Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 05:38:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153351.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_SRR1153351 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153351.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 05:38:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153351.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	47,783,886
Mapped reads	47,463,123 / 99.33%
Unmapped reads	320,763 / 0.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	258,451 / 0.54%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	32,744,209 / 68.53%
Duplication rate	59.83%
Clipped reads	6,061,531 / 12.69%

2.2. ACGT Content

Number/percentage of A's	1,221,840,016 / 26.44%
Number/percentage of C's	1,080,974,846 / 23.39%
Number/percentage of T's	1,255,681,368 / 27.18%
Number/percentage of G's	1,060,766,497 / 22.96%
Number/percentage of N's	1,365,282 / 0.03%
GC Percentage	46.35%

2.3. Coverage

Mean	1.4928

Standard Deviation	17.8553

2.4. Mapping Quality

Mean Mapping Quality	50.75

2.5. Mismatches and indels

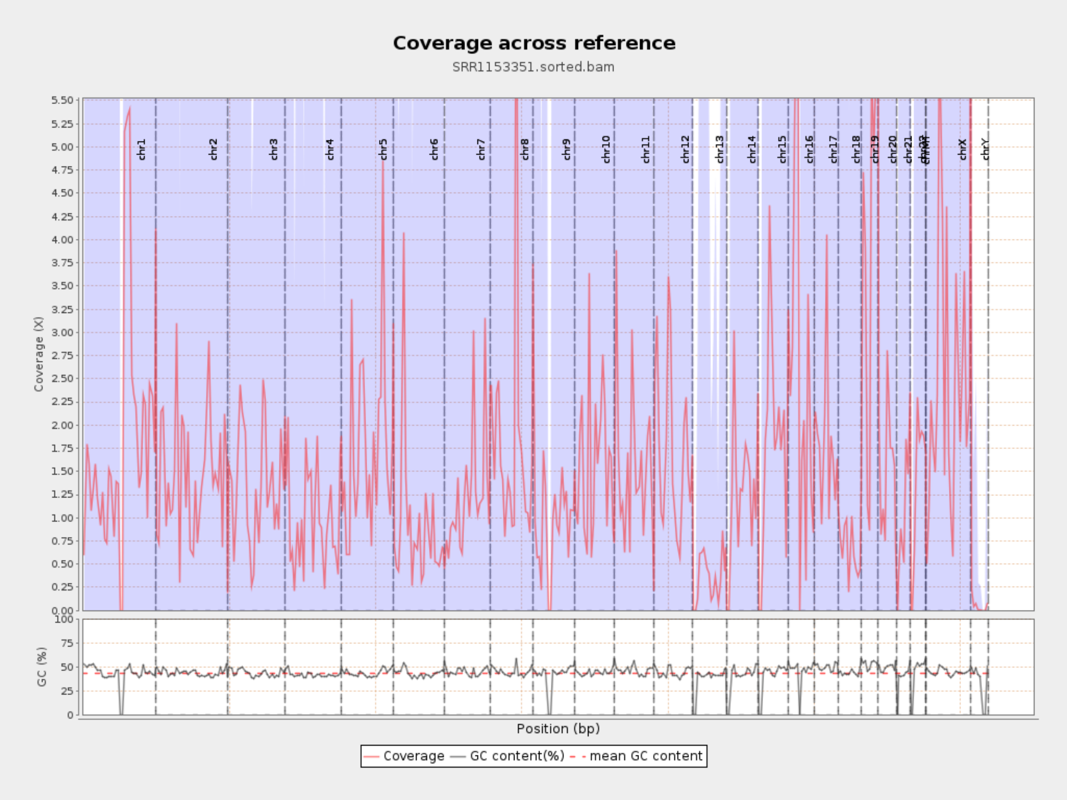
General error rate	0.27%
Mismatches	12,121,625
Insertions	324,234
Mapped reads with at least one insertion	0.68%
Deletions	279,275
Mapped reads with at least one deletion	0.58%
Homopolymer indels	49.77%

2.6. Chromosome stats

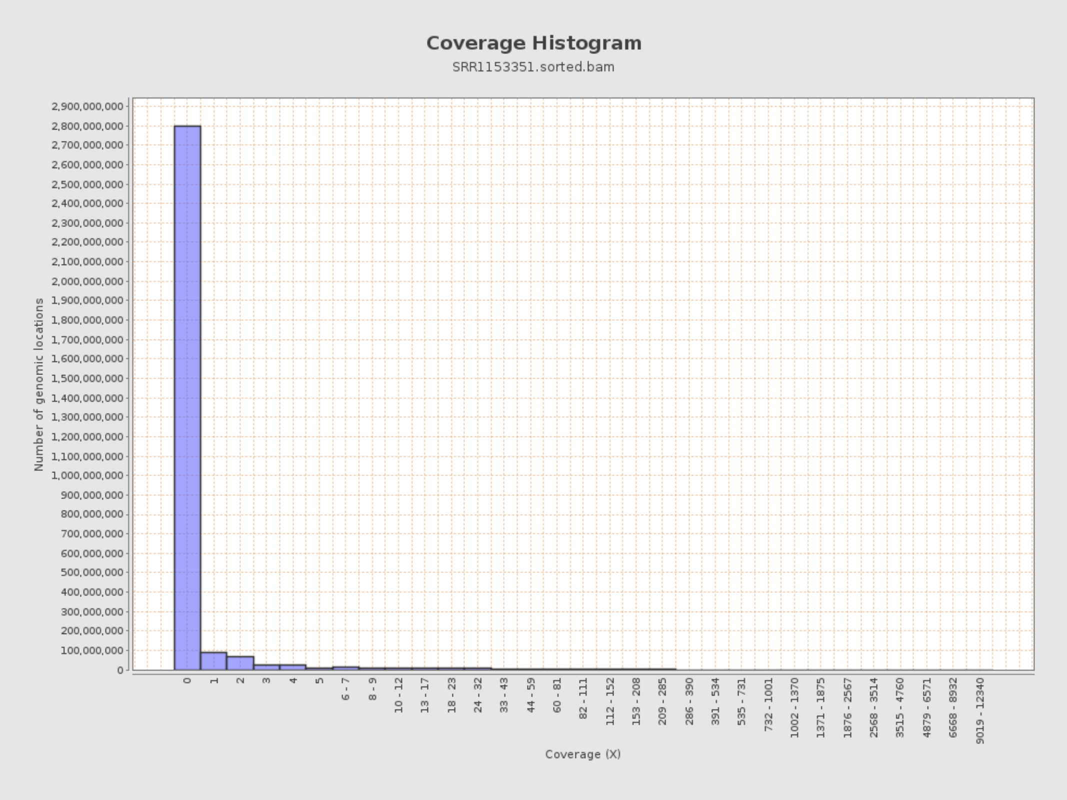
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	448853195	1.8008	18.1653
chr2	243199373	359233177	1.4771	16.0699
chr3	198022430	262511892	1.3257	14.7399
chr4	191154276	187364230	0.9802	12.1459
chr5	180915260	320803565	1.7732	18.9399
chr6	171115067	152038644	0.8885	11.5959
chr7	159138663	196933690	1.2375	14.4101

chr8	146364022	270252492	1.8464	34.2116
chr9	141213431	129656495	0.9182	10.9812
chr10	135534747	220067948	1.6237	17.3858
chr11	135006516	211934132	1.5698	16.3839
chr12	133851895	236739115	1.7687	17.0924
chr13	115169878	41619588	0.3614	5.4814
chr14	107349540	134370910	1.2517	13.6443
chr15	102531392	176795436	1.7243	16.4805
chr16	90354753	229873186	2.5441	25.9781
chr17	81195210	150012333	1.8476	15.0363
chr18	78077248	51312191	0.6572	8.9172
chr19	59128983	234018243	3.9578	30.0446
chr20	63025520	95195473	1.5104	14.9255
chr21	48129895	51180256	1.0634	13.1495
chr22	51304566	69826989	1.361	14.7826
chrMT	16571	11483	0.693	1.6873
chrX	155270560	387752081	2.4973	27.7826
chrY	59373566	2826744	0.0476	1.9052

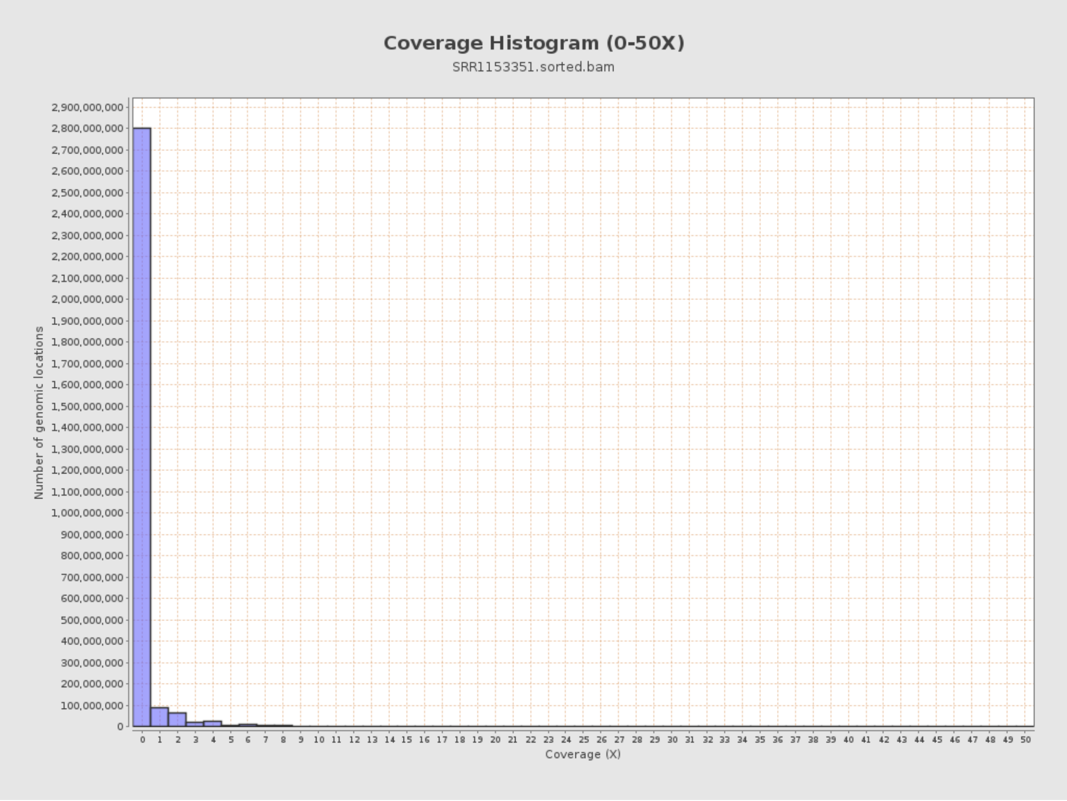
3. Results : Coverage across reference



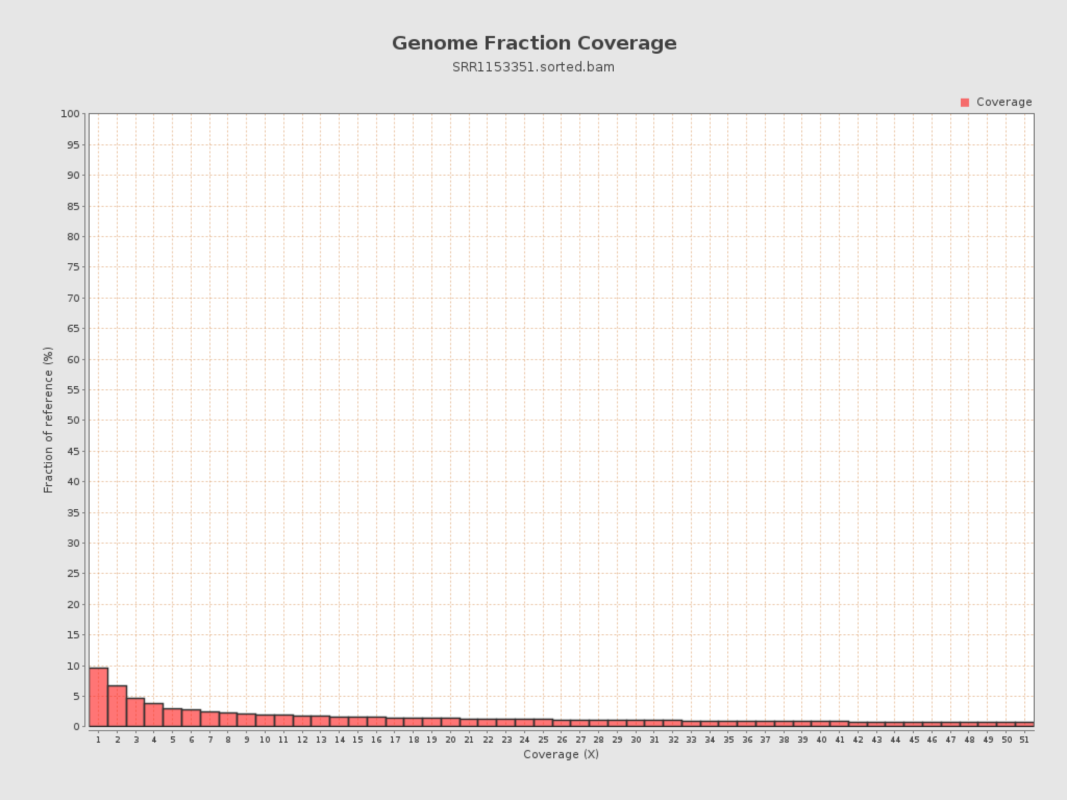
4. Results : Coverage Histogram



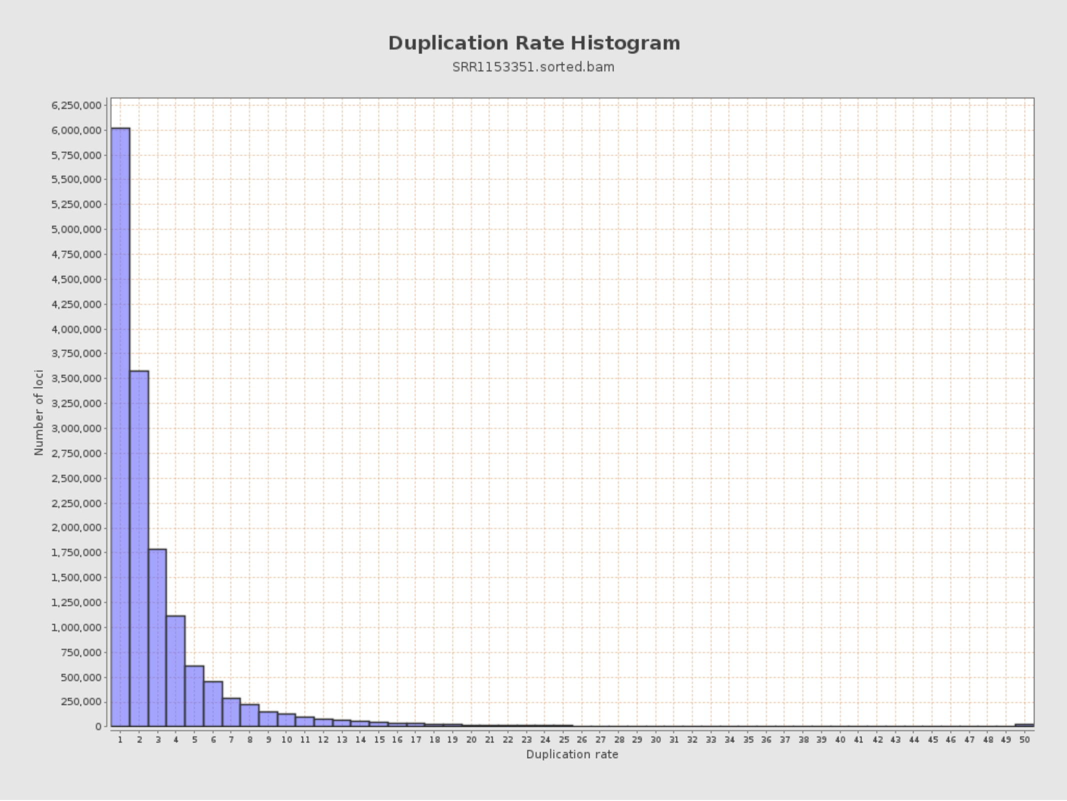
5. Results : Coverage Histogram (0-50X)



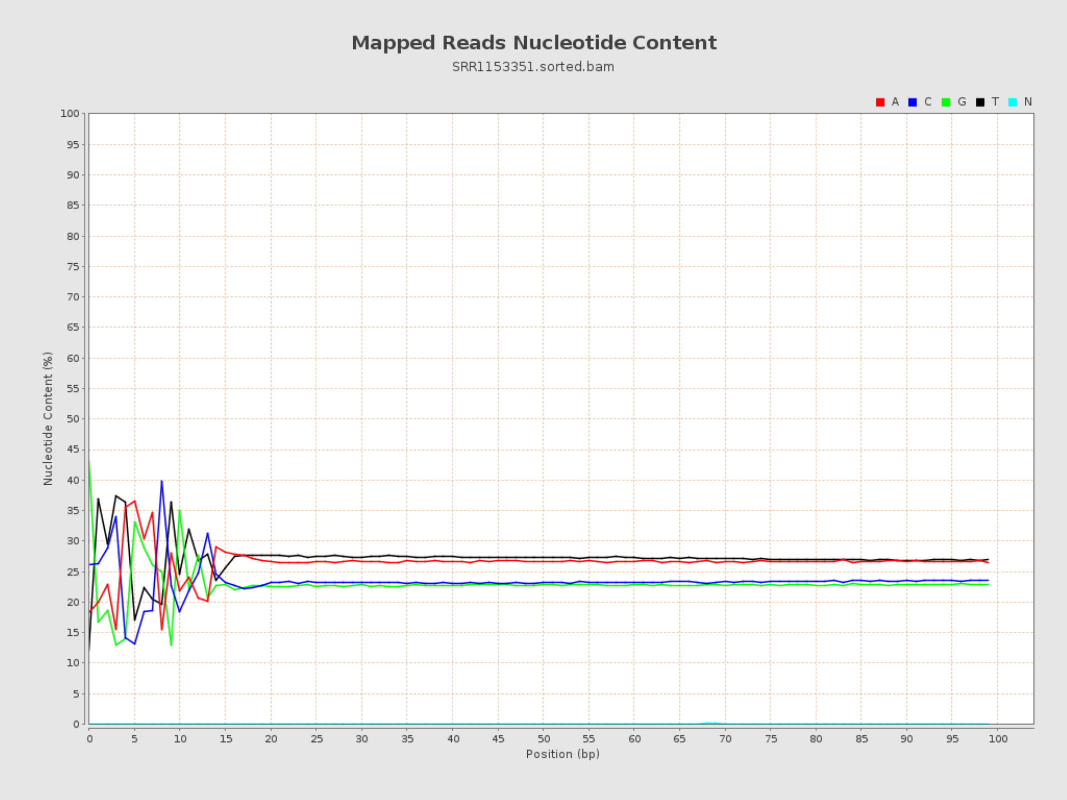
6. Results : Genome Fraction Coverage



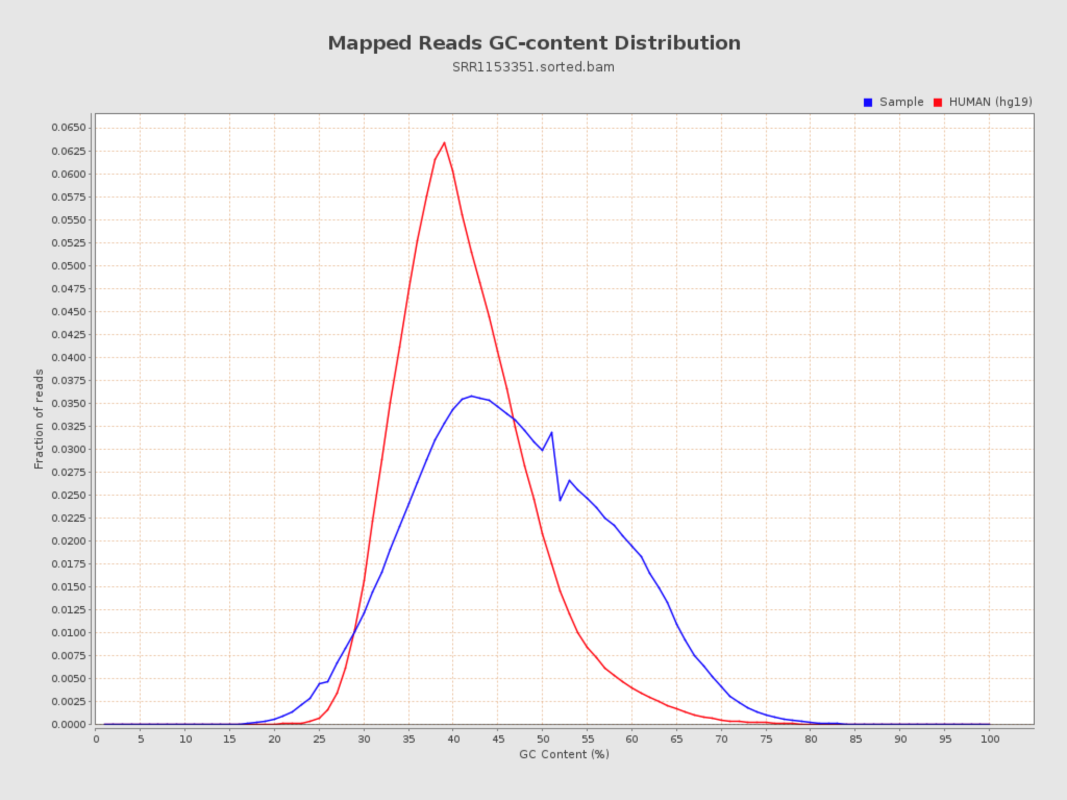
7. Results : Duplication Rate Histogram



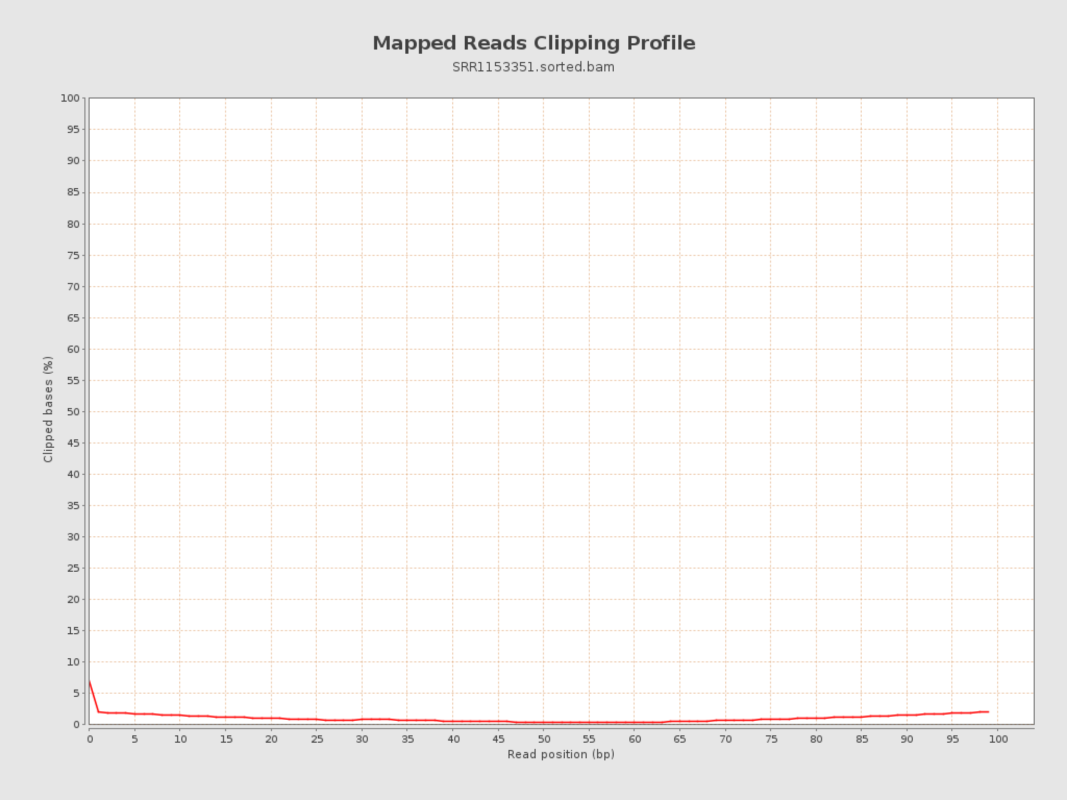
8. Results : Mapped Reads Nucleotide Content



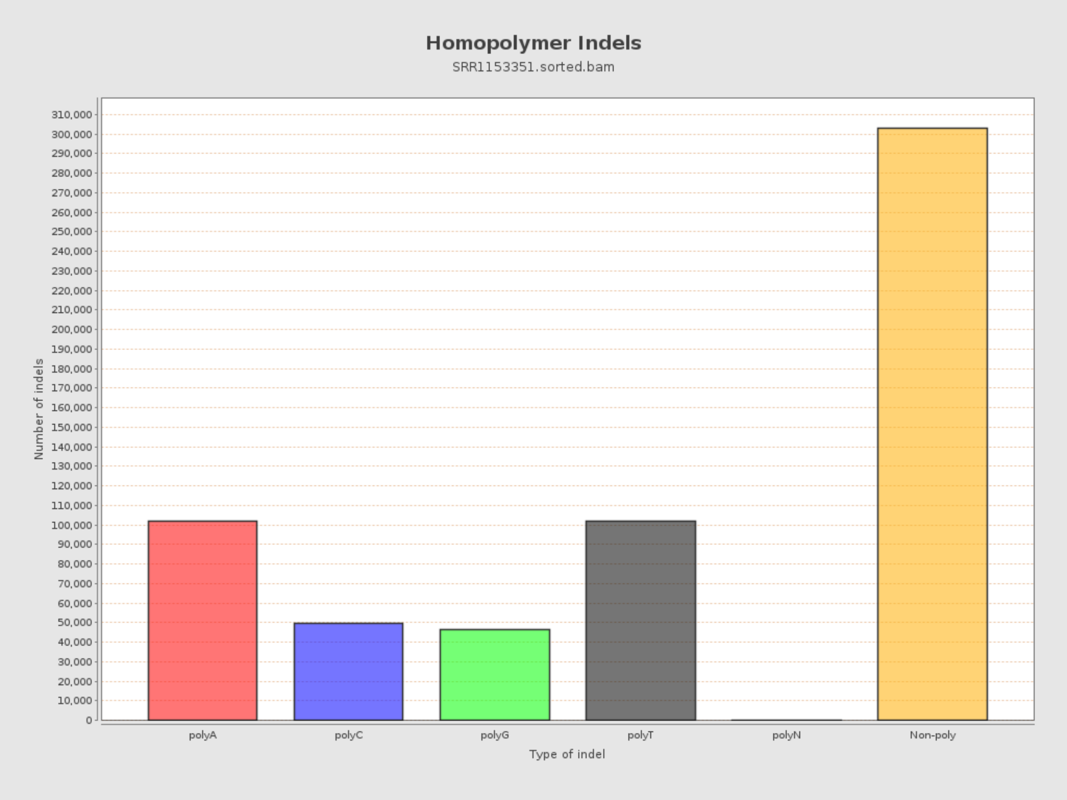
9. Results : Mapped Reads GC-content Distribution



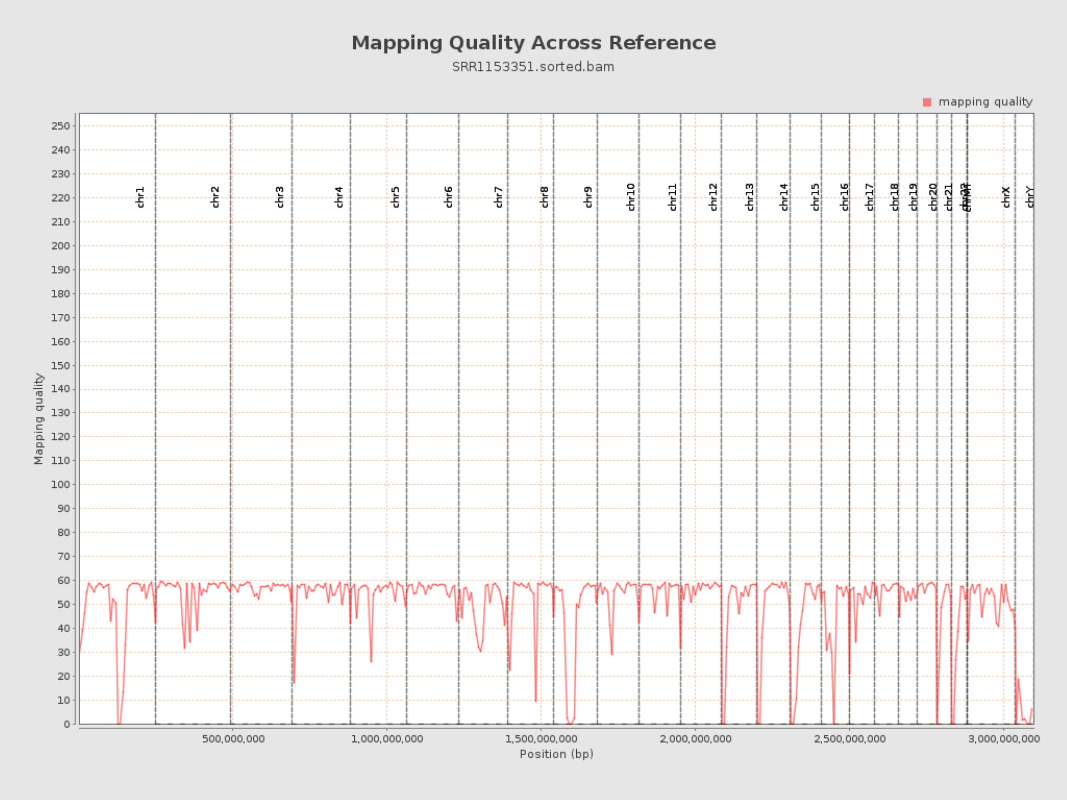
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram