Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:18:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013194.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_SRR6013194 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013194.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:18:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013194.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,903,569
Mapped reads	1,599,696 / 84.04%
Unmapped reads	303,873 / 15.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,158 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	99,896 / 5.25%
Duplication rate	5.1%
Clipped reads	820,341 / 43.09%

2.2. ACGT Content

Number/percentage of A's	28,097,627 / 27.09%
Number/percentage of C's	18,738,945 / 18.06%
Number/percentage of T's	33,397,823 / 32.2%
Number/percentage of G's	23,500,202 / 22.65%
Number/percentage of N's	1,382 / 0%
GC Percentage	40.72%

2.3. Coverage

Mean	0.0335

Standard Deviation	0.345

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

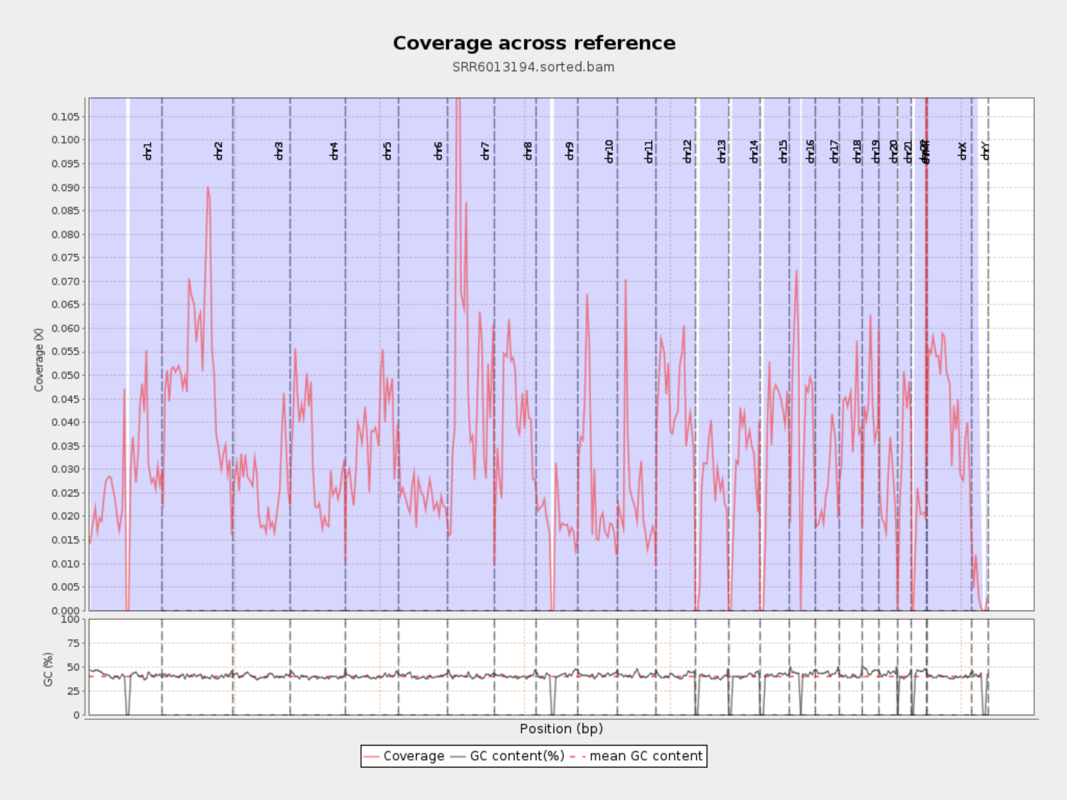
General error rate	0.74%
Mismatches	758,871
Insertions	6,709
Mapped reads with at least one insertion	0.42%
Deletions	27,360
Mapped reads with at least one deletion	1.69%
Homopolymer indels	46.62%

2.6. Chromosome stats

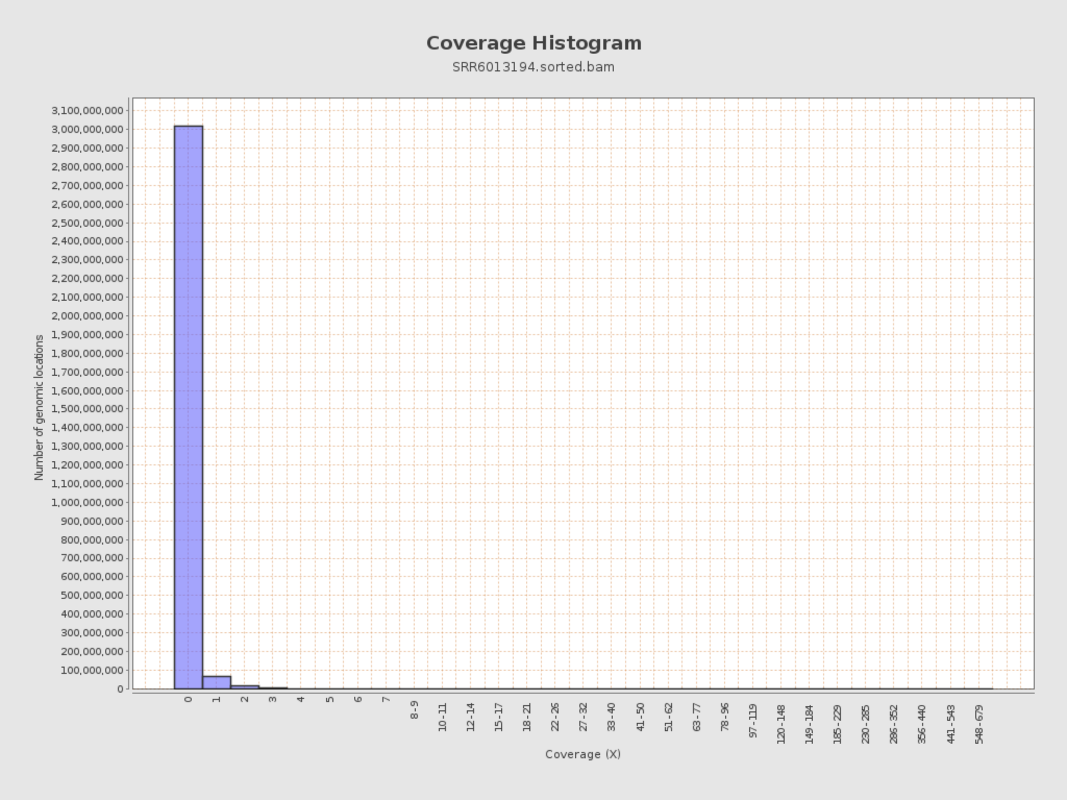
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6703794	0.0269	0.5908
chr2	243199373	12300431	0.0506	0.4205
chr3	198022430	5217338	0.0263	0.2024
chr4	191154276	6150705	0.0322	0.2267
chr5	180915260	6734605	0.0372	0.2455
chr6	171115067	4143343	0.0242	0.2209
chr7	159138663	8478012	0.0533	0.6597

chr8	146364022	6037622	0.0413	0.3614
chr9	141213431	2494524	0.0177	0.245
chr10	135534747	3737808	0.0276	0.3074
chr11	135006516	3257925	0.0241	0.2441
chr12	133851895	6081446	0.0454	0.2689
chr13	115169878	2759785	0.024	0.1918
chr14	107349540	3068975	0.0286	0.2171
chr15	102531392	3633696	0.0354	0.2368
chr16	90354753	3868338	0.0428	0.2657
chr17	81195210	2118581	0.0261	0.2144
chr18	78077248	3229289	0.0414	0.4701
chr19	59128983	2576683	0.0436	0.4322
chr20	63025520	1498353	0.0238	0.1988
chr21	48129895	1711250	0.0356	0.2399
chr22	51304566	822031	0.016	0.154
chrMT	16571	14483	0.874	1.3208
chrX	155270560	6916161	0.0445	0.2907
chrY	59373566	228062	0.0038	0.0899

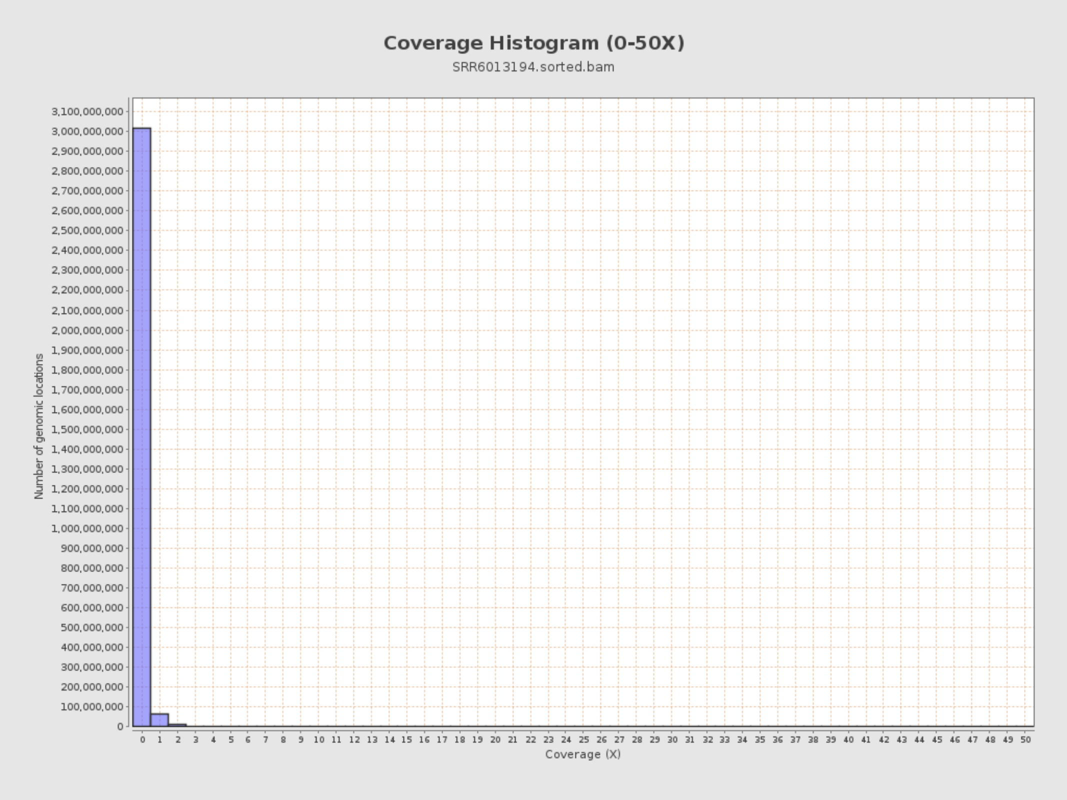
3. Results : Coverage across reference



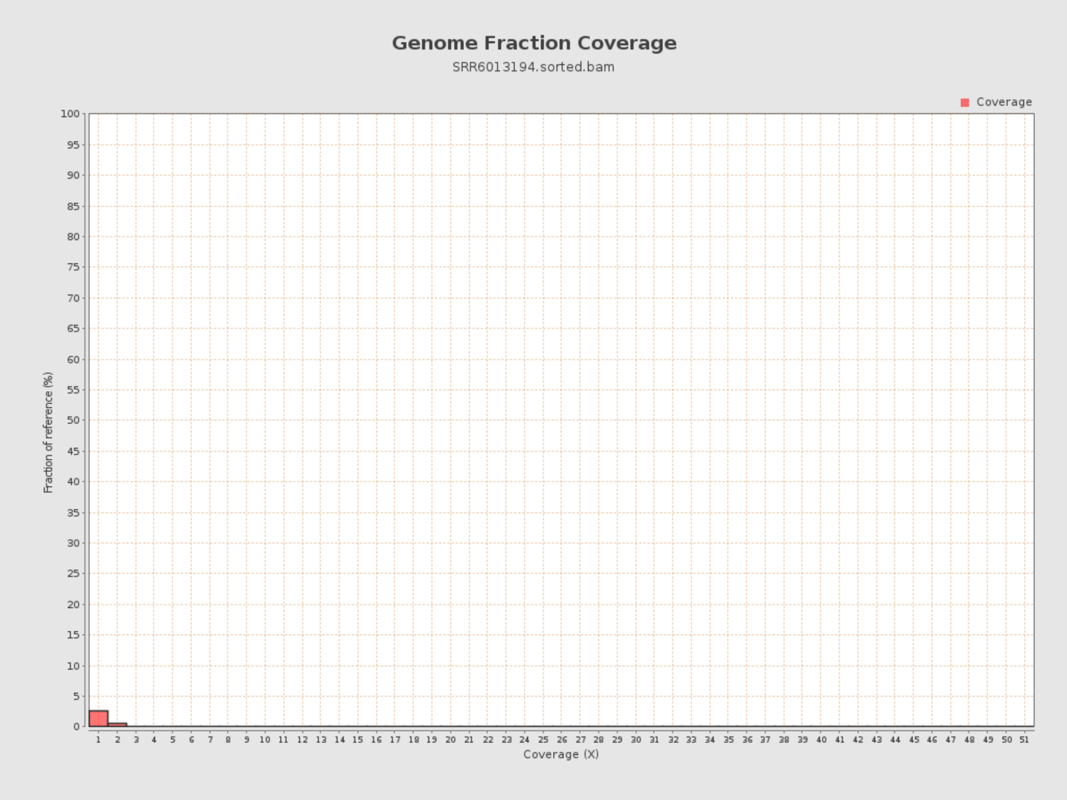
4. Results : Coverage Histogram



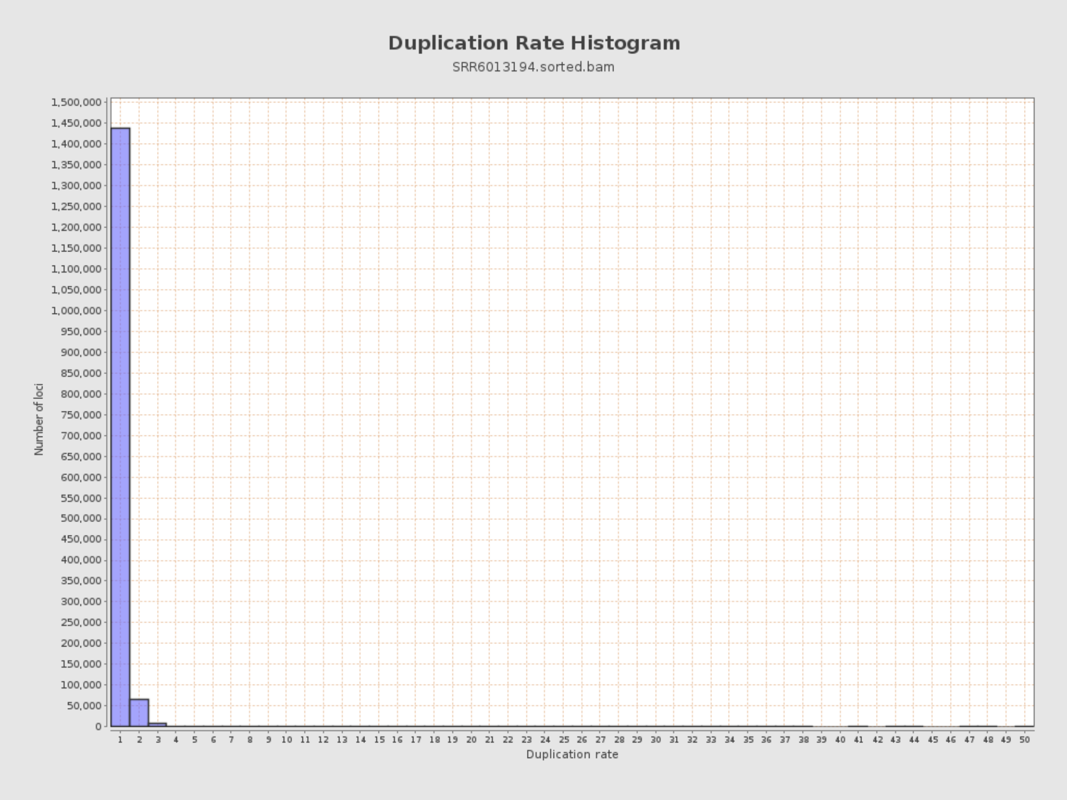
5. Results : Coverage Histogram (0-50X)



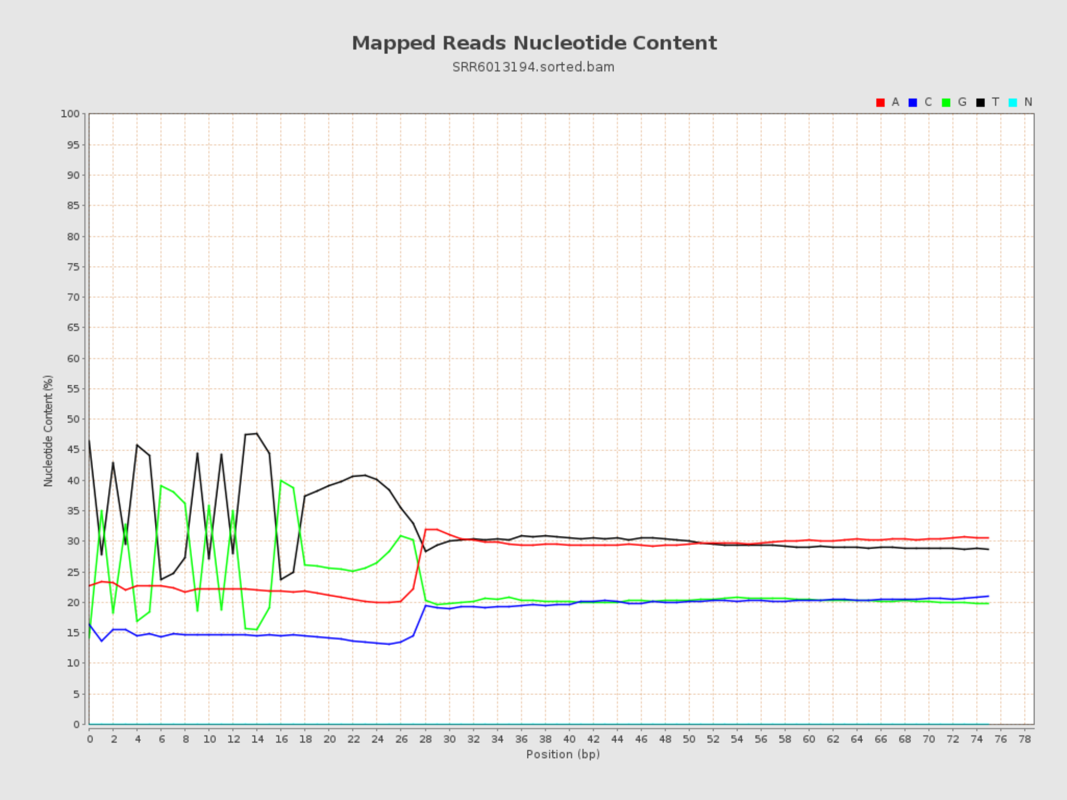
6. Results : Genome Fraction Coverage



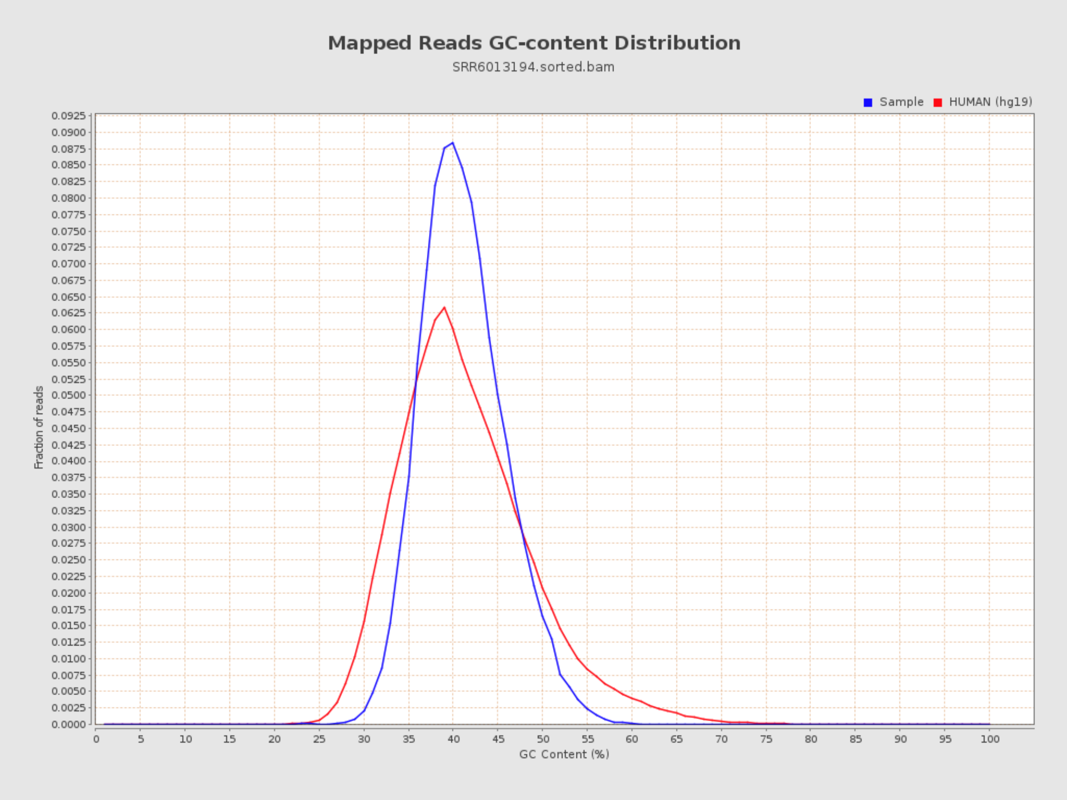
7. Results : Duplication Rate Histogram



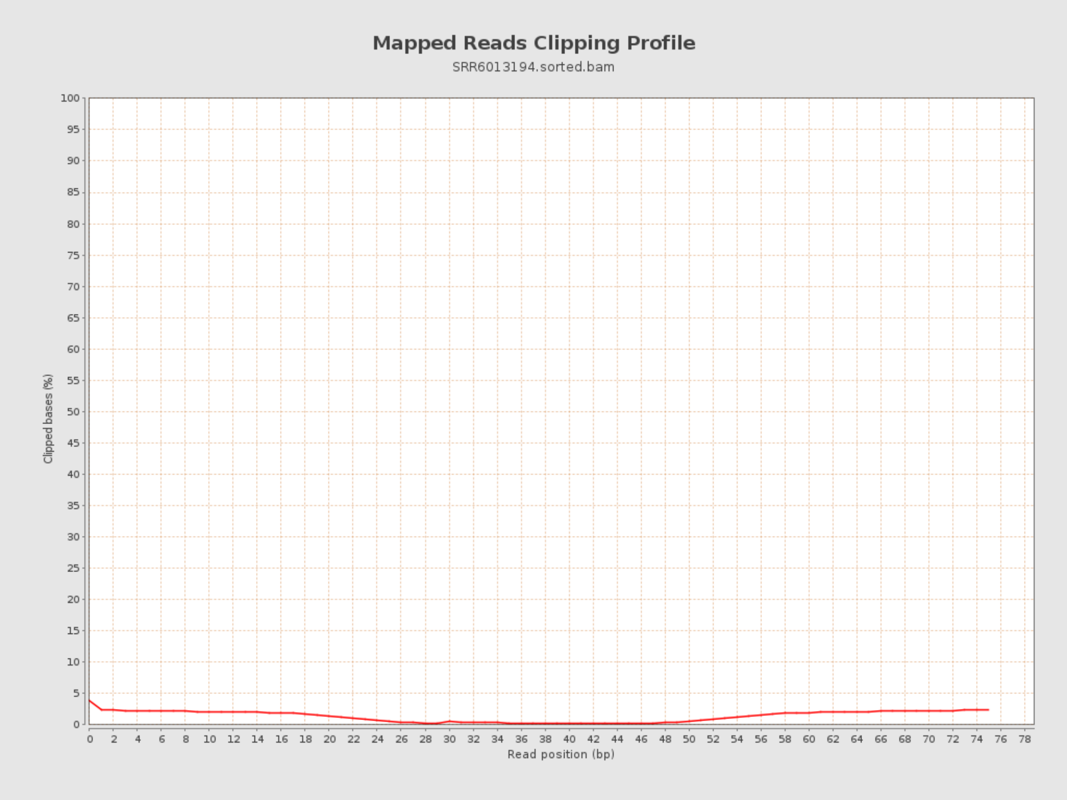
8. Results : Mapped Reads Nucleotide Content



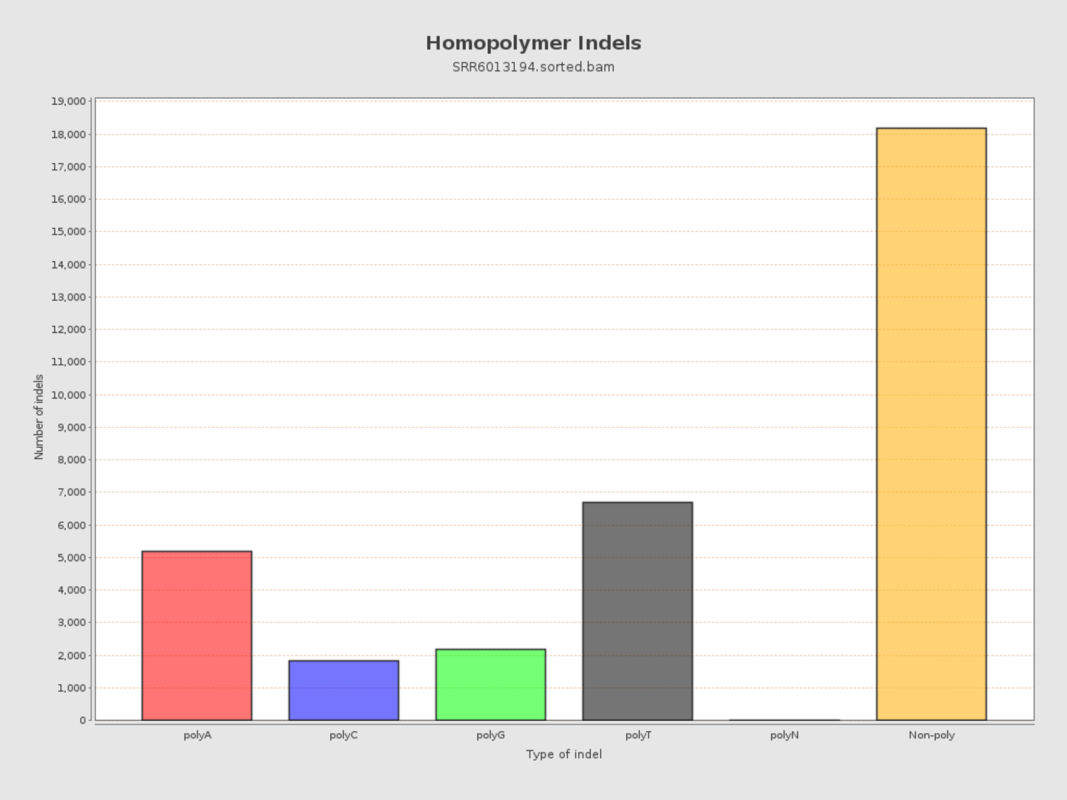
9. Results : Mapped Reads GC-content Distribution



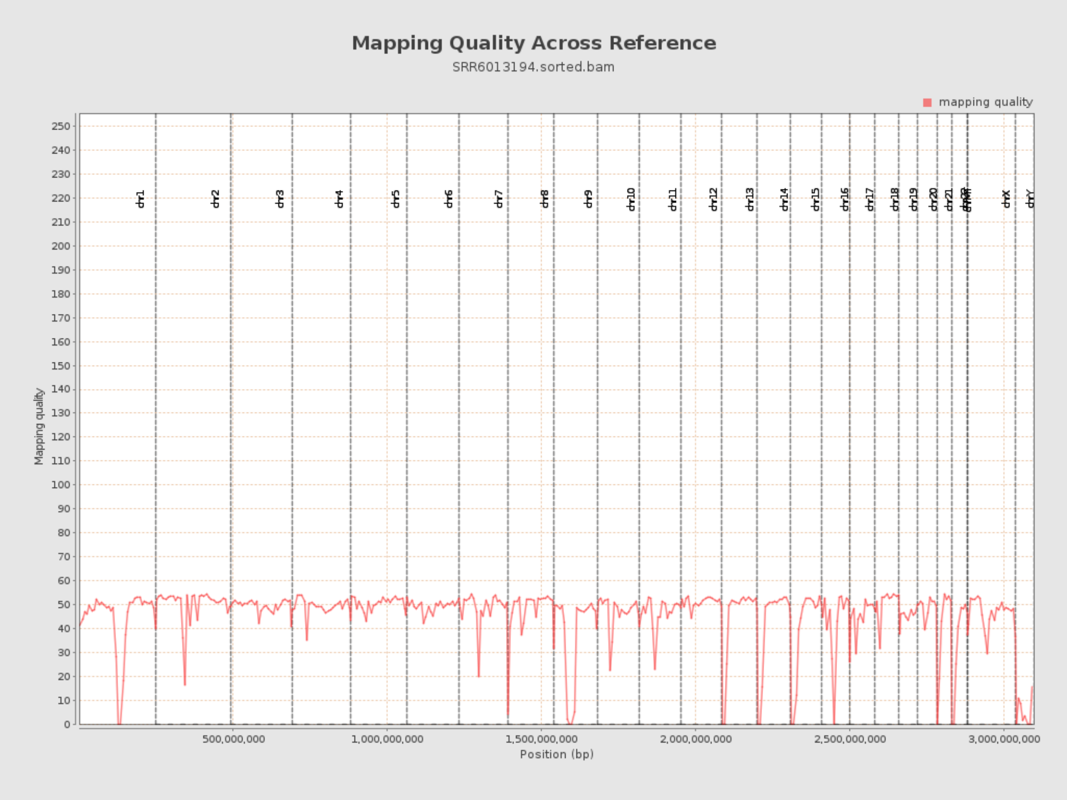
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram