Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 04:54:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506342.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_SRR1506342 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506342.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 04:54:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506342.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,414,035
Mapped reads	10,085,087 / 65.43%
Unmapped reads	5,328,948 / 34.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	174,397 / 1.13%
Read min/max/mean length	30 / 94 / 94.41
Duplicated reads (estimated)	1,495,006 / 9.7%
Duplication rate	10.53%
Clipped reads	6,409,889 / 41.58%

2.2. ACGT Content

Number/percentage of A's	225,020,028 / 28.69%
Number/percentage of C's	149,083,531 / 19.01%
Number/percentage of T's	219,793,037 / 28.03%
Number/percentage of G's	190,083,379 / 24.24%
Number/percentage of N's	203,801 / 0.03%
GC Percentage	43.25%

2.3. Coverage

Mean	0.2534

Standard Deviation	1.5224

2.4. Mapping Quality

Mean Mapping Quality	47.57

2.5. Mismatches and indels

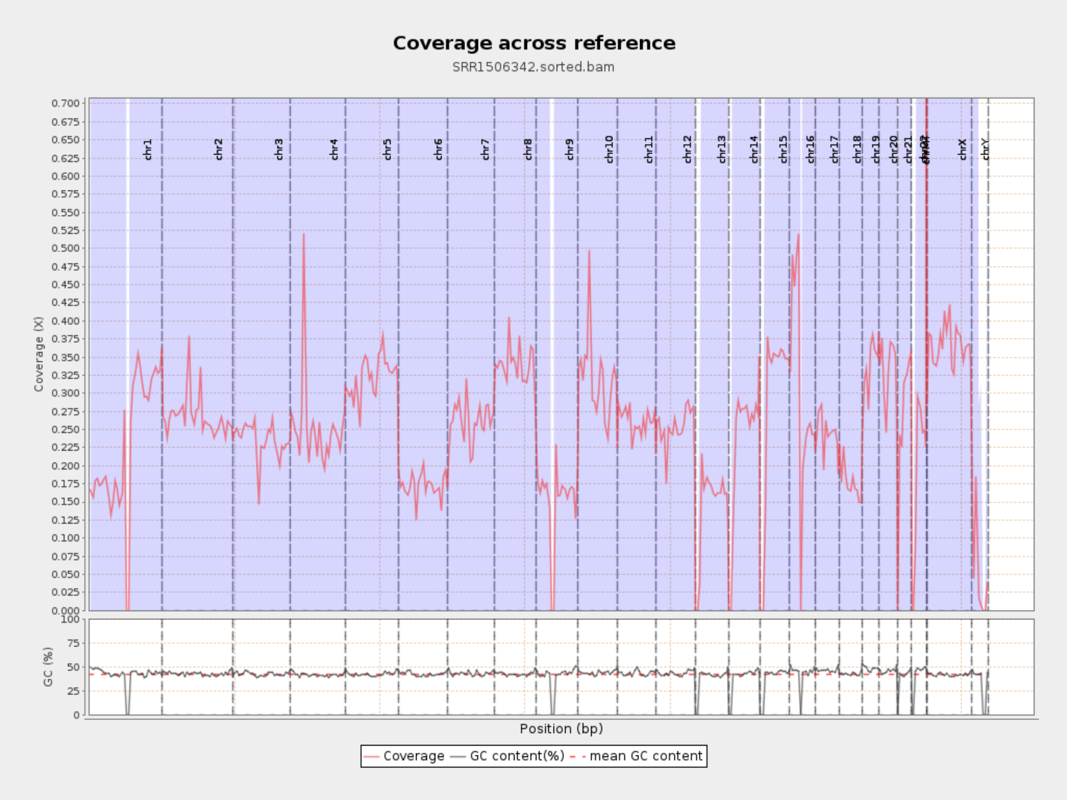
General error rate	0.75%
Mismatches	5,700,542
Insertions	65,055
Mapped reads with at least one insertion	0.63%
Deletions	163,153
Mapped reads with at least one deletion	1.59%
Homopolymer indels	43.37%

2.6. Chromosome stats

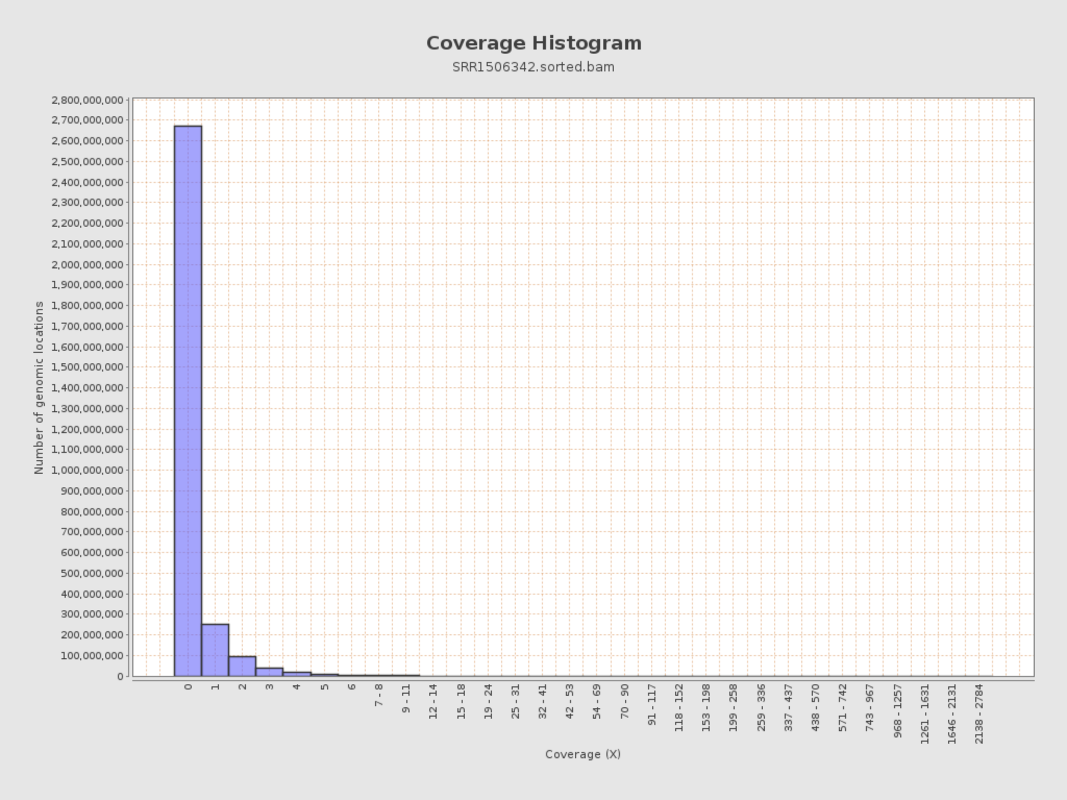
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	56380097	0.2262	2.594
chr2	243199373	65389040	0.2689	1.6337
chr3	198022430	46557536	0.2351	0.786
chr4	191154276	47942960	0.2508	1.4388
chr5	180915260	58520577	0.3235	0.9627
chr6	171115067	29567863	0.1728	0.745
chr7	159138663	41707666	0.2621	1.9026

chr8	146364022	49729371	0.3398	2.1323
chr9	141213431	21122673	0.1496	1.3987
chr10	135534747	43545661	0.3213	1.8482
chr11	135006516	35323290	0.2616	1.4523
chr12	133851895	33839198	0.2528	0.869
chr13	115169878	16521260	0.1435	0.6081
chr14	107349540	24605471	0.2292	0.9578
chr15	102531392	29418502	0.2869	0.9142
chr16	90354753	27864971	0.3084	1.2483
chr17	81195210	19767428	0.2435	1.0347
chr18	78077248	13873955	0.1777	2.3373
chr19	59128983	19937766	0.3372	2.0156
chr20	63025520	20829763	0.3305	1.086
chr21	48129895	13003376	0.2702	1.3184
chr22	51304566	9391333	0.1831	0.778
chrMT	16571	38895	2.3472	3.7548
chrX	155270560	56757070	0.3655	1.2048
chrY	59373566	2876421	0.0484	1.602

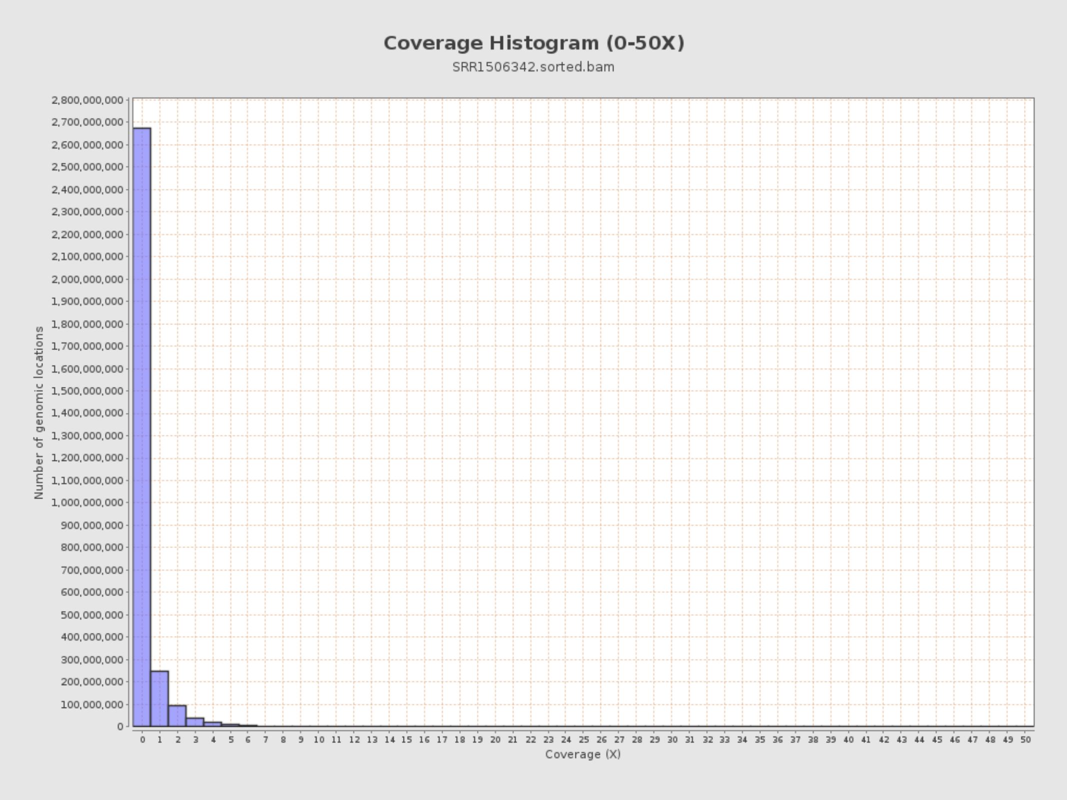
3. Results : Coverage across reference



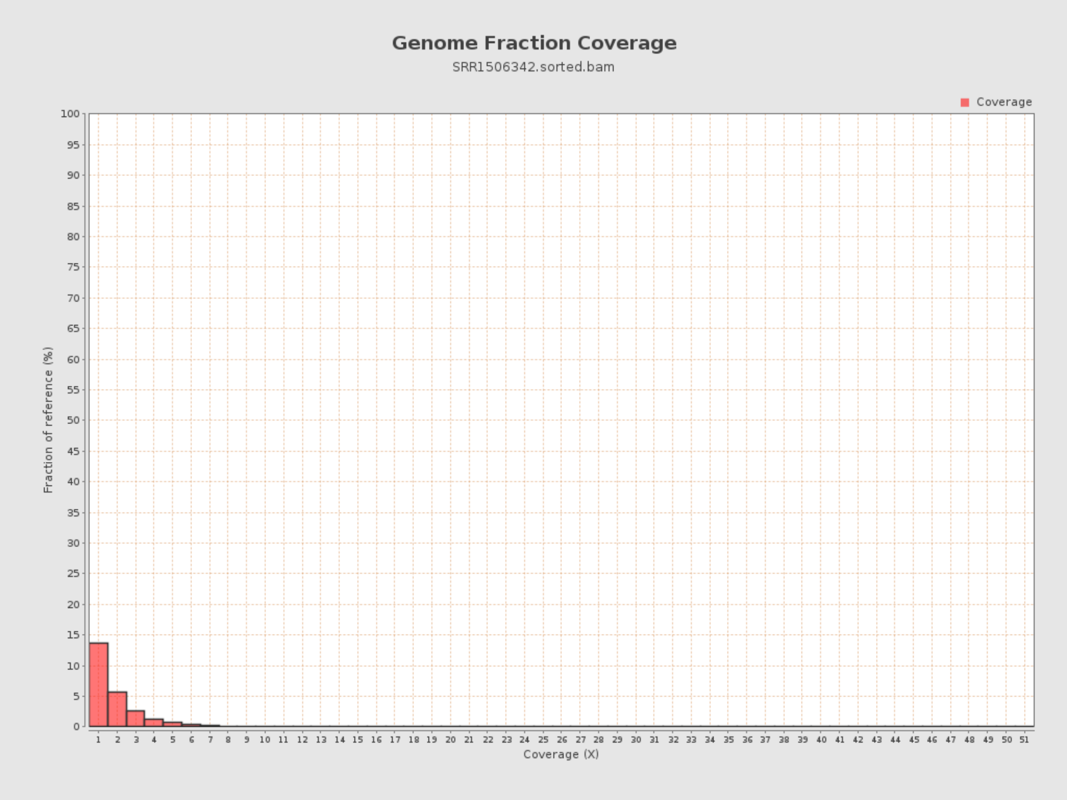
4. Results : Coverage Histogram



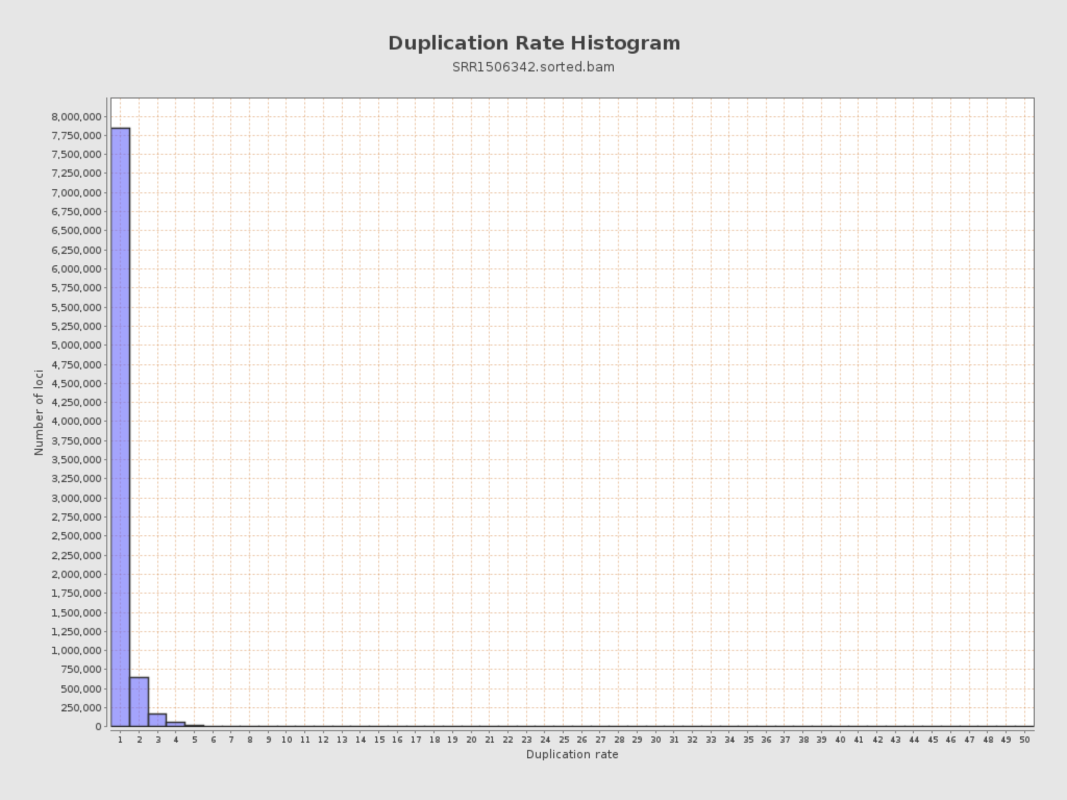
5. Results : Coverage Histogram (0-50X)



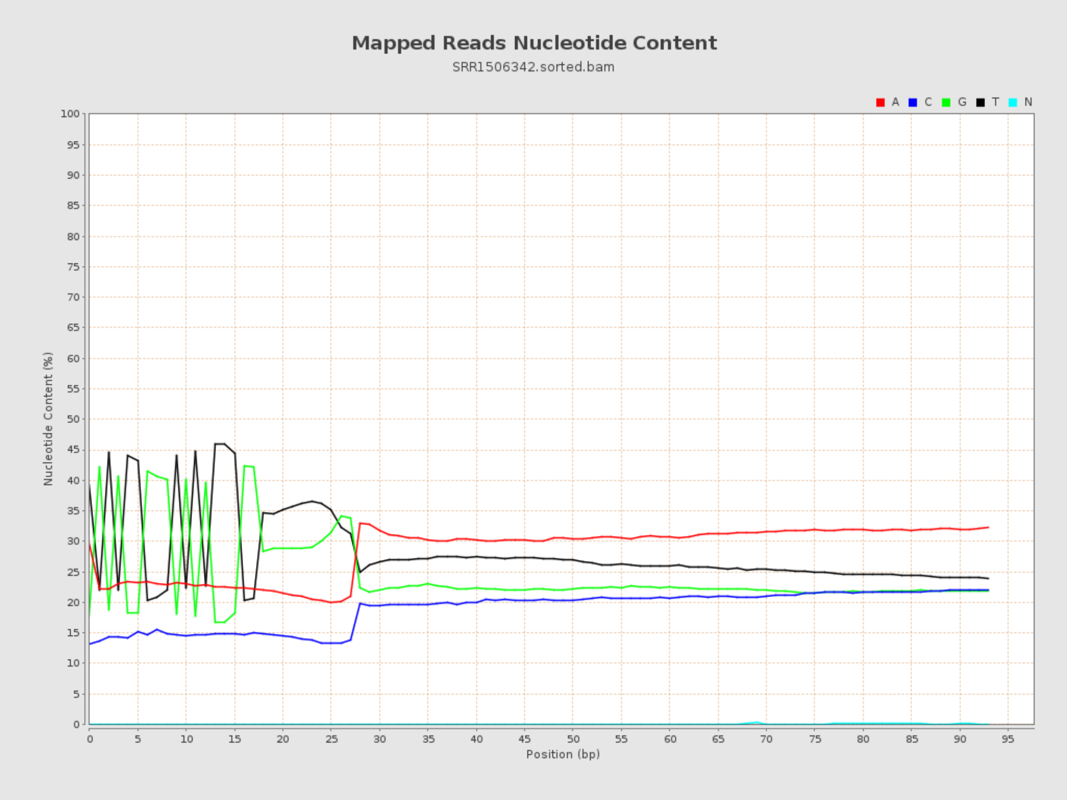
6. Results : Genome Fraction Coverage



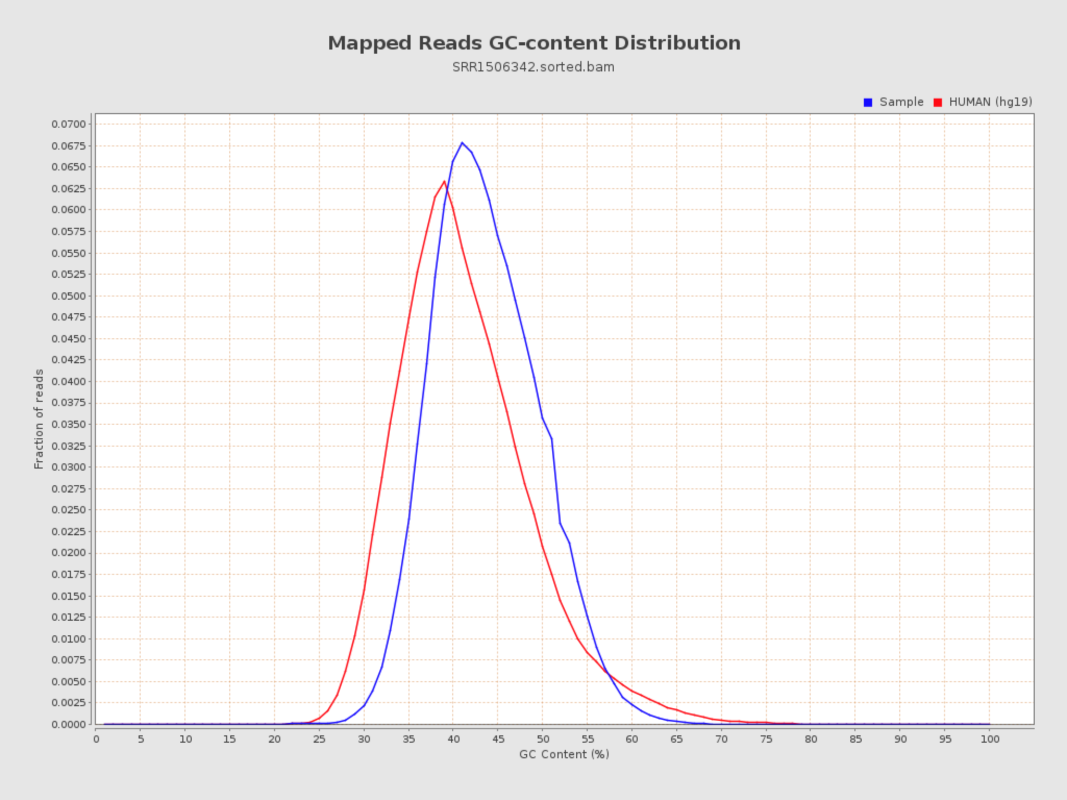
7. Results : Duplication Rate Histogram



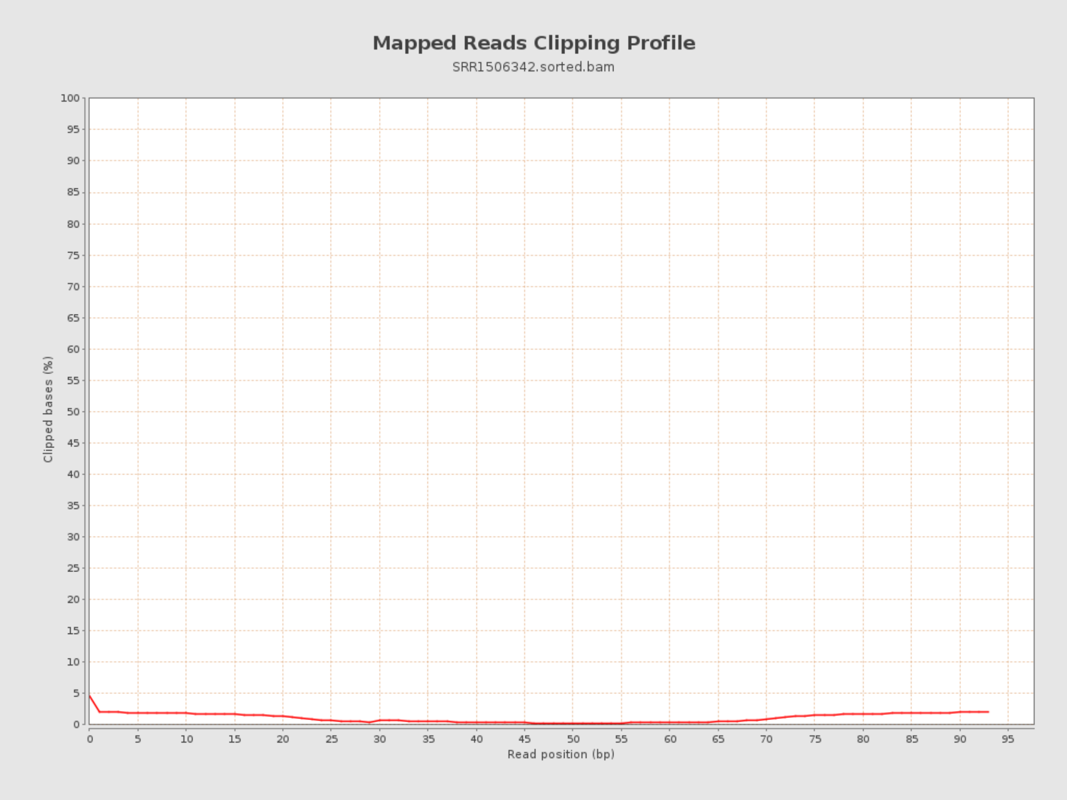
8. Results : Mapped Reads Nucleotide Content



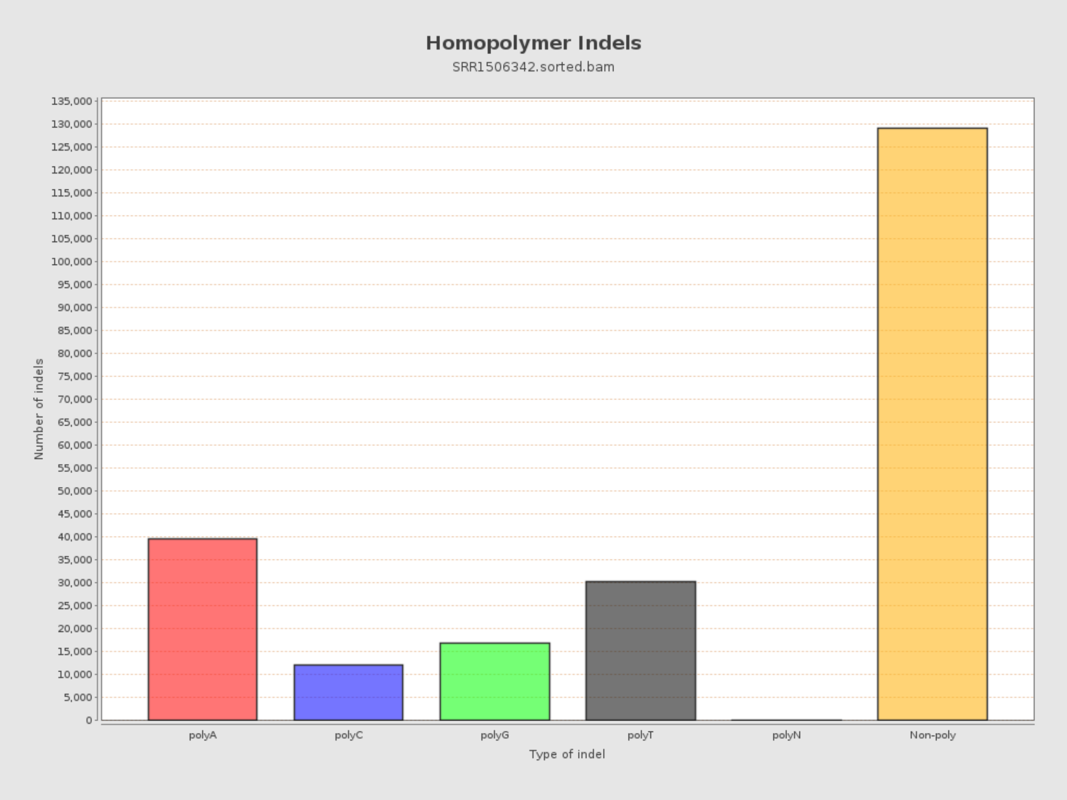
9. Results : Mapped Reads GC-content Distribution



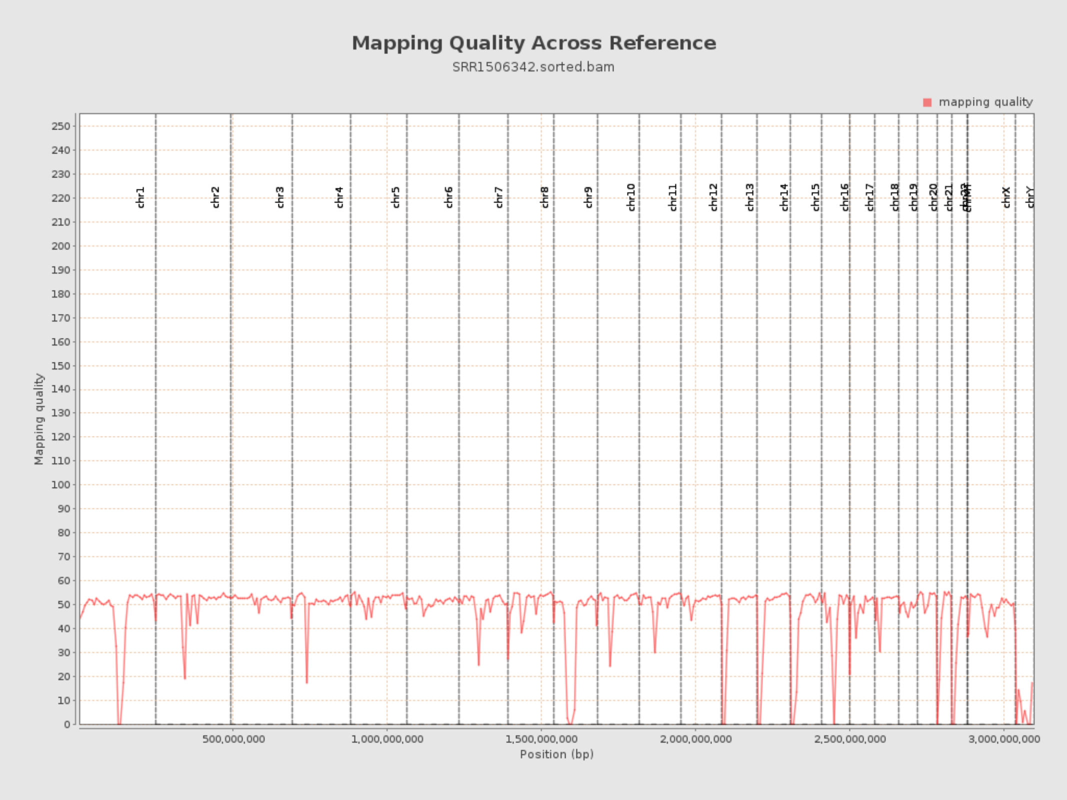
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram