Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:32:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548997.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_SRR1548997 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548997.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:32:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548997.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,798,132
Mapped reads	10,171,850 / 86.22%
Unmapped reads	1,626,282 / 13.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	981,467 / 8.32%
Duplication rate	8.85%
Clipped reads	549,784 / 4.66%

2.2. ACGT Content

Number/percentage of A's	120,939,127 / 29.97%
Number/percentage of C's	79,986,441 / 19.82%
Number/percentage of T's	121,525,958 / 30.11%
Number/percentage of G's	81,097,485 / 20.1%
Number/percentage of N's	4,268 / 0%
GC Percentage	39.92%

2.3. Coverage

Mean	0.1304
Standard Deviation	1.0733

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Mismatches and indels

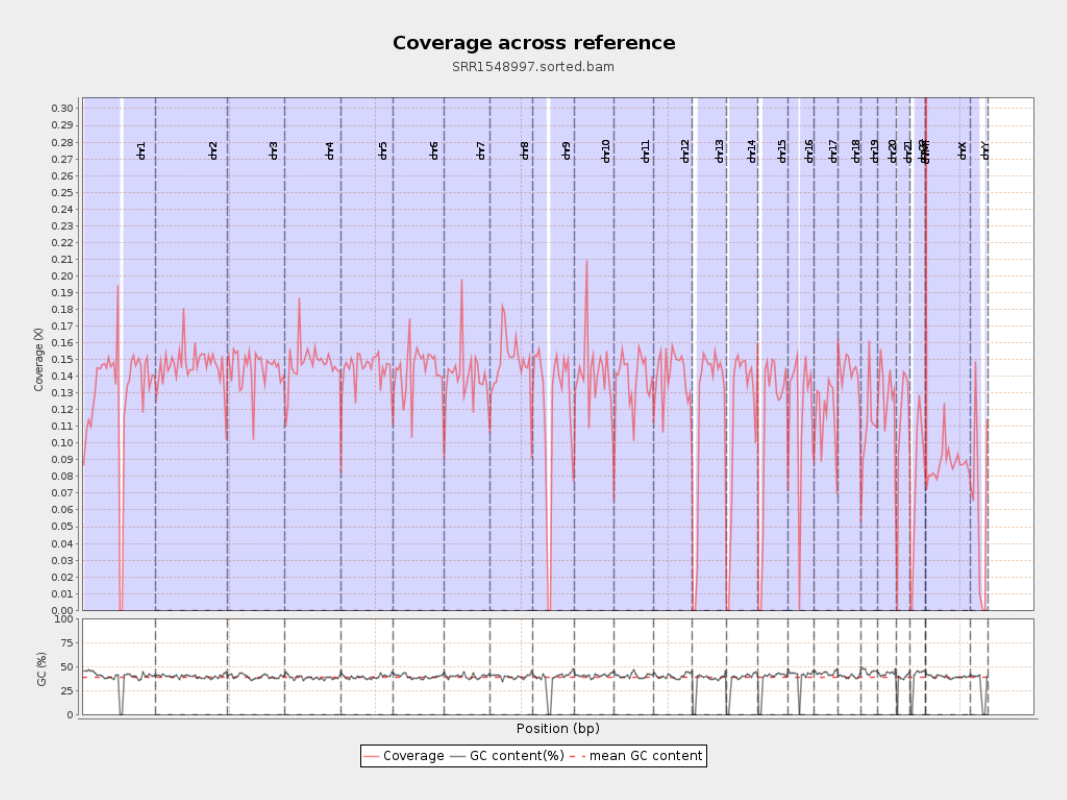
General error rate	0.3%
Mismatches	1,194,322
Insertions	12,594
Mapped reads with at least one insertion	0.12%
Deletions	35,247
Mapped reads with at least one deletion	0.35%
Homopolymer indels	43.18%

2.6. Chromosome stats

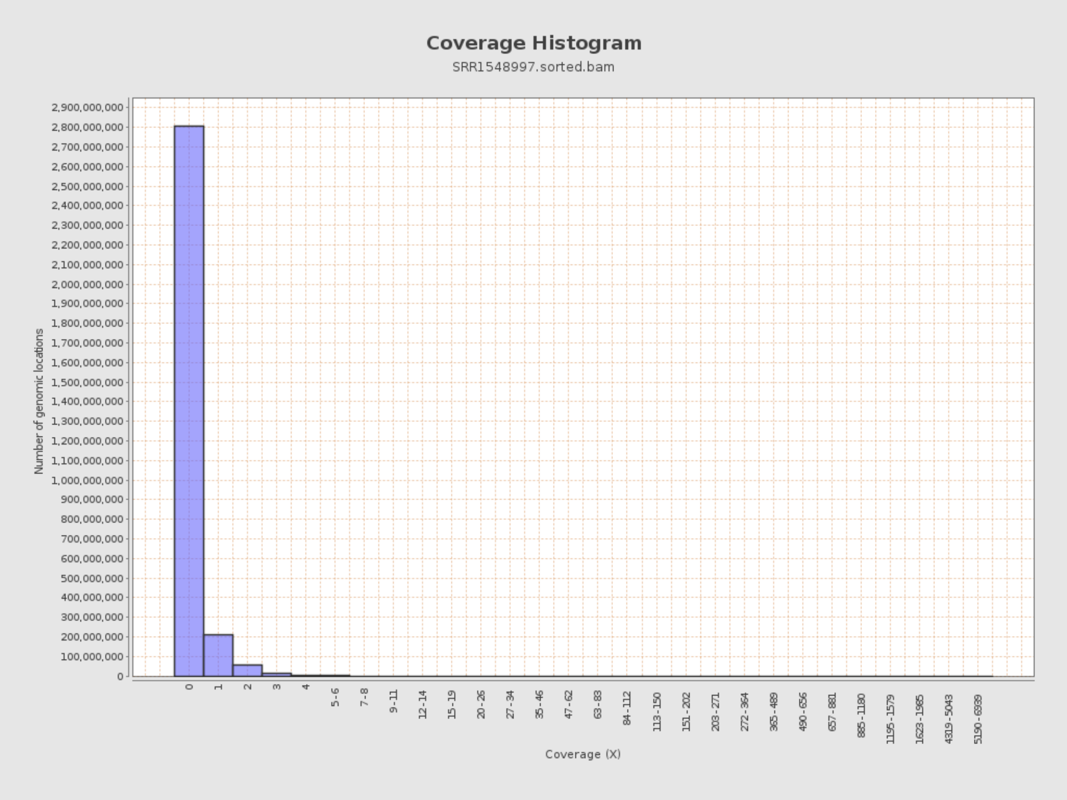
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32238870	0.1293	1.5768
chr2	243199373	35604152	0.1464	0.7224
chr3	198022430	28632492	0.1446	0.4989
chr4	191154276	28233298	0.1477	0.5698
chr5	180915260	25982753	0.1436	0.5043
chr6	171115067	24660208	0.1441	0.5963
chr7	159138663	22189278	0.1394	1.0257
chr8	146364022	21636961	0.1478	3.4268

chr9	141213431	17189265	0.1217	0.6902
chr10	135534747	19143109	0.1412	0.7906
chr11	135006516	18656553	0.1382	0.679
chr12	133851895	18781491	0.1403	0.5133
chr13	115169878	13787874	0.1197	0.4466
chr14	107349540	12543941	0.1169	0.5511
chr15	102531392	11433253	0.1115	0.4313
chr16	90354753	10674573	0.1181	0.514
chr17	81195210	9648307	0.1188	0.5082
chr18	78077248	11216055	0.1437	1.4188
chr19	59128983	6578553	0.1113	1.1787
chr20	63025520	8148163	0.1293	0.5051
chr21	48129895	5303341	0.1102	0.5566
chr22	51304566	3981282	0.0776	0.3967
chrMT	16571	37821	2.2824	3.049
chrX	155270560	13622000	0.0877	0.521
chrY	59373566	3675313	0.0619	0.6376

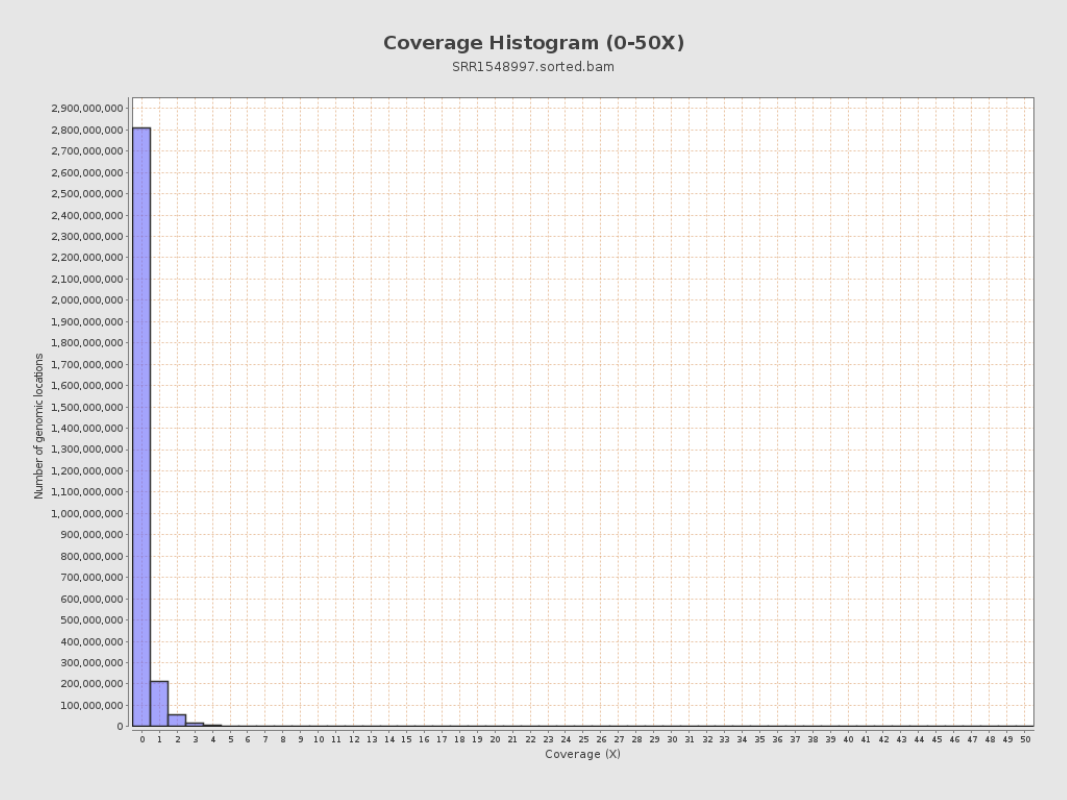
3. Results : Coverage across reference



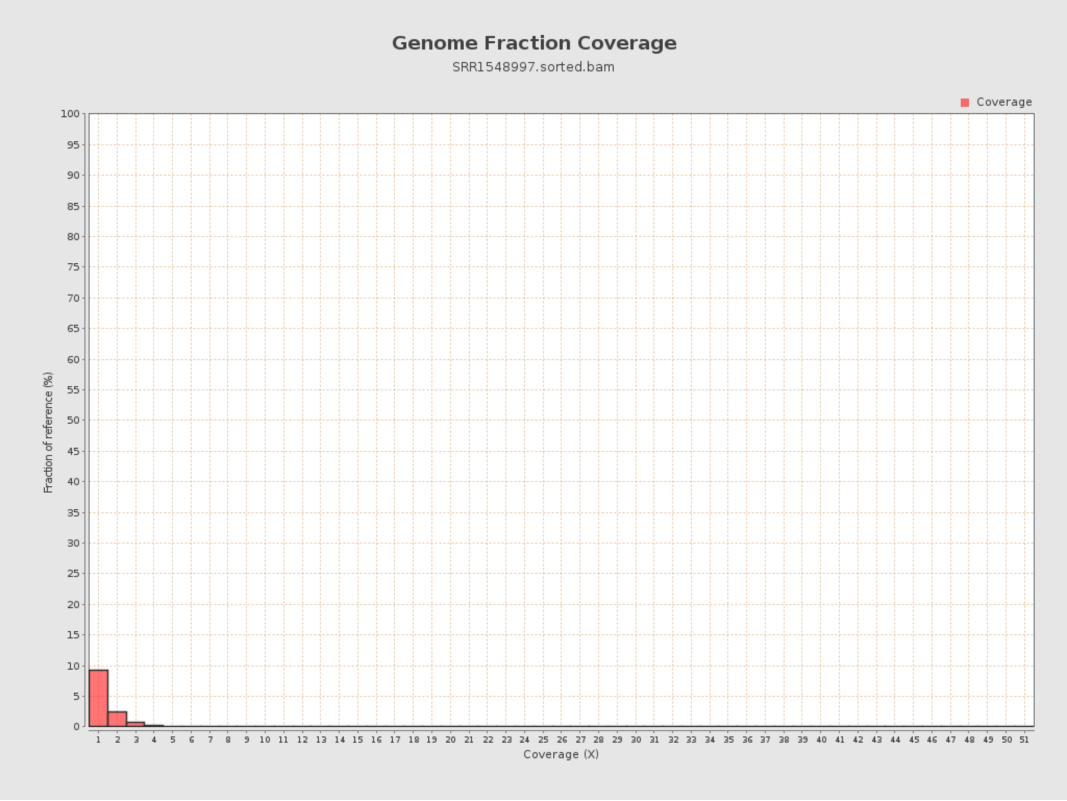
4. Results : Coverage Histogram



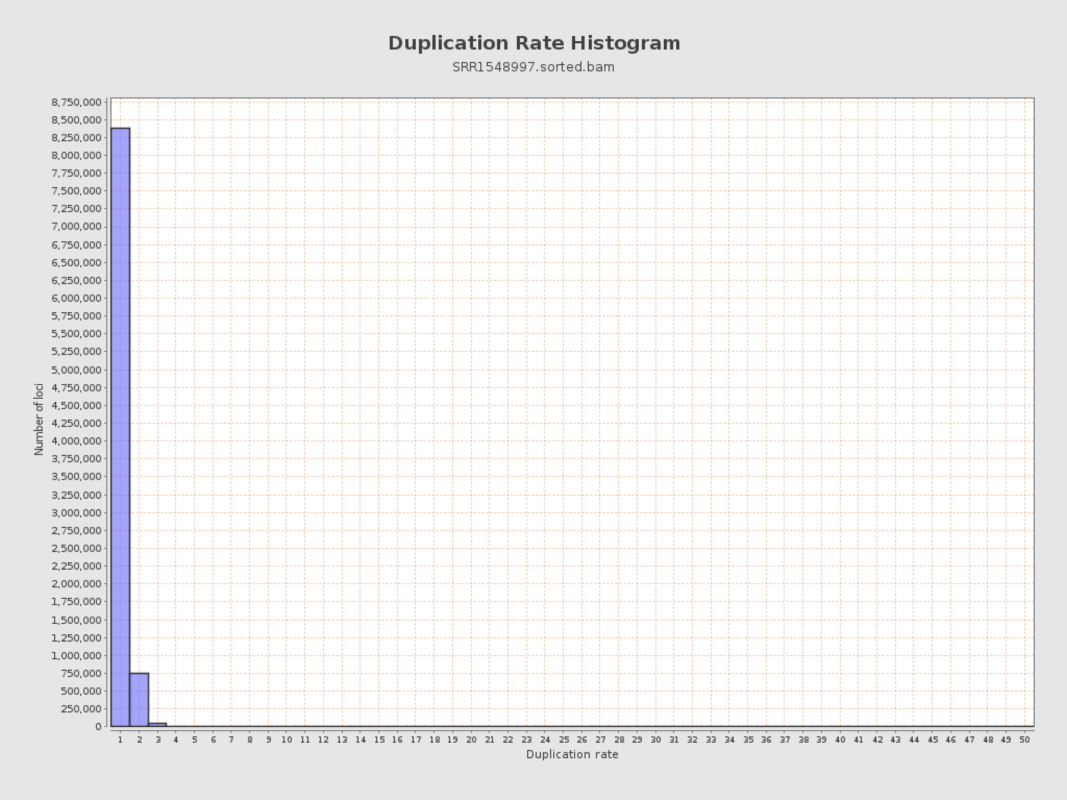
5. Results : Coverage Histogram (0-50X)



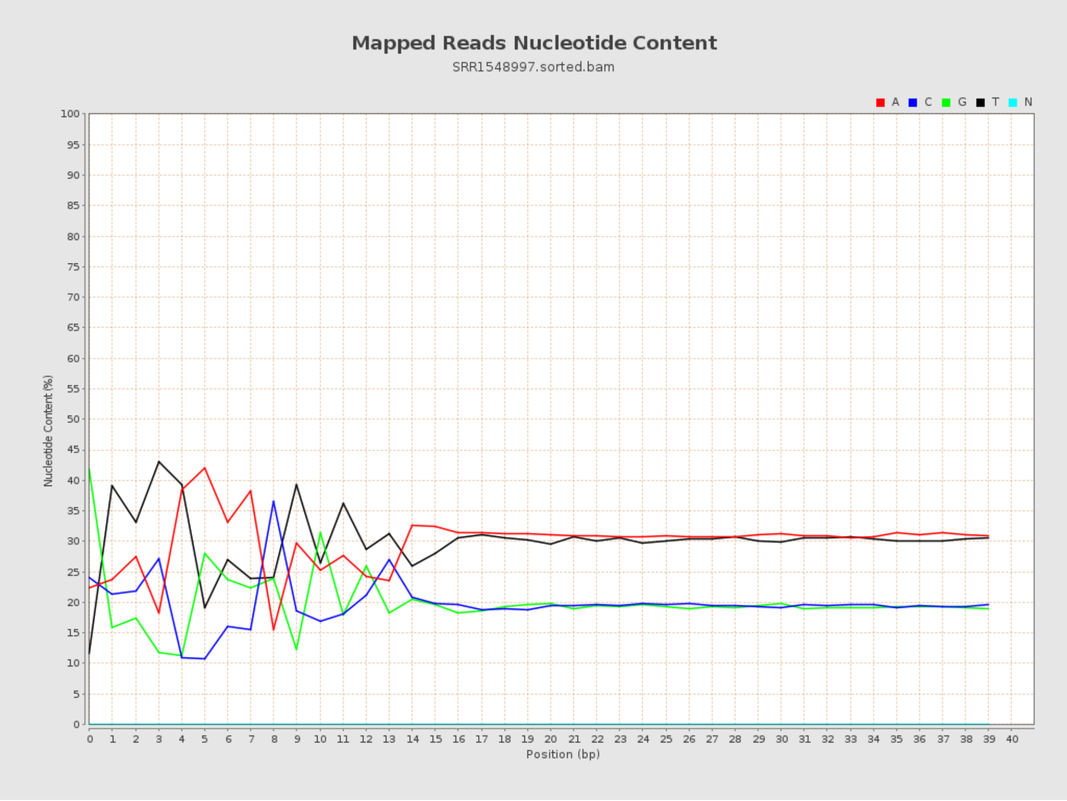
6. Results : Genome Fraction Coverage



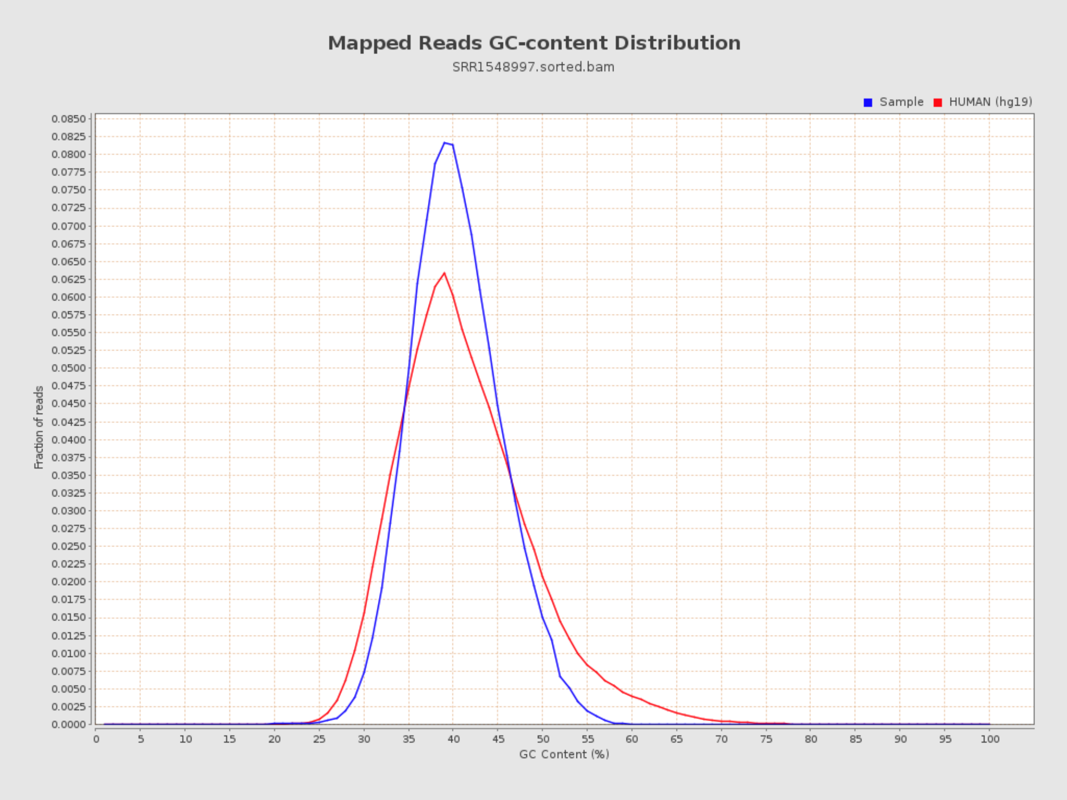
7. Results : Duplication Rate Histogram



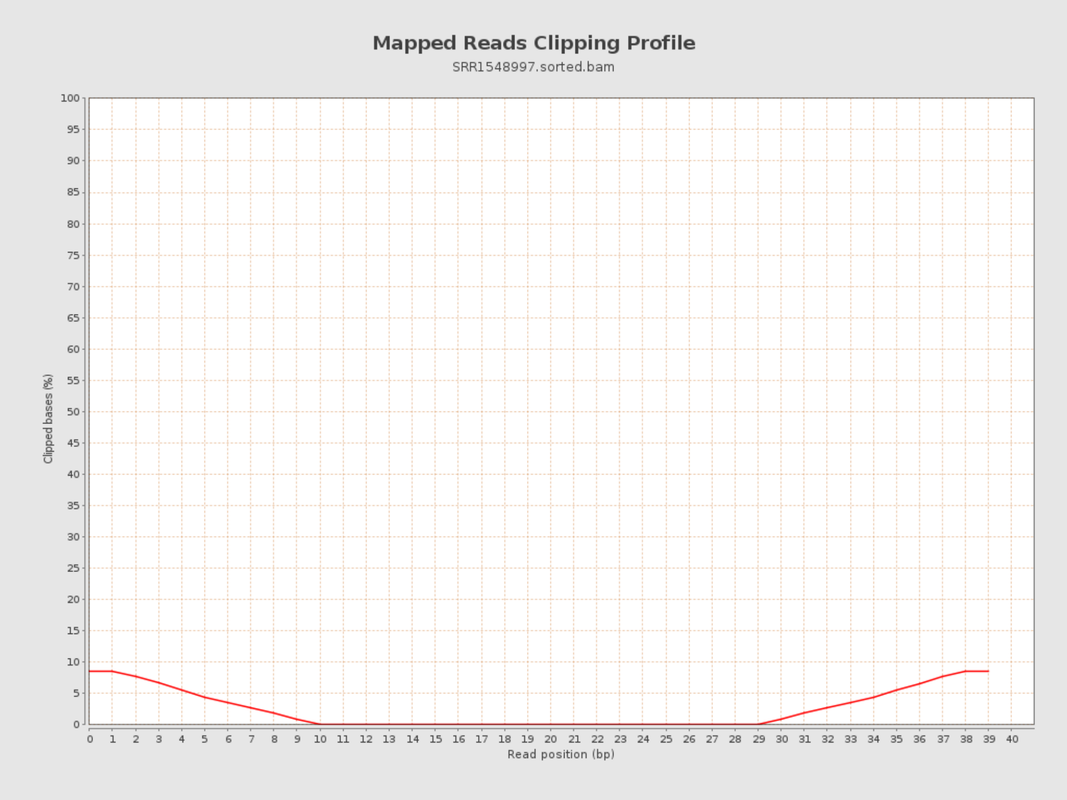
8. Results : Mapped Reads Nucleotide Content



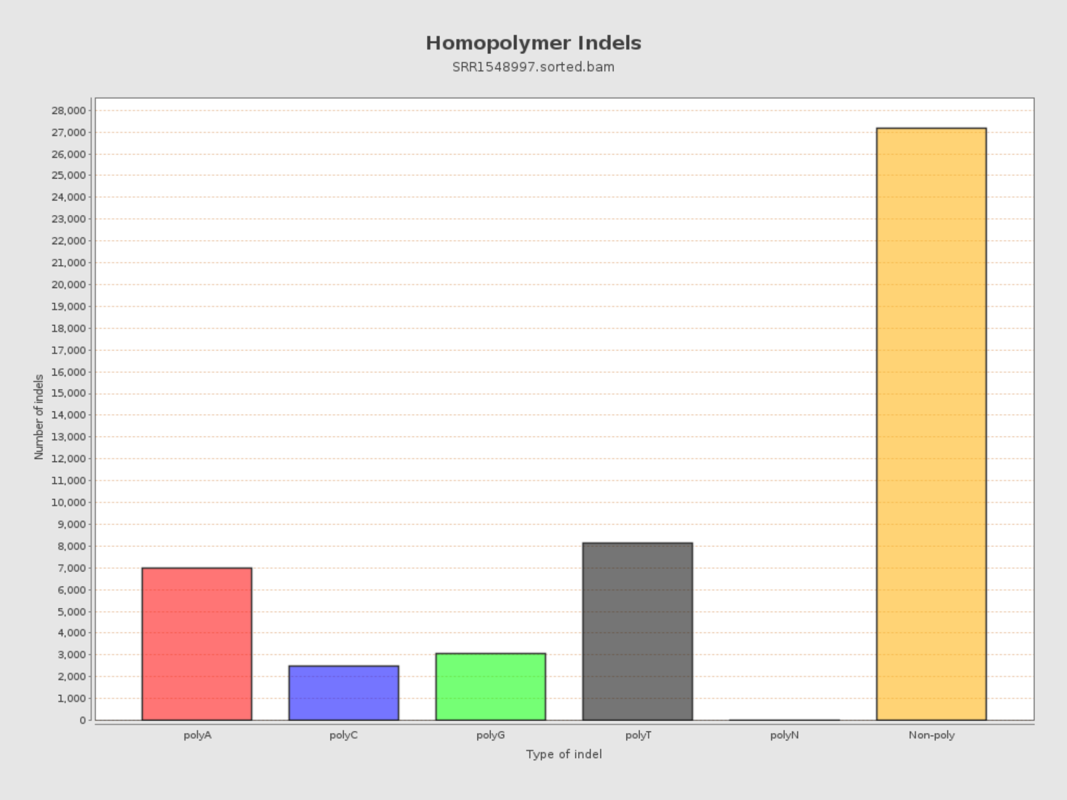
9. Results : Mapped Reads GC-content Distribution



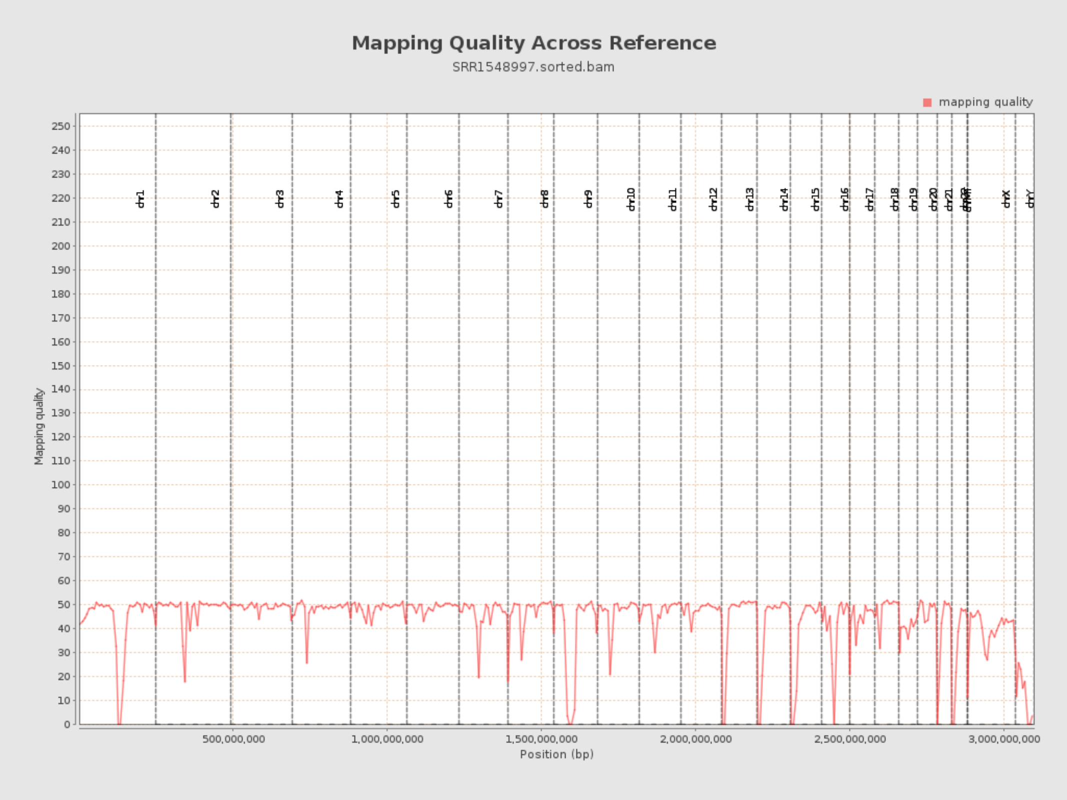
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram