Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:05:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085053.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_SRR3085053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085053.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:05:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,391,903
Mapped reads	1,244,163 / 89.39%
Unmapped reads	147,740 / 10.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,349 / 1.17%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	47,286 / 3.4%
Duplication rate	2.02%
Clipped reads	549,322 / 39.47%

2.2. ACGT Content

Number/percentage of A's	24,341,621 / 28.95%
Number/percentage of C's	15,978,399 / 19%
Number/percentage of T's	24,840,991 / 29.54%
Number/percentage of G's	18,911,382 / 22.49%
Number/percentage of N's	9,305 / 0.01%
GC Percentage	41.5%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.4398

2.4. Mapping Quality

Mean Mapping Quality	43.1

2.5. Mismatches and indels

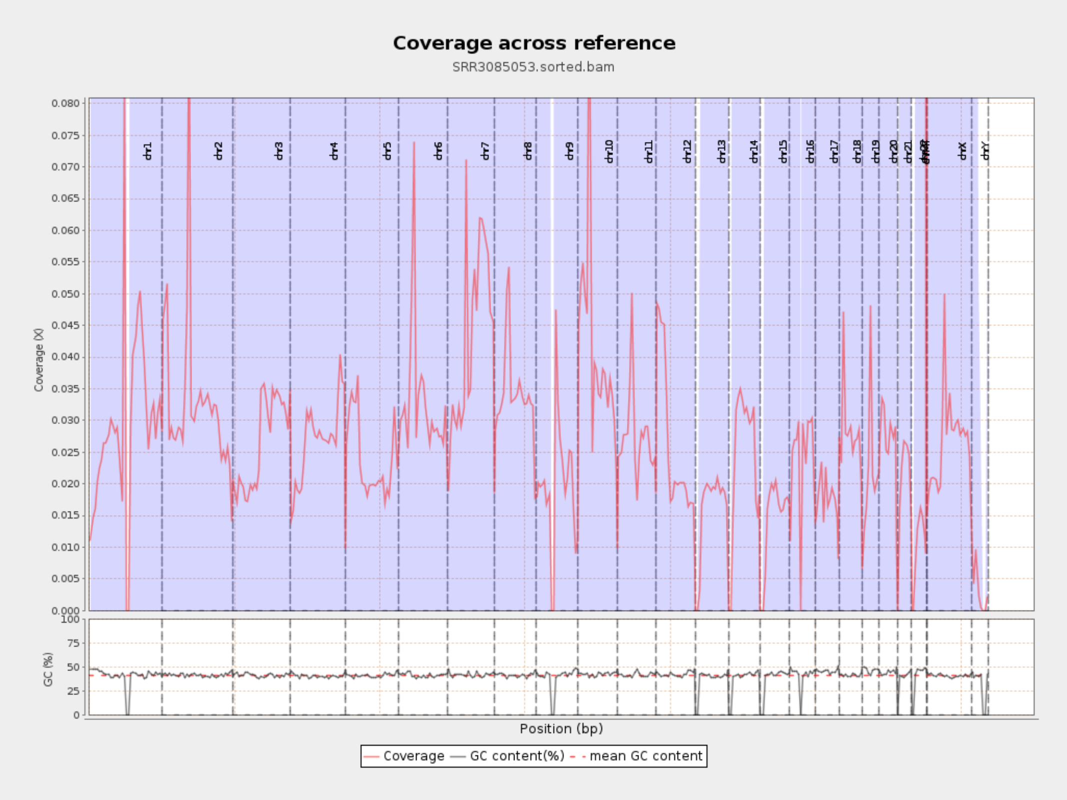
General error rate	0.98%
Mismatches	815,356
Insertions	7,169
Mapped reads with at least one insertion	0.57%
Deletions	15,515
Mapped reads with at least one deletion	1.23%
Homopolymer indels	42.88%

2.6. Chromosome stats

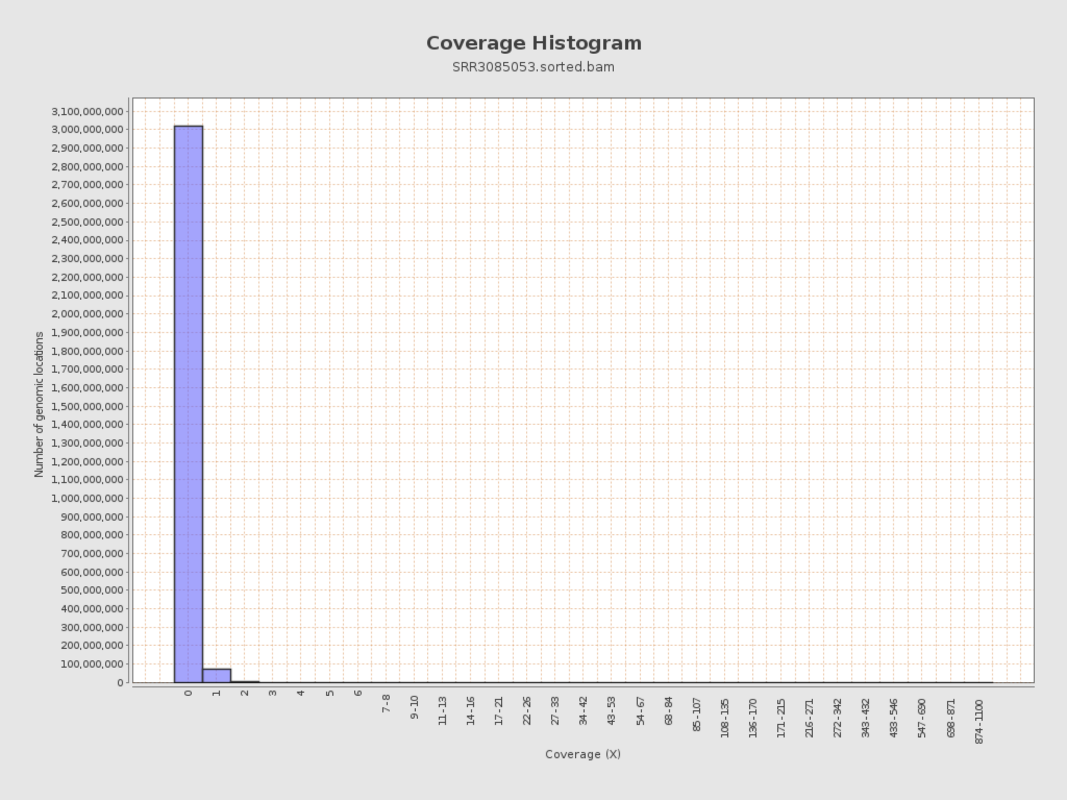
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7321992	0.0294	0.9379
chr2	243199373	8194806	0.0337	0.4776
chr3	198022430	5206876	0.0263	0.1894
chr4	191154276	5149347	0.0269	0.1777
chr5	180915260	4350463	0.024	0.1682
chr6	171115067	5670882	0.0331	0.3994
chr7	159138663	6991347	0.0439	0.4726

chr8	146364022	5003379	0.0342	0.5175
chr9	141213431	2819664	0.02	0.3897
chr10	135534747	5722619	0.0422	0.615
chr11	135006516	3668045	0.0272	0.4547
chr12	133851895	3486591	0.026	0.183
chr13	115169878	1794953	0.0156	0.1285
chr14	107349540	2614954	0.0244	0.2081
chr15	102531392	1467699	0.0143	0.1268
chr16	90354753	2150131	0.0238	0.2309
chr17	81195210	1412027	0.0174	0.2188
chr18	78077248	2225803	0.0285	0.7526
chr19	59128983	1309284	0.0221	0.6241
chr20	63025520	1745991	0.0277	0.1815
chr21	48129895	976986	0.0203	0.1914
chr22	51304566	503527	0.0098	0.1035
chrMT	16571	14243	0.8595	1.1041
chrX	155270560	4120135	0.0265	0.2479
chrY	59373566	185103	0.0031	0.0772

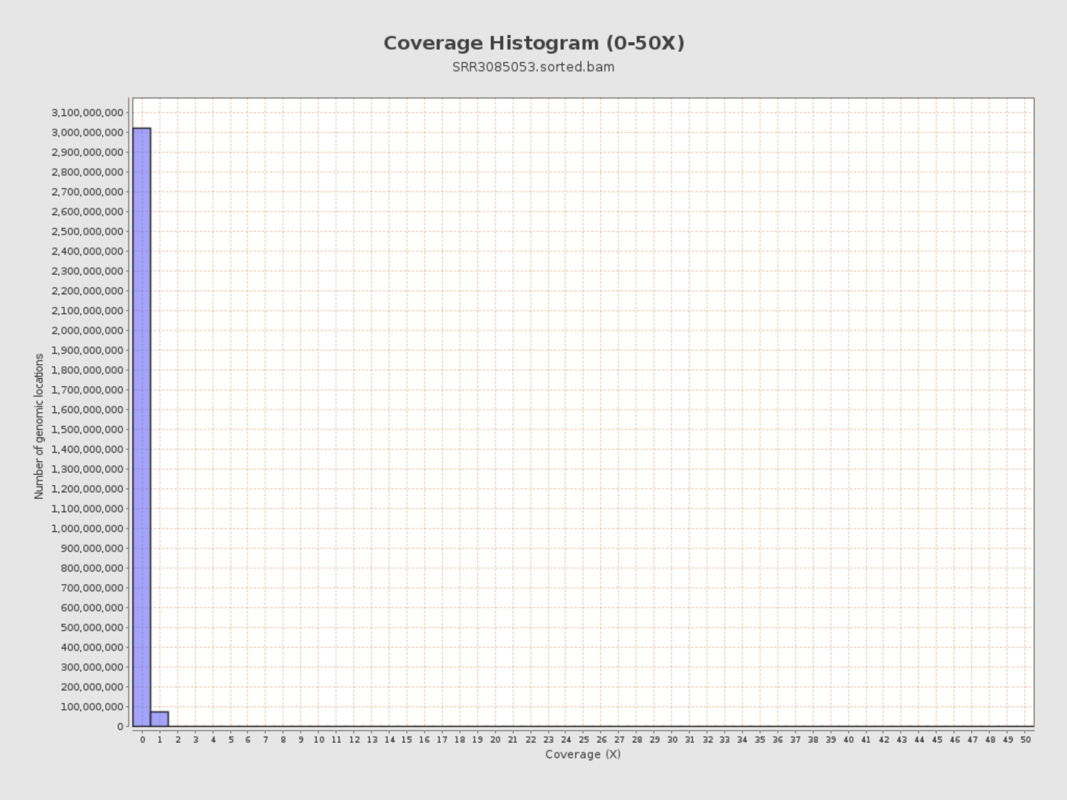
3. Results : Coverage across reference



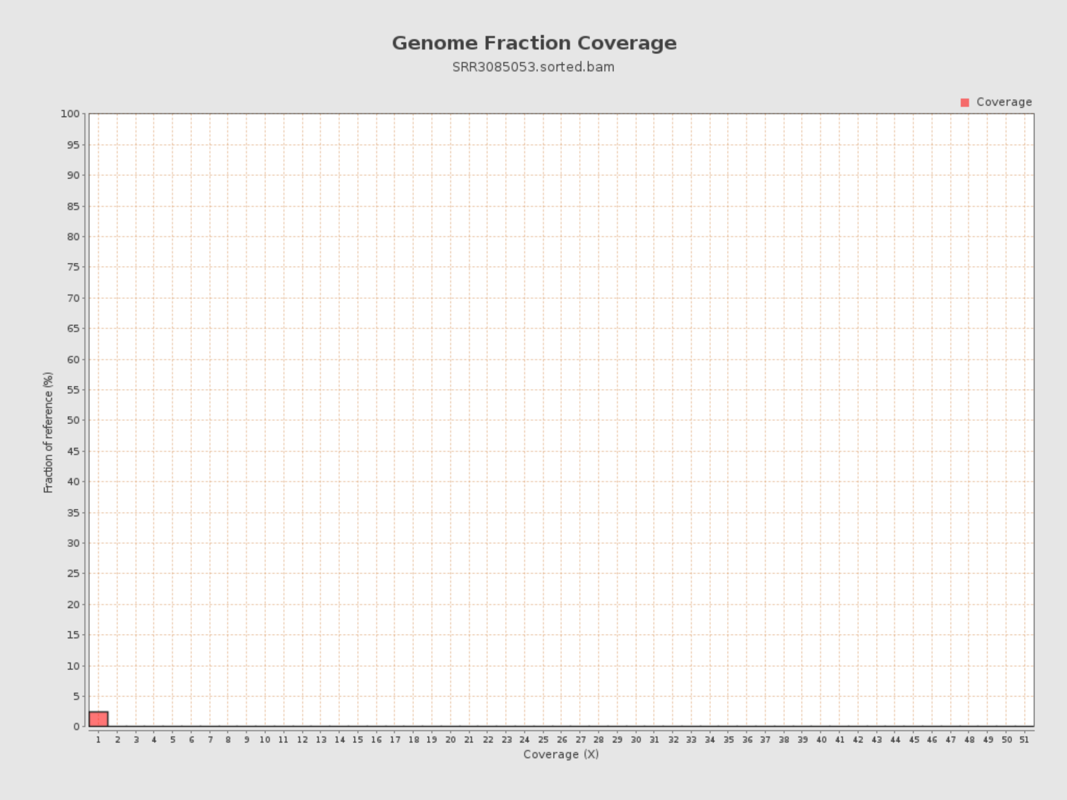
4. Results : Coverage Histogram



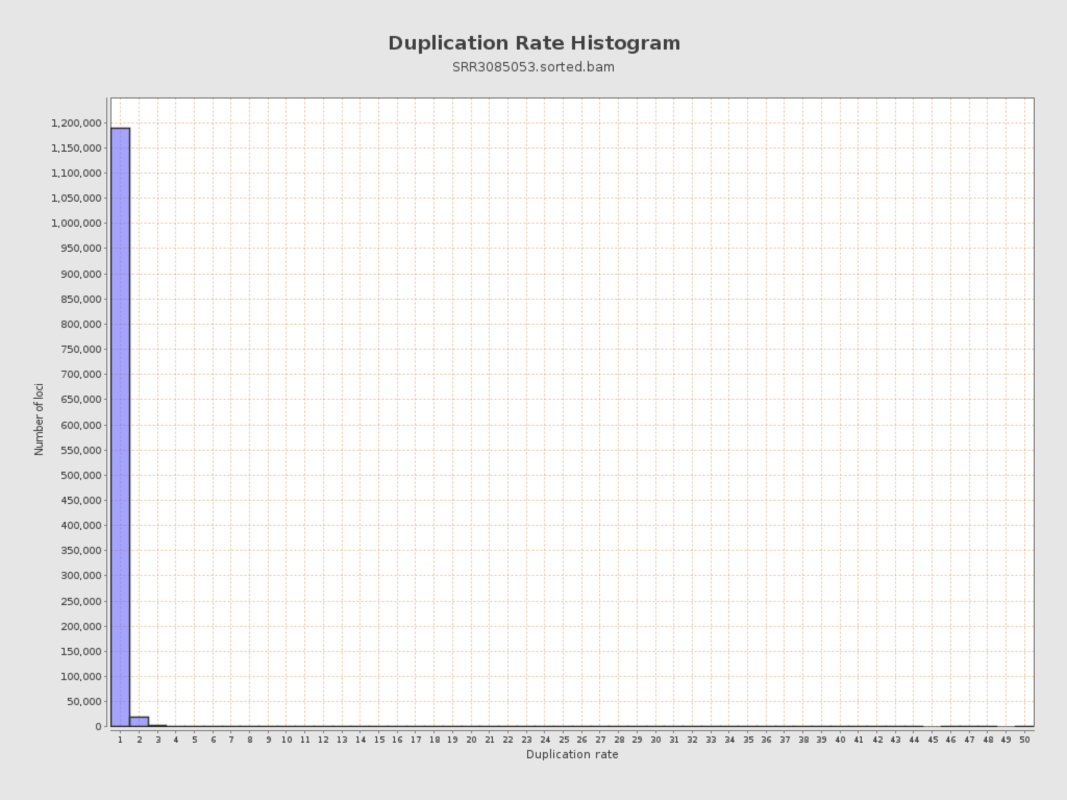
5. Results : Coverage Histogram (0-50X)



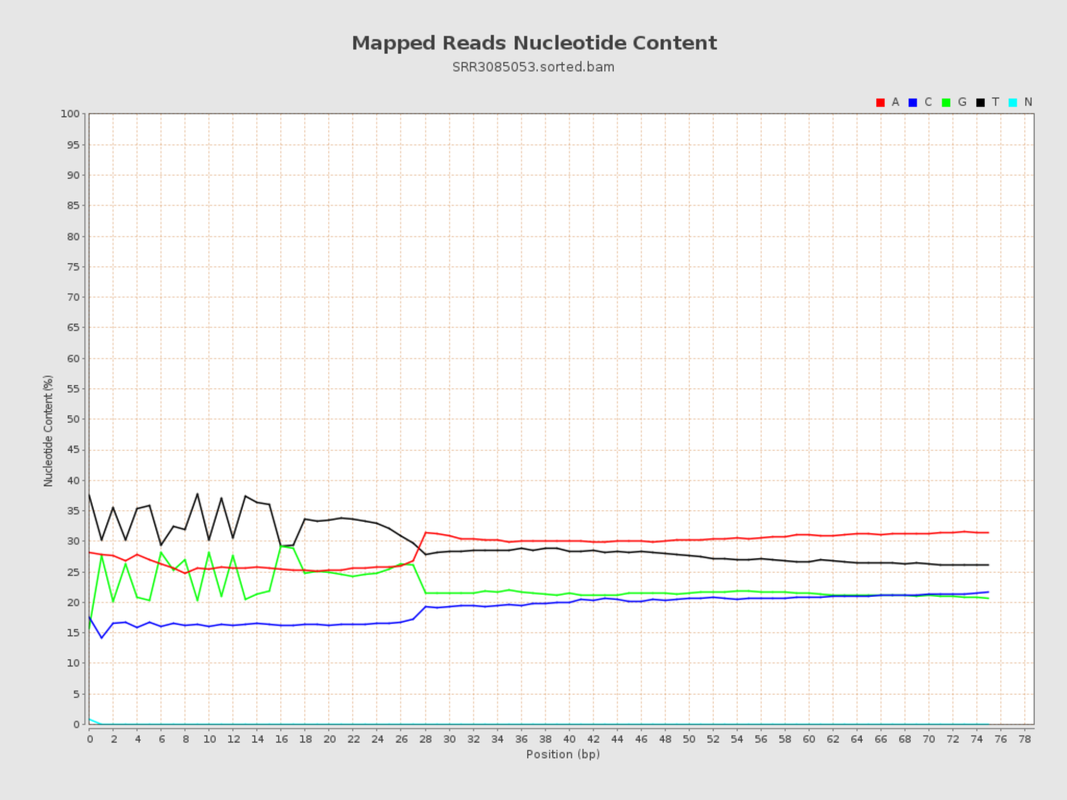
6. Results : Genome Fraction Coverage



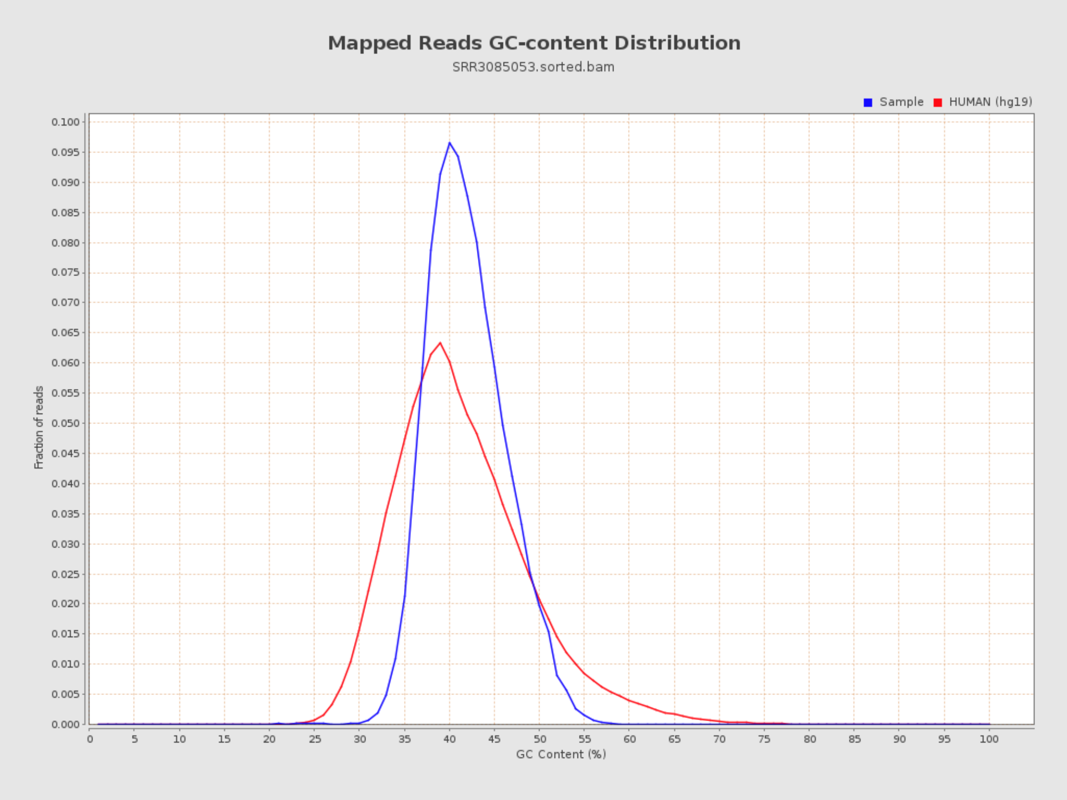
7. Results : Duplication Rate Histogram



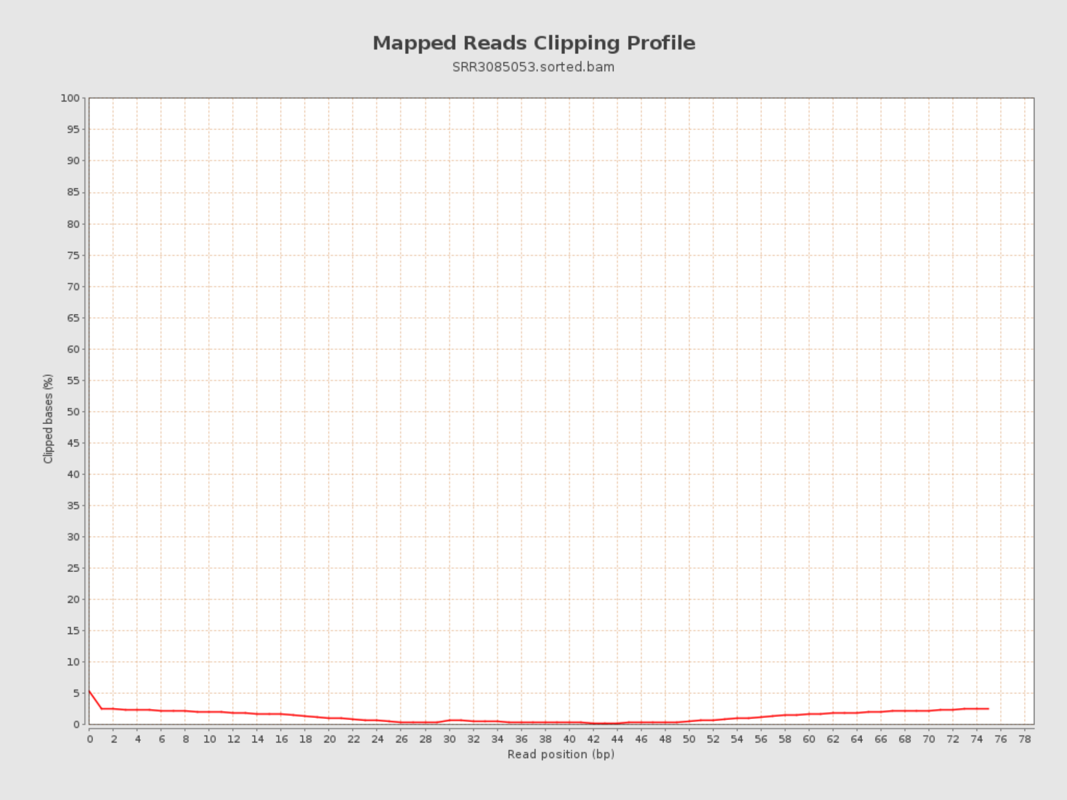
8. Results : Mapped Reads Nucleotide Content



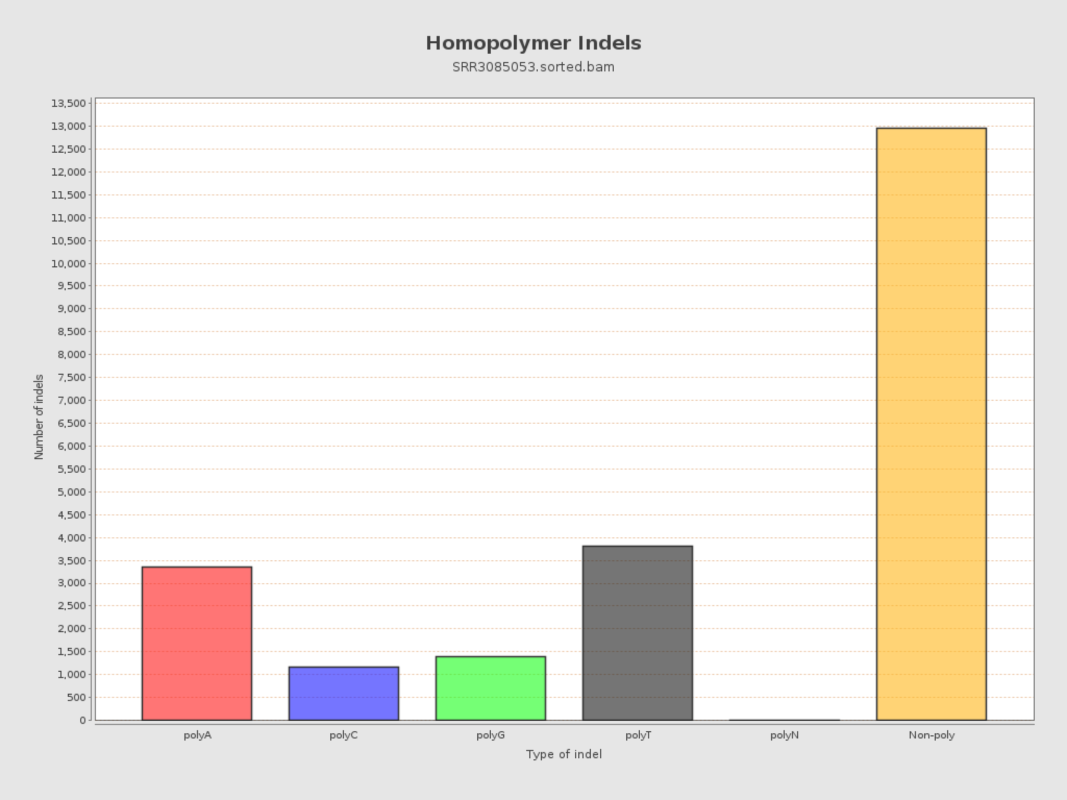
9. Results : Mapped Reads GC-content Distribution



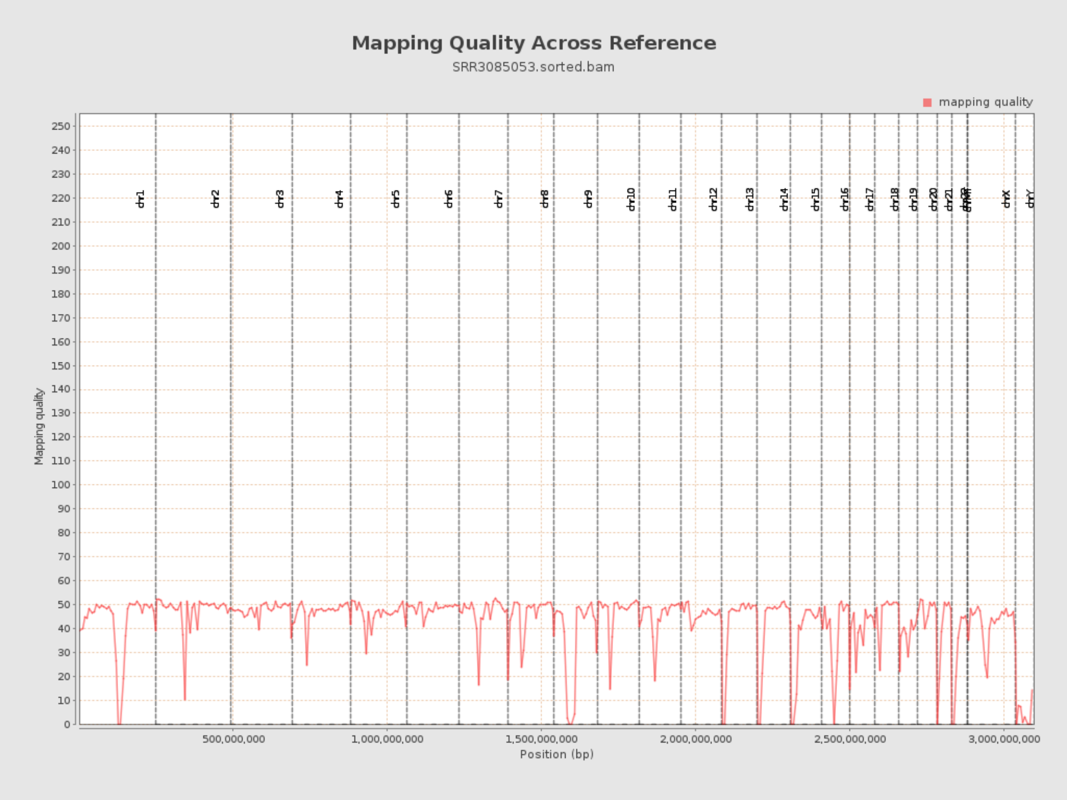
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram