Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 22:09:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536755.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_SRR536755 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536755.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 22:09:24 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536755.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,565,000
Mapped reads	22,720,707 / 96.42%
Unmapped reads	844,293 / 3.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	552 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	207,477 / 0.88%
Duplication rate	0.9%
Clipped reads	361,887 / 1.54%

2.2. ACGT Content

Number/percentage of A's	353,216,851 / 31.18%
Number/percentage of C's	211,421,810 / 18.66%
Number/percentage of T's	352,944,678 / 31.15%
Number/percentage of G's	214,922,542 / 18.97%
Number/percentage of N's	479,947 / 0.04%
GC Percentage	37.63%

2.3. Coverage

Mean	0.366

Standard Deviation	0.6762

2.4. Mapping Quality

Mean Mapping Quality	46.59

2.5. Mismatches and indels

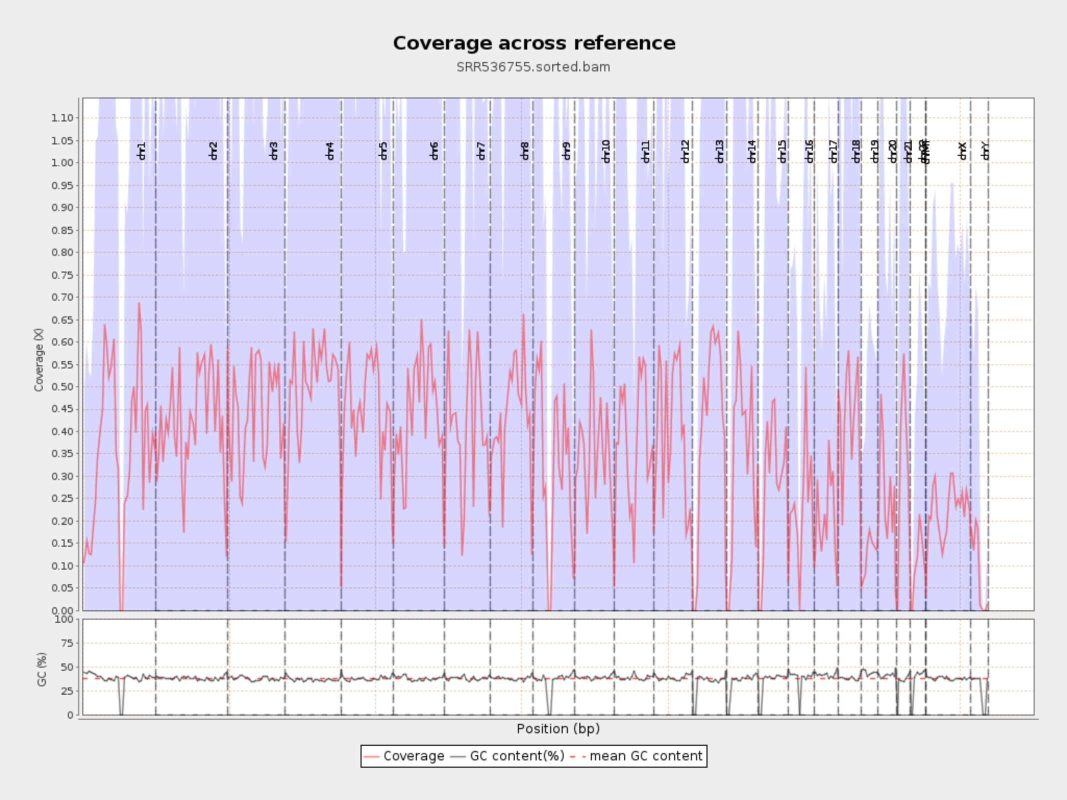
General error rate	0.36%
Mismatches	3,964,998
Insertions	63,168
Mapped reads with at least one insertion	0.28%
Deletions	58,578
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.36%

2.6. Chromosome stats

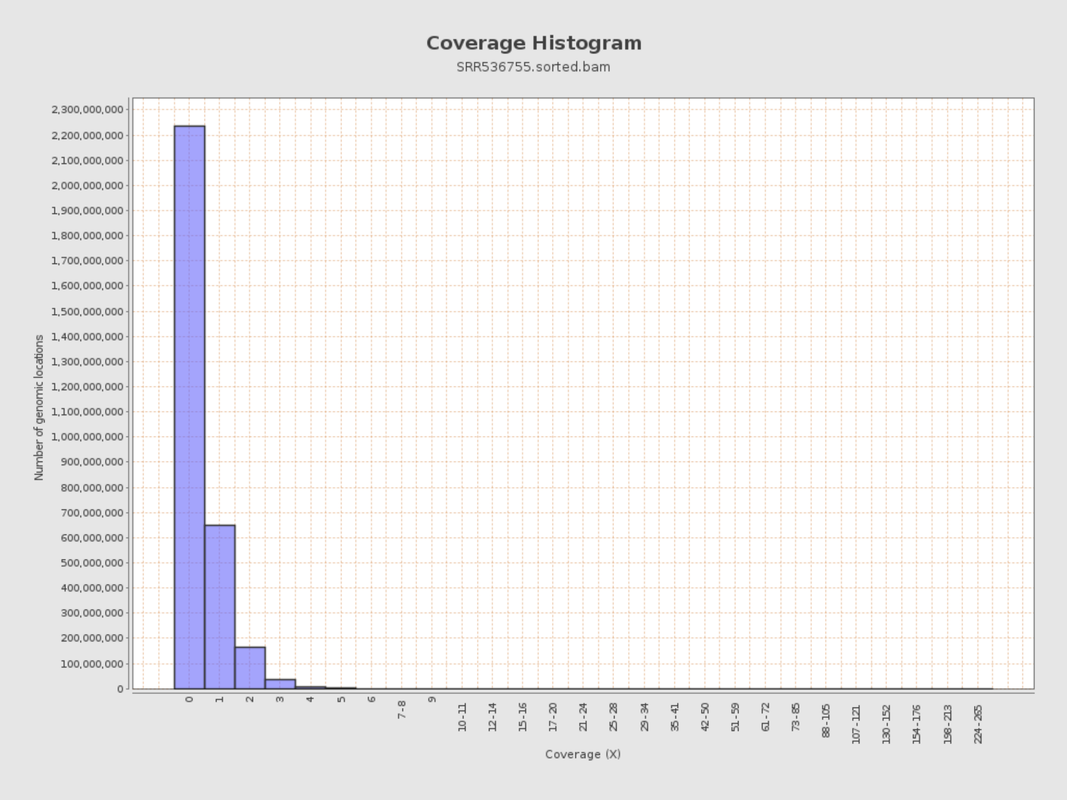
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	88635174	0.3556	0.6808
chr2	243199373	103011454	0.4236	0.7117
chr3	198022430	88000049	0.4444	0.7257
chr4	191154276	95608206	0.5002	0.7671
chr5	180915260	80375038	0.4443	0.7254
chr6	171115067	76576807	0.4475	0.7322
chr7	159138663	64743508	0.4068	0.709

chr8	146364022	64179455	0.4385	0.7248
chr9	141213431	47082814	0.3334	0.6518
chr10	135534747	48891216	0.3607	0.6592
chr11	135006516	51197993	0.3792	0.6887
chr12	133851895	52866034	0.395	0.7012
chr13	115169878	48073102	0.4174	0.7235
chr14	107349540	37155993	0.3461	0.6696
chr15	102531392	29625007	0.2889	0.6101
chr16	90354753	20561130	0.2276	0.5351
chr17	81195210	17307953	0.2132	0.5213
chr18	78077248	33954925	0.4349	0.7228
chr19	59128983	7569359	0.128	0.3908
chr20	63025520	16906988	0.2683	0.5794
chr21	48129895	14986115	0.3114	0.6546
chr22	51304566	5625306	0.1096	0.3697
chrMT	16571	504	0.0304	0.2015
chrX	155270560	34999494	0.2254	0.5002
chrY	59373566	5148402	0.0867	0.3314

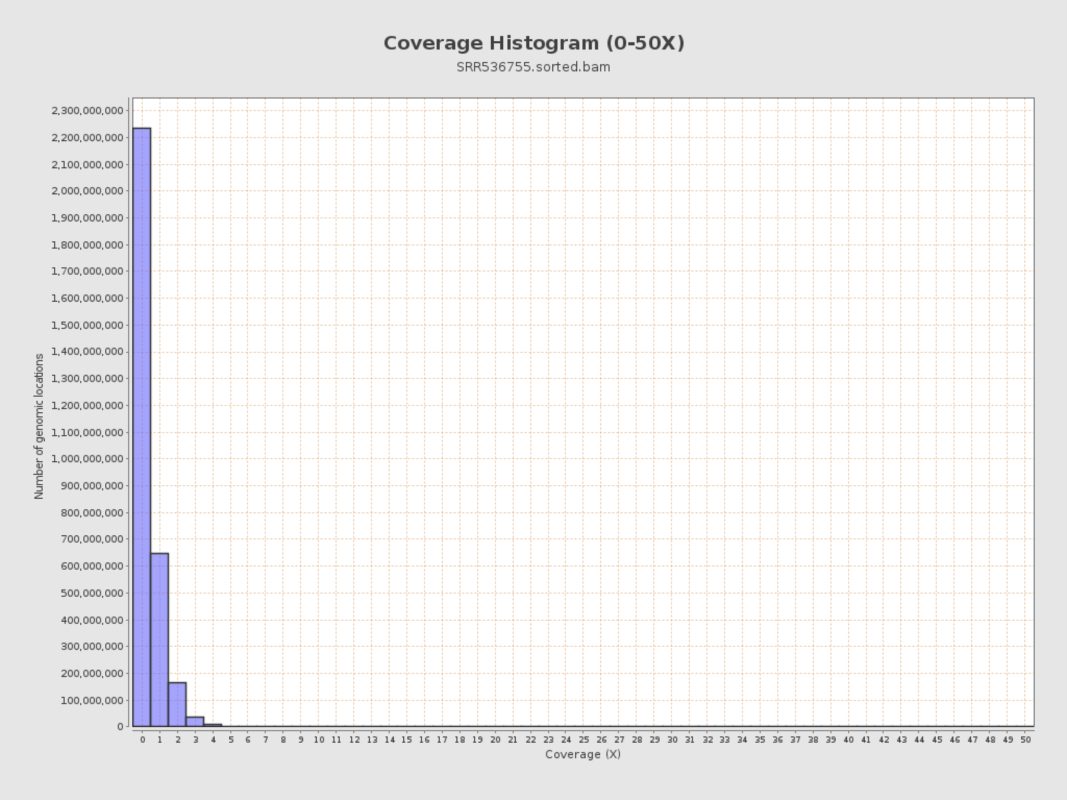
3. Results : Coverage across reference



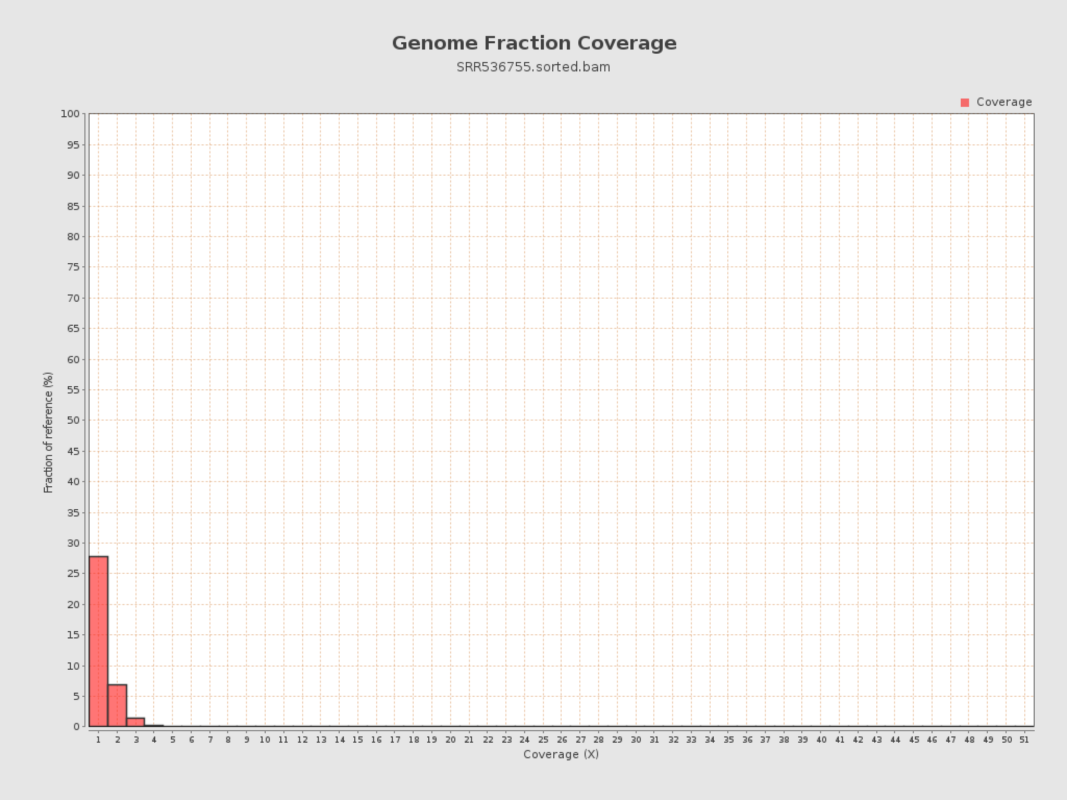
4. Results : Coverage Histogram



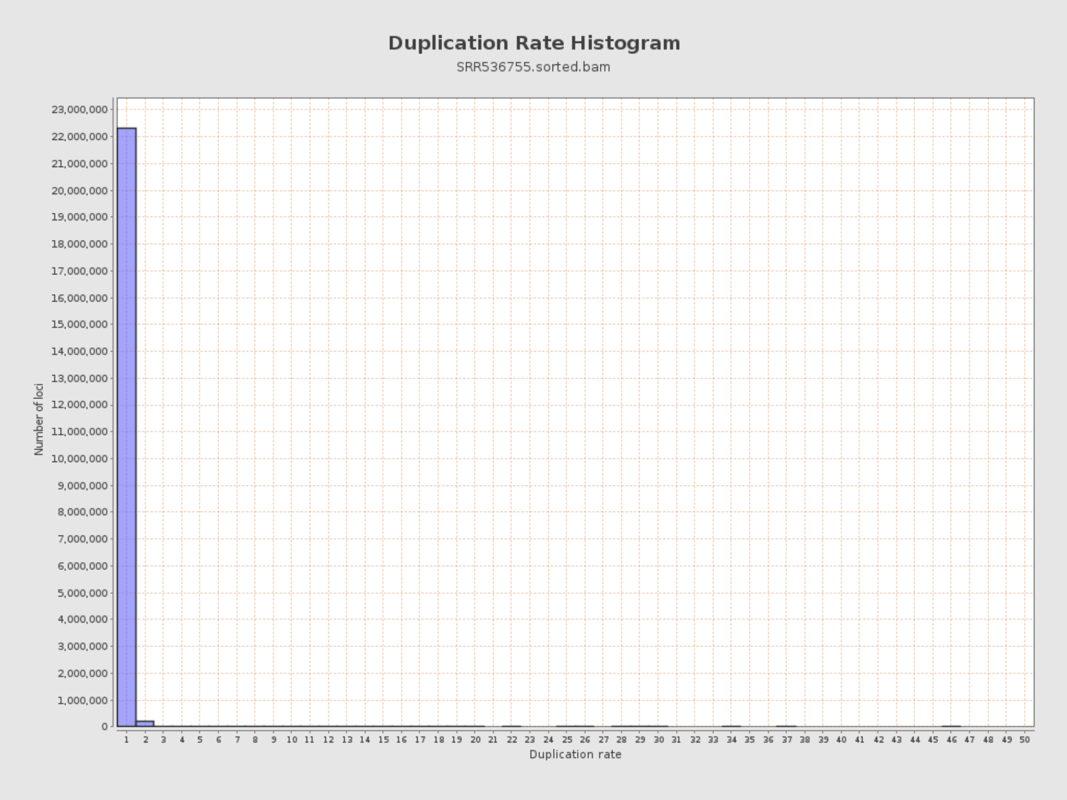
5. Results : Coverage Histogram (0-50X)



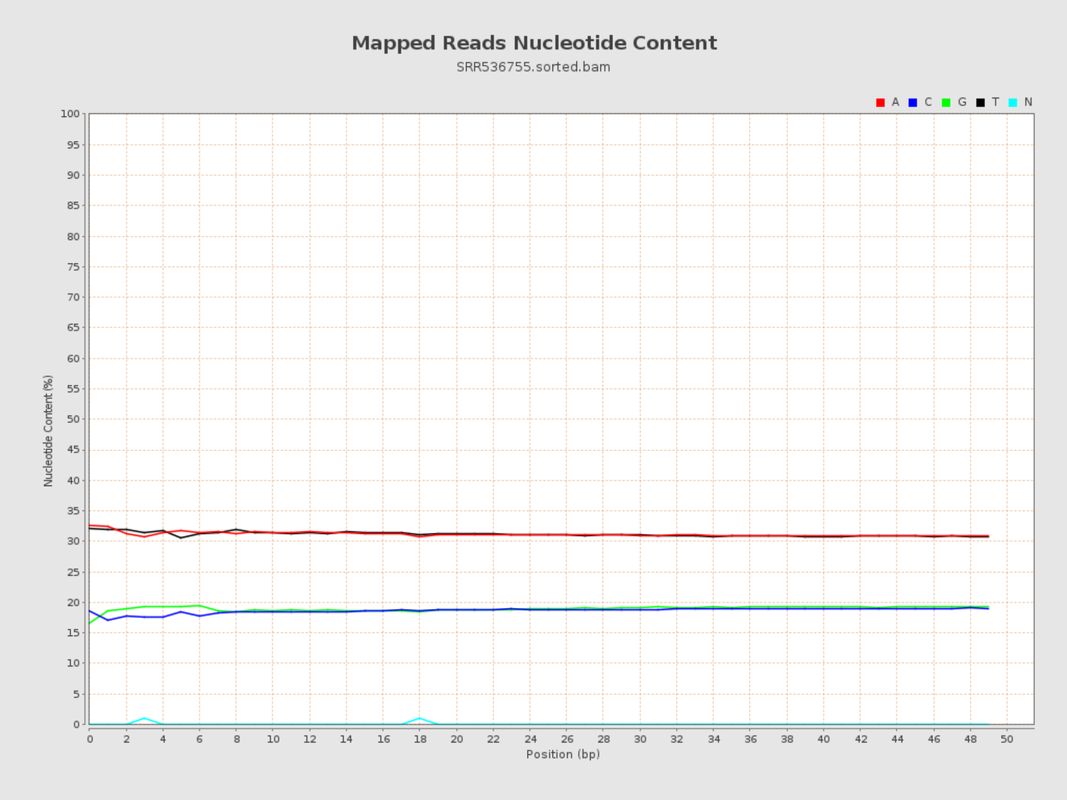
6. Results : Genome Fraction Coverage



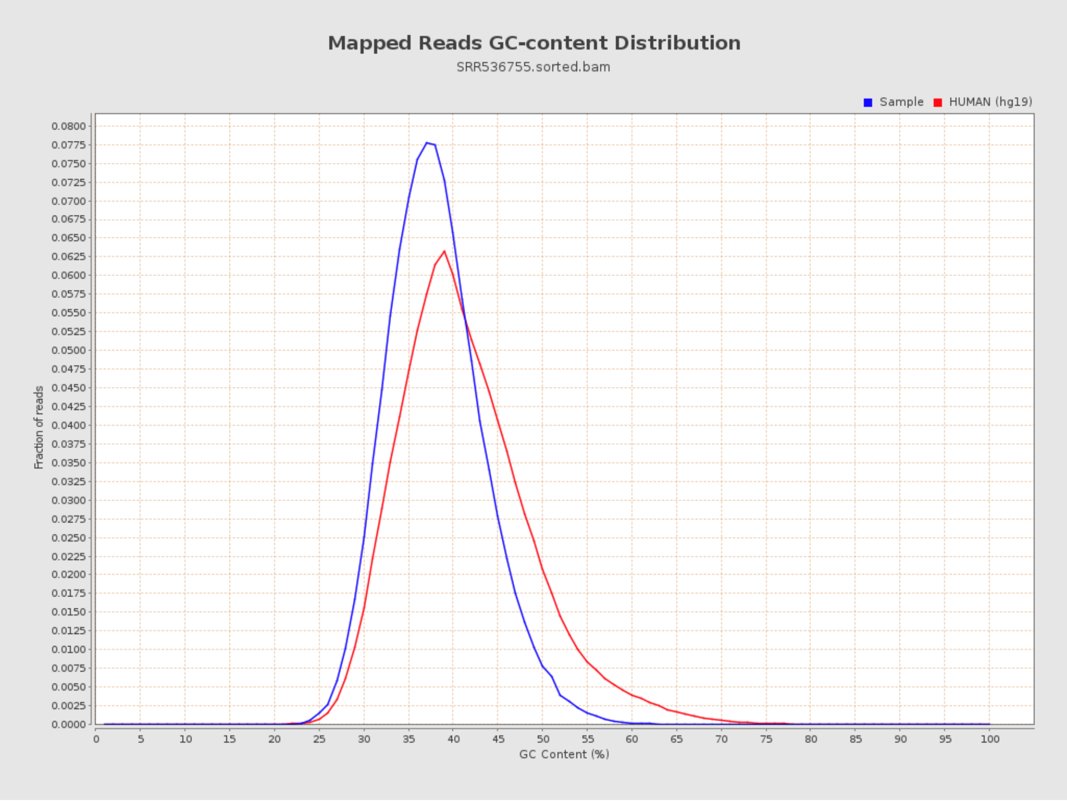
7. Results : Duplication Rate Histogram



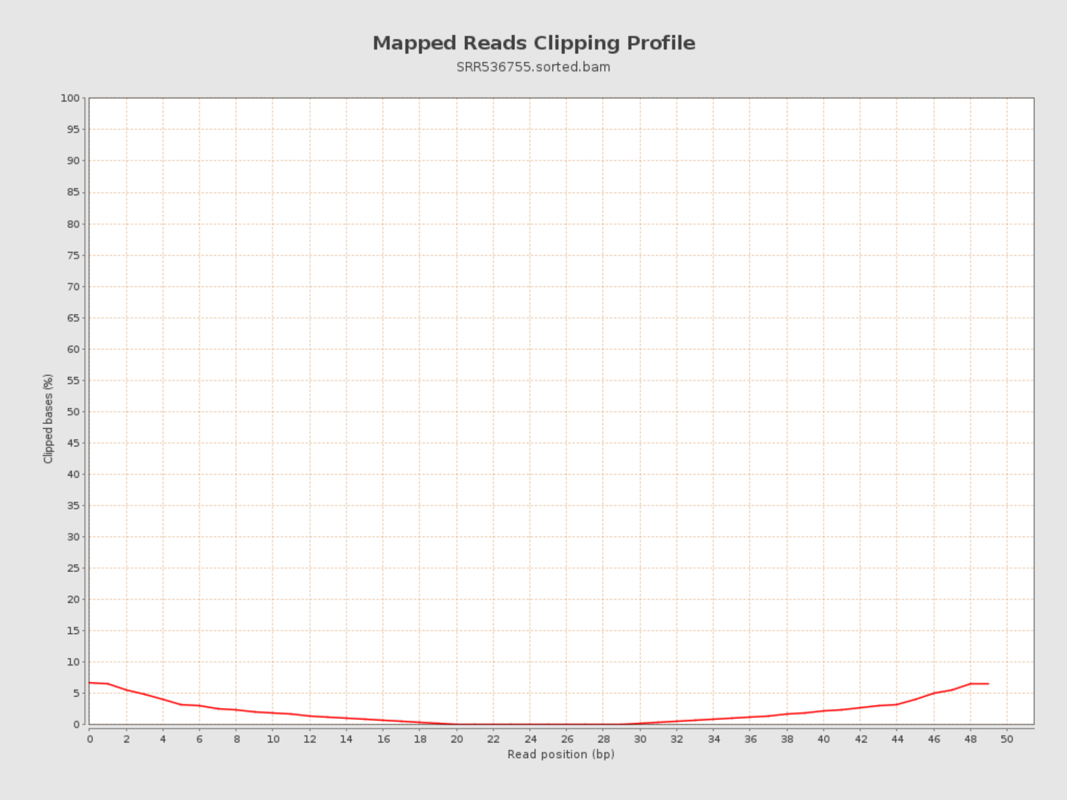
8. Results : Mapped Reads Nucleotide Content



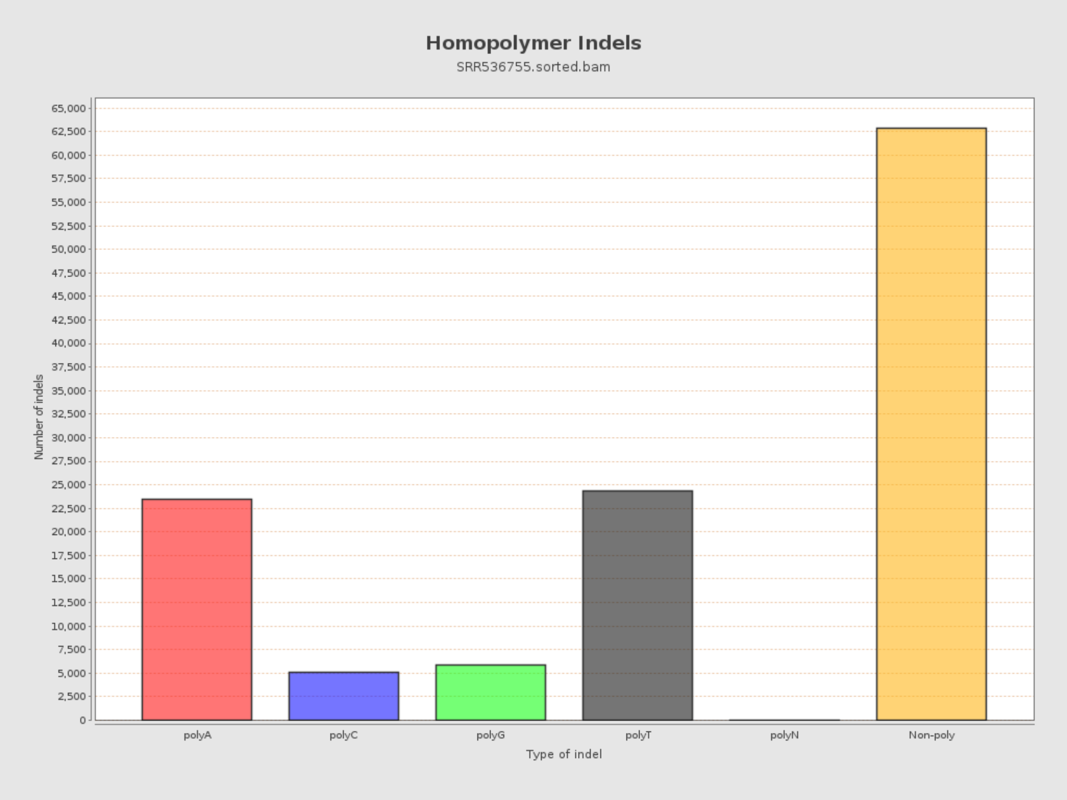
9. Results : Mapped Reads GC-content Distribution



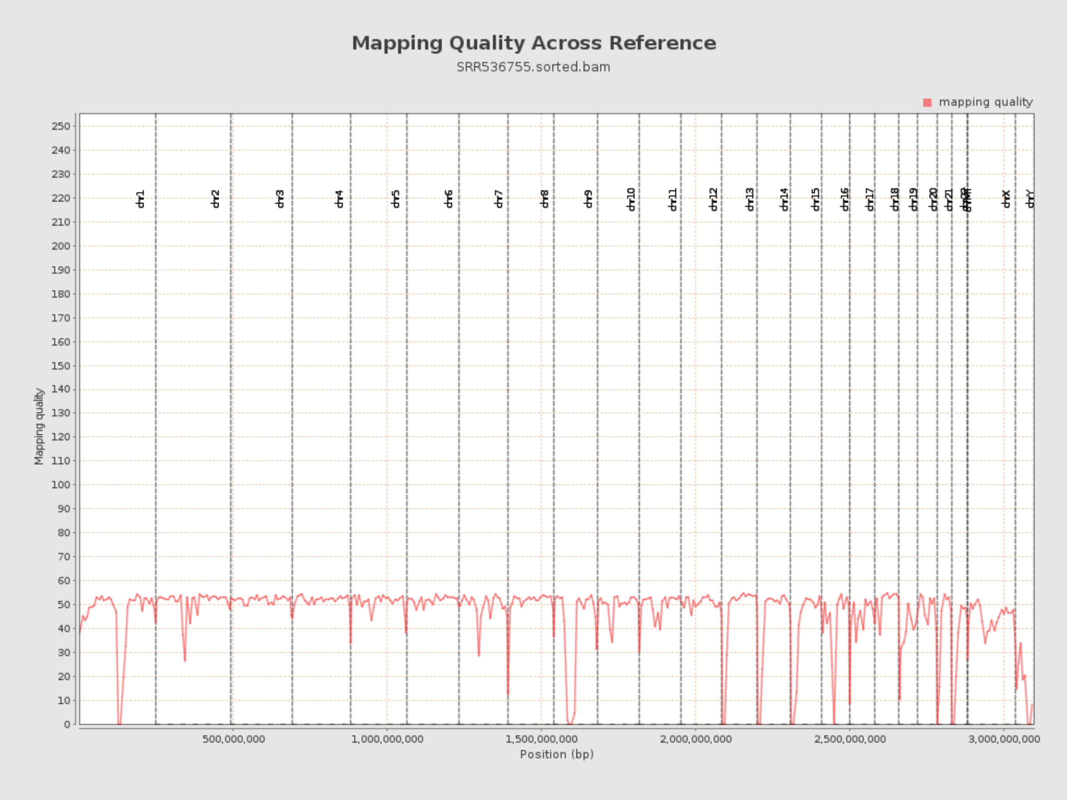
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram