Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:01:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013313.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_SRR6013313 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013313.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:01:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013313.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,454,104
Mapped reads	1,179,884 / 81.14%
Unmapped reads	274,220 / 18.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,243 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	58,695 / 4.04%
Duplication rate	4.23%
Clipped reads	651,022 / 44.77%

2.2. ACGT Content

Number/percentage of A's	20,025,183 / 26.5%
Number/percentage of C's	14,151,725 / 18.73%
Number/percentage of T's	23,744,542 / 31.42%
Number/percentage of G's	17,645,895 / 23.35%
Number/percentage of N's	9,073 / 0.01%
GC Percentage	42.07%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2375

2.4. Mapping Quality

Mean Mapping Quality	45.33

2.5. Mismatches and indels

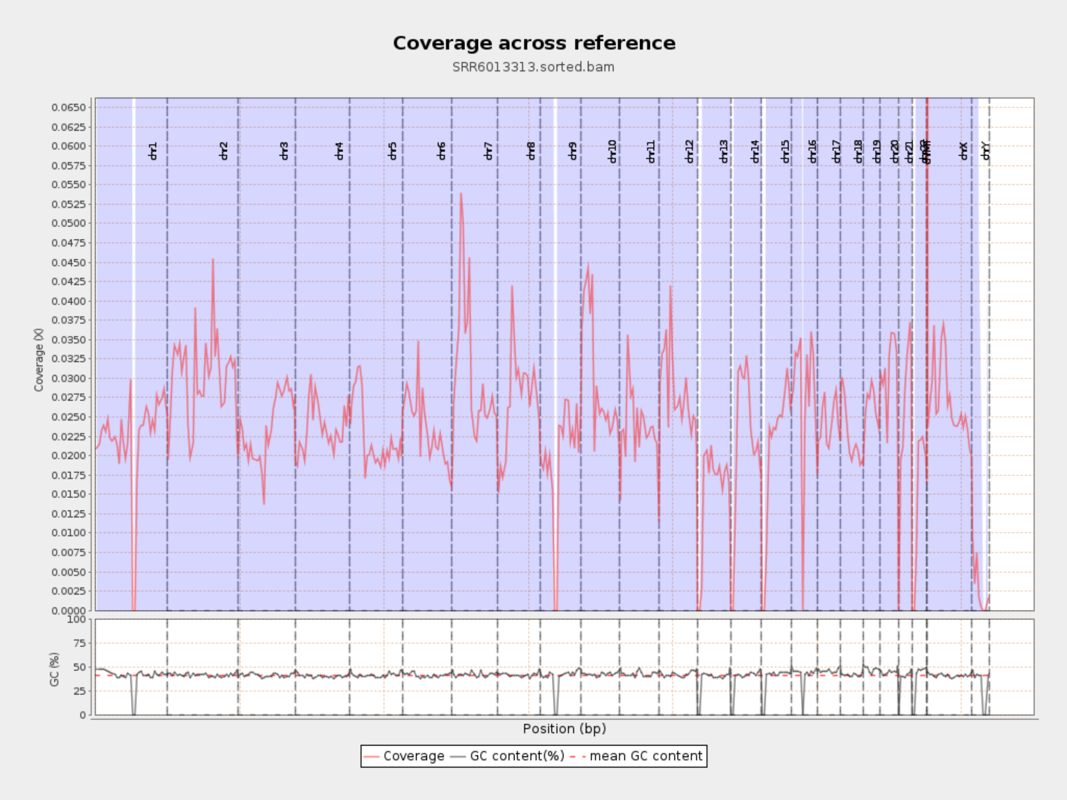
General error rate	0.78%
Mismatches	577,351
Insertions	4,825
Mapped reads with at least one insertion	0.41%
Deletions	19,545
Mapped reads with at least one deletion	1.64%
Homopolymer indels	45.11%

2.6. Chromosome stats

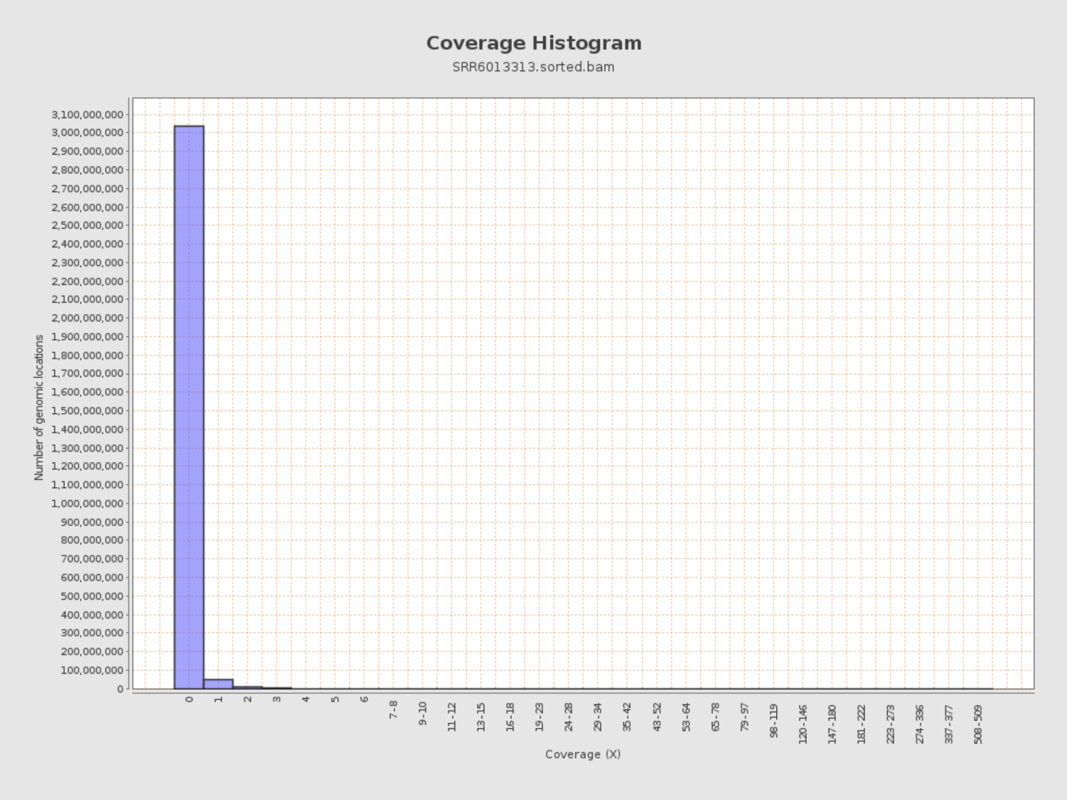
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5534634	0.0222	0.3257
chr2	243199373	7403850	0.0304	0.3111
chr3	198022430	4678668	0.0236	0.1827
chr4	191154276	4500753	0.0235	0.1843
chr5	180915260	4079757	0.0226	0.1784
chr6	171115067	4037963	0.0236	0.2182
chr7	159138663	4907531	0.0308	0.3673

chr8	146364022	4006524	0.0274	0.2389
chr9	141213431	2746167	0.0194	0.1943
chr10	135534747	4095936	0.0302	0.2636
chr11	135006516	3237508	0.024	0.2031
chr12	133851895	3845862	0.0287	0.2025
chr13	115169878	1757902	0.0153	0.147
chr14	107349540	2349603	0.0219	0.1815
chr15	102531392	2117566	0.0207	0.1712
chr16	90354753	2499972	0.0277	0.2058
chr17	81195210	1986036	0.0245	0.1954
chr18	78077248	1768413	0.0226	0.2864
chr19	59128983	1569568	0.0265	0.2828
chr20	63025520	1952328	0.031	0.213
chr21	48129895	1237132	0.0257	0.1941
chr22	51304566	758647	0.0148	0.1434
chrMT	16571	158272	9.5511	6.619
chrX	155270560	4216656	0.0272	0.2071
chrY	59373566	162829	0.0027	0.068

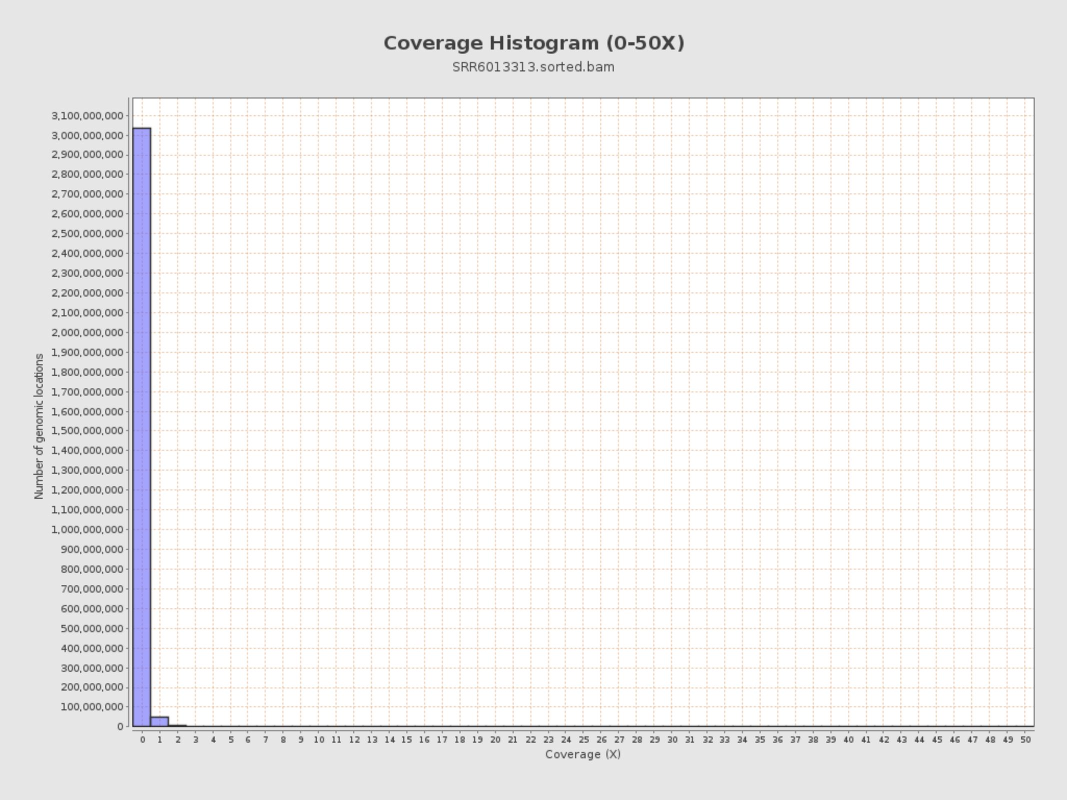
3. Results : Coverage across reference



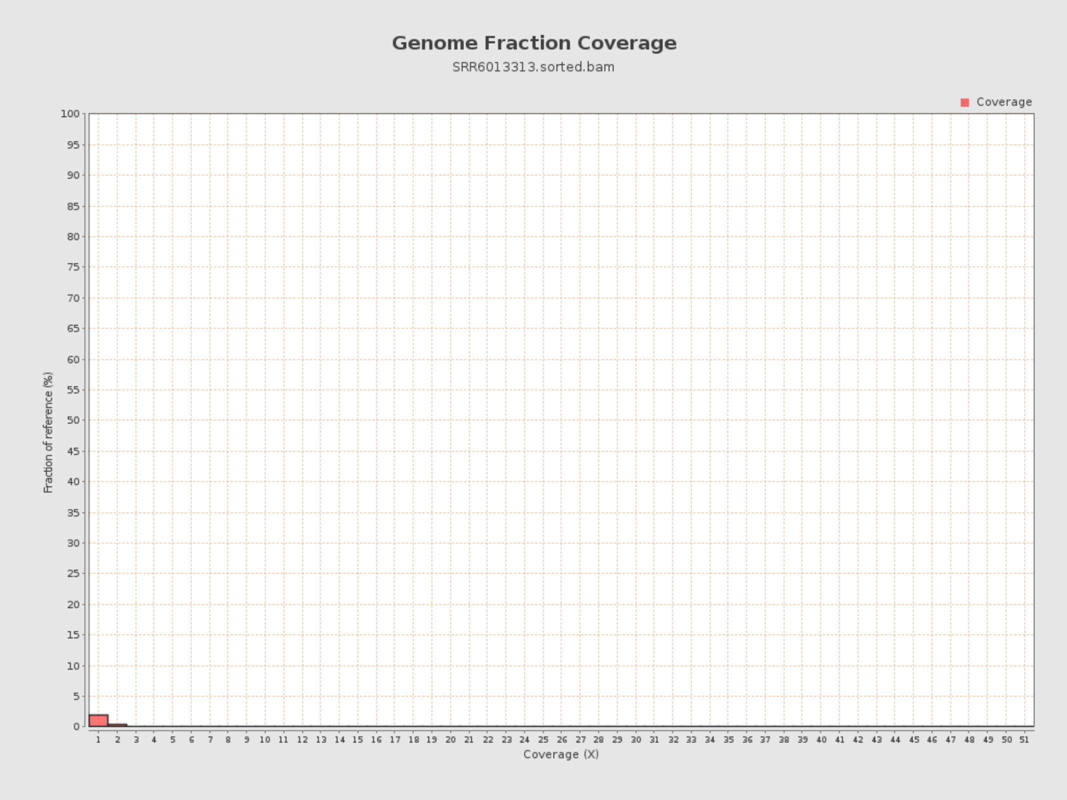
4. Results : Coverage Histogram



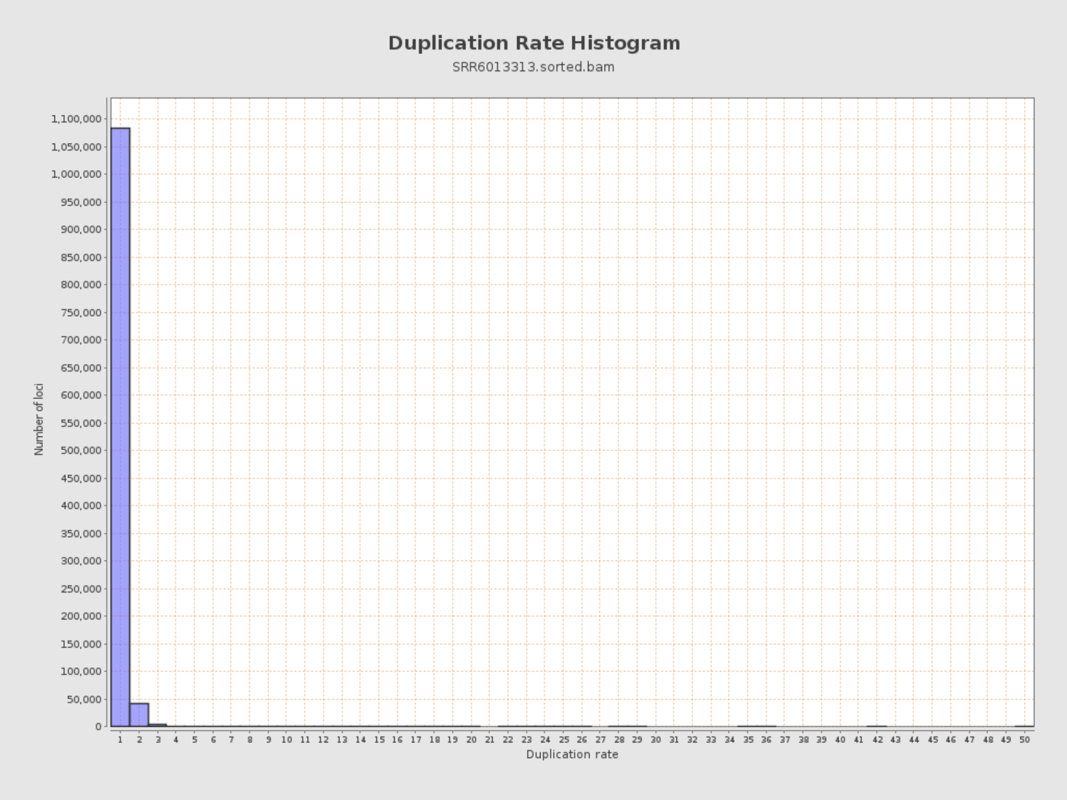
5. Results : Coverage Histogram (0-50X)



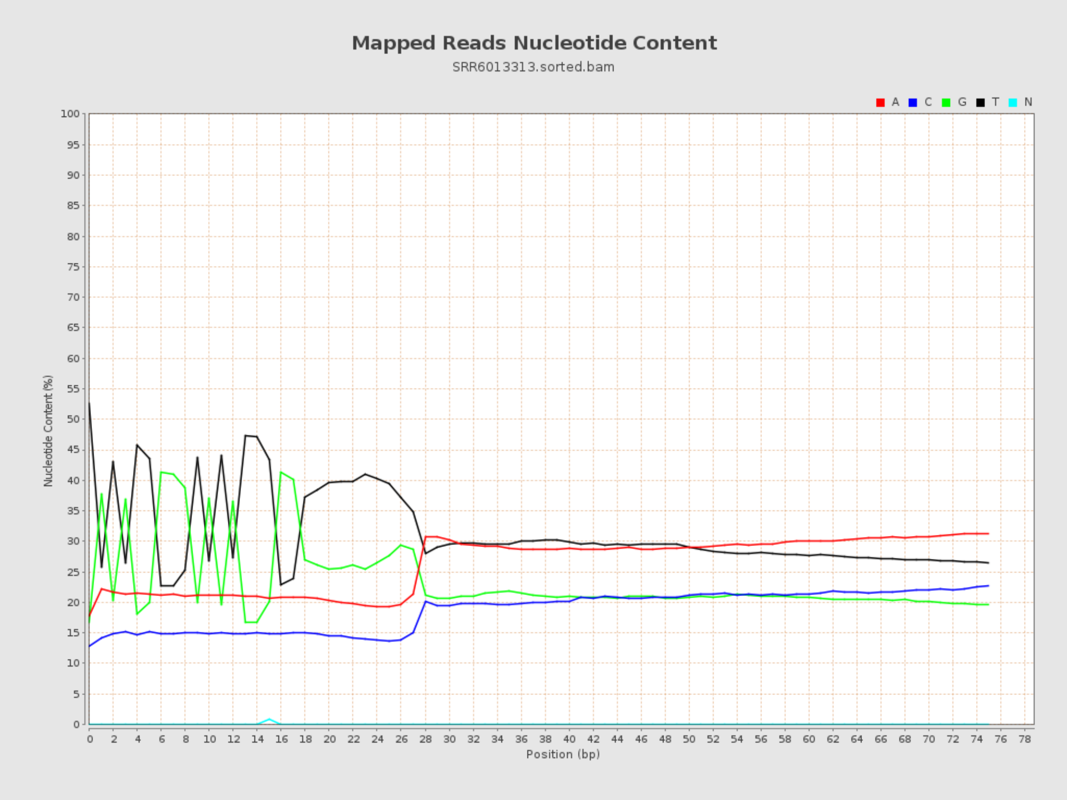
6. Results : Genome Fraction Coverage



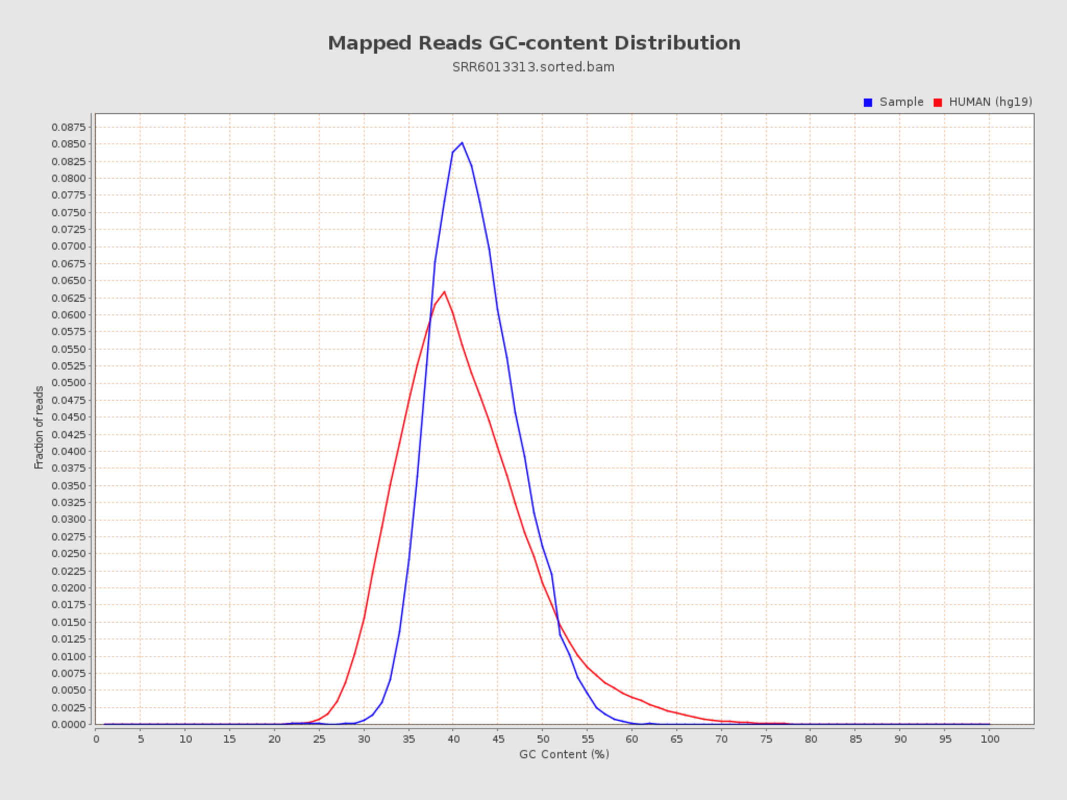
7. Results : Duplication Rate Histogram



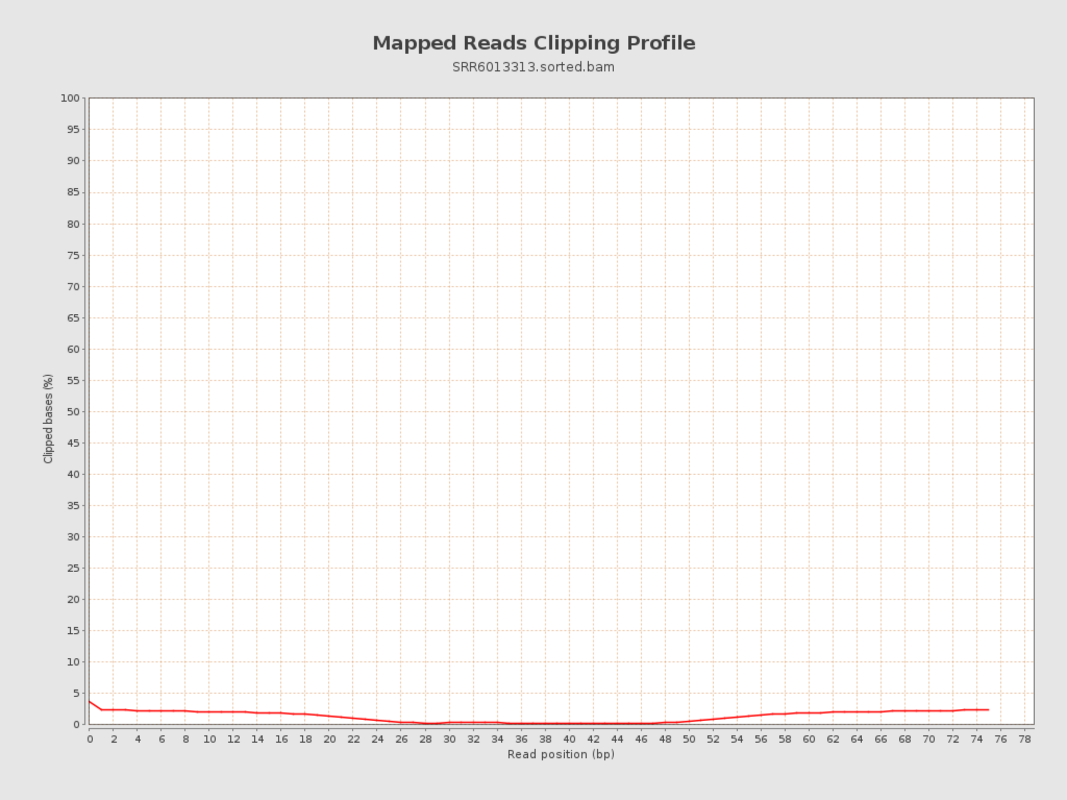
8. Results : Mapped Reads Nucleotide Content



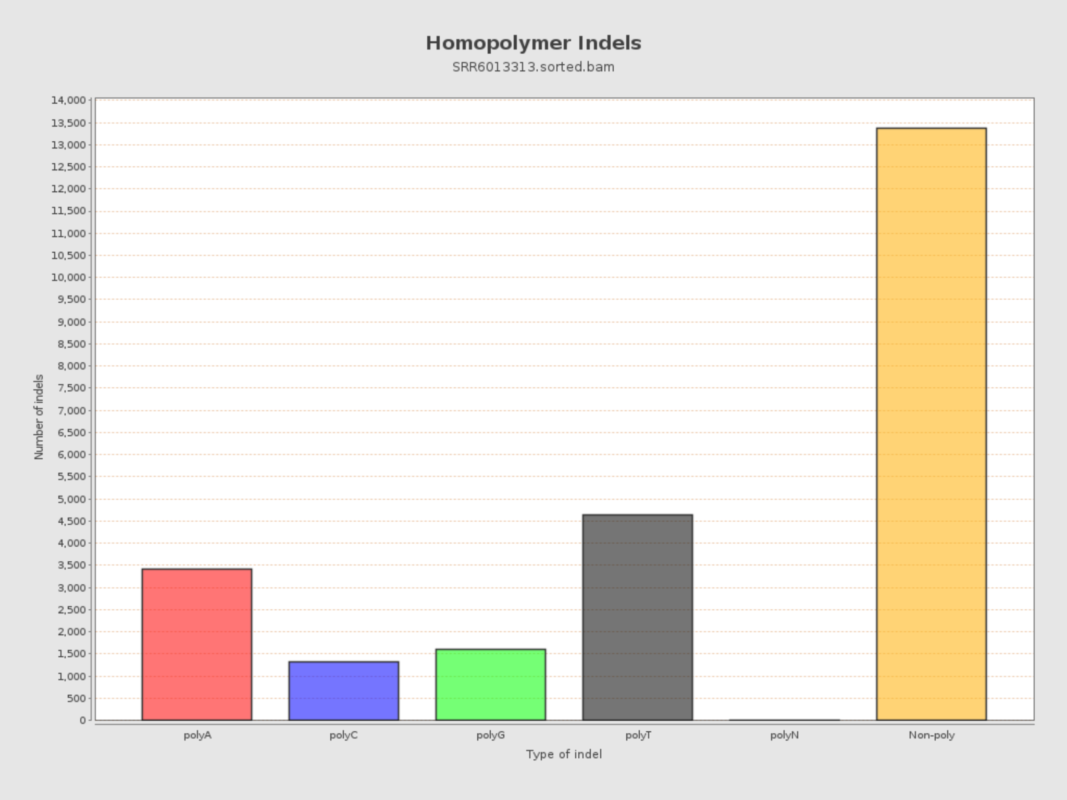
9. Results : Mapped Reads GC-content Distribution



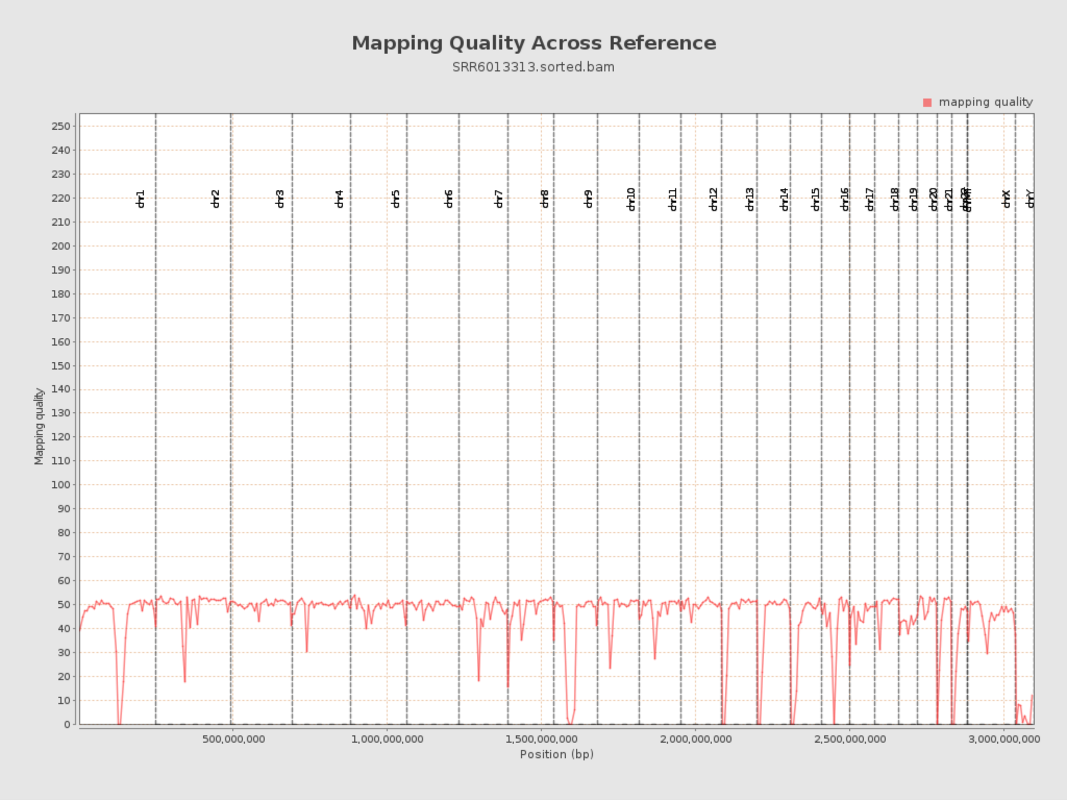
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram