Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:24:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013321.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_SRR6013321 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013321.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:24:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013321.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,715,170
Mapped reads	1,356,737 / 79.1%
Unmapped reads	358,433 / 20.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,827 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	141,572 / 8.25%
Duplication rate	8.3%
Clipped reads	728,128 / 42.45%

2.2. ACGT Content

Number/percentage of A's	23,516,812 / 26.85%
Number/percentage of C's	16,510,306 / 18.85%
Number/percentage of T's	27,376,037 / 31.26%
Number/percentage of G's	20,162,186 / 23.02%
Number/percentage of N's	10,793 / 0.01%
GC Percentage	41.87%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.3094

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

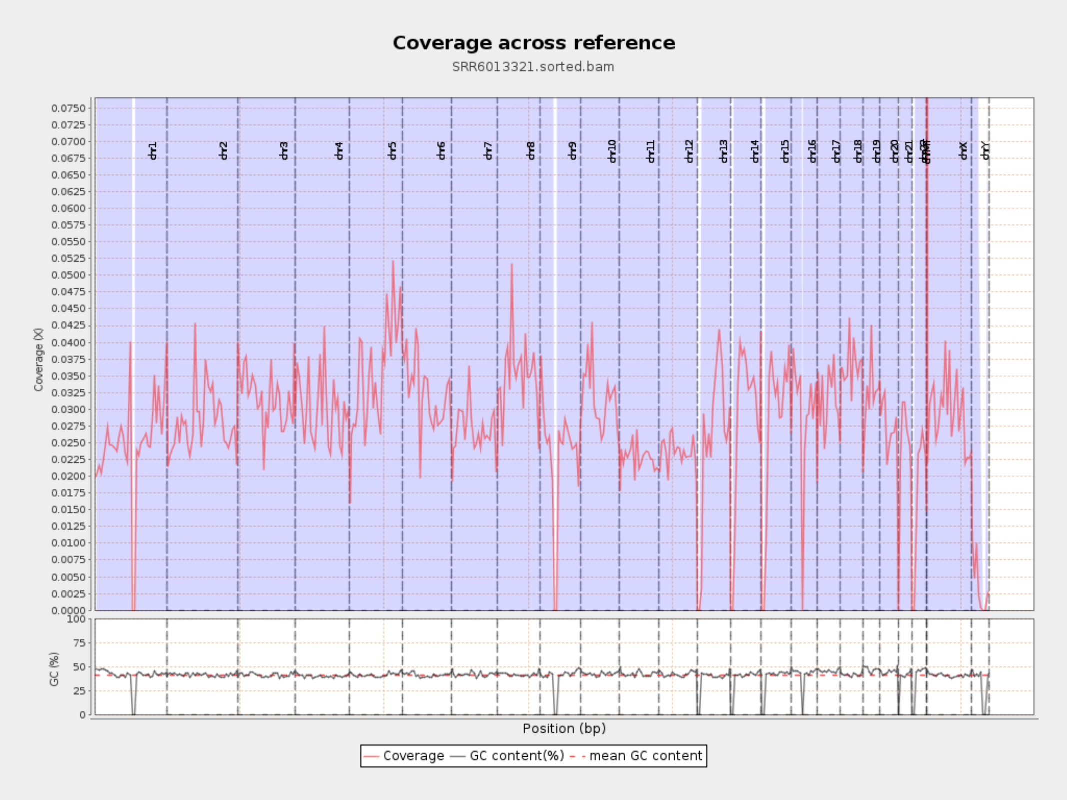
General error rate	0.79%
Mismatches	681,460
Insertions	6,026
Mapped reads with at least one insertion	0.44%
Deletions	21,972
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.68%

2.6. Chromosome stats

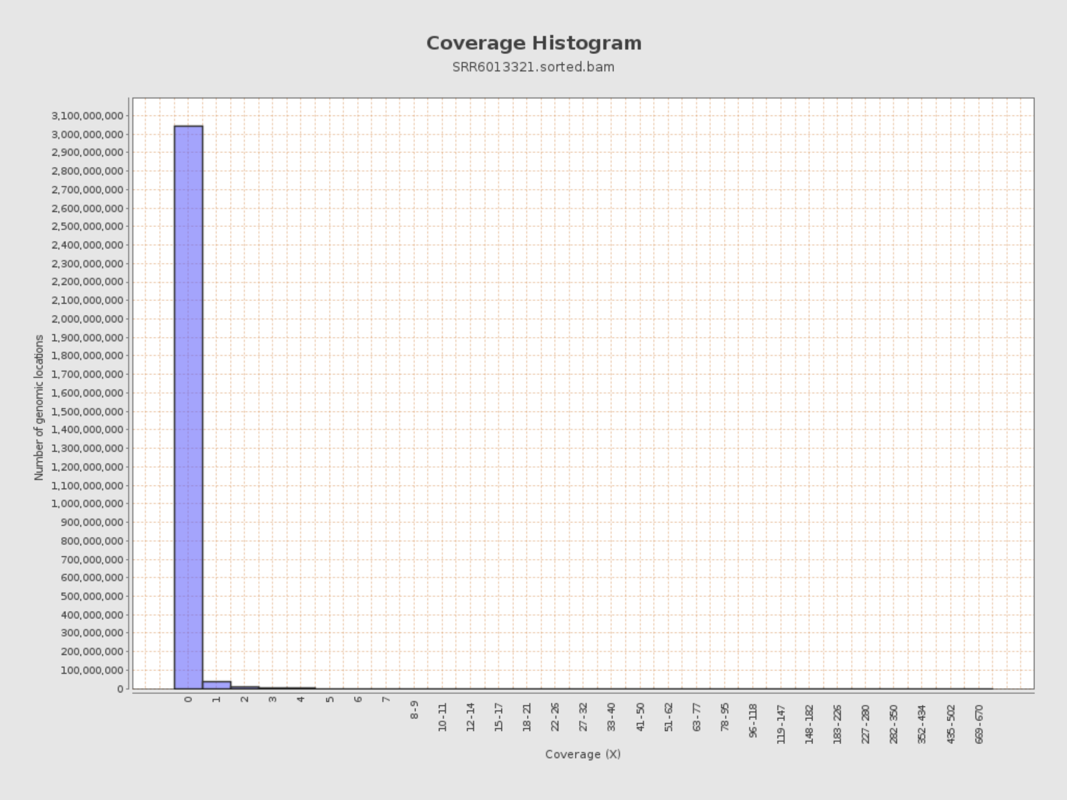
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6187449	0.0248	0.4782
chr2	243199373	6815909	0.028	0.4009
chr3	198022430	6246168	0.0315	0.2677
chr4	191154276	5757840	0.0301	0.2616
chr5	180915260	6516563	0.036	0.2868
chr6	171115067	5551699	0.0324	0.3011
chr7	159138663	4280872	0.0269	0.307

chr8	146364022	5171900	0.0353	0.346
chr9	141213431	3265592	0.0231	0.2593
chr10	135534747	4302914	0.0317	0.3097
chr11	135006516	3080757	0.0228	0.2456
chr12	133851895	3167475	0.0237	0.2337
chr13	115169878	2892130	0.0251	0.2405
chr14	107349540	3020255	0.0281	0.258
chr15	102531392	2823484	0.0275	0.2486
chr16	90354753	2618284	0.029	0.2632
chr17	81195210	2554487	0.0315	0.277
chr18	78077248	2870911	0.0368	0.3744
chr19	59128983	1916059	0.0324	0.3818
chr20	63025520	1709871	0.0271	0.2534
chr21	48129895	1155373	0.024	0.2336
chr22	51304566	872957	0.017	0.195
chrMT	16571	42729	2.5785	3.0624
chrX	155270560	4580779	0.0295	0.2602
chrY	59373566	211477	0.0036	0.0949

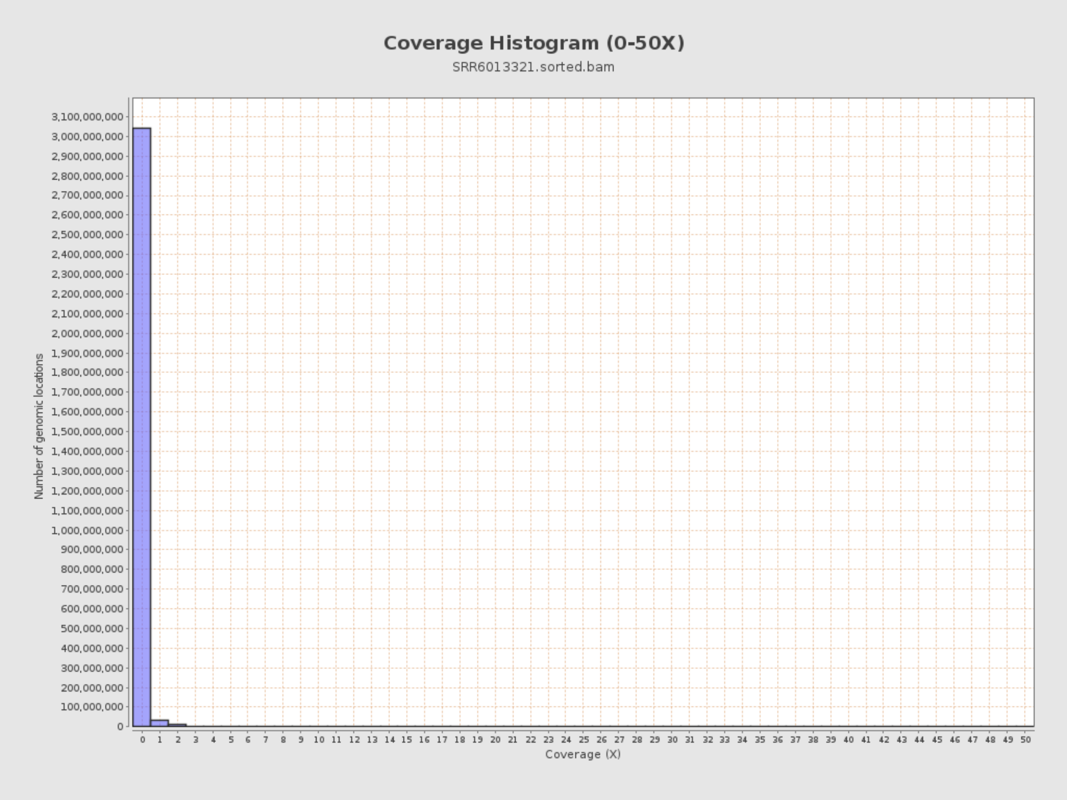
3. Results : Coverage across reference



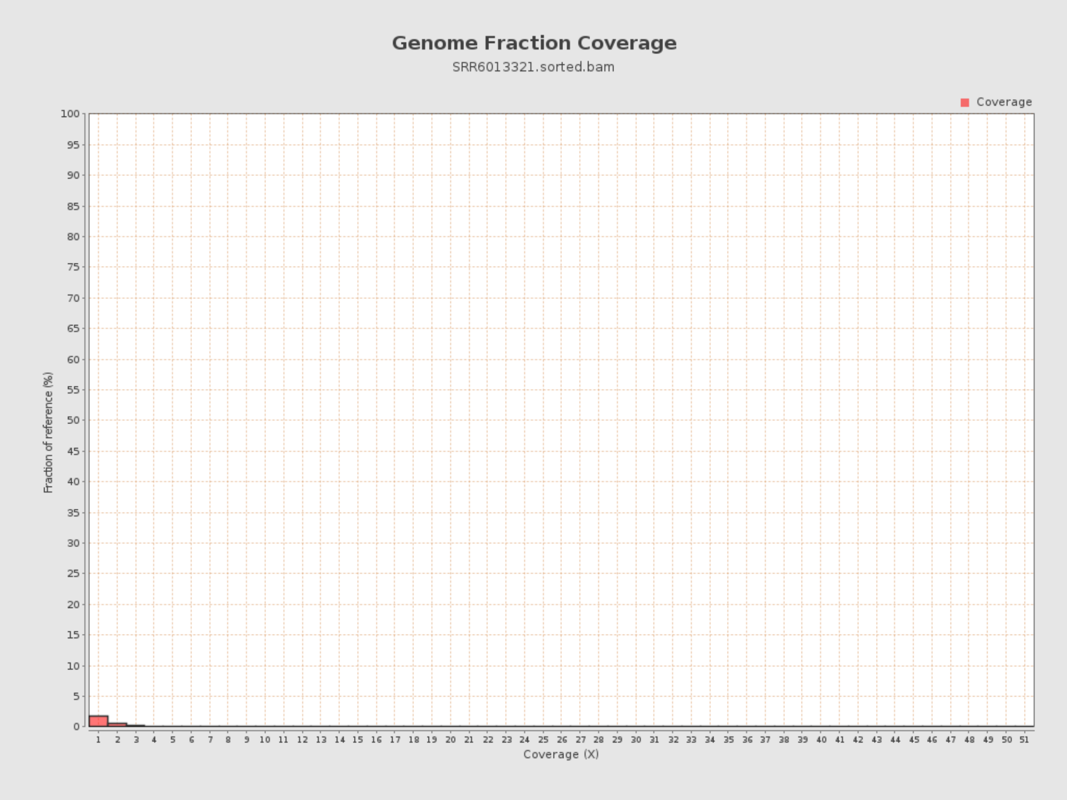
4. Results : Coverage Histogram



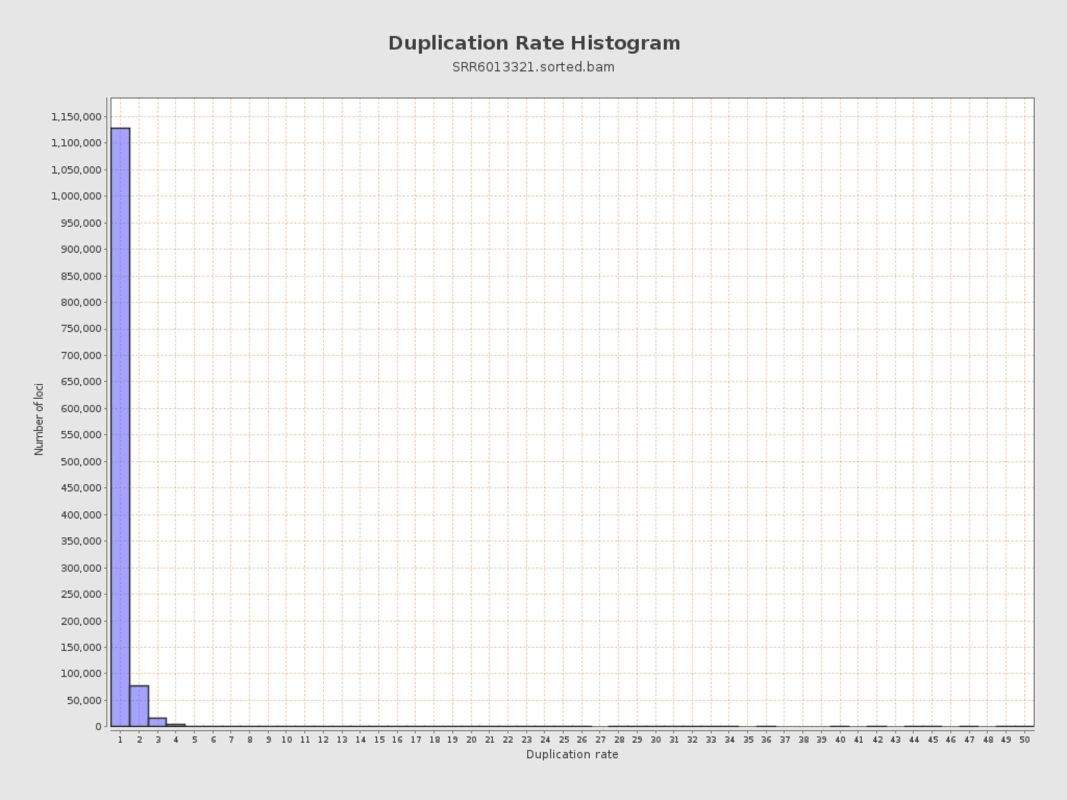
5. Results : Coverage Histogram (0-50X)



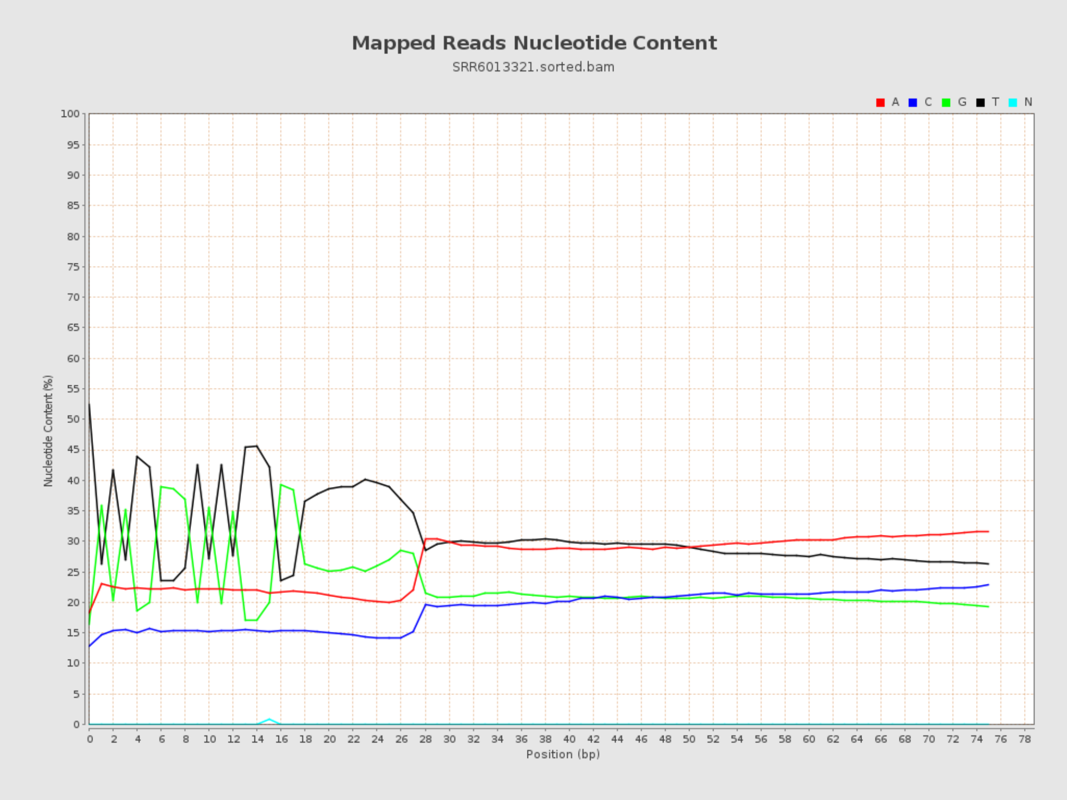
6. Results : Genome Fraction Coverage



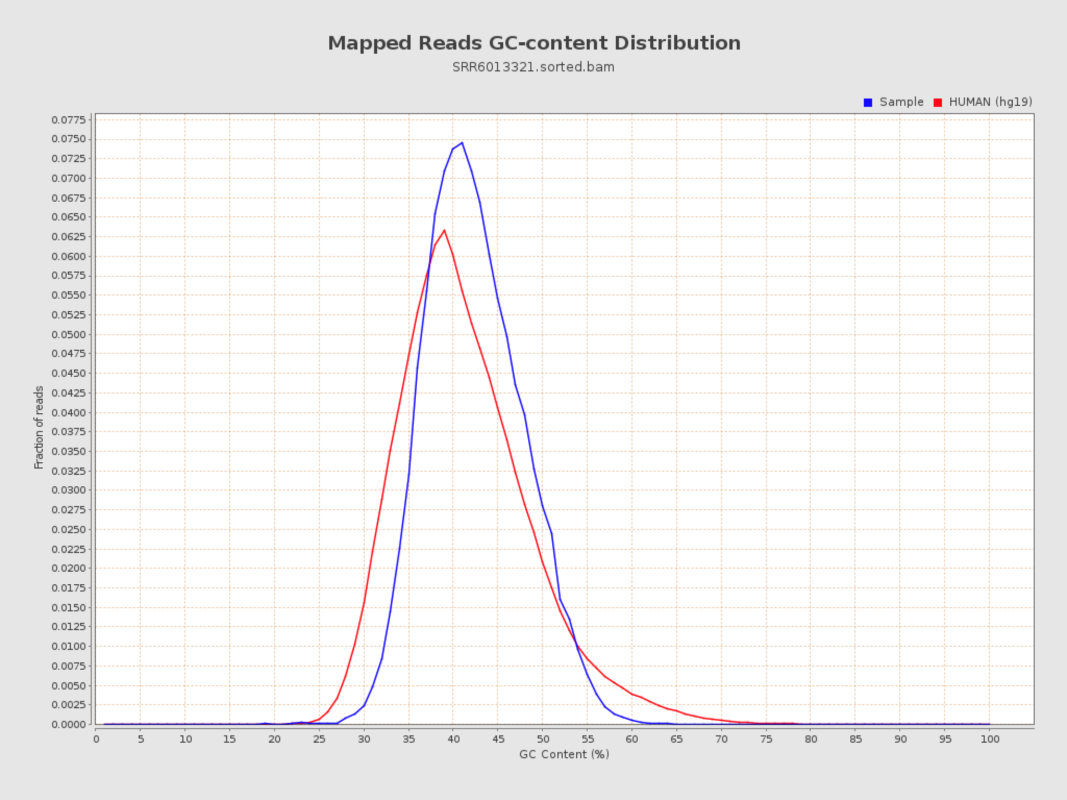
7. Results : Duplication Rate Histogram



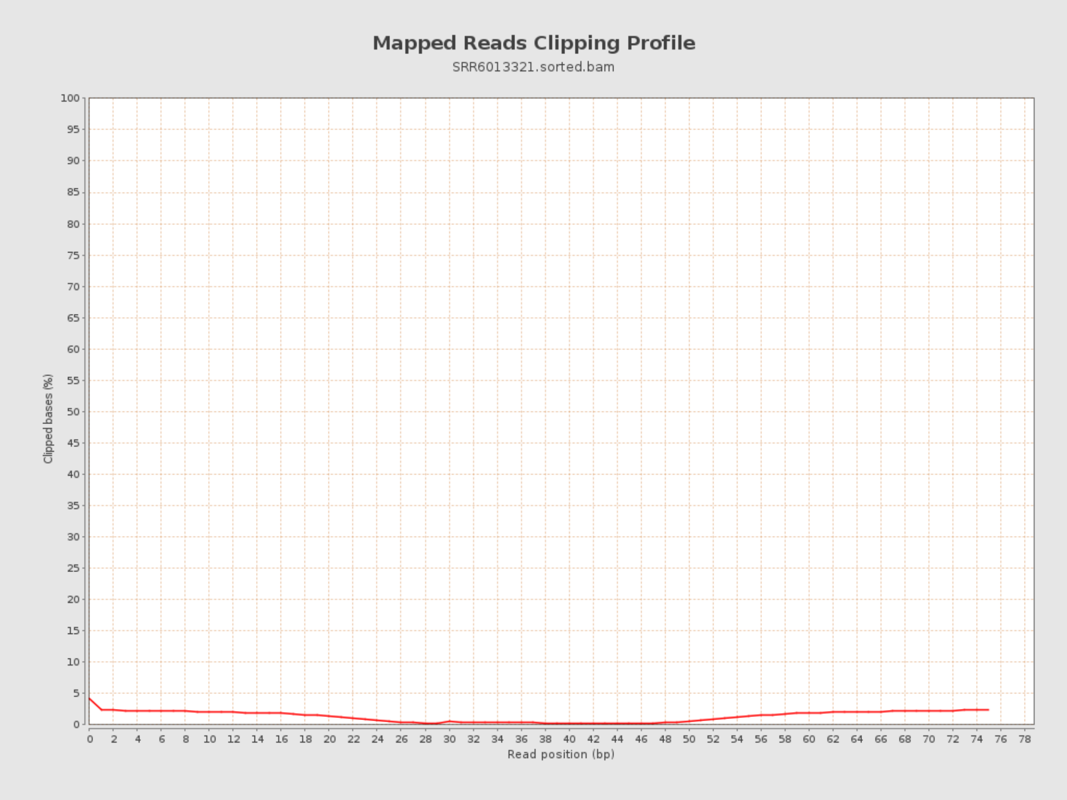
8. Results : Mapped Reads Nucleotide Content



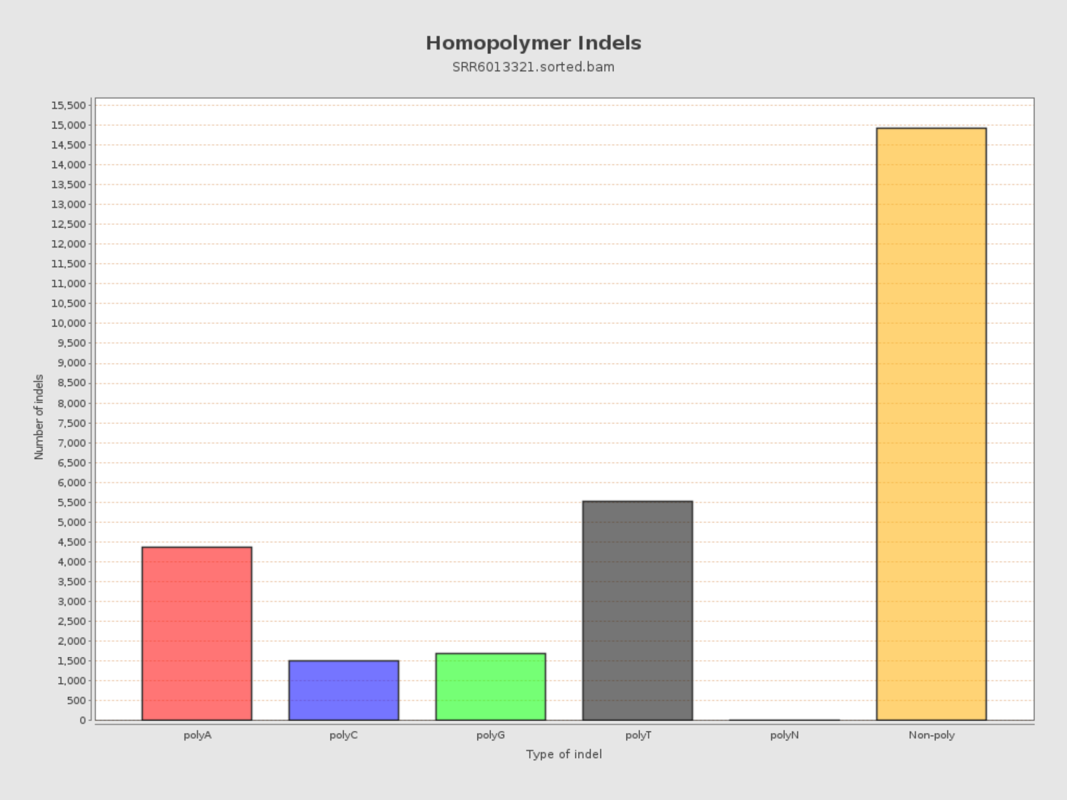
9. Results : Mapped Reads GC-content Distribution



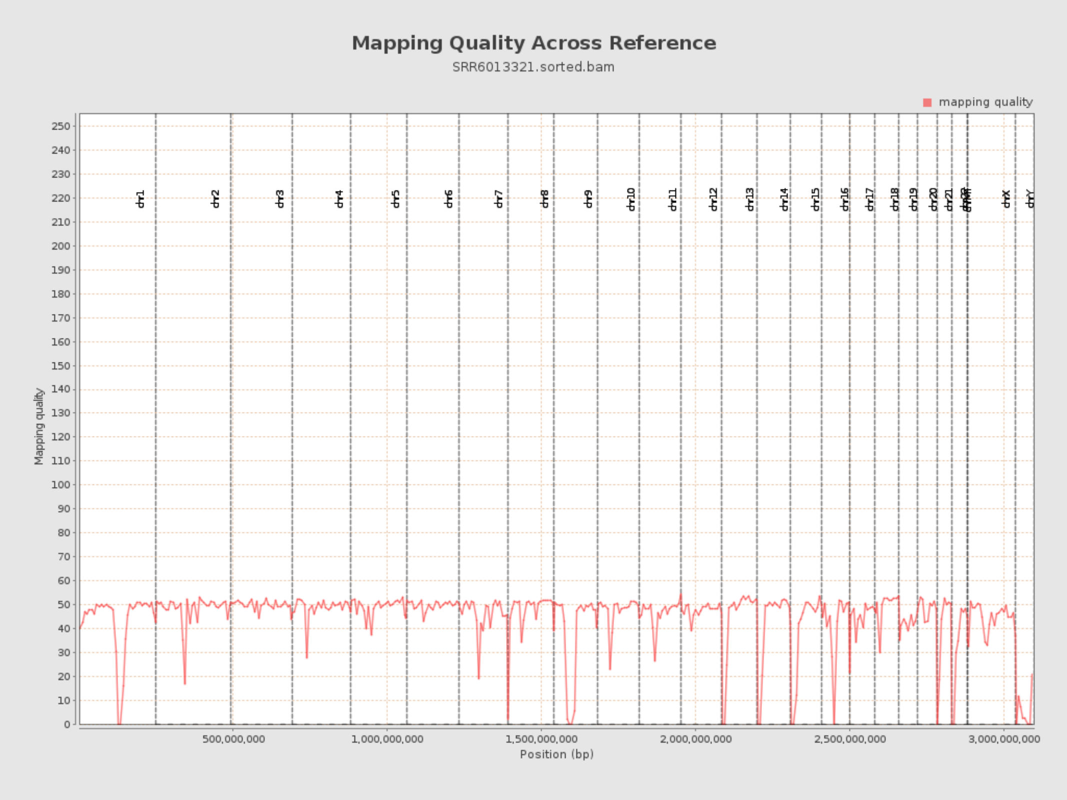
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram