Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/09 14:21:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514701.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_SRR5514701 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514701.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 09 14:21:52 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514701.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,394,214
Mapped reads	58,898,209 / 99.16%
Unmapped reads	496,005 / 0.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,804,135 / 9.77%
Read min/max/mean length	30 / 100 / 101.27
Duplicated reads (estimated)	58,565,718 / 98.61%
Duplication rate	48.01%
Clipped reads	21,725,542 / 36.58%

2.2. ACGT Content

Number/percentage of A's	1,615,476,477 / 29.11%
Number/percentage of C's	1,148,901,800 / 20.7%
Number/percentage of T's	1,612,620,624 / 29.06%
Number/percentage of G's	1,170,232,364 / 21.09%
Number/percentage of N's	2,209,626 / 0.04%
GC Percentage	41.79%

2.3. Coverage

Mean	1.7947

Standard Deviation	291.3494

2.4. Mapping Quality

Mean Mapping Quality	48.37

2.5. Mismatches and indels

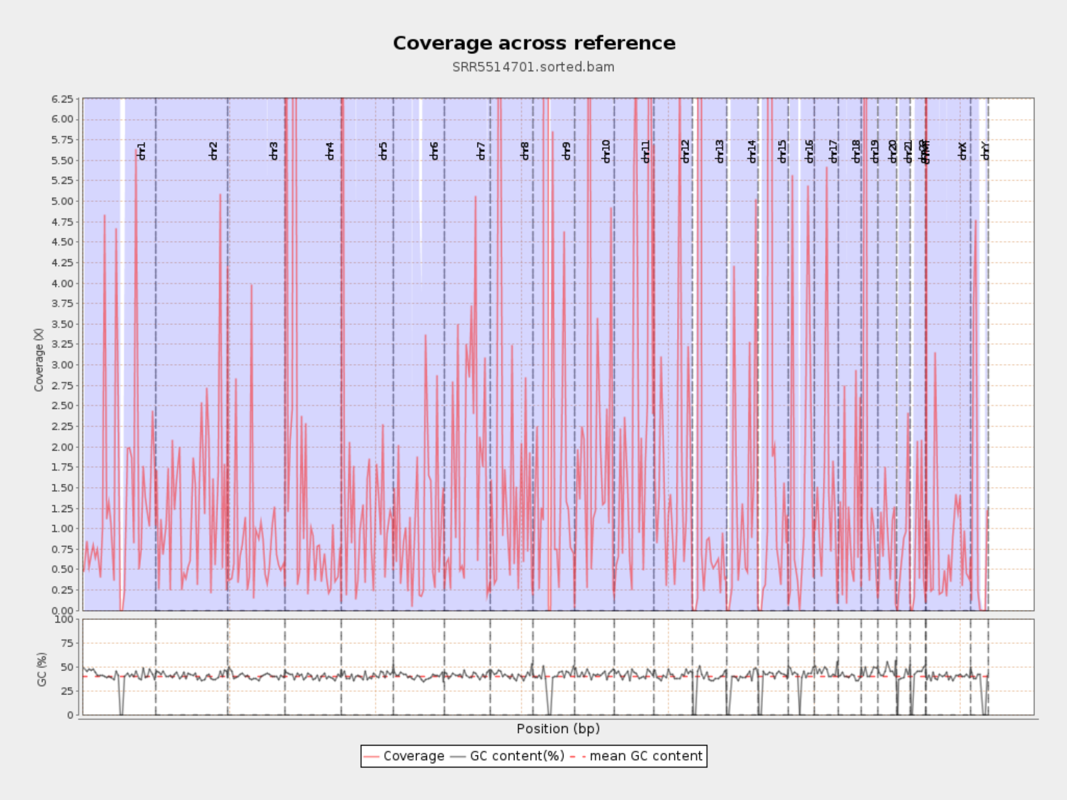
General error rate	0.87%
Mismatches	43,328,854
Insertions	2,941,283
Mapped reads with at least one insertion	4.81%
Deletions	2,346,628
Mapped reads with at least one deletion	3.74%
Homopolymer indels	39.83%

2.6. Chromosome stats

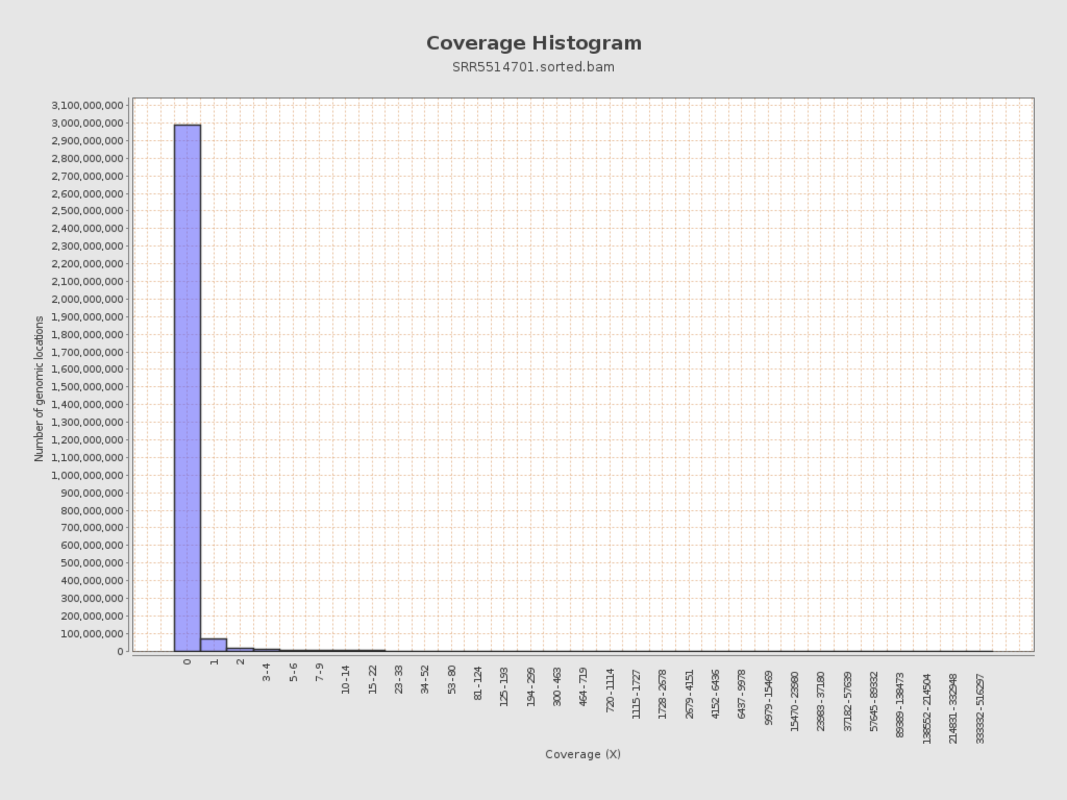
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	352534582	1.4144	87.4041
chr2	243199373	318084813	1.3079	56.9419
chr3	198022430	179938112	0.9087	58.0665
chr4	191154276	339145041	1.7742	146.4341
chr5	180915260	280415127	1.55	149.3365
chr6	171115067	179570681	1.0494	58.7255
chr7	159138663	275725993	1.7326	84.0637

chr8	146364022	265649370	1.815	225.9658
chr9	141213431	805081471	5.7012	900.0189
chr10	135534747	318401372	2.3492	159.4611
chr11	135006516	328899431	2.4362	195.6991
chr12	133851895	228637291	1.7081	98.7434
chr13	115169878	404108911	3.5088	939.5941
chr14	107349540	157921471	1.4711	153.8177
chr15	102531392	281086019	2.7415	297.9899
chr16	90354753	144072210	1.5945	103.8278
chr17	81195210	125238245	1.5424	82.006
chr18	78077248	92569336	1.1856	63.3643
chr19	59128983	137155710	2.3196	174.5099
chr20	63025520	59550520	0.9449	38.3923
chr21	48129895	38948704	0.8092	34.8573
chr22	51304566	39461235	0.7692	59.6137
chrMT	16571	1614620	97.4365	196.5748
chrX	155270560	123826958	0.7975	47.2308
chrY	59373566	78191718	1.3169	49.4806

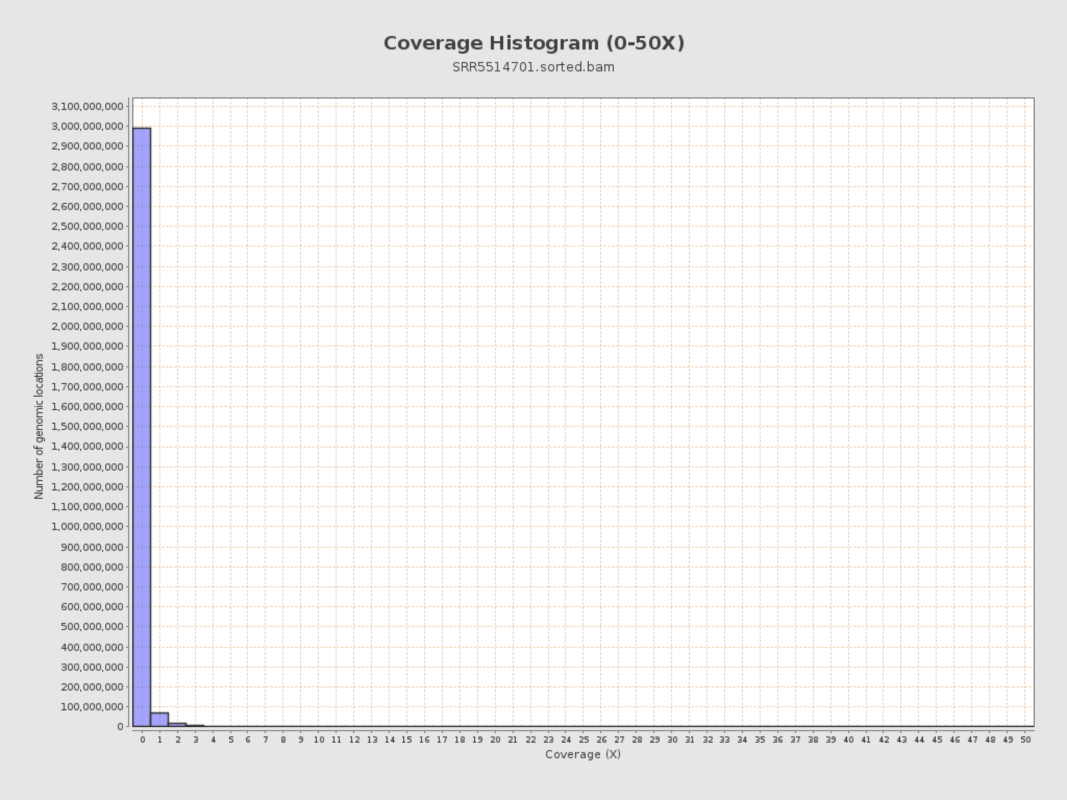
3. Results : Coverage across reference



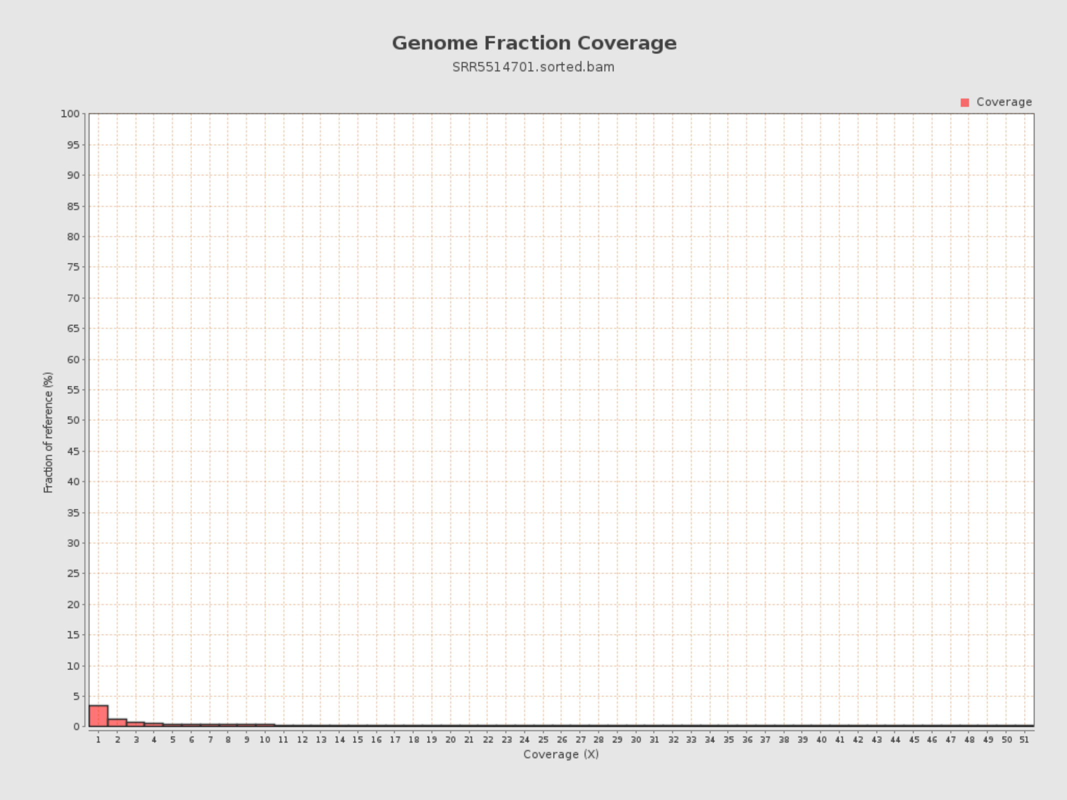
4. Results : Coverage Histogram



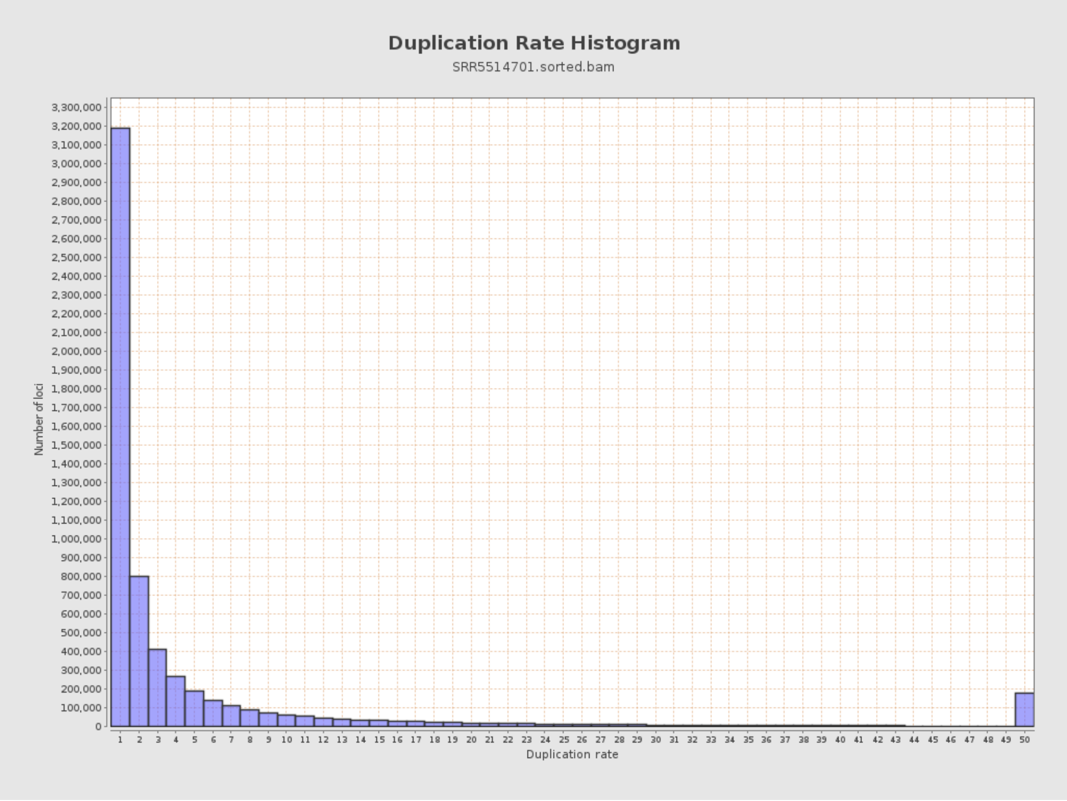
5. Results : Coverage Histogram (0-50X)



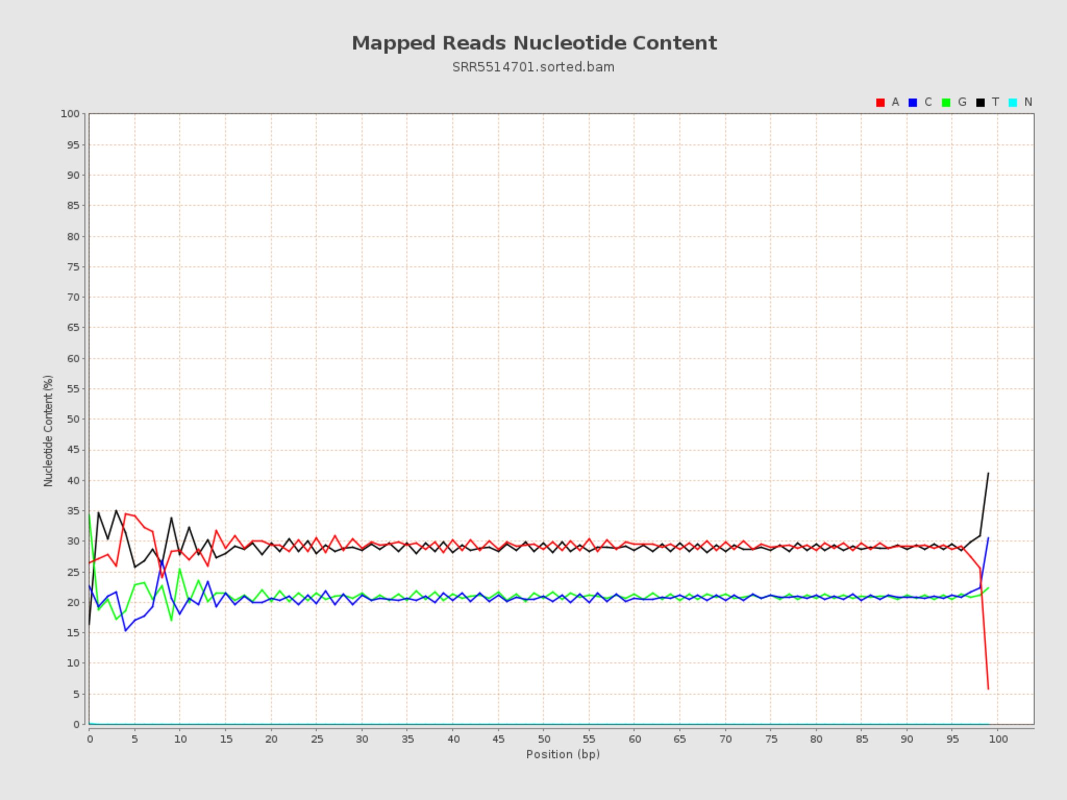
6. Results : Genome Fraction Coverage



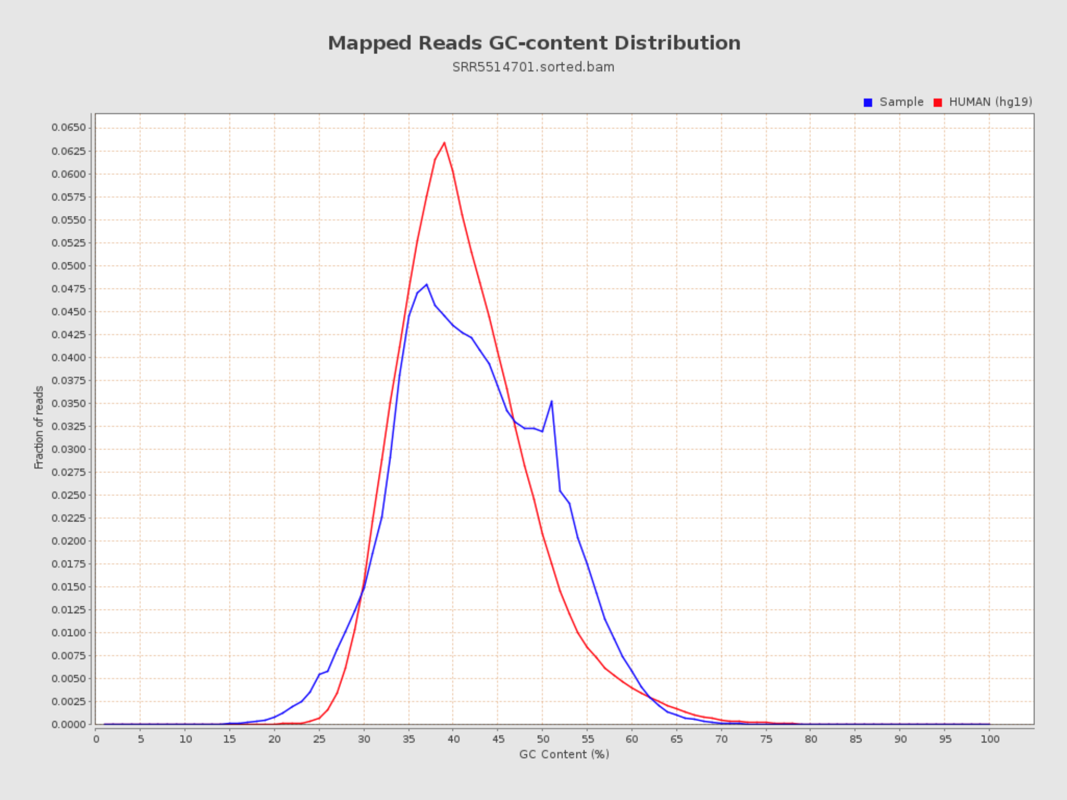
7. Results : Duplication Rate Histogram



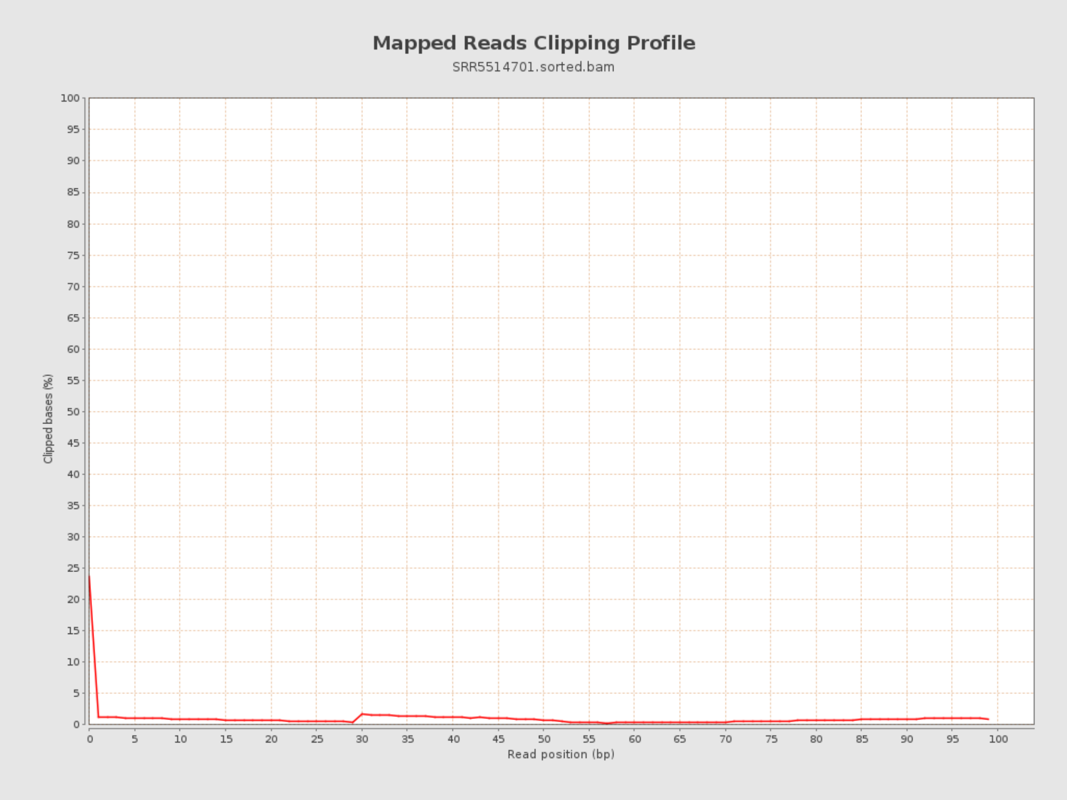
8. Results : Mapped Reads Nucleotide Content



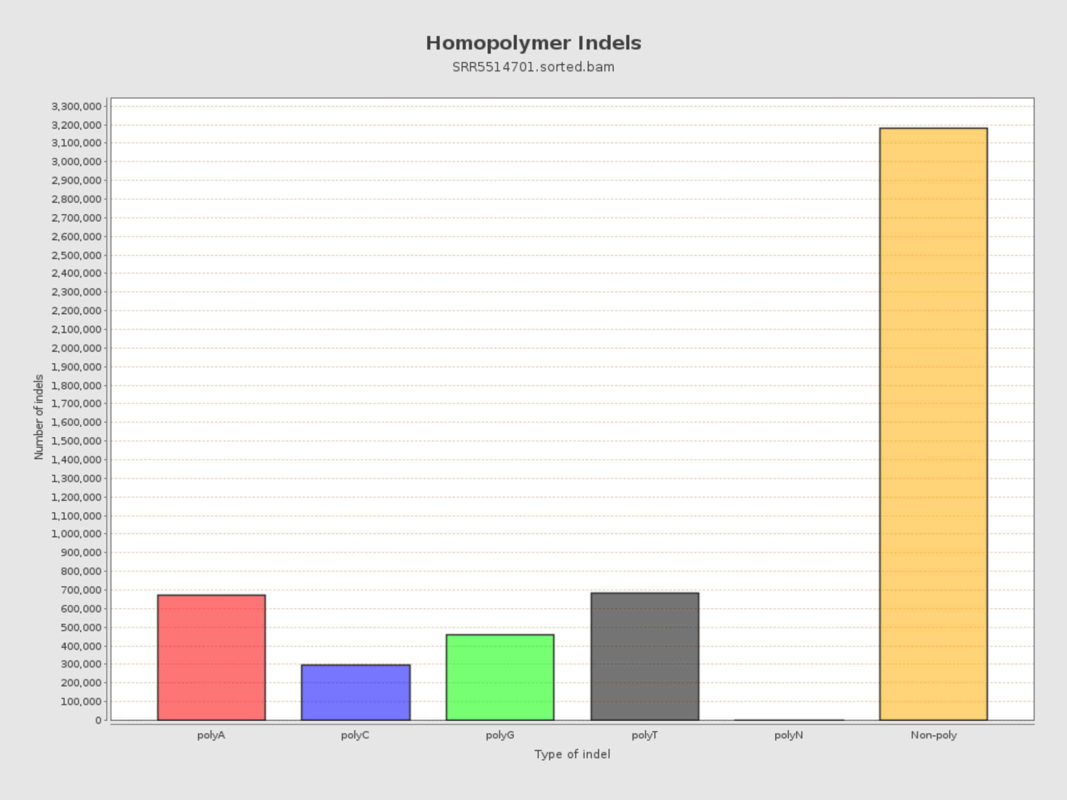
9. Results : Mapped Reads GC-content Distribution



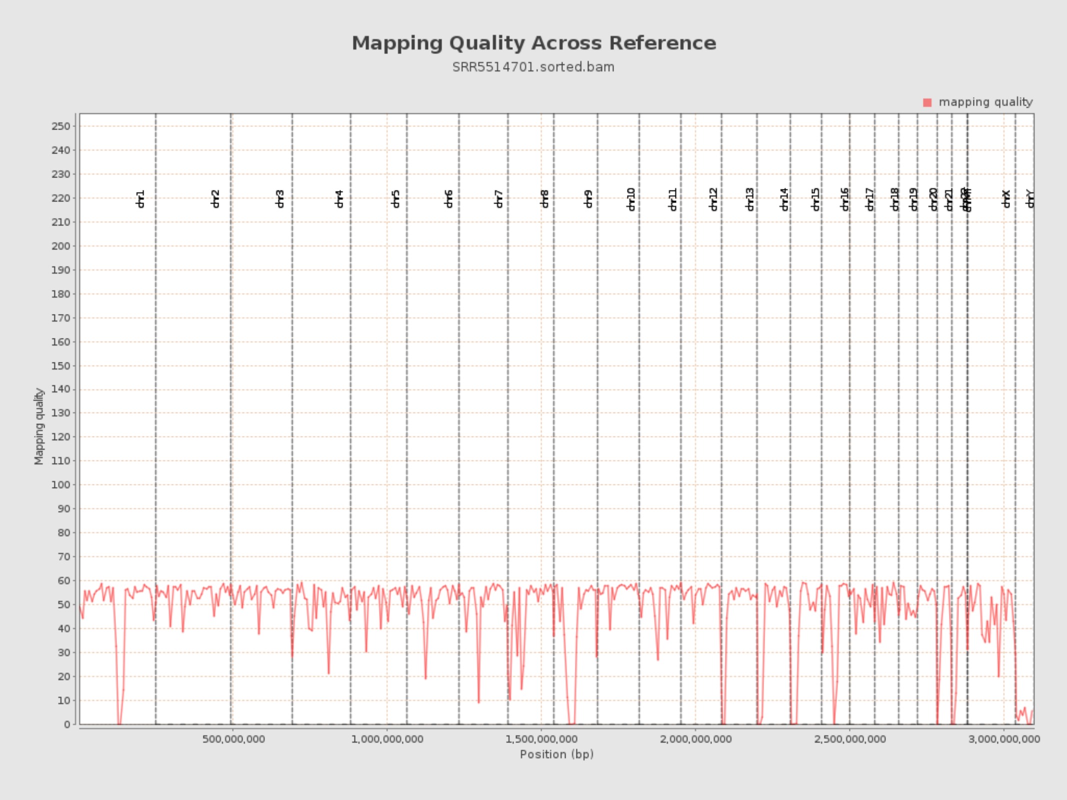
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram