Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:34:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230344.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_SRR6230344 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230344.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:34:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230344.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,950,889
Mapped reads	3,766,903 / 95.34%
Unmapped reads	183,986 / 4.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,618 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	229,437 / 5.81%
Duplication rate	5.09%
Clipped reads	969,579 / 24.54%

2.2. ACGT Content

Number/percentage of A's	80,262,842 / 29.6%
Number/percentage of C's	55,586,670 / 20.5%
Number/percentage of T's	79,002,355 / 29.13%
Number/percentage of G's	56,127,862 / 20.7%
Number/percentage of N's	220,860 / 0.08%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0876

Standard Deviation	0.7783

2.4. Mapping Quality

Mean Mapping Quality	47.61

2.5. Mismatches and indels

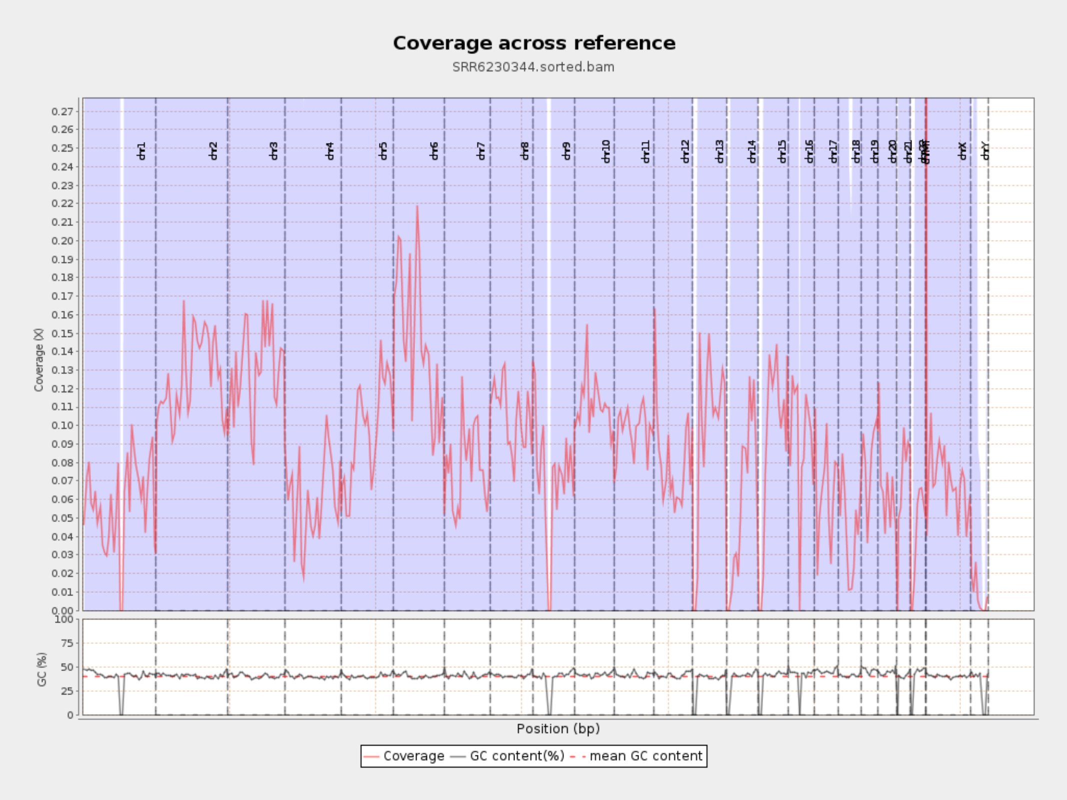
General error rate	0.89%
Mismatches	2,382,777
Insertions	21,342
Mapped reads with at least one insertion	0.56%
Deletions	67,796
Mapped reads with at least one deletion	1.78%
Homopolymer indels	47.92%

2.6. Chromosome stats

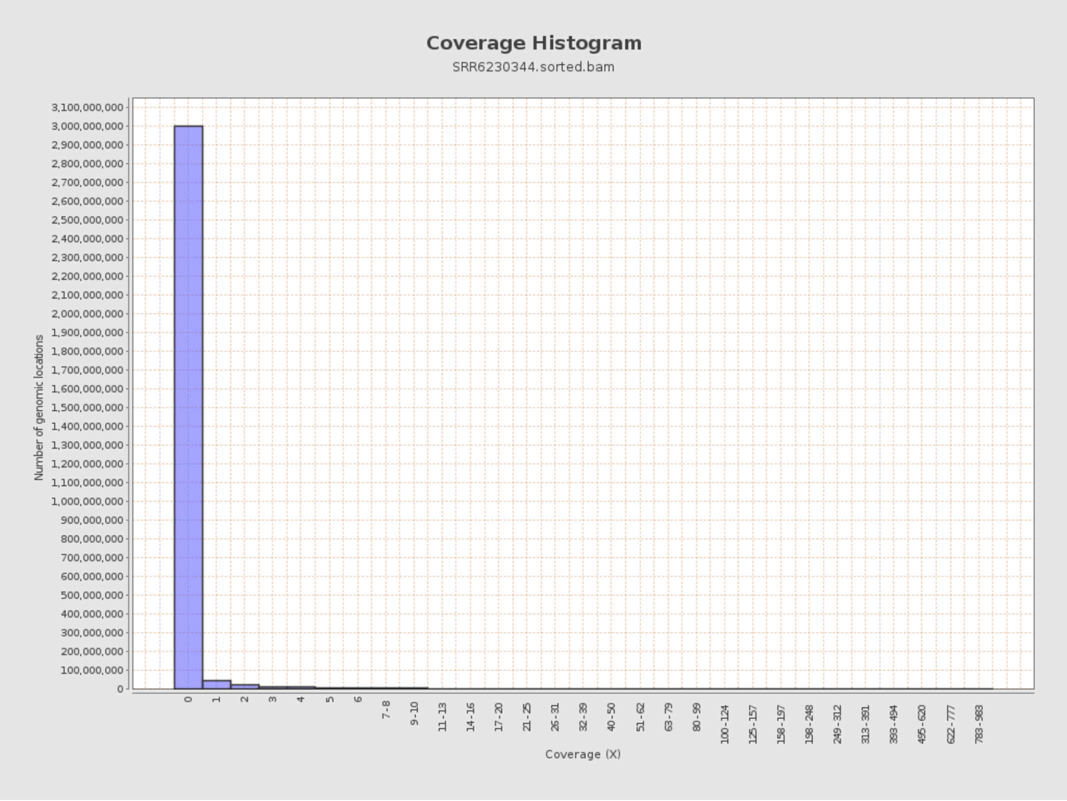
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14238433	0.0571	0.8838
chr2	243199373	30700858	0.1262	0.9033
chr3	198022430	25728105	0.1299	0.7719
chr4	191154276	11644156	0.0609	0.5303
chr5	180915260	17715623	0.0979	0.6704
chr6	171115067	24956531	0.1458	1.057
chr7	159138663	12402769	0.0779	0.8231

chr8	146364022	15306761	0.1046	0.9263
chr9	141213431	9877831	0.0699	0.6725
chr10	135534747	15119336	0.1116	0.8911
chr11	135006516	13187143	0.0977	0.9757
chr12	133851895	10837555	0.081	0.6131
chr13	115169878	11307309	0.0982	0.671
chr14	107349540	6466434	0.0602	0.5475
chr15	102531392	9238830	0.0901	0.6403
chr16	90354753	8192391	0.0907	0.6727
chr17	81195210	5194322	0.064	0.5853
chr18	78077248	3529175	0.0452	1.1913
chr19	59128983	4758795	0.0805	0.8121
chr20	63025520	4075020	0.0647	0.5624
chr21	48129895	3341367	0.0694	0.5712
chr22	51304566	2142270	0.0418	0.4281
chrMT	16571	37678	2.2737	2.7606
chrX	155270560	10827107	0.0697	0.6176
chrY	59373566	487832	0.0082	0.1985

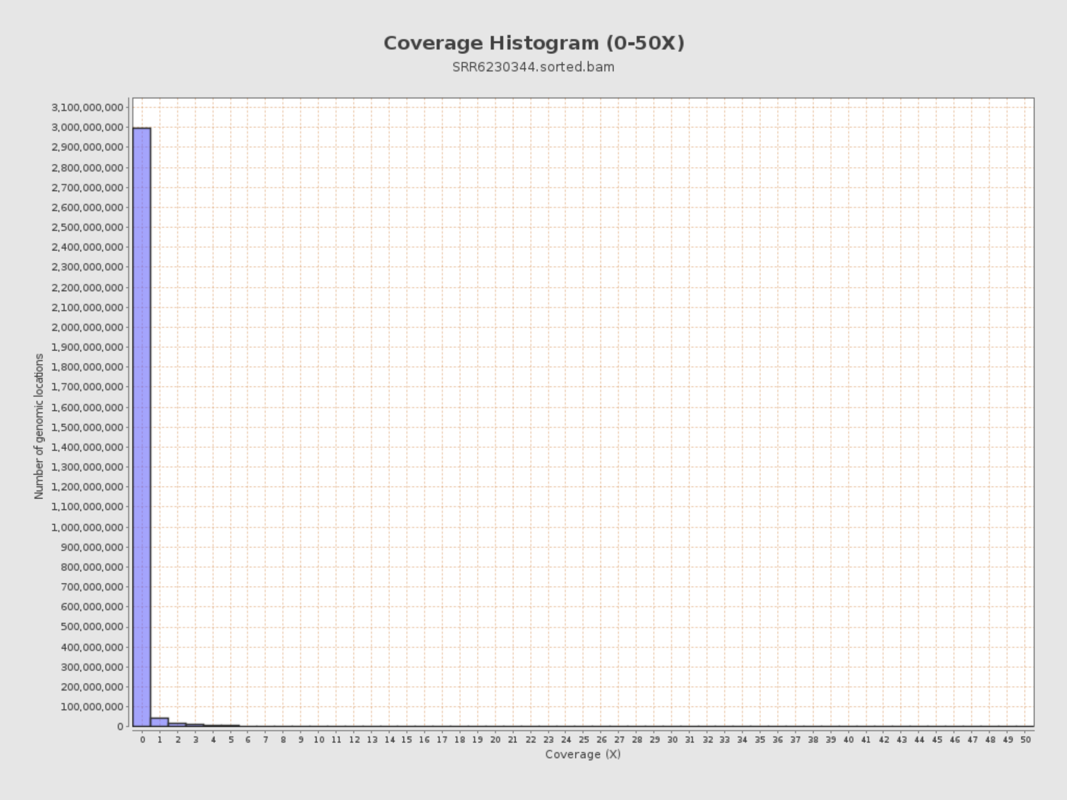
3. Results : Coverage across reference



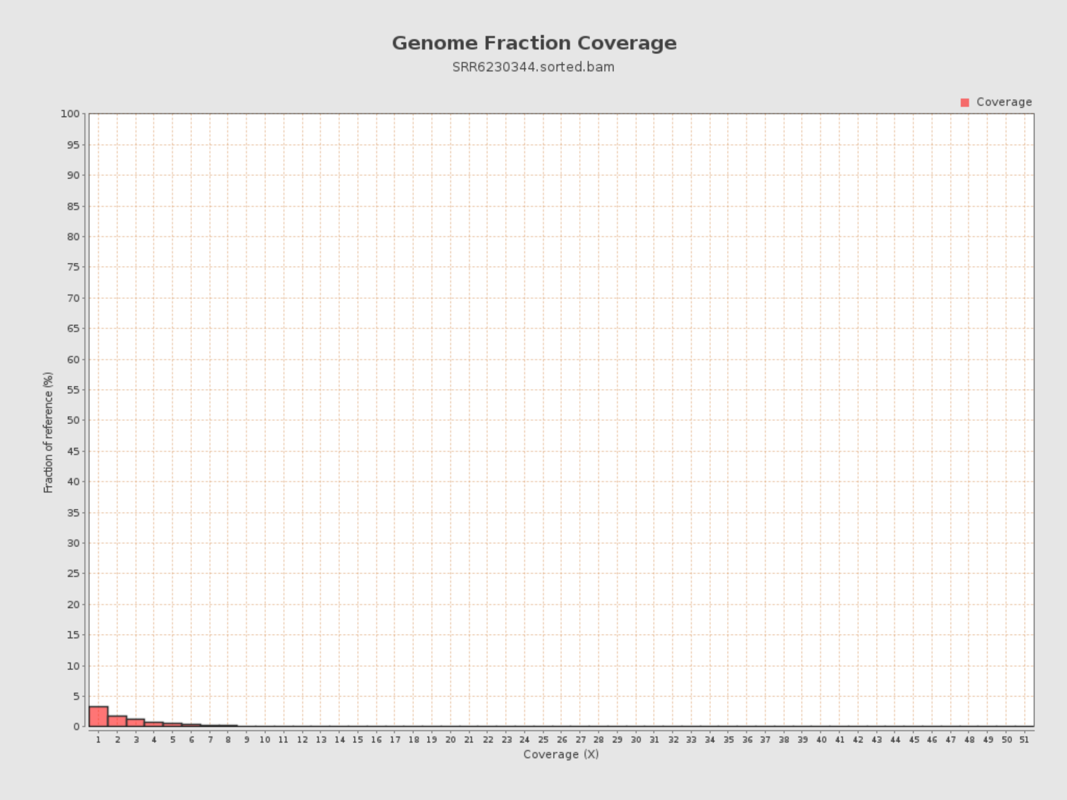
4. Results : Coverage Histogram



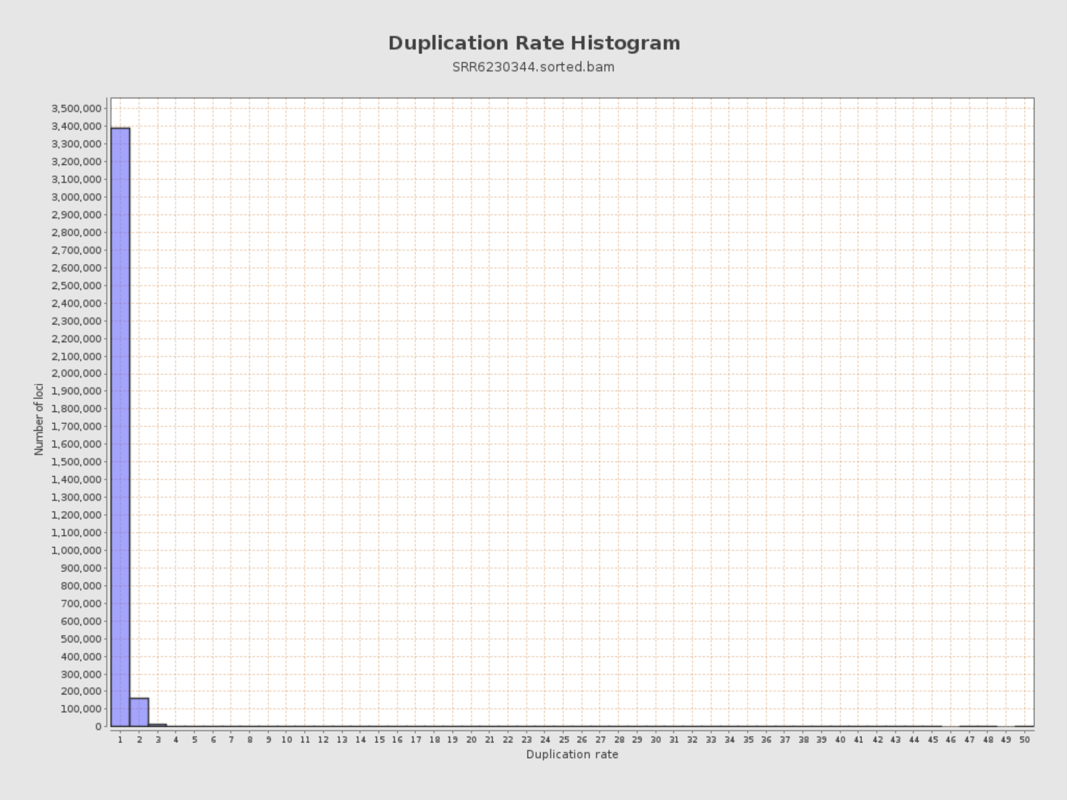
5. Results : Coverage Histogram (0-50X)



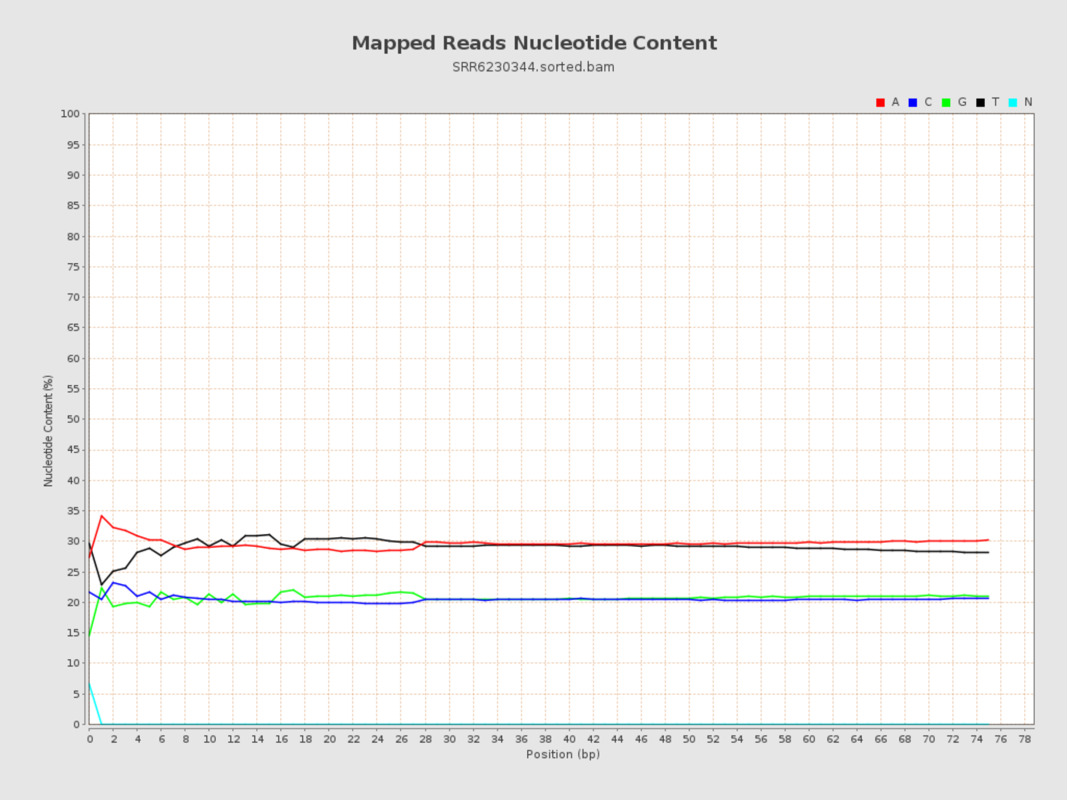
6. Results : Genome Fraction Coverage



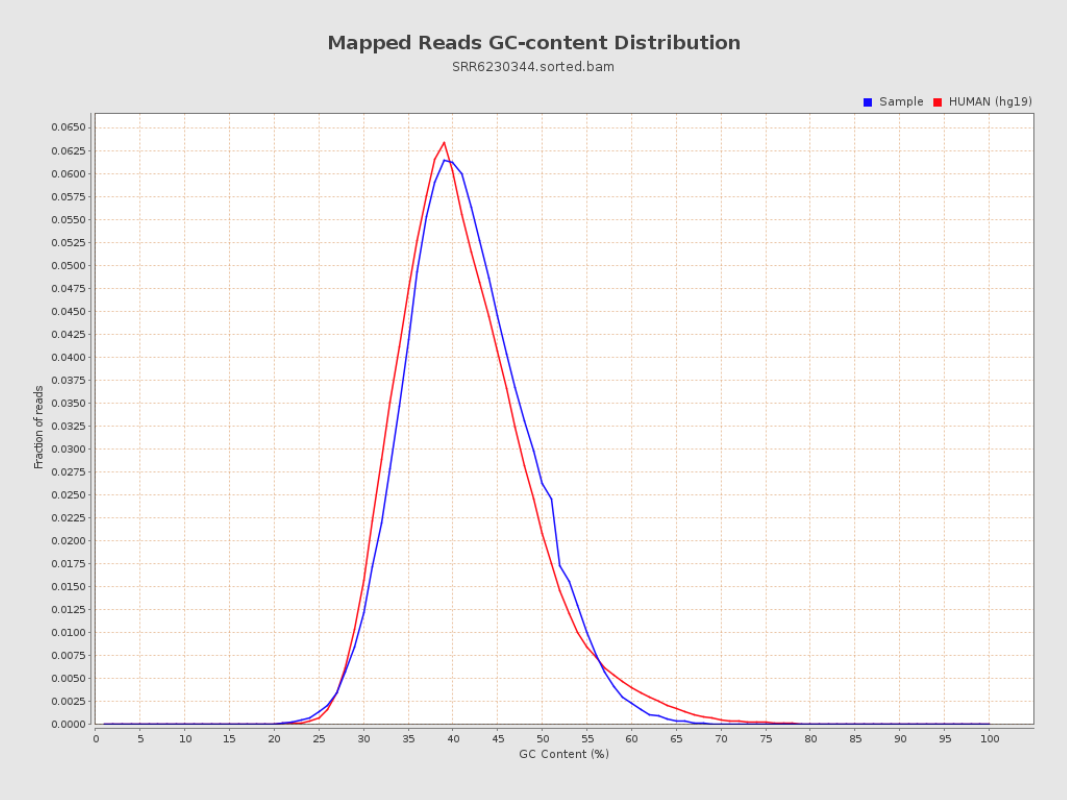
7. Results : Duplication Rate Histogram



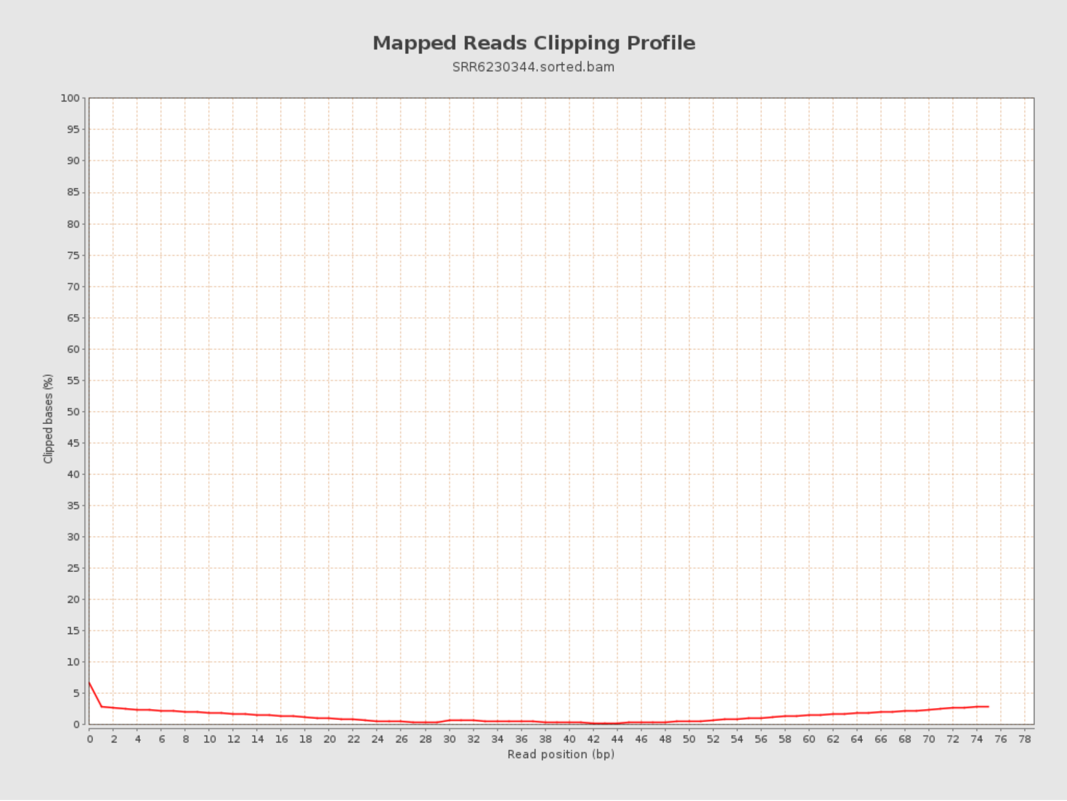
8. Results : Mapped Reads Nucleotide Content



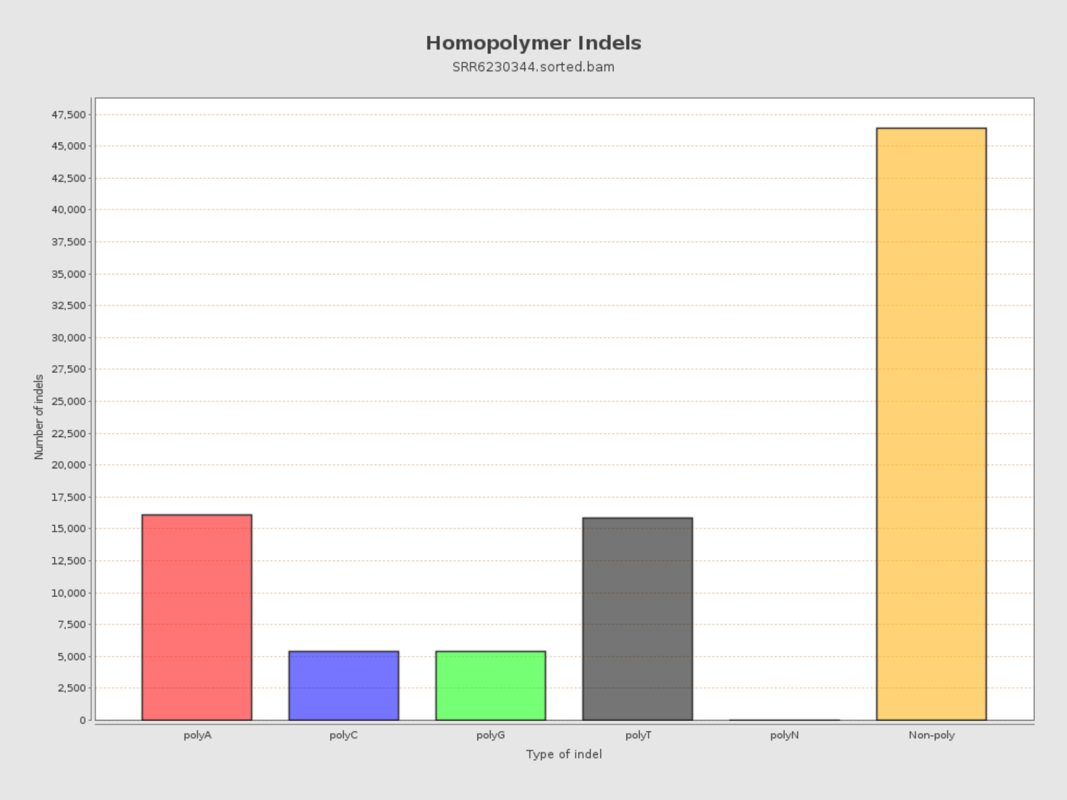
9. Results : Mapped Reads GC-content Distribution



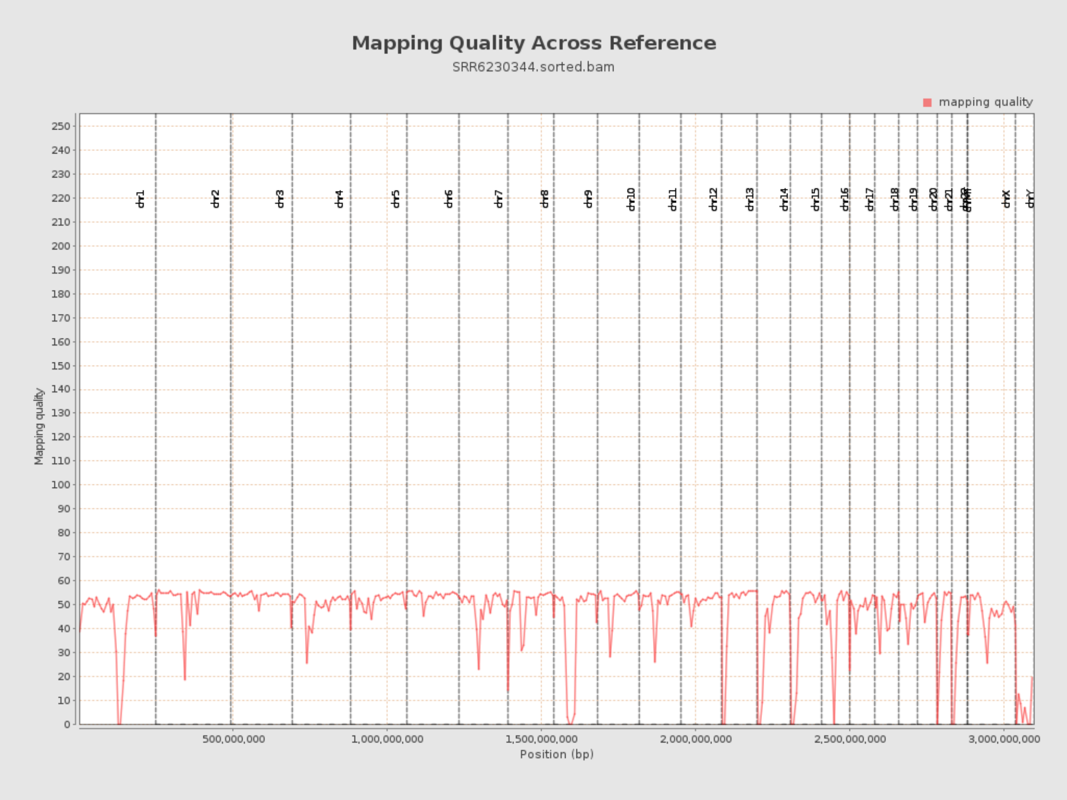
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram