Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:40:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013306.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_SRR6013306 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013306.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:40:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013306.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,366,524
Mapped reads	2,126,523 / 89.86%
Unmapped reads	240,001 / 10.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,063 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	80,372 / 3.4%
Duplication rate	3%
Clipped reads	1,031,475 / 43.59%

2.2. ACGT Content

Number/percentage of A's	37,873,801 / 27.14%
Number/percentage of C's	26,735,529 / 19.16%
Number/percentage of T's	42,942,704 / 30.77%
Number/percentage of G's	31,976,178 / 22.91%
Number/percentage of N's	32,231 / 0.02%
GC Percentage	42.07%

2.3. Coverage

Mean	0.0451

Standard Deviation	0.3522

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

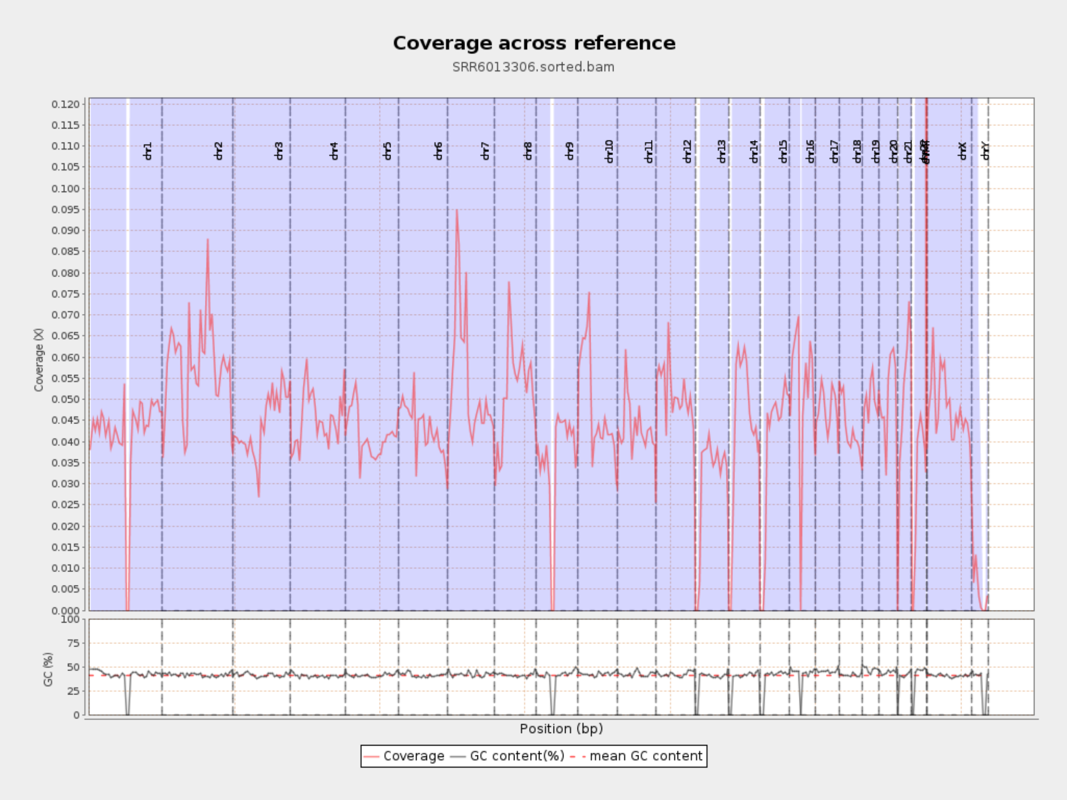
General error rate	0.8%
Mismatches	1,099,581
Insertions	9,290
Mapped reads with at least one insertion	0.43%
Deletions	33,809
Mapped reads with at least one deletion	1.57%
Homopolymer indels	45.27%

2.6. Chromosome stats

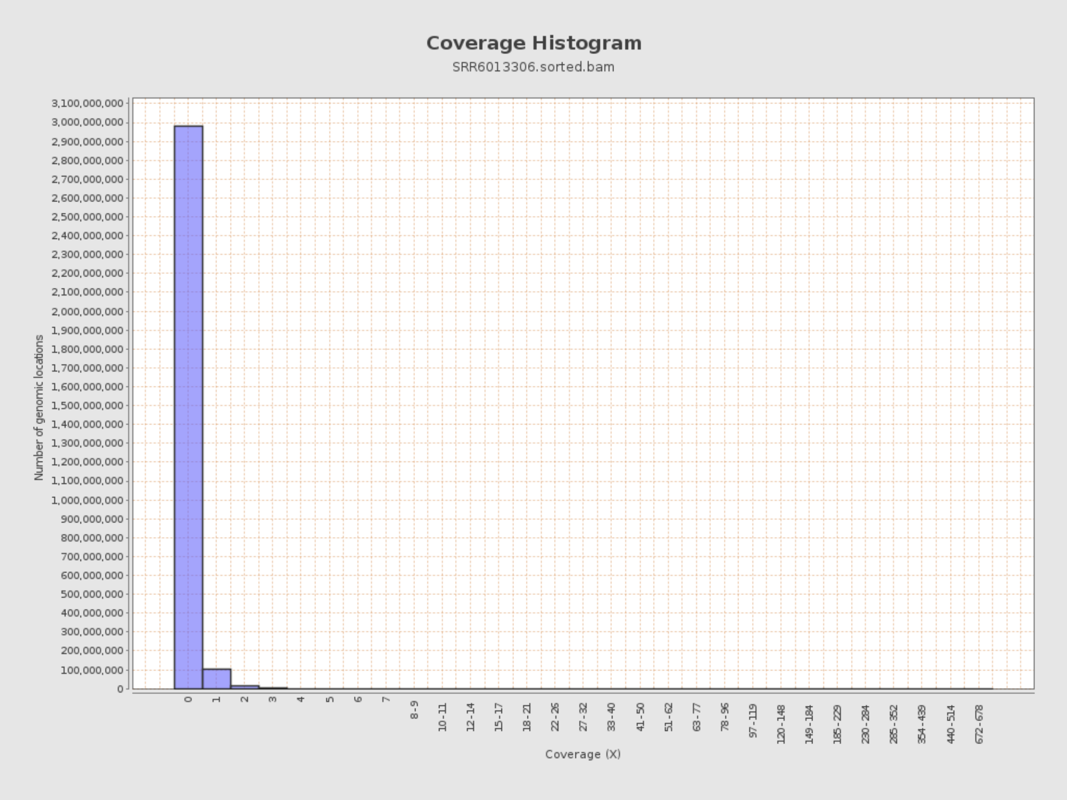
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10382618	0.0417	0.5023
chr2	243199373	14161129	0.0582	0.4608
chr3	198022430	8720847	0.044	0.241
chr4	191154276	8641134	0.0452	0.2513
chr5	180915260	7516110	0.0415	0.235
chr6	171115067	7402989	0.0433	0.2866
chr7	159138663	8714629	0.0548	0.6175

chr8	146364022	7649603	0.0523	0.3459
chr9	141213431	5019536	0.0355	0.2982
chr10	135534747	6619489	0.0488	0.3746
chr11	135006516	5853746	0.0434	0.2819
chr12	133851895	6887728	0.0515	0.2664
chr13	115169878	3509067	0.0305	0.2058
chr14	107349540	4634090	0.0432	0.2548
chr15	102531392	3970699	0.0387	0.2294
chr16	90354753	4731454	0.0524	0.285
chr17	81195210	3843114	0.0473	0.2747
chr18	78077248	3374282	0.0432	0.5022
chr19	59128983	2921645	0.0494	0.4447
chr20	63025520	3179088	0.0504	0.2645
chr21	48129895	2373327	0.0493	0.2679
chr22	51304566	1484735	0.0289	0.1941
chrMT	16571	288848	17.4309	12.2325
chrX	155270560	7436001	0.0479	0.2716
chrY	59373566	303356	0.0051	0.1133

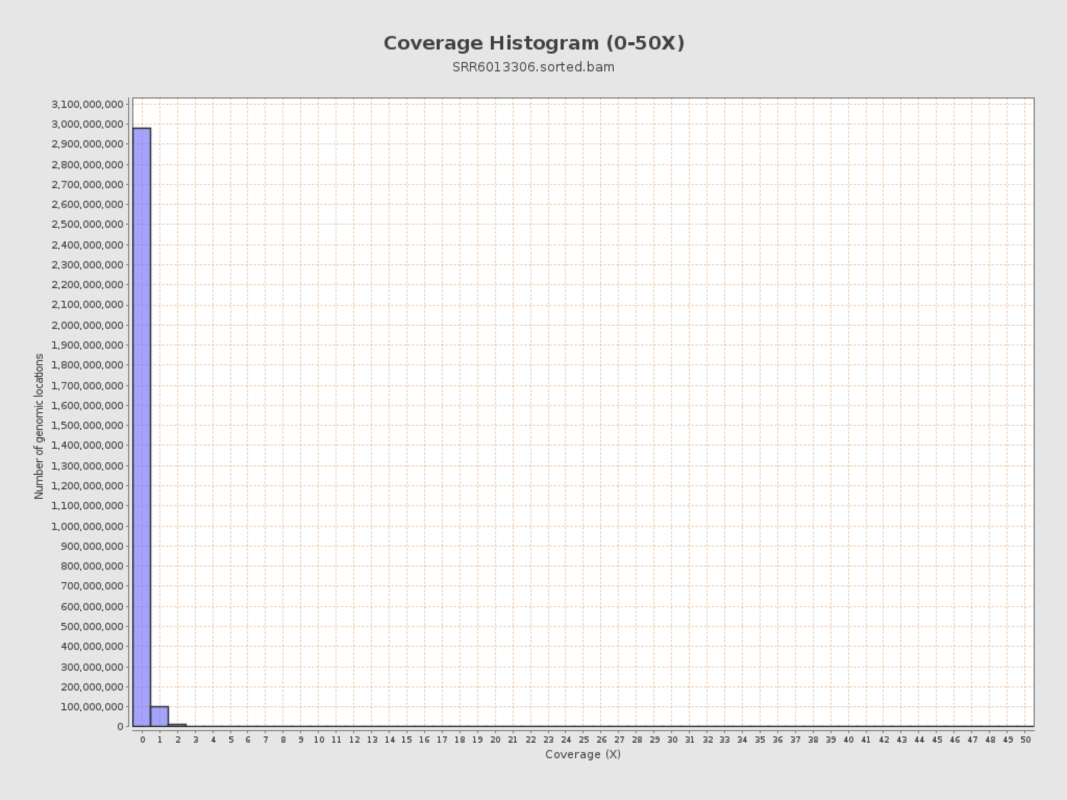
3. Results : Coverage across reference



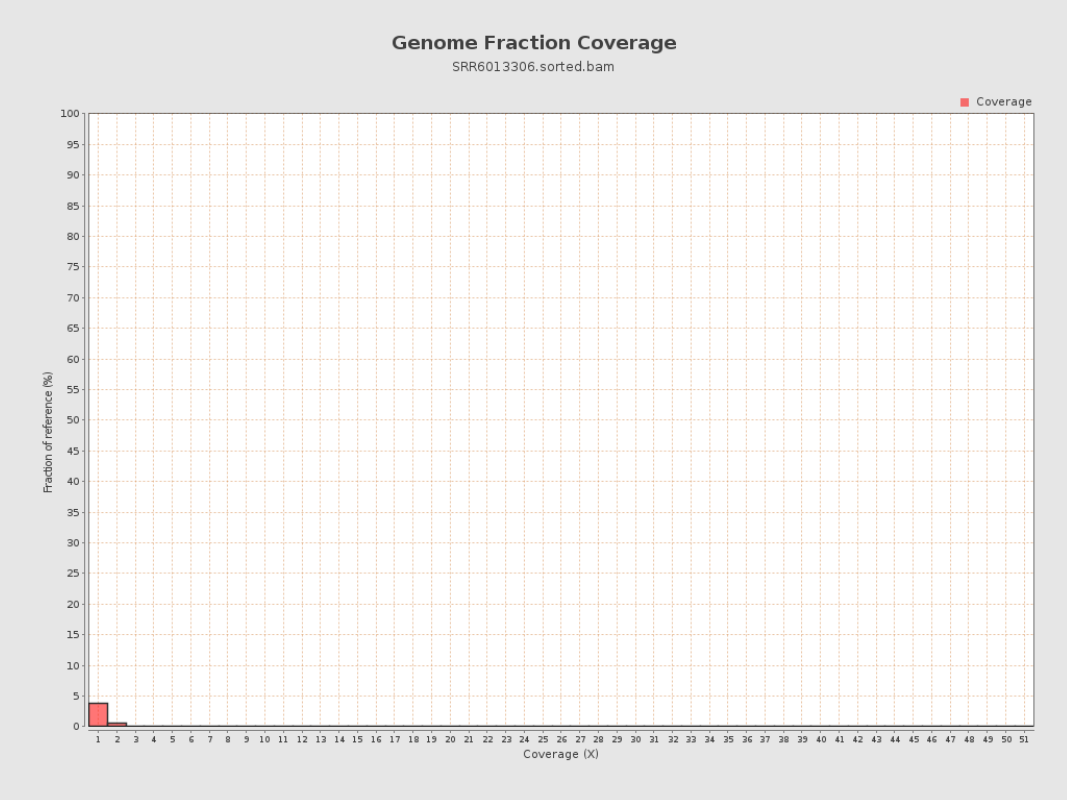
4. Results : Coverage Histogram



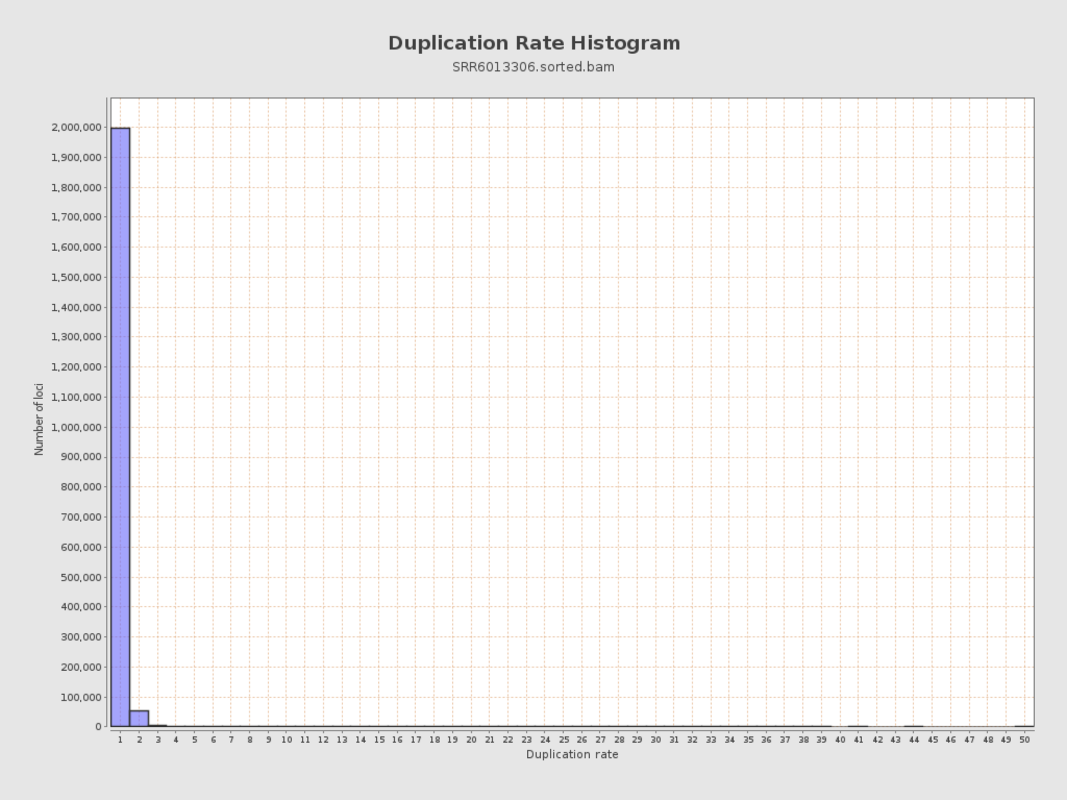
5. Results : Coverage Histogram (0-50X)



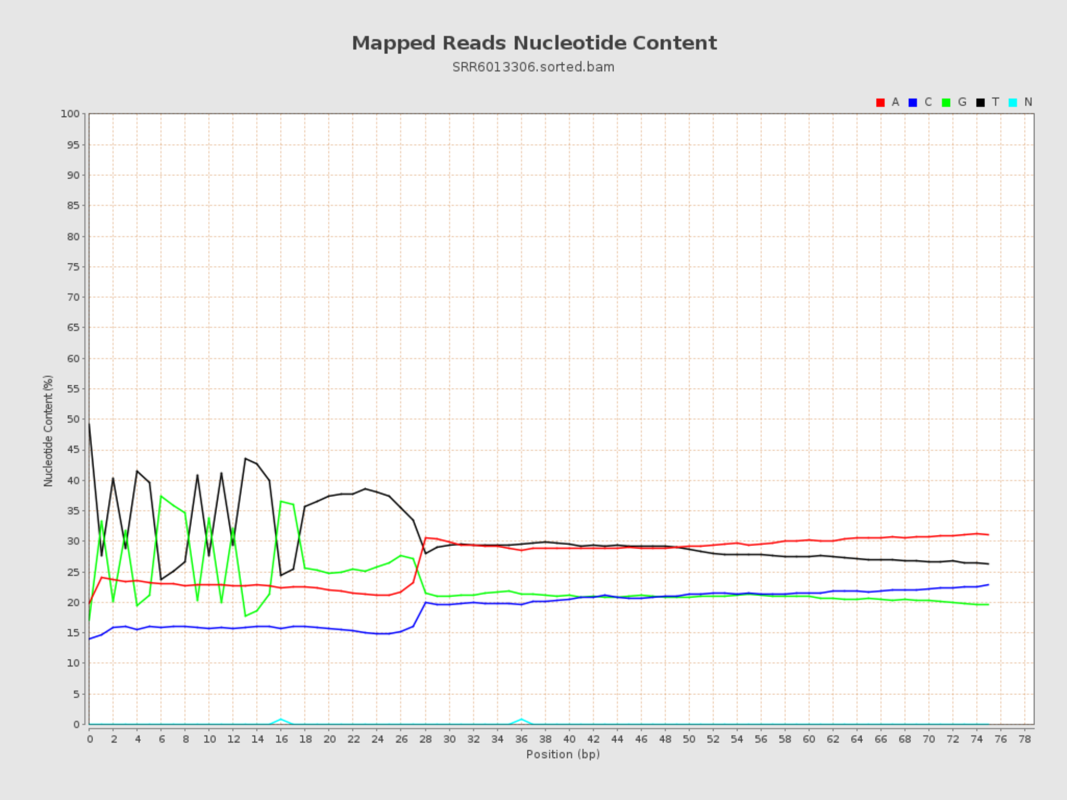
6. Results : Genome Fraction Coverage



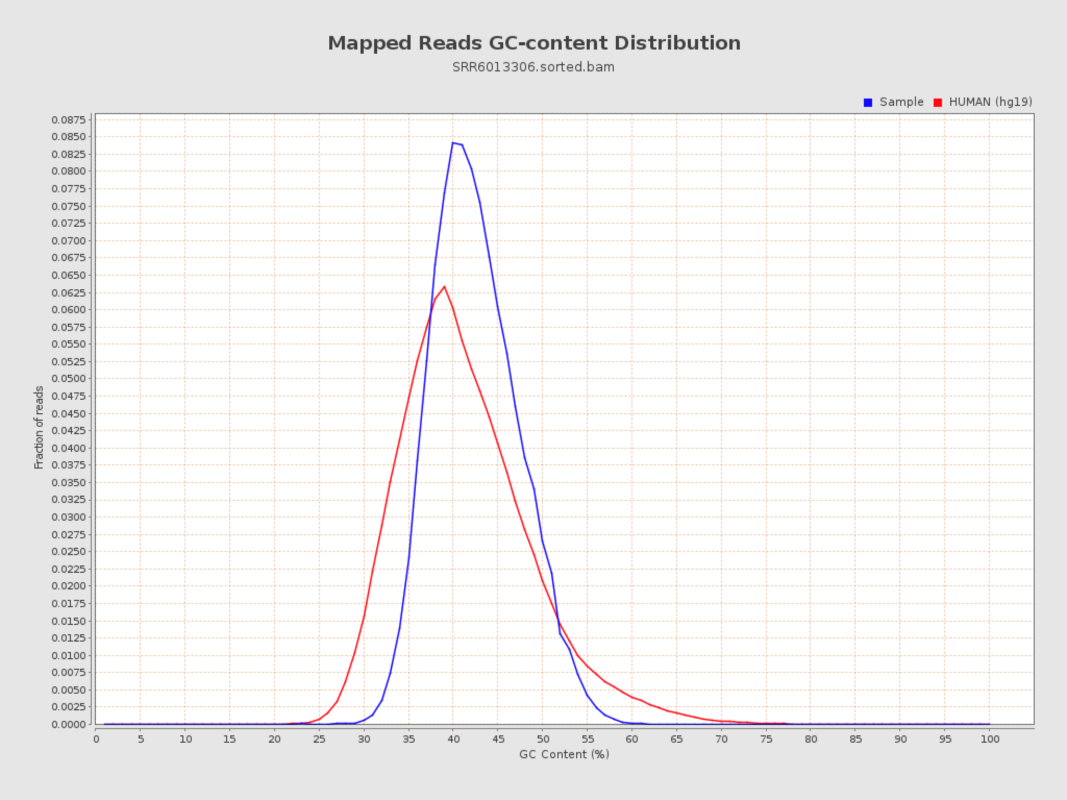
7. Results : Duplication Rate Histogram



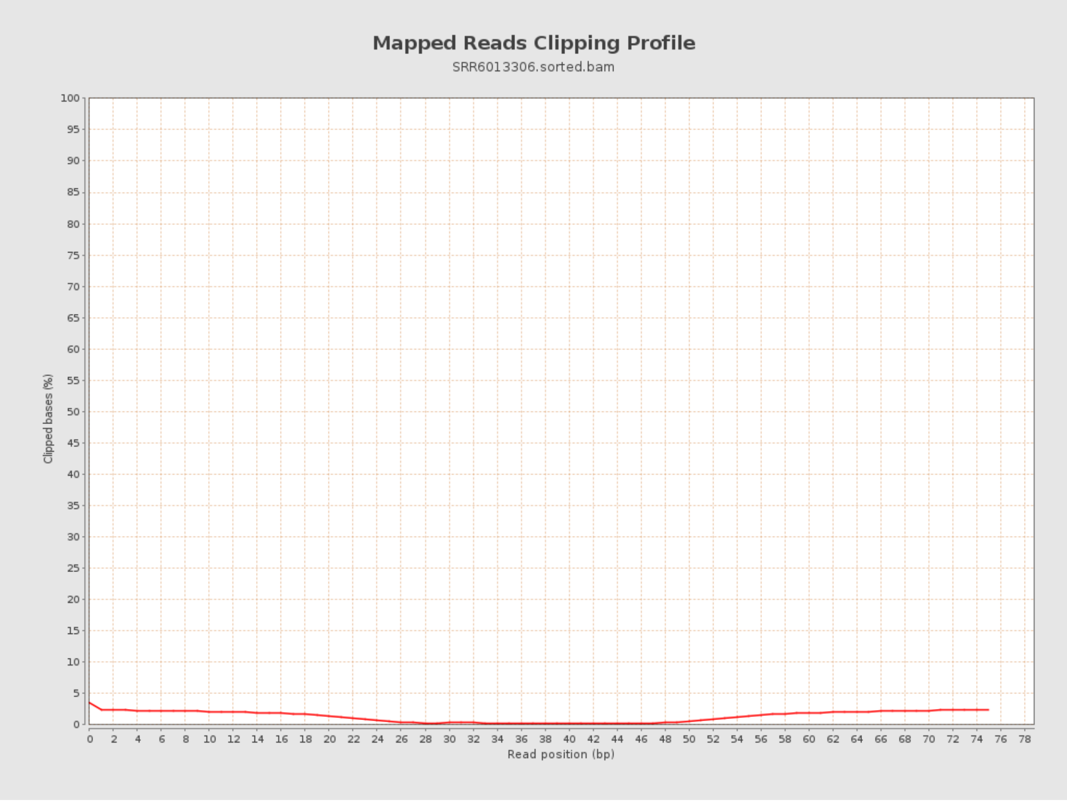
8. Results : Mapped Reads Nucleotide Content



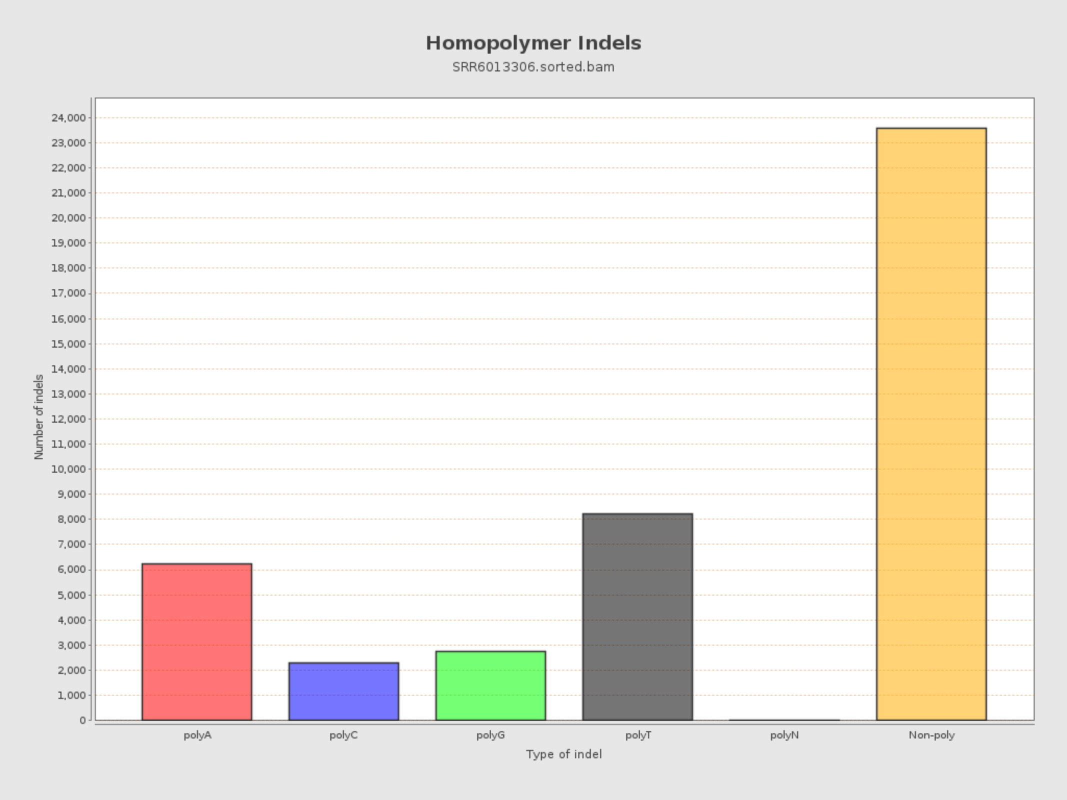
9. Results : Mapped Reads GC-content Distribution



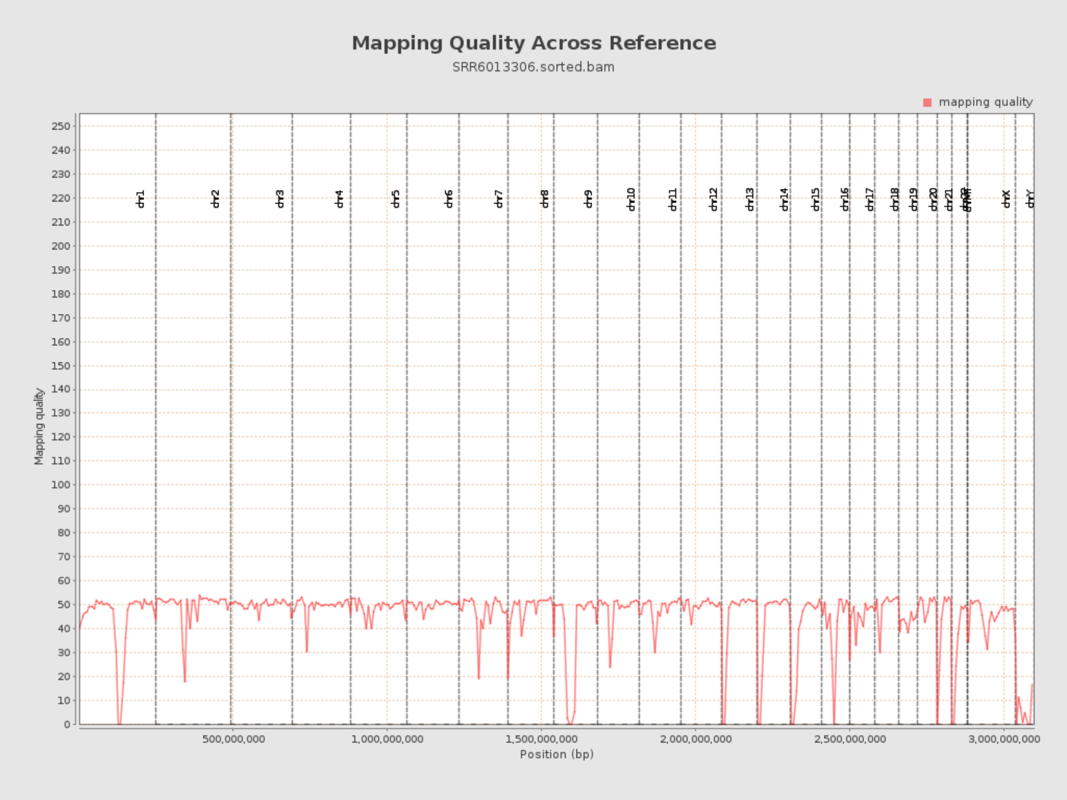
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram