Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:32:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013365.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_SRR6013365 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013365.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:32:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013365.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,749,647
Mapped reads	1,581,012 / 90.36%
Unmapped reads	168,635 / 9.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,131 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	63,257 / 3.62%
Duplication rate	2.75%
Clipped reads	643,923 / 36.8%

2.2. ACGT Content

Number/percentage of A's	30,706,723 / 28.7%
Number/percentage of C's	19,427,256 / 18.16%
Number/percentage of T's	34,008,120 / 31.79%
Number/percentage of G's	22,827,701 / 21.34%
Number/percentage of N's	23,458 / 0.02%
GC Percentage	39.49%

2.3. Coverage

Mean	0.0346

Standard Deviation	0.402

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

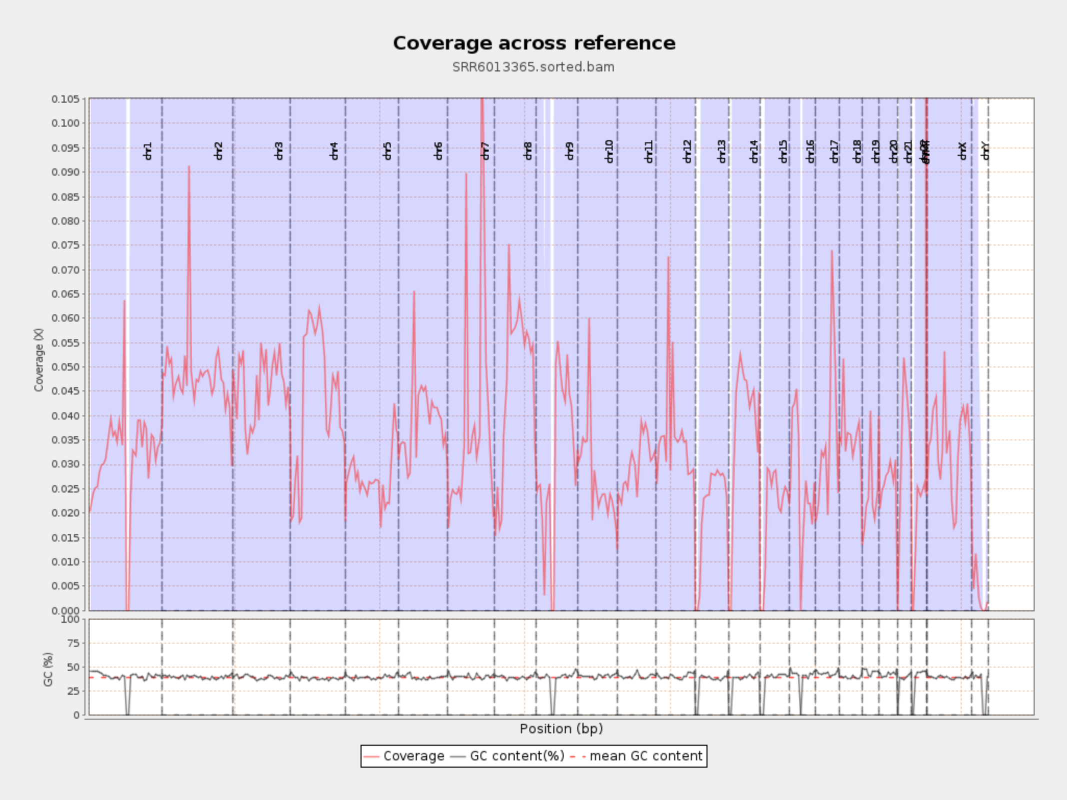
General error rate	0.84%
Mismatches	882,619
Insertions	8,508
Mapped reads with at least one insertion	0.53%
Deletions	26,321
Mapped reads with at least one deletion	1.64%
Homopolymer indels	47.11%

2.6. Chromosome stats

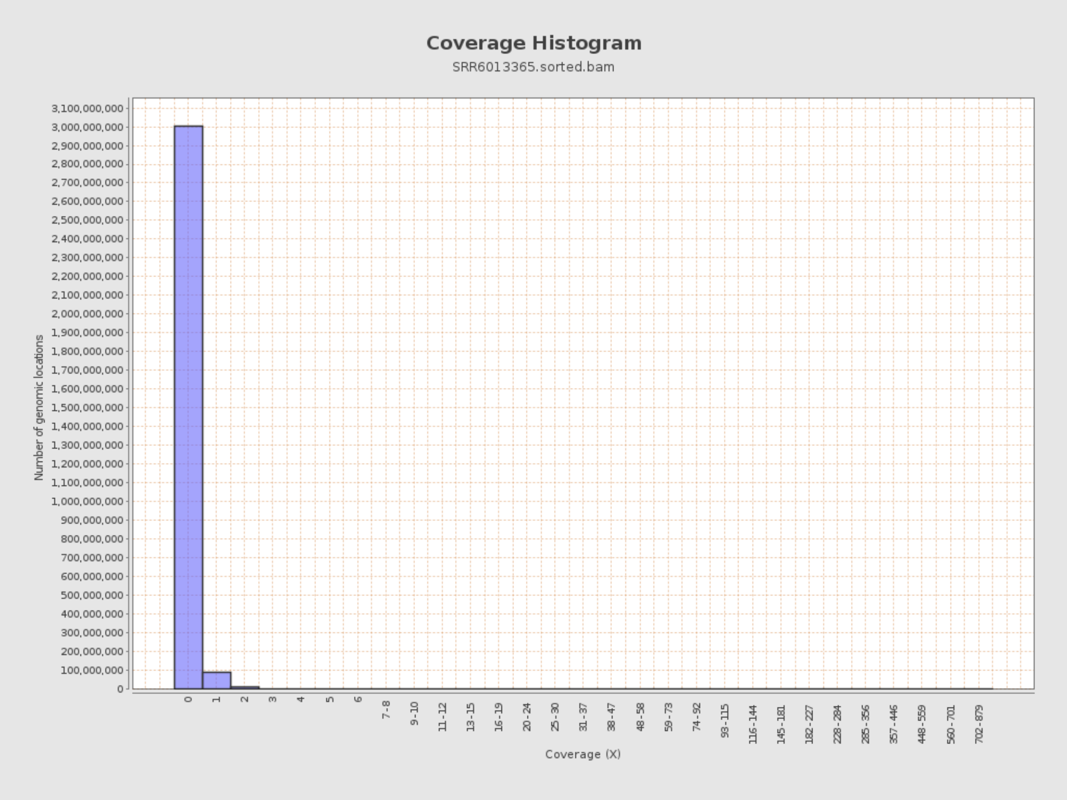
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7863777	0.0315	0.6498
chr2	243199373	11830383	0.0486	0.4732
chr3	198022430	9091700	0.0459	0.2335
chr4	191154276	8324728	0.0435	0.2463
chr5	180915260	4946983	0.0273	0.1822
chr6	171115067	6750735	0.0395	0.2861
chr7	159138663	6480284	0.0407	0.8122

chr8	146364022	6923959	0.0473	0.5827
chr9	141213431	4429413	0.0314	0.3746
chr10	135534747	3753952	0.0277	0.3551
chr11	135006516	4047760	0.03	0.2759
chr12	133851895	4812557	0.036	0.2174
chr13	115169878	2427042	0.0211	0.1576
chr14	107349540	4034363	0.0376	0.2385
chr15	102531392	2109878	0.0206	0.1626
chr16	90354753	2402325	0.0266	0.2089
chr17	81195210	2832728	0.0349	0.2215
chr18	78077248	2841941	0.0364	0.7405
chr19	59128983	1419936	0.024	0.4548
chr20	63025520	1673506	0.0266	0.1883
chr21	48129895	1606844	0.0334	0.2215
chr22	51304566	909379	0.0177	0.143
chrMT	16571	40929	2.4699	2.1592
chrX	155270560	5275492	0.034	0.2332
chrY	59373566	207967	0.0035	0.1252

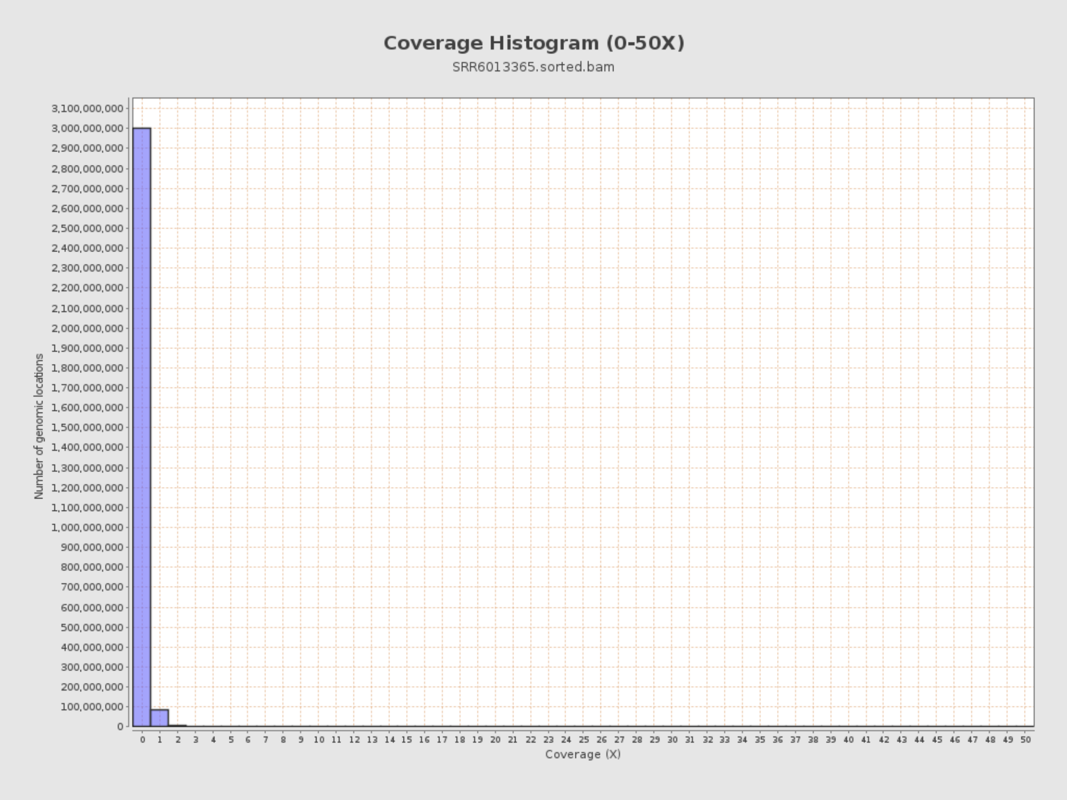
3. Results : Coverage across reference



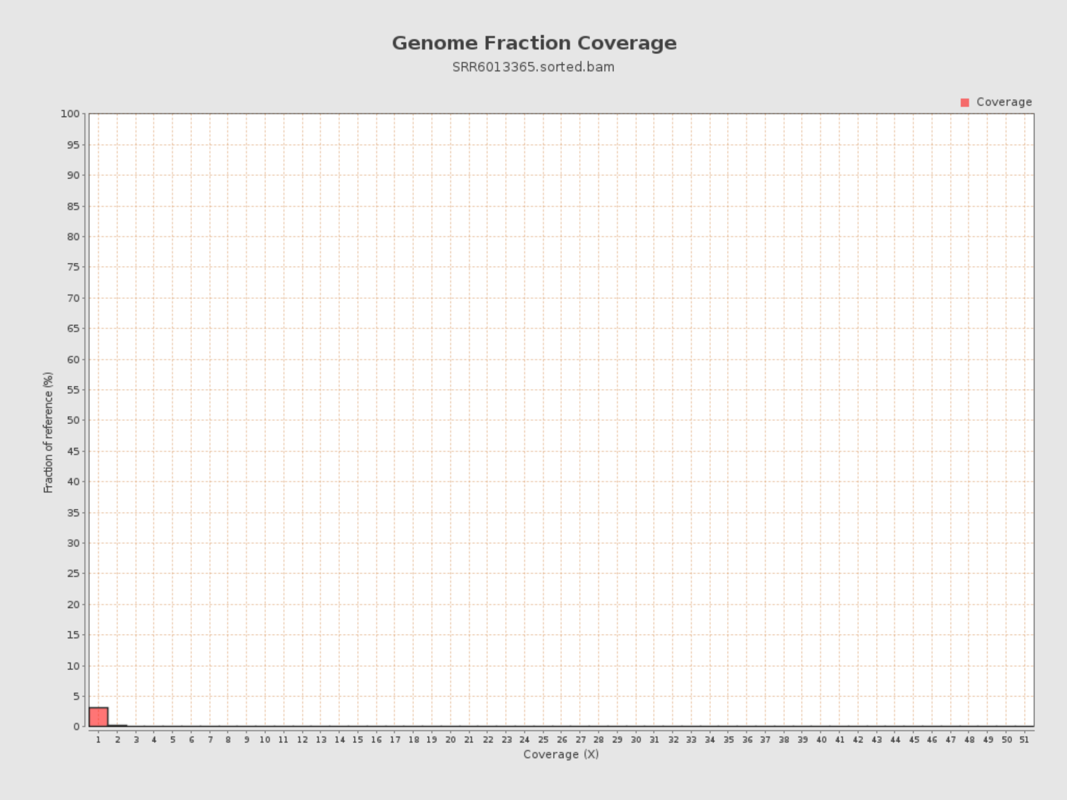
4. Results : Coverage Histogram



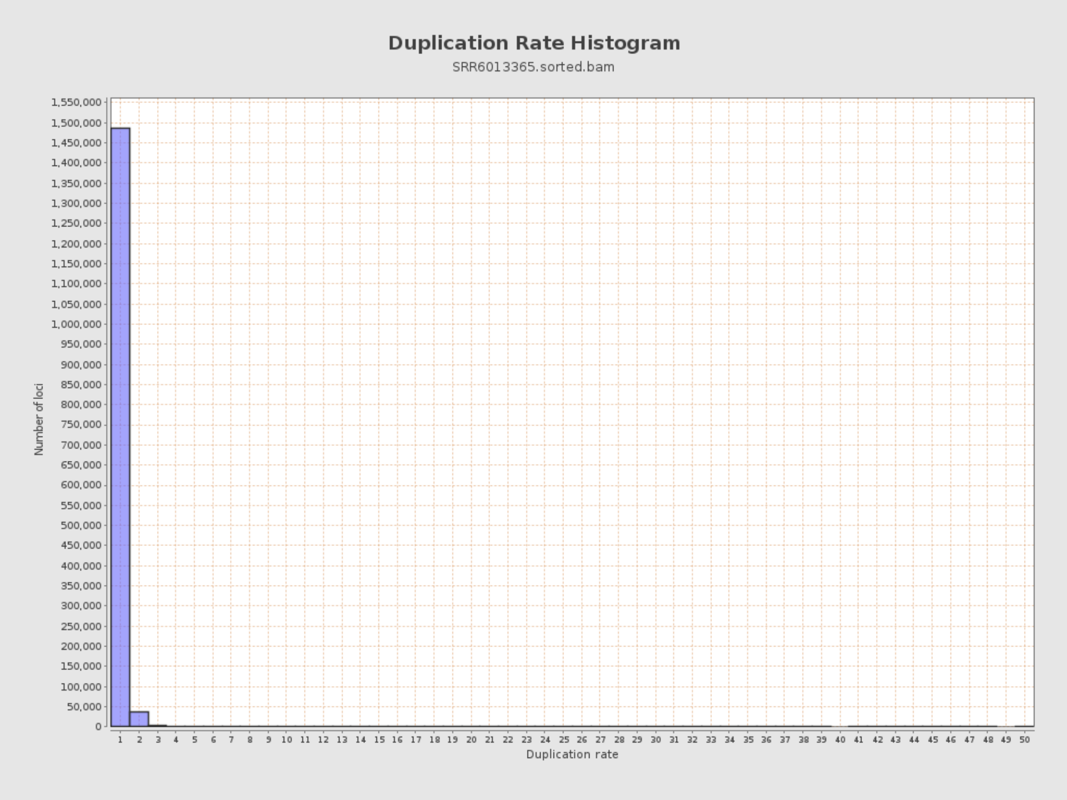
5. Results : Coverage Histogram (0-50X)



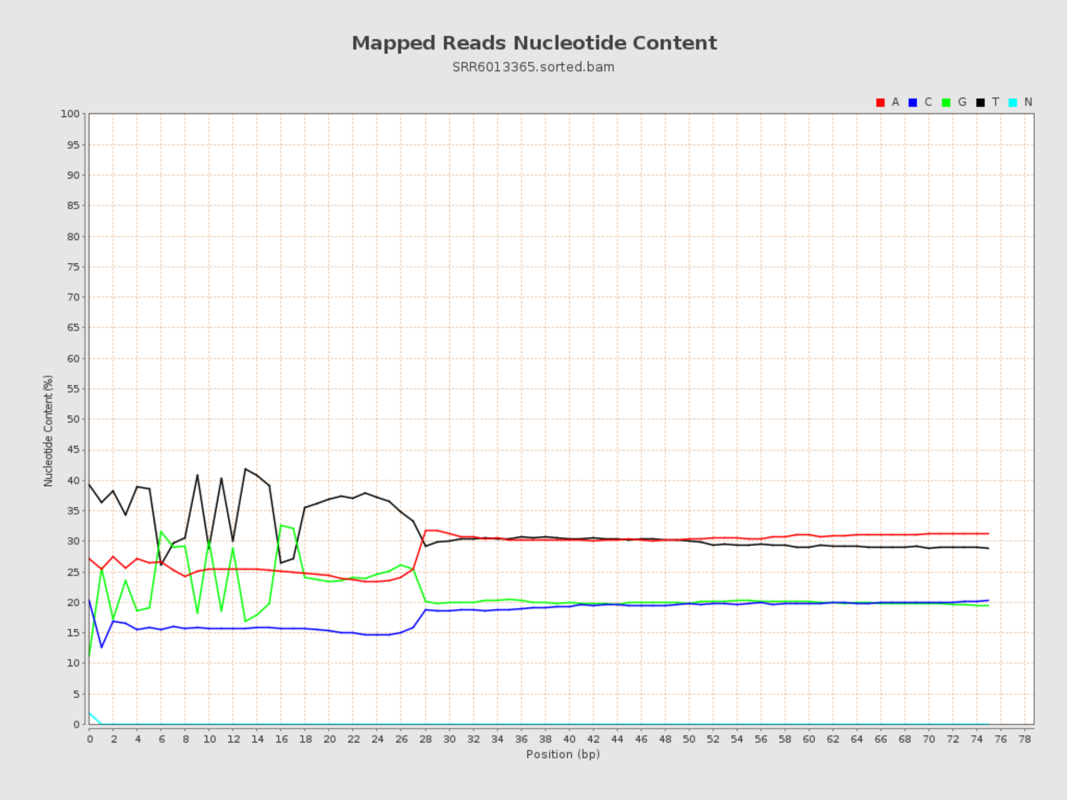
6. Results : Genome Fraction Coverage



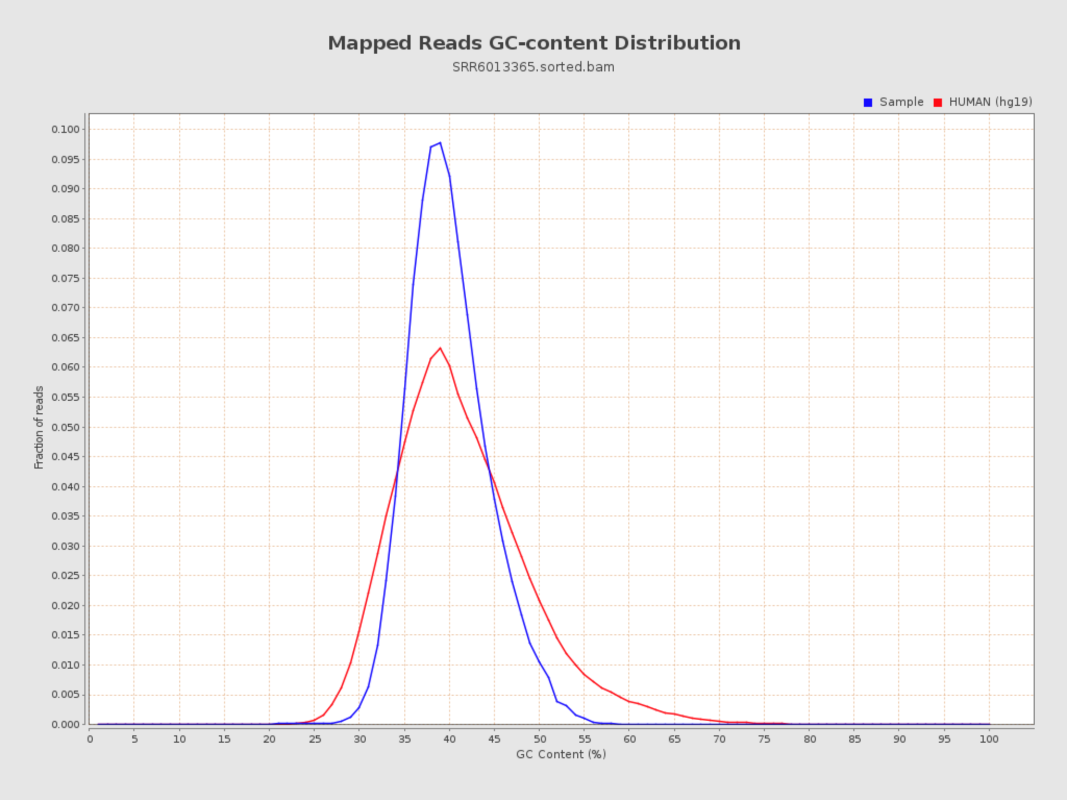
7. Results : Duplication Rate Histogram



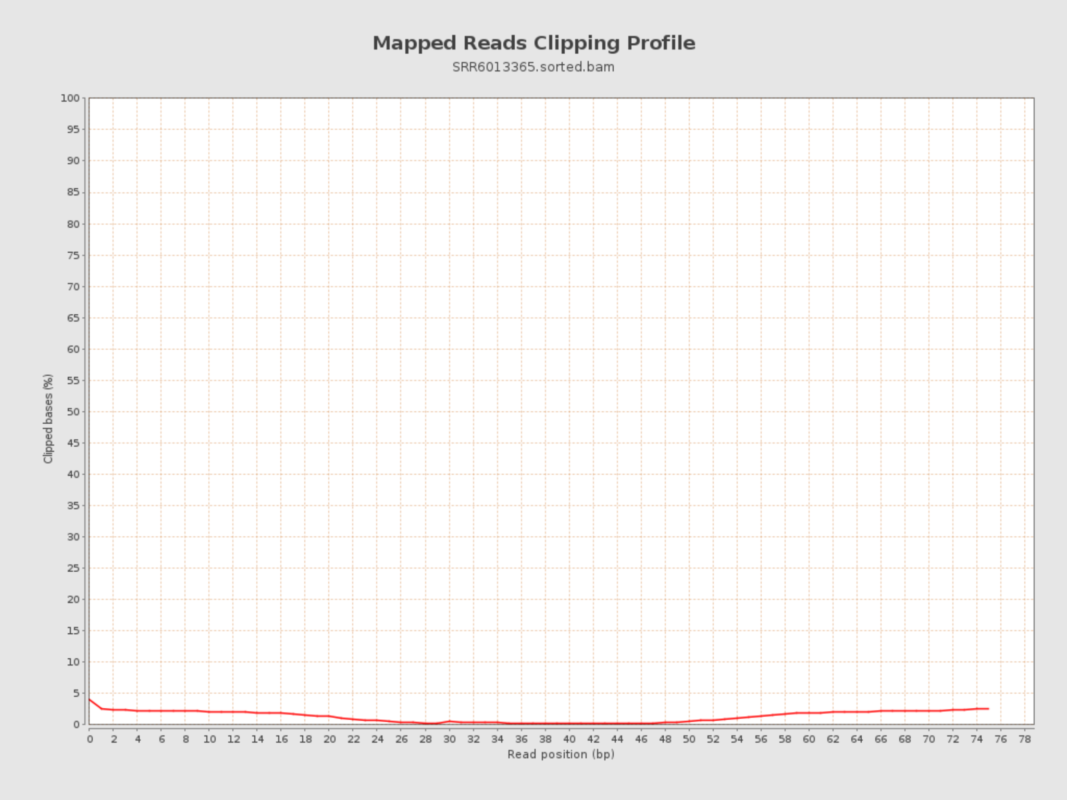
8. Results : Mapped Reads Nucleotide Content



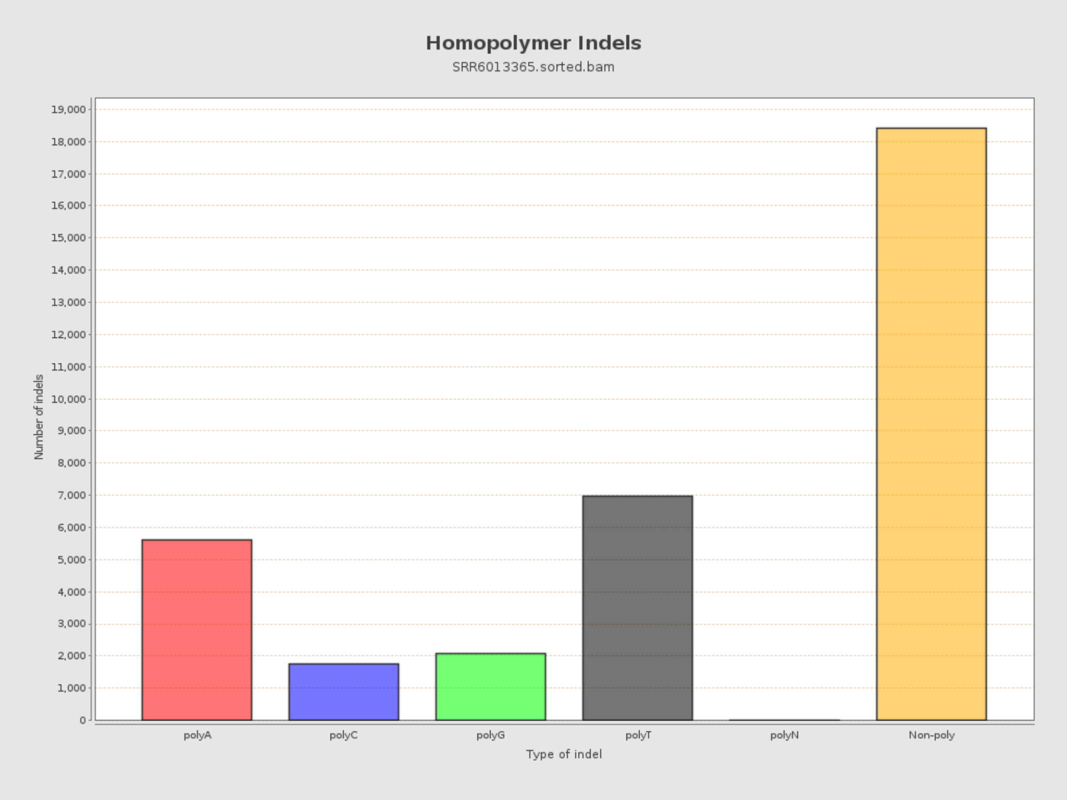
9. Results : Mapped Reads GC-content Distribution



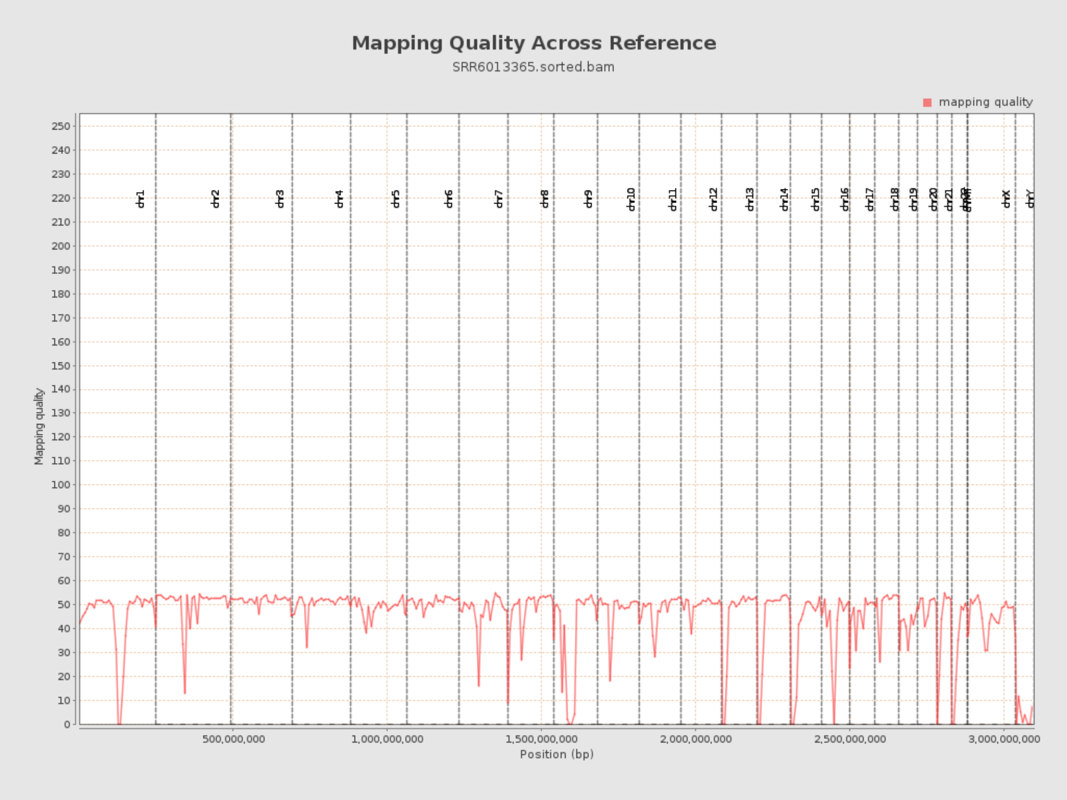
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram