Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:05:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013314.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_SRR6013314 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013314.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:05:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013314.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,529,761
Mapped reads	2,292,681 / 90.63%
Unmapped reads	237,080 / 9.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,611 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	79,218 / 3.13%
Duplication rate	2.64%
Clipped reads	1,105,173 / 43.69%

2.2. ACGT Content

Number/percentage of A's	41,269,423 / 27.36%
Number/percentage of C's	28,726,435 / 19.04%
Number/percentage of T's	46,235,284 / 30.65%
Number/percentage of G's	34,583,420 / 22.93%
Number/percentage of N's	37,237 / 0.02%
GC Percentage	41.97%

2.3. Coverage

Mean	0.0487

Standard Deviation	0.3703

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Mismatches and indels

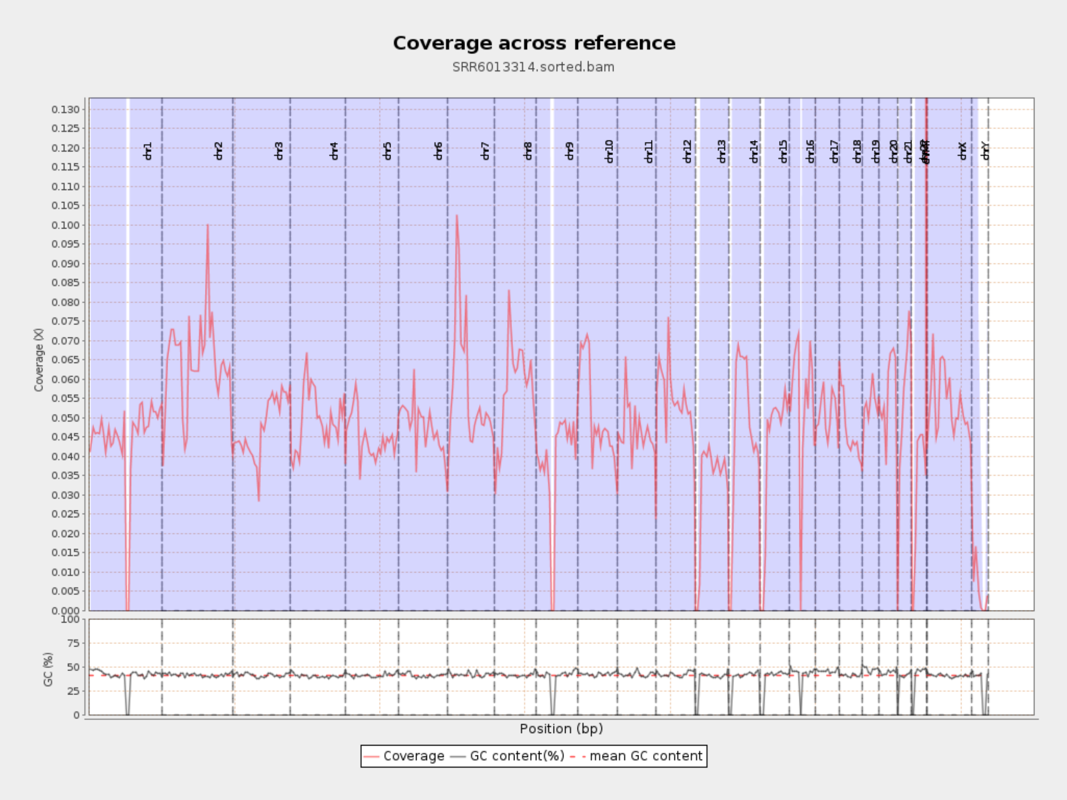
General error rate	0.77%
Mismatches	1,138,404
Insertions	10,498
Mapped reads with at least one insertion	0.45%
Deletions	34,497
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.13%

2.6. Chromosome stats

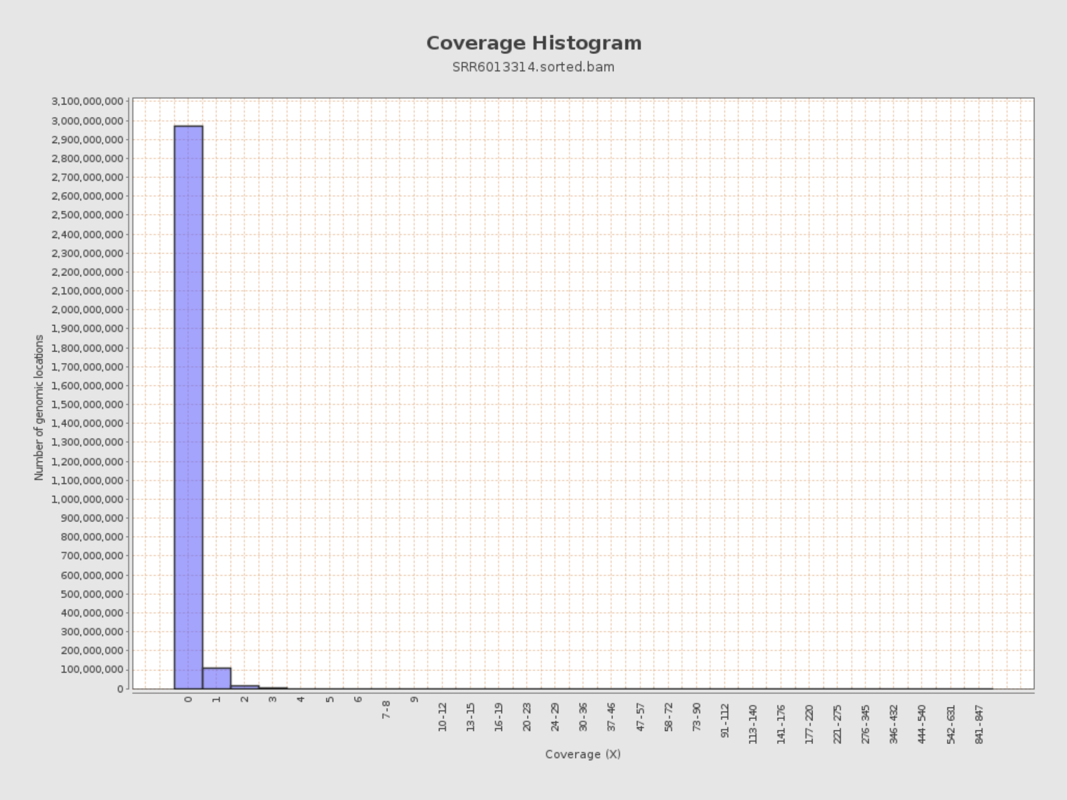
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11027656	0.0442	0.4647
chr2	243199373	15589772	0.0641	0.5114
chr3	198022430	9400440	0.0475	0.2489
chr4	191154276	9474732	0.0496	0.2668
chr5	180915260	8121477	0.0449	0.243
chr6	171115067	8120806	0.0475	0.2973
chr7	159138663	9255447	0.0582	0.6374

chr8	146364022	8427240	0.0576	0.4527
chr9	141213431	5386103	0.0381	0.3008
chr10	135534747	7021927	0.0518	0.3685
chr11	135006516	6274360	0.0465	0.2995
chr12	133851895	7389772	0.0552	0.2743
chr13	115169878	3698514	0.0321	0.2161
chr14	107349540	4976602	0.0464	0.2625
chr15	102531392	4249012	0.0414	0.2456
chr16	90354753	4891242	0.0541	0.2851
chr17	81195210	4118987	0.0507	0.2831
chr18	78077248	3653994	0.0468	0.5144
chr19	59128983	3153503	0.0533	0.4088
chr20	63025520	3540117	0.0562	0.2766
chr21	48129895	2550187	0.053	0.278
chr22	51304566	1549613	0.0302	0.1973
chrMT	16571	395499	23.8669	25.3308
chrX	155270560	8289527	0.0534	0.28
chrY	59373566	355889	0.006	0.1289

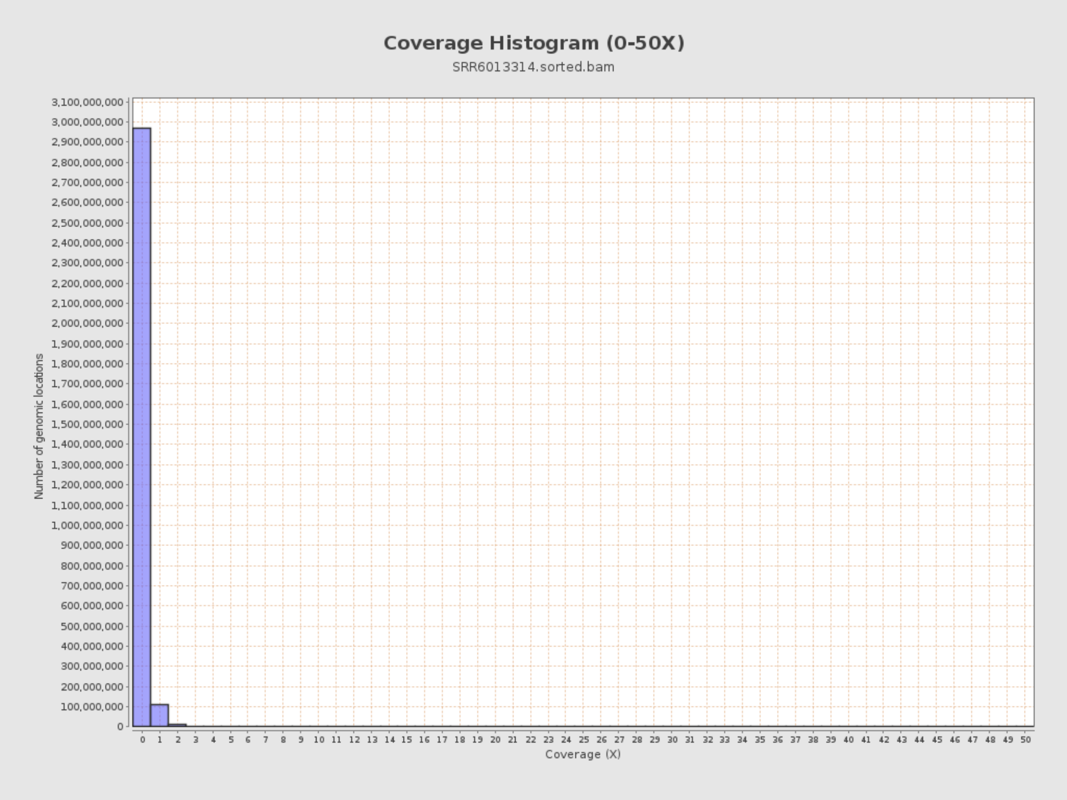
3. Results : Coverage across reference



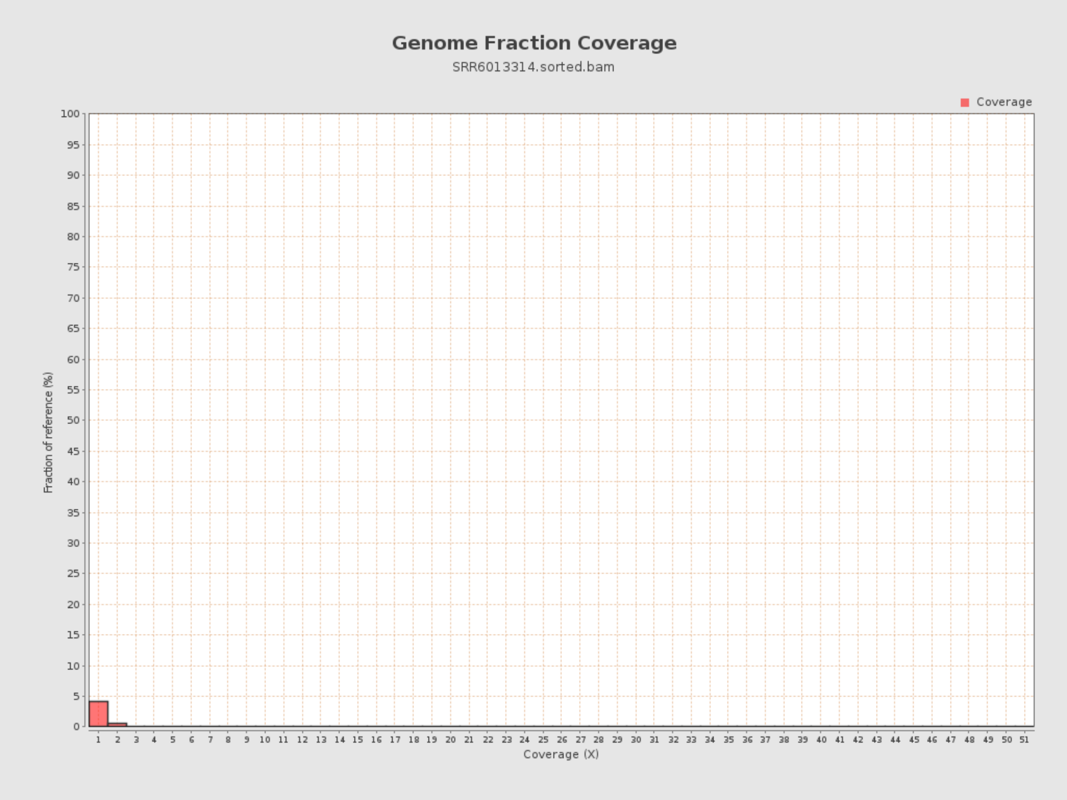
4. Results : Coverage Histogram



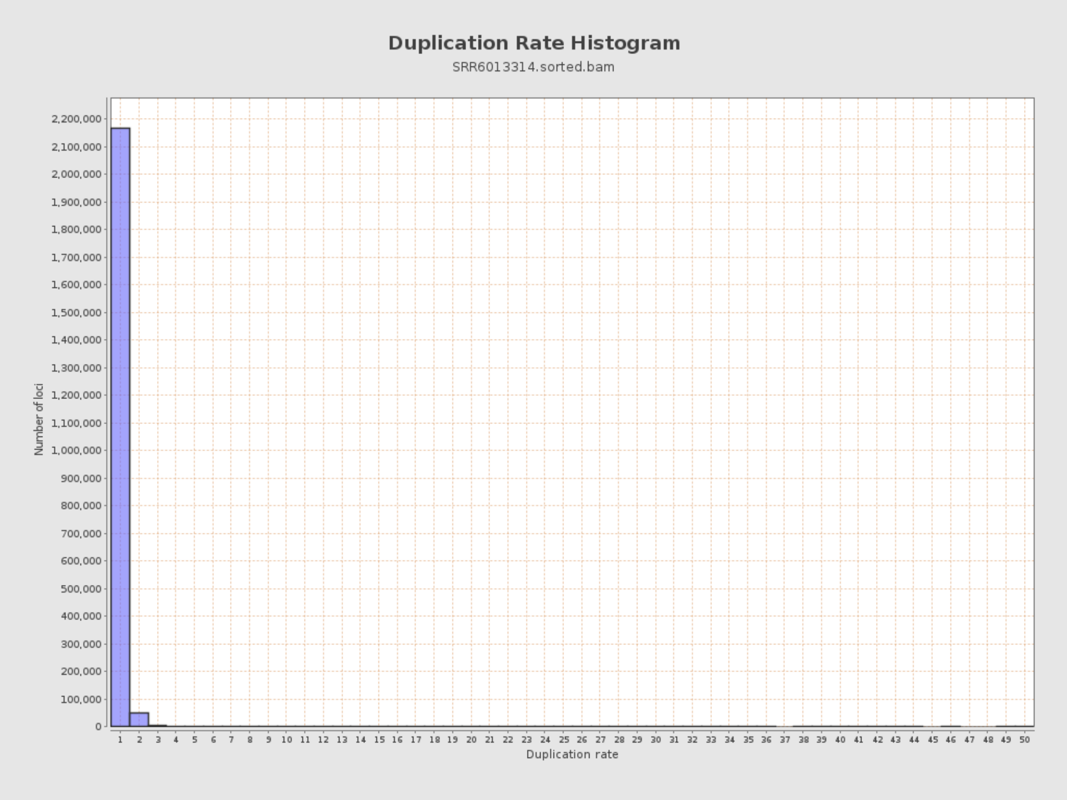
5. Results : Coverage Histogram (0-50X)



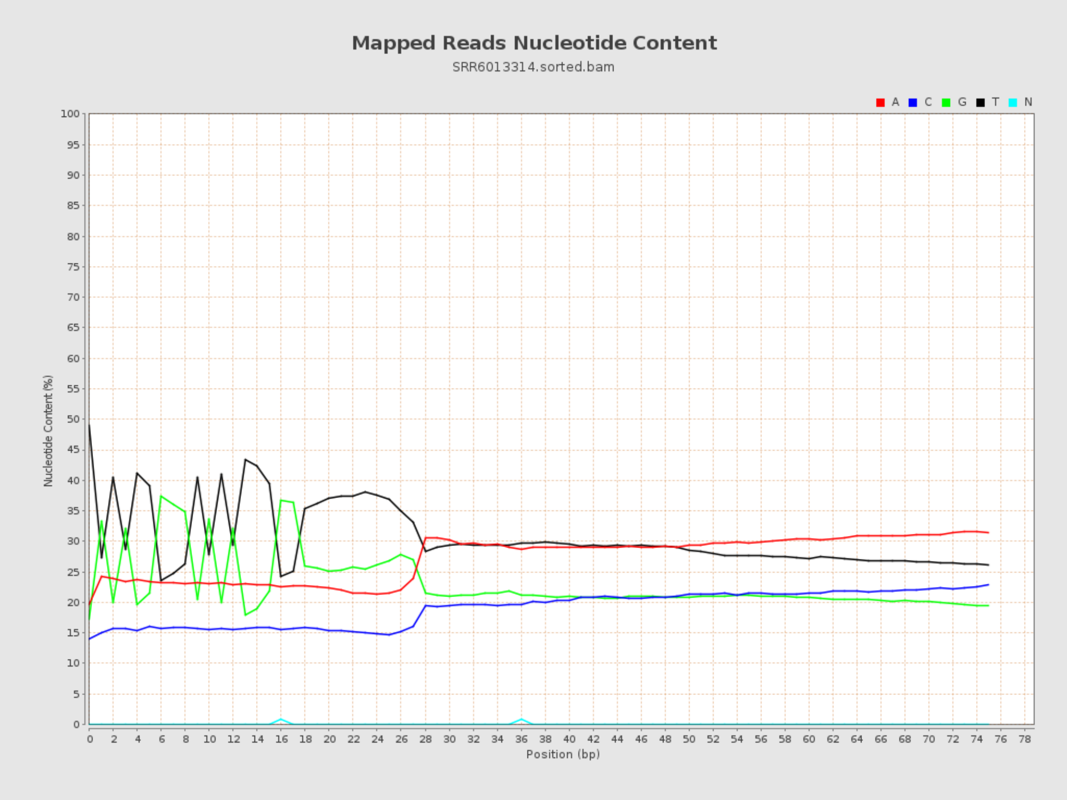
6. Results : Genome Fraction Coverage



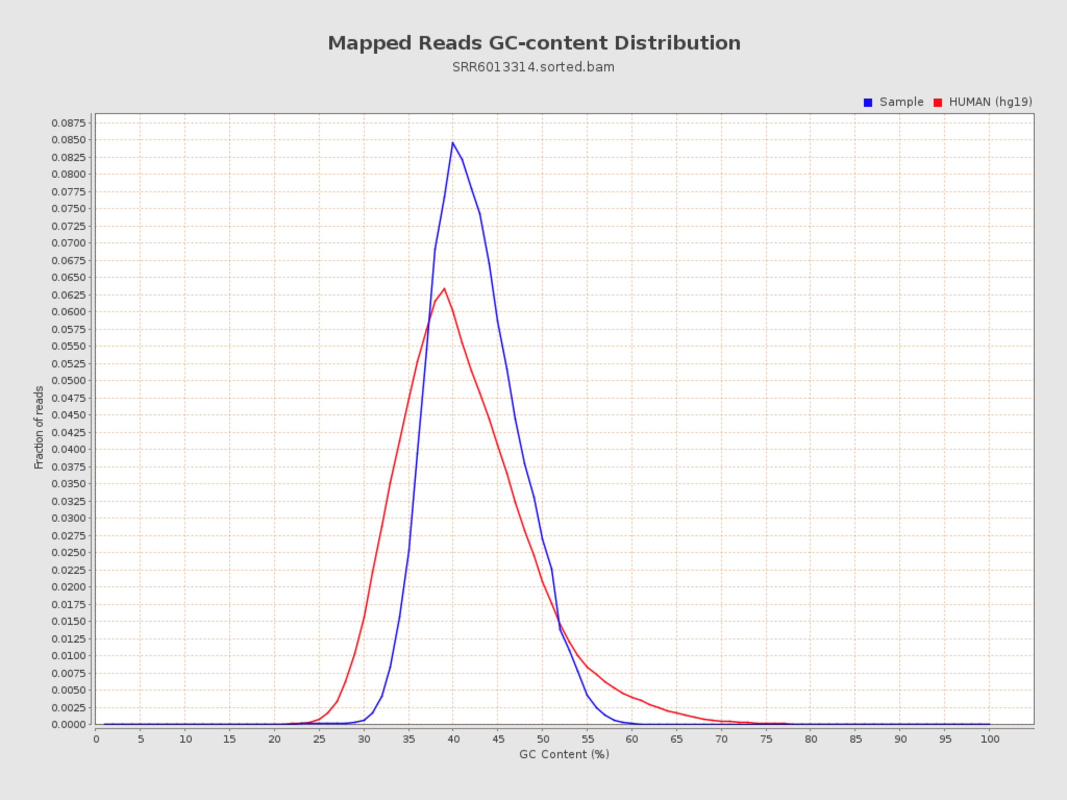
7. Results : Duplication Rate Histogram



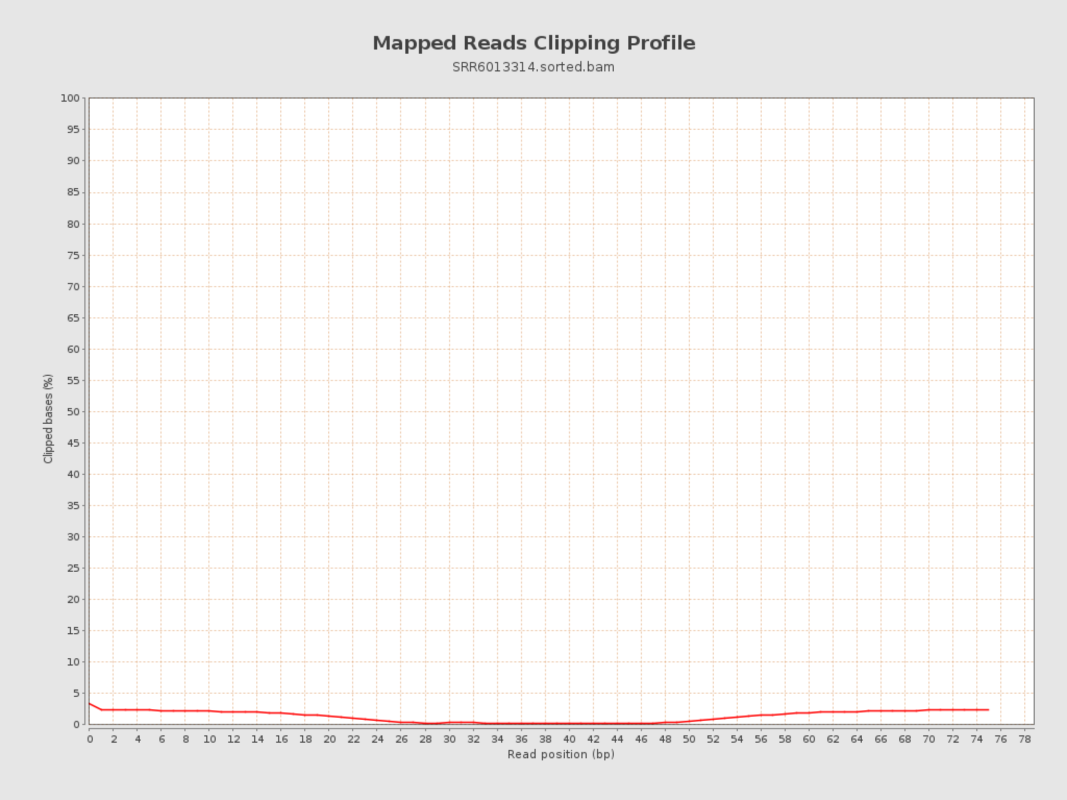
8. Results : Mapped Reads Nucleotide Content



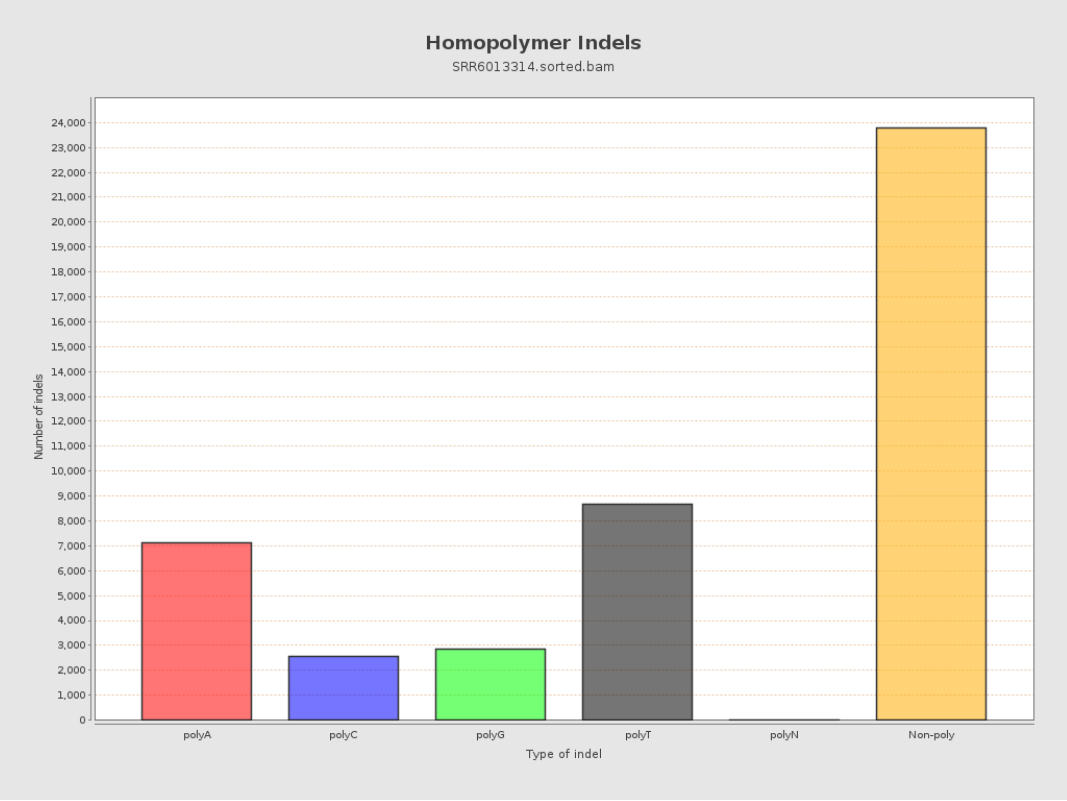
9. Results : Mapped Reads GC-content Distribution



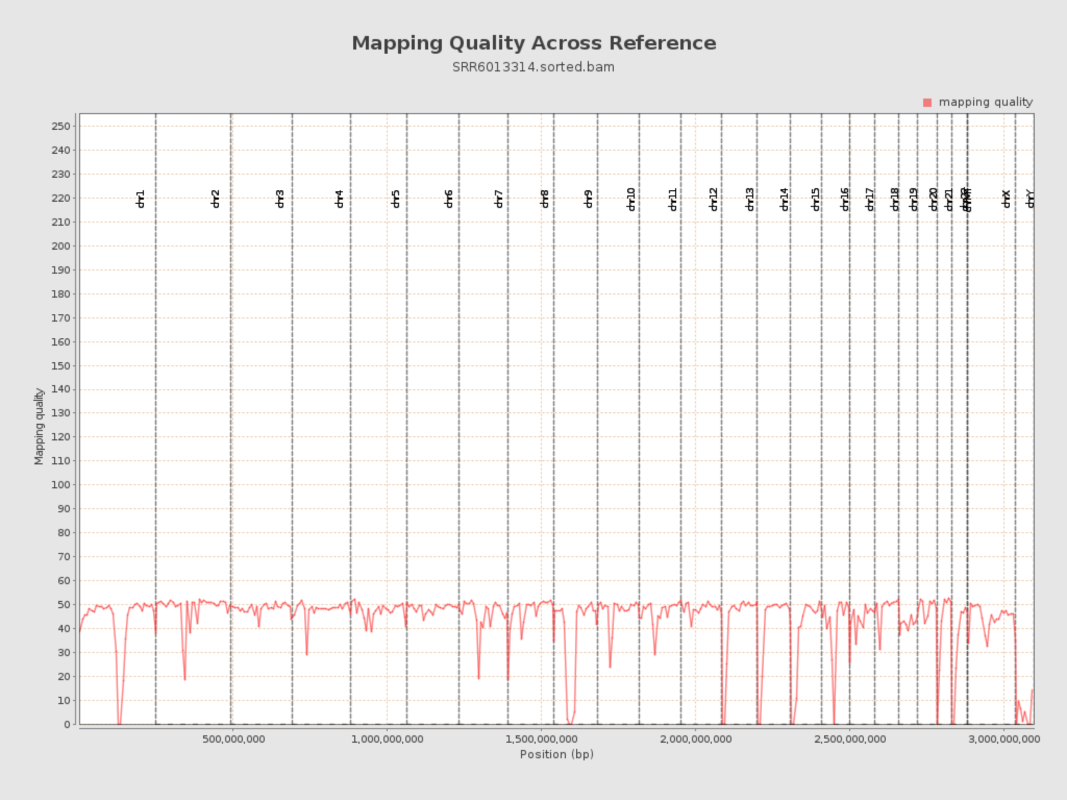
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram