Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:26:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549055.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_SRR1549055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549055.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:25:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,771,430
Mapped reads	37,455,790 / 87.57%
Unmapped reads	5,315,640 / 12.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	4,061,913 / 9.5%
Duplication rate	8.65%
Clipped reads	2,810,489 / 6.57%

2.2. ACGT Content

Number/percentage of A's	417,324,372 / 28.15%
Number/percentage of C's	318,828,551 / 21.51%
Number/percentage of T's	425,716,113 / 28.72%
Number/percentage of G's	320,362,026 / 21.61%
Number/percentage of N's	12,151 / 0%
GC Percentage	43.12%

2.3. Coverage

Mean	0.4789
Standard Deviation	3.7101

2.4. Mapping Quality

Mean Mapping Quality	39.92

2.5. Mismatches and indels

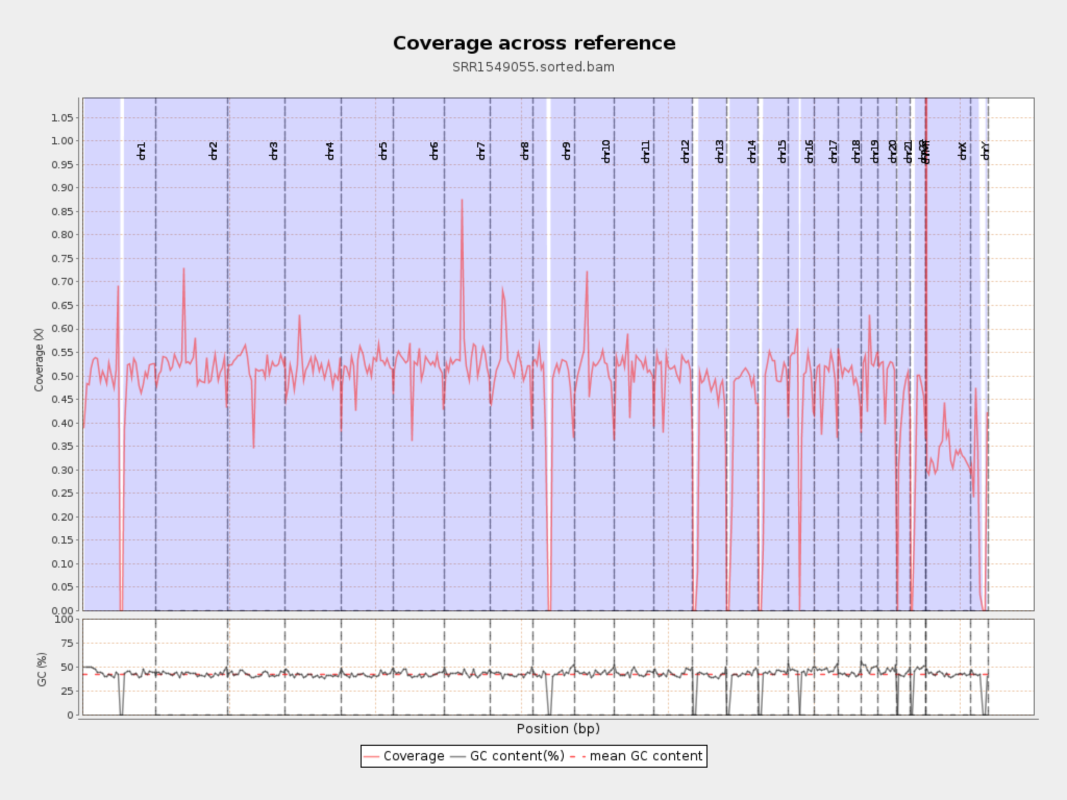
General error rate	0.27%
Mismatches	3,898,918
Insertions	45,359
Mapped reads with at least one insertion	0.12%
Deletions	112,968
Mapped reads with at least one deletion	0.3%
Homopolymer indels	40.63%

2.6. Chromosome stats

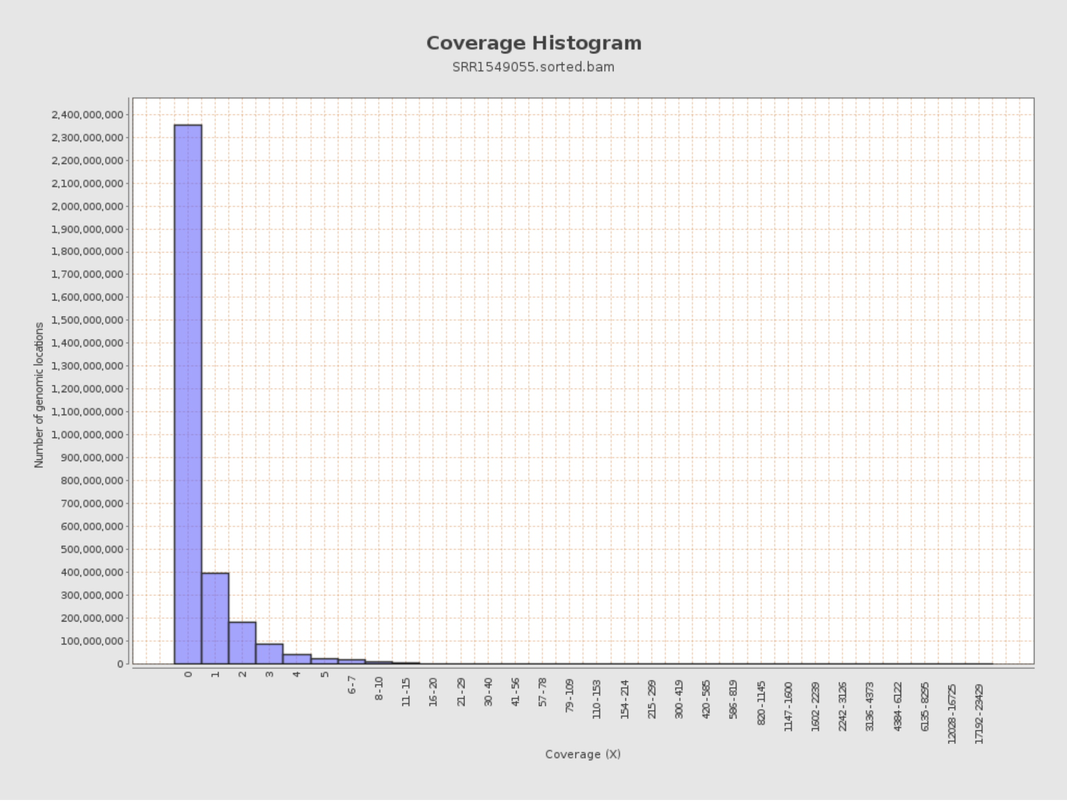
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	118215834	0.4743	5.8691
chr2	243199373	127349213	0.5236	2.5905
chr3	198022430	102686277	0.5186	1.2165
chr4	191154276	98408244	0.5148	1.4832
chr5	180915260	94103128	0.5202	1.2622
chr6	171115067	89198911	0.5213	1.4427
chr7	159138663	86958320	0.5464	4.7417
chr8	146364022	76645732	0.5237	11.4804

chr9	141213431	63186008	0.4475	2.544
chr10	135534747	70937959	0.5234	2.5051
chr11	135006516	69708808	0.5163	1.9819
chr12	133851895	68301125	0.5103	1.3308
chr13	115169878	46056875	0.3999	1.0433
chr14	107349540	44159747	0.4114	1.6181
chr15	102531392	42367312	0.4132	1.095
chr16	90354753	41573118	0.4601	1.4812
chr17	81195210	40192743	0.495	1.288
chr18	78077248	39241068	0.5026	4.8659
chr19	59128983	31013872	0.5245	5.5427
chr20	63025520	31382448	0.4979	1.3511
chr21	48129895	18771357	0.39	1.7322
chr22	51304566	16977916	0.3309	1.8557
chrMT	16571	126848	7.6548	7.8851
chrX	155270560	51504864	0.3317	1.6281
chrY	59373566	13325829	0.2244	2.0247

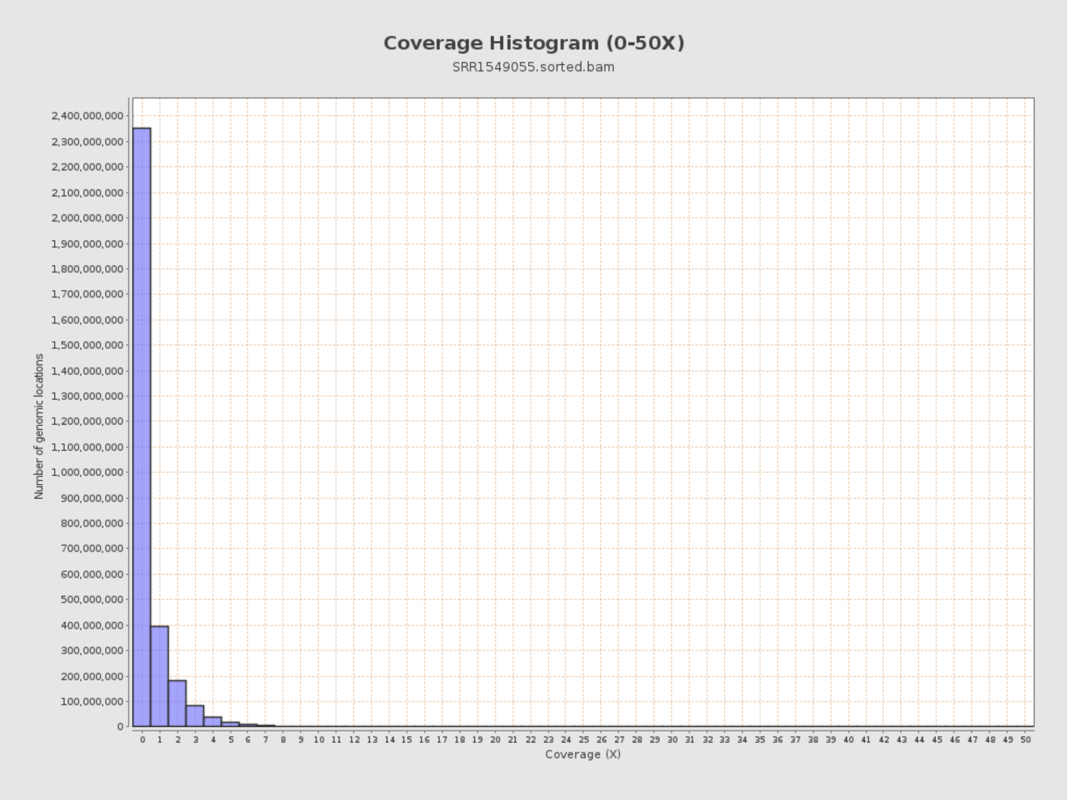
3. Results : Coverage across reference



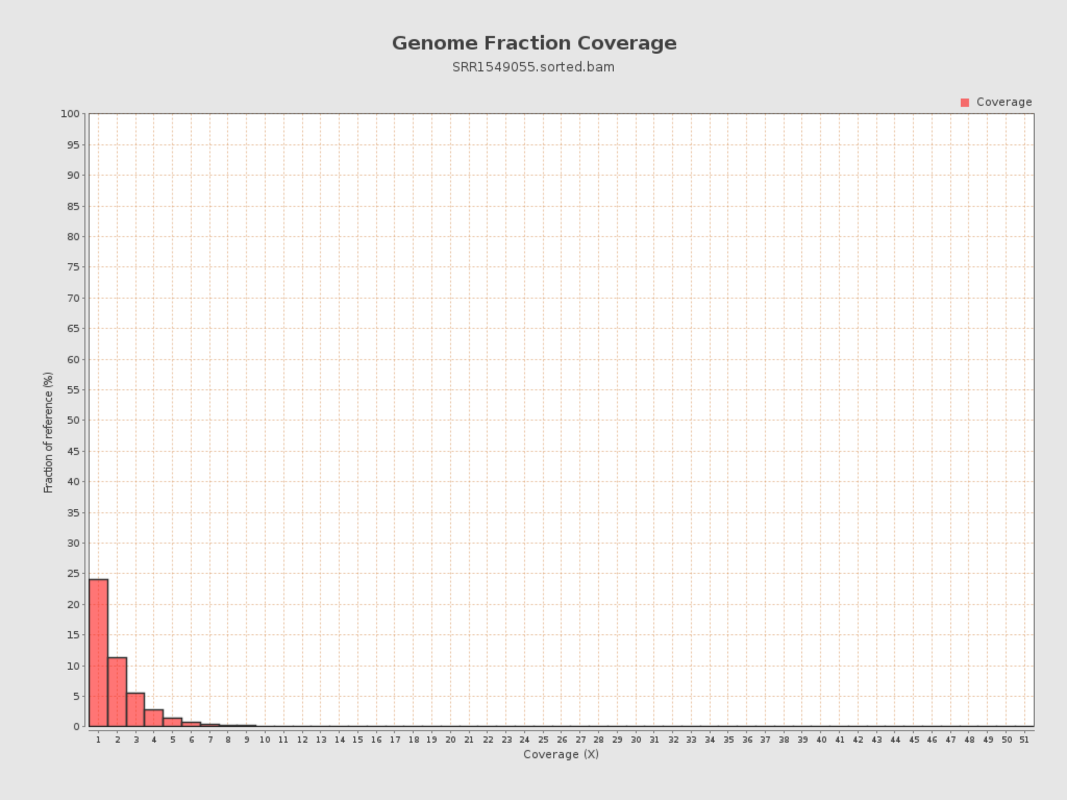
4. Results : Coverage Histogram



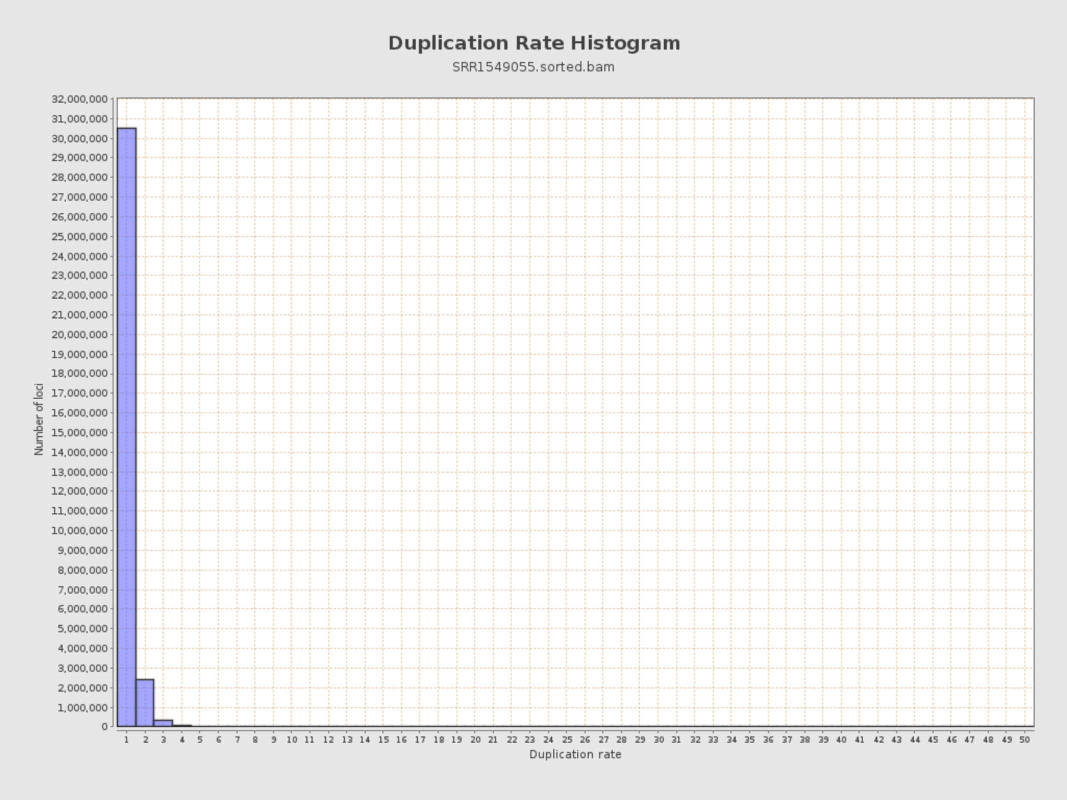
5. Results : Coverage Histogram (0-50X)



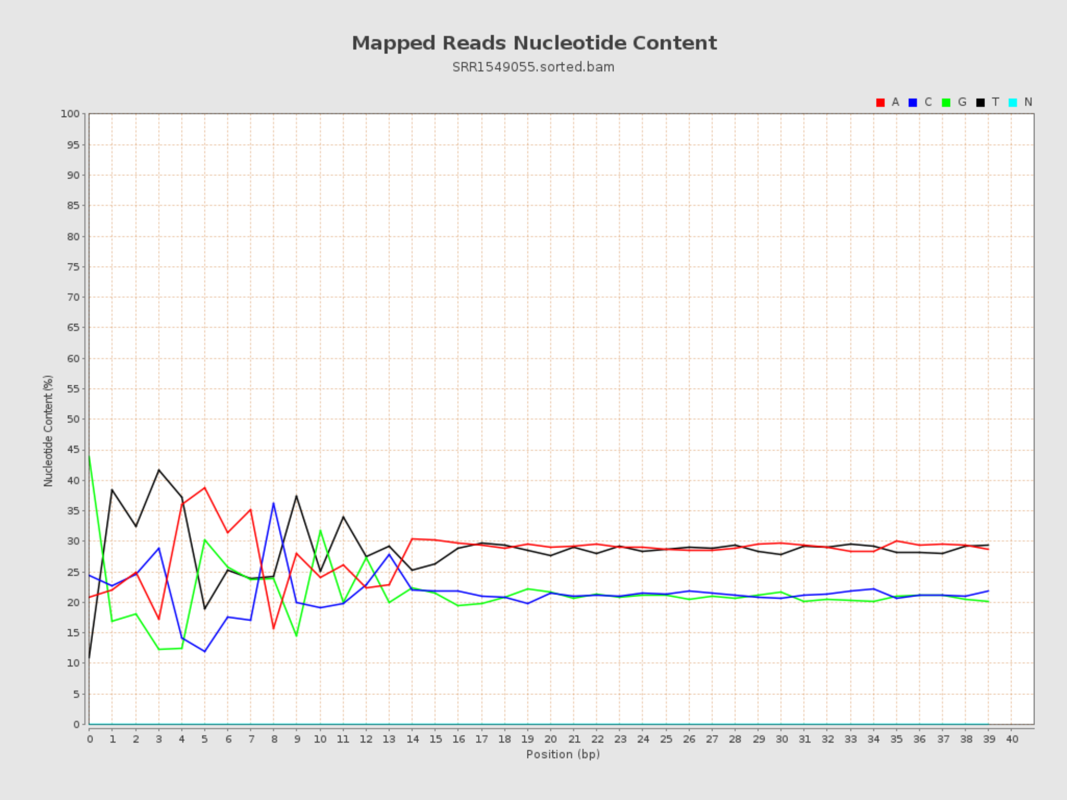
6. Results : Genome Fraction Coverage



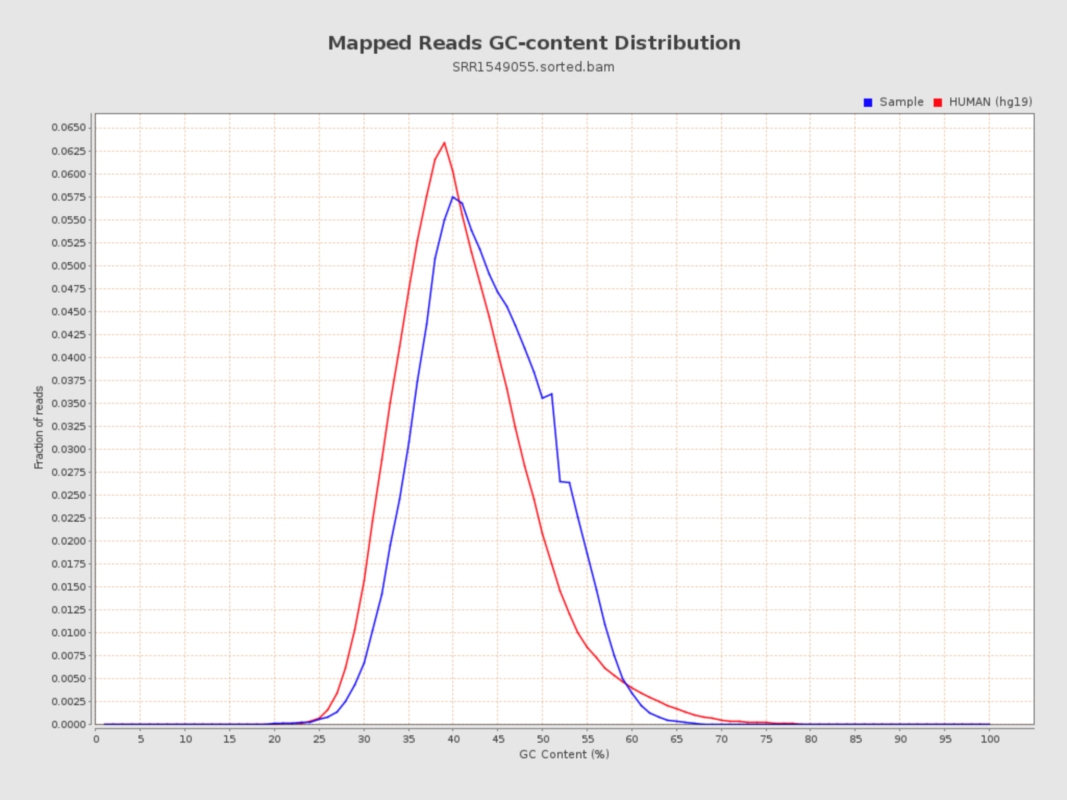
7. Results : Duplication Rate Histogram



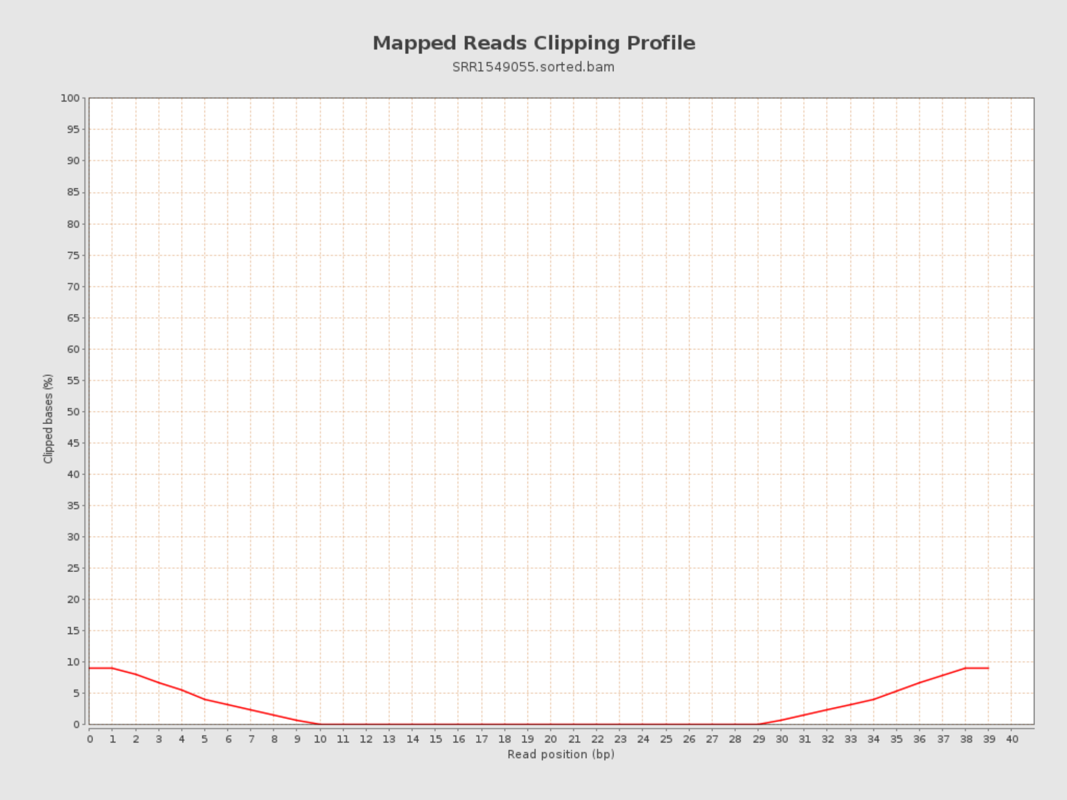
8. Results : Mapped Reads Nucleotide Content



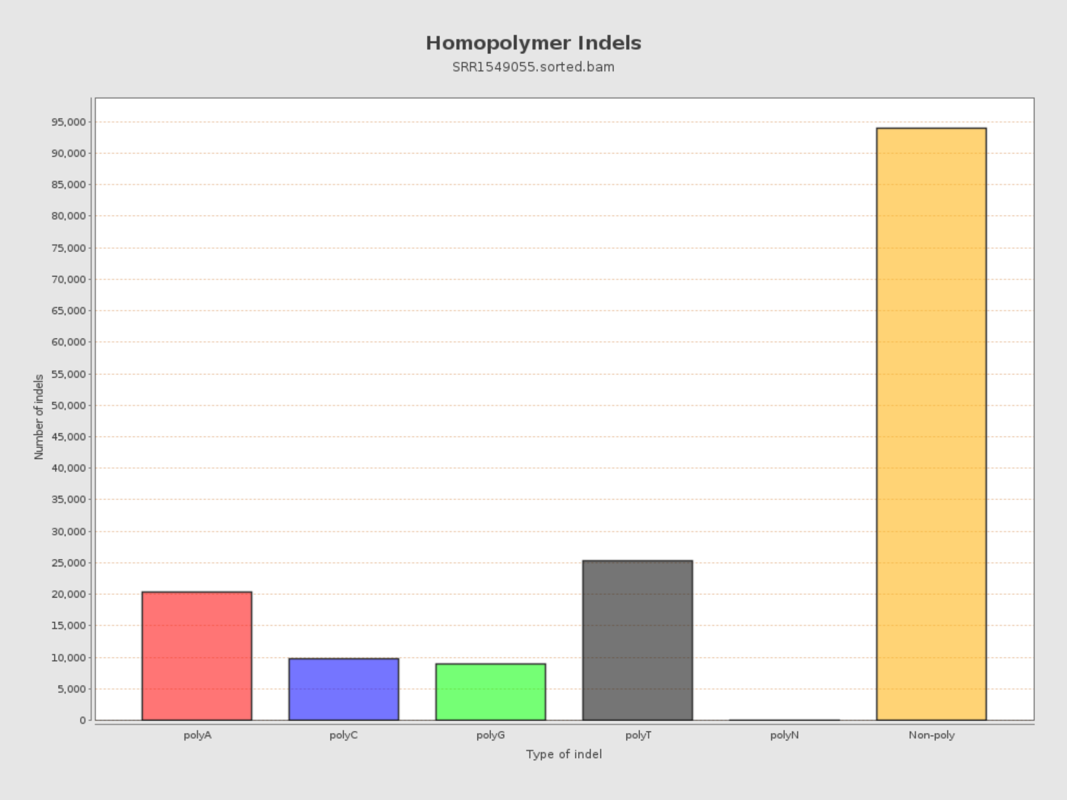
9. Results : Mapped Reads GC-content Distribution



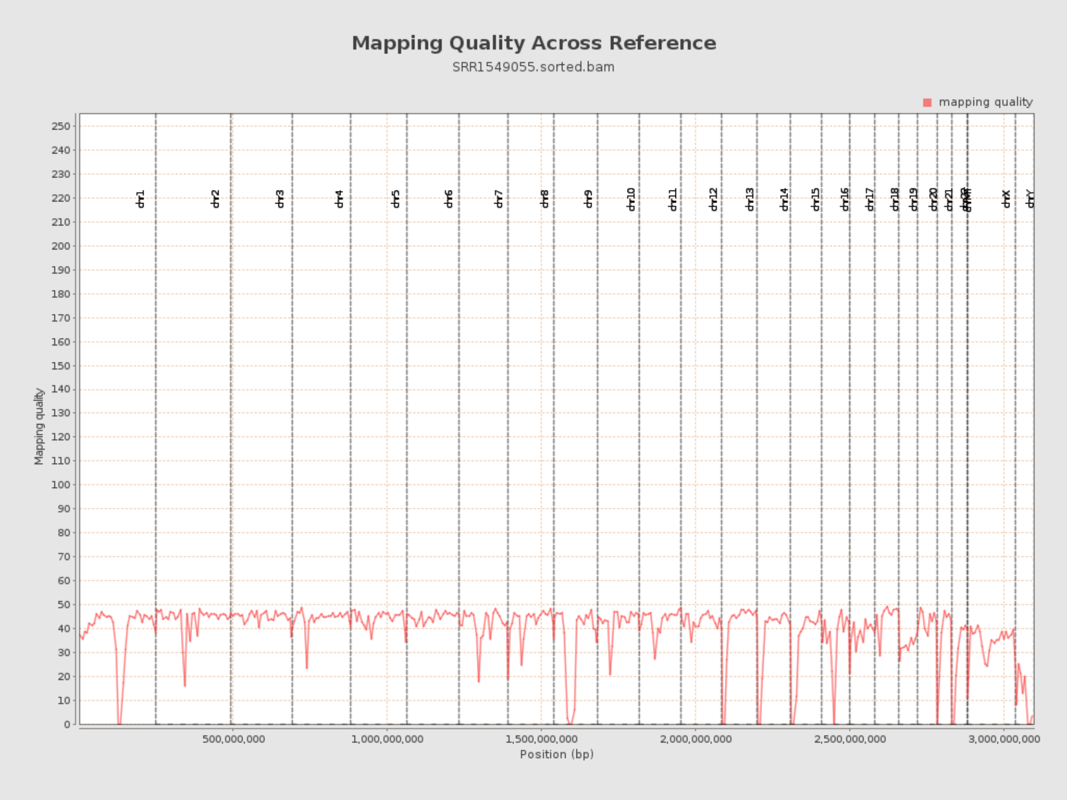
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram