Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:14:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549058.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_SRR1549058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549058.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:14:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,694,440
Mapped reads	8,335,228 / 85.98%
Unmapped reads	1,359,212 / 14.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	458,461 / 4.73%
Duplication rate	4.05%
Clipped reads	334,470 / 3.45%

2.2. ACGT Content

Number/percentage of A's	96,169,071 / 29.02%
Number/percentage of C's	69,310,898 / 20.92%
Number/percentage of T's	96,418,904 / 29.1%
Number/percentage of G's	69,483,723 / 20.97%
Number/percentage of N's	6,121 / 0%
GC Percentage	41.88%

2.3. Coverage

Mean	0.1071
Standard Deviation	1.1649

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

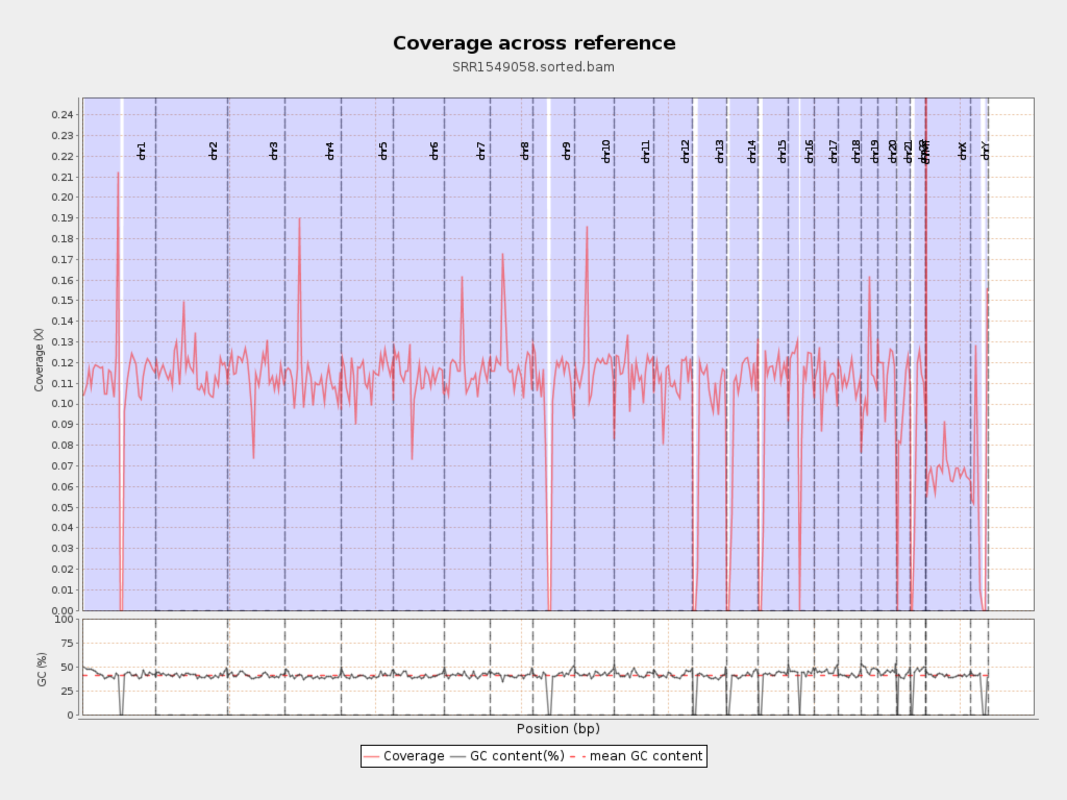
General error rate	0.3%
Mismatches	997,307
Insertions	7,740
Mapped reads with at least one insertion	0.09%
Deletions	24,346
Mapped reads with at least one deletion	0.29%
Homopolymer indels	45.25%

2.6. Chromosome stats

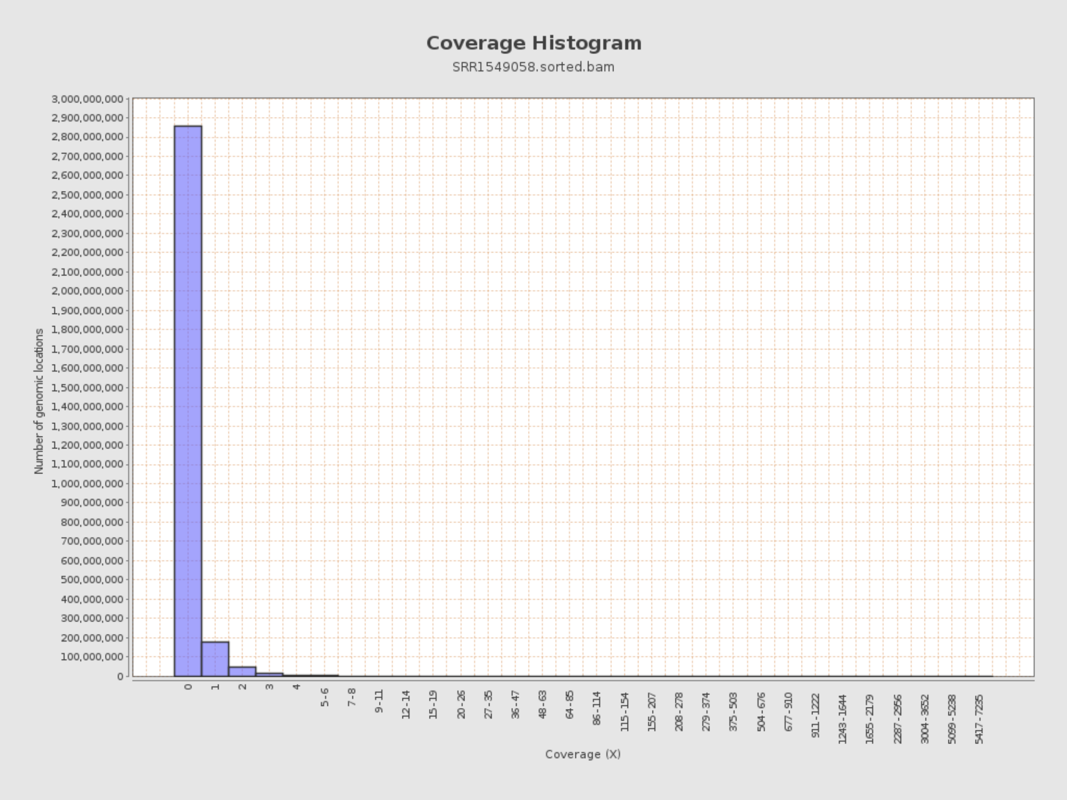
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27401026	0.1099	2.2428
chr2	243199373	28303591	0.1164	0.6626
chr3	198022430	22654776	0.1144	0.4471
chr4	191154276	21701495	0.1135	0.5778
chr5	180915260	20628388	0.114	0.4514
chr6	171115067	19354650	0.1131	0.489
chr7	159138663	18469985	0.1161	0.8879
chr8	146364022	17692019	0.1209	3.5597

chr9	141213431	14014921	0.0992	0.5906
chr10	135534747	16273410	0.1201	0.824
chr11	135006516	15611542	0.1156	0.6553
chr12	133851895	15009945	0.1121	0.4573
chr13	115169878	10572440	0.0918	0.3899
chr14	107349540	10214237	0.0951	0.4481
chr15	102531392	9760919	0.0952	0.3965
chr16	90354753	9569364	0.1059	0.4913
chr17	81195210	9085037	0.1119	0.4852
chr18	78077248	8745565	0.112	1.1758
chr19	59128983	6607811	0.1118	1.5464
chr20	63025520	7279036	0.1155	0.487
chr21	48129895	4436310	0.0922	0.5437
chr22	51304566	4089886	0.0797	0.3946
chrMT	16571	8842	0.5336	1.0364
chrX	155270560	10430556	0.0672	0.4231
chrY	59373566	3503510	0.059	0.8252

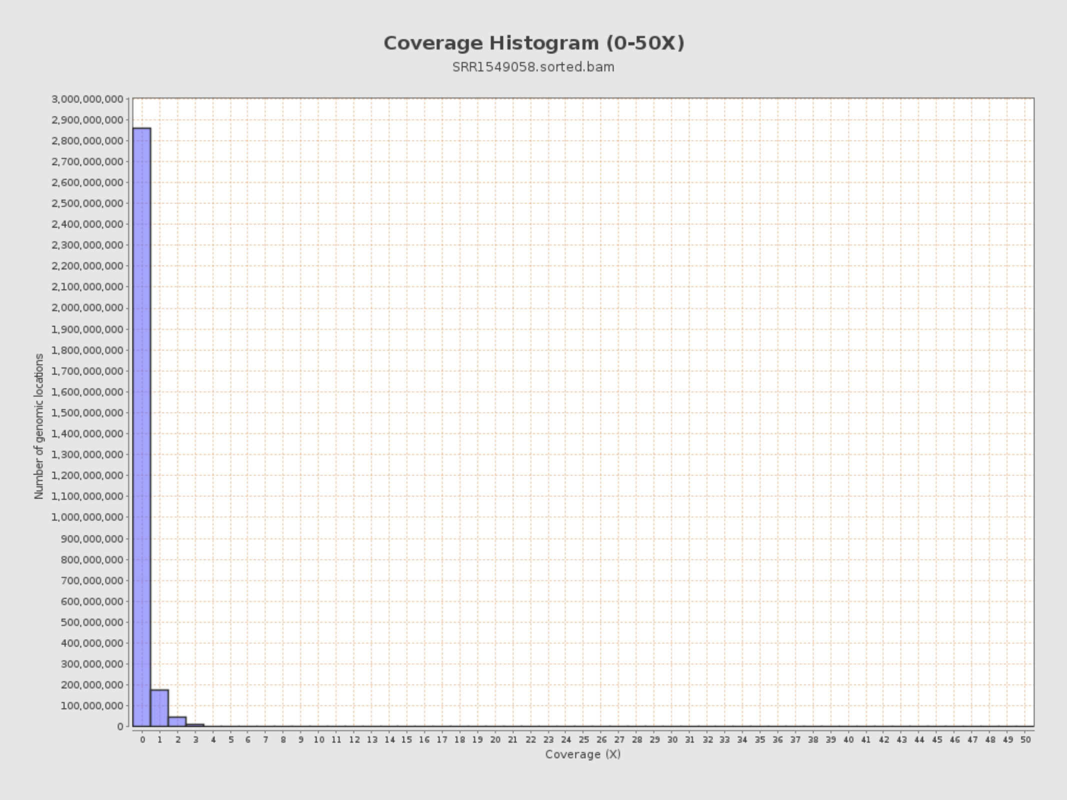
3. Results : Coverage across reference



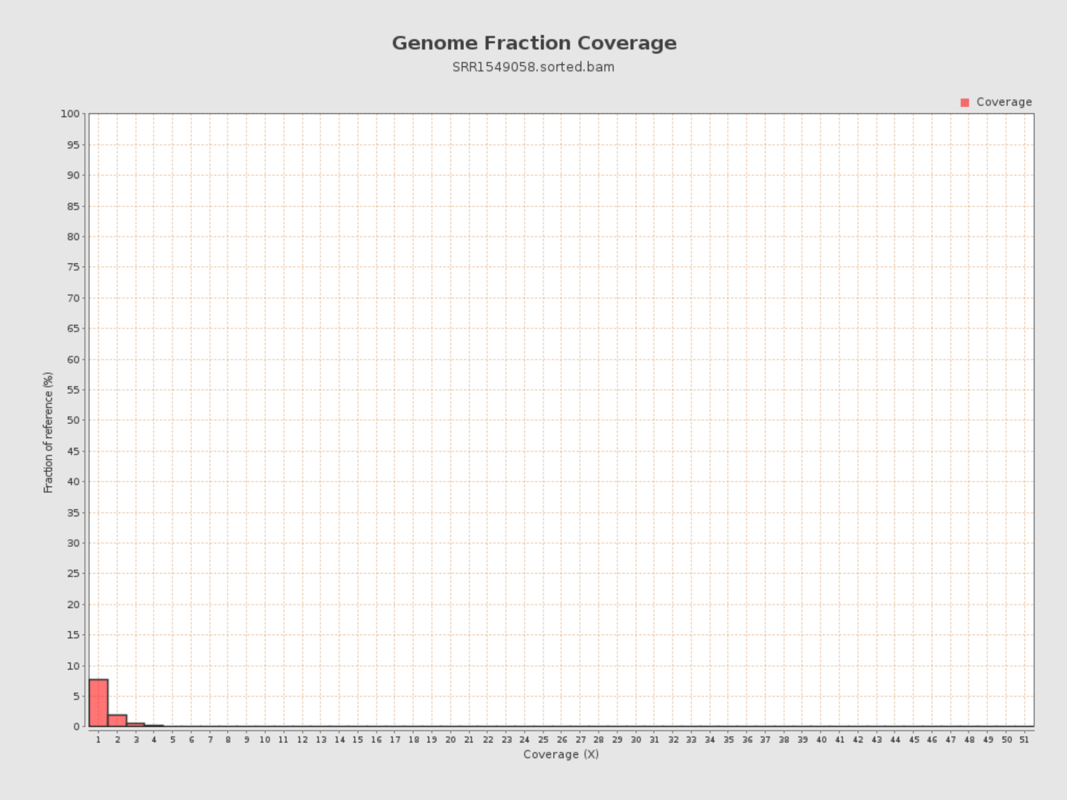
4. Results : Coverage Histogram



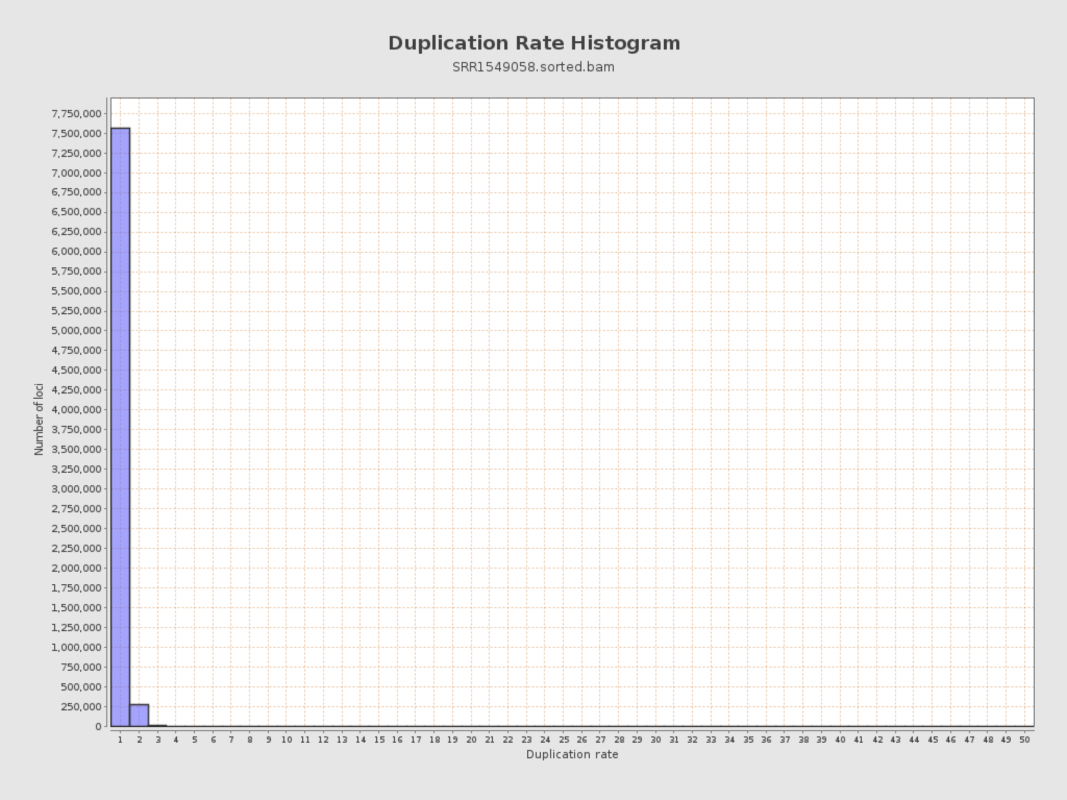
5. Results : Coverage Histogram (0-50X)



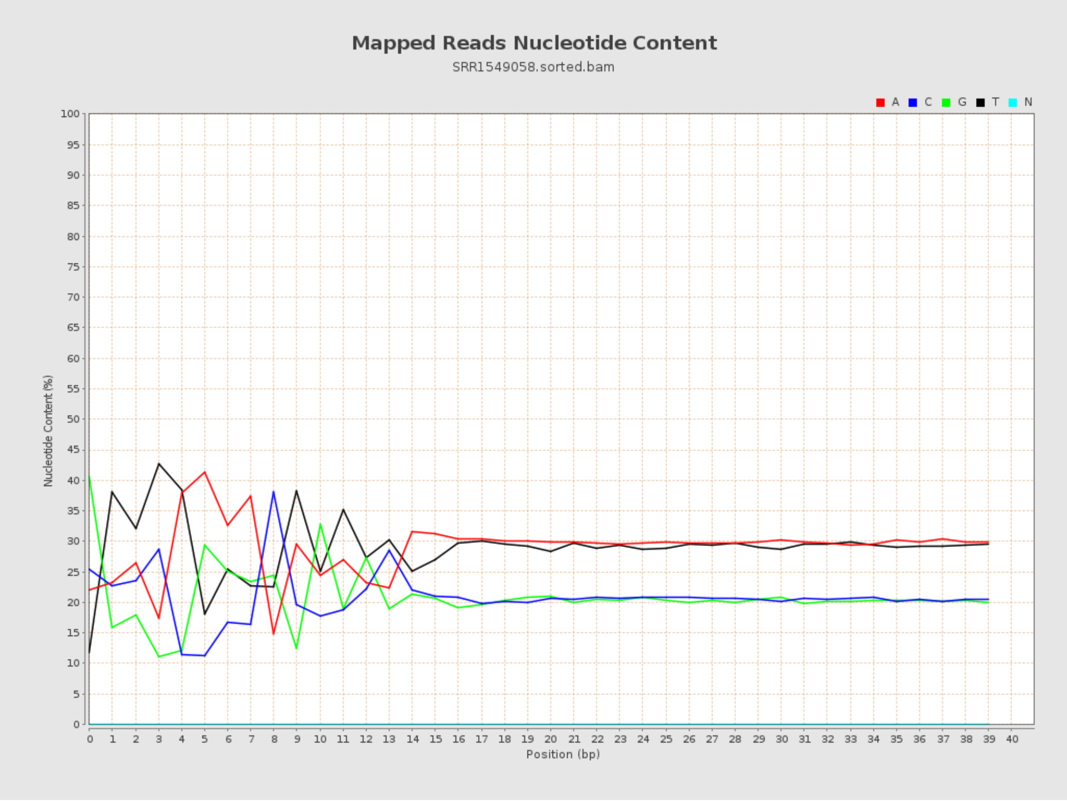
6. Results : Genome Fraction Coverage



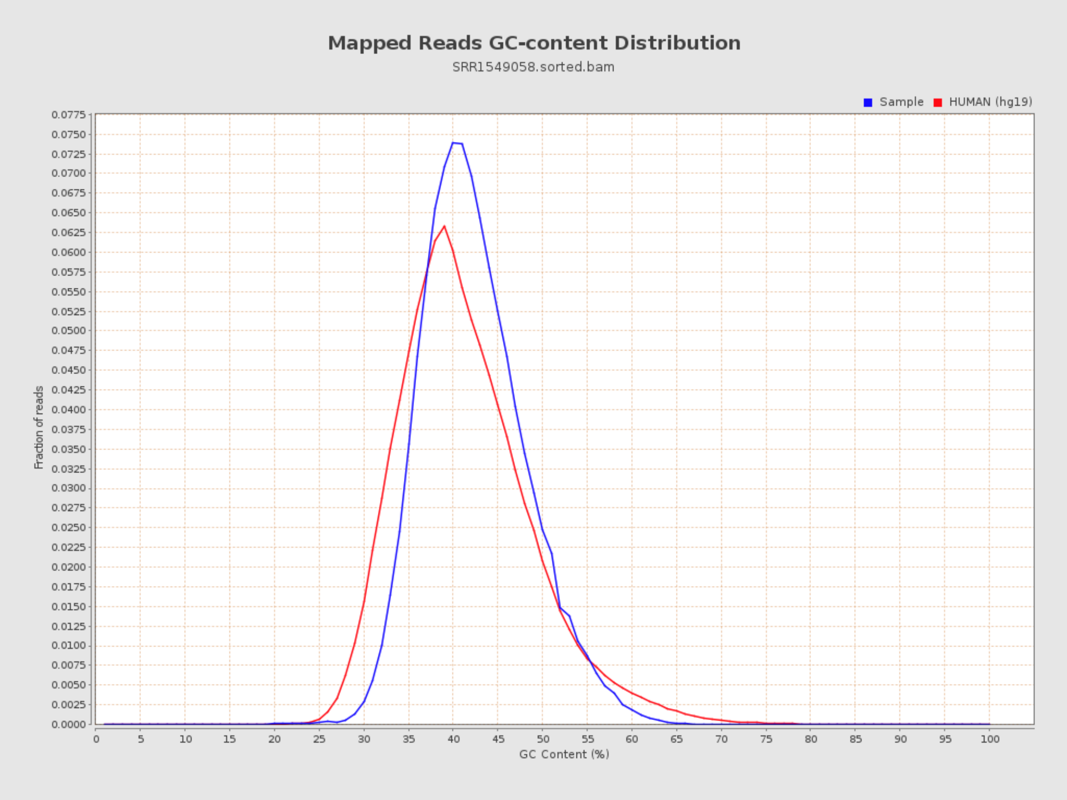
7. Results : Duplication Rate Histogram



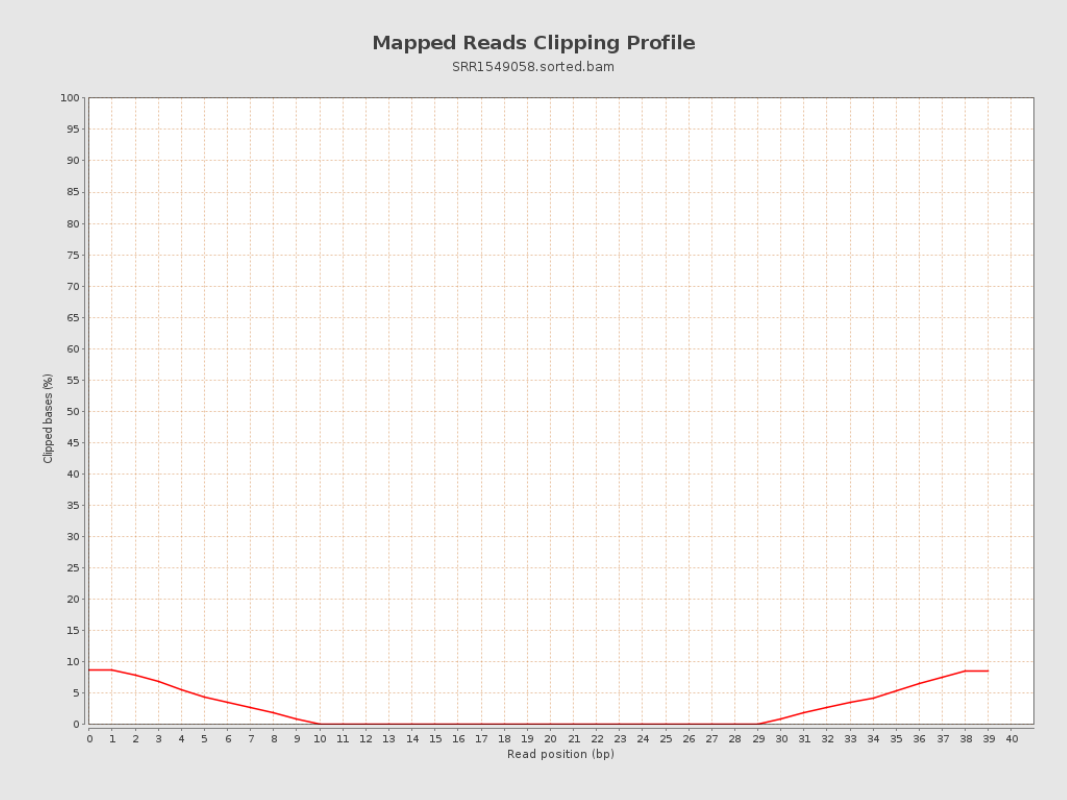
8. Results : Mapped Reads Nucleotide Content



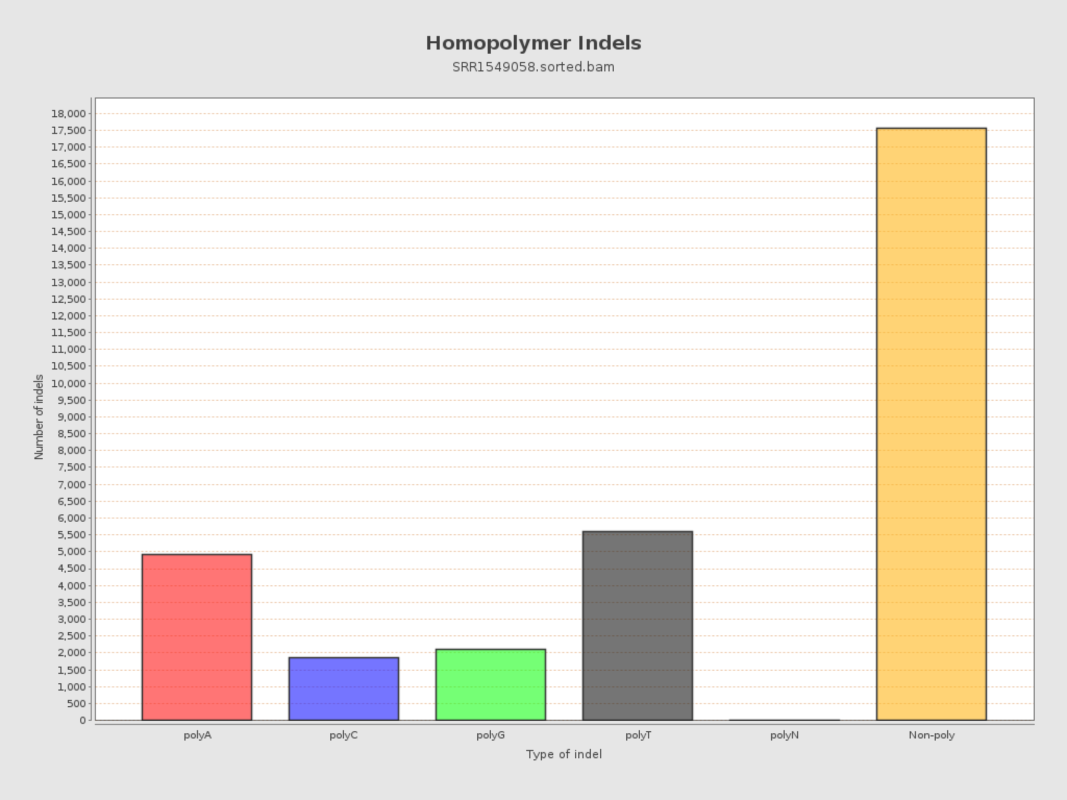
9. Results : Mapped Reads GC-content Distribution



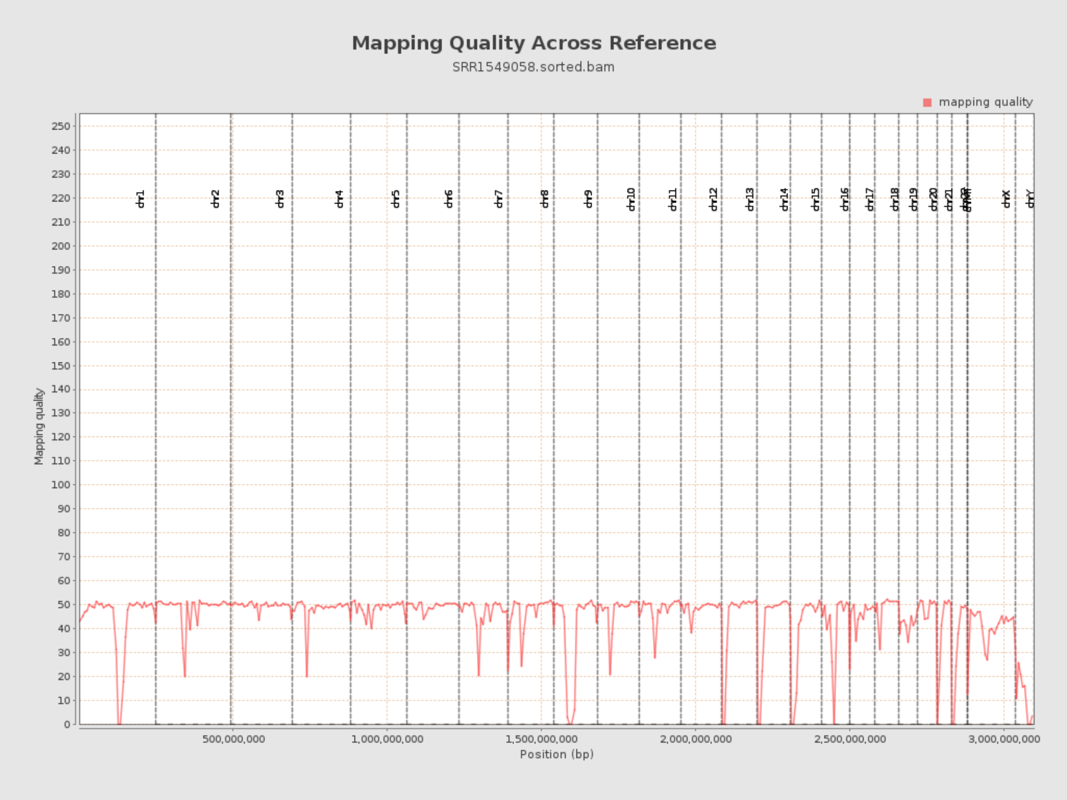
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram