Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:50:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082440.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_SRR3082440 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082440.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:50:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082440.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,958,054
Mapped reads	2,679,940 / 90.6%
Unmapped reads	278,114 / 9.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,671 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	103,844 / 3.51%
Duplication rate	2.88%
Clipped reads	1,101,199 / 37.23%

2.2. ACGT Content

Number/percentage of A's	51,752,112 / 28.4%
Number/percentage of C's	34,193,697 / 18.76%
Number/percentage of T's	56,746,344 / 31.14%
Number/percentage of G's	39,549,152 / 21.7%
Number/percentage of N's	3,726 / 0%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0589

Standard Deviation	0.4877

2.4. Mapping Quality

Mean Mapping Quality	46.48

2.5. Mismatches and indels

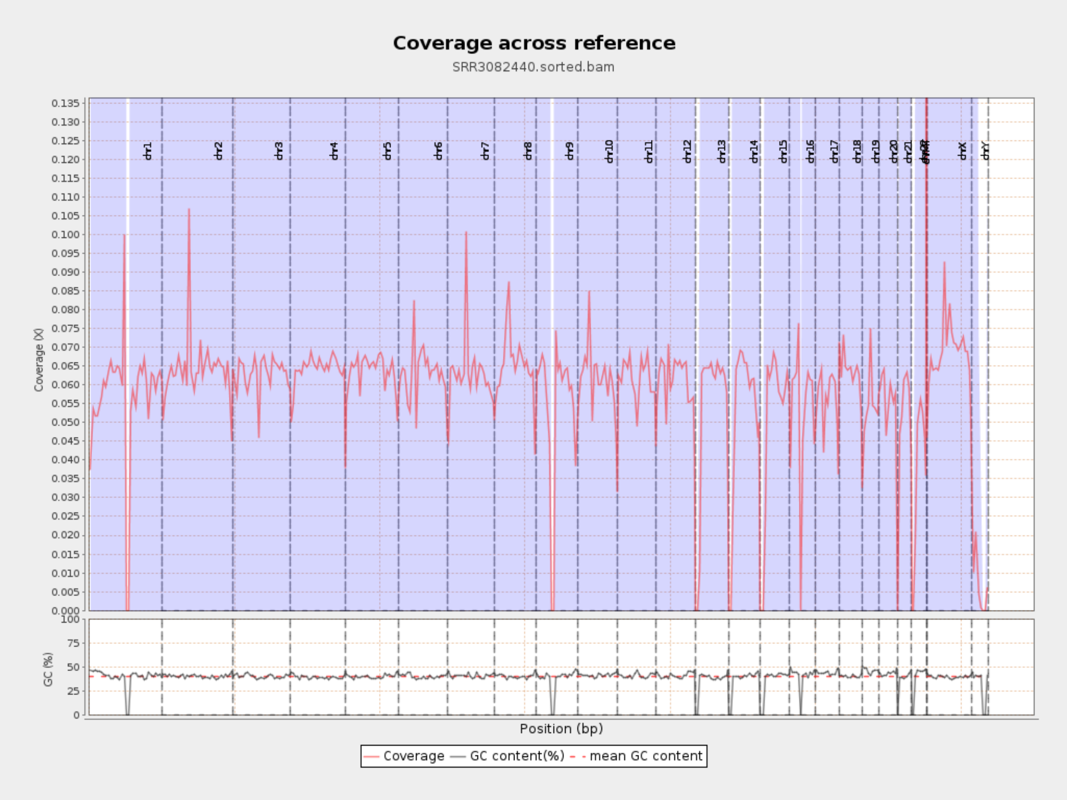
General error rate	0.84%
Mismatches	1,506,859
Insertions	14,560
Mapped reads with at least one insertion	0.54%
Deletions	41,016
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.67%

2.6. Chromosome stats

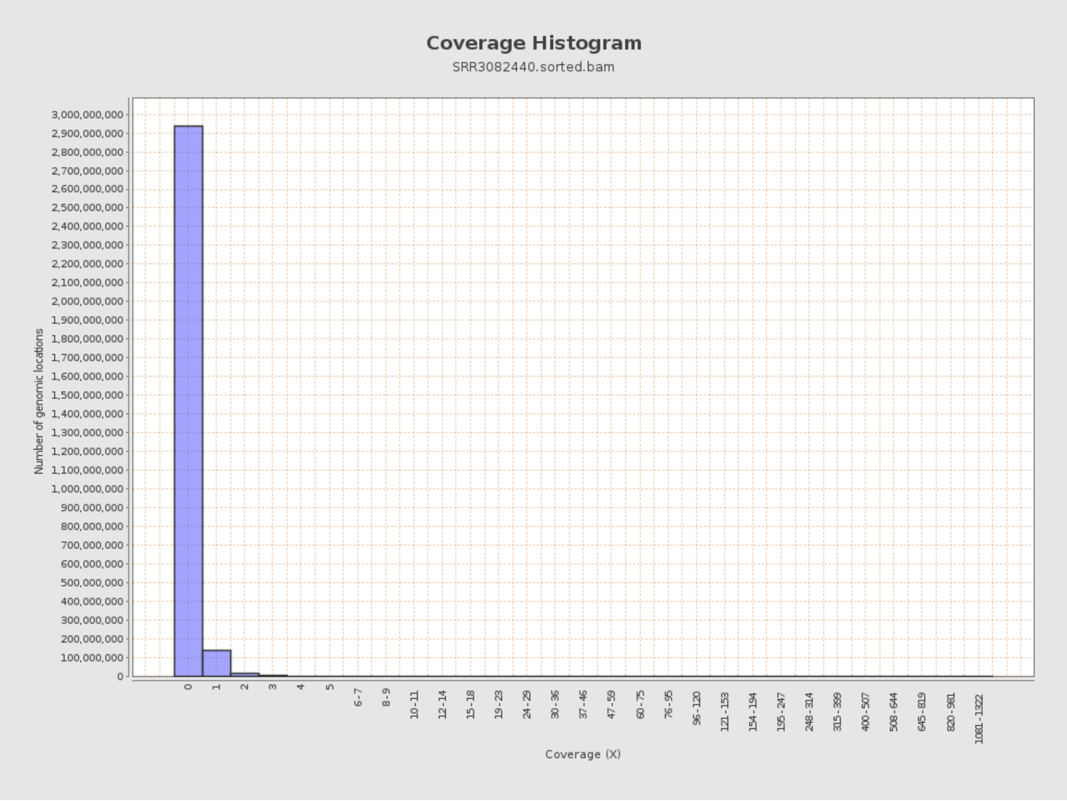
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14166511	0.0568	0.8787
chr2	243199373	15647242	0.0643	0.5819
chr3	198022430	12501076	0.0631	0.2796
chr4	191154276	12287534	0.0643	0.2922
chr5	180915260	11537894	0.0638	0.2842
chr6	171115067	10780472	0.063	0.3533
chr7	159138663	10120632	0.0636	0.623

chr8	146364022	9545691	0.0652	0.8473
chr9	141213431	7607913	0.0539	0.4368
chr10	135534747	8421829	0.0621	0.4214
chr11	135006516	8286844	0.0614	0.3953
chr12	133851895	8236535	0.0615	0.2831
chr13	115169878	6040732	0.0525	0.2549
chr14	107349540	5547790	0.0517	0.2752
chr15	102531392	5142390	0.0502	0.2548
chr16	90354753	4822042	0.0534	0.2901
chr17	81195210	4512391	0.0556	0.2974
chr18	78077248	5003318	0.0641	0.8262
chr19	59128983	3230523	0.0546	0.6379
chr20	63025520	3533660	0.0561	0.2707
chr21	48129895	2393820	0.0497	0.2693
chr22	51304566	1802283	0.0351	0.2063
chrMT	16571	7240	0.4369	0.7719
chrX	155270560	10695549	0.0689	0.3386
chrY	59373566	439142	0.0074	0.1454

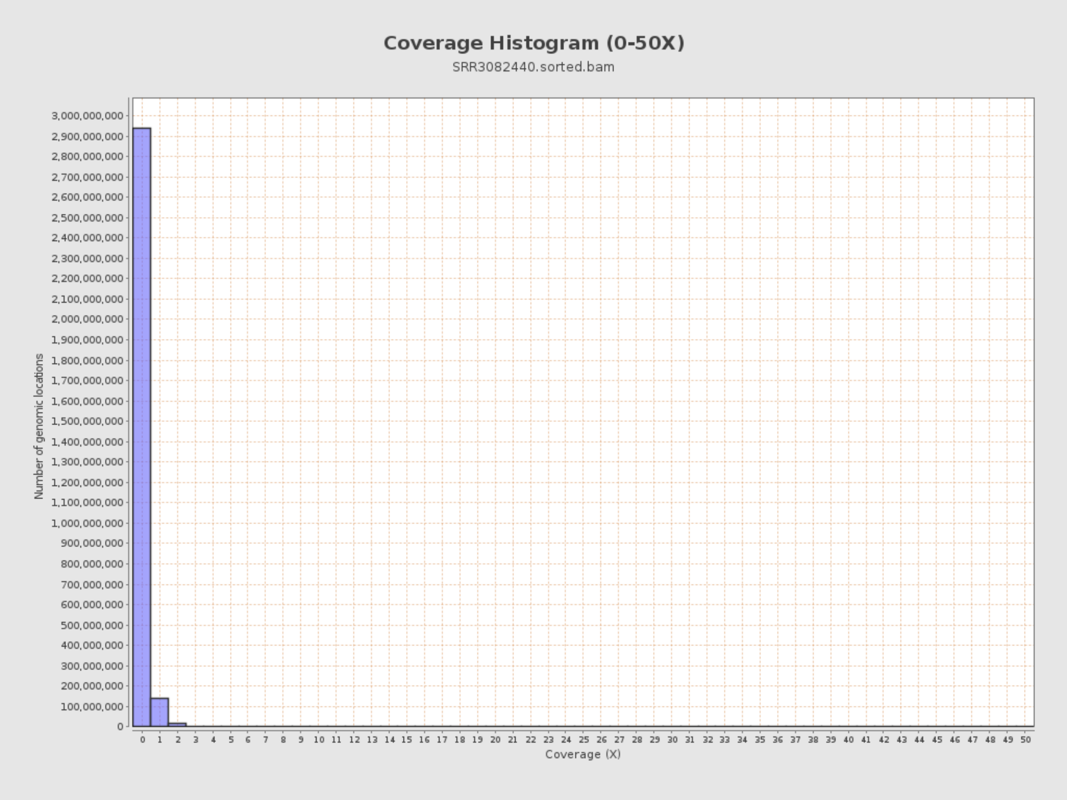
3. Results : Coverage across reference



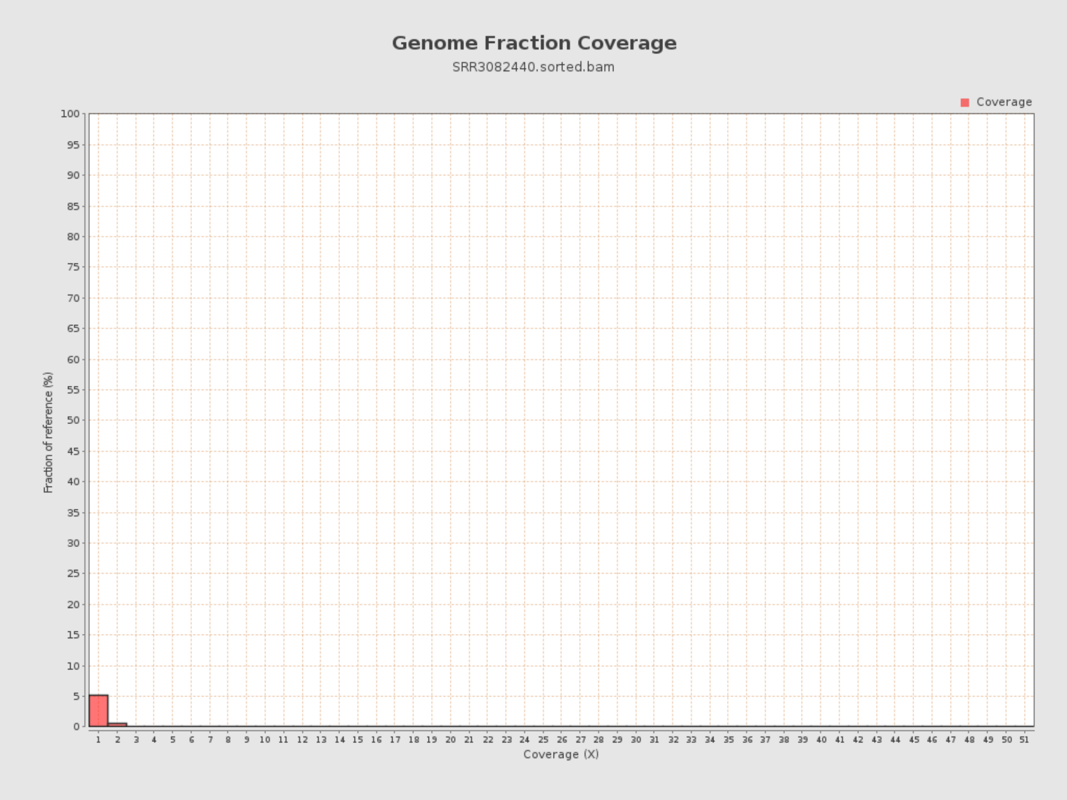
4. Results : Coverage Histogram



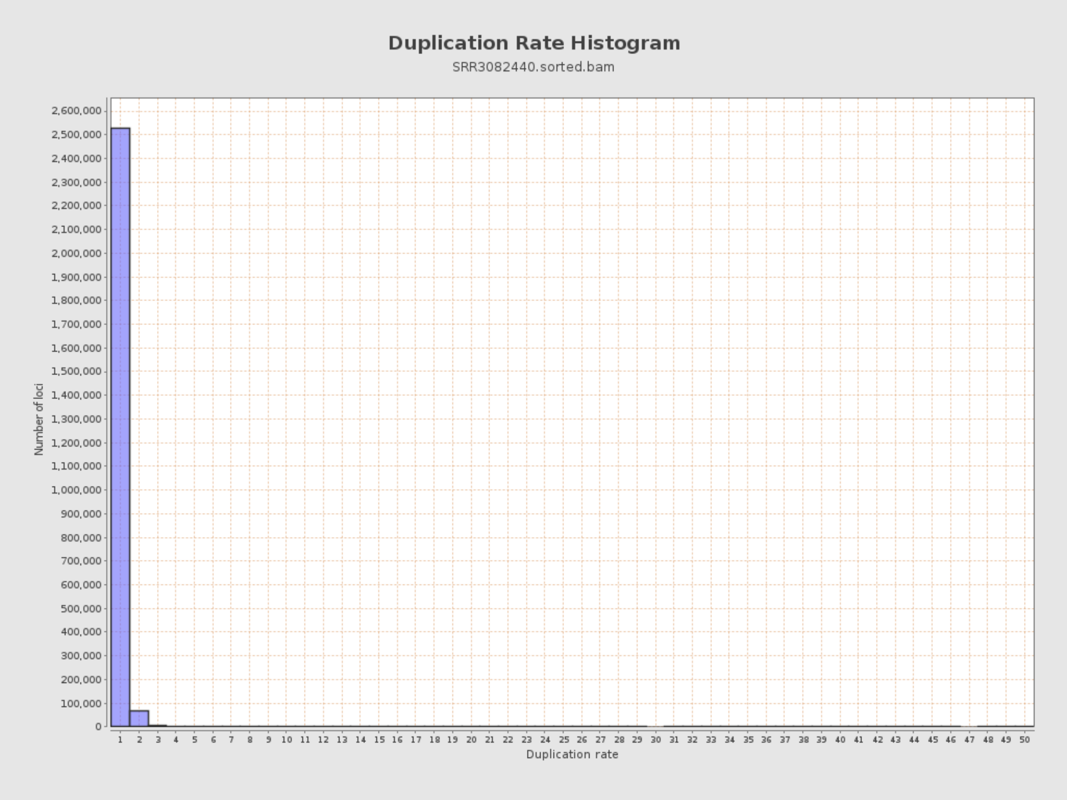
5. Results : Coverage Histogram (0-50X)



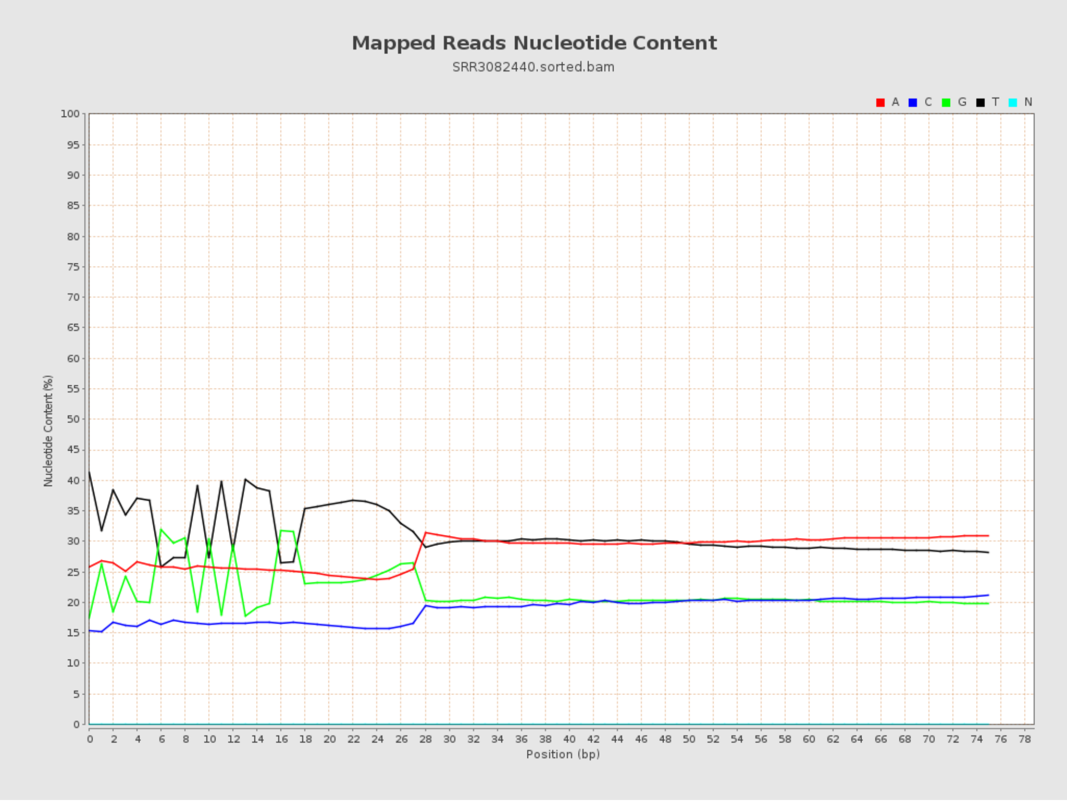
6. Results : Genome Fraction Coverage



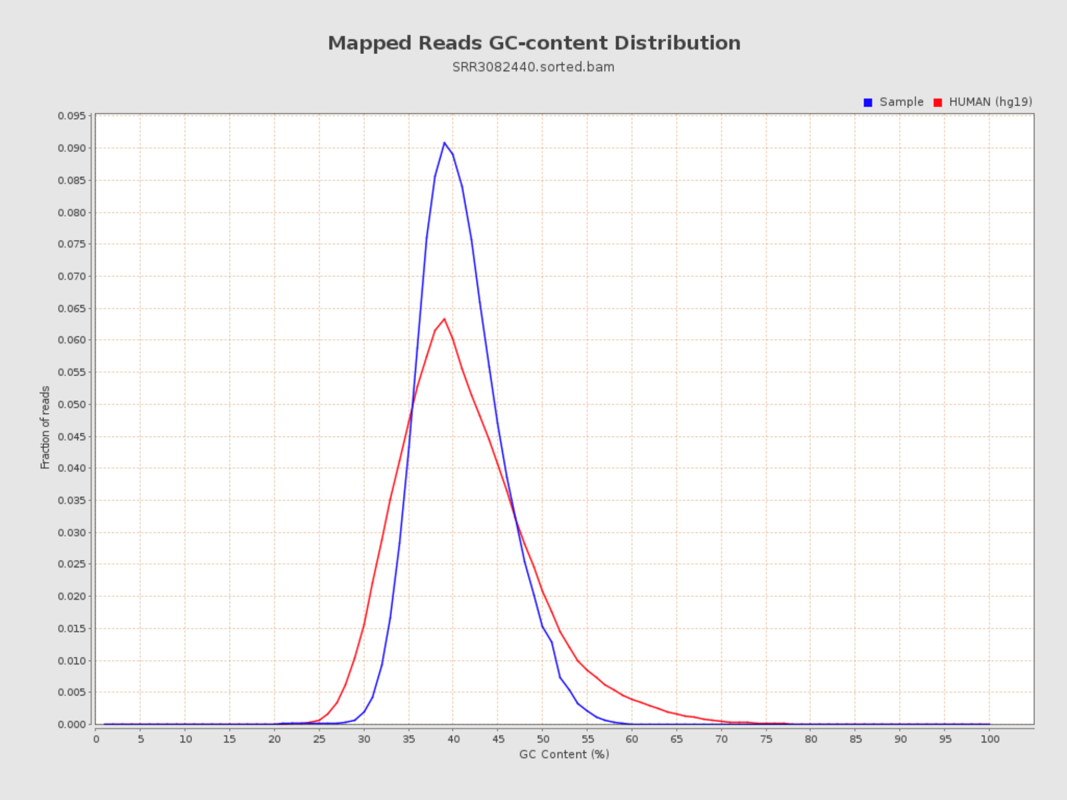
7. Results : Duplication Rate Histogram



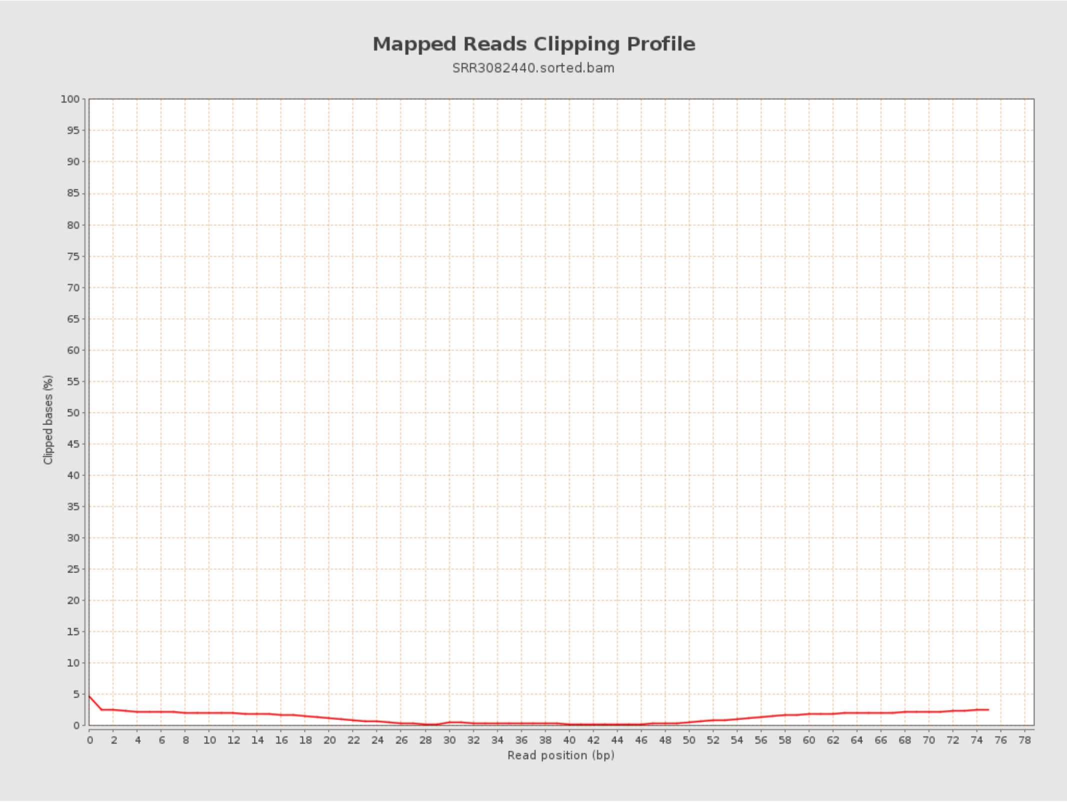
8. Results : Mapped Reads Nucleotide Content



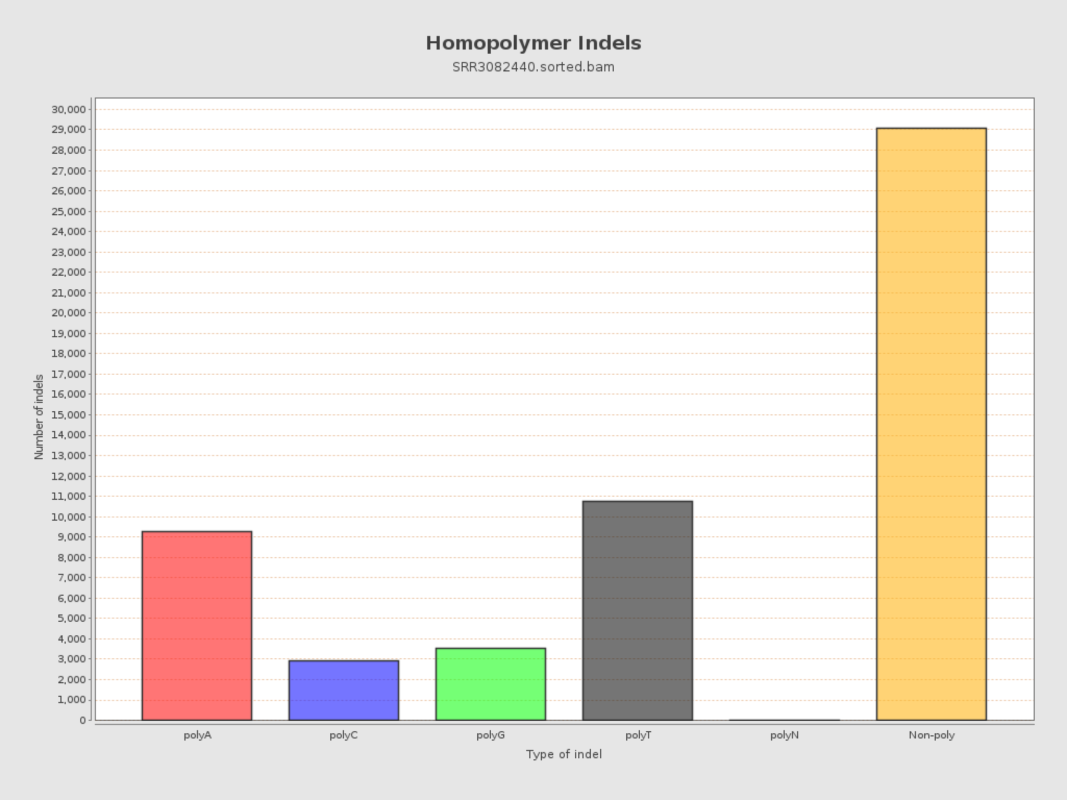
9. Results : Mapped Reads GC-content Distribution



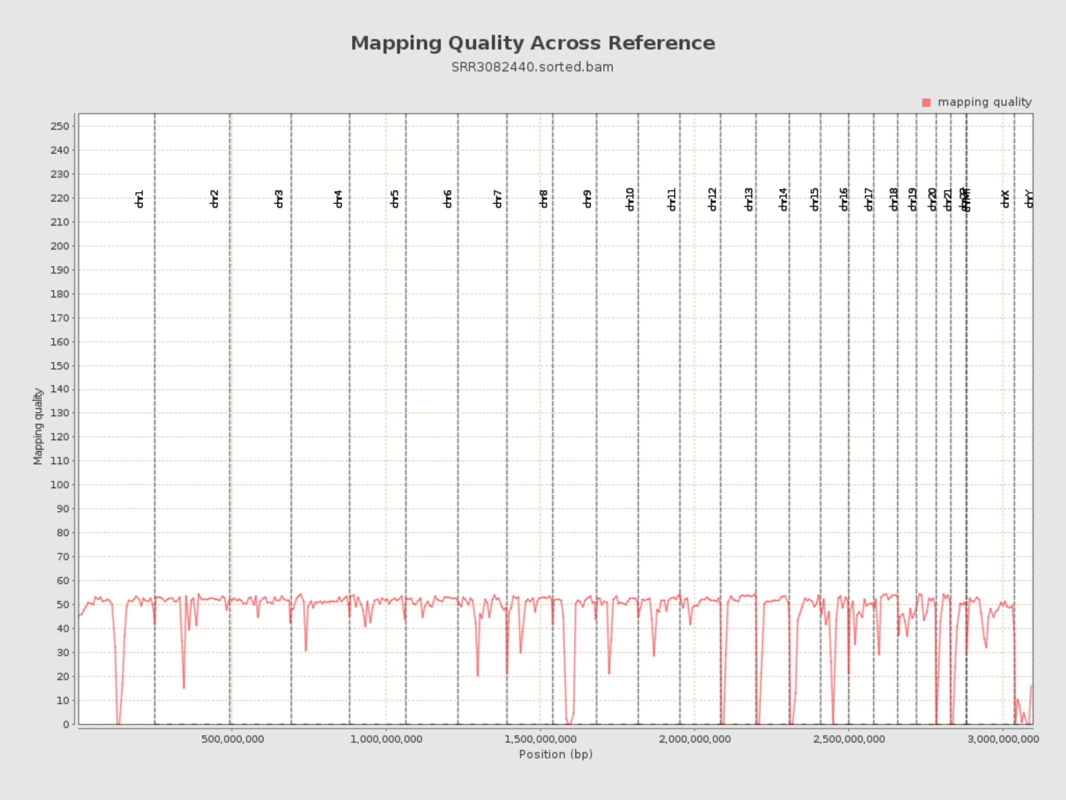
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram