Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:39:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548992.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_SRR1548992 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548992.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:39:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548992.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,757,062
Mapped reads	4,969,522 / 86.32%
Unmapped reads	787,540 / 13.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	295,985 / 5.14%
Duplication rate	5.24%
Clipped reads	248,023 / 4.31%

2.2. ACGT Content

Number/percentage of A's	60,351,001 / 30.59%
Number/percentage of C's	38,361,518 / 19.44%
Number/percentage of T's	59,184,546 / 30%
Number/percentage of G's	39,390,598 / 19.97%
Number/percentage of N's	1,538 / 0%
GC Percentage	39.41%

2.3. Coverage

Mean	0.0637
Standard Deviation	0.5245

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

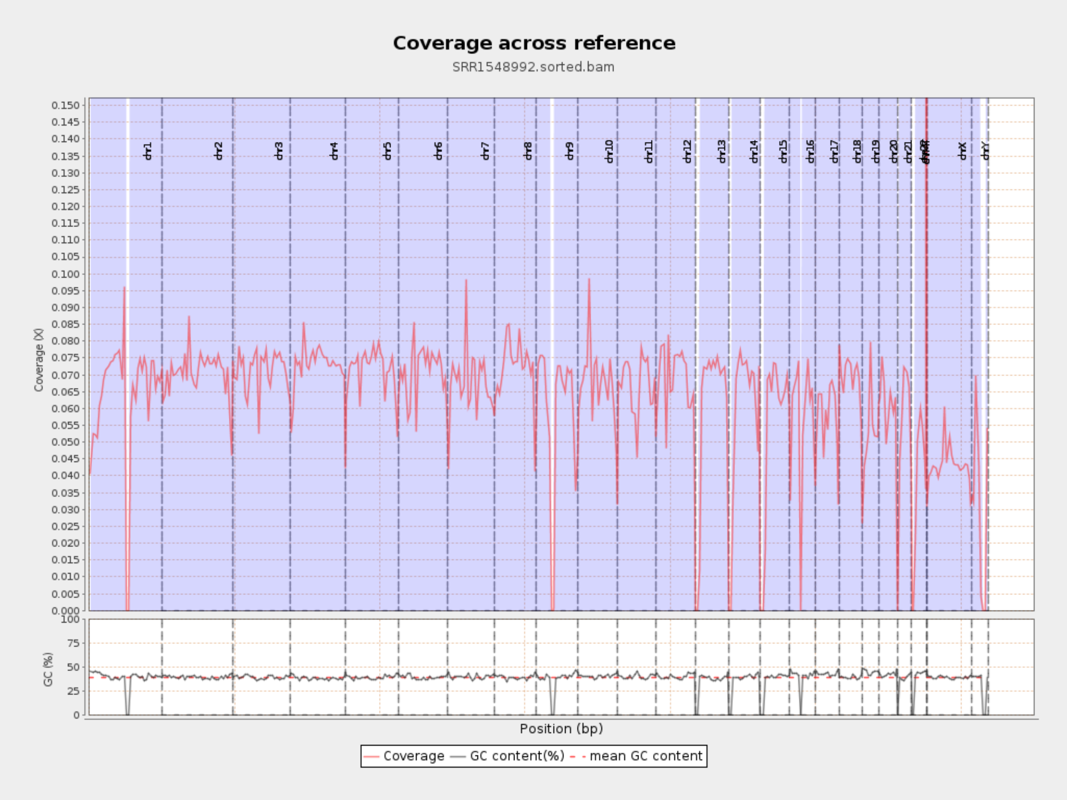
General error rate	0.31%
Mismatches	613,097
Insertions	5,681
Mapped reads with at least one insertion	0.11%
Deletions	16,546
Mapped reads with at least one deletion	0.33%
Homopolymer indels	43.41%

2.6. Chromosome stats

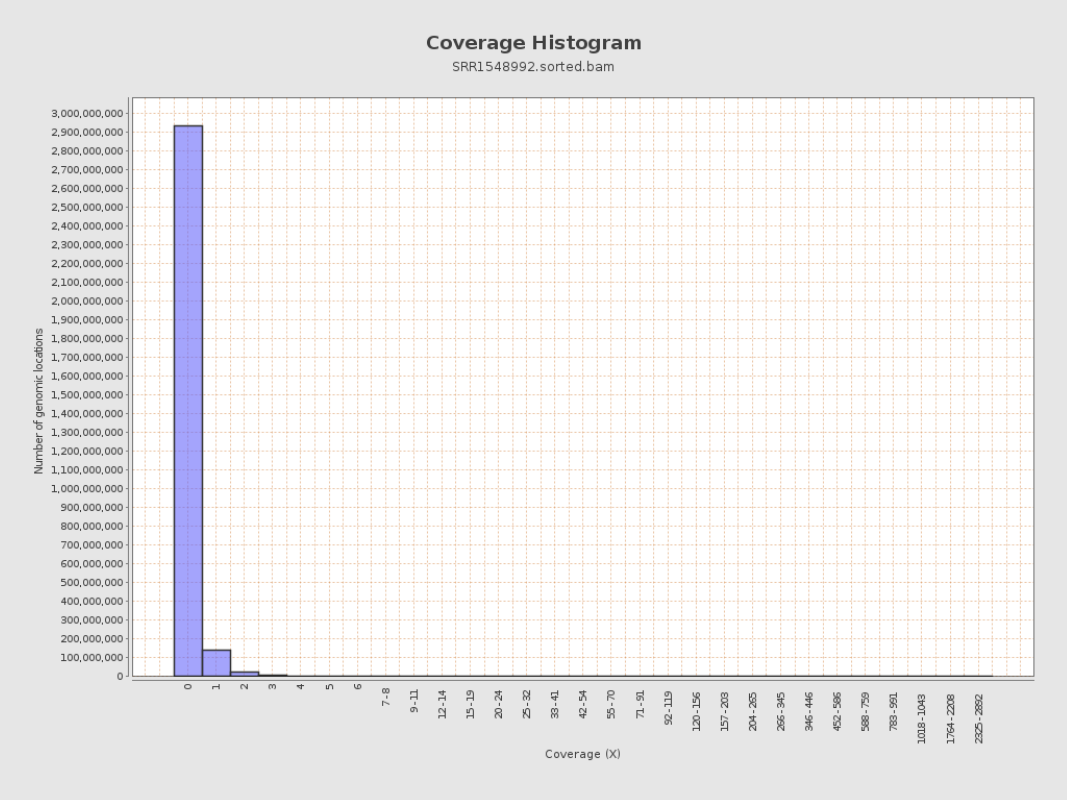
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15887346	0.0637	0.8006
chr2	243199373	17190504	0.0707	0.3995
chr3	198022430	14179733	0.0716	0.3106
chr4	191154276	13965027	0.0731	0.3316
chr5	180915260	12961716	0.0716	0.3143
chr6	171115067	12176230	0.0712	0.3488
chr7	159138663	10871966	0.0683	0.5546
chr8	146364022	10567365	0.0722	1.4471

chr9	141213431	8344902	0.0591	0.3664
chr10	135534747	9278226	0.0685	0.4257
chr11	135006516	9000285	0.0667	0.373
chr12	133851895	9244980	0.0691	0.3157
chr13	115169878	6780856	0.0589	0.279
chr14	107349540	6176636	0.0575	0.3343
chr15	102531392	5524490	0.0539	0.2669
chr16	90354753	5136588	0.0568	0.3067
chr17	81195210	4646103	0.0572	0.3021
chr18	78077248	5460610	0.0699	0.7383
chr19	59128983	3149945	0.0533	0.6277
chr20	63025520	3821718	0.0606	0.302
chr21	48129895	2611766	0.0543	0.3185
chr22	51304566	1856836	0.0362	0.2328
chrMT	16571	13236	0.7987	1.3147
chrX	155270560	6713078	0.0432	0.2926
chrY	59373566	1750406	0.0295	0.3196

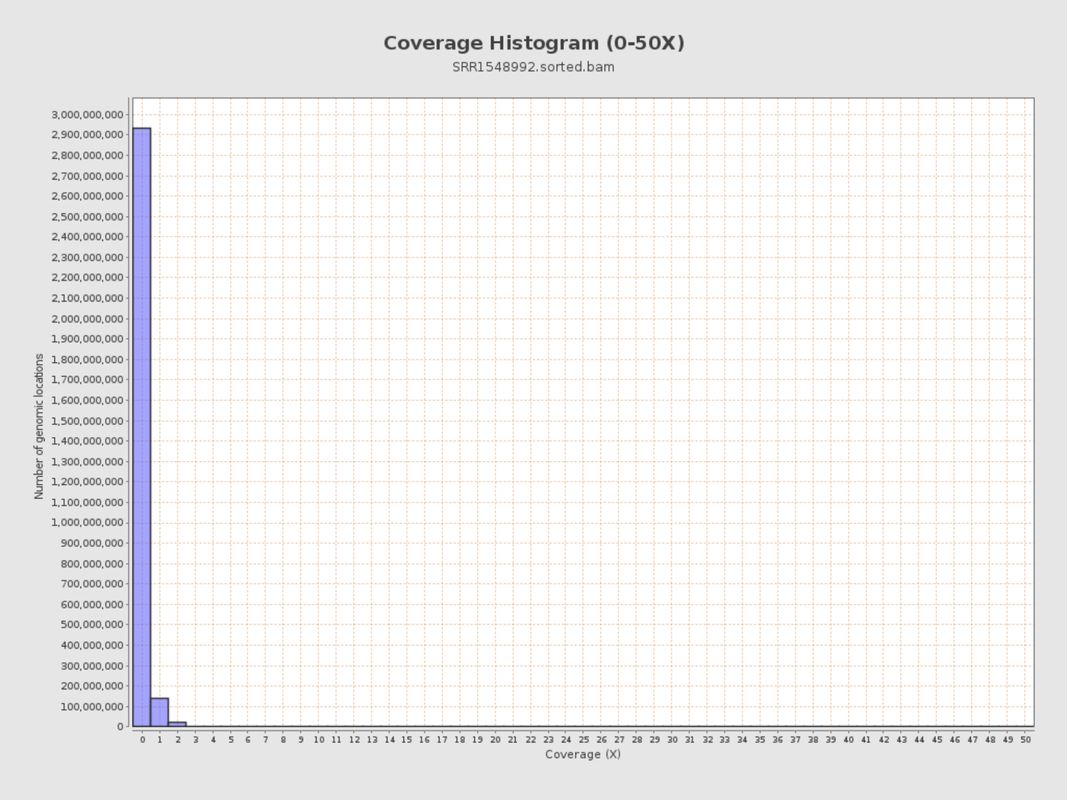
3. Results : Coverage across reference



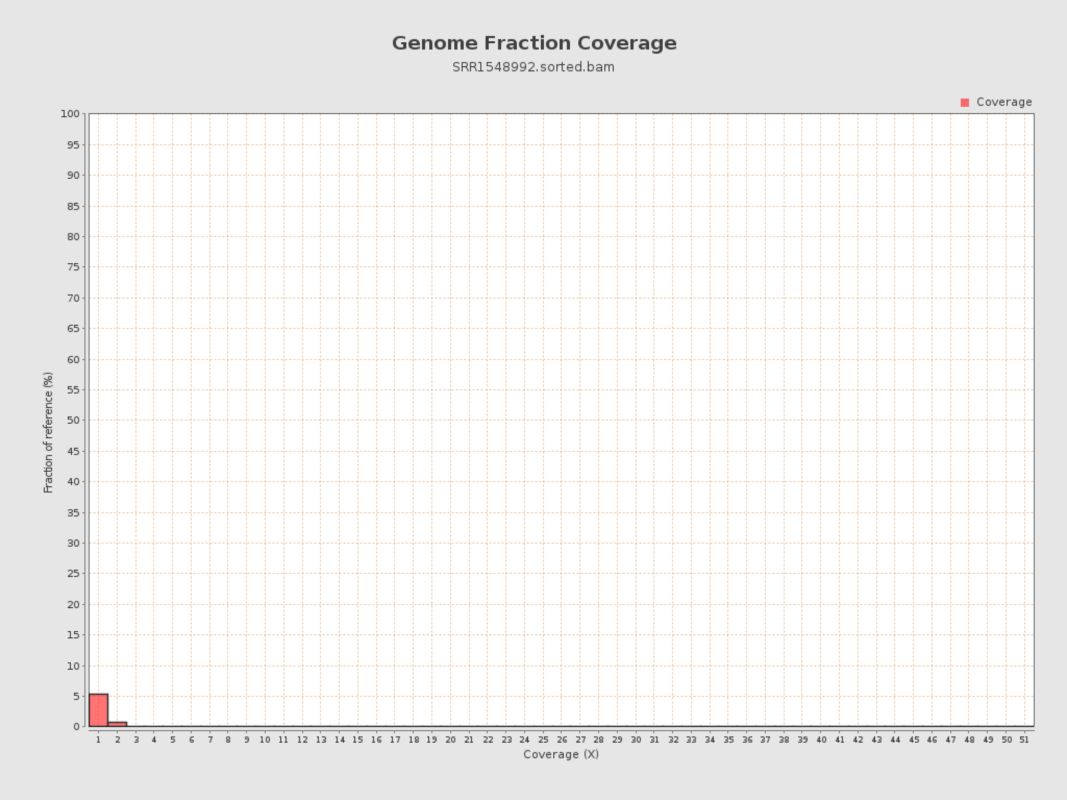
4. Results : Coverage Histogram



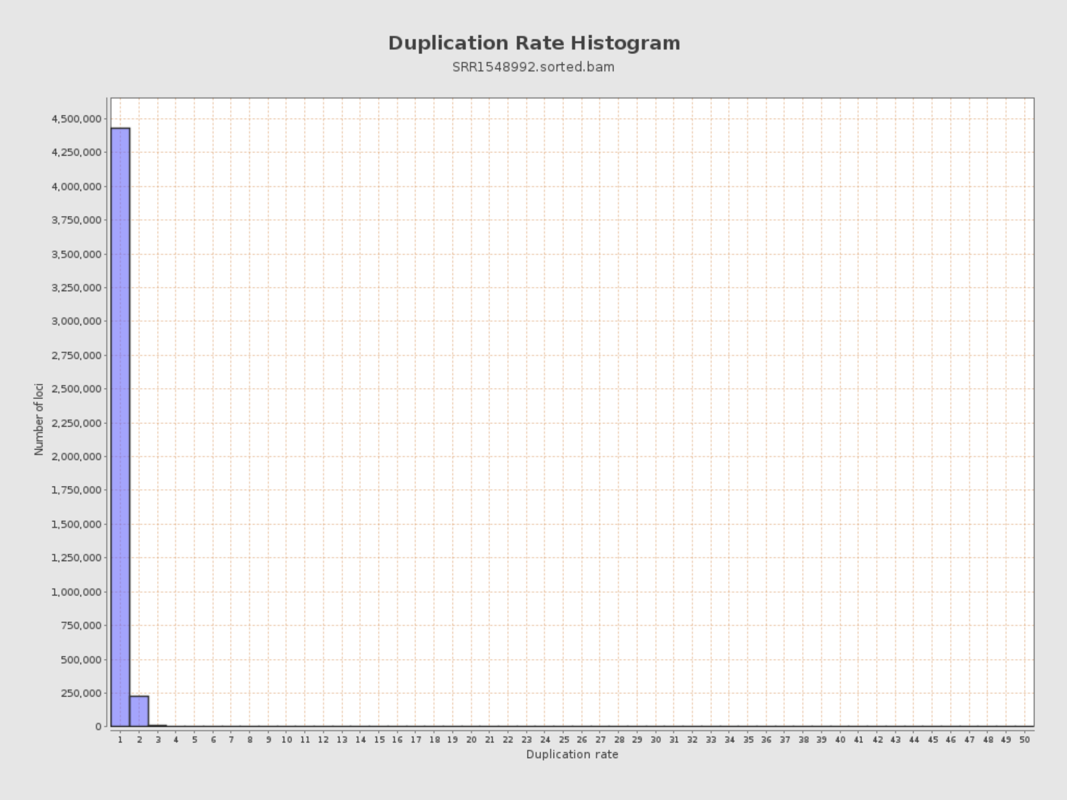
5. Results : Coverage Histogram (0-50X)



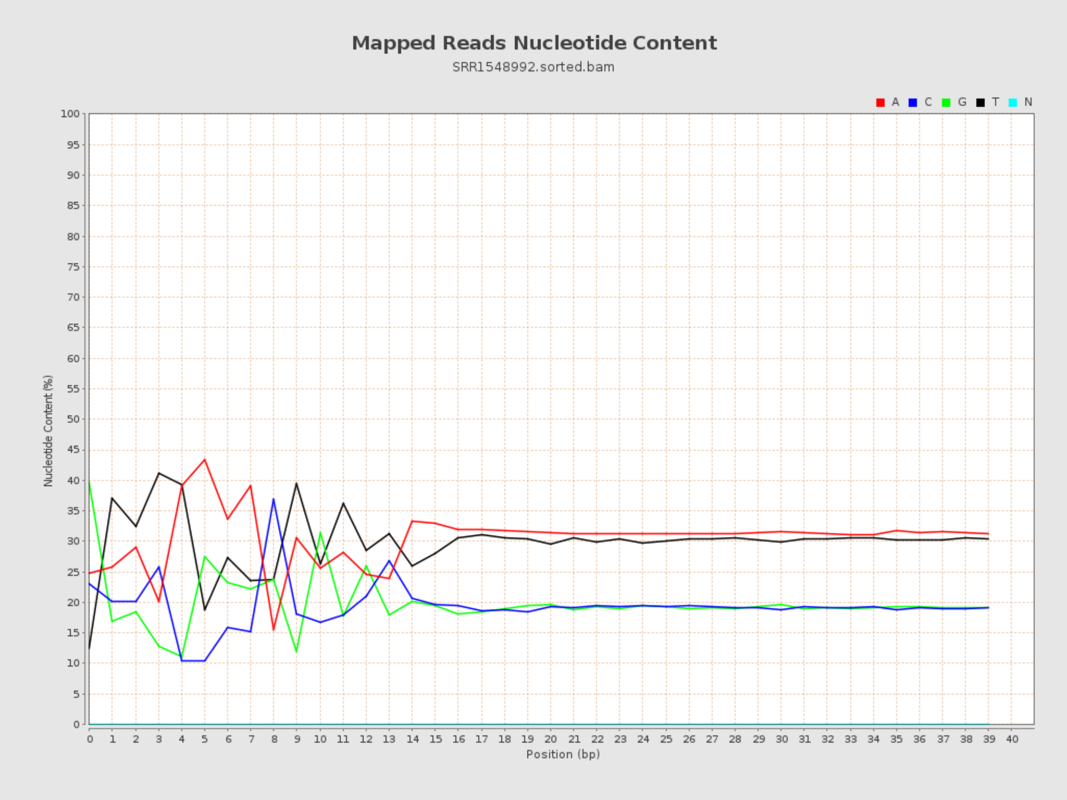
6. Results : Genome Fraction Coverage



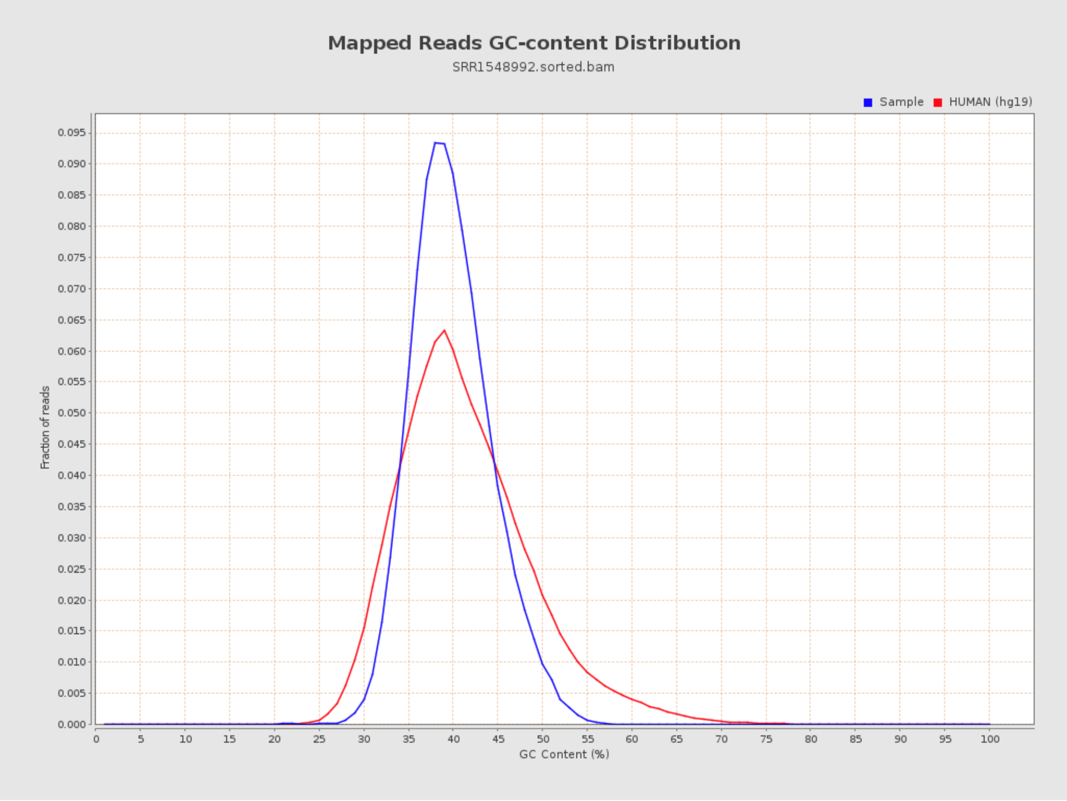
7. Results : Duplication Rate Histogram



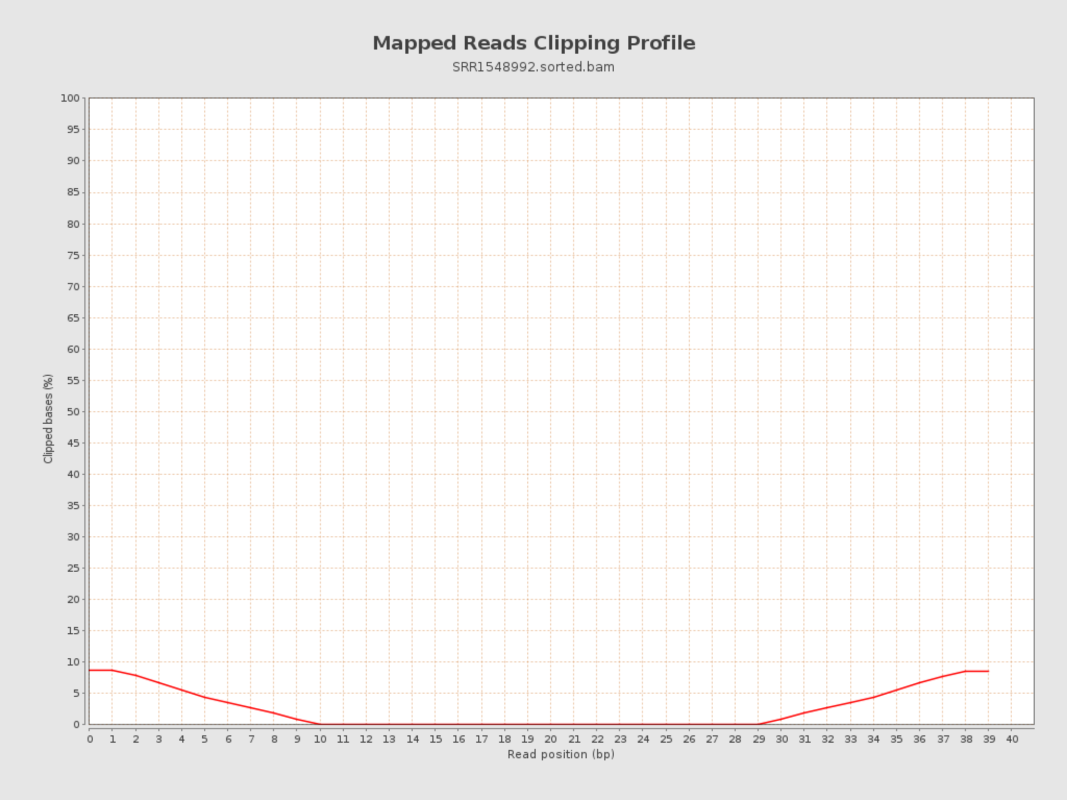
8. Results : Mapped Reads Nucleotide Content



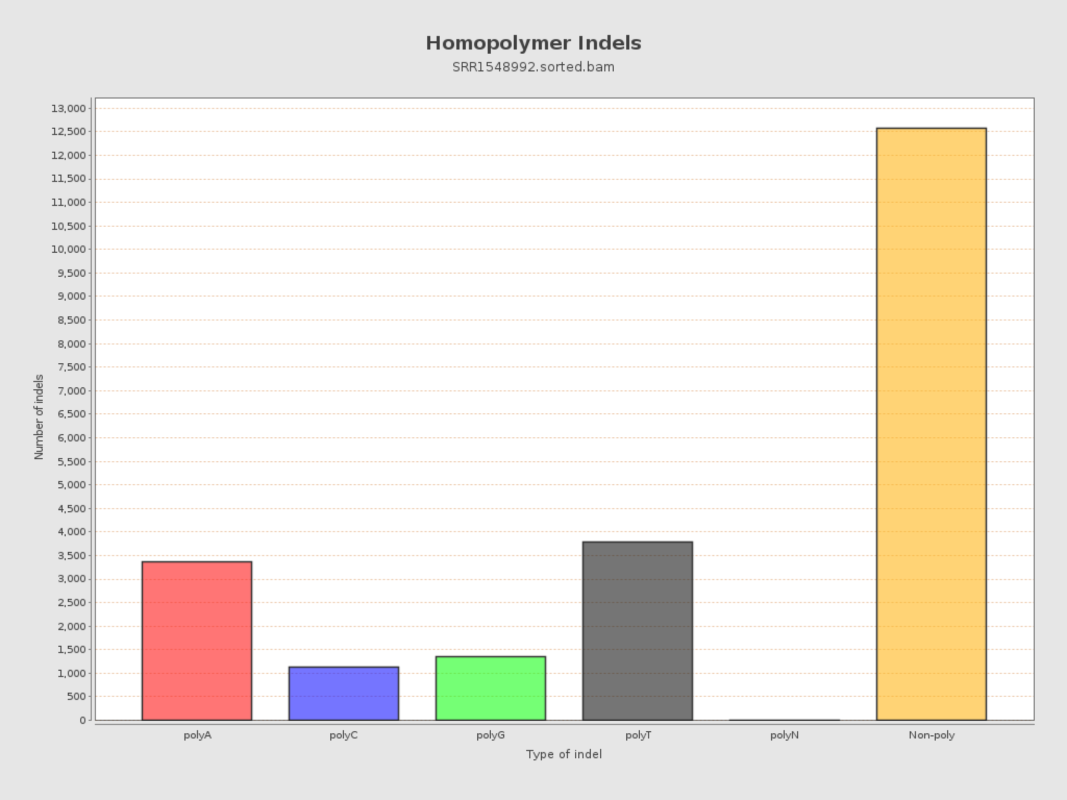
9. Results : Mapped Reads GC-content Distribution



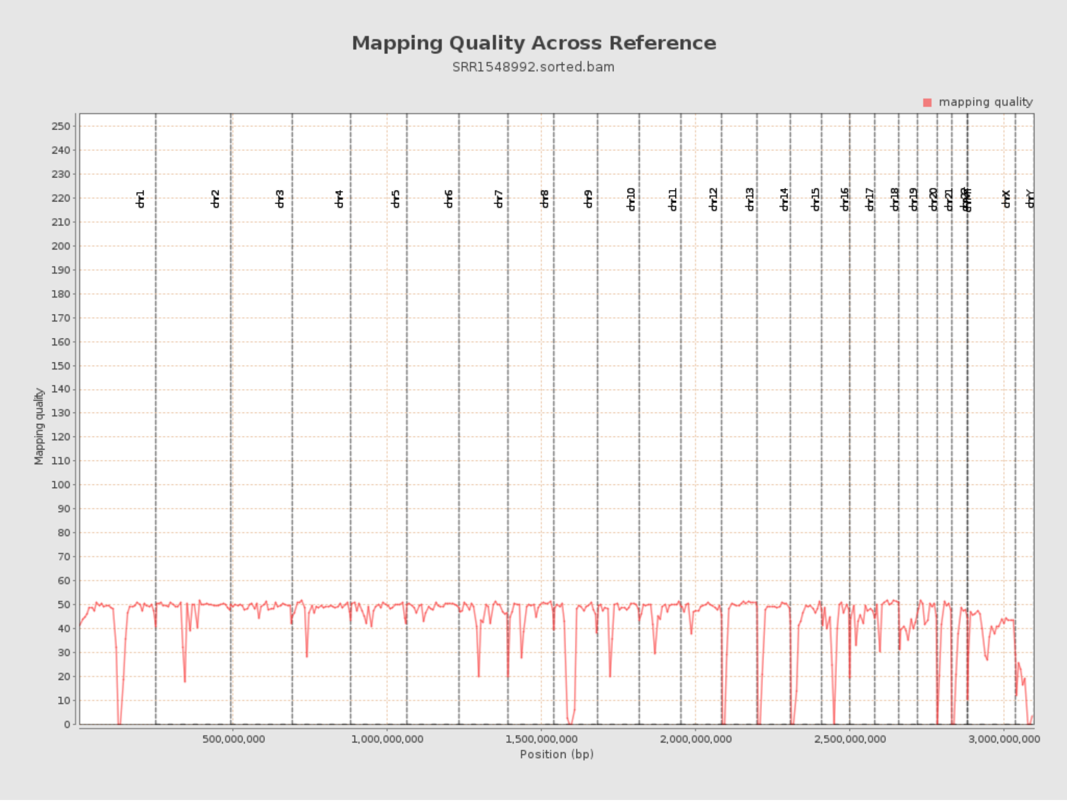
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram