Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:26:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013363.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_SRR6013363 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013363.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:26:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013363.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,154,361
Mapped reads	1,863,578 / 86.5%
Unmapped reads	290,783 / 13.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,697 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	106,147 / 4.93%
Duplication rate	4.37%
Clipped reads	835,627 / 38.79%

2.2. ACGT Content

Number/percentage of A's	33,760,141 / 27.16%
Number/percentage of C's	23,260,945 / 18.71%
Number/percentage of T's	39,164,519 / 31.51%
Number/percentage of G's	28,086,673 / 22.6%
Number/percentage of N's	26,646 / 0.02%
GC Percentage	41.31%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.4308

2.4. Mapping Quality

Mean Mapping Quality	45.3

2.5. Mismatches and indels

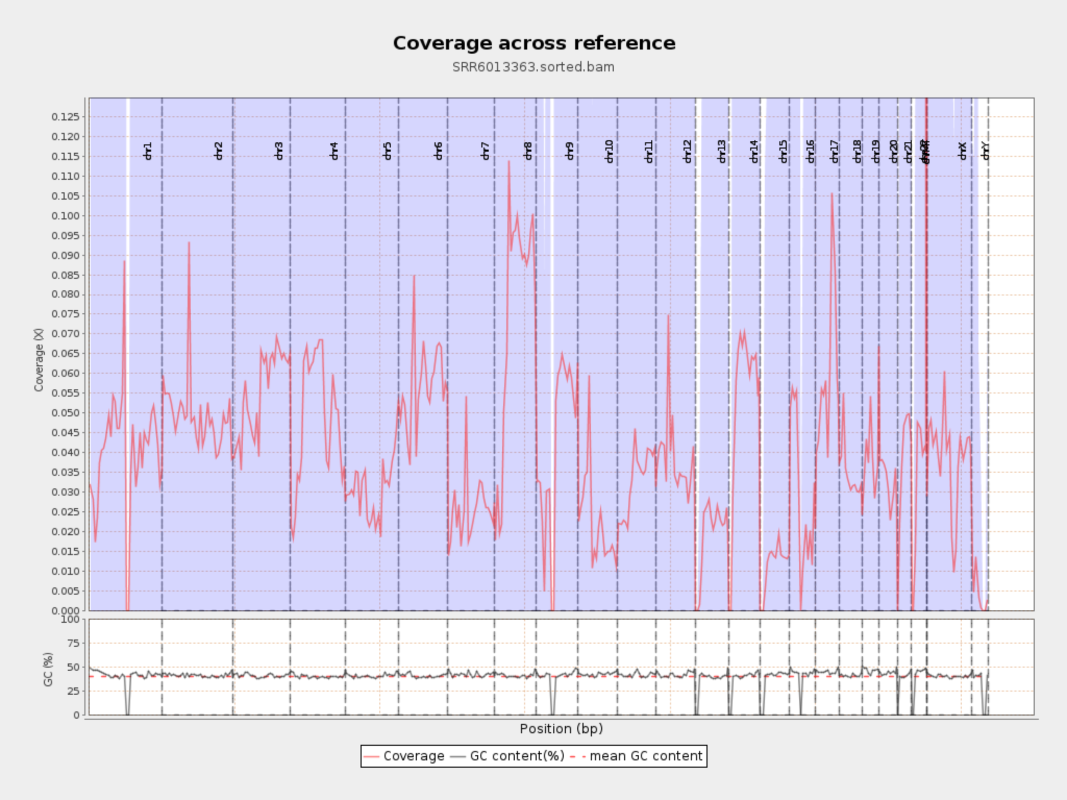
General error rate	0.84%
Mismatches	1,022,792
Insertions	9,151
Mapped reads with at least one insertion	0.49%
Deletions	29,291
Mapped reads with at least one deletion	1.55%
Homopolymer indels	46.31%

2.6. Chromosome stats

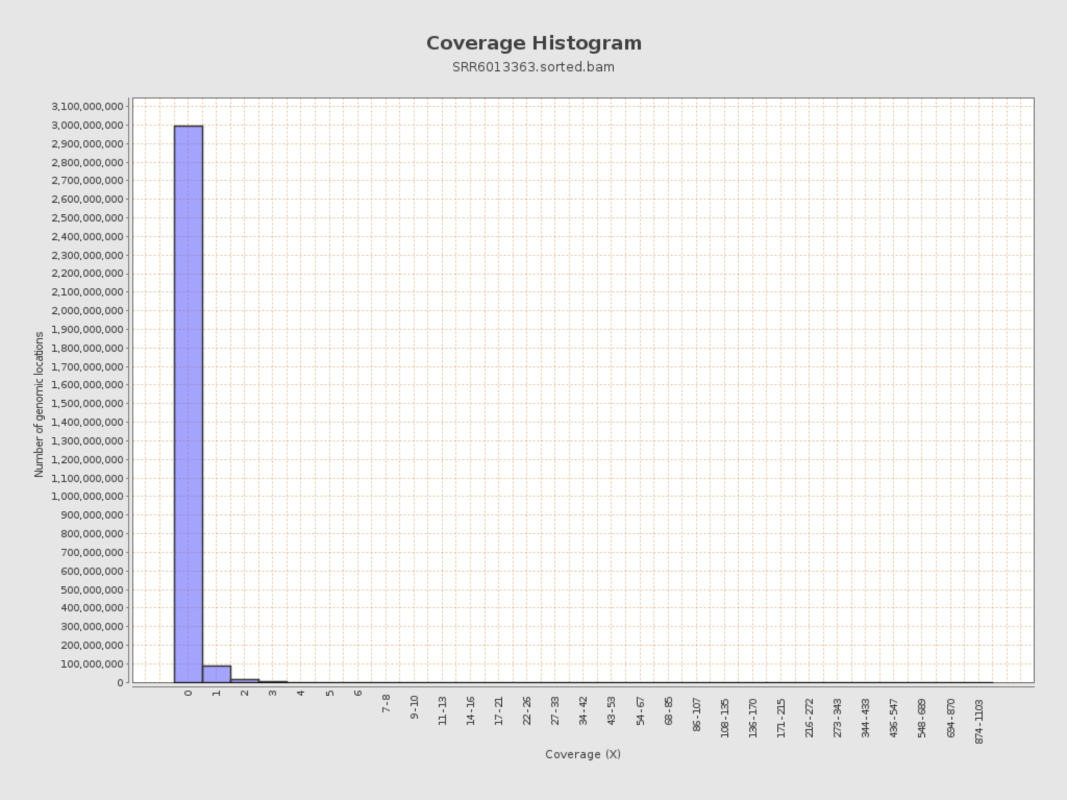
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9993349	0.0401	0.8864
chr2	243199373	12077716	0.0497	0.5507
chr3	198022430	10869619	0.0549	0.2731
chr4	191154276	9225144	0.0483	0.2816
chr5	180915260	5526359	0.0305	0.2042
chr6	171115067	9772118	0.0571	0.3863
chr7	159138663	4079494	0.0256	0.4436

chr8	146364022	11013374	0.0752	0.4886
chr9	141213431	5785469	0.041	0.4076
chr10	135534747	3024516	0.0223	0.3946
chr11	135006516	4394737	0.0326	0.3117
chr12	133851895	5200913	0.0389	0.2403
chr13	115169878	2191265	0.019	0.1612
chr14	107349540	5752921	0.0536	0.291
chr15	102531392	1190625	0.0116	0.1349
chr16	90354753	2641253	0.0292	0.2272
chr17	81195210	4864103	0.0599	0.3292
chr18	78077248	2746932	0.0352	0.7241
chr19	59128983	2321434	0.0393	0.5907
chr20	63025520	2079717	0.033	0.2207
chr21	48129895	1799272	0.0374	0.2448
chr22	51304566	1548804	0.0302	0.2001
chrMT	16571	36939	2.2291	2.0638
chrX	155270560	5969054	0.0384	0.2712
chrY	59373566	244267	0.0041	0.132

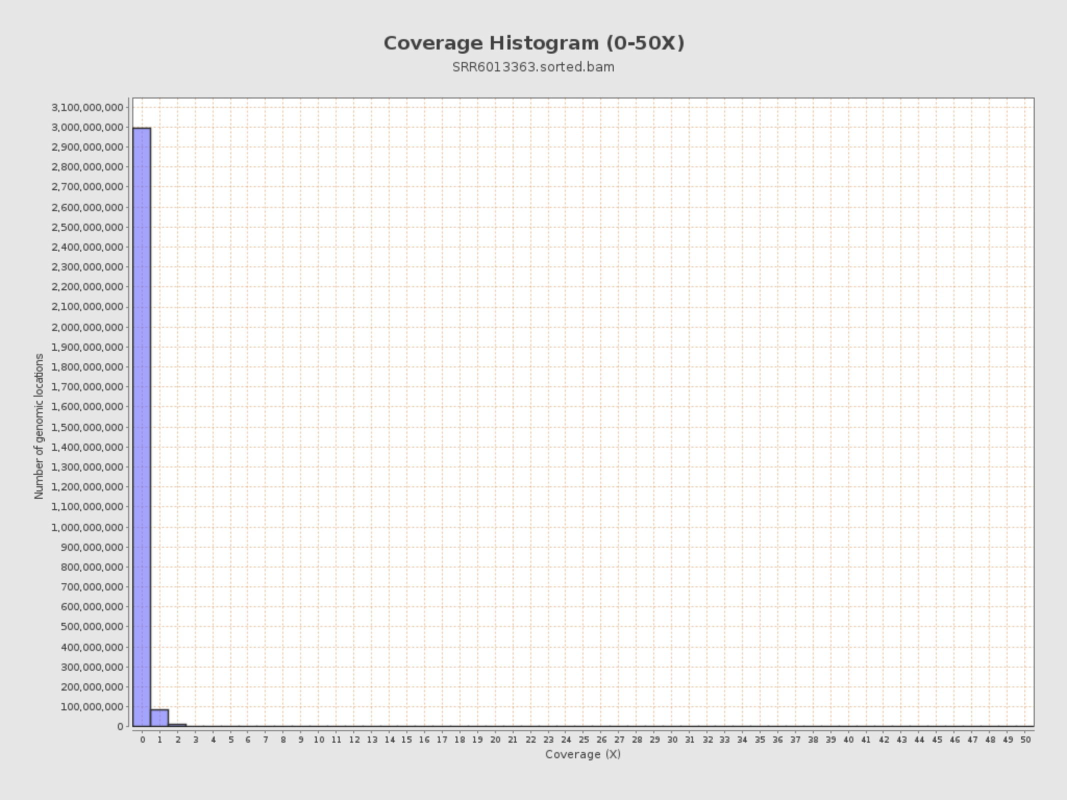
3. Results : Coverage across reference



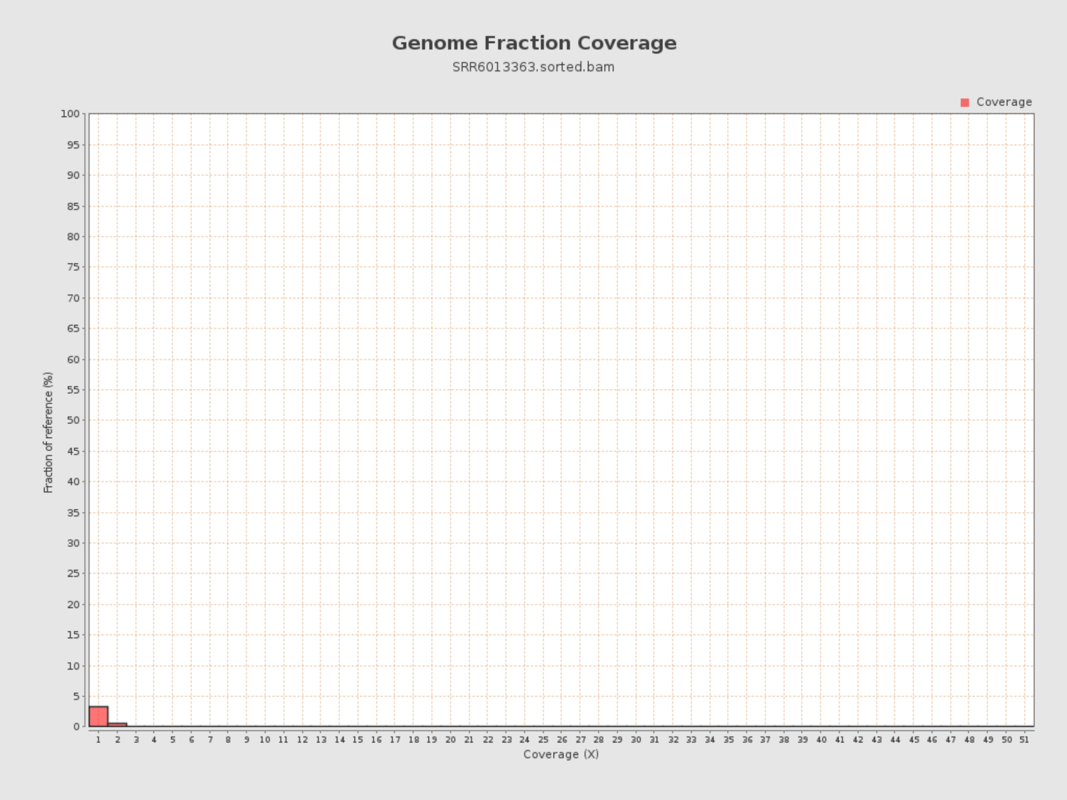
4. Results : Coverage Histogram



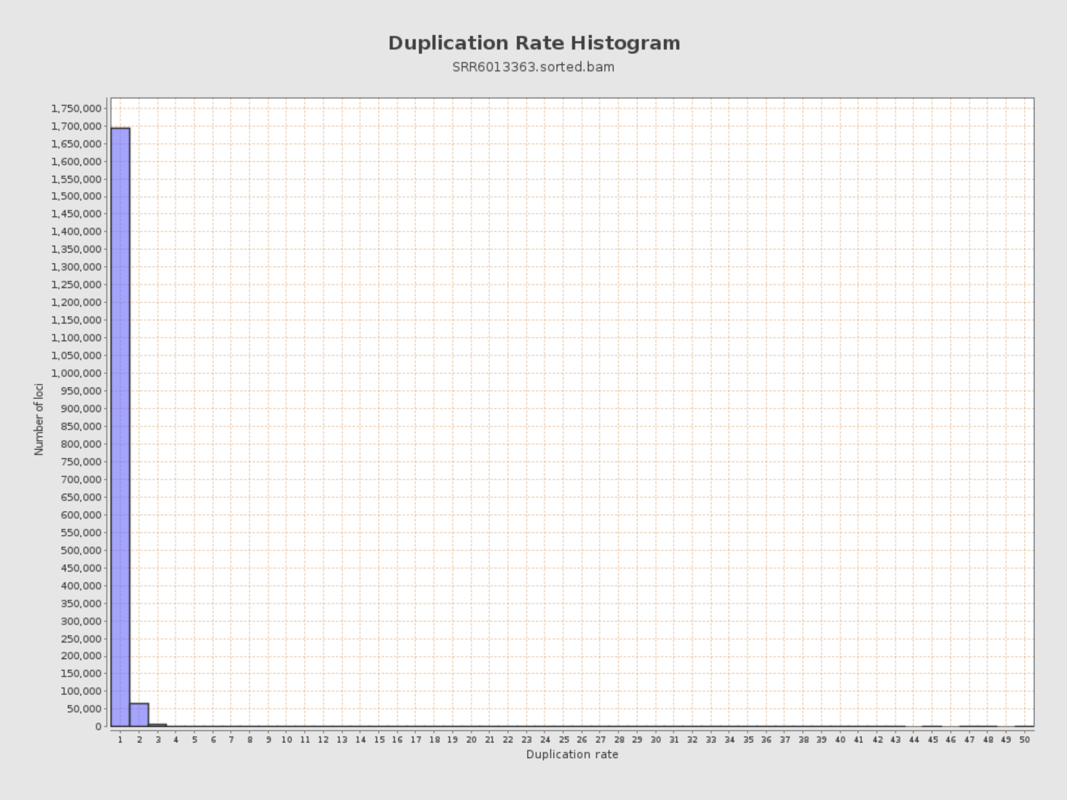
5. Results : Coverage Histogram (0-50X)



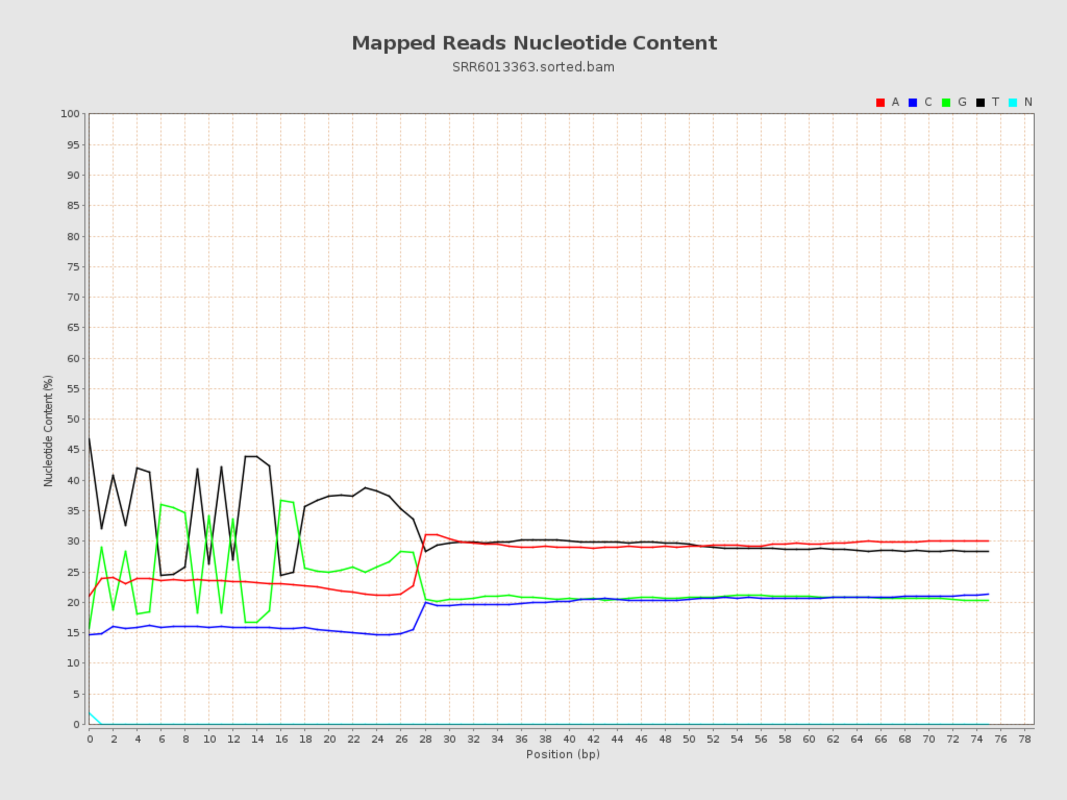
6. Results : Genome Fraction Coverage



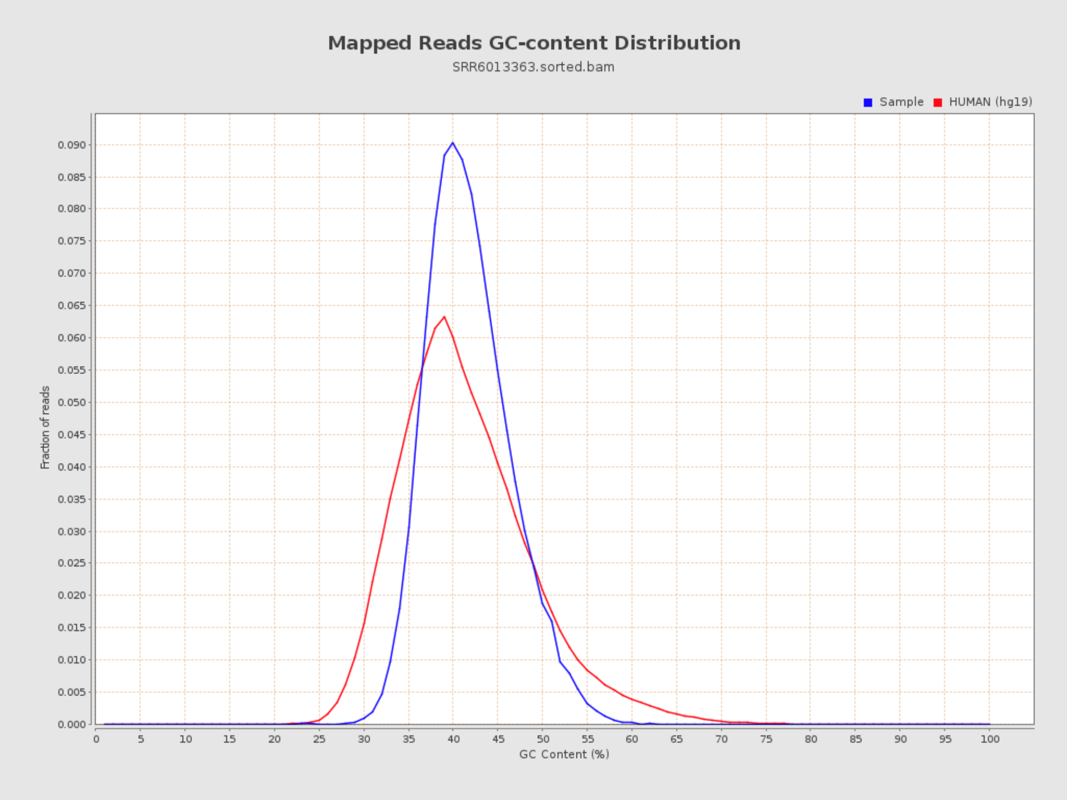
7. Results : Duplication Rate Histogram



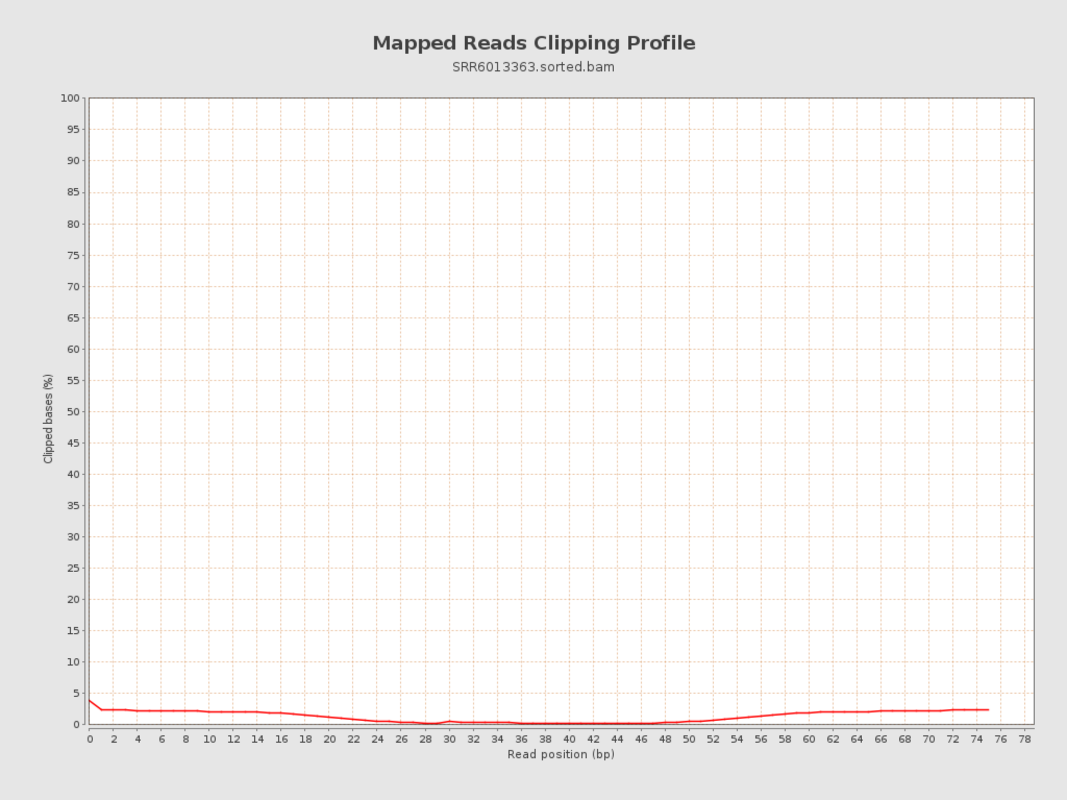
8. Results : Mapped Reads Nucleotide Content



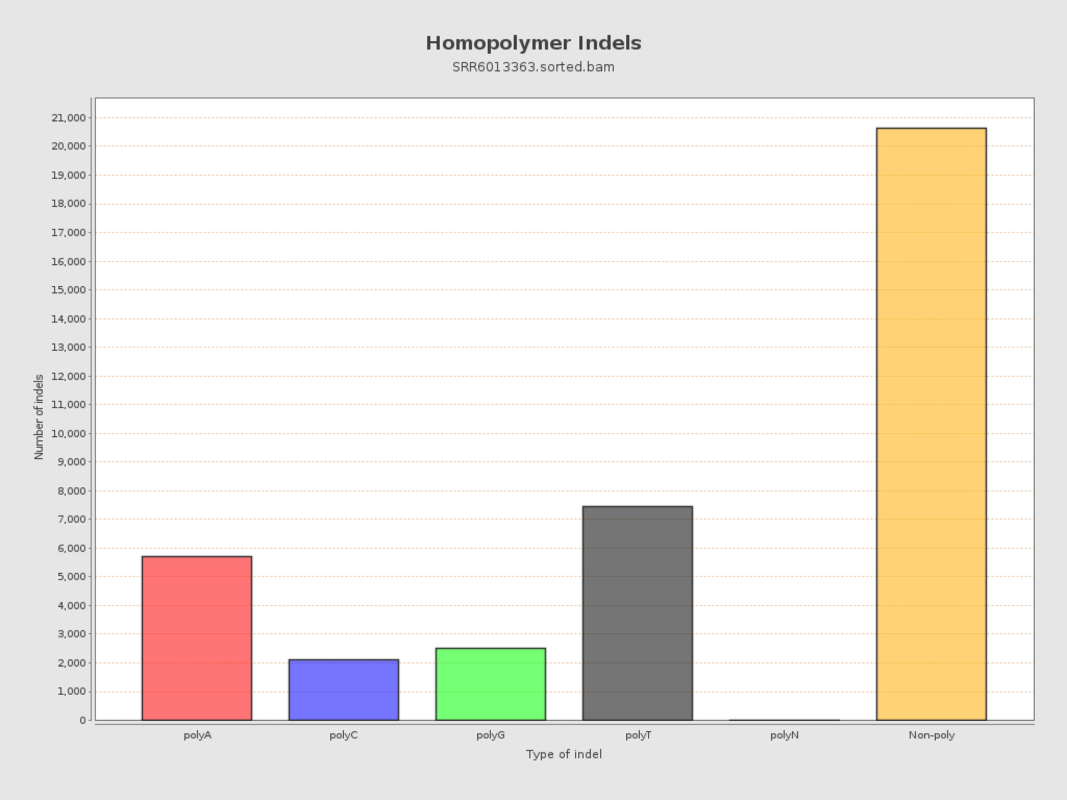
9. Results : Mapped Reads GC-content Distribution



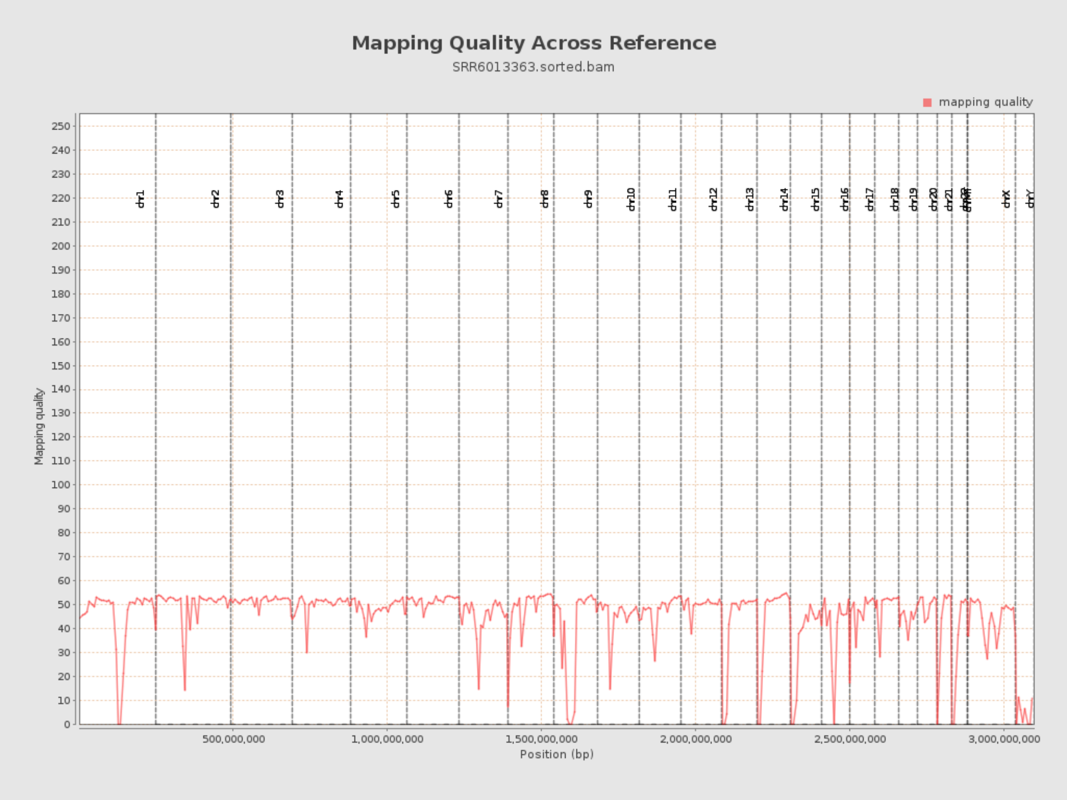
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram