Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 23:18:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536758.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_SRR536758 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536758.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 23:18:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536758.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,194,632
Mapped reads	24,622,441 / 97.73%
Unmapped reads	572,191 / 2.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	597 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	282,691 / 1.12%
Duplication rate	1.14%
Clipped reads	295,060 / 1.17%

2.2. ACGT Content

Number/percentage of A's	379,172,012 / 30.87%
Number/percentage of C's	233,344,032 / 19%
Number/percentage of T's	379,086,464 / 30.86%
Number/percentage of G's	236,607,532 / 19.26%
Number/percentage of N's	43,067 / 0%
GC Percentage	38.26%

2.3. Coverage

Mean	0.3968

Standard Deviation	0.7361

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Mismatches and indels

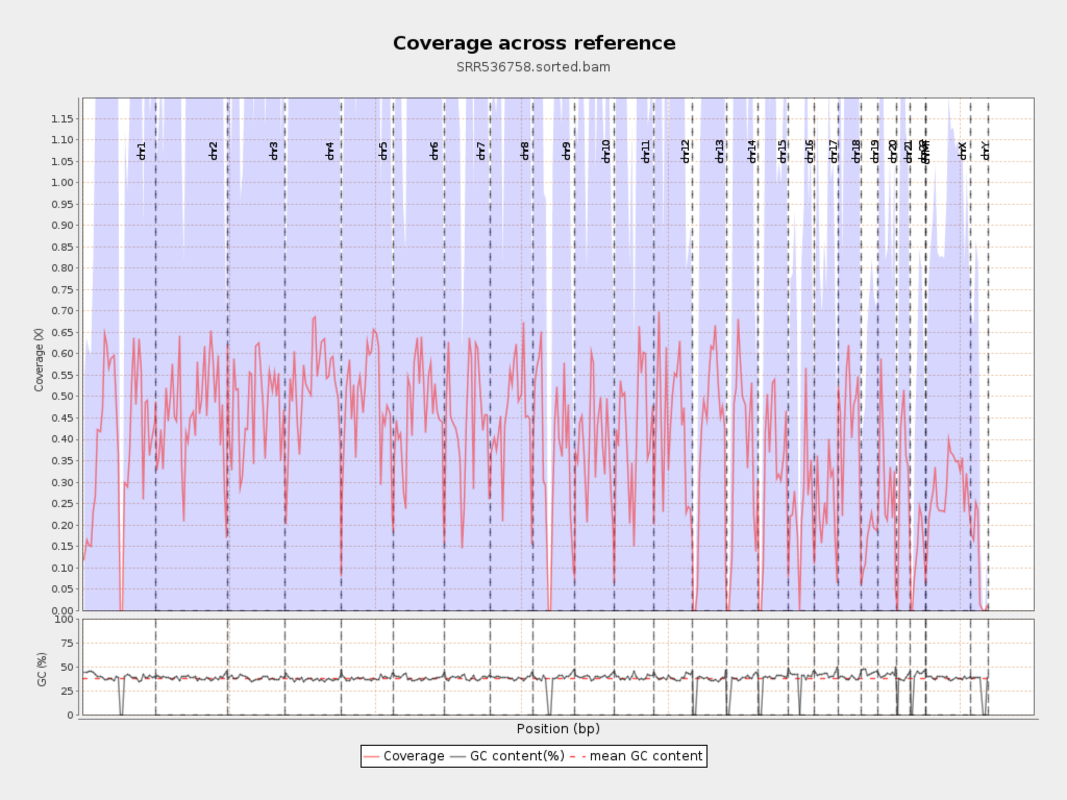
General error rate	0.2%
Mismatches	2,306,357
Insertions	70,620
Mapped reads with at least one insertion	0.29%
Deletions	64,490
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.37%

2.6. Chromosome stats

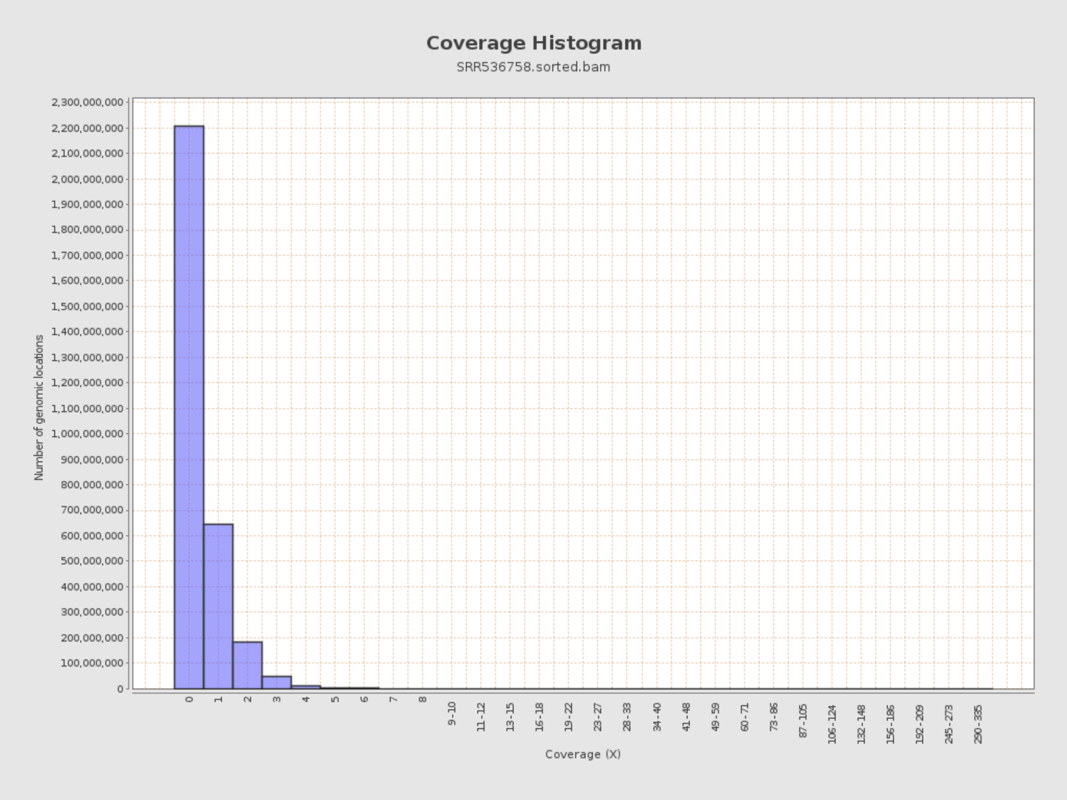
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	97778405	0.3923	0.7534
chr2	243199373	111292303	0.4576	0.7744
chr3	198022430	94249535	0.476	0.7881
chr4	191154276	100271790	0.5246	0.8253
chr5	180915260	87795479	0.4853	0.7962
chr6	171115067	80654388	0.4713	0.7869
chr7	159138663	69525591	0.4369	0.7693

chr8	146364022	66780559	0.4563	0.7738
chr9	141213431	52131795	0.3692	0.7183
chr10	135534747	53511974	0.3948	0.7167
chr11	135006516	57434881	0.4254	0.7724
chr12	133851895	57787350	0.4317	0.766
chr13	115169878	47237269	0.4102	0.7474
chr14	107349540	39395735	0.367	0.7202
chr15	102531392	33496319	0.3267	0.6861
chr16	90354753	21648271	0.2396	0.5673
chr17	81195210	20208057	0.2489	0.5812
chr18	78077248	35777418	0.4582	0.7699
chr19	59128983	9727720	0.1645	0.4578
chr20	63025520	19783293	0.3139	0.6542
chr21	48129895	14583536	0.303	0.6709
chr22	51304566	6628367	0.1292	0.4128
chrMT	16571	1384	0.0835	0.3053
chrX	155270560	44483002	0.2865	0.5955
chrY	59373566	6176138	0.104	0.3775

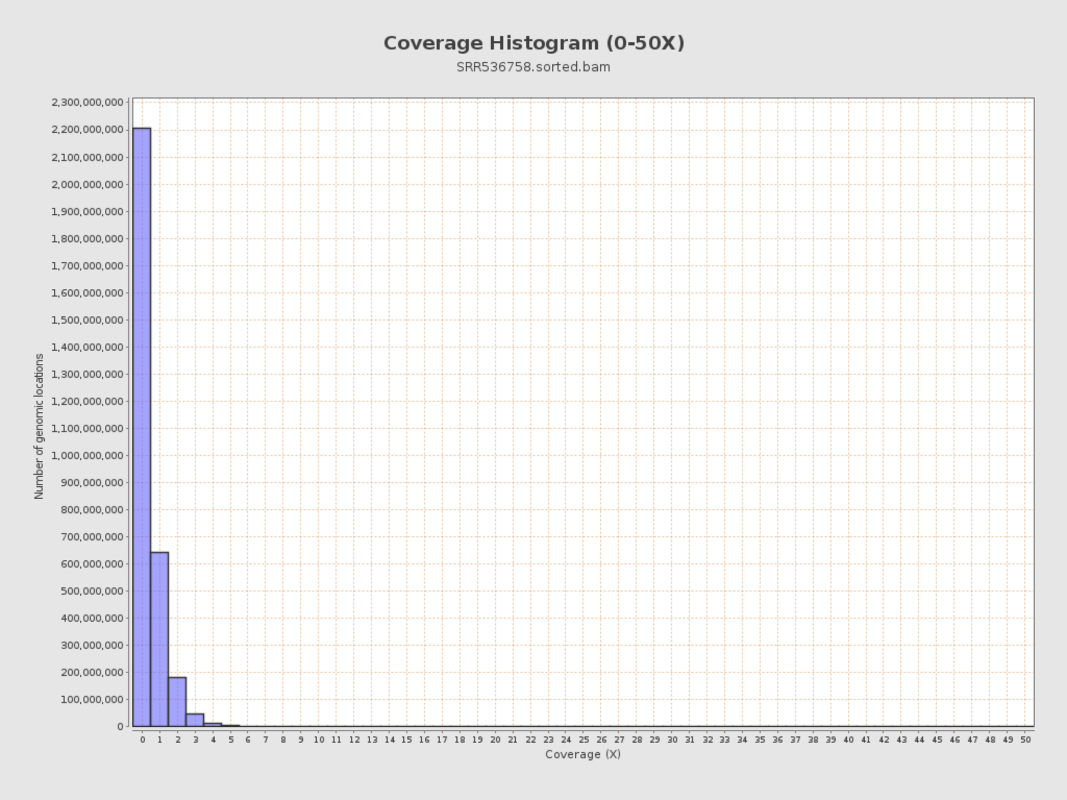
3. Results : Coverage across reference



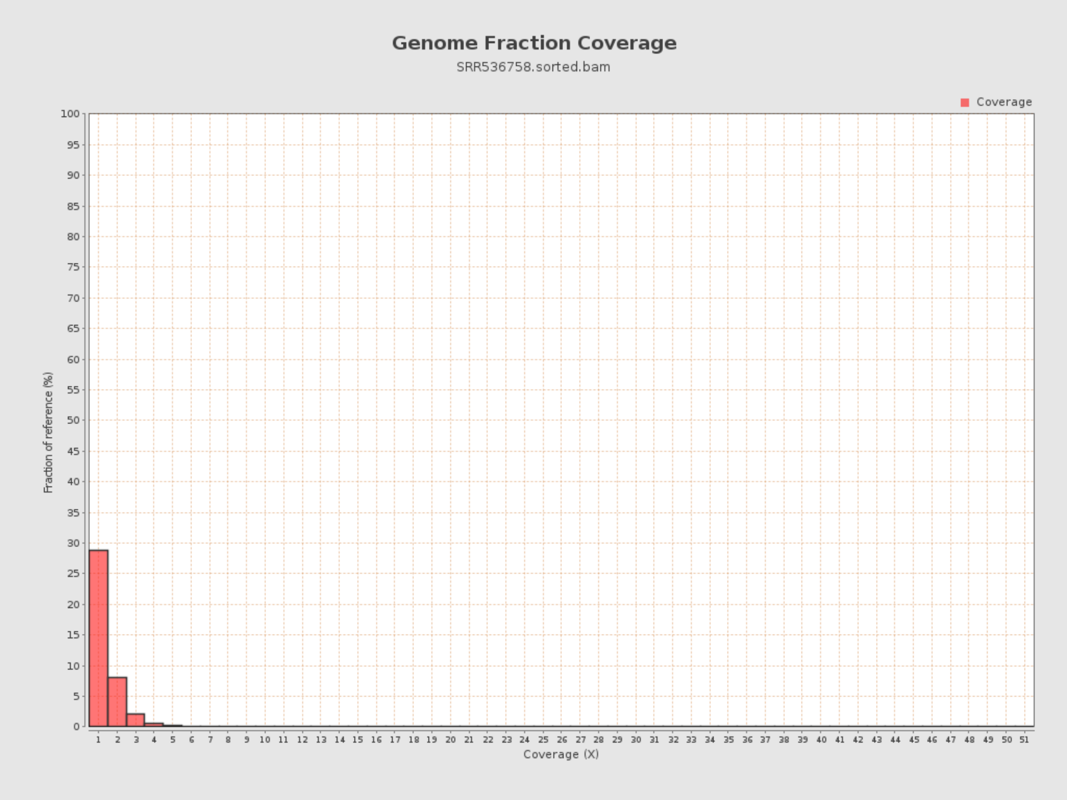
4. Results : Coverage Histogram



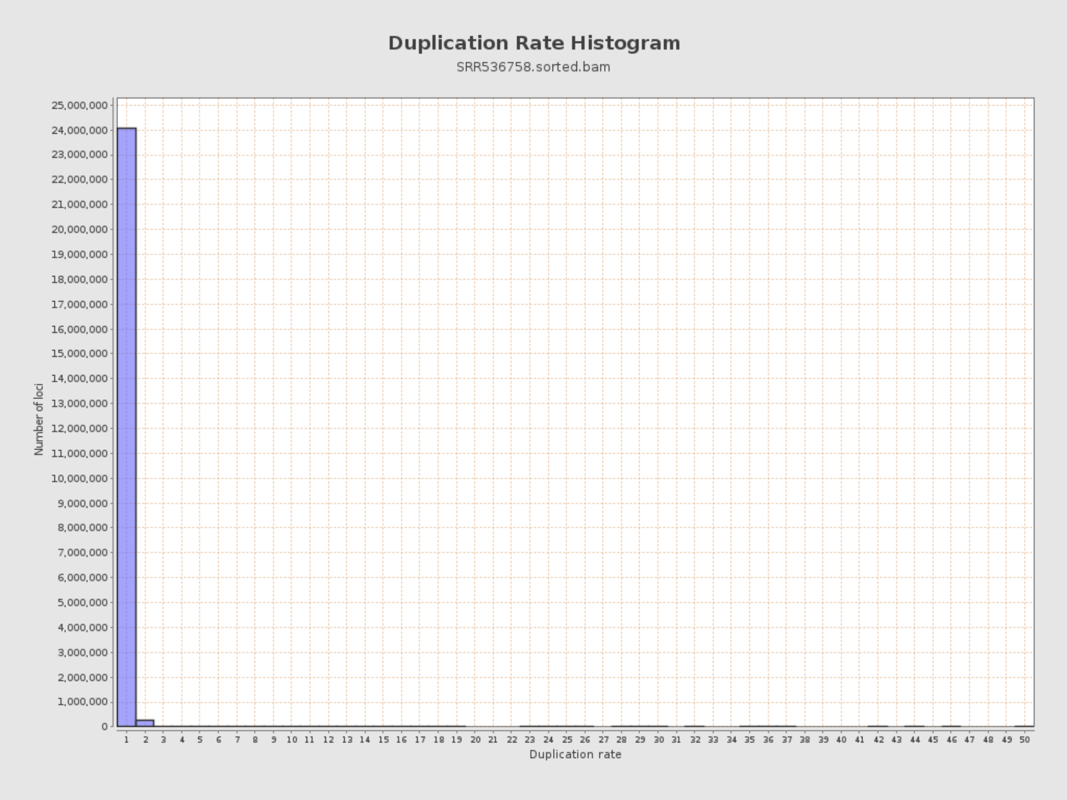
5. Results : Coverage Histogram (0-50X)



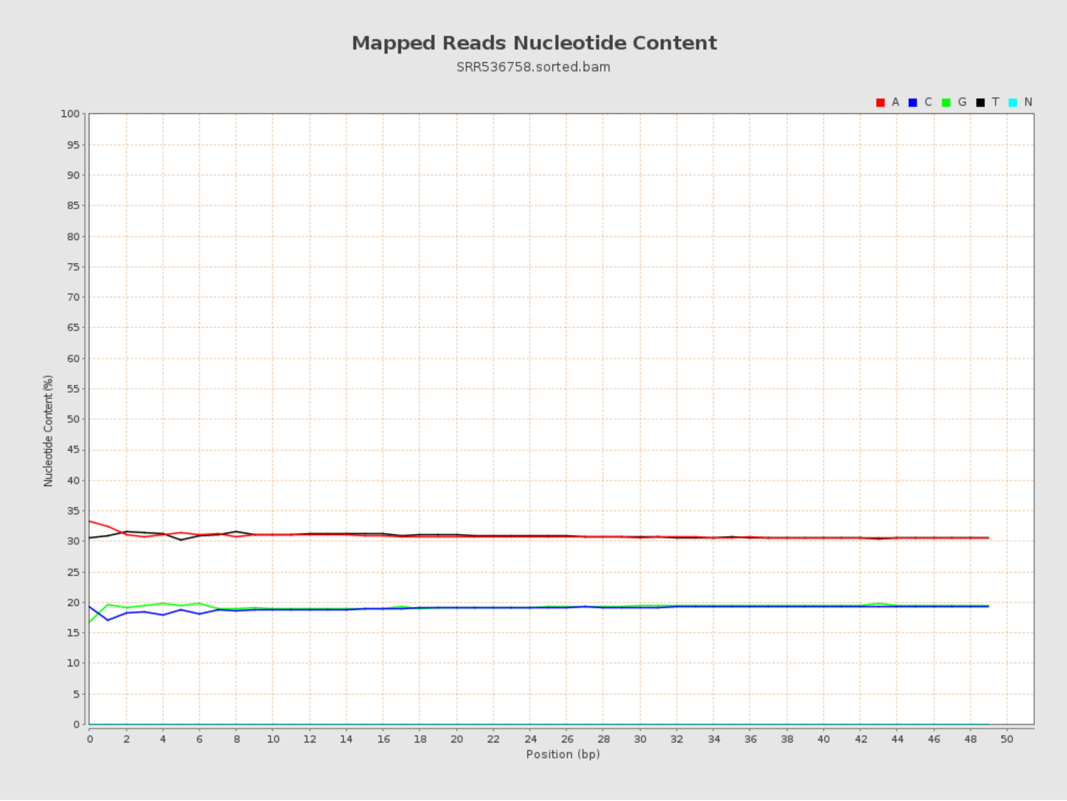
6. Results : Genome Fraction Coverage



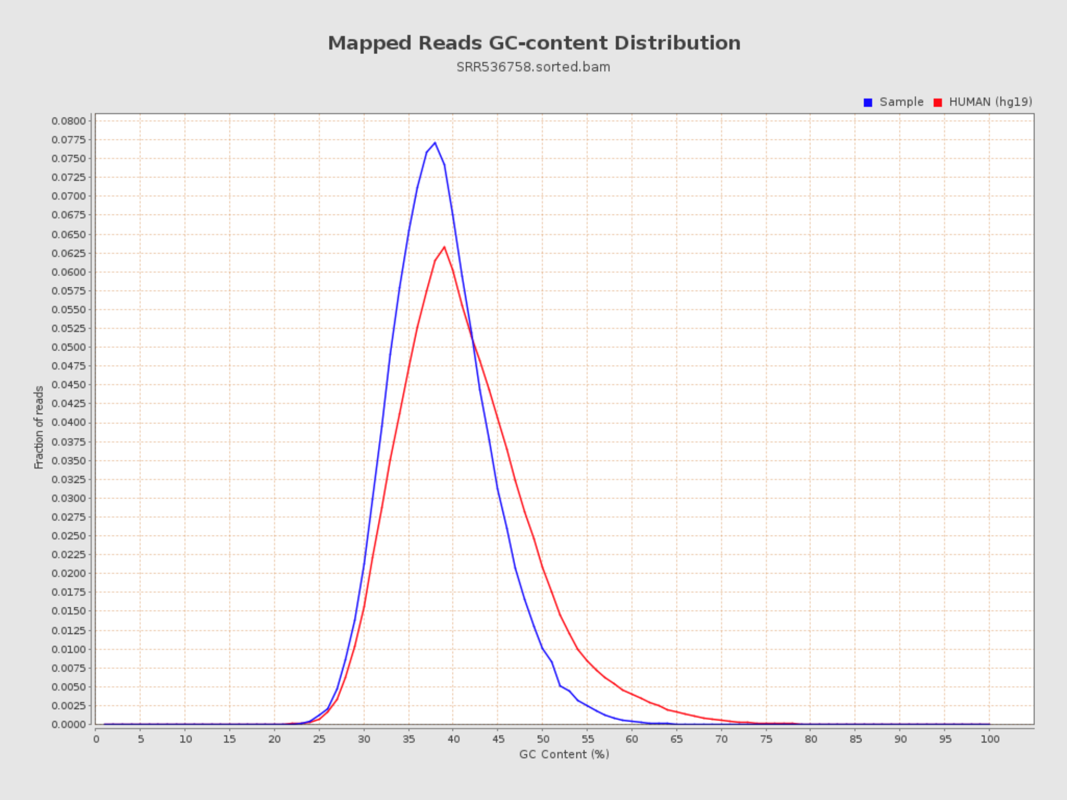
7. Results : Duplication Rate Histogram



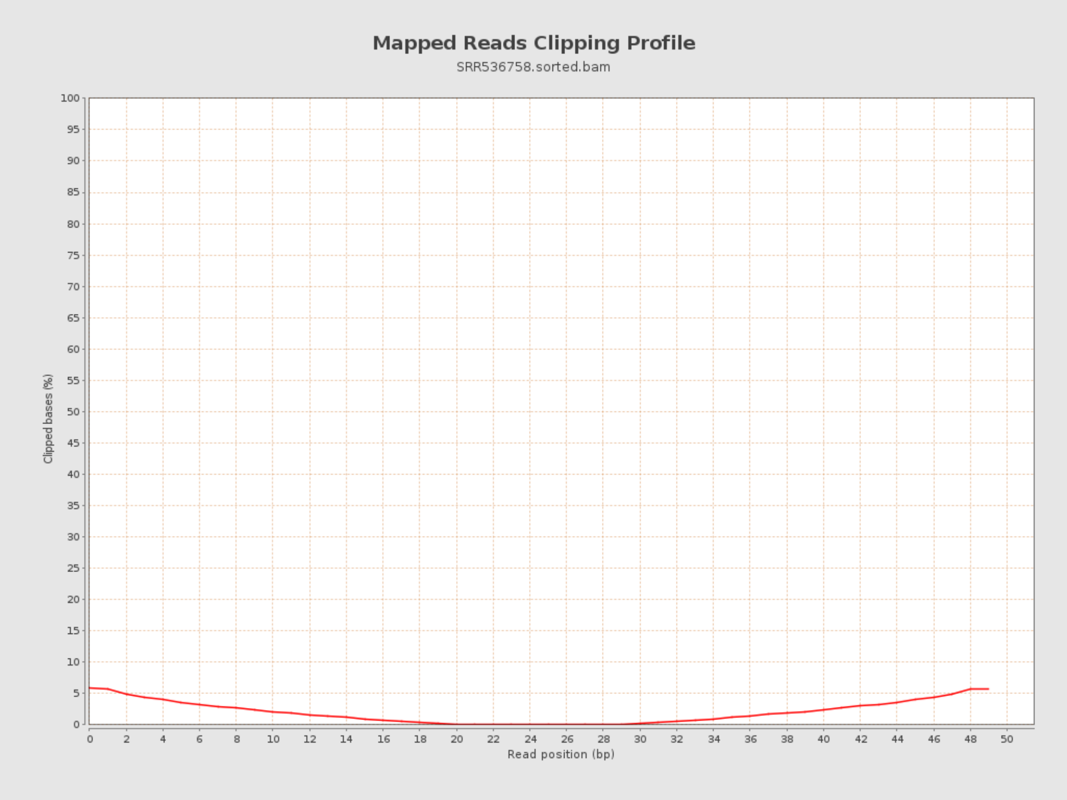
8. Results : Mapped Reads Nucleotide Content



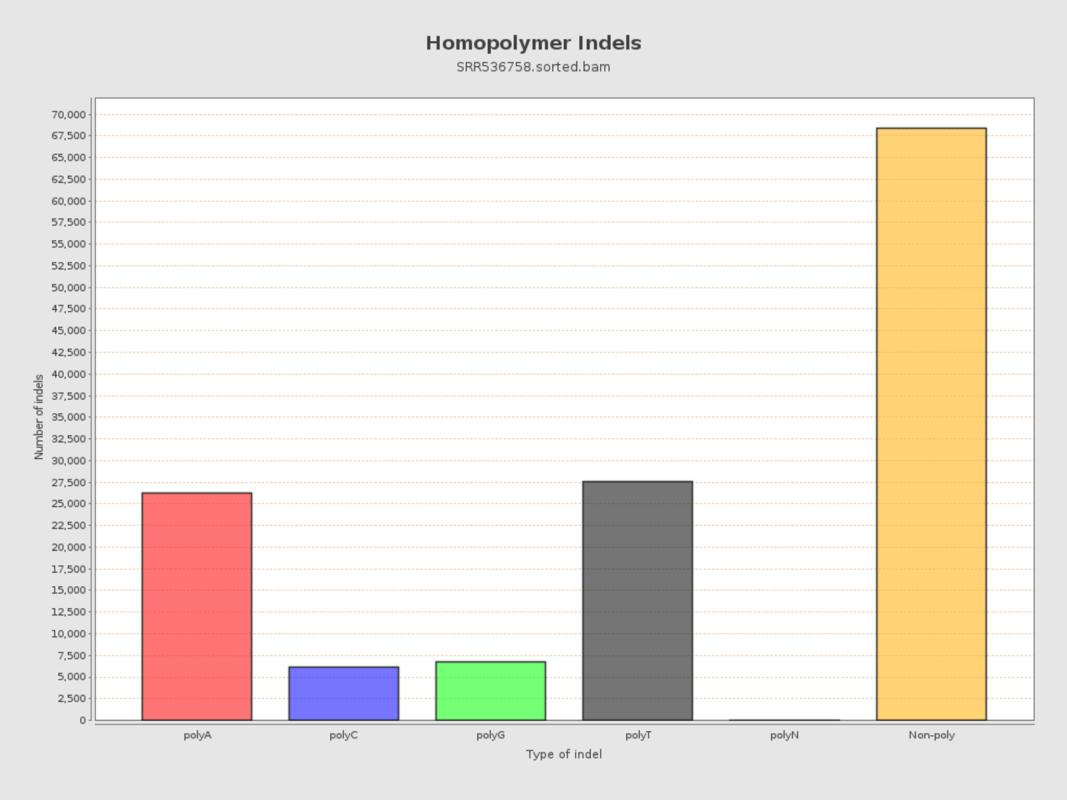
9. Results : Mapped Reads GC-content Distribution



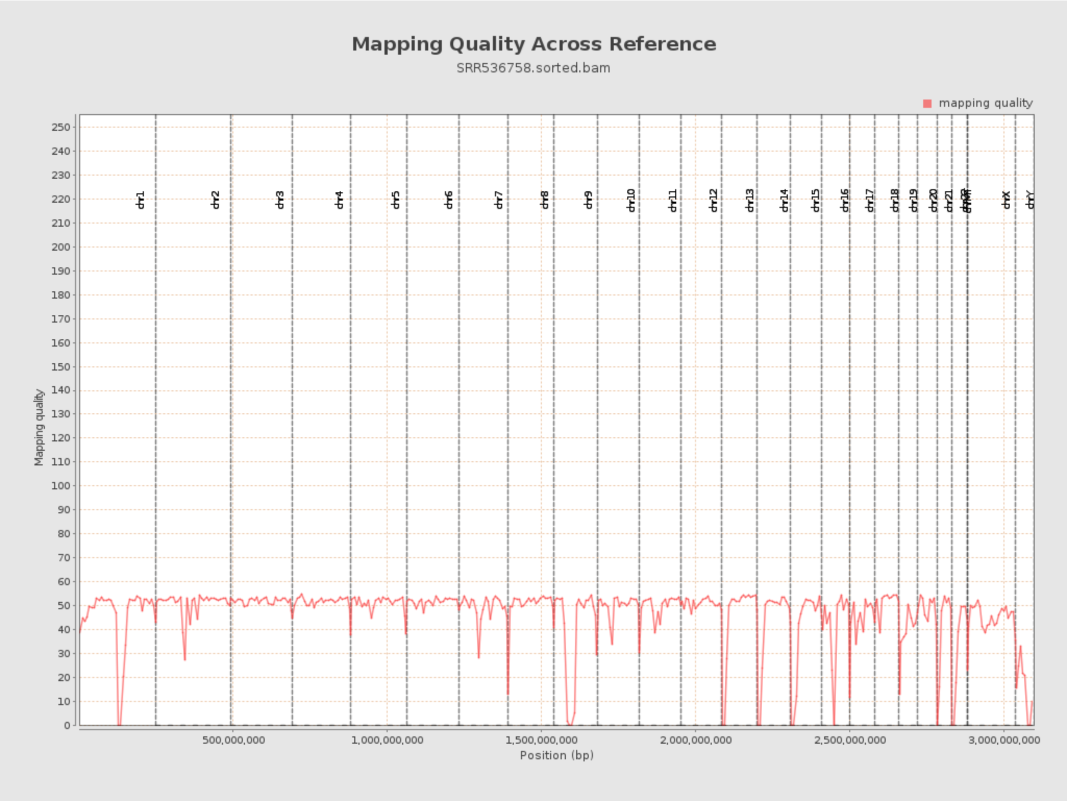
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram