Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:06:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013294.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_SRR6013294 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013294.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:06:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013294.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,482,577
Mapped reads	1,101,744 / 74.31%
Unmapped reads	380,833 / 25.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,705 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	134,043 / 9.04%
Duplication rate	9.08%
Clipped reads	673,685 / 45.44%

2.2. ACGT Content

Number/percentage of A's	18,598,157 / 26.83%
Number/percentage of C's	12,185,491 / 17.58%
Number/percentage of T's	22,807,082 / 32.91%
Number/percentage of G's	15,702,179 / 22.66%
Number/percentage of N's	13,128 / 0.02%
GC Percentage	40.24%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.2925

2.4. Mapping Quality

Mean Mapping Quality	44.26

2.5. Mismatches and indels

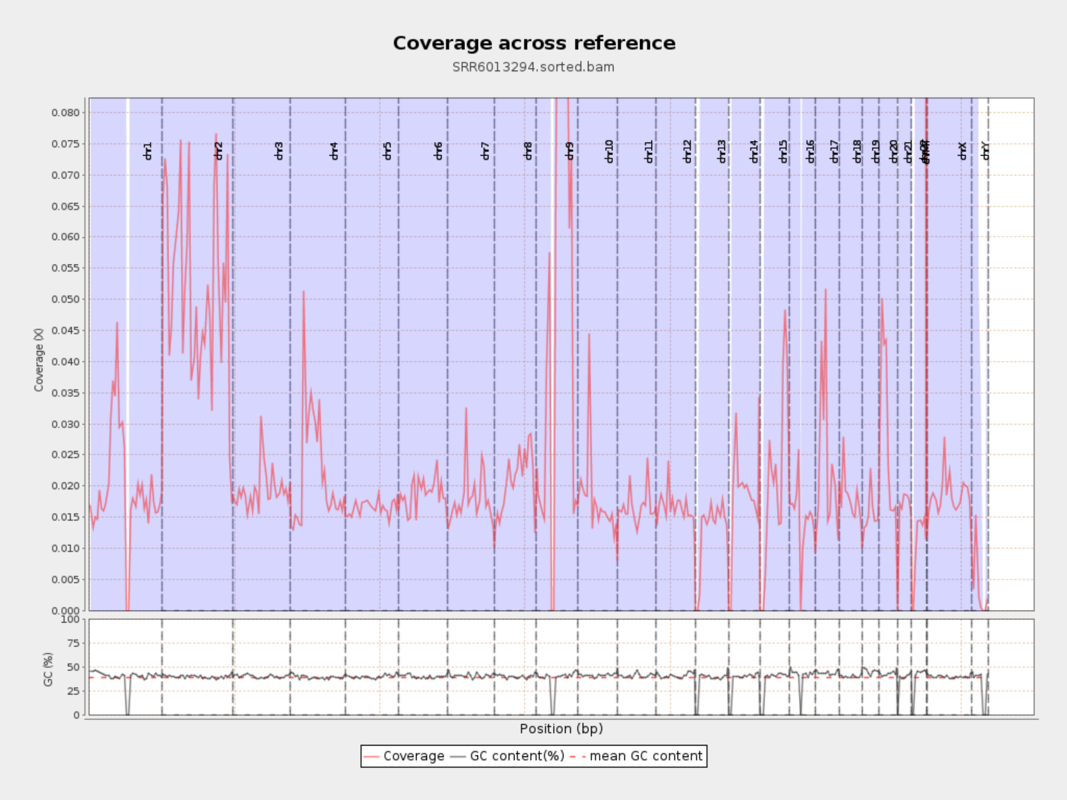
General error rate	1.01%
Mismatches	688,173
Insertions	6,096
Mapped reads with at least one insertion	0.55%
Deletions	20,281
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.39%

2.6. Chromosome stats

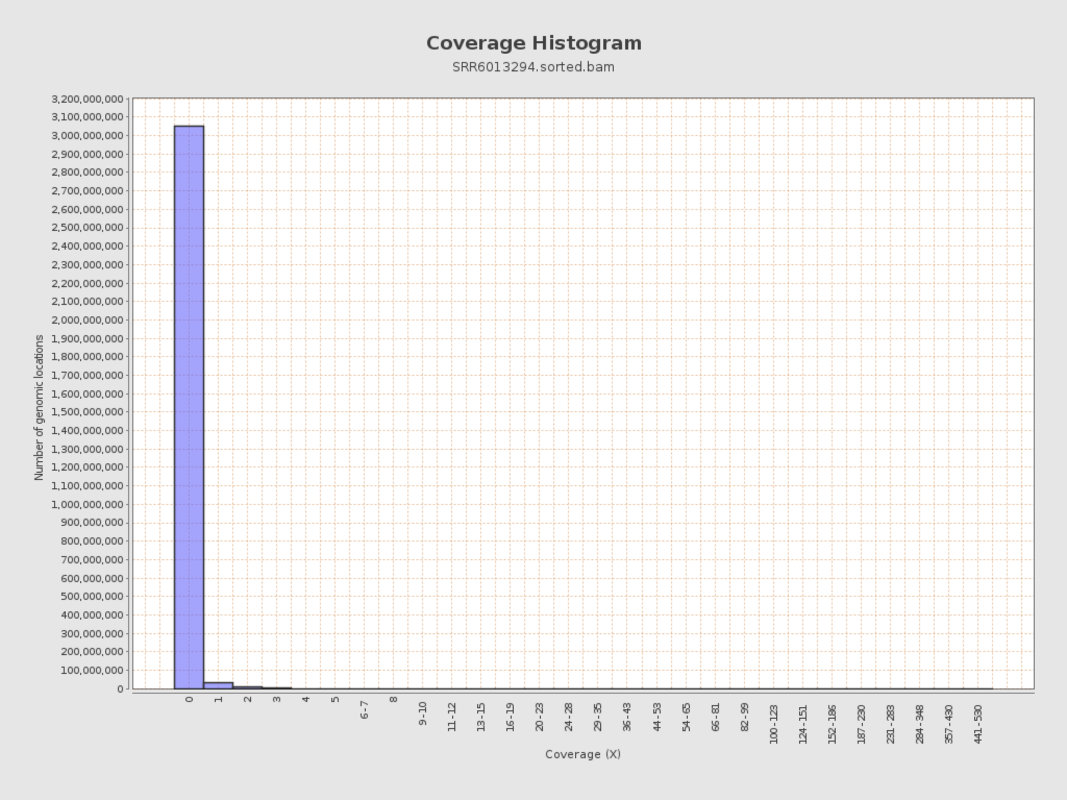
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4913830	0.0197	0.2713
chr2	243199373	12665898	0.0521	0.4935
chr3	198022430	3854950	0.0195	0.2089
chr4	191154276	4217952	0.0221	0.2773
chr5	180915260	2988504	0.0165	0.2042
chr6	171115067	3209241	0.0188	0.2184
chr7	159138663	2896078	0.0182	0.2842

chr8	146364022	3057628	0.0209	0.2875
chr9	141213431	7227967	0.0512	0.4253
chr10	135534747	2433616	0.018	0.34
chr11	135006516	2225456	0.0165	0.2173
chr12	133851895	2229646	0.0167	0.2104
chr13	115169878	1458565	0.0127	0.1685
chr14	107349540	1870090	0.0174	0.247
chr15	102531392	2162637	0.0211	0.2041
chr16	90354753	1338941	0.0148	0.2264
chr17	81195210	1922119	0.0237	0.2329
chr18	78077248	1430349	0.0183	0.5499
chr19	59128983	921367	0.0156	0.2284
chr20	63025520	1816359	0.0288	0.2458
chr21	48129895	761773	0.0158	0.2589
chr22	51304566	529075	0.0103	0.1458
chrMT	16571	143277	8.6462	6.3758
chrX	155270560	2856549	0.0184	0.2202
chrY	59373566	209860	0.0035	0.1823

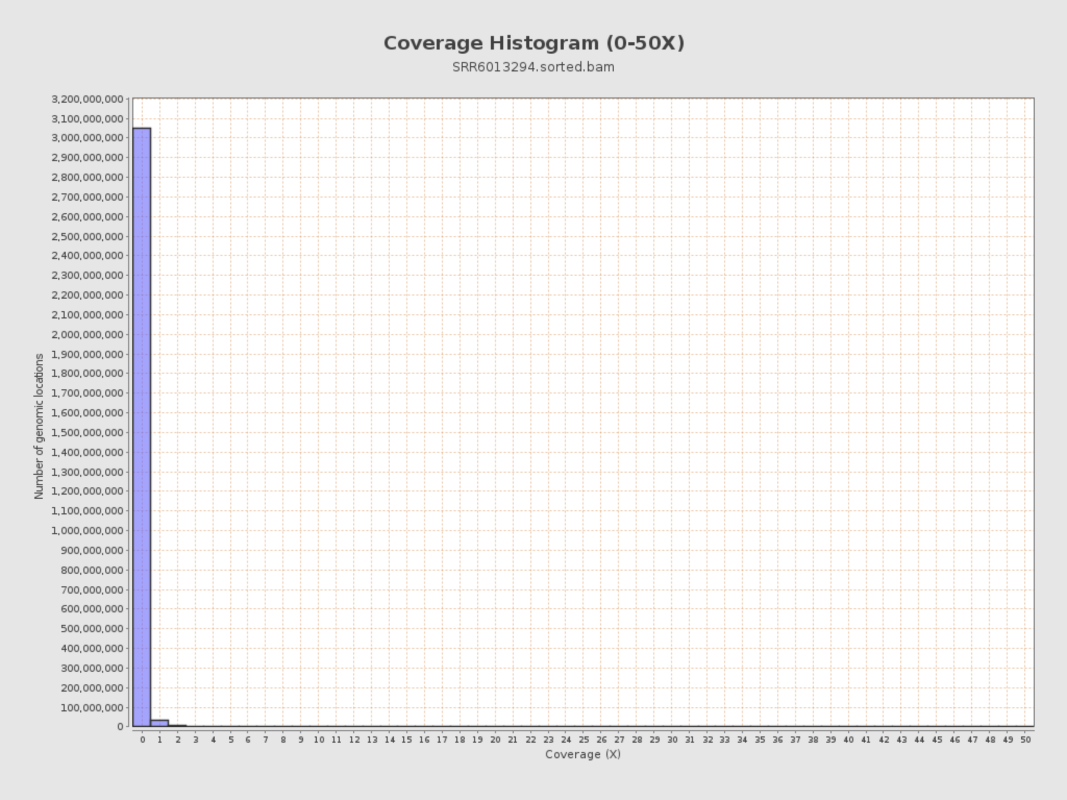
3. Results : Coverage across reference



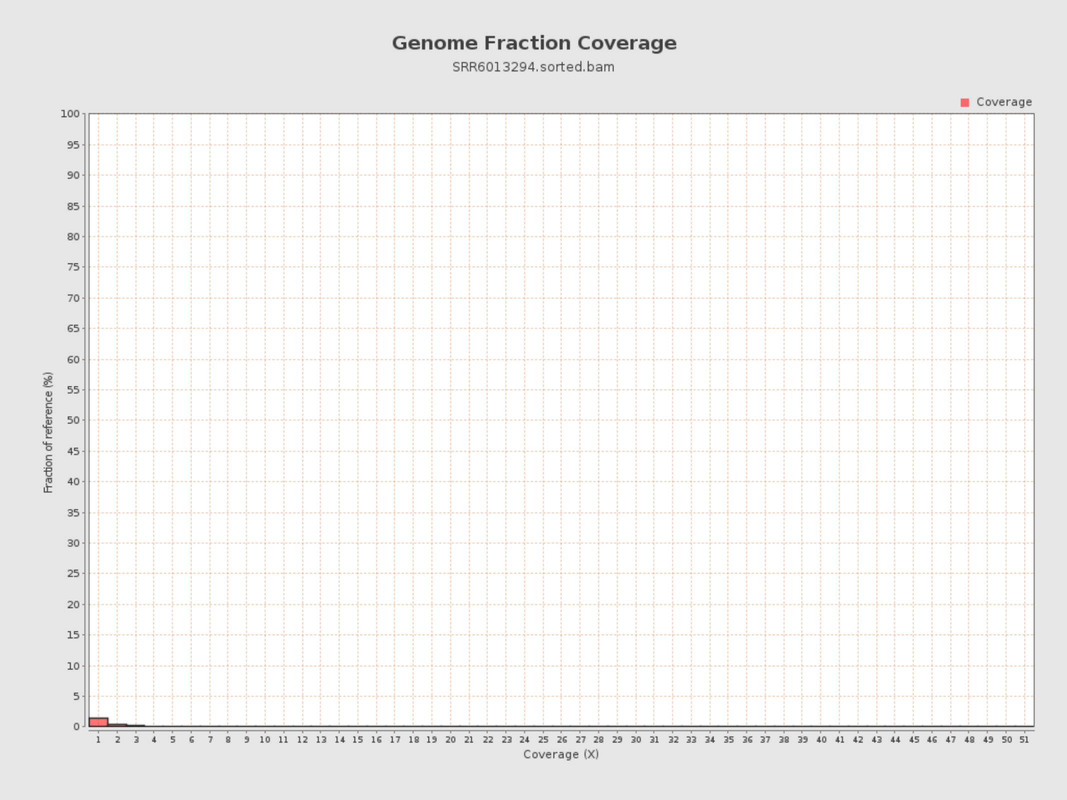
4. Results : Coverage Histogram



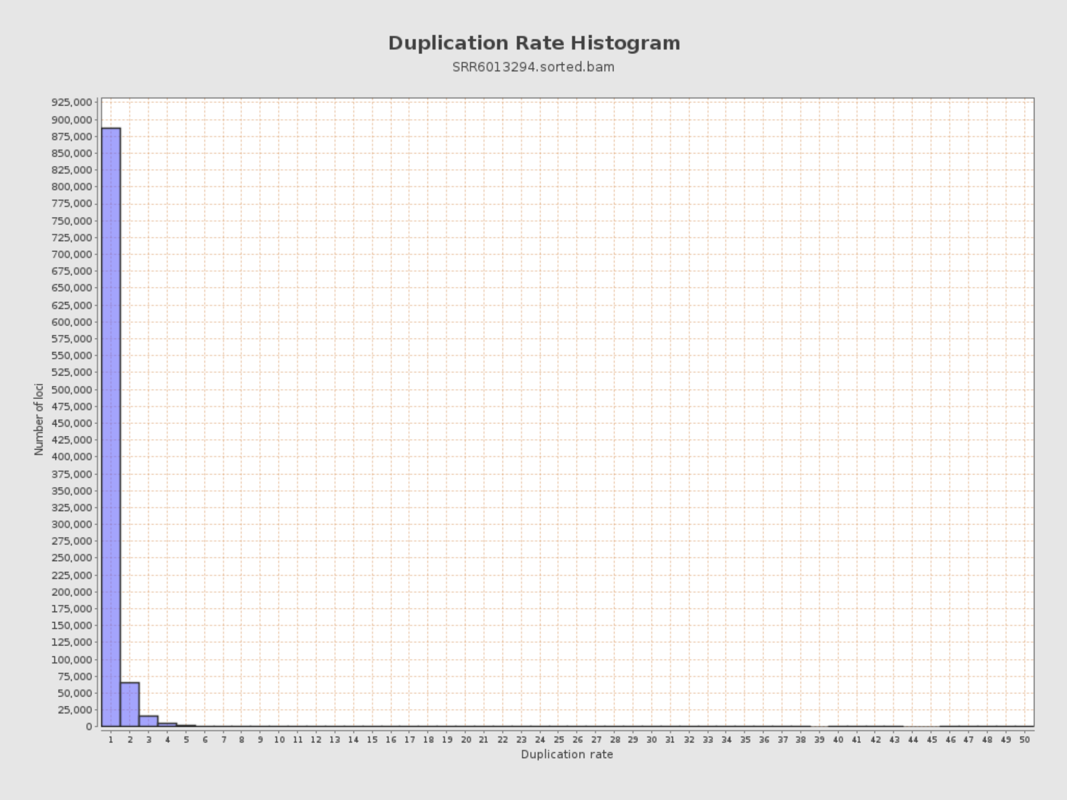
5. Results : Coverage Histogram (0-50X)



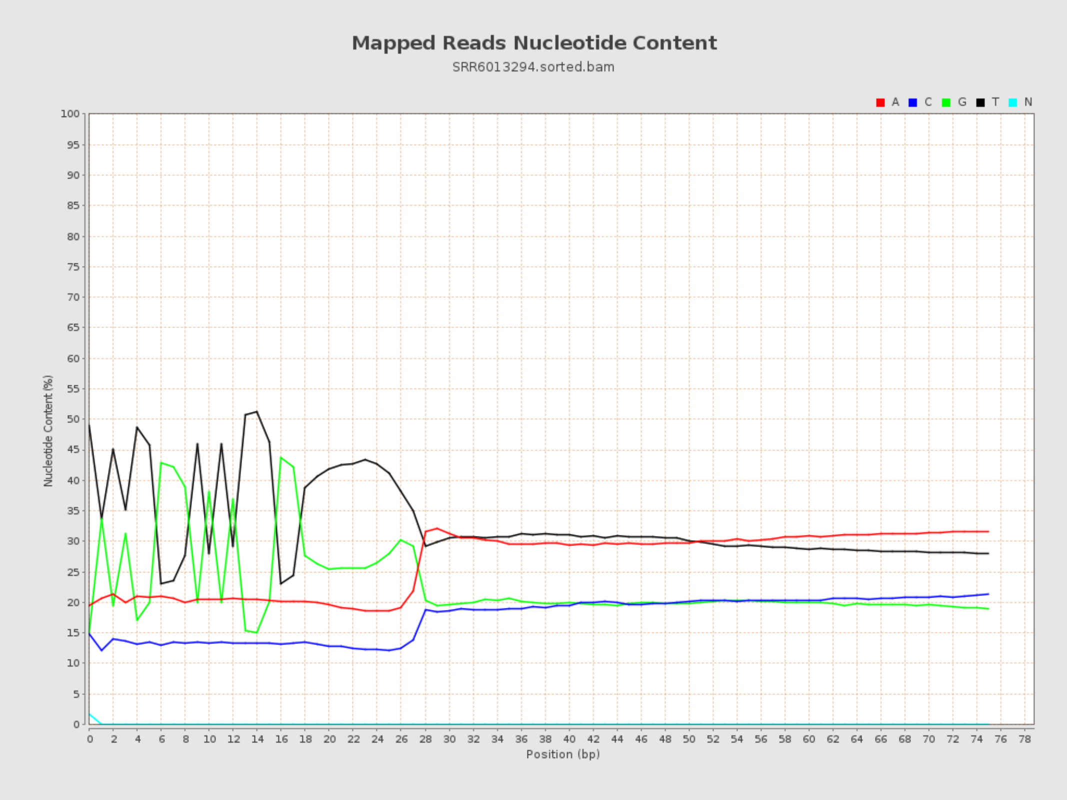
6. Results : Genome Fraction Coverage



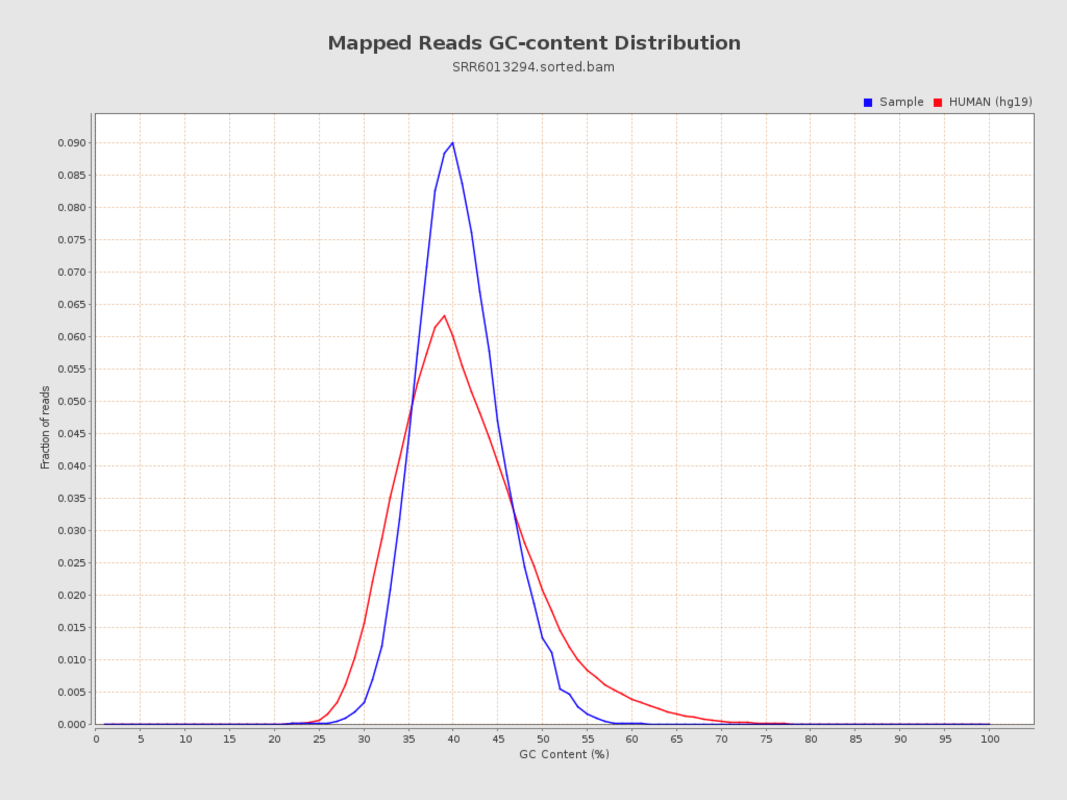
7. Results : Duplication Rate Histogram



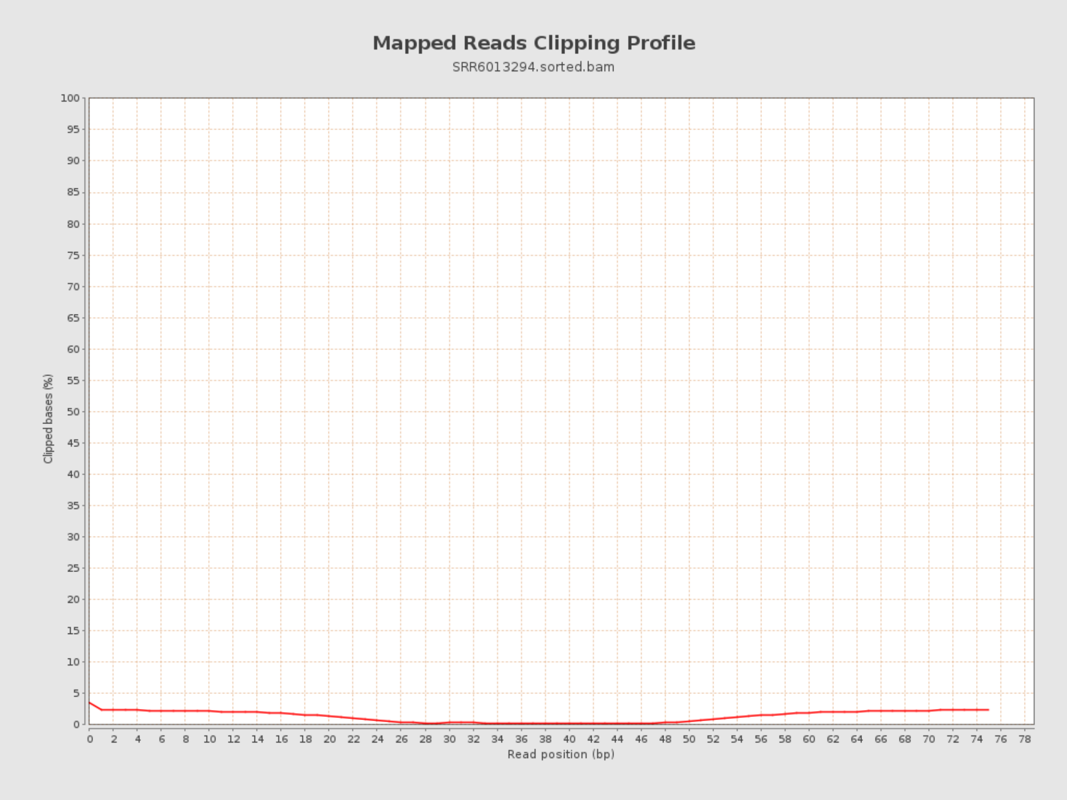
8. Results : Mapped Reads Nucleotide Content



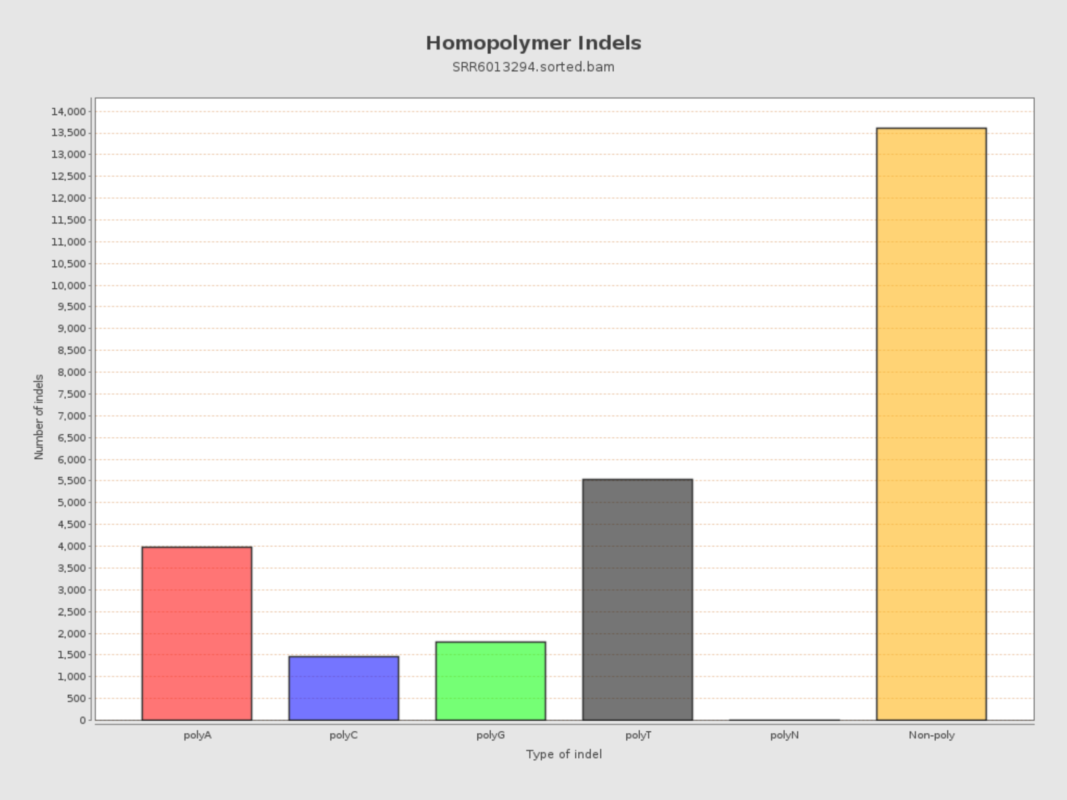
9. Results : Mapped Reads GC-content Distribution



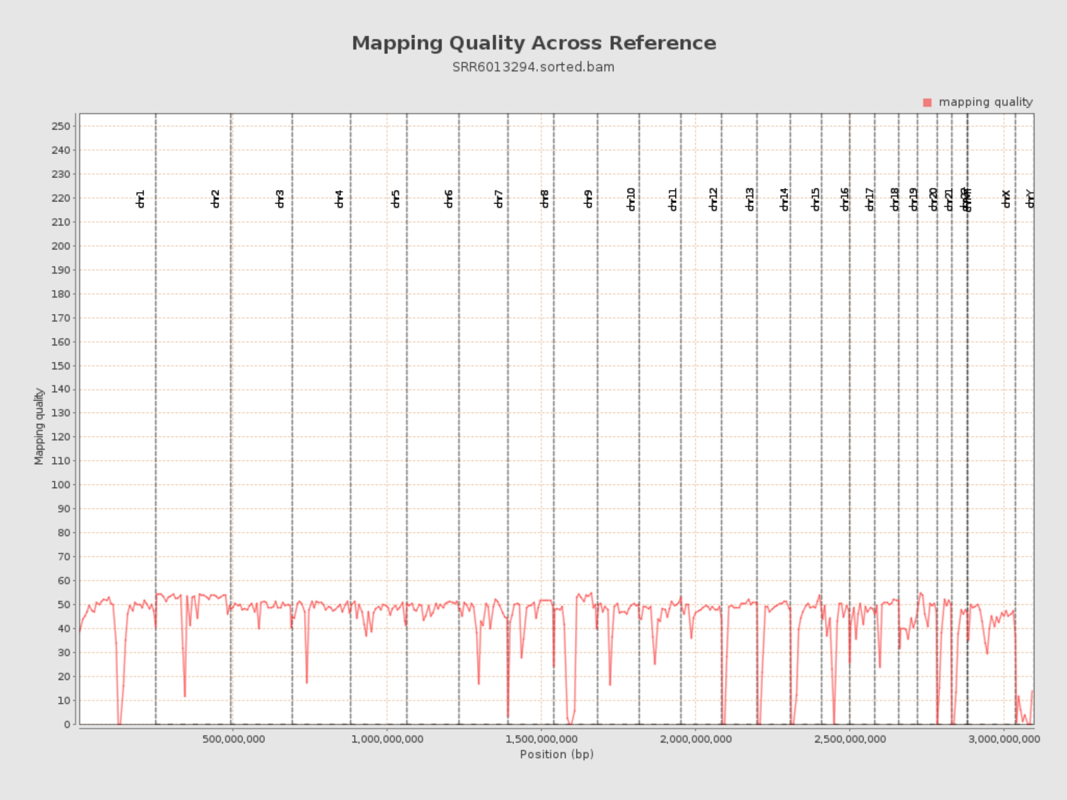
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram