Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:35:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013325.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_SRR6013325 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013325.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:35:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013325.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,859,009
Mapped reads	2,438,245 / 85.28%
Unmapped reads	420,764 / 14.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,825 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	145,130 / 5.08%
Duplication rate	4.62%
Clipped reads	1,318,262 / 46.11%

2.2. ACGT Content

Number/percentage of A's	41,287,667 / 26.37%
Number/percentage of C's	28,671,262 / 18.31%
Number/percentage of T's	49,409,052 / 31.55%
Number/percentage of G's	37,227,157 / 23.77%
Number/percentage of N's	2,167 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0506

Standard Deviation	0.472

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

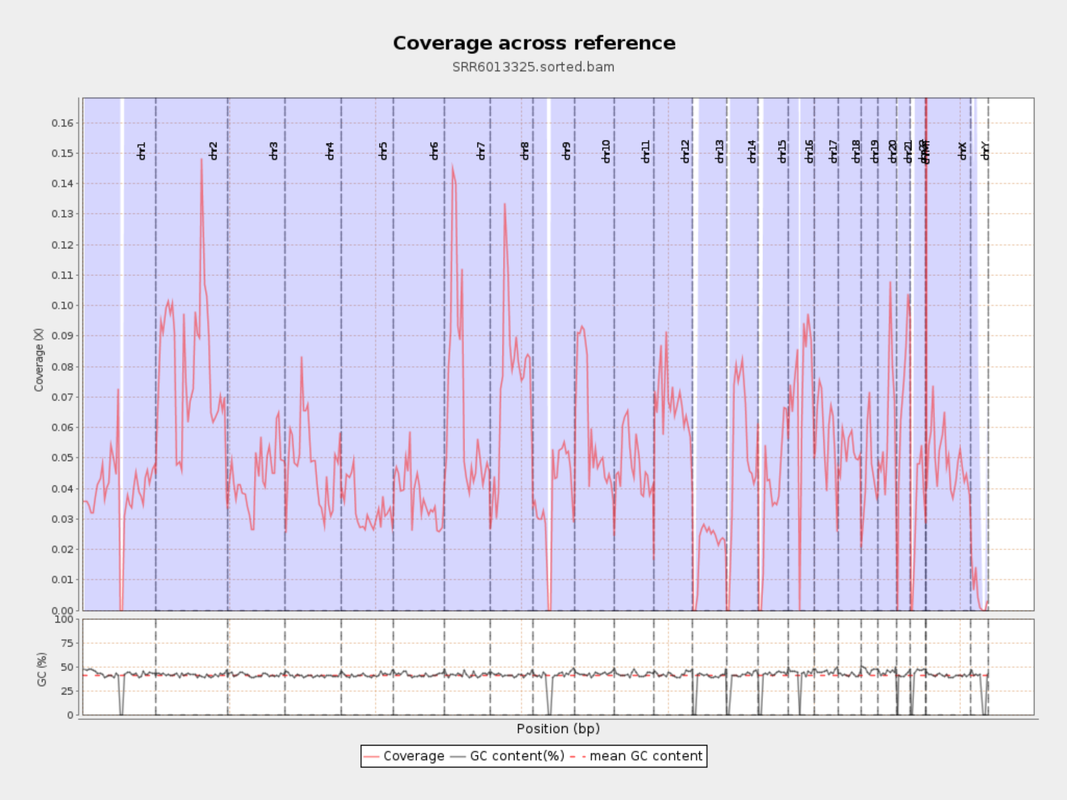
General error rate	0.79%
Mismatches	1,212,602
Insertions	10,266
Mapped reads with at least one insertion	0.42%
Deletions	45,581
Mapped reads with at least one deletion	1.85%
Homopolymer indels	47.06%

2.6. Chromosome stats

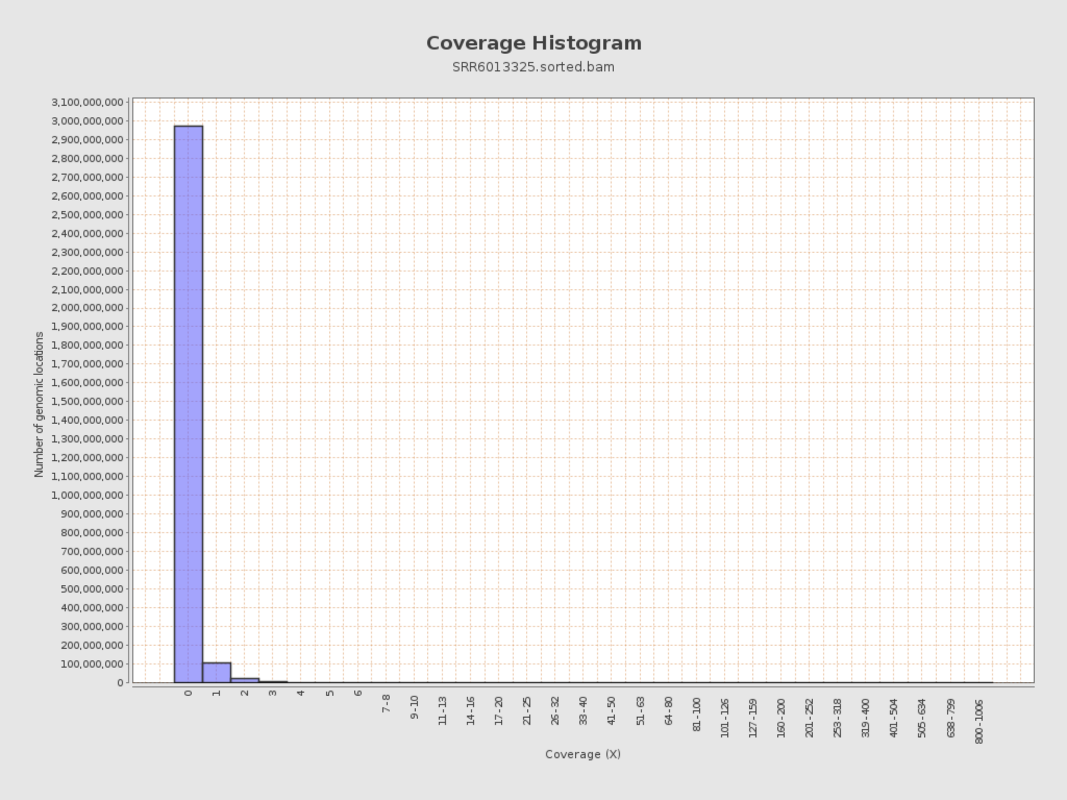
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9656215	0.0387	0.7883
chr2	243199373	19551614	0.0804	0.5803
chr3	198022430	8701942	0.0439	0.2521
chr4	191154276	9228855	0.0483	0.2818
chr5	180915260	6040411	0.0334	0.2276
chr6	171115067	6463474	0.0378	0.3081
chr7	159138663	10646663	0.0669	0.977

chr8	146364022	10904755	0.0745	0.4744
chr9	141213431	5244015	0.0371	0.3953
chr10	135534747	8132249	0.06	0.4524
chr11	135006516	6397189	0.0474	0.4101
chr12	133851895	9115816	0.0681	0.3209
chr13	115169878	2405324	0.0209	0.1747
chr14	107349540	5596477	0.0521	0.2958
chr15	102531392	3869837	0.0377	0.2721
chr16	90354753	6419501	0.071	0.3404
chr17	81195210	4724561	0.0582	0.3701
chr18	78077248	4096969	0.0525	0.704
chr19	59128983	2701395	0.0457	0.5269
chr20	63025520	3869423	0.0614	0.316
chr21	48129895	3321095	0.069	0.3312
chr22	51304566	1647175	0.0321	0.2138
chrMT	16571	23957	1.4457	1.8137
chrX	155270560	7604099	0.049	0.3154
chrY	59373566	313568	0.0053	0.1117

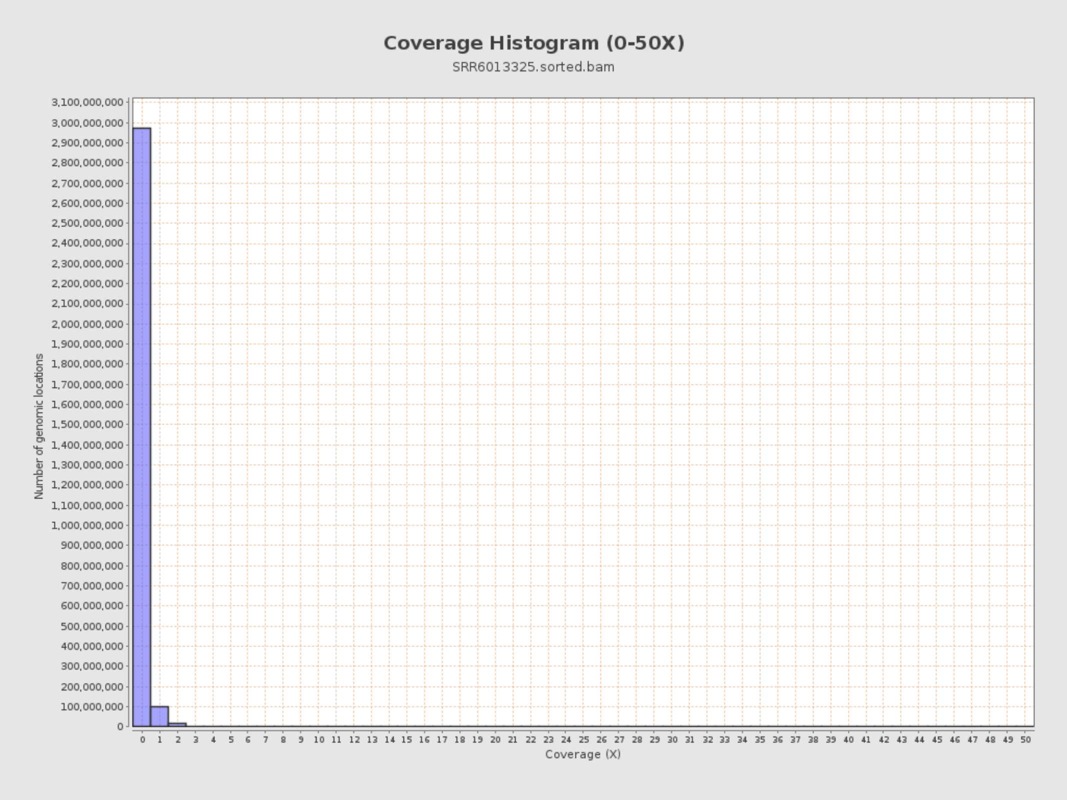
3. Results : Coverage across reference



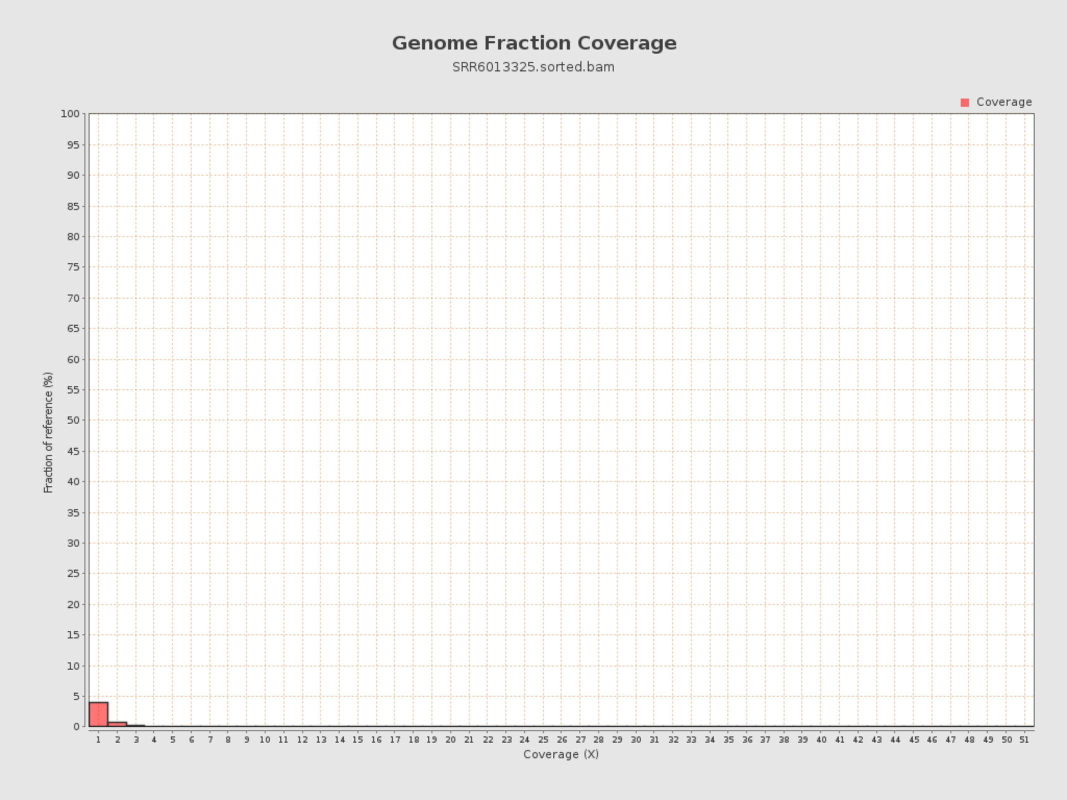
4. Results : Coverage Histogram



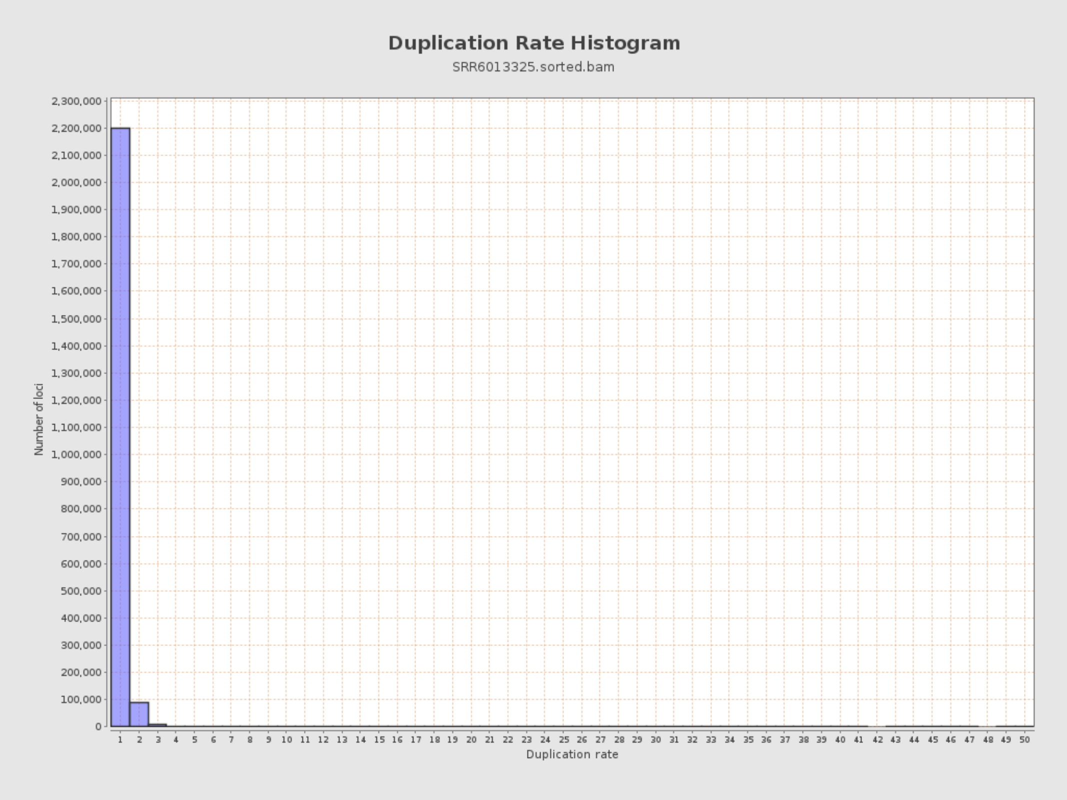
5. Results : Coverage Histogram (0-50X)



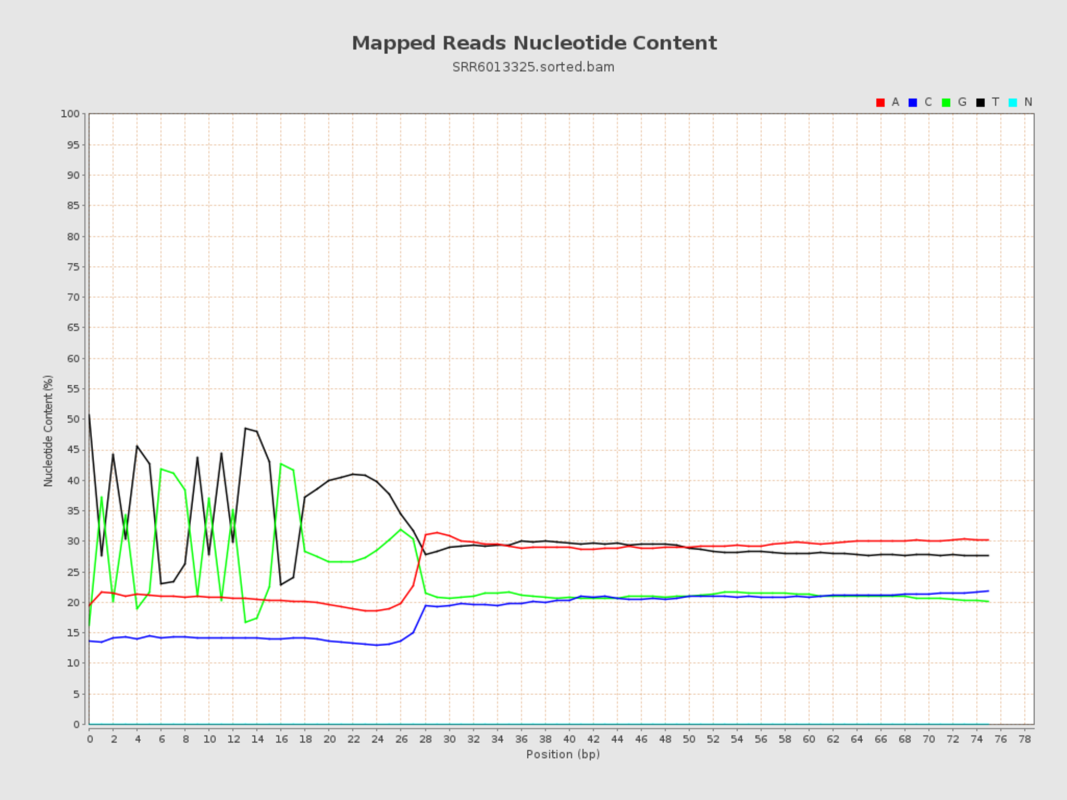
6. Results : Genome Fraction Coverage



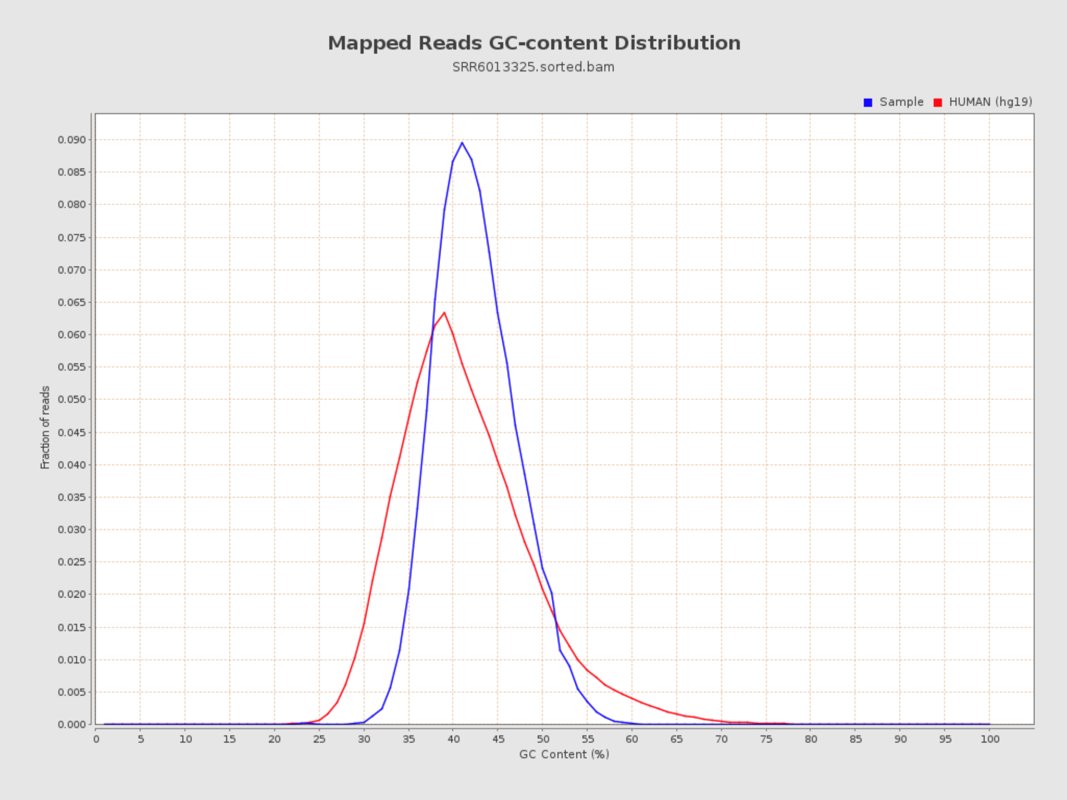
7. Results : Duplication Rate Histogram



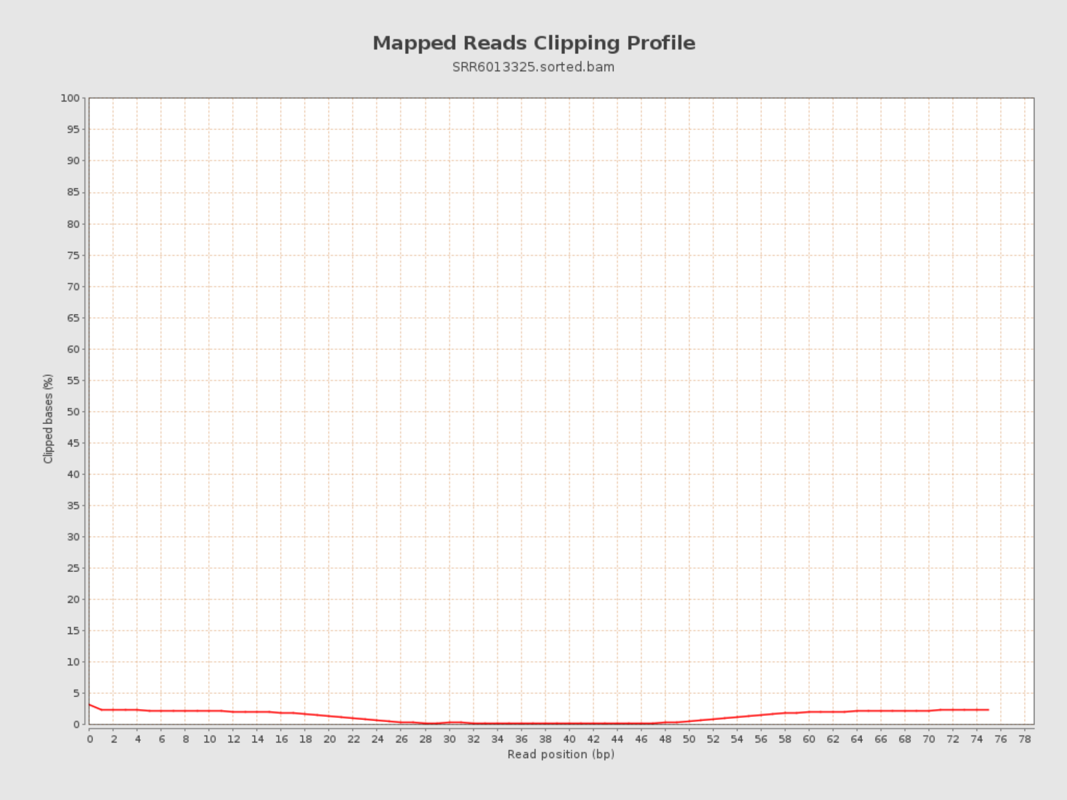
8. Results : Mapped Reads Nucleotide Content



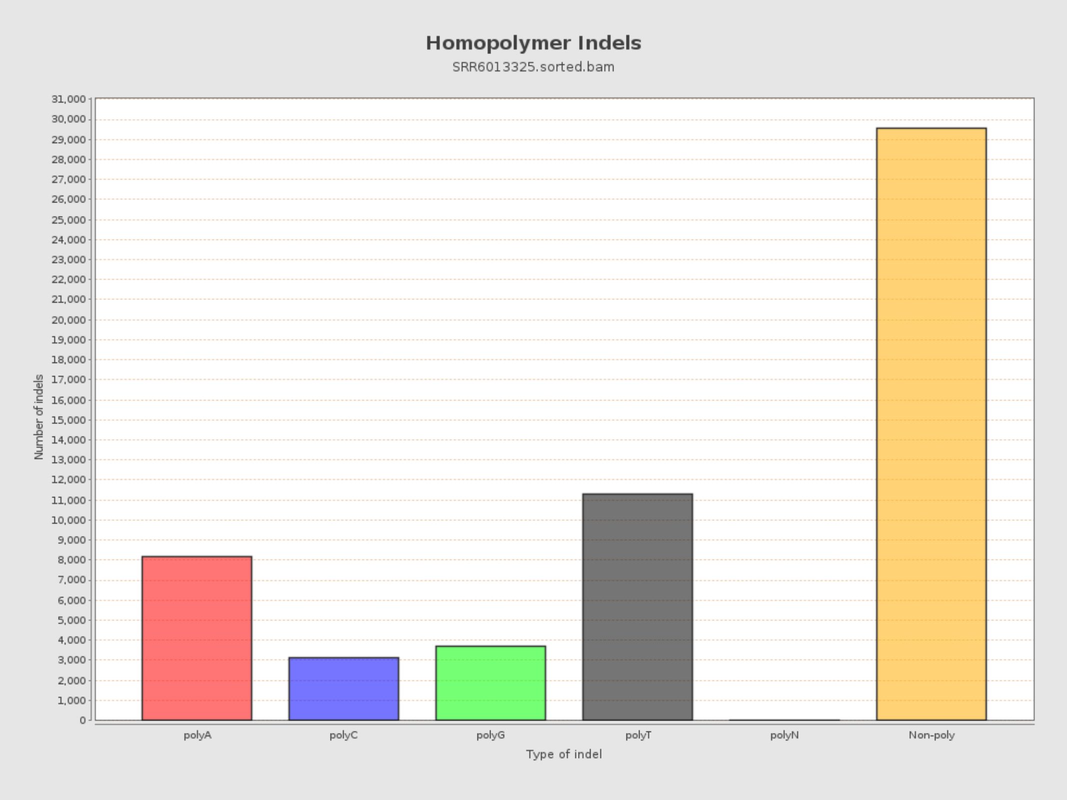
9. Results : Mapped Reads GC-content Distribution



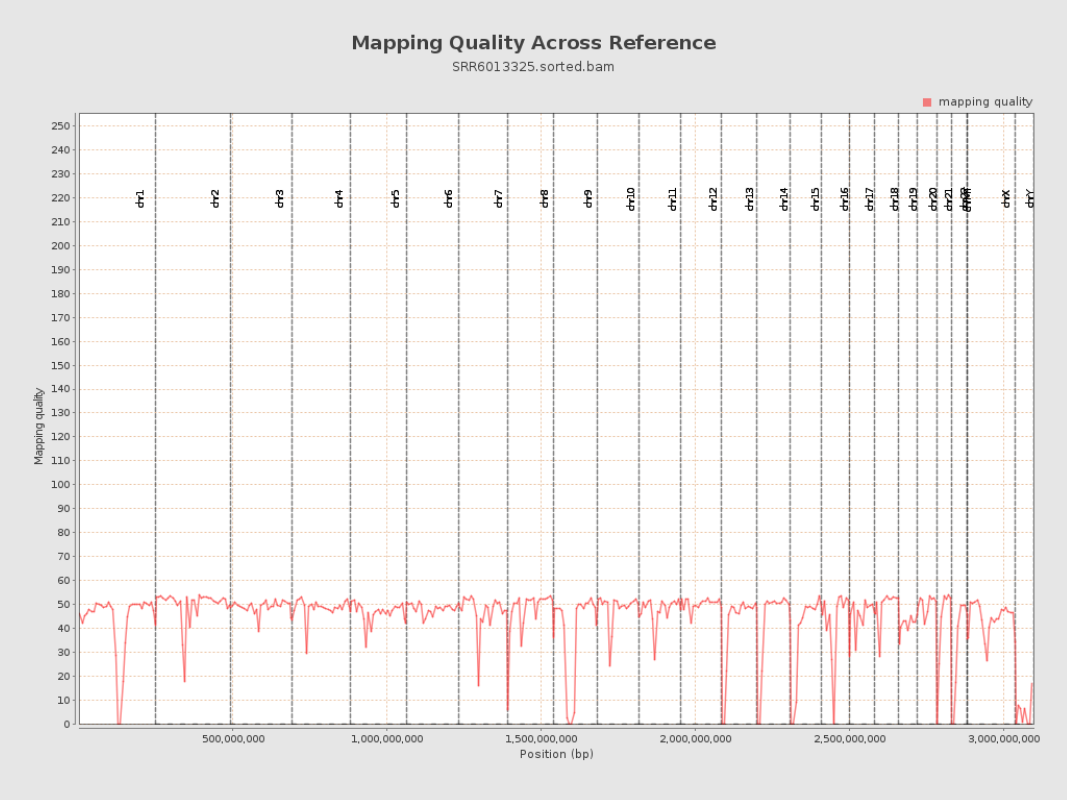
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram