Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:43:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549114.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_SRR1549114 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549114.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:43:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,907,364
Mapped reads	5,112,906 / 57.4%
Unmapped reads	3,794,458 / 42.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	231,300 / 2.6%
Duplication rate	3.34%
Clipped reads	267,417 / 3%

2.2. ACGT Content

Number/percentage of A's	60,283,168 / 29.71%
Number/percentage of C's	41,330,568 / 20.37%
Number/percentage of T's	60,174,254 / 29.66%
Number/percentage of G's	41,105,074 / 20.26%
Number/percentage of N's	8,240 / 0%
GC Percentage	40.63%

2.3. Coverage

Mean	0.0656
Standard Deviation	0.9527

2.4. Mapping Quality

Mean Mapping Quality	44.2

2.5. Mismatches and indels

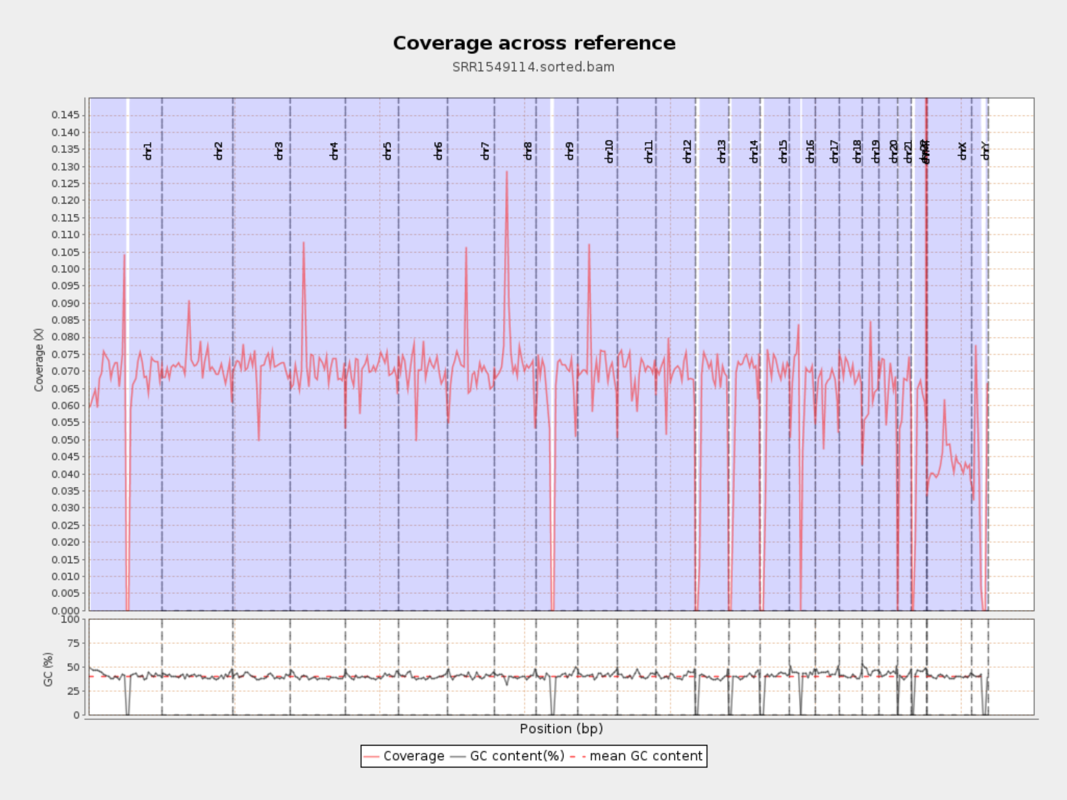
General error rate	0.32%
Mismatches	650,673
Insertions	5,229
Mapped reads with at least one insertion	0.1%
Deletions	17,003
Mapped reads with at least one deletion	0.33%
Homopolymer indels	44.4%

2.6. Chromosome stats

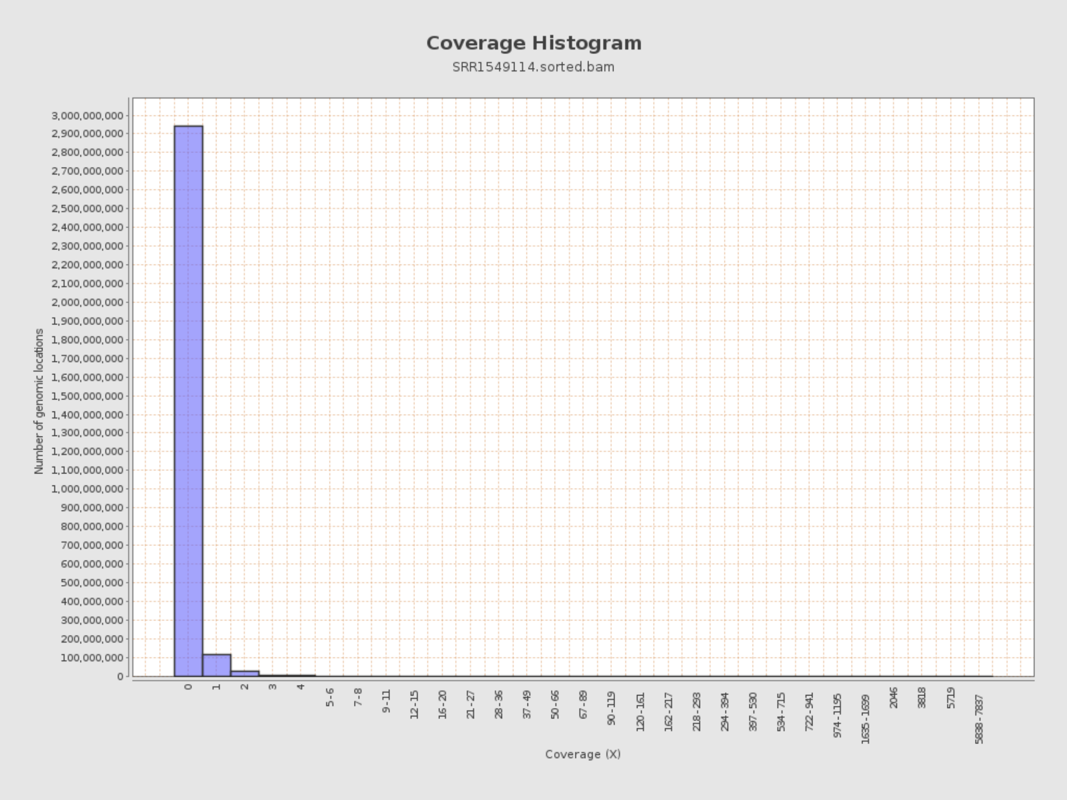
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16456130	0.066	0.9168
chr2	243199373	17462211	0.0718	0.4461
chr3	198022430	14120844	0.0713	0.3369
chr4	191154276	13686028	0.0716	0.3868
chr5	180915260	12754562	0.0705	0.339
chr6	171115067	12036763	0.0703	0.346
chr7	159138663	11279199	0.0709	0.6112
chr8	146364022	10954409	0.0748	3.8247

chr9	141213431	8587942	0.0608	0.3919
chr10	135534747	9759097	0.072	0.4964
chr11	135006516	9472734	0.0702	0.4077
chr12	133851895	9302315	0.0695	0.3418
chr13	115169878	6745194	0.0586	0.3052
chr14	107349540	6363085	0.0593	0.3585
chr15	102531392	5973346	0.0583	0.2997
chr16	90354753	5597680	0.062	0.3393
chr17	81195210	5201200	0.0641	0.3317
chr18	78077248	5490084	0.0703	0.7075
chr19	59128983	3714590	0.0628	0.7075
chr20	63025520	4190230	0.0665	0.3489
chr21	48129895	2764694	0.0574	0.3596
chr22	51304566	2255567	0.044	0.2672
chrMT	16571	103676	6.2565	7.9388
chrX	155270560	6705930	0.0432	0.314
chrY	59373566	1945538	0.0328	0.4016

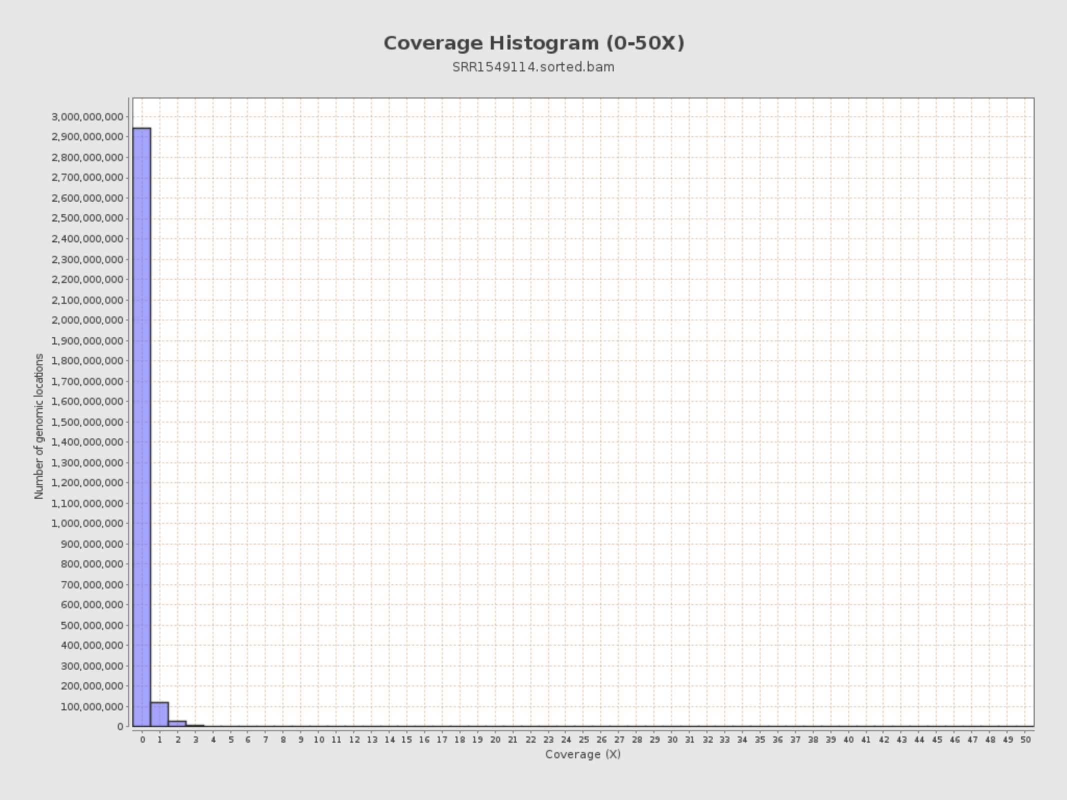
3. Results : Coverage across reference



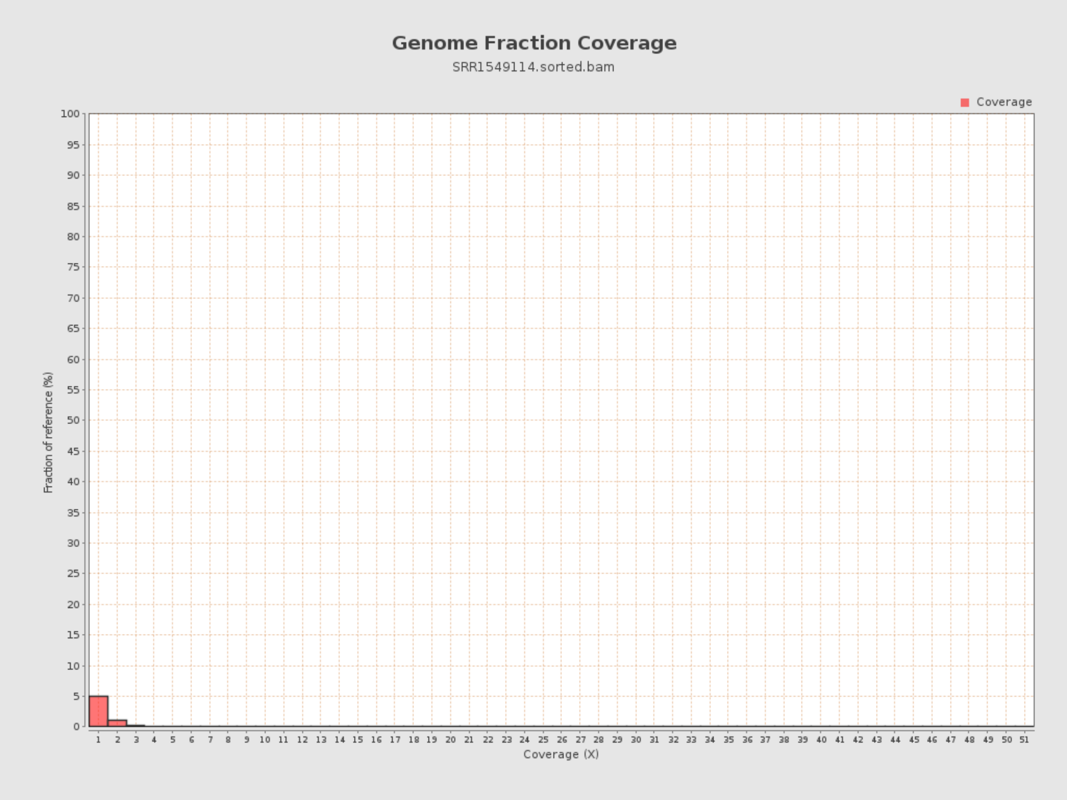
4. Results : Coverage Histogram



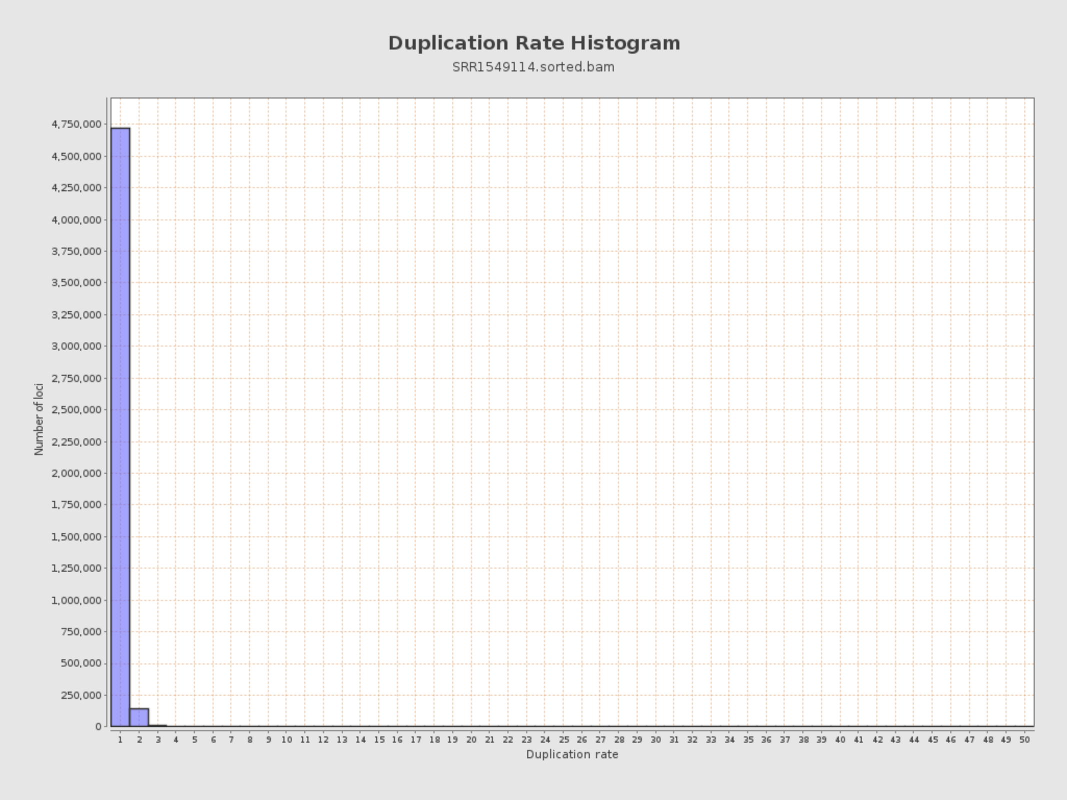
5. Results : Coverage Histogram (0-50X)



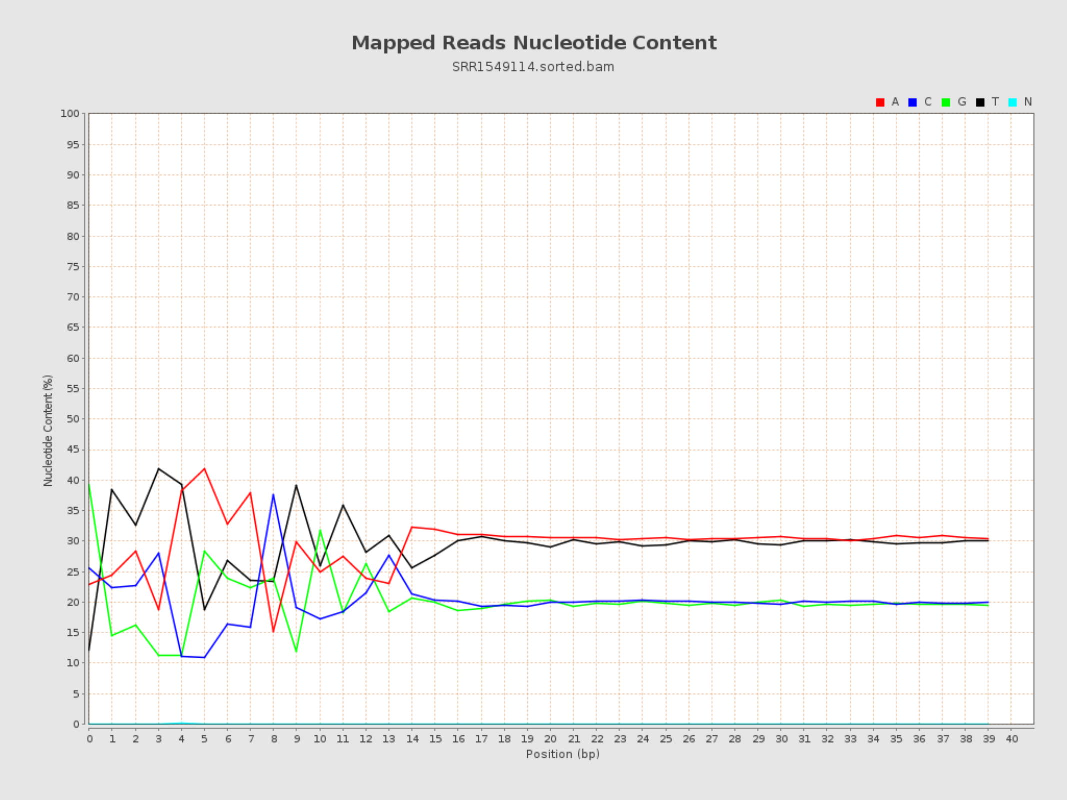
6. Results : Genome Fraction Coverage



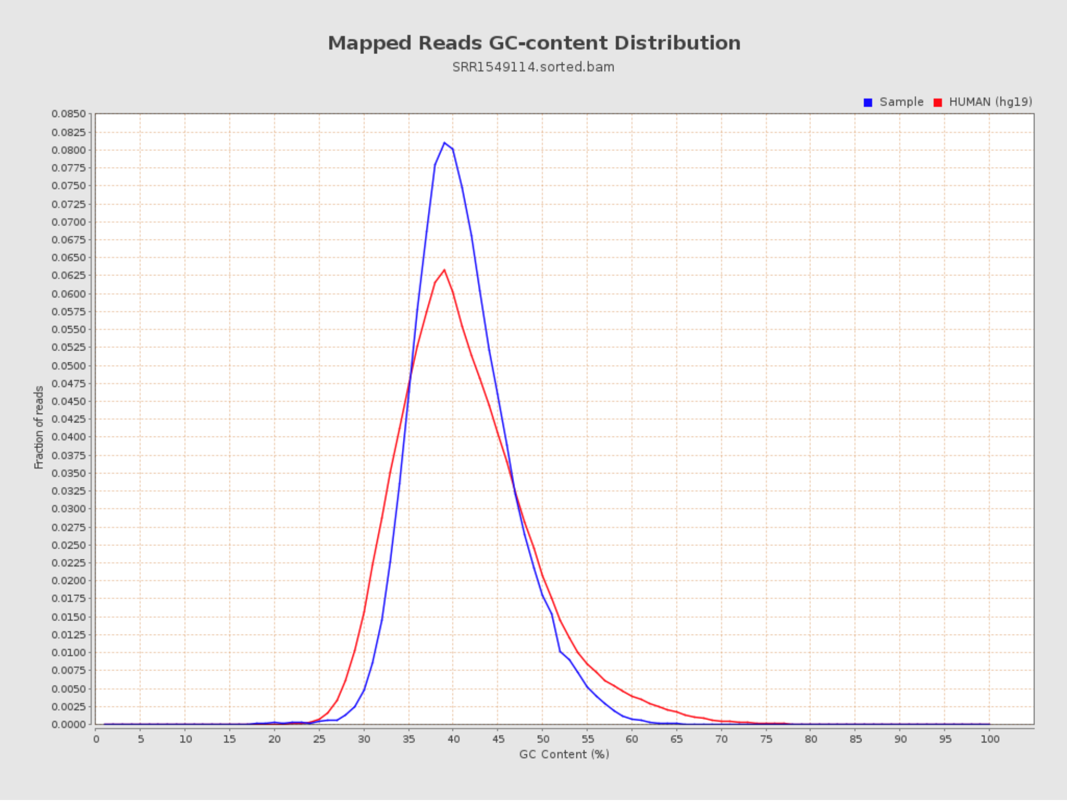
7. Results : Duplication Rate Histogram



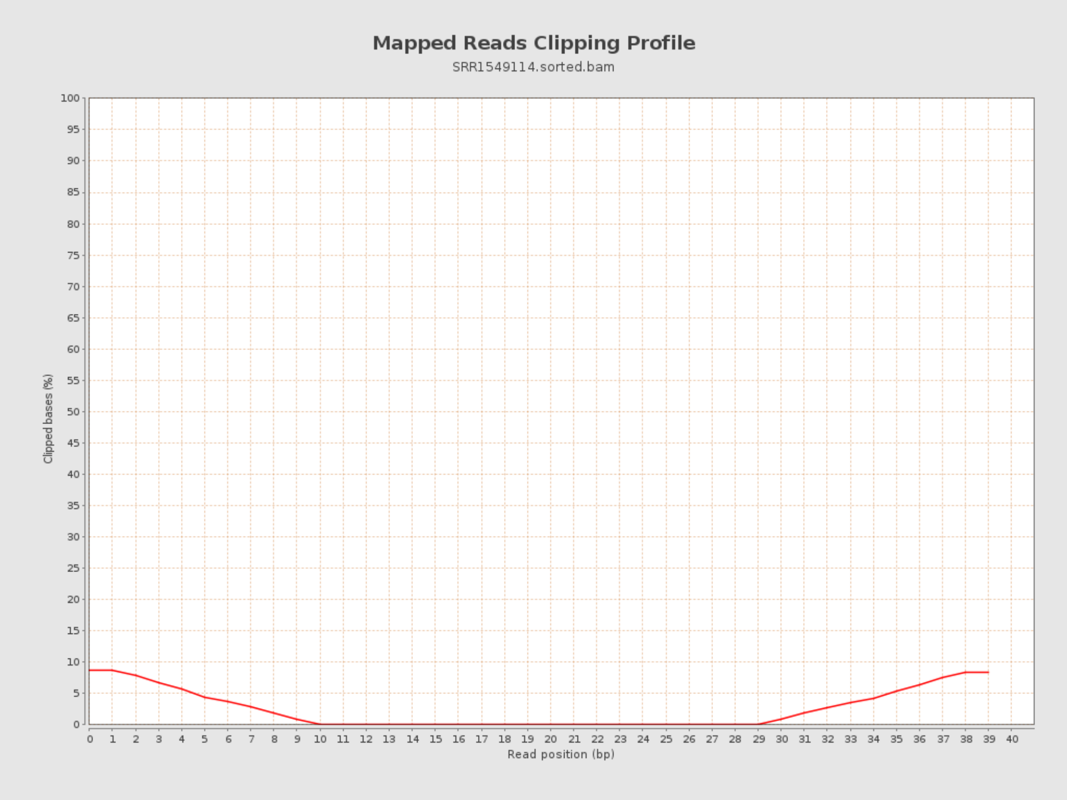
8. Results : Mapped Reads Nucleotide Content



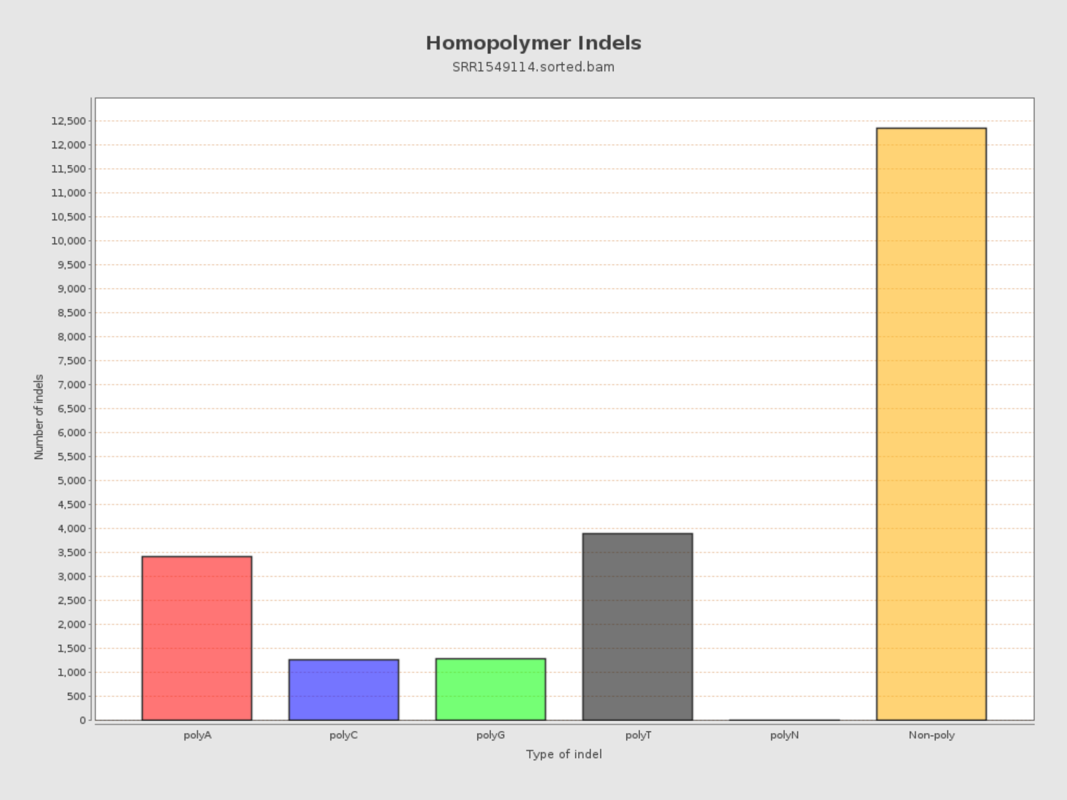
9. Results : Mapped Reads GC-content Distribution



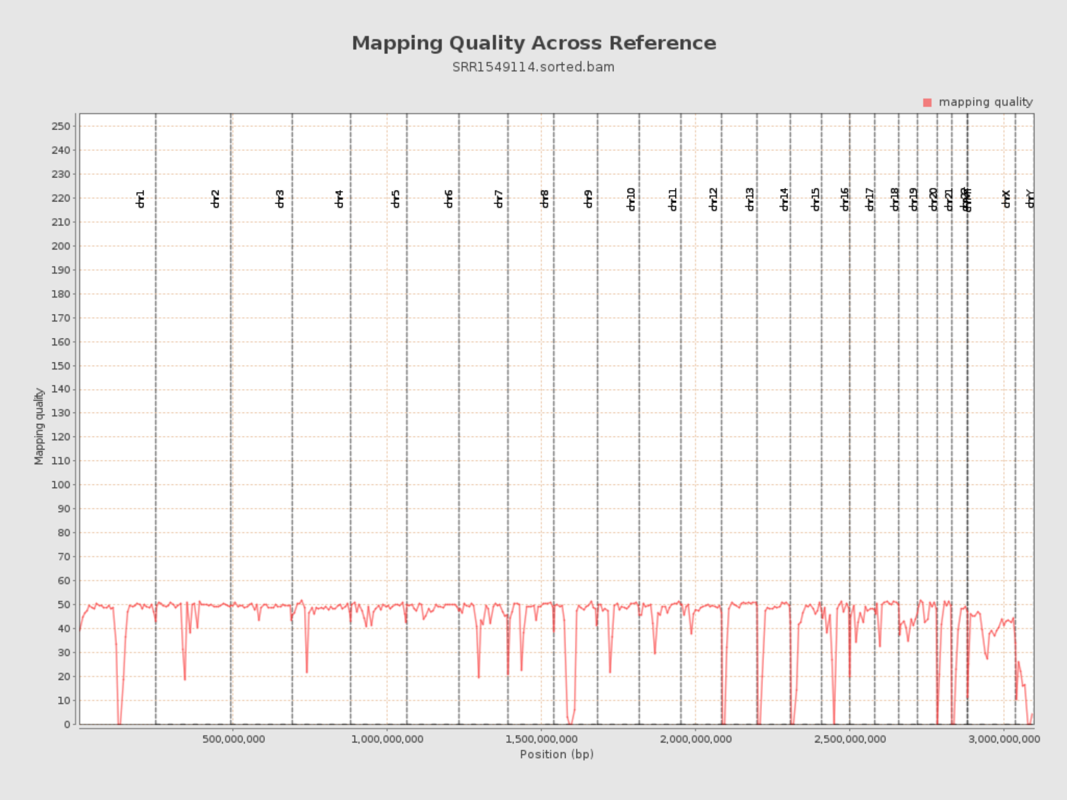
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram