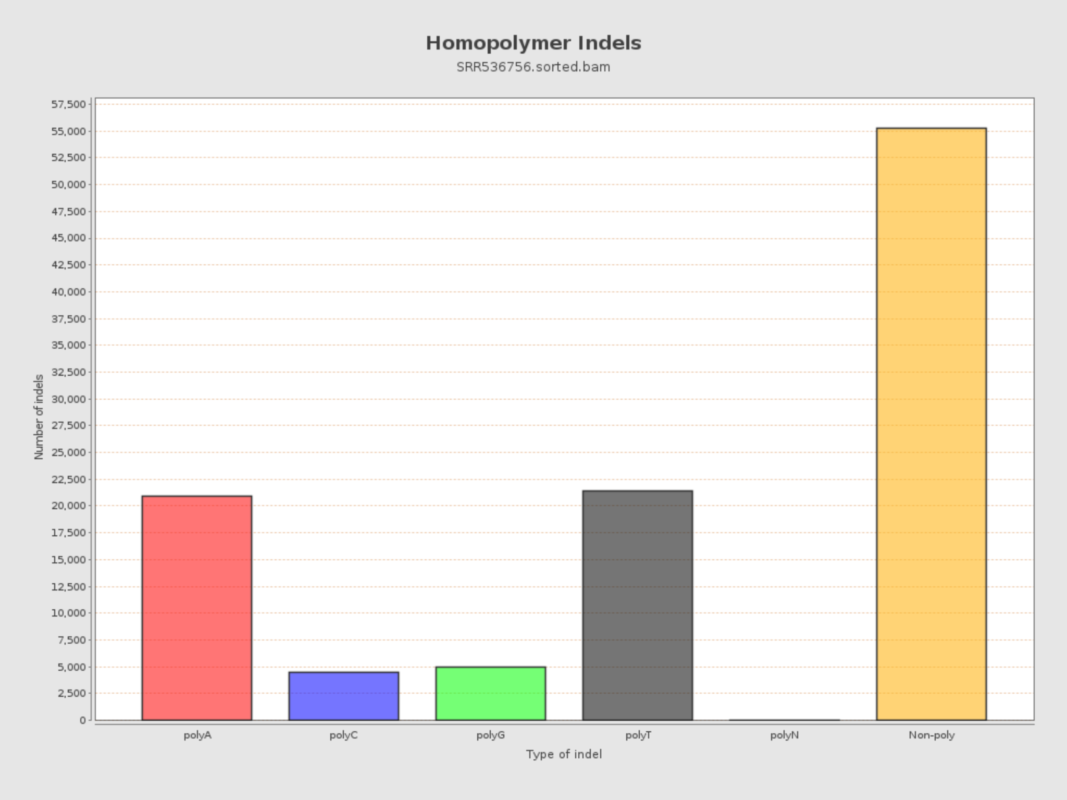
9. Results : Mapped Reads GC-content Distribution



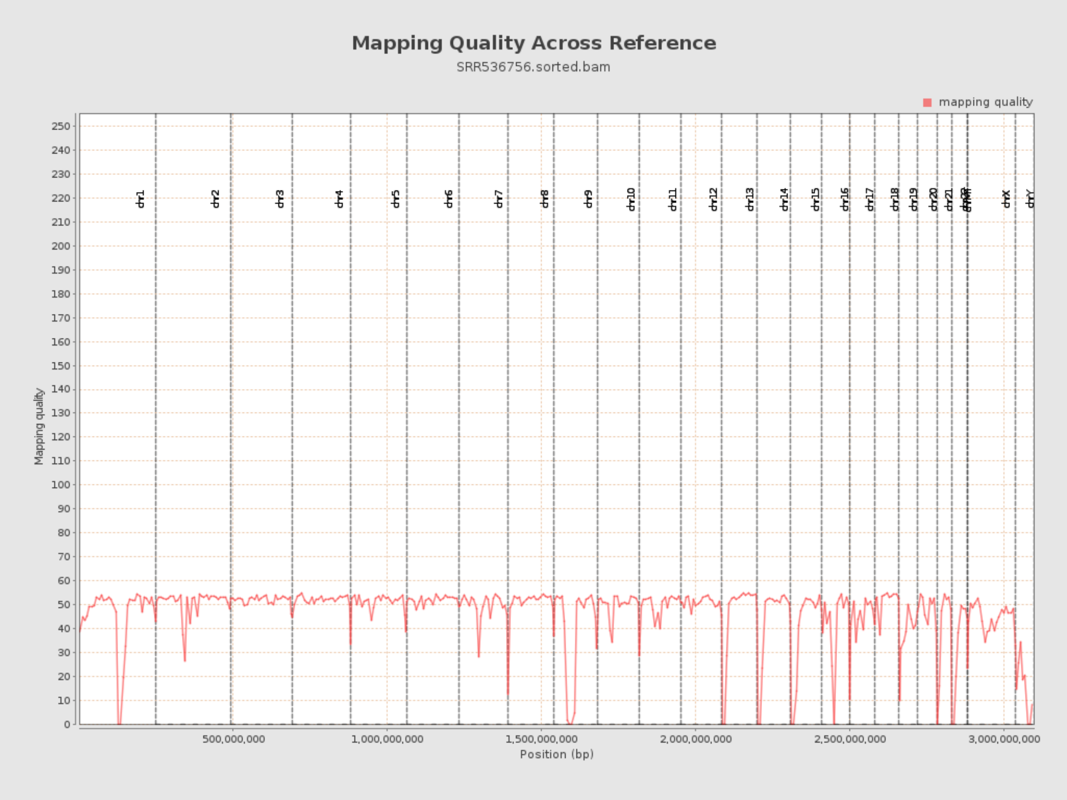
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram