Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:52:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013247.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_SRR6013247 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013247.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:52:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013247.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,219,870
Mapped reads	926,906 / 75.98%
Unmapped reads	292,964 / 24.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,237 / 1.09%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	87,780 / 7.2%
Duplication rate	7.85%
Clipped reads	547,091 / 44.85%

2.2. ACGT Content

Number/percentage of A's	16,350,447 / 27.86%
Number/percentage of C's	10,346,836 / 17.63%
Number/percentage of T's	19,210,973 / 32.73%
Number/percentage of G's	12,770,164 / 21.76%
Number/percentage of N's	12,210 / 0.02%
GC Percentage	39.39%

2.3. Coverage

Mean	0.019

Standard Deviation	0.246

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

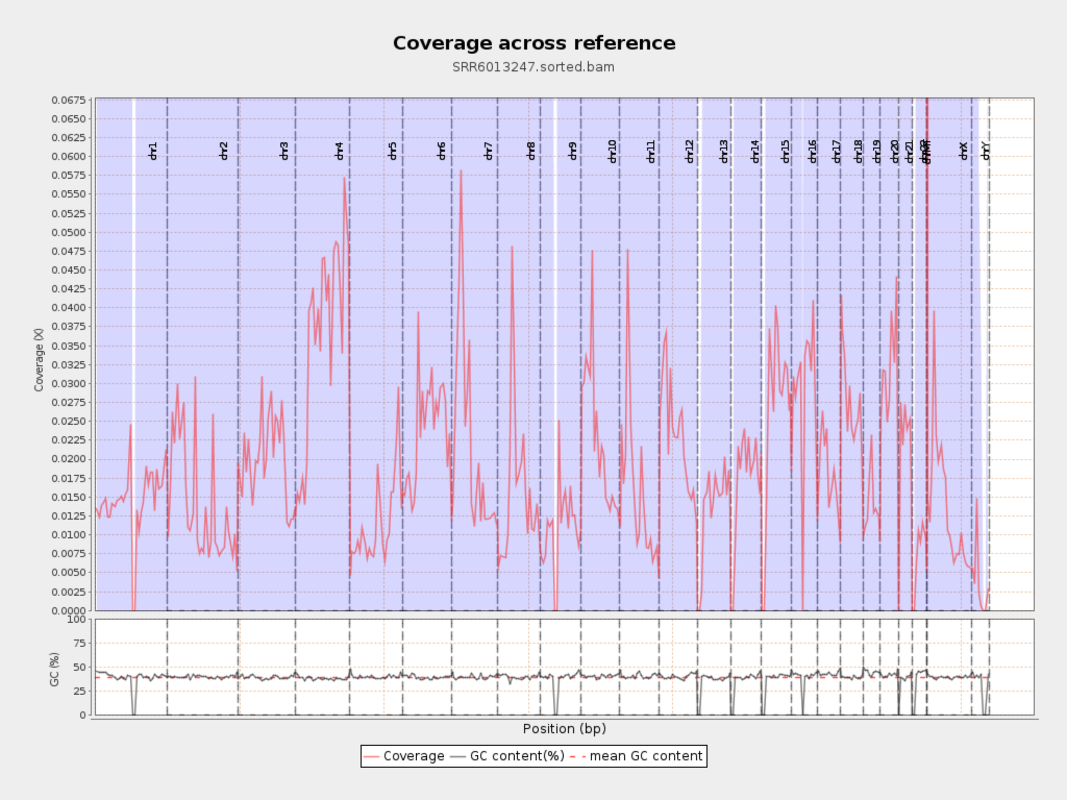
General error rate	1.01%
Mismatches	583,065
Insertions	4,533
Mapped reads with at least one insertion	0.49%
Deletions	27,379
Mapped reads with at least one deletion	2.91%
Homopolymer indels	42.25%

2.6. Chromosome stats

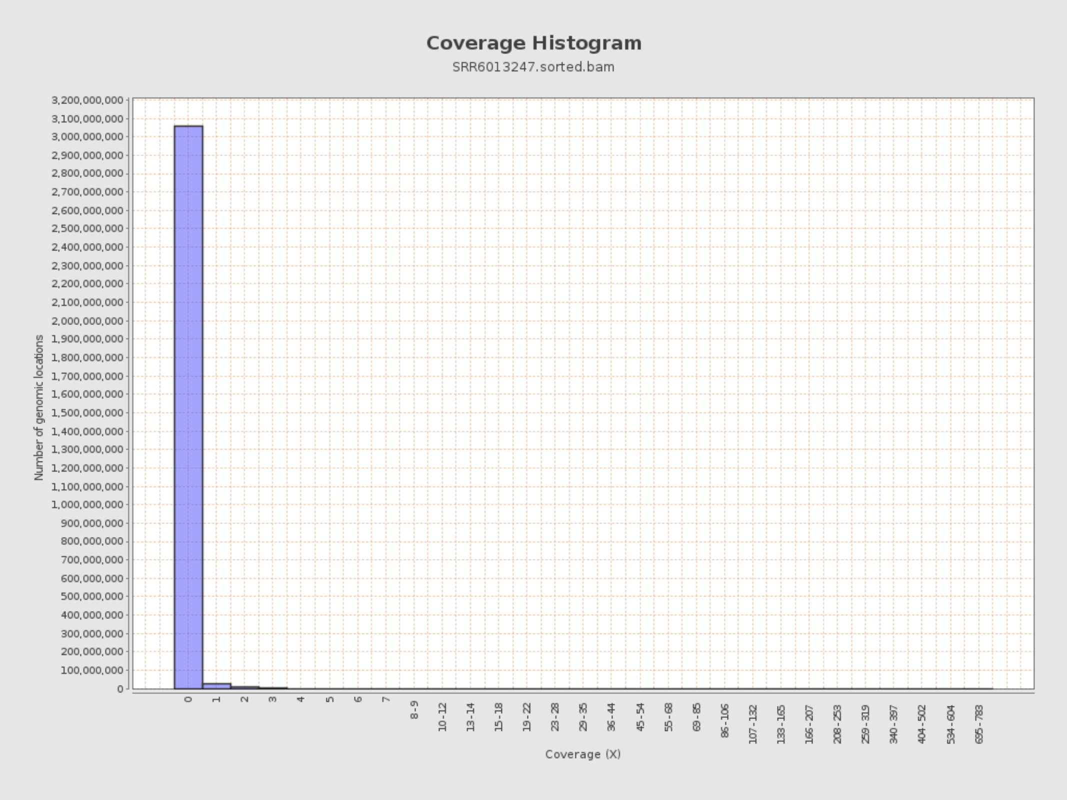
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3621982	0.0145	0.2685
chr2	243199373	3419410	0.0141	0.2643
chr3	198022430	3975472	0.0201	0.1957
chr4	191154276	7006435	0.0367	0.2739
chr5	180915260	2094714	0.0116	0.1498
chr6	171115067	4056920	0.0237	0.2455
chr7	159138663	3494089	0.022	0.279

chr8	146364022	2356143	0.0161	0.4628
chr9	141213431	1518503	0.0108	0.2096
chr10	135534747	3093393	0.0228	0.2545
chr11	135006516	2115326	0.0157	0.1878
chr12	133851895	3129104	0.0234	0.2126
chr13	115169878	1550562	0.0135	0.1642
chr14	107349540	1799633	0.0168	0.1834
chr15	102531392	2674571	0.0261	0.2209
chr16	90354753	2572625	0.0285	0.2434
chr17	81195210	1480111	0.0182	0.2012
chr18	78077248	2168117	0.0278	0.3646
chr19	59128983	843527	0.0143	0.2441
chr20	63025520	2015528	0.032	0.2507
chr21	48129895	1058953	0.022	0.2152
chr22	51304566	374825	0.0073	0.1151
chrMT	16571	11792	0.7116	1.1546
chrX	155270560	2090950	0.0135	0.1689
chrY	59373566	216366	0.0036	0.1195

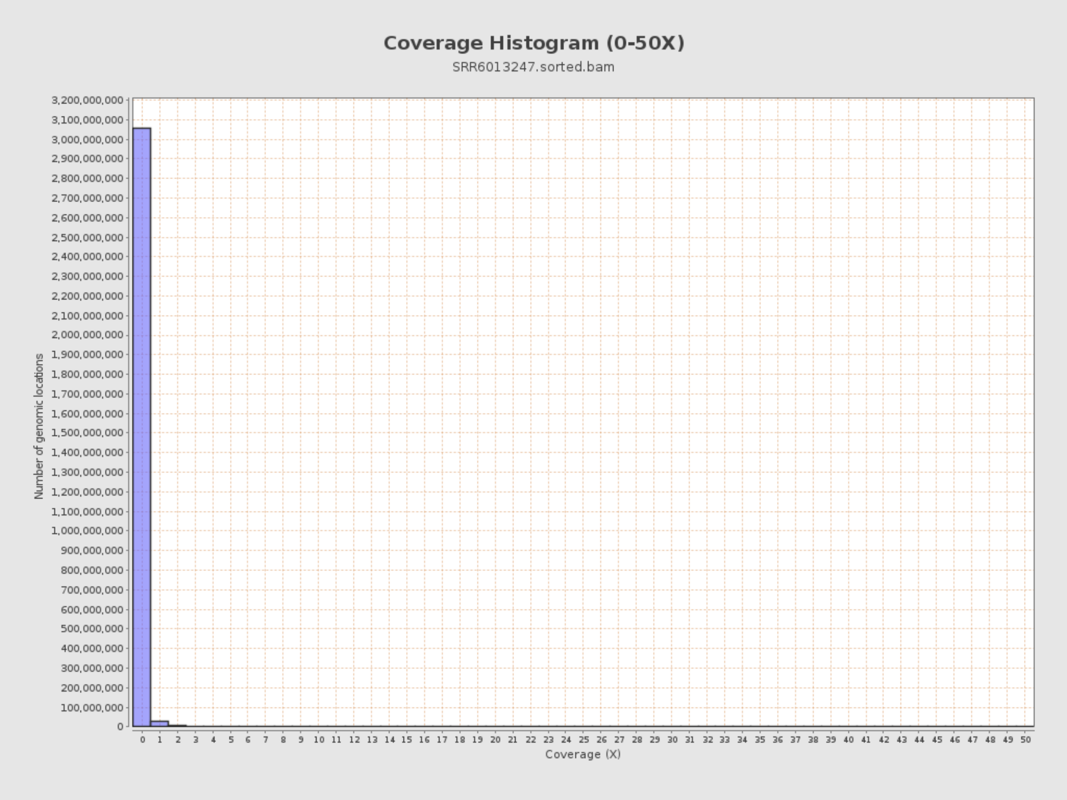
3. Results : Coverage across reference



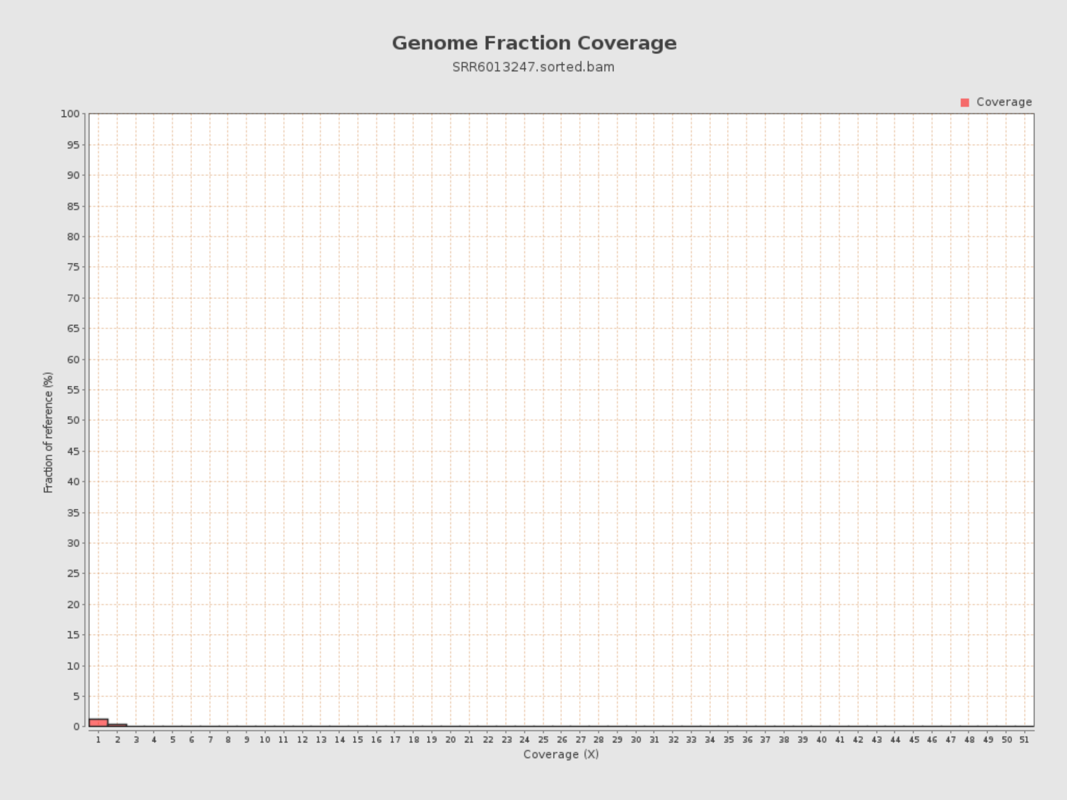
4. Results : Coverage Histogram



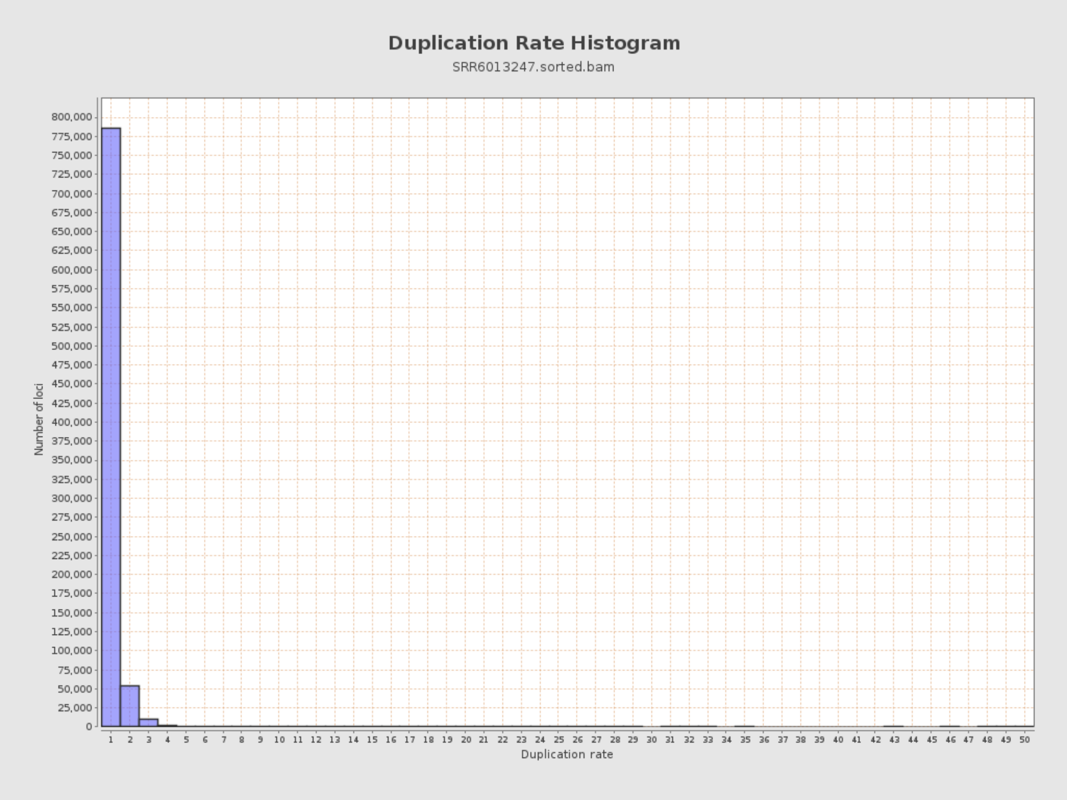
5. Results : Coverage Histogram (0-50X)



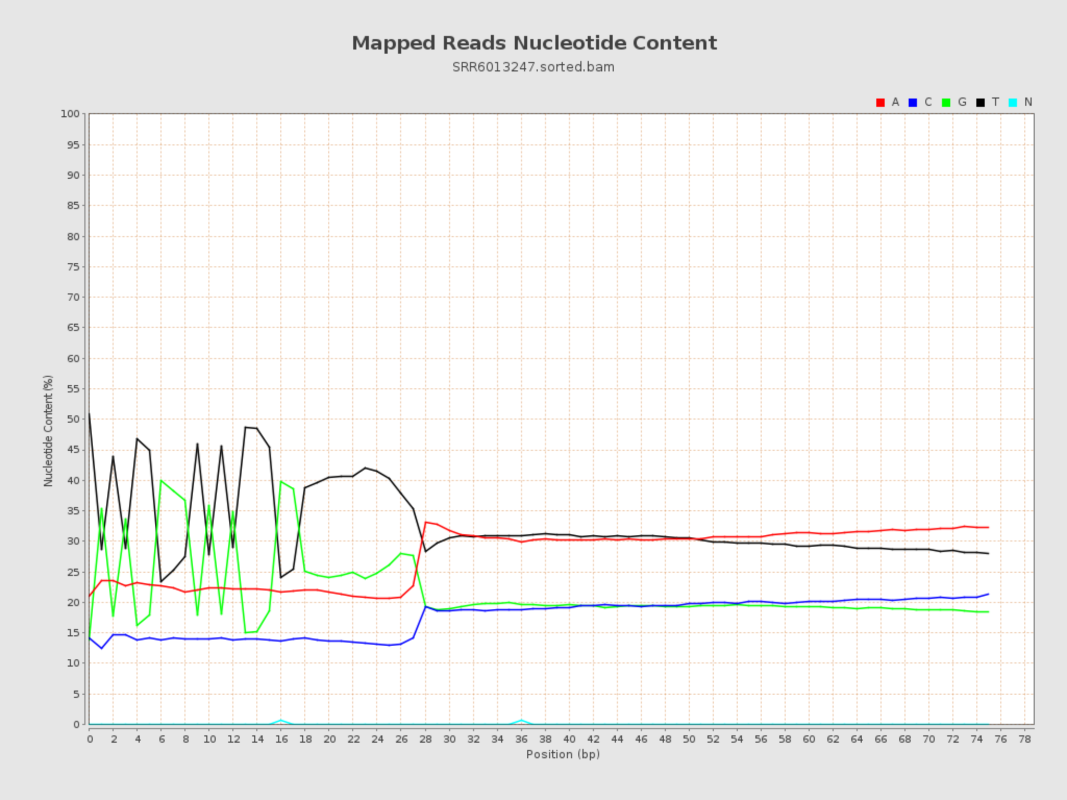
6. Results : Genome Fraction Coverage



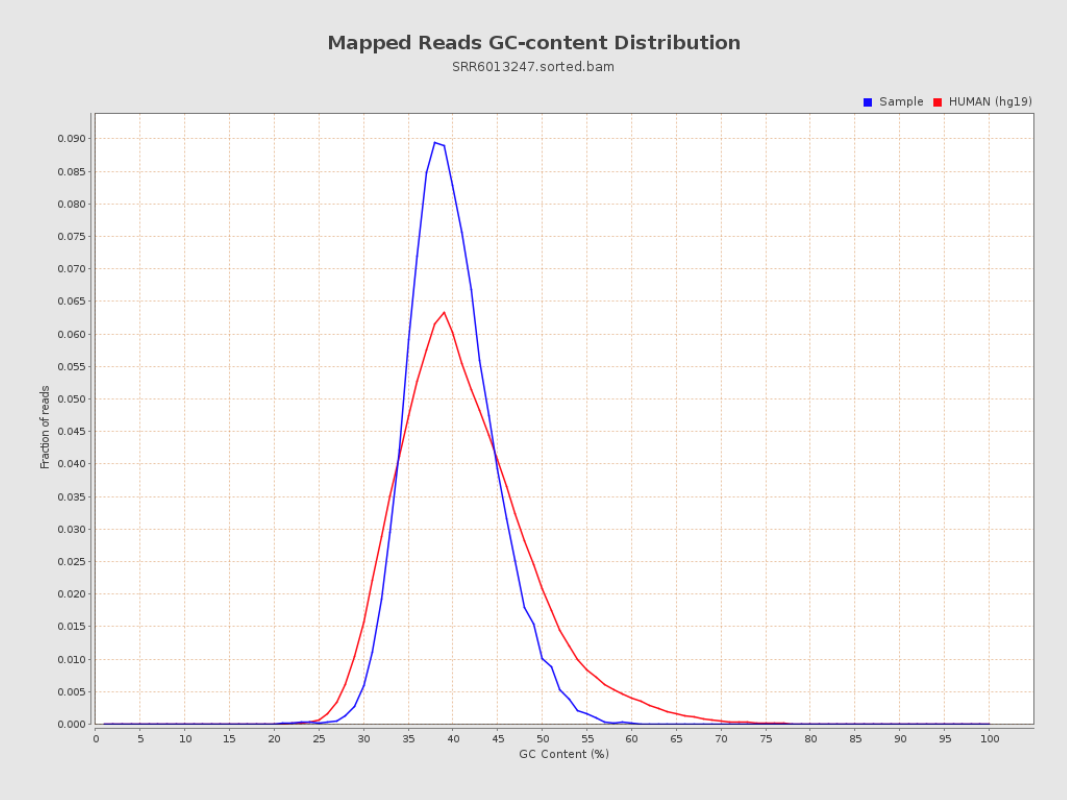
7. Results : Duplication Rate Histogram



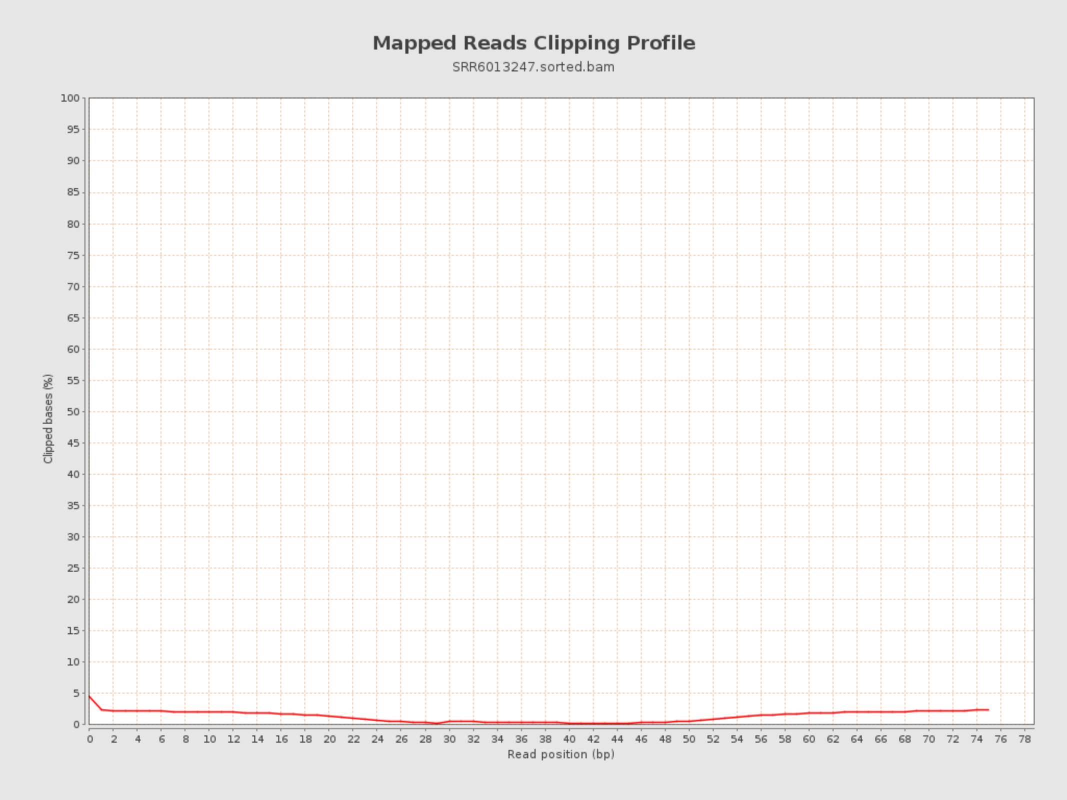
8. Results : Mapped Reads Nucleotide Content



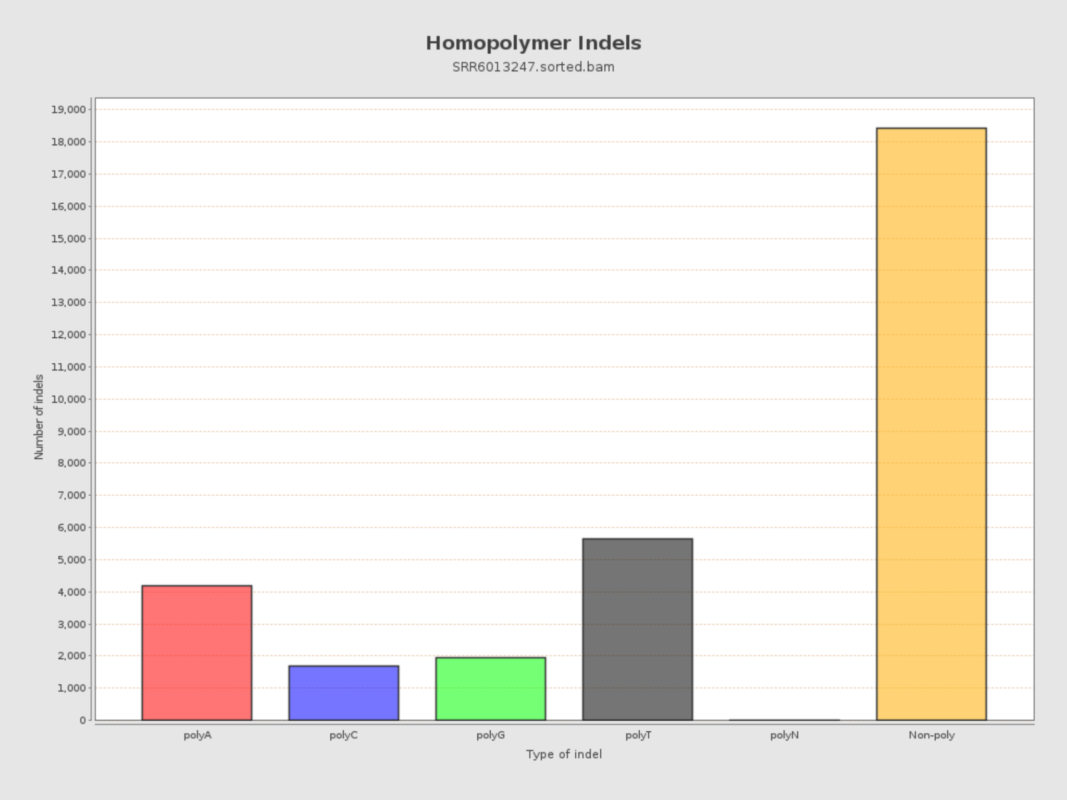
9. Results : Mapped Reads GC-content Distribution



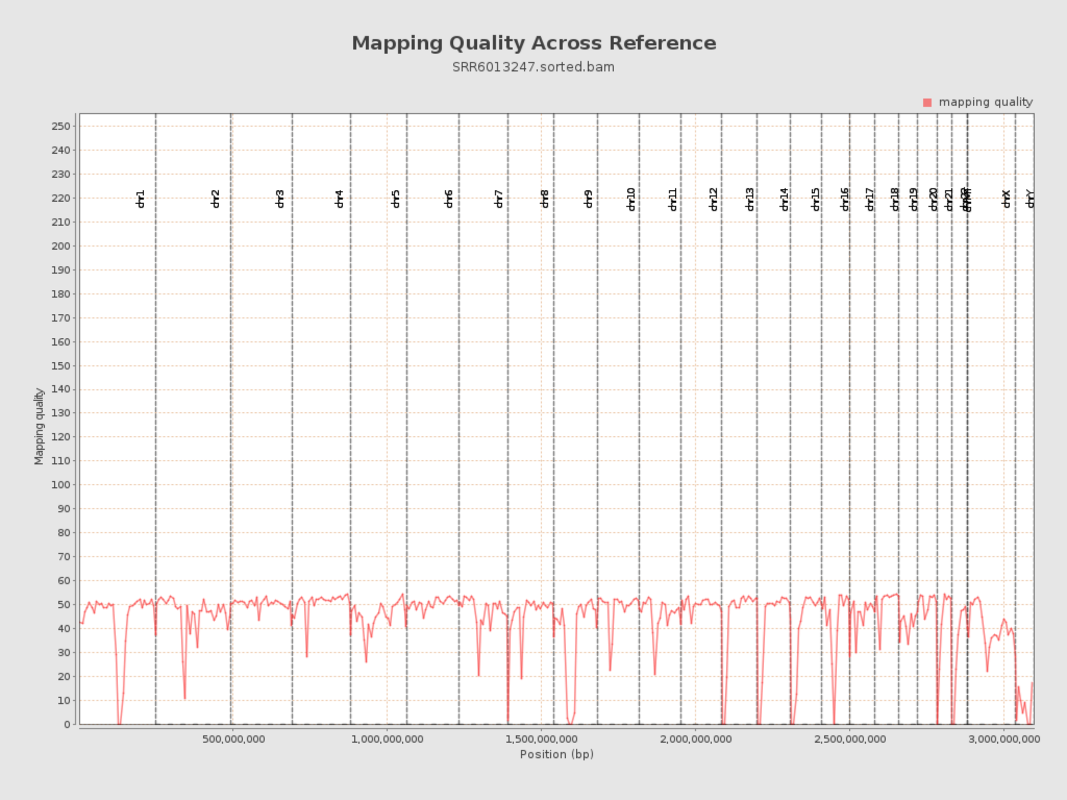
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram