Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:15:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013339.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_SRR6013339 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013339.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:15:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013339.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,321,519
Mapped reads	2,065,943 / 88.99%
Unmapped reads	255,576 / 11.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,035 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	91,248 / 3.93%
Duplication rate	3.52%
Clipped reads	957,164 / 41.23%

2.2. ACGT Content

Number/percentage of A's	37,002,558 / 27.05%
Number/percentage of C's	26,153,436 / 19.12%
Number/percentage of T's	42,392,093 / 30.99%
Number/percentage of G's	31,221,644 / 22.82%
Number/percentage of N's	31,879 / 0.02%
GC Percentage	41.94%

2.3. Coverage

Mean	0.0442

Standard Deviation	0.3757

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

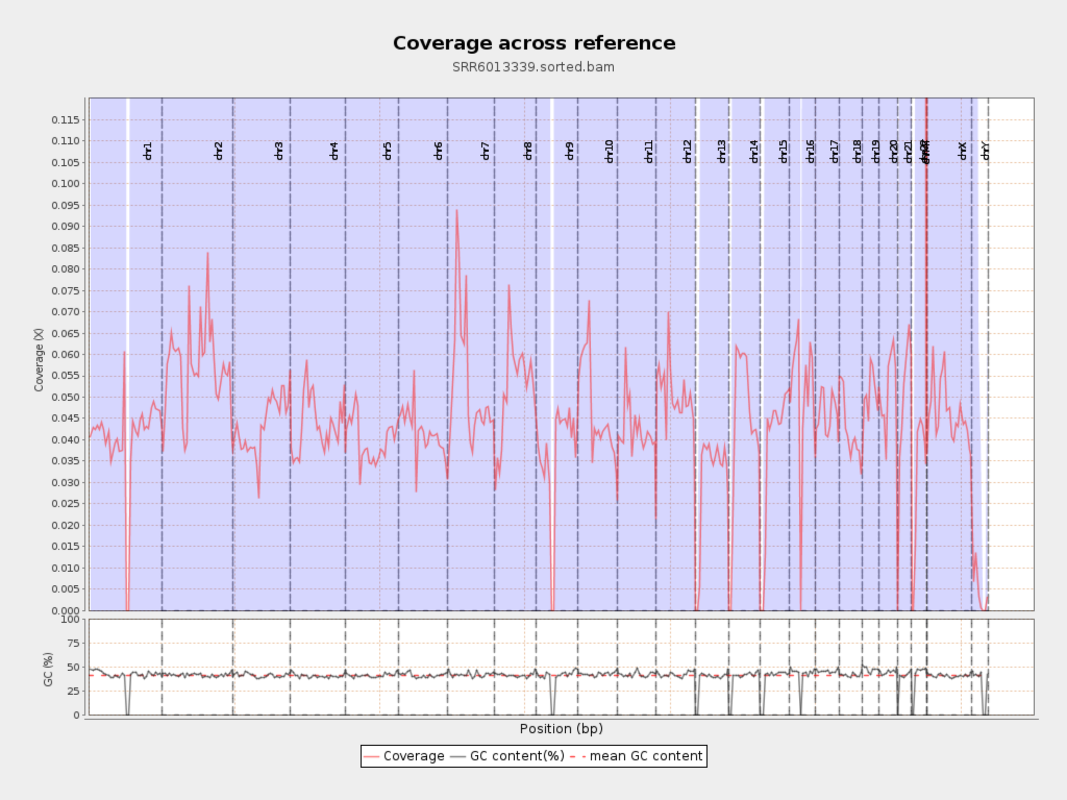
General error rate	0.81%
Mismatches	1,093,369
Insertions	9,258
Mapped reads with at least one insertion	0.44%
Deletions	34,554
Mapped reads with at least one deletion	1.65%
Homopolymer indels	45.08%

2.6. Chromosome stats

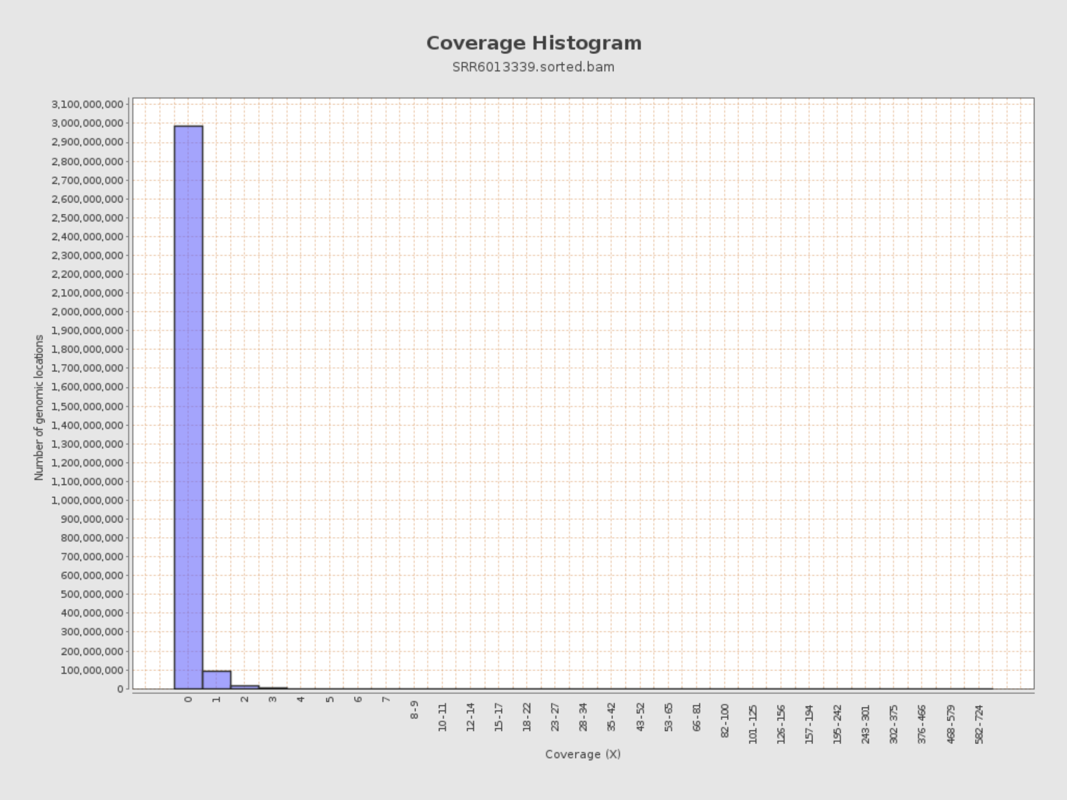
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10021141	0.0402	0.6187
chr2	243199373	13884424	0.0571	0.481
chr3	198022430	8555836	0.0432	0.2441
chr4	191154276	8318162	0.0435	0.2513
chr5	180915260	7205877	0.0398	0.2357
chr6	171115067	7140192	0.0417	0.2923
chr7	159138663	8465978	0.0532	0.6039

chr8	146364022	7646858	0.0522	0.3657
chr9	141213431	5076394	0.0359	0.3087
chr10	135534747	6435013	0.0475	0.3782
chr11	135006516	5719357	0.0424	0.2852
chr12	133851895	6794979	0.0508	0.2683
chr13	115169878	3484859	0.0303	0.2058
chr14	107349540	4664732	0.0435	0.2613
chr15	102531392	3830926	0.0374	0.2272
chr16	90354753	4590885	0.0508	0.2977
chr17	81195210	3726489	0.0459	0.2749
chr18	78077248	3312826	0.0424	0.5238
chr19	59128983	3002278	0.0508	0.4784
chr20	63025520	3224660	0.0512	0.2728
chr21	48129895	2308994	0.048	0.2727
chr22	51304566	1499498	0.0292	0.2003
chrMT	16571	451039	27.2186	15.4933
chrX	155270560	7201278	0.0464	0.2738
chrY	59373566	299103	0.005	0.1134

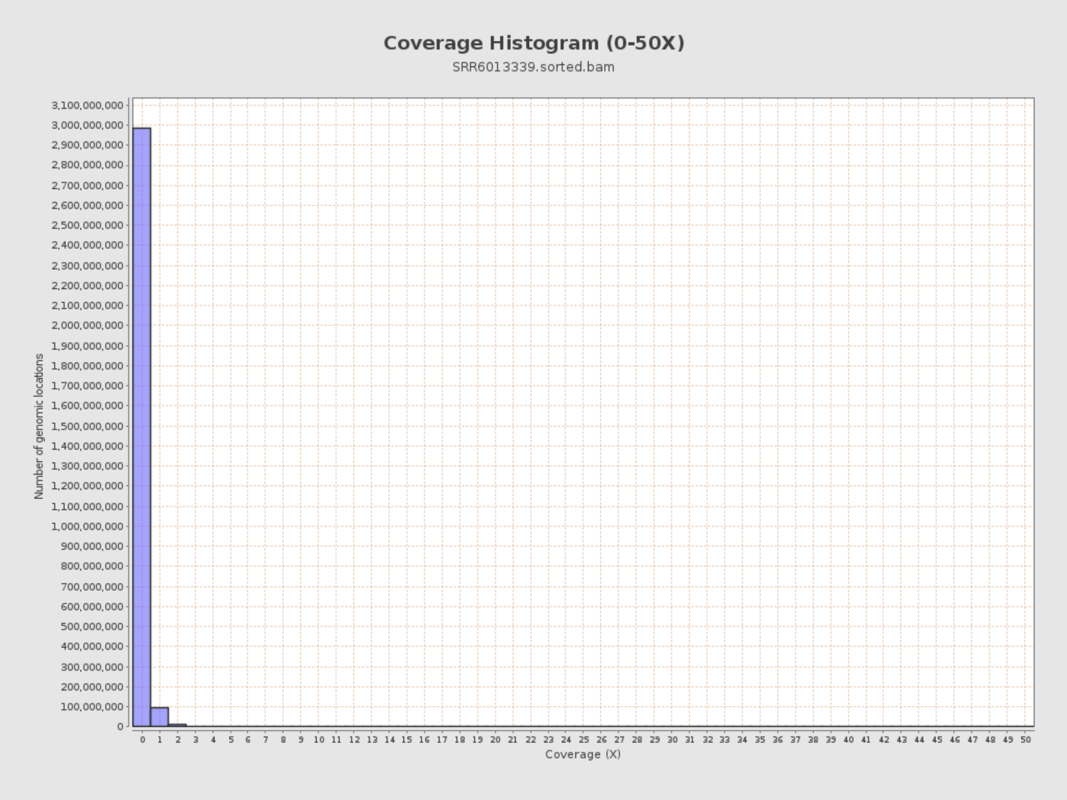
3. Results : Coverage across reference



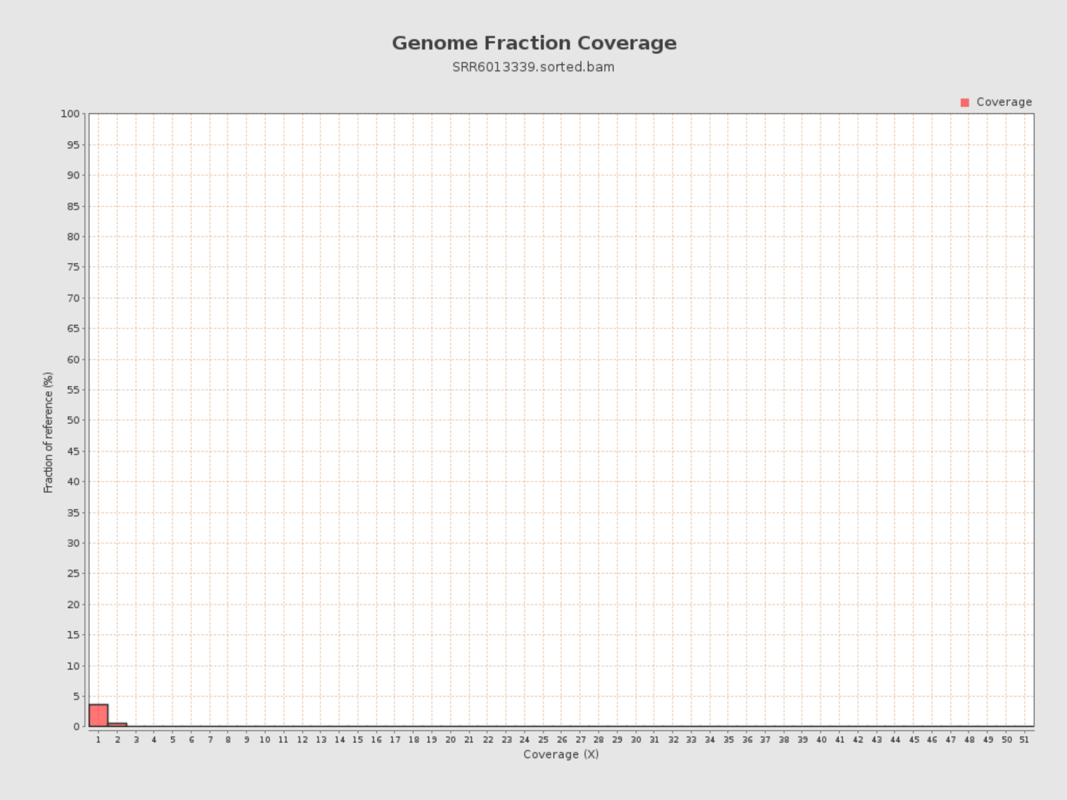
4. Results : Coverage Histogram



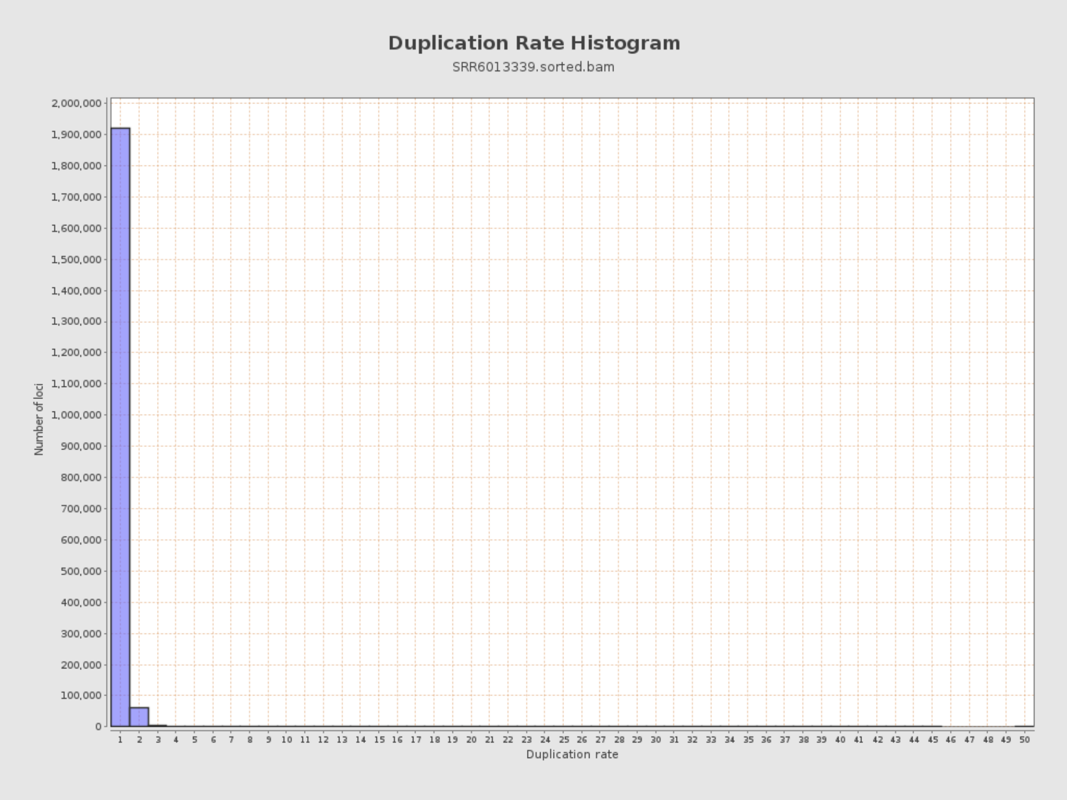
5. Results : Coverage Histogram (0-50X)



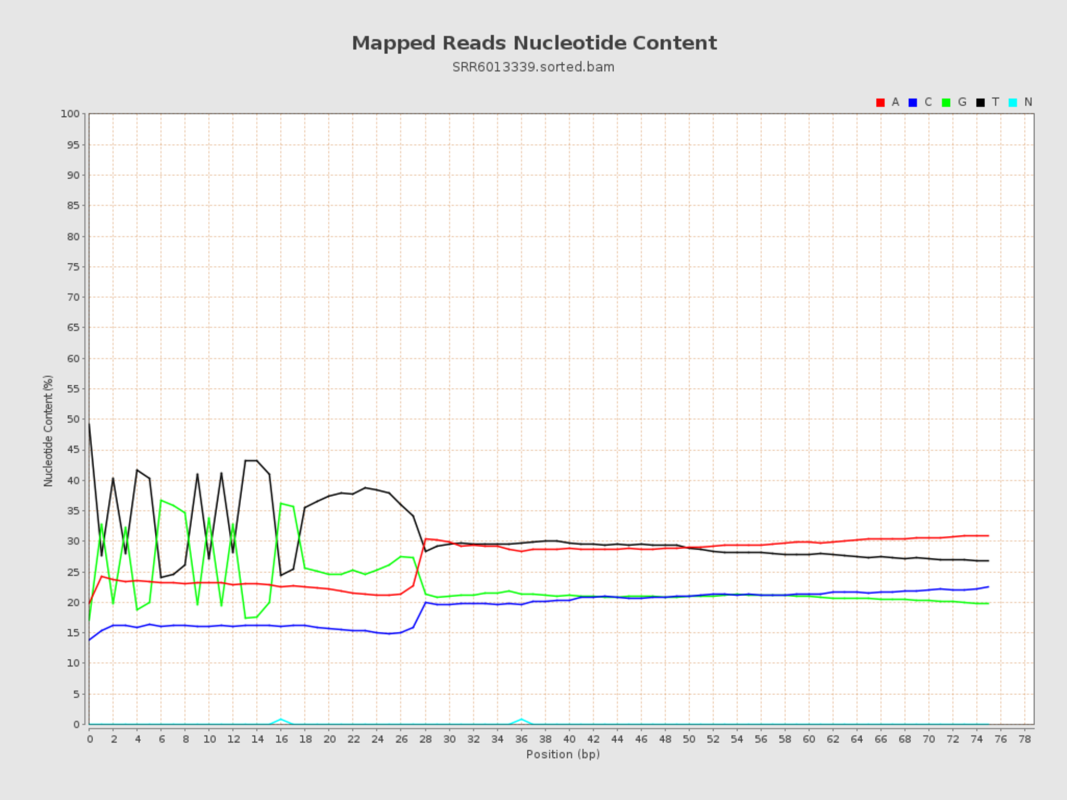
6. Results : Genome Fraction Coverage



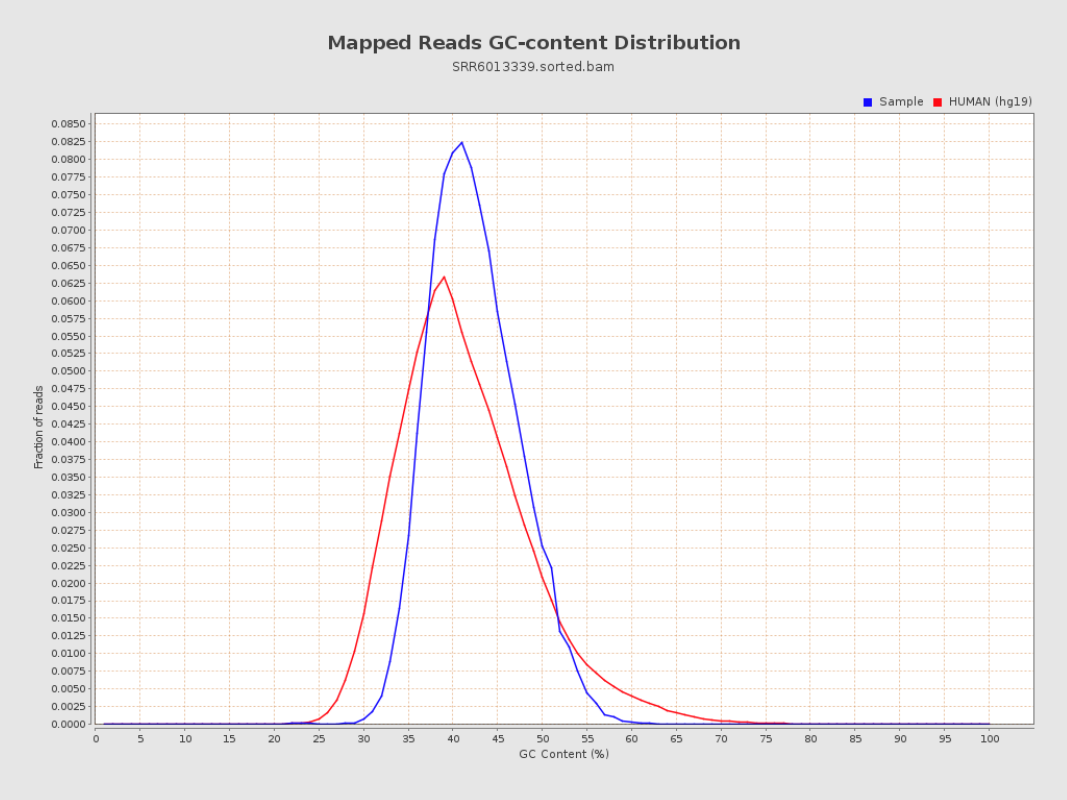
7. Results : Duplication Rate Histogram



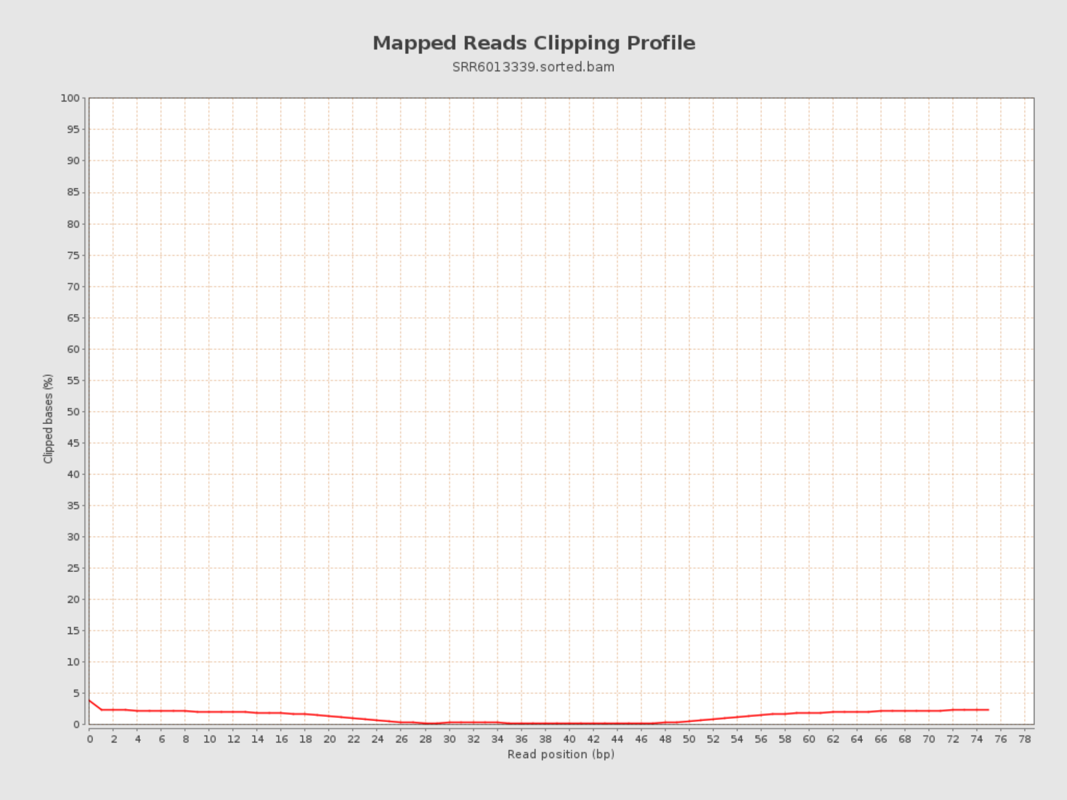
8. Results : Mapped Reads Nucleotide Content



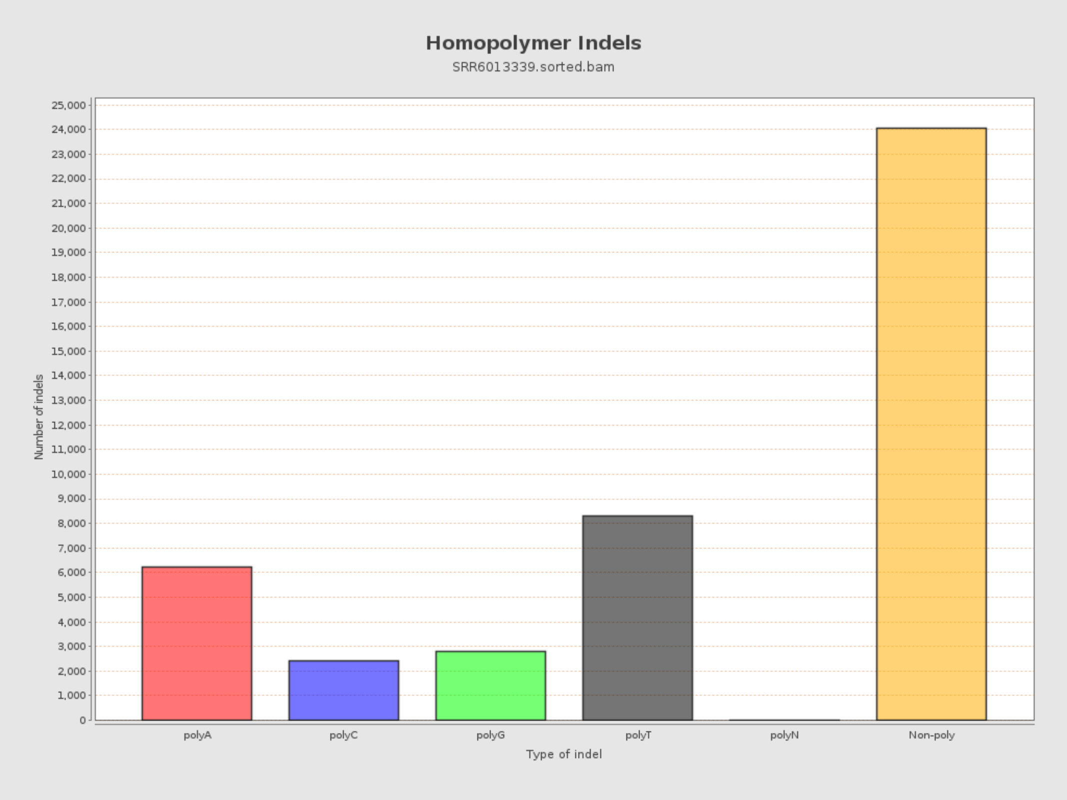
9. Results : Mapped Reads GC-content Distribution



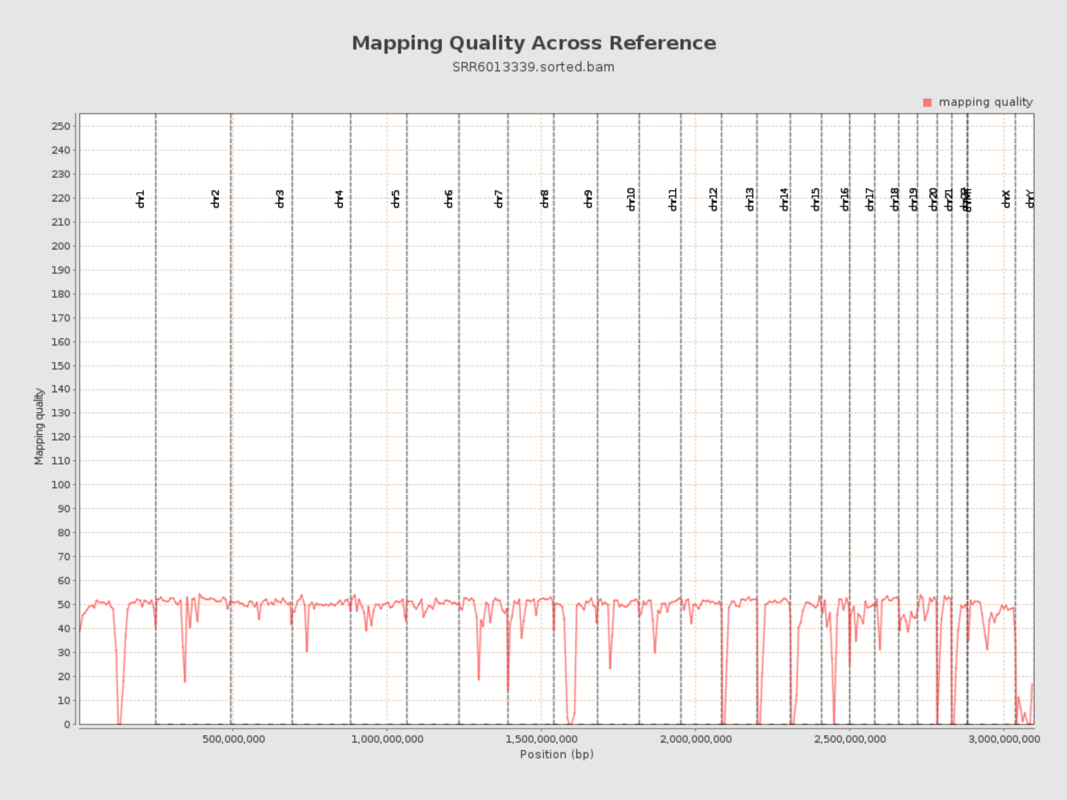
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram