Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:18:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013234.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_SRR6013234 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013234.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:18:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013234.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,887,655
Mapped reads	1,691,189 / 89.59%
Unmapped reads	196,466 / 10.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,683 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	100,449 / 5.32%
Duplication rate	4.67%
Clipped reads	680,906 / 36.07%

2.2. ACGT Content

Number/percentage of A's	32,335,011 / 28.22%
Number/percentage of C's	20,954,501 / 18.29%
Number/percentage of T's	36,758,231 / 32.08%
Number/percentage of G's	24,498,836 / 21.38%
Number/percentage of N's	24,871 / 0.02%
GC Percentage	39.67%

2.3. Coverage

Mean	0.037

Standard Deviation	0.3929

2.4. Mapping Quality

Mean Mapping Quality	47.22

2.5. Mismatches and indels

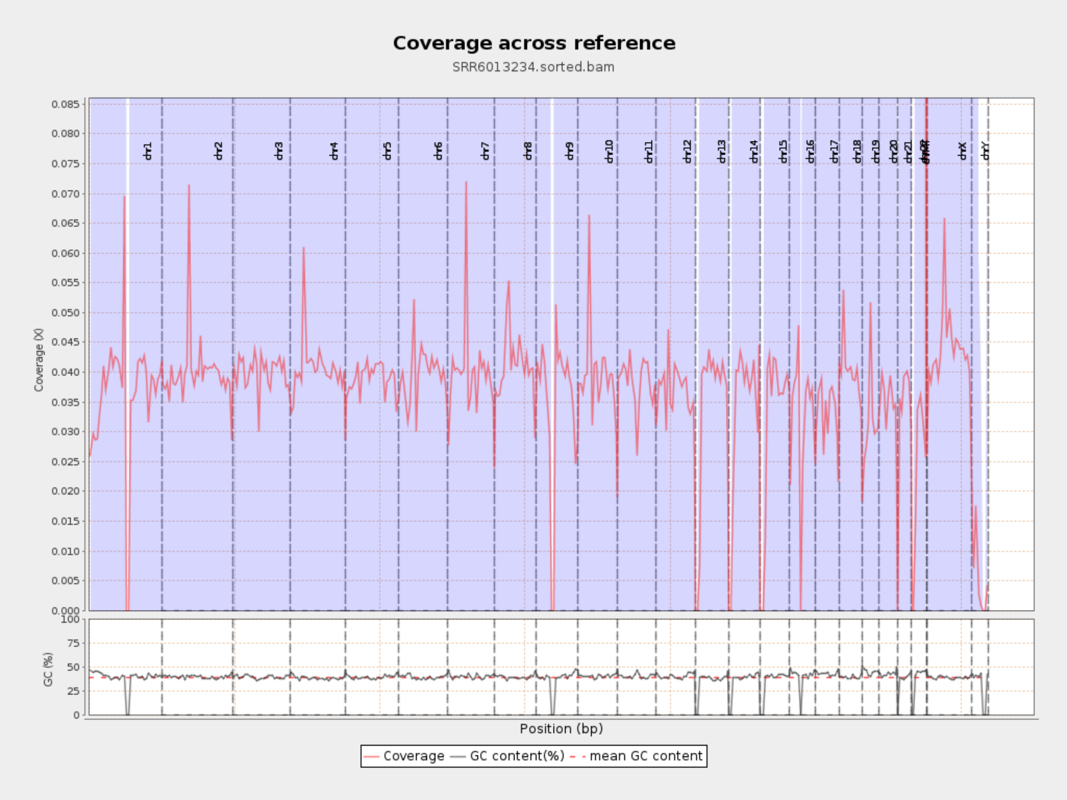
General error rate	0.8%
Mismatches	902,697
Insertions	8,708
Mapped reads with at least one insertion	0.51%
Deletions	25,752
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.59%

2.6. Chromosome stats

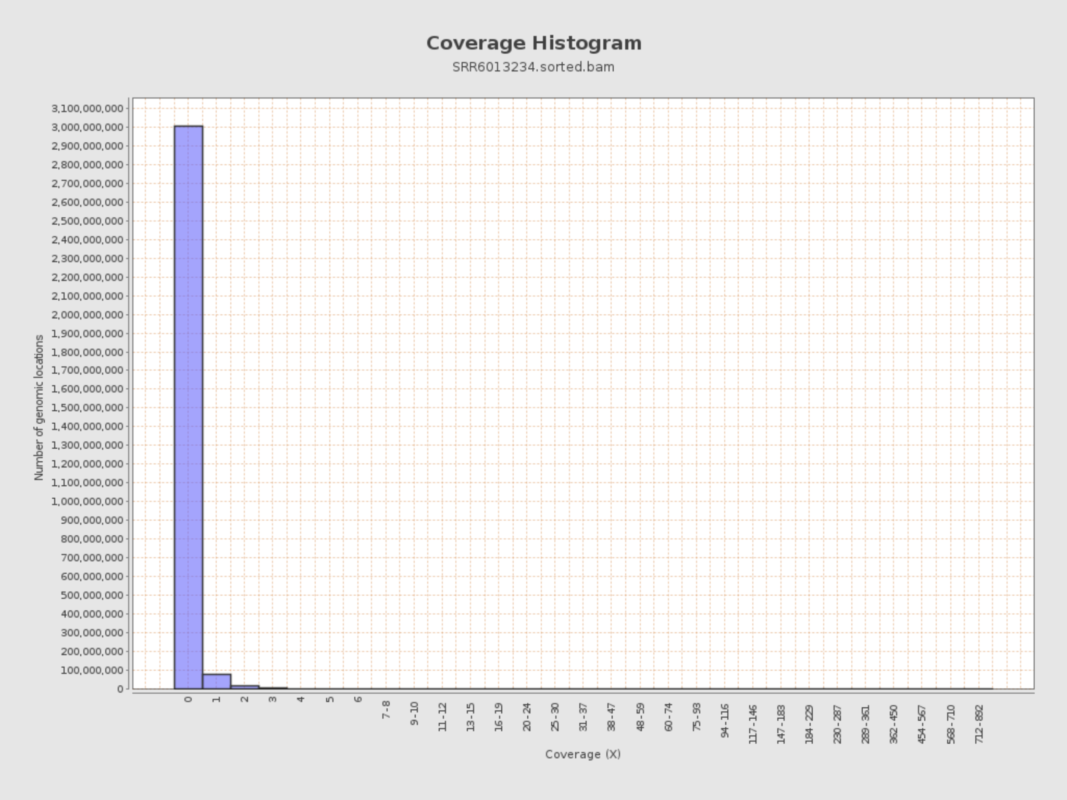
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9040024	0.0363	0.7384
chr2	243199373	9773933	0.0402	0.4249
chr3	198022430	7932194	0.0401	0.2387
chr4	191154276	7777851	0.0407	0.2641
chr5	180915260	7046476	0.0389	0.2379
chr6	171115067	6798821	0.0397	0.2792
chr7	159138663	6428041	0.0404	0.5246

chr8	146364022	6028661	0.0412	0.5961
chr9	141213431	4906986	0.0347	0.3548
chr10	135534747	5384984	0.0397	0.3529
chr11	135006516	5127086	0.038	0.2863
chr12	133851895	4946259	0.037	0.2361
chr13	115169878	3853782	0.0335	0.2186
chr14	107349540	3505168	0.0327	0.2257
chr15	102531392	3228563	0.0315	0.2115
chr16	90354753	2933147	0.0325	0.2443
chr17	81195210	2679014	0.033	0.2433
chr18	78077248	3177196	0.0407	0.6901
chr19	59128983	1889644	0.032	0.5202
chr20	63025520	2215560	0.0352	0.2317
chr21	48129895	1598632	0.0332	0.2423
chr22	51304566	1168692	0.0228	0.1769
chrMT	16571	80434	4.8539	3.5389
chrX	155270560	6781542	0.0437	0.2792
chrY	59373566	313919	0.0053	0.1527

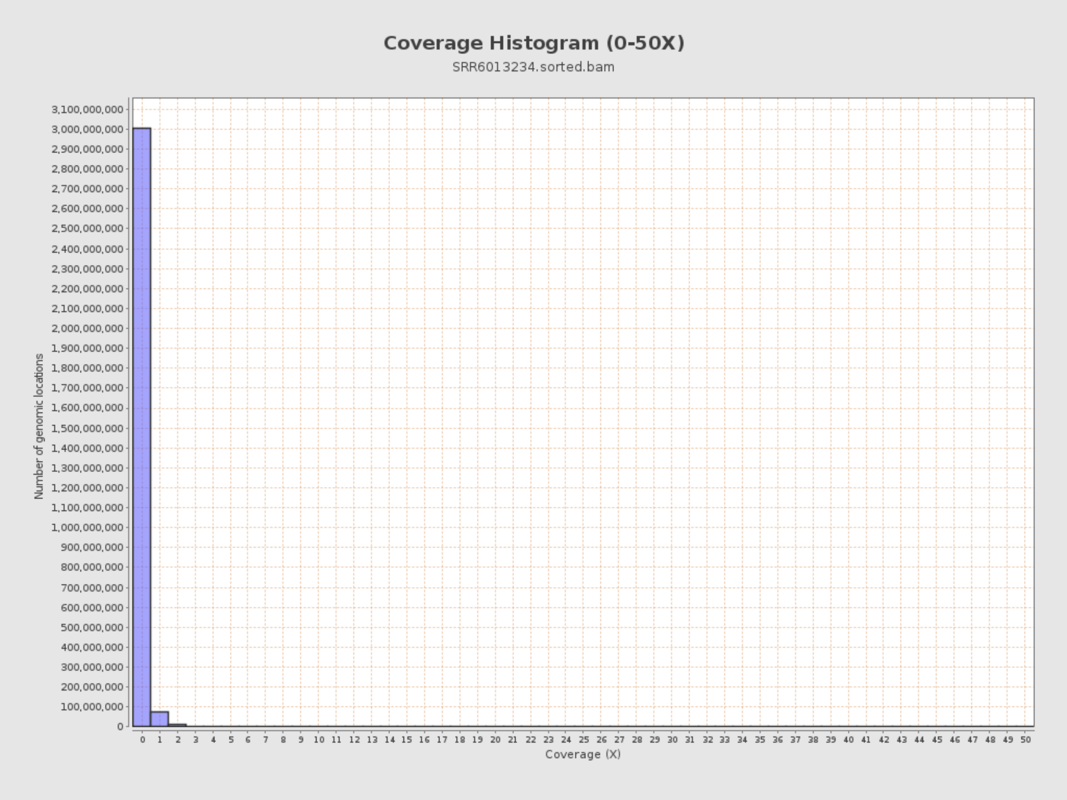
3. Results : Coverage across reference



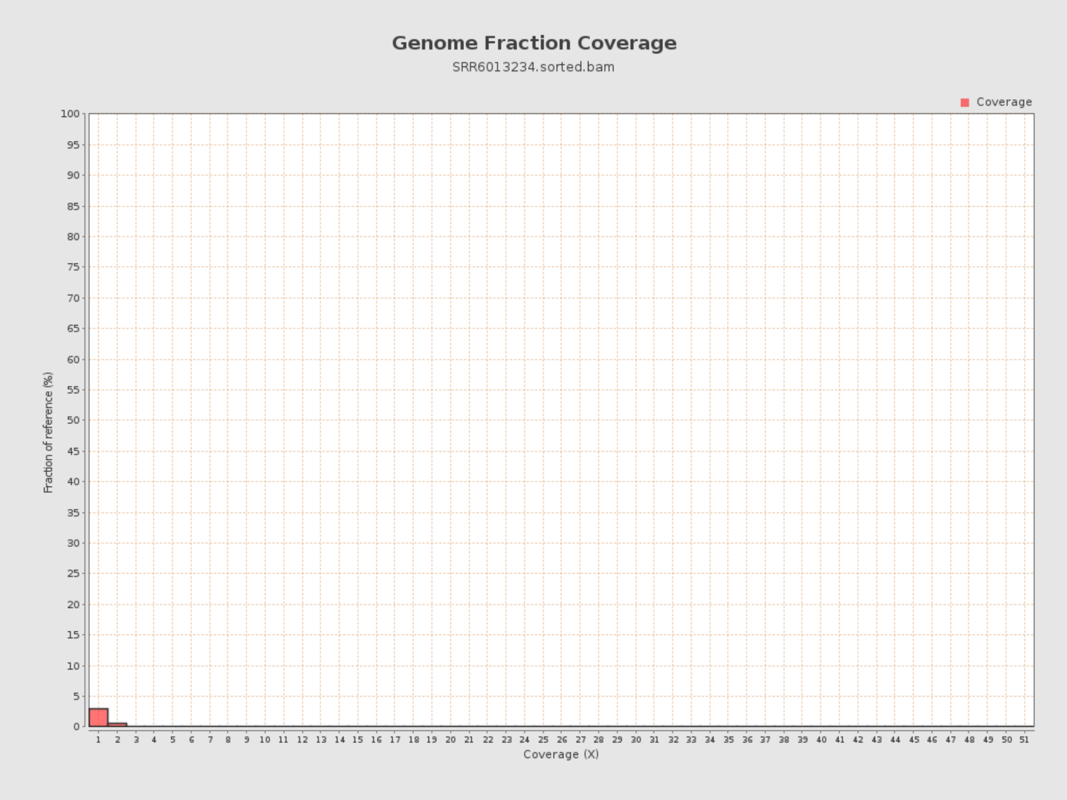
4. Results : Coverage Histogram



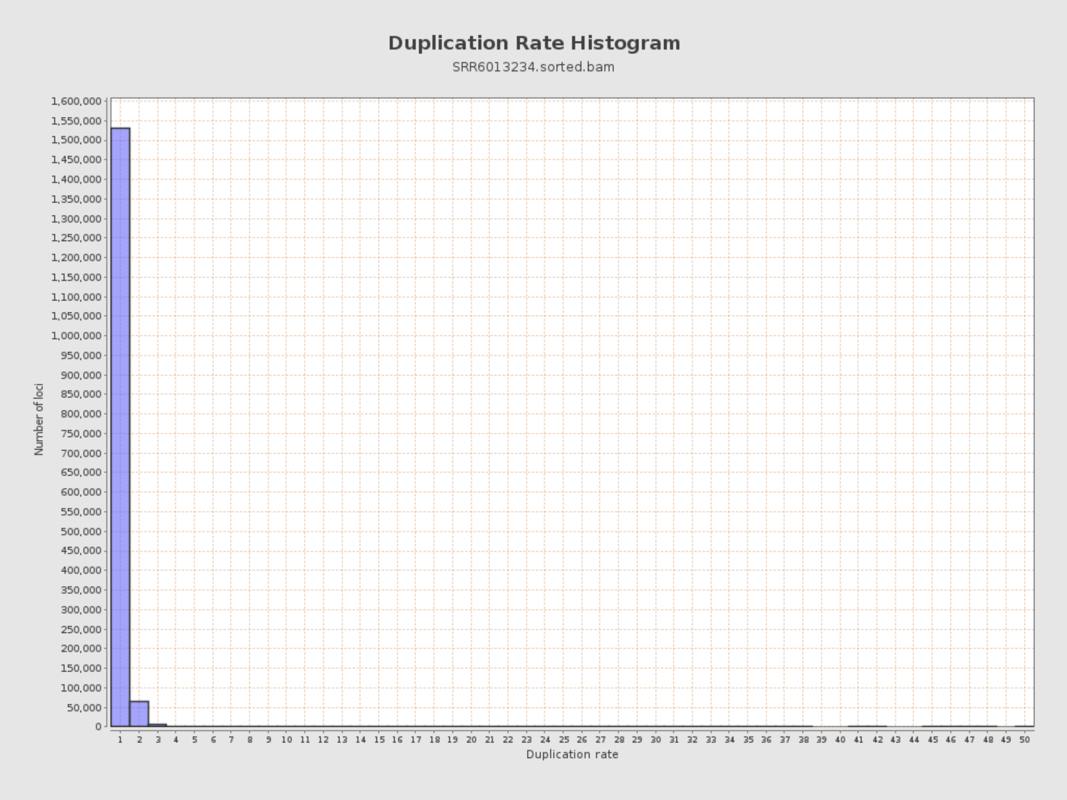
5. Results : Coverage Histogram (0-50X)



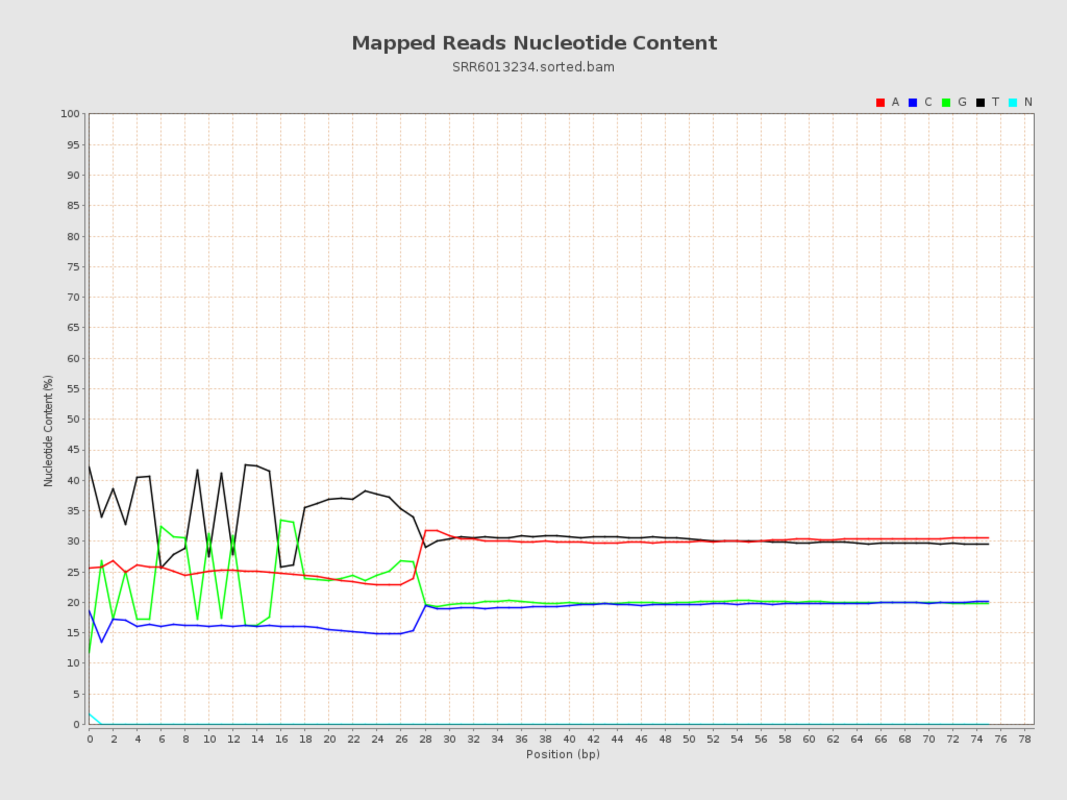
6. Results : Genome Fraction Coverage



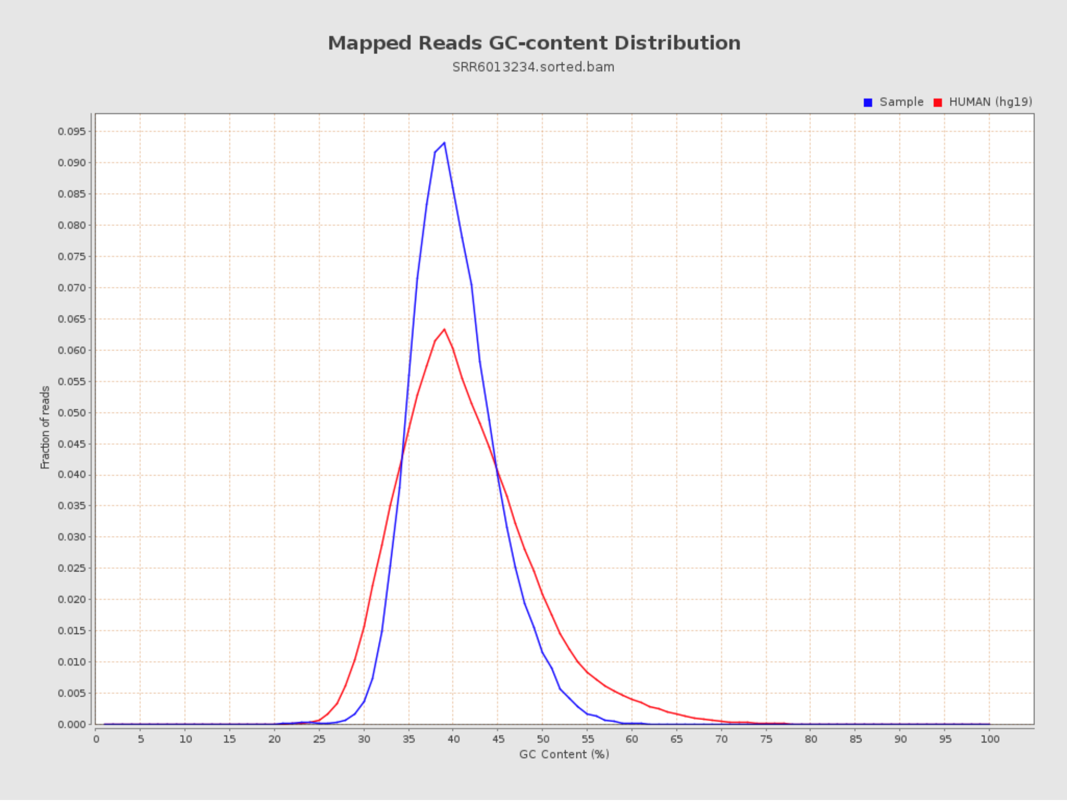
7. Results : Duplication Rate Histogram



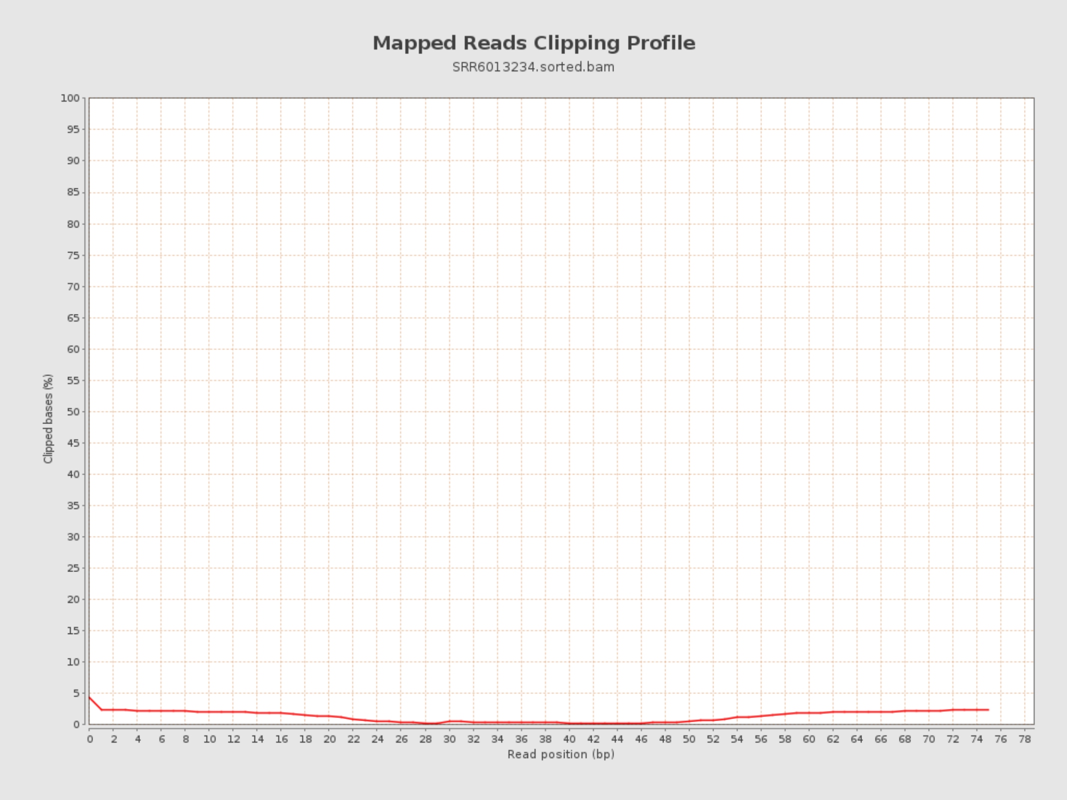
8. Results : Mapped Reads Nucleotide Content



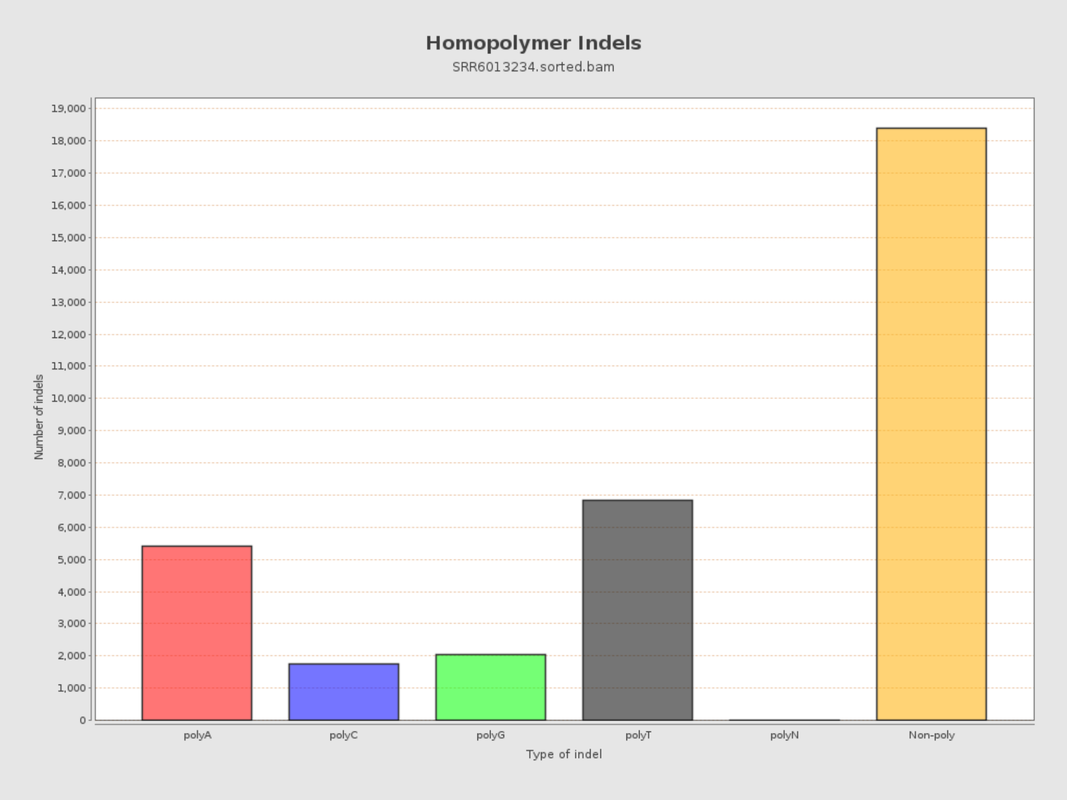
9. Results : Mapped Reads GC-content Distribution



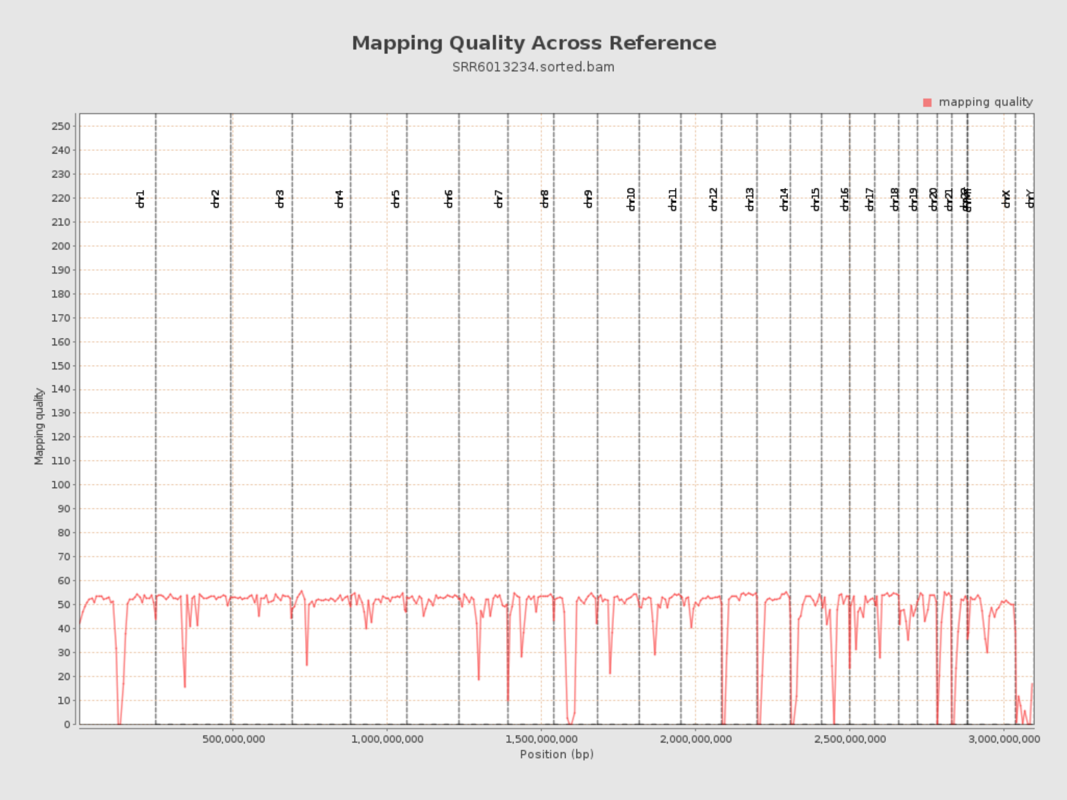
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram