Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 23:28:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514747.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_SRR5514747 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514747.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 23:28:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514747.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,016,483
Mapped reads	30,318,387 / 91.83%
Unmapped reads	2,698,096 / 8.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,943,434 / 14.97%
Read min/max/mean length	30 / 100 / 105.31
Duplicated reads (estimated)	23,527,676 / 71.26%
Duplication rate	39.69%
Clipped reads	17,317,392 / 52.45%

2.2. ACGT Content

Number/percentage of A's	861,292,221 / 30.45%
Number/percentage of C's	530,505,993 / 18.75%
Number/percentage of T's	865,266,185 / 30.59%
Number/percentage of G's	571,568,494 / 20.21%
Number/percentage of N's	189,783 / 0.01%
GC Percentage	38.96%

2.3. Coverage

Mean	0.9149

Standard Deviation	98.7938

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

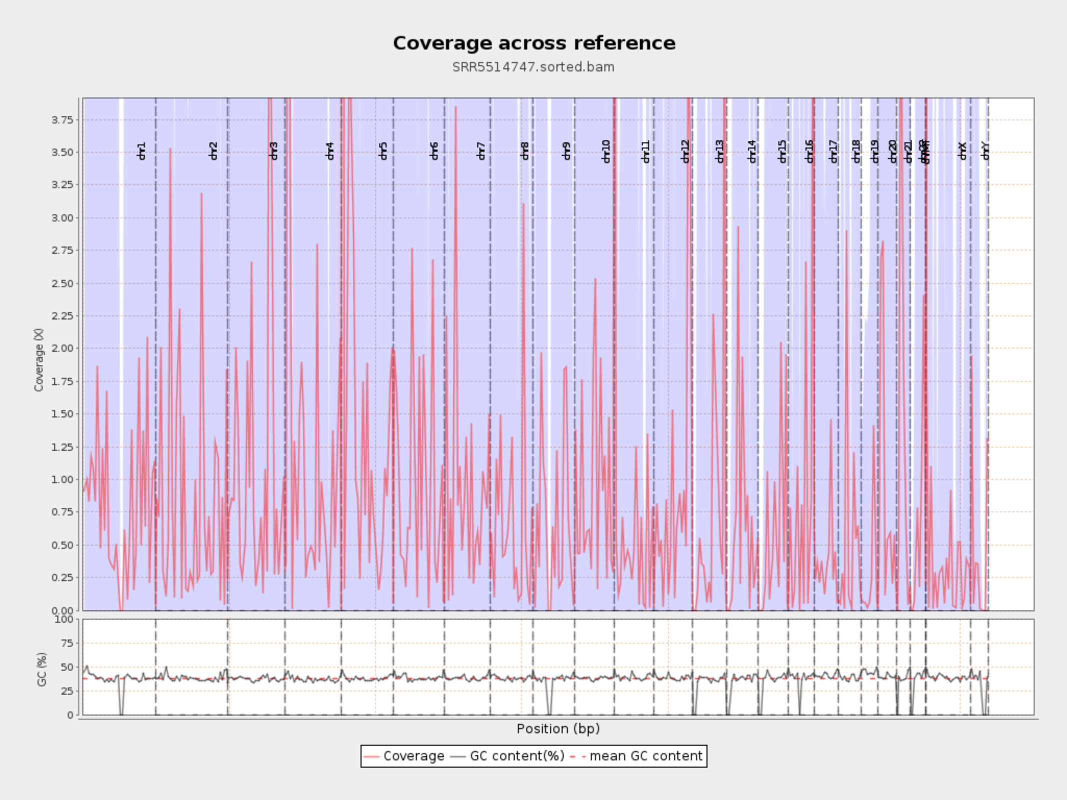
General error rate	0.81%
Mismatches	19,176,814
Insertions	2,088,665
Mapped reads with at least one insertion	6.5%
Deletions	1,025,067
Mapped reads with at least one deletion	3.12%
Homopolymer indels	43.83%

2.6. Chromosome stats

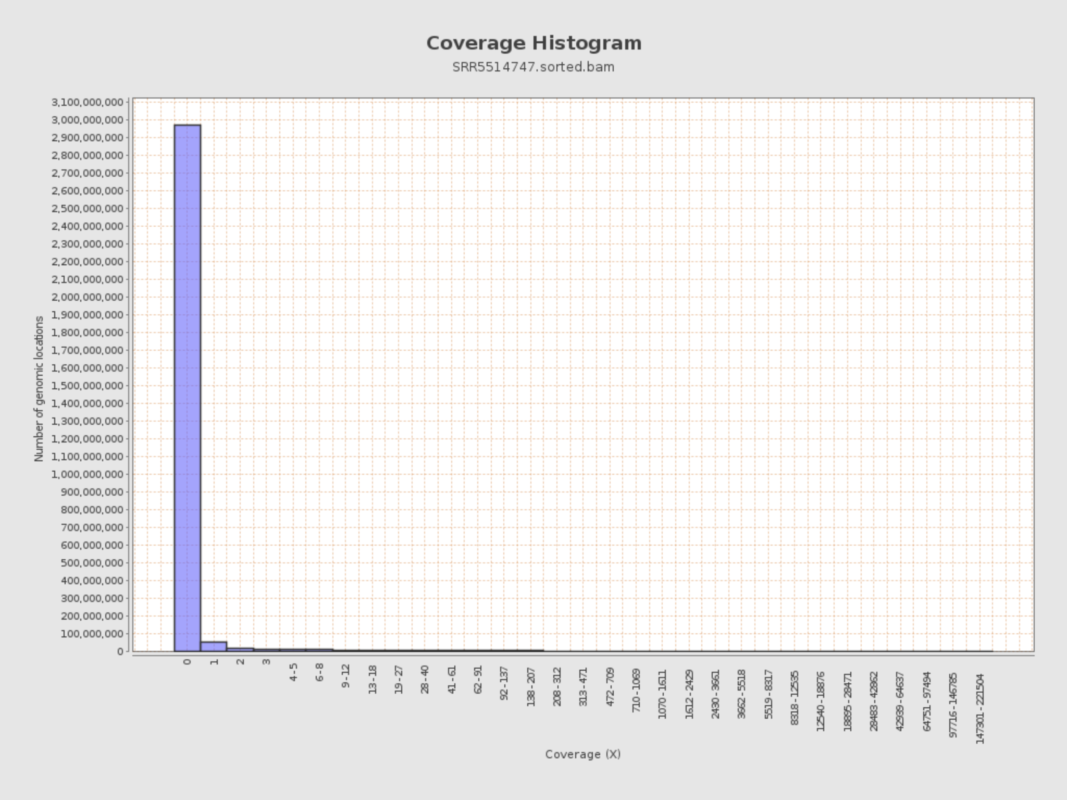
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	199206486	0.7992	27.4916
chr2	243199373	205062880	0.8432	30.4599
chr3	198022430	214306193	1.0822	18.8705
chr4	191154276	239629935	1.2536	93.1479
chr5	180915260	403529424	2.2305	367.6571
chr6	171115067	175217044	1.024	29.1493
chr7	159138663	148521799	0.9333	22.8828

chr8	146364022	101044718	0.6904	18.9851
chr9	141213431	98026071	0.6942	17.2268
chr10	135534747	130078628	0.9597	18.7579
chr11	135006516	82392204	0.6103	54.309
chr12	133851895	128354609	0.9589	60.7736
chr13	115169878	102018544	0.8858	68.9347
chr14	107349540	71542212	0.6664	14.3599
chr15	102531392	60701912	0.592	20.4012
chr16	90354753	93095971	1.0303	111.8622
chr17	81195210	32983535	0.4062	8.552
chr18	78077248	46062909	0.59	16.1426
chr19	59128983	15120533	0.2557	7.7614
chr20	63025520	61272096	0.9722	21.264
chr21	48129895	62527155	1.2991	19.3577
chr22	51304566	35221721	0.6865	43.8469
chrMT	16571	46894897	2,829.9377	3,064.3551
chrX	155270560	53250652	0.343	22.2705
chrY	59373566	26327353	0.4434	34.2968

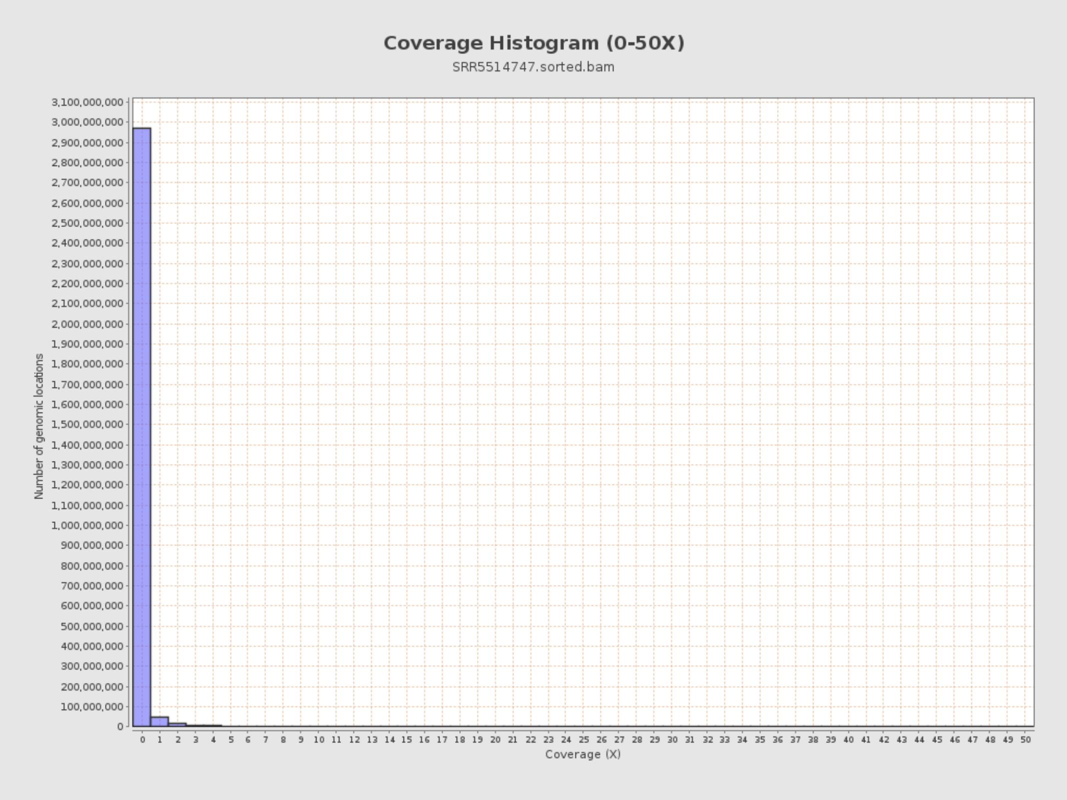
3. Results : Coverage across reference



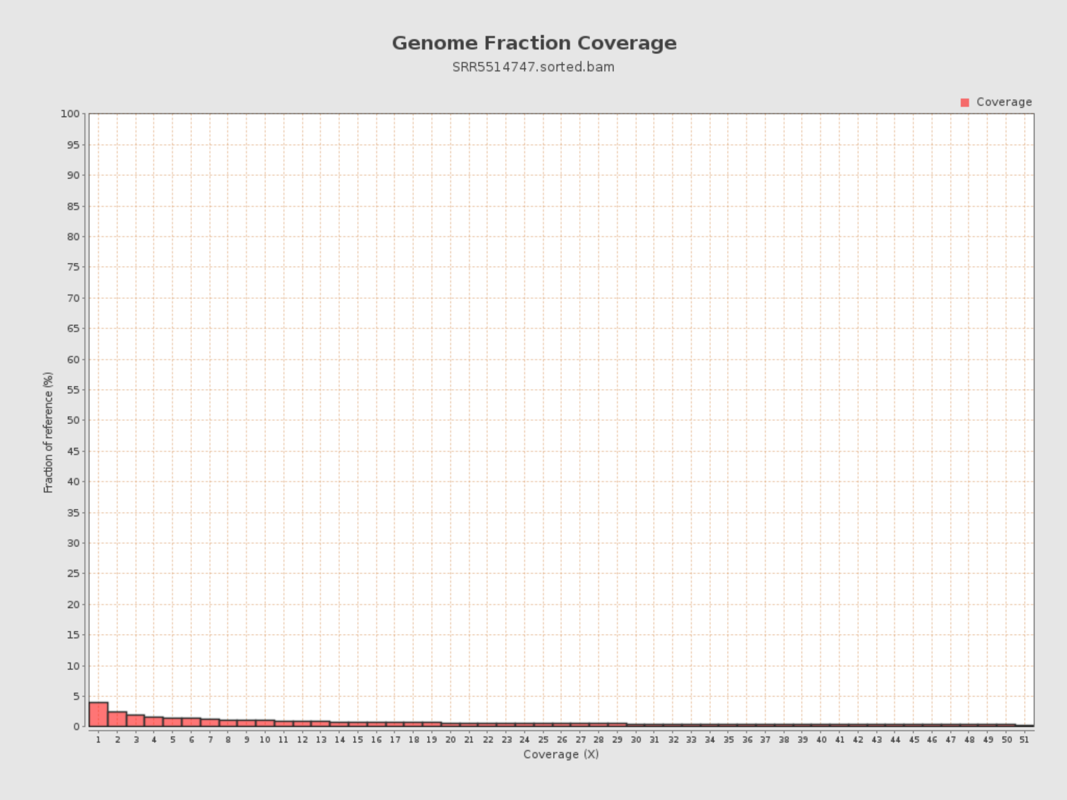
4. Results : Coverage Histogram



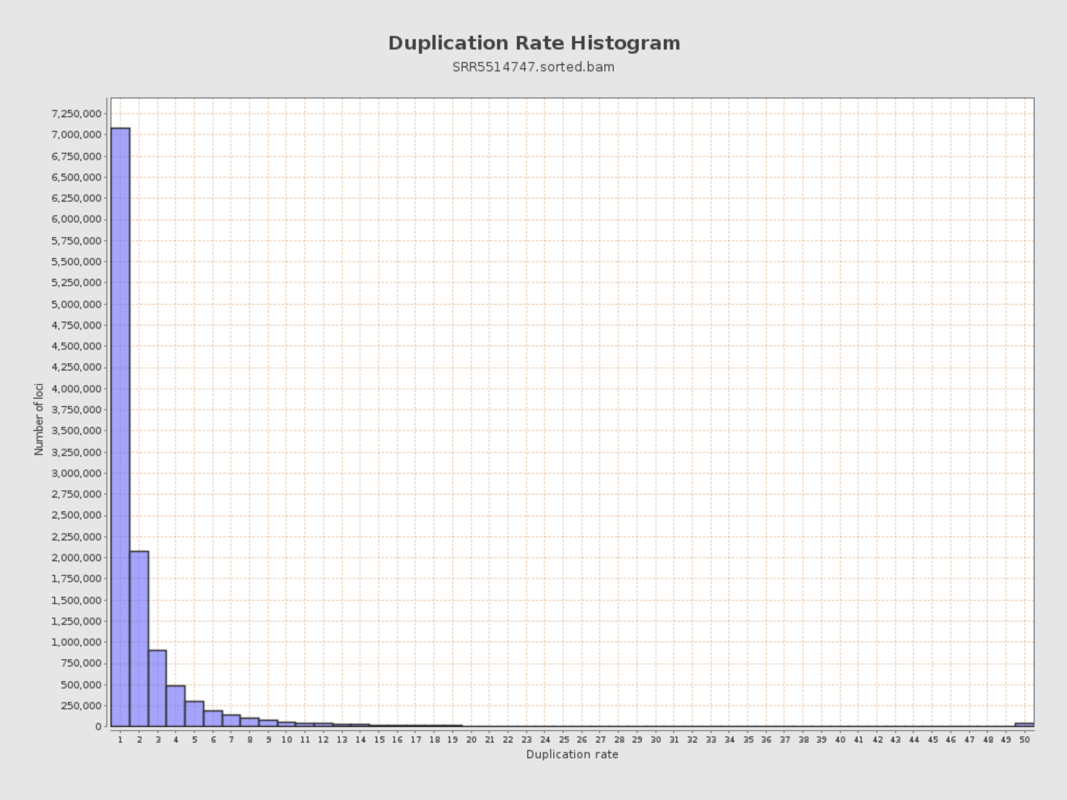
5. Results : Coverage Histogram (0-50X)



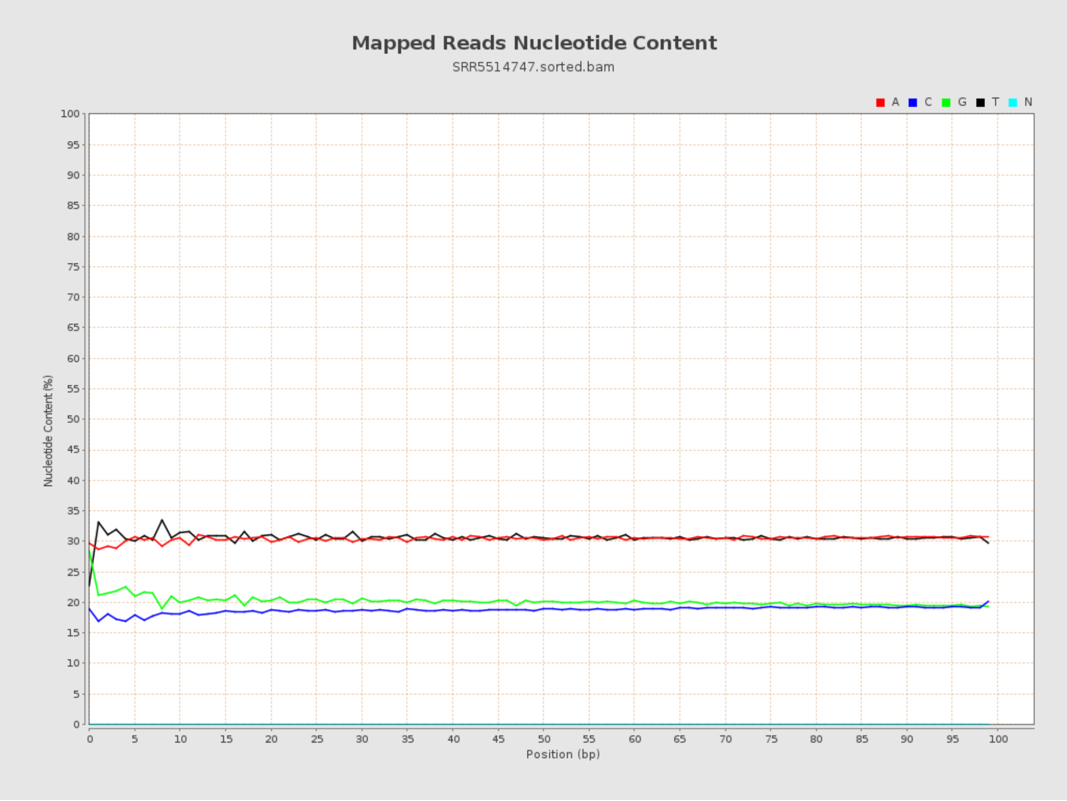
6. Results : Genome Fraction Coverage



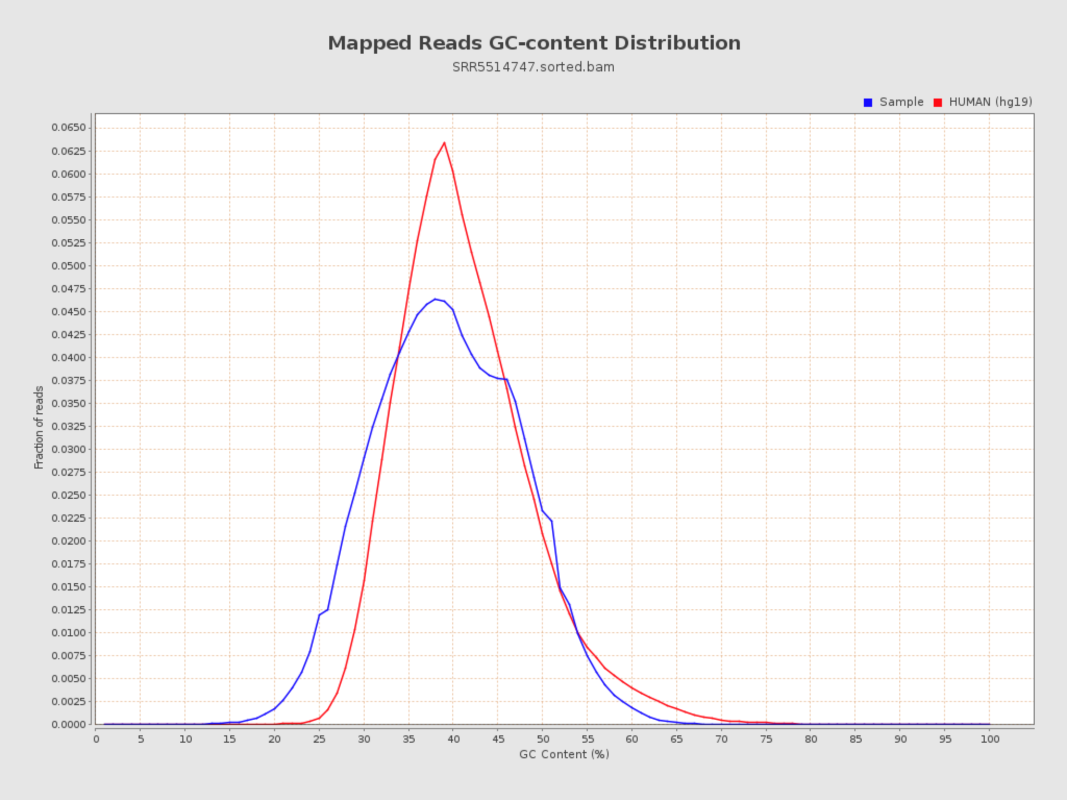
7. Results : Duplication Rate Histogram



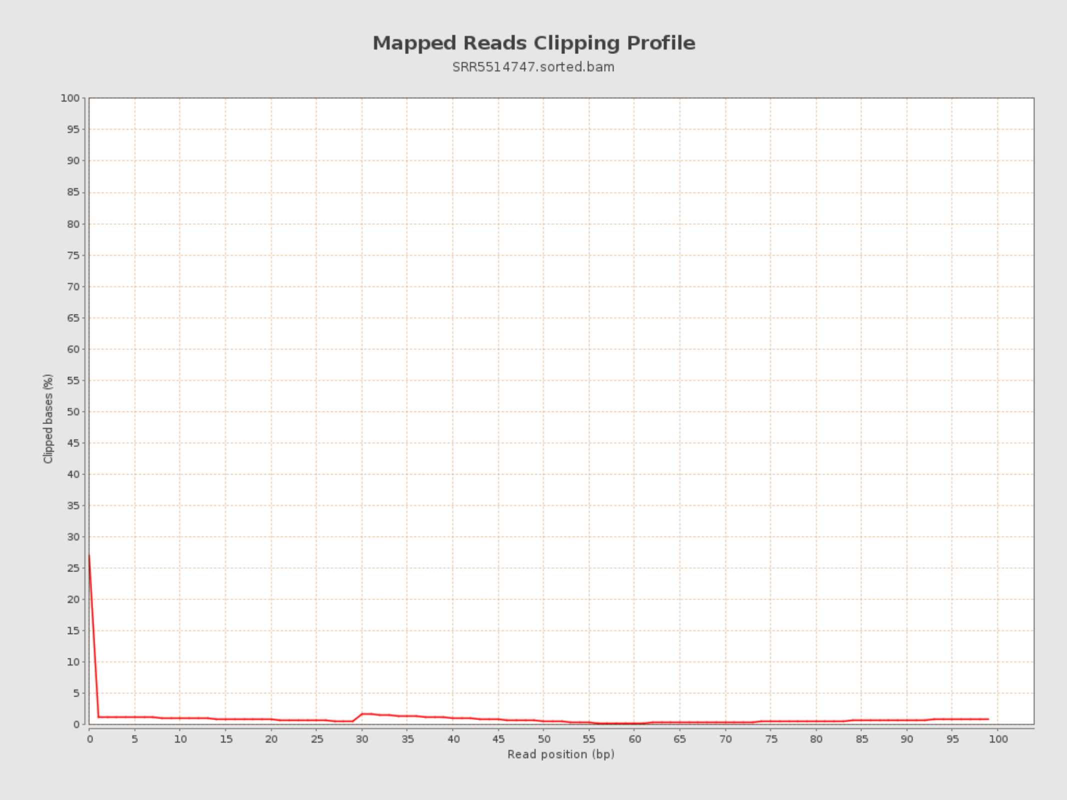
8. Results : Mapped Reads Nucleotide Content



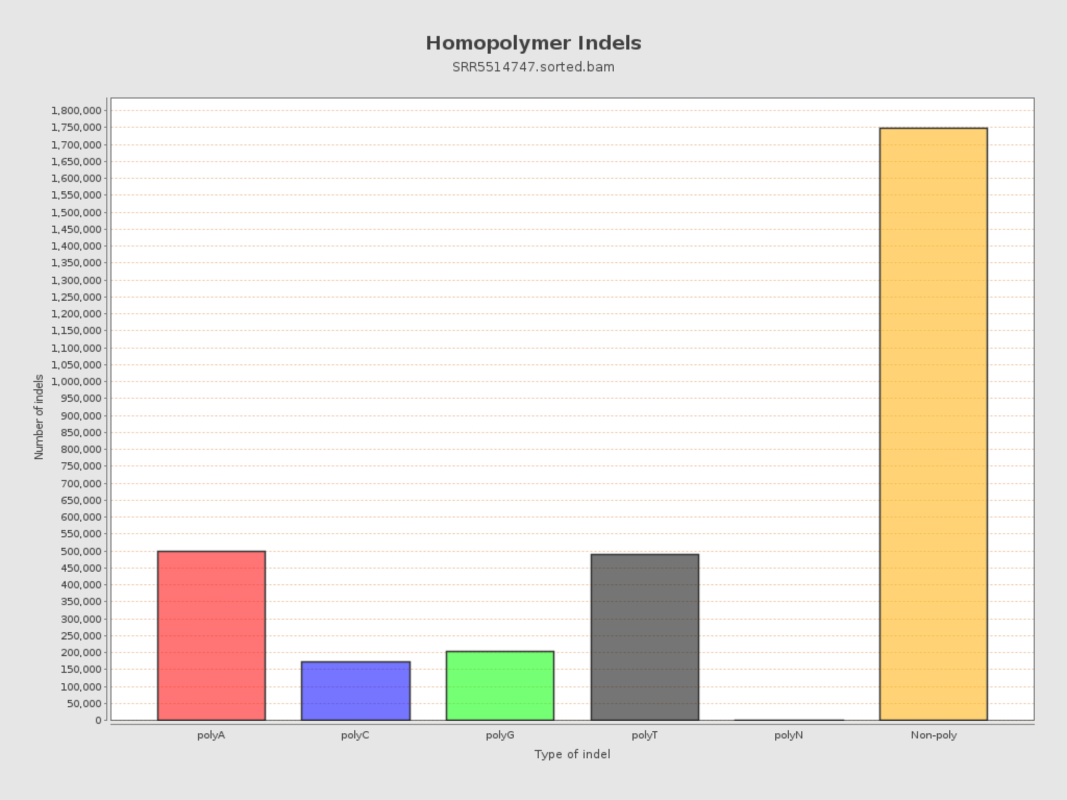
9. Results : Mapped Reads GC-content Distribution



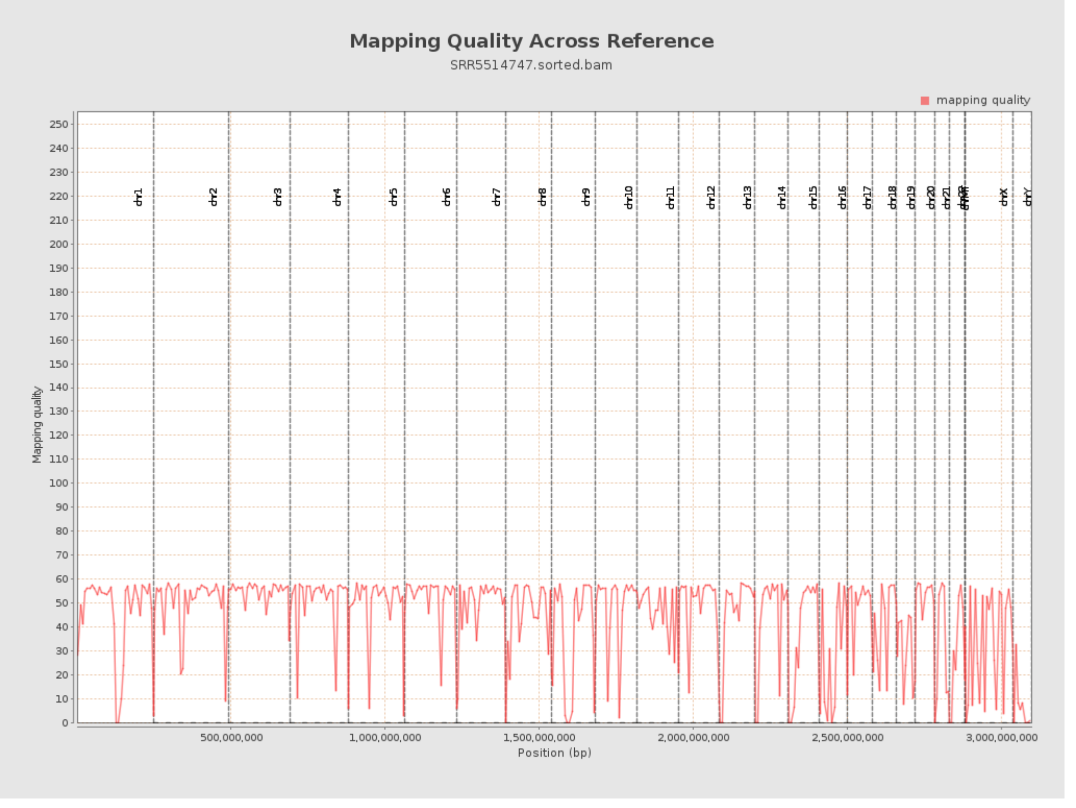
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram