Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:50:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013330.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_SRR6013330 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013330.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:50:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013330.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,361,804
Mapped reads	945,328 / 69.42%
Unmapped reads	416,476 / 30.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,201 / 0.16%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	70,786 / 5.2%
Duplication rate	6.52%
Clipped reads	795,367 / 58.41%

2.2. ACGT Content

Number/percentage of A's	13,917,054 / 26.01%
Number/percentage of C's	7,716,590 / 14.42%
Number/percentage of T's	18,065,132 / 33.76%
Number/percentage of G's	13,789,329 / 25.77%
Number/percentage of N's	16,552 / 0.03%
GC Percentage	40.19%

2.3. Coverage

Mean	0.0173

Standard Deviation	0.1657

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

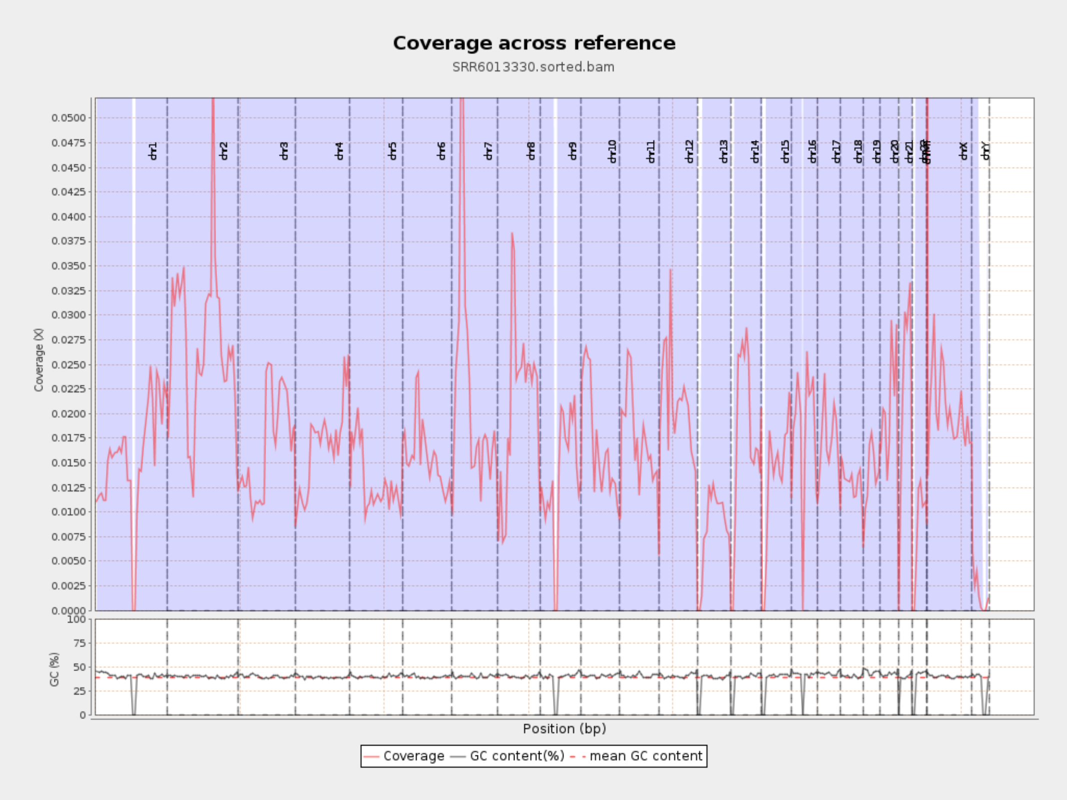
General error rate	1.06%
Mismatches	560,309
Insertions	2,970
Mapped reads with at least one insertion	0.31%
Deletions	13,932
Mapped reads with at least one deletion	1.46%
Homopolymer indels	51.18%

2.6. Chromosome stats

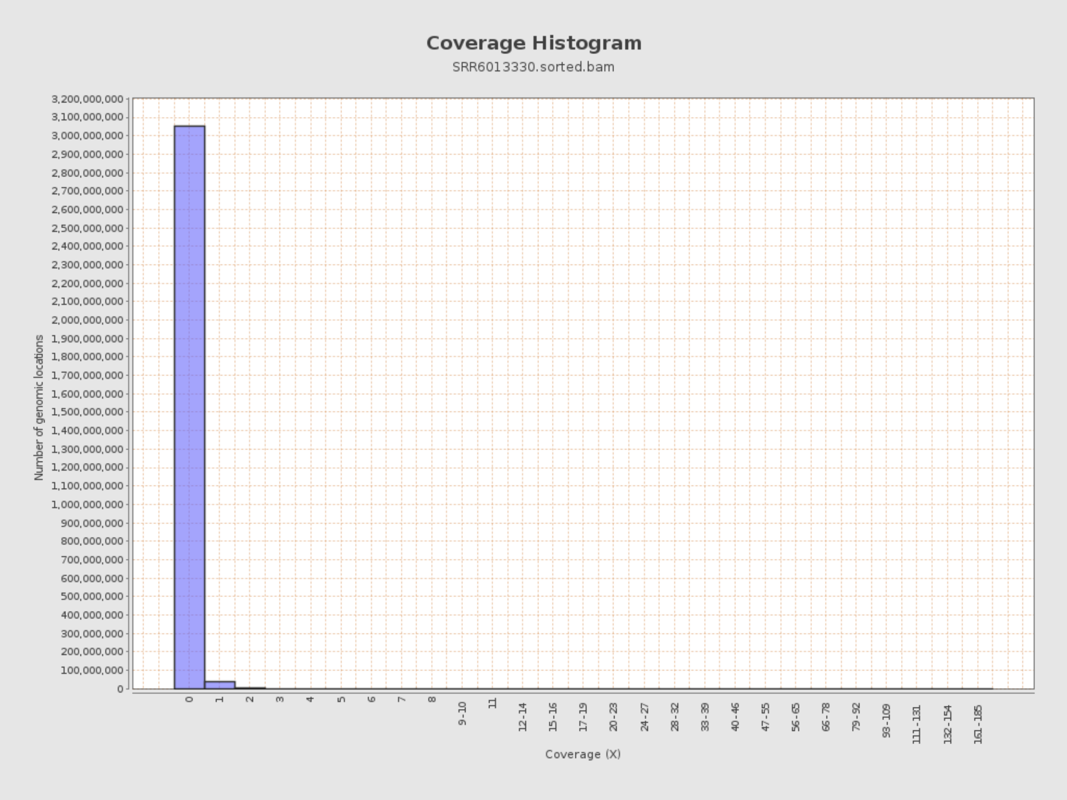
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3904515	0.0157	0.1702
chr2	243199373	6691179	0.0275	0.2166
chr3	198022430	3297842	0.0167	0.1487
chr4	191154276	3203946	0.0168	0.1543
chr5	180915260	2378786	0.0131	0.1342
chr6	171115067	2683579	0.0157	0.159
chr7	159138663	3543815	0.0223	0.2333

chr8	146364022	3103465	0.0212	0.1905
chr9	141213431	1926213	0.0136	0.146
chr10	135534747	2334241	0.0172	0.1603
chr11	135006516	2357727	0.0175	0.1574
chr12	133851895	2817410	0.021	0.1691
chr13	115169878	966753	0.0084	0.1045
chr14	107349540	1918756	0.0179	0.1568
chr15	102531392	1373925	0.0134	0.14
chr16	90354753	1649238	0.0183	0.1575
chr17	81195210	1399652	0.0172	0.1556
chr18	78077248	1033395	0.0132	0.1601
chr19	59128983	828252	0.014	0.1511
chr20	63025520	1303780	0.0207	0.1705
chr21	48129895	1102410	0.0229	0.1803
chr22	51304566	424721	0.0083	0.1021
chrMT	16571	7705	0.465	1.0895
chrX	155270560	3172555	0.0204	0.1724
chrY	59373566	102825	0.0017	0.0481

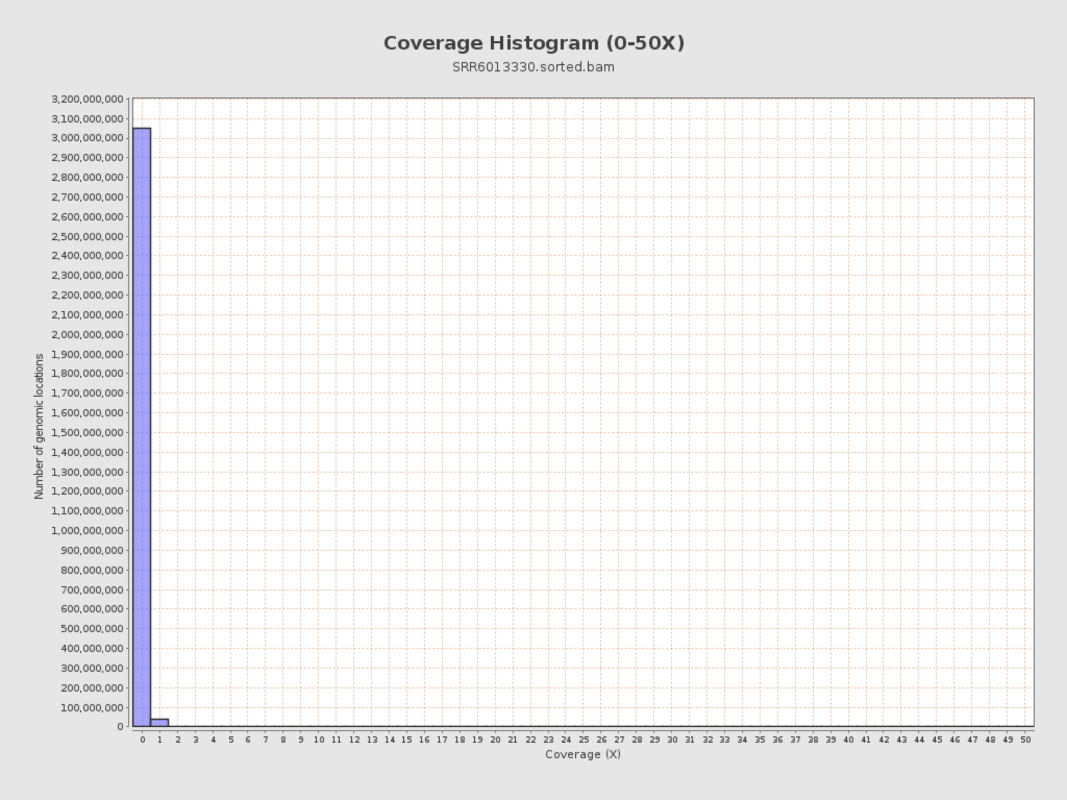
3. Results : Coverage across reference



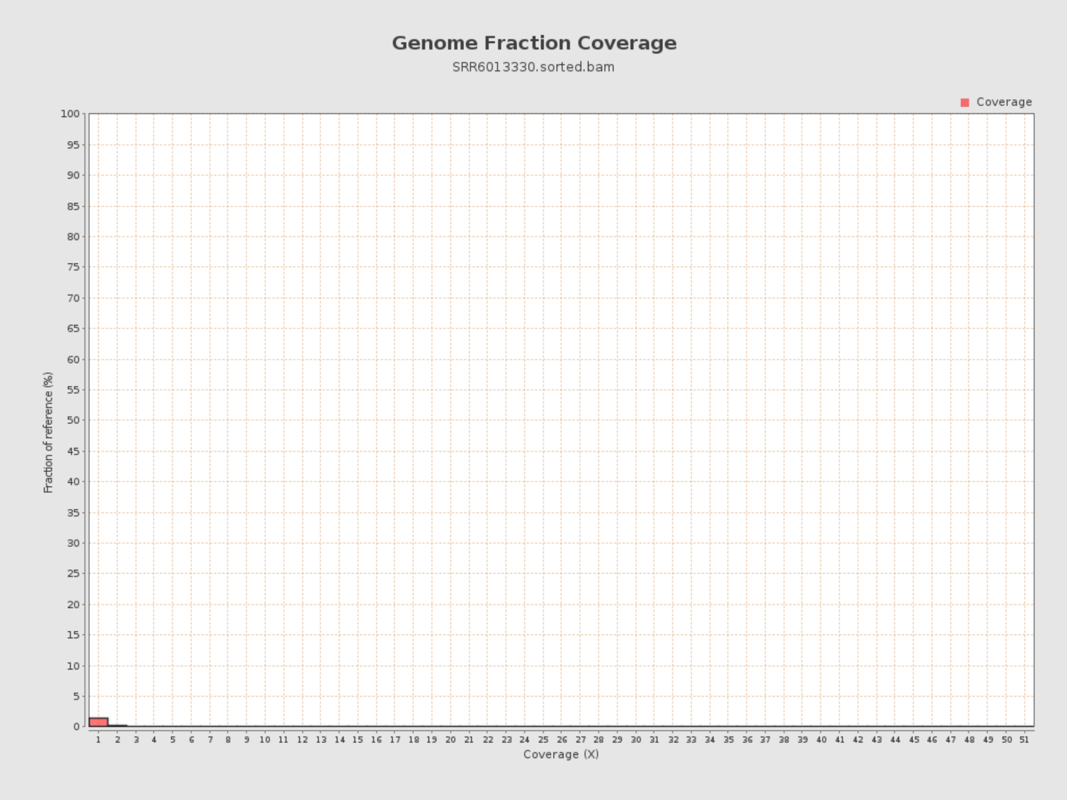
4. Results : Coverage Histogram



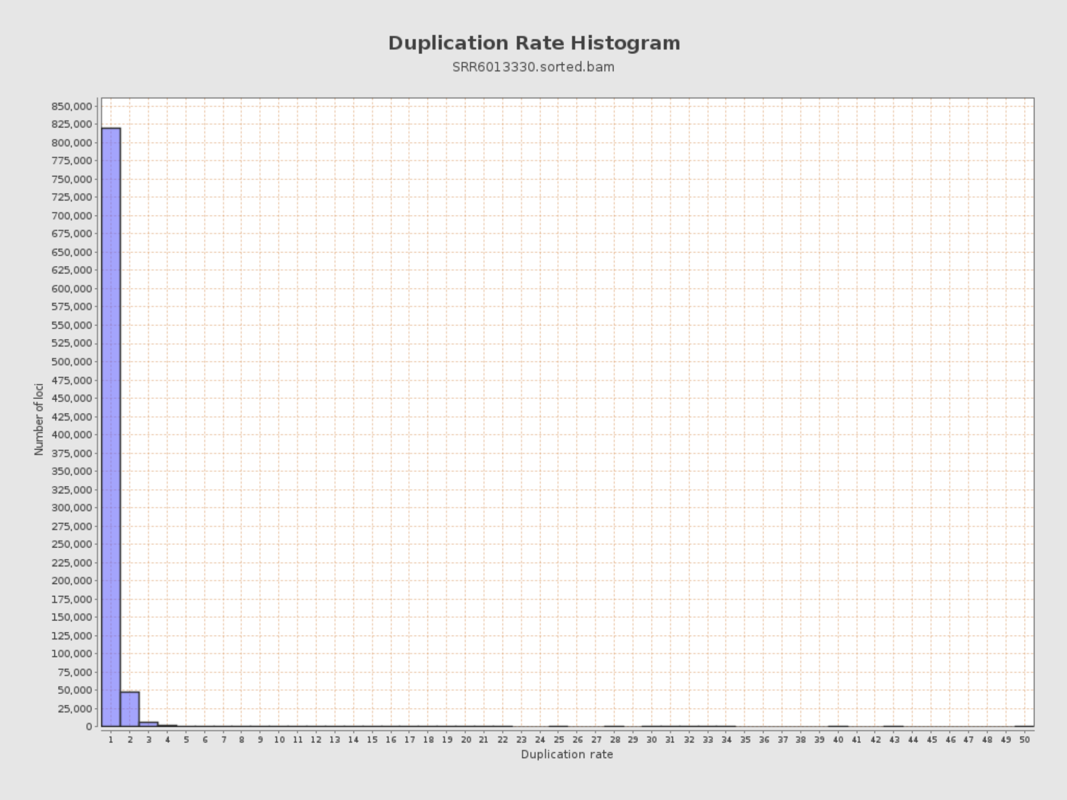
5. Results : Coverage Histogram (0-50X)



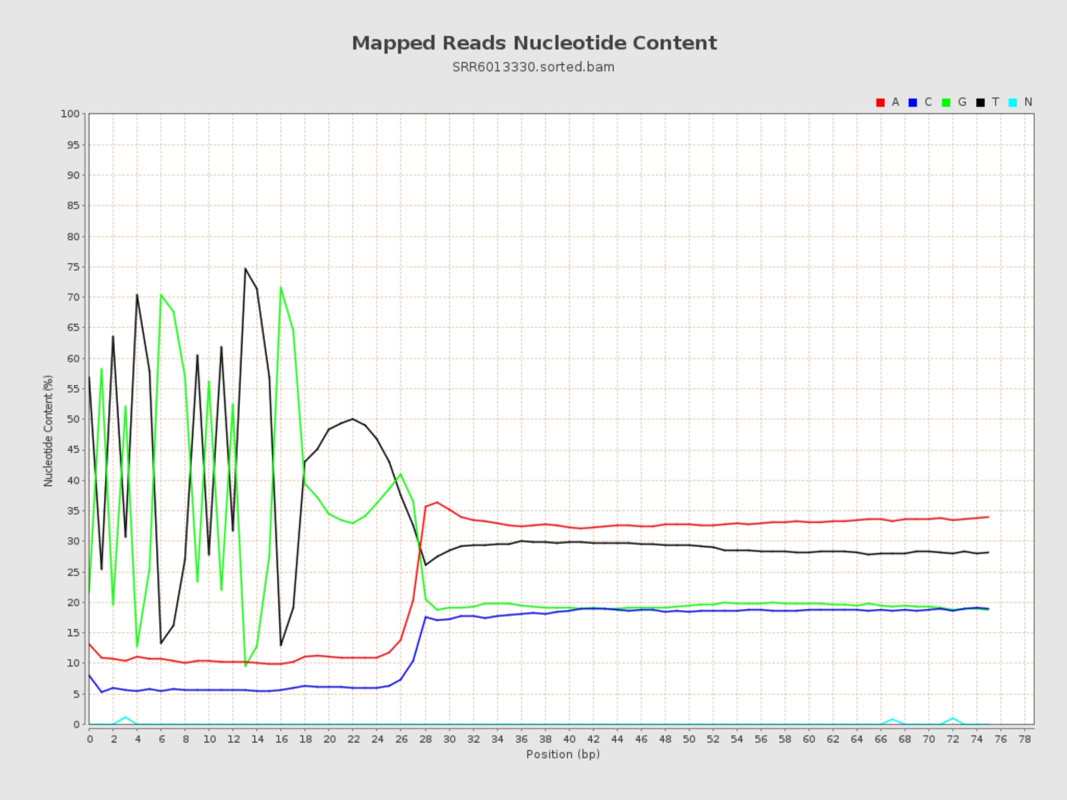
6. Results : Genome Fraction Coverage



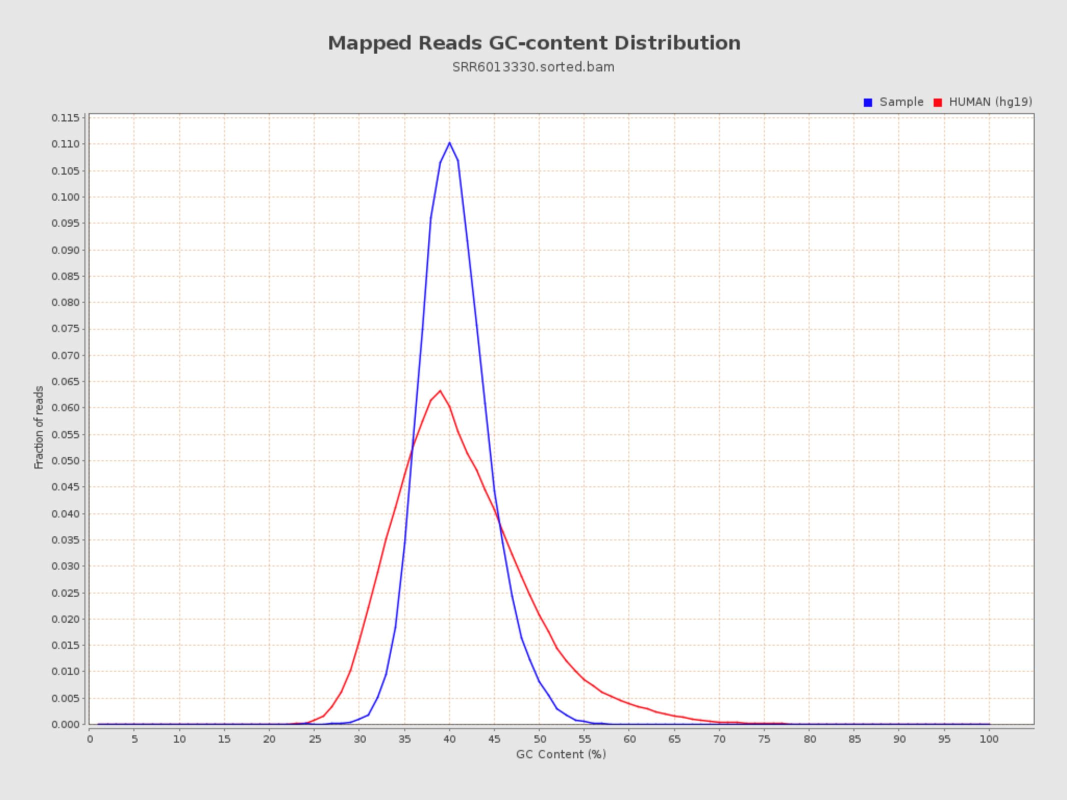
7. Results : Duplication Rate Histogram



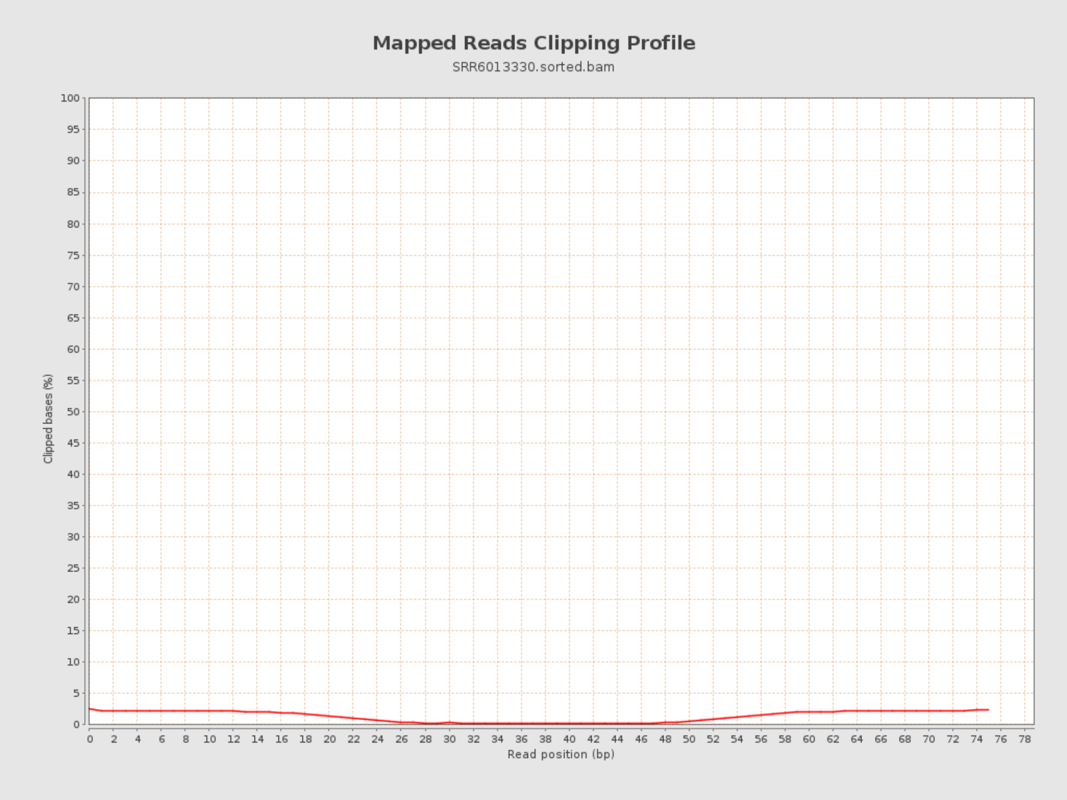
8. Results : Mapped Reads Nucleotide Content



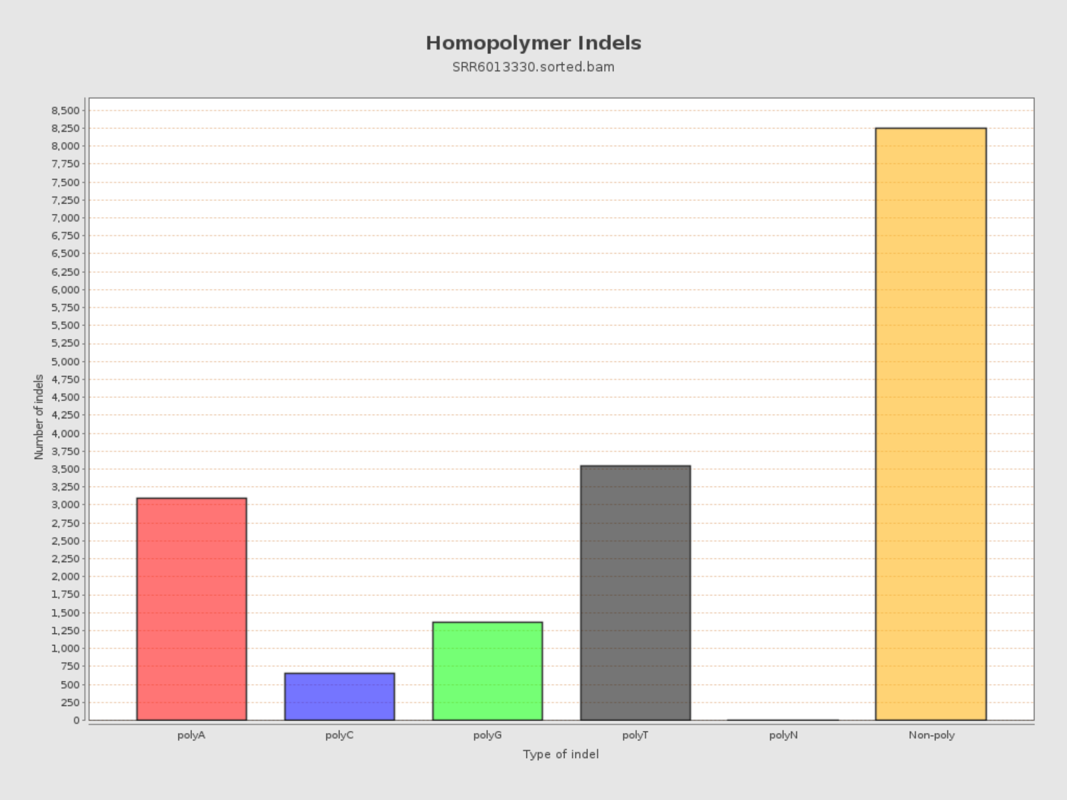
9. Results : Mapped Reads GC-content Distribution



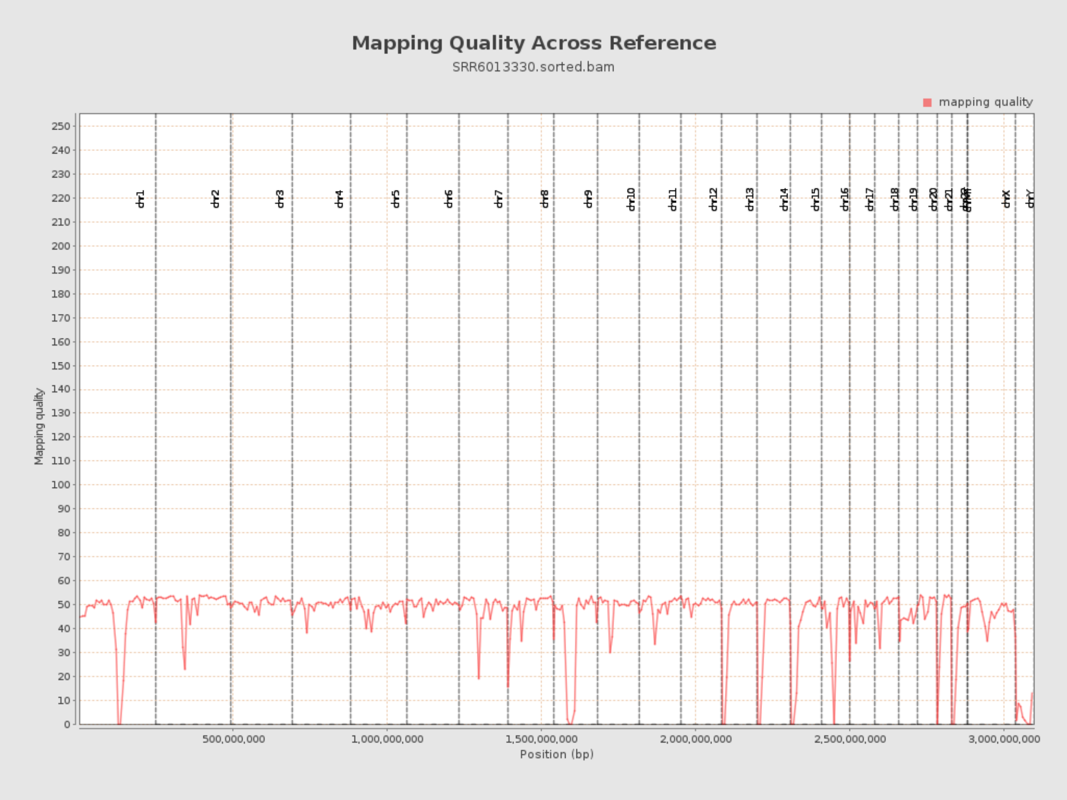
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram