Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:46:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013328.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_SRR6013328 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013328.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:46:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013328.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,269,271
Mapped reads	1,996,400 / 87.98%
Unmapped reads	272,871 / 12.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,553 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	85,427 / 3.76%
Duplication rate	2.86%
Clipped reads	963,264 / 42.45%

2.2. ACGT Content

Number/percentage of A's	36,728,639 / 28.07%
Number/percentage of C's	23,865,808 / 18.24%
Number/percentage of T's	41,312,434 / 31.57%
Number/percentage of G's	28,941,526 / 22.12%
Number/percentage of N's	1,713 / 0%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0423

Standard Deviation	0.4781

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

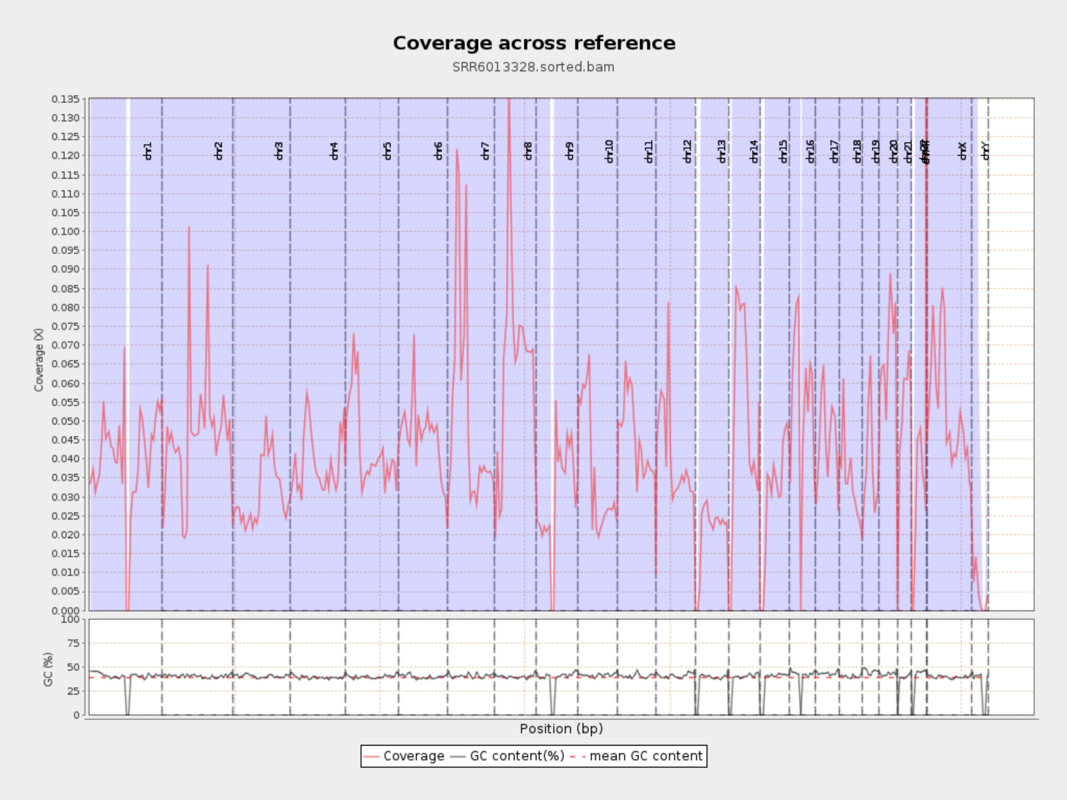
General error rate	0.8%
Mismatches	1,026,912
Insertions	9,644
Mapped reads with at least one insertion	0.48%
Deletions	39,061
Mapped reads with at least one deletion	1.94%
Homopolymer indels	46.99%

2.6. Chromosome stats

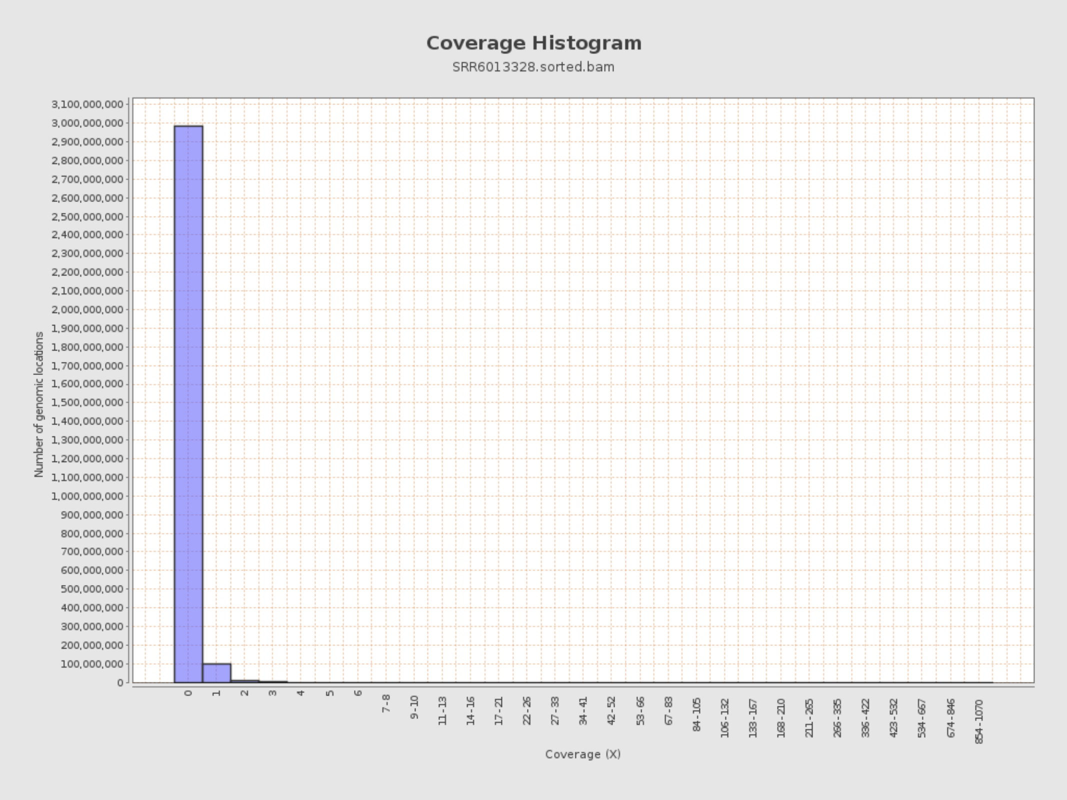
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9971513	0.04	0.8614
chr2	243199373	11309820	0.0465	0.5585
chr3	198022430	6099445	0.0308	0.1957
chr4	191154276	7514466	0.0393	0.2367
chr5	180915260	7898120	0.0437	0.2409
chr6	171115067	7886721	0.0461	0.3899
chr7	159138663	8388554	0.0527	0.8928

chr8	146364022	9640666	0.0659	0.5931
chr9	141213431	4261174	0.0302	0.4376
chr10	135534747	5006376	0.0369	0.3508
chr11	135006516	6106037	0.0452	0.4363
chr12	133851895	5467620	0.0408	0.2348
chr13	115169878	2330660	0.0202	0.1604
chr14	107349540	5411217	0.0504	0.268
chr15	102531392	3141454	0.0306	0.2094
chr16	90354753	4993095	0.0553	0.2981
chr17	81195210	3658253	0.0451	0.3392
chr18	78077248	2702425	0.0346	0.8346
chr19	59128983	2330825	0.0394	0.5913
chr20	63025520	4296747	0.0682	0.3008
chr21	48129895	2447953	0.0509	0.2712
chr22	51304566	1450975	0.0283	0.1849
chrMT	16571	14232	0.8588	1.1767
chrX	155270560	8275153	0.0533	0.332
chrY	59373566	313610	0.0053	0.1053

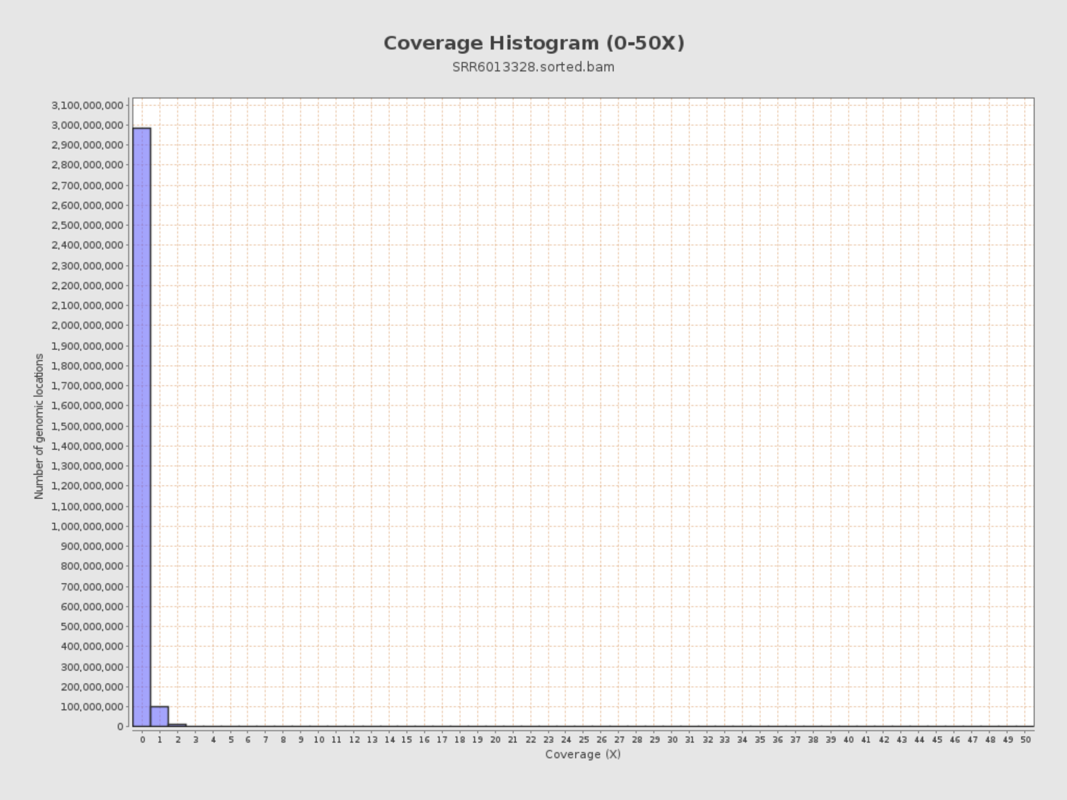
3. Results : Coverage across reference



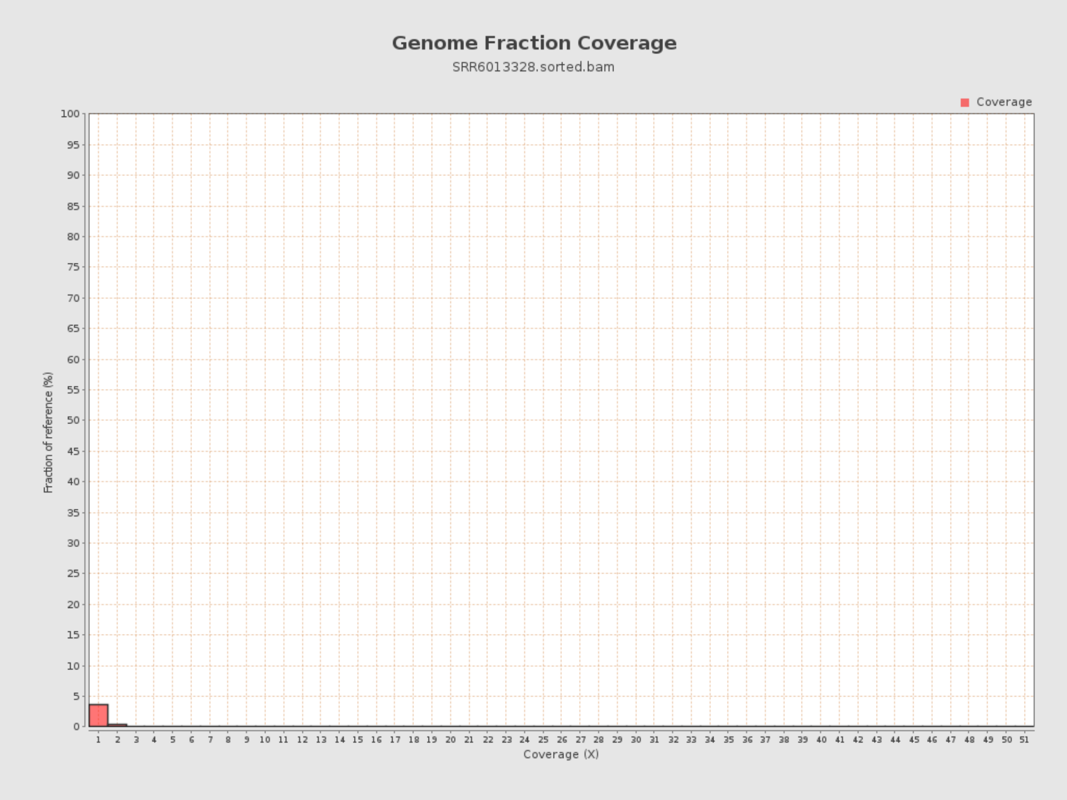
4. Results : Coverage Histogram



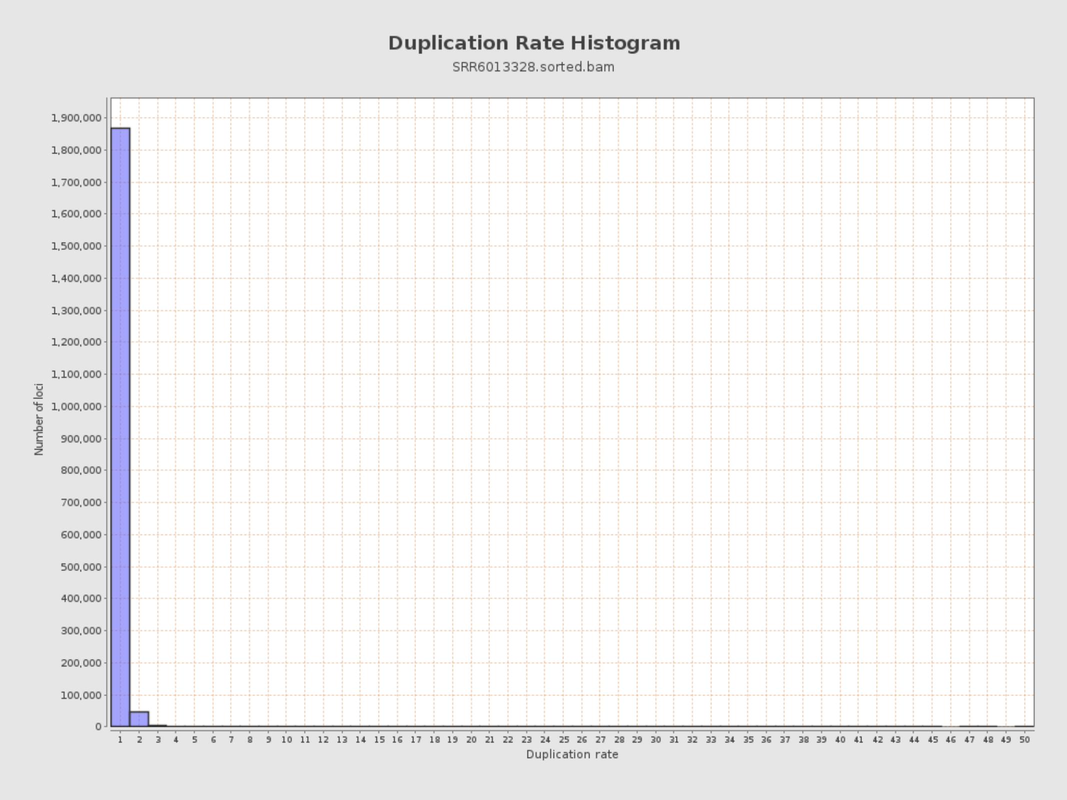
5. Results : Coverage Histogram (0-50X)



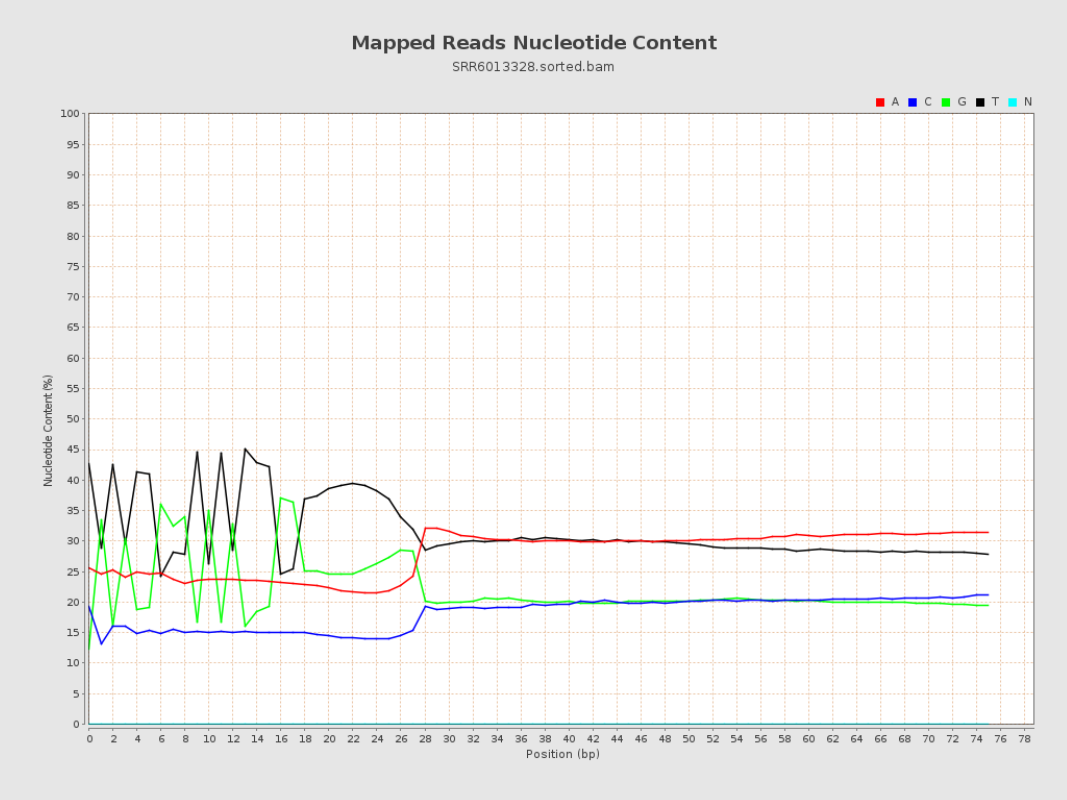
6. Results : Genome Fraction Coverage



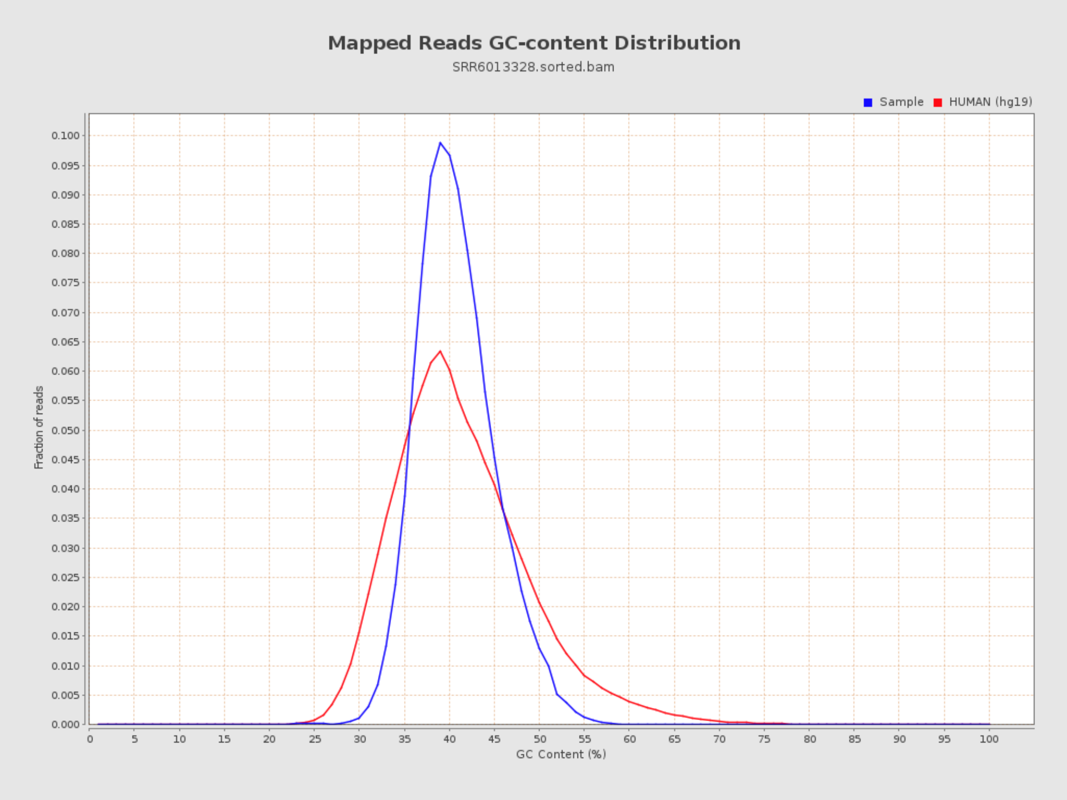
7. Results : Duplication Rate Histogram



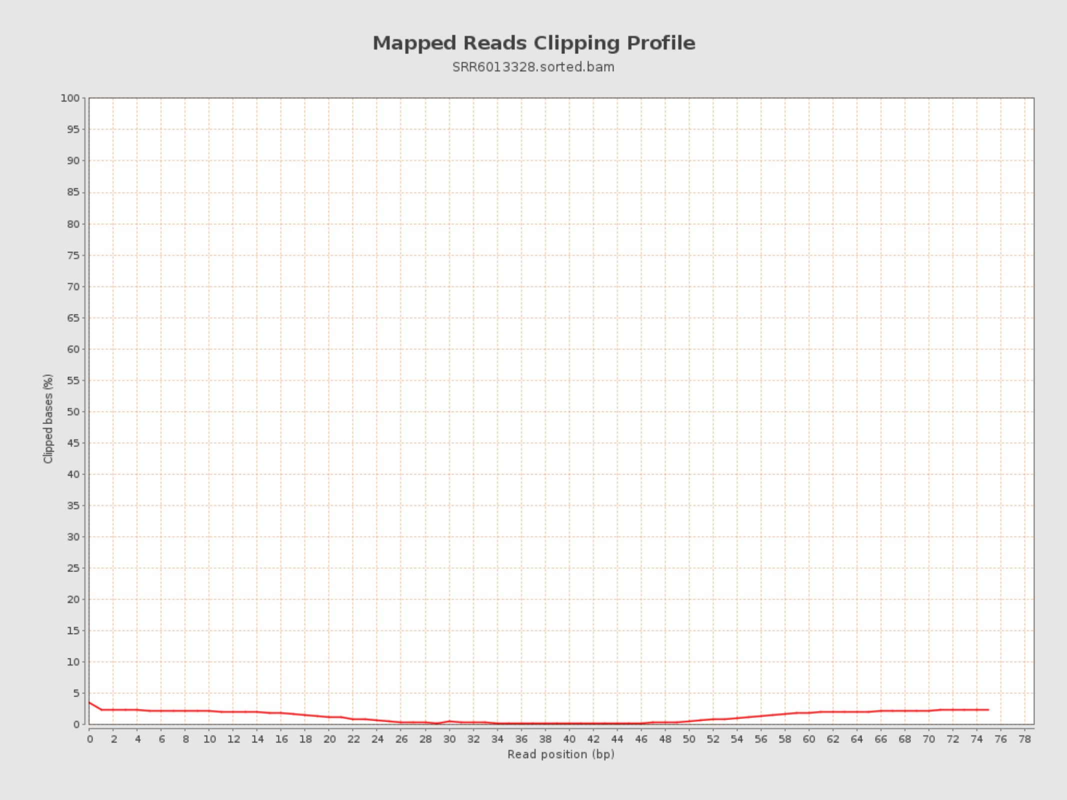
8. Results : Mapped Reads Nucleotide Content



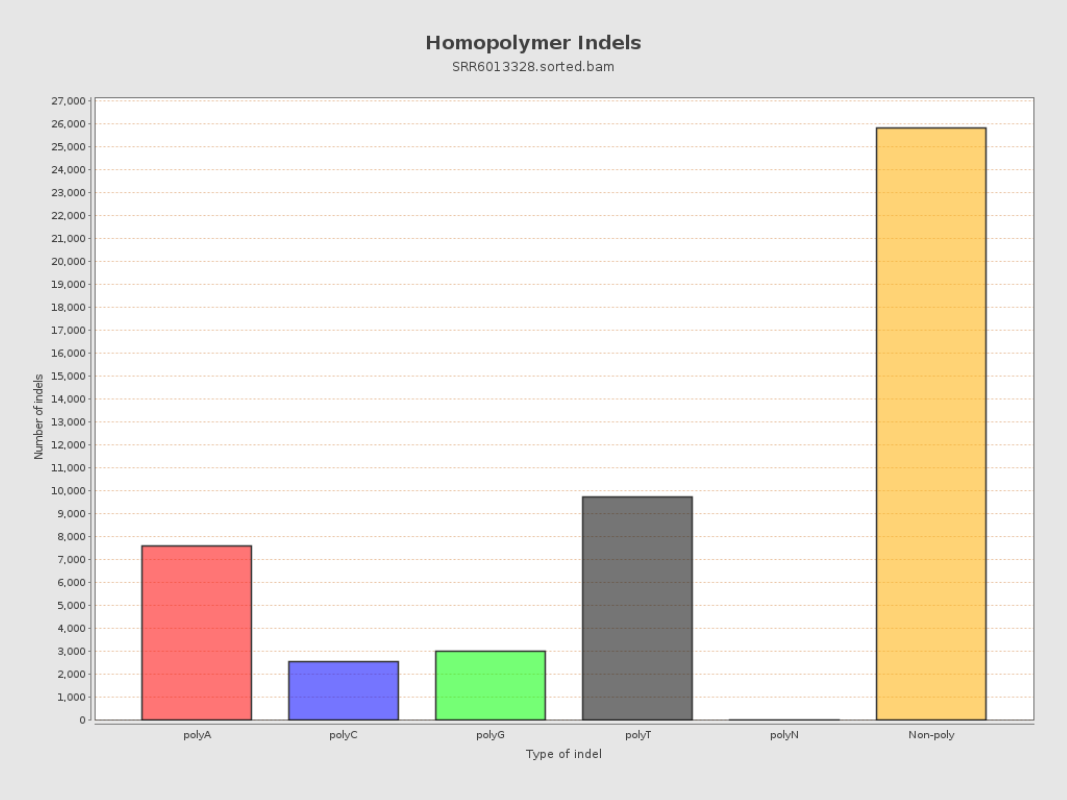
9. Results : Mapped Reads GC-content Distribution



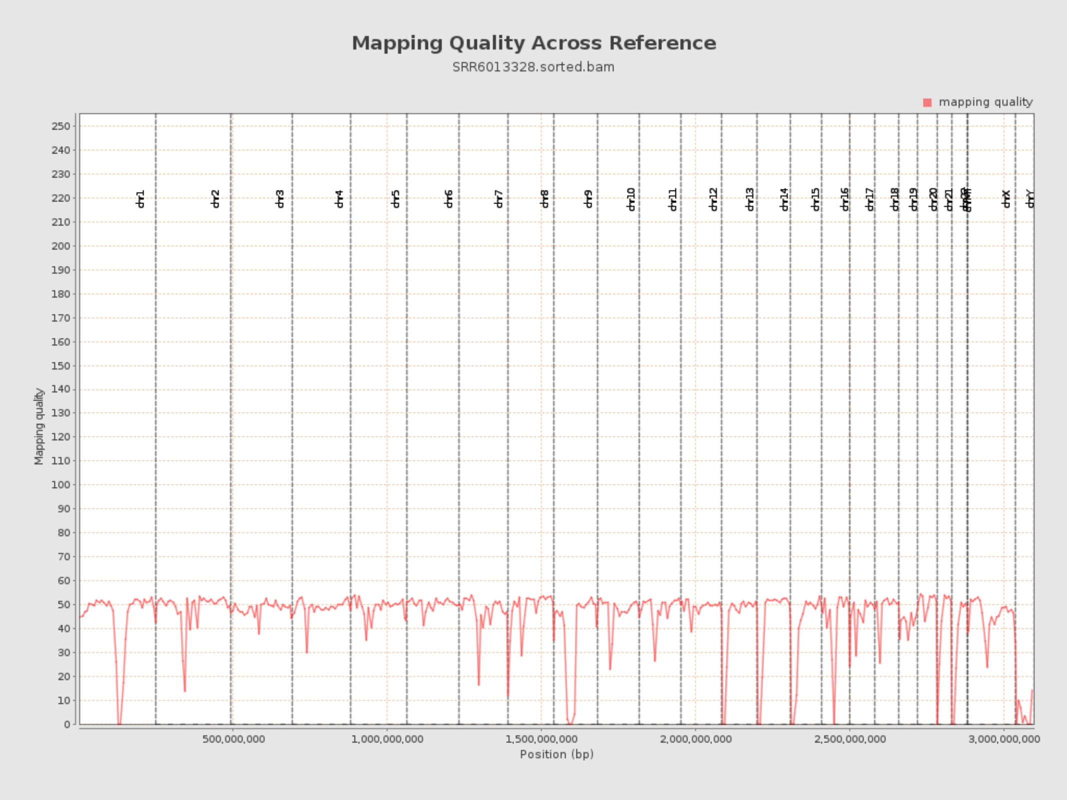
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram