

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 15:04:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514741.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_SRR5514741 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514741.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 15:04:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514741.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,090,679
Mapped reads	34,170,549 / 94.68%
Unmapped reads	1,920,130 / 5.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,368,022 / 3.79%
Read min/max/mean length	30 / 100 / 99.87
Duplicated reads (estimated)	21,561,963 / 59.74%
Duplication rate	35.83%
Clipped reads	8,242,285 / 22.84%

2.2. ACGT Content

Number/percentage of A's	820,199,401 / 25.76%
Number/percentage of C's	756,637,866 / 23.77%
Number/percentage of T's	826,870,423 / 25.97%
Number/percentage of G's	759,209,010 / 23.85%
Number/percentage of N's	20,772,017 / 0.65%
GC Percentage	47.61%

2.3. Coverage

Mean	1.0296

Standard Deviation	40.0592
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2.4. Mapping Quality

Mean Mapping Quality	40.89
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2.5. Mismatches and indels

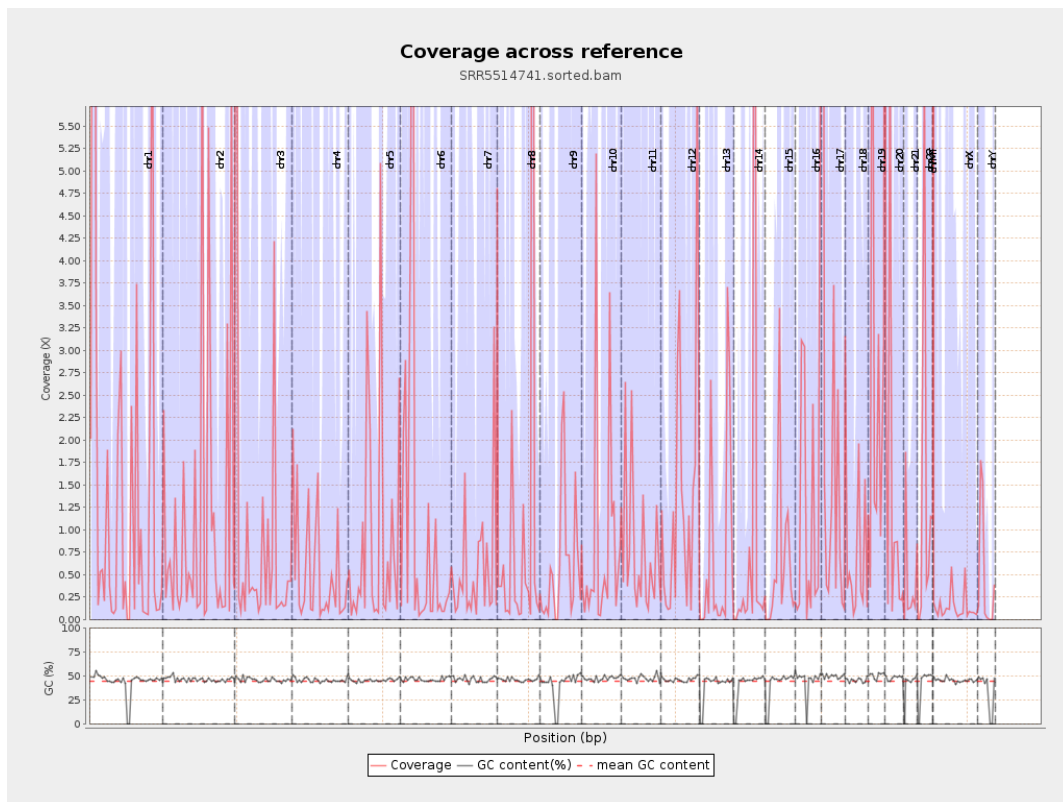
General error rate	1.24%
Mismatches	36,081,205
Insertions	1,489,080
Mapped reads with at least one insertion	4.08%
Deletions	1,225,586
Mapped reads with at least one deletion	3.39%
Homopolymer indels	37.97%

2.6. Chromosome stats

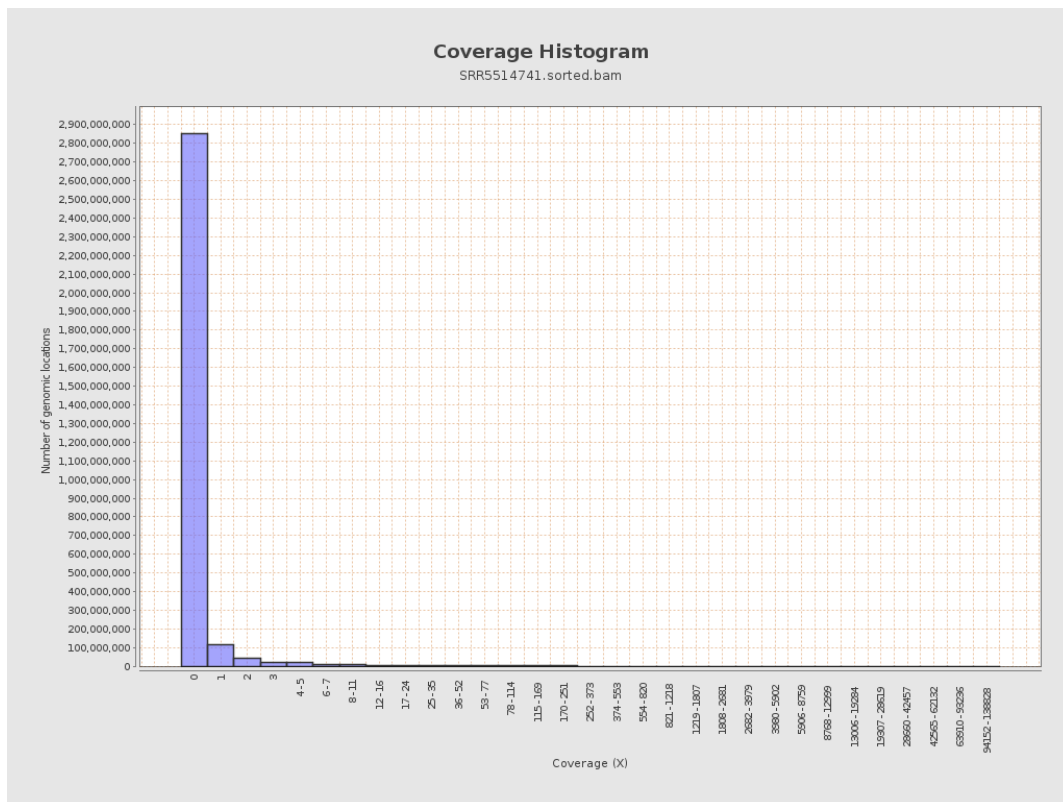
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	394111390	1.5812	22.9507
chr2	243199373	284667648	1.1705	101.0832
chr3	198022430	205329964	1.0369	20.4601
chr4	191154276	98048490	0.5129	20.0185
chr5	180915260	156760896	0.8665	21.2035
chr6	171115067	193082995	1.1284	25.2565
chr7	159138663	91698139	0.5762	13.5052

chr8	146364022	160915668	1.0994	18.7365
chr9	141213431	87599176	0.6203	19.22
chr10	135534747	116893793	0.8625	64.8972
chr11	135006516	100746398	0.7462	17.3038
chr12	133851895	182449575	1.3631	17.4797
chr13	115169878	88474292	0.7682	15.1324
chr14	107349540	111720814	1.0407	23.7538
chr15	102531392	61733153	0.6021	11.3379
chr16	90354753	145487057	1.6102	68.7645
chr17	81195210	228224427	2.8108	37.2356
chr18	78077248	54234606	0.6946	40.1611
chr19	59128983	189105792	3.1982	35.1656
chr20	63025520	86784886	1.377	18.3652
chr21	48129895	23475071	0.4877	12.1192
chr22	51304566	67974476	1.3249	18.8293
chrMT	16571	5862226	353.7642	186.8733
chrX	155270560	21783524	0.1403	10.1878
chrY	59373566	30024524	0.5057	72.4389

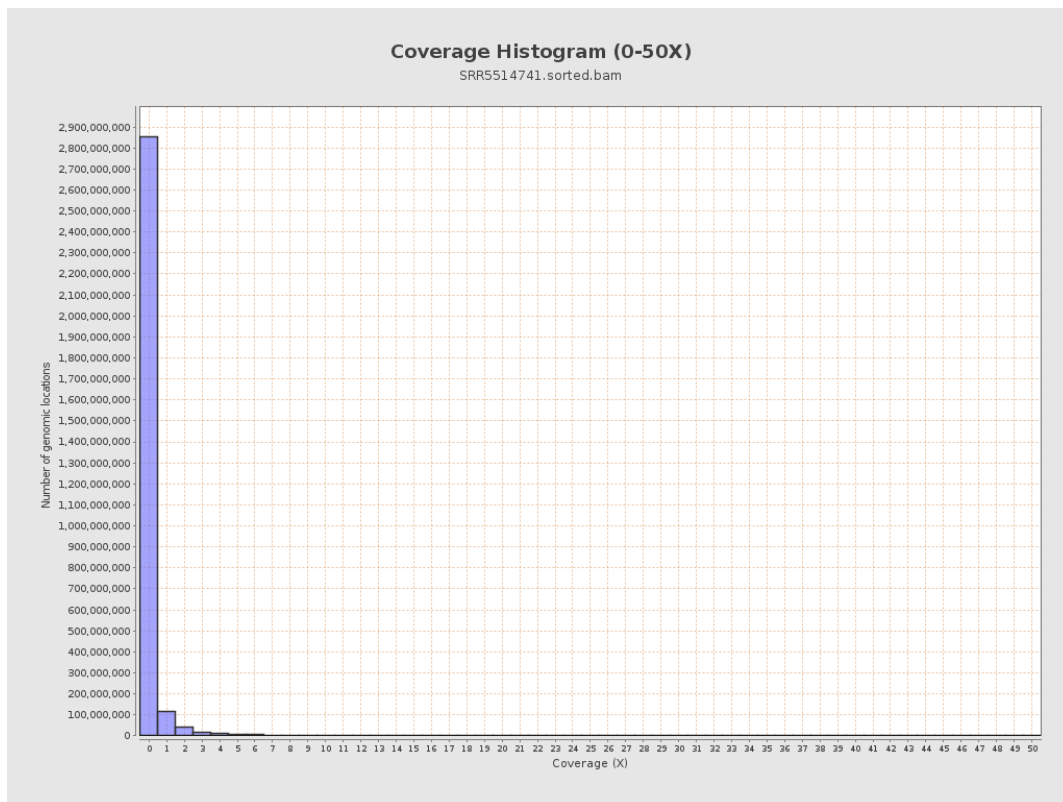
3. Results : Coverage across reference



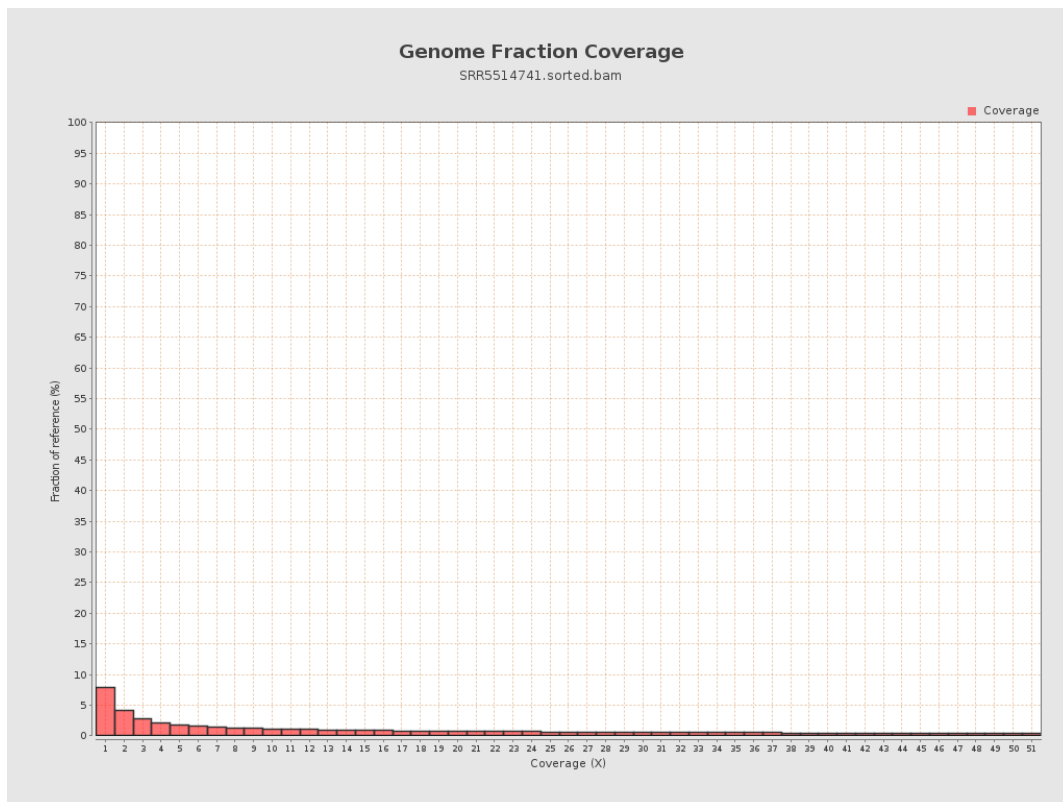
4. Results : Coverage Histogram



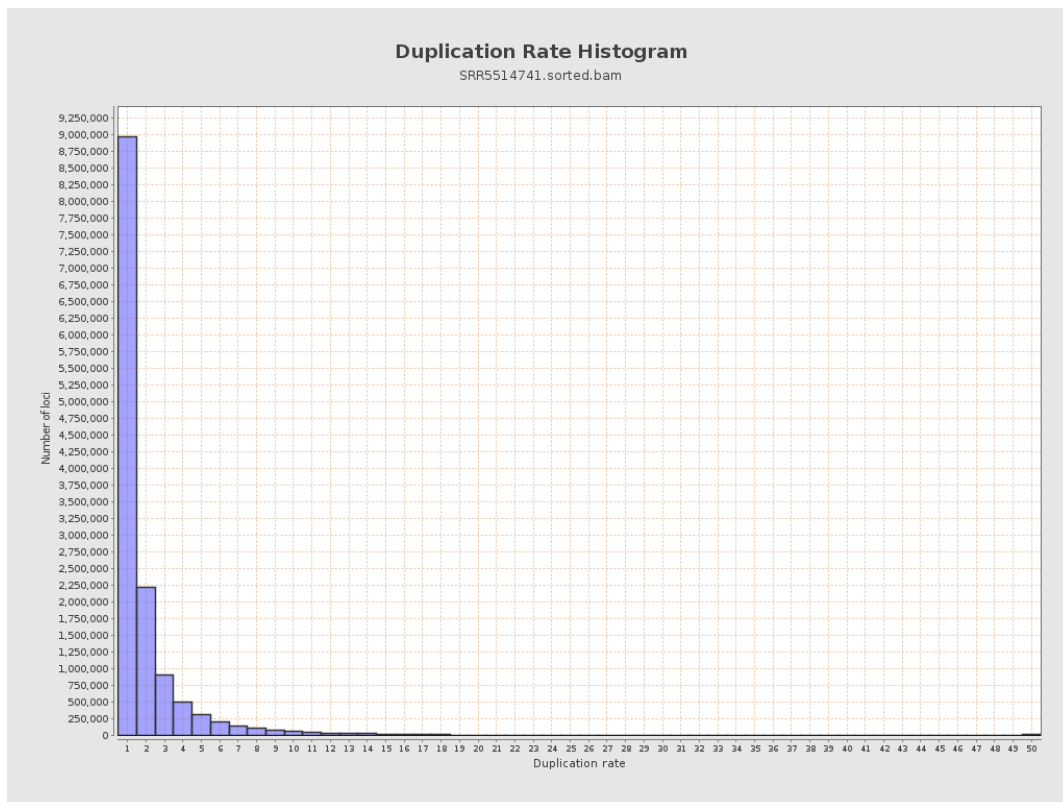
5. Results : Coverage Histogram (0-50X)



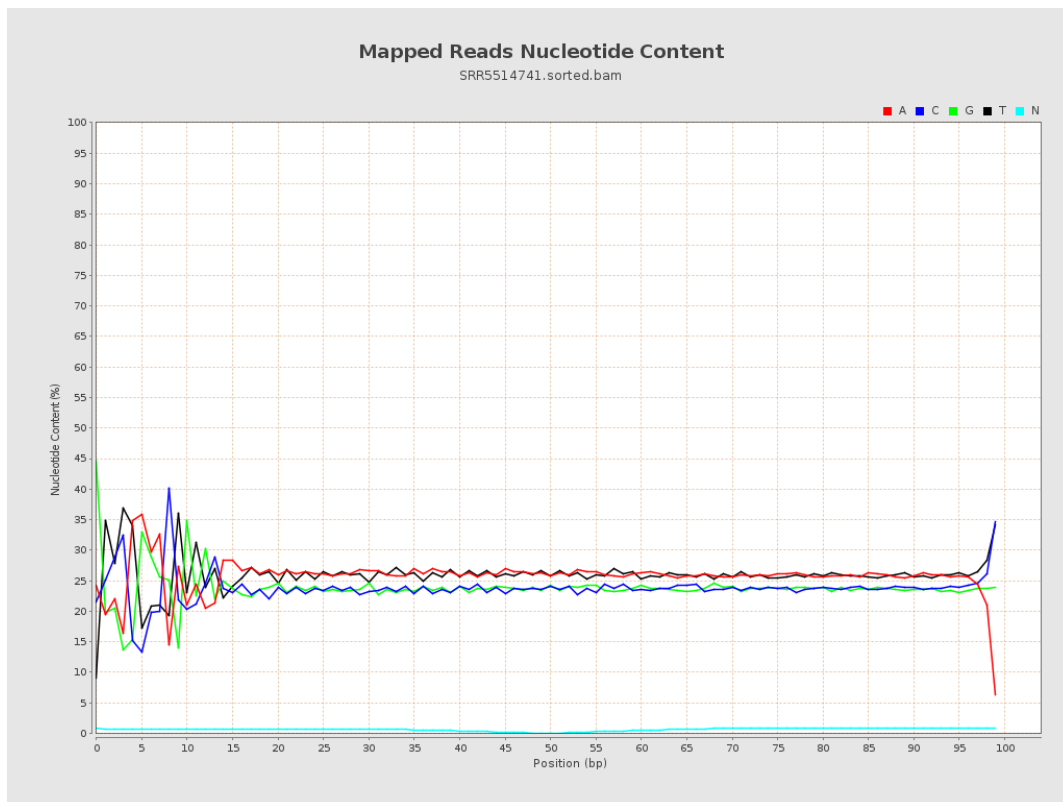
6. Results : Genome Fraction Coverage



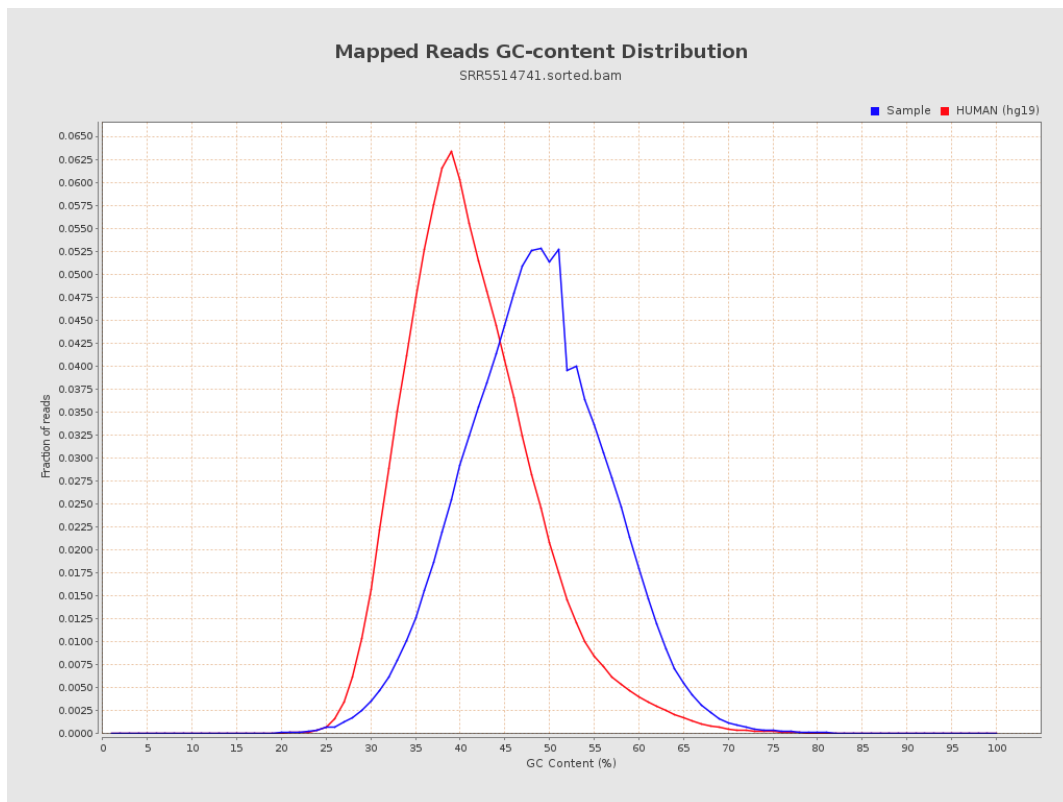
7. Results : Duplication Rate Histogram



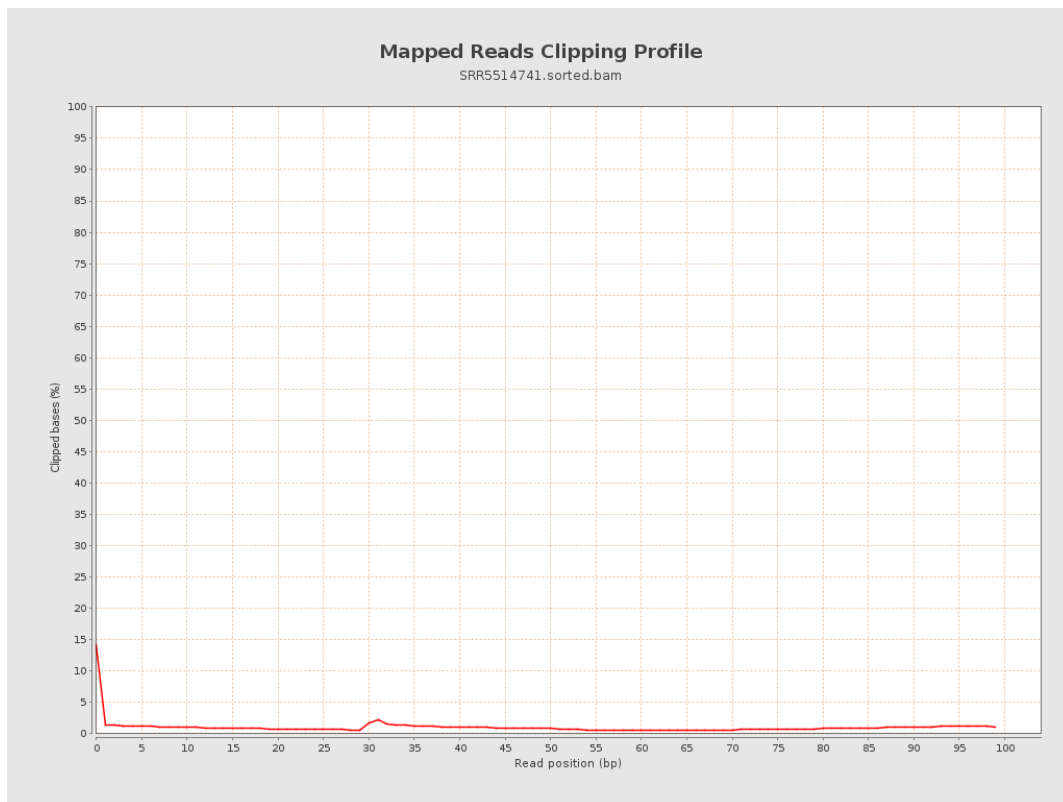
8. Results : Mapped Reads Nucleotide Content



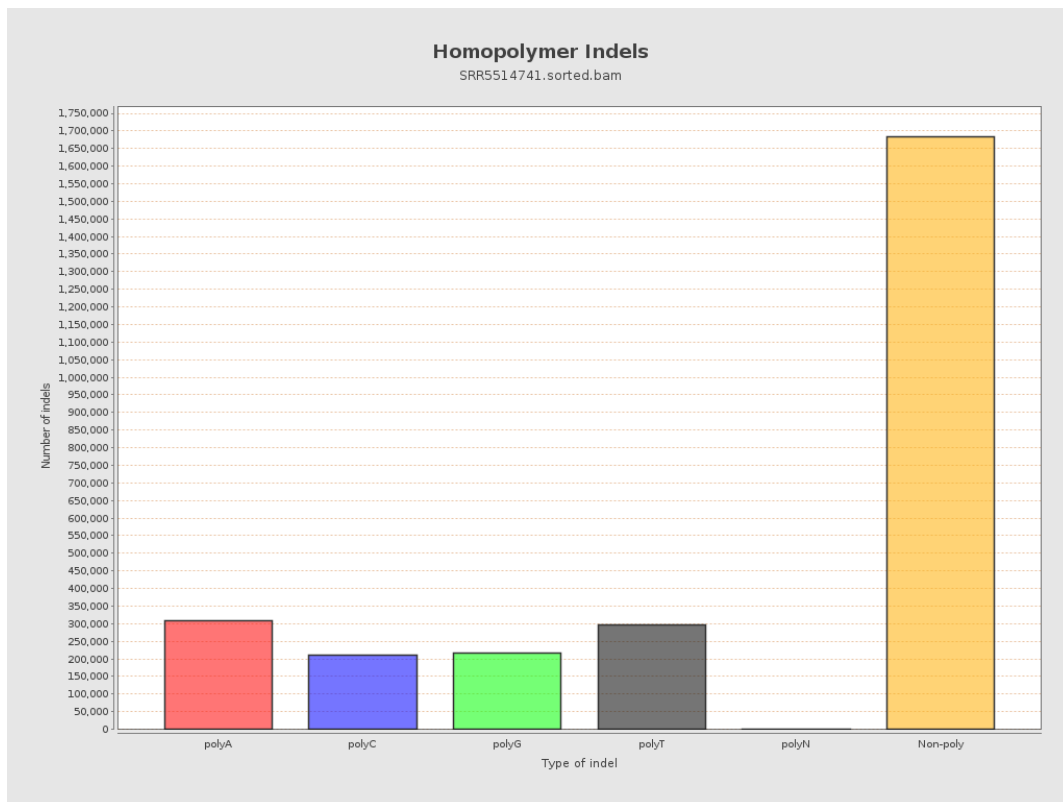
9. Results : Mapped Reads GC-content Distribution



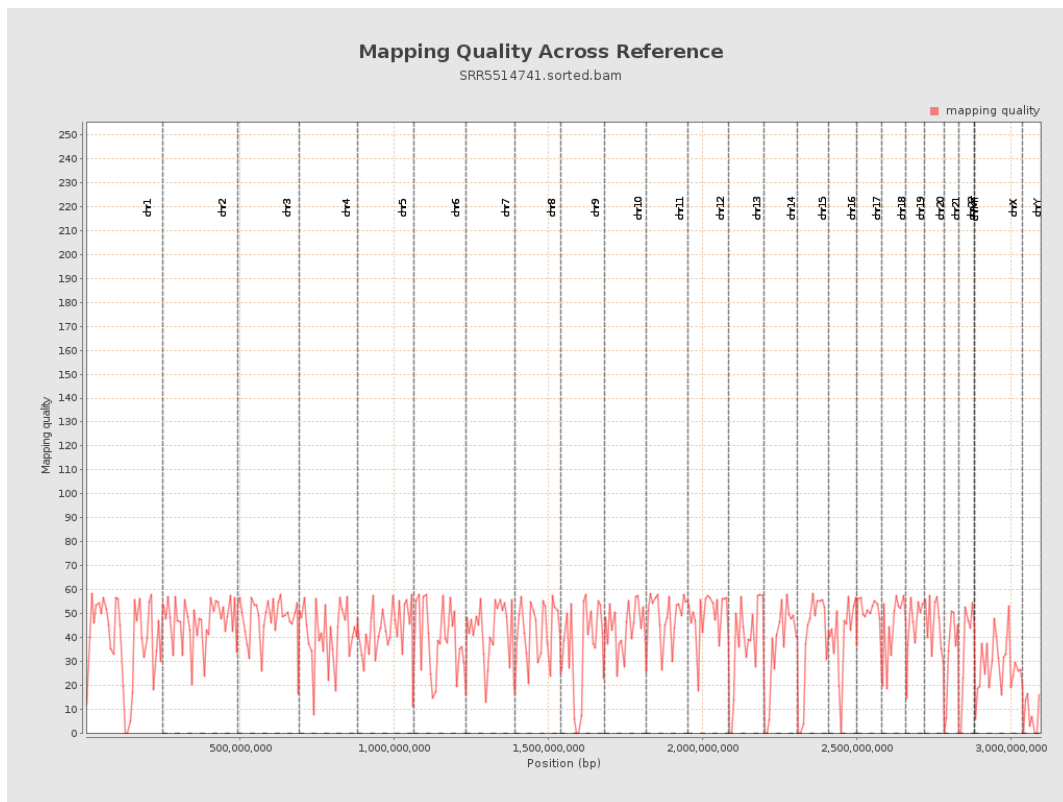
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

