Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 06:32:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472753.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_SRR3472753 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472753_1.fastq.gz SRR3472753_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 06:32:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472753.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,394,096
Mapped reads	15,250,073 / 99.06%
Unmapped reads	144,023 / 0.94%
Mapped paired reads	15,250,073 / 99.06%
Mapped reads, first in pair	7,661,119 / 49.77%
Mapped reads, second in pair	7,588,954 / 49.3%
Mapped reads, both in pair	15,151,280 / 98.42%
Mapped reads, singletons	98,793 / 0.64%
Secondary alignments	0
Supplementary alignments	56,019 / 0.36%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	9,236,331 / 60%
Duplication rate	46.72%
Clipped reads	1,086,667 / 7.06%

2.2. ACGT Content

Number/percentage of A's	422,358,594 / 28.06%
Number/percentage of C's	332,330,293 / 22.08%
Number/percentage of T's	419,118,643 / 27.84%
Number/percentage of G's	331,145,981 / 22%
Number/percentage of N's	286,834 / 0.02%

GC Percentage	44.08%

2.3. Coverage

Mean	0.4863
Standard Deviation	15.5

2.4. Mapping Quality

Mean Mapping Quality	55.41

2.5. Insert size

Mean	23,904.34
Standard Deviation	1,517,700.51
P25/Median/P75	191 / 268 / 361

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	9,988,635
Insertions	95,653
Mapped reads with at least one insertion	0.62%
Deletions	94,686
Mapped reads with at least one deletion	0.61%
Homopolymer indels	46.03%

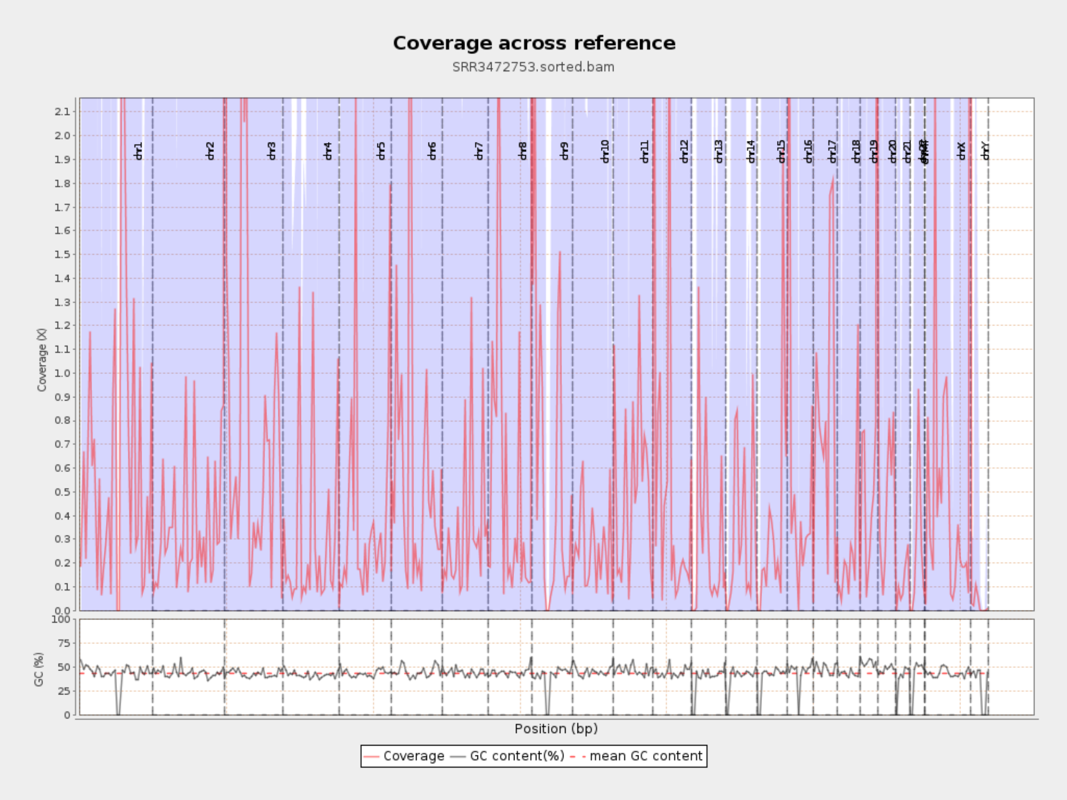
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

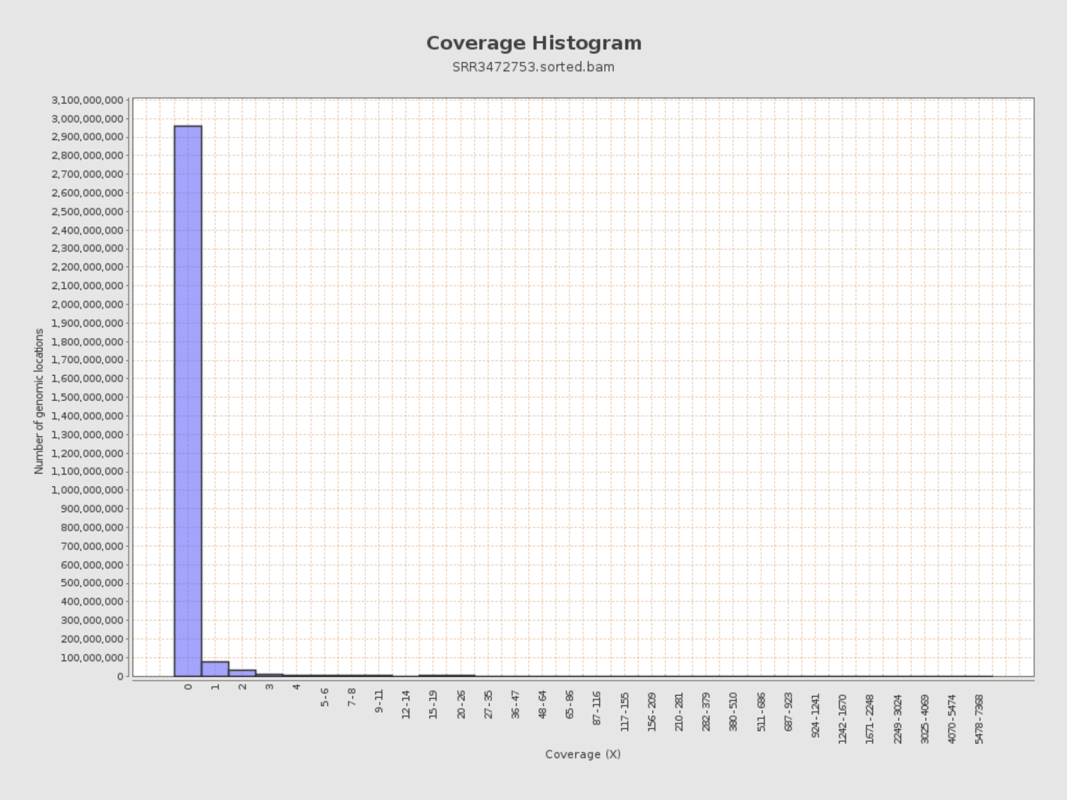
		bases	coverage	deviation
chr1	249250621	161457316	0.6478	18.7834
chr2	243199373	83436300	0.3431	10.3728
chr3	198022430	187645580	0.9476	20.8795
chr4	191154276	55584470	0.2908	11.892
chr5	180915260	77494728	0.4283	19.4484
chr6	171115067	103286890	0.6036	16.3509
chr7	159138663	54963908	0.3454	9.2113
chr8	146364022	80502129	0.55	16.2298
chr9	141213431	89061275	0.6307	16.2605
chr10	135534747	36286503	0.2677	8.9543
chr11	135006516	69582723	0.5154	15.5723
chr12	133851895	84484263	0.6312	19.7411
chr13	115169878	35271515	0.3063	10.2752
chr14	107349540	34994595	0.326	11.7834
chr15	102531392	38639771	0.3769	12.2135
chr16	90354753	52492675	0.581	18.8627
chr17	81195210	65222661	0.8033	17.8199
chr18	78077248	21071612	0.2699	9.6265
chr19	59128983	34279184	0.5797	18.0473
chr20	63025520	30003723	0.4761	12.1698
chr21	48129895	5733538	0.1191	4.5828
chr22	51304566	13239036	0.258	8.6072
chrMT	16571	1543	0.0931	0.3305
chrX	155270560	89015307	0.5733	22.0964

chrY	59373566	1712664	0.0288	1.0271

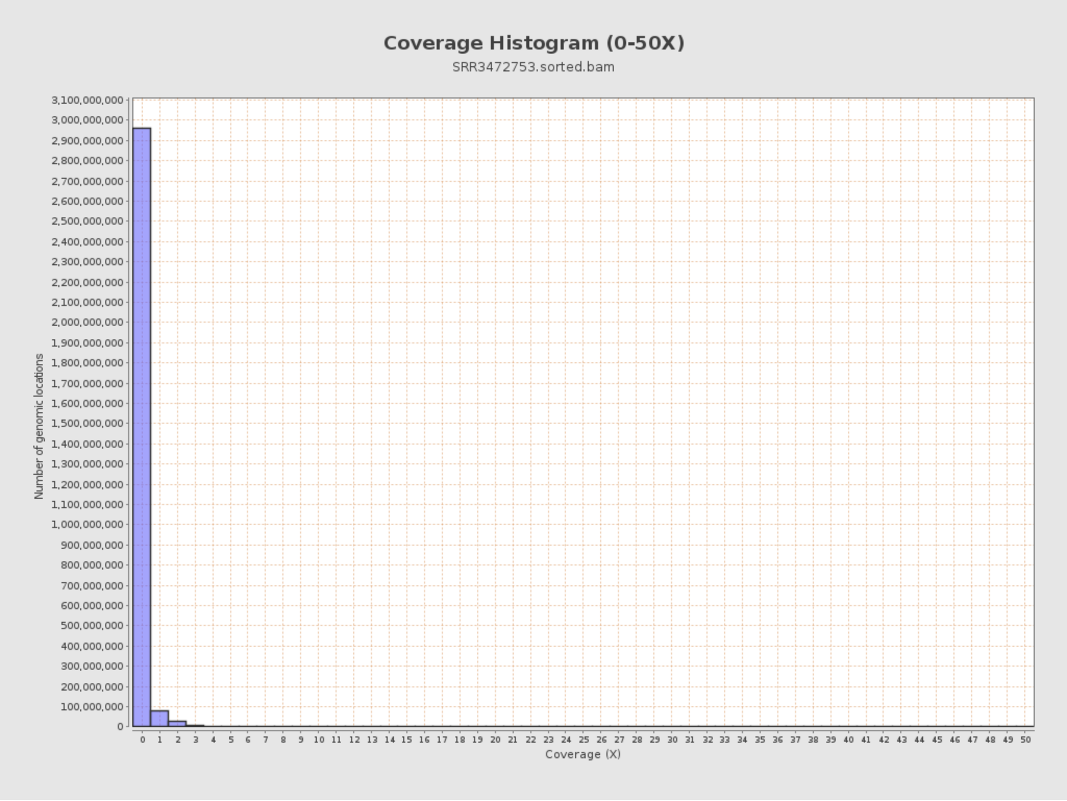
3. Results : Coverage across reference



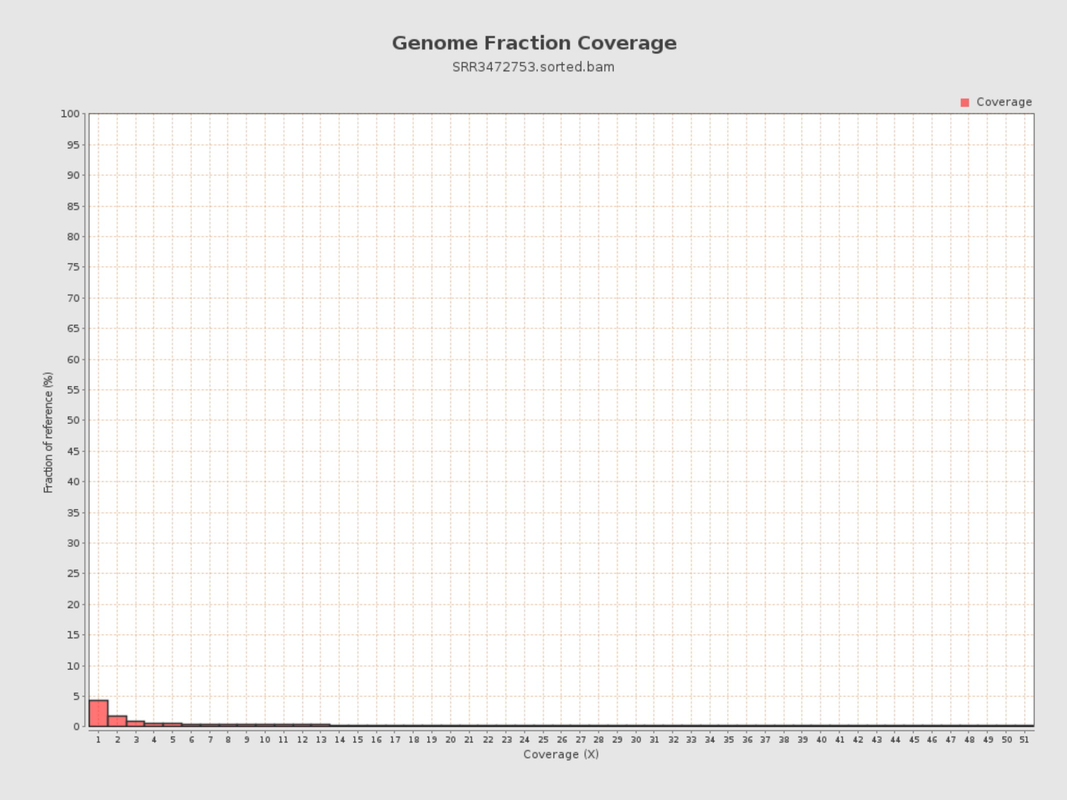
4. Results : Coverage Histogram



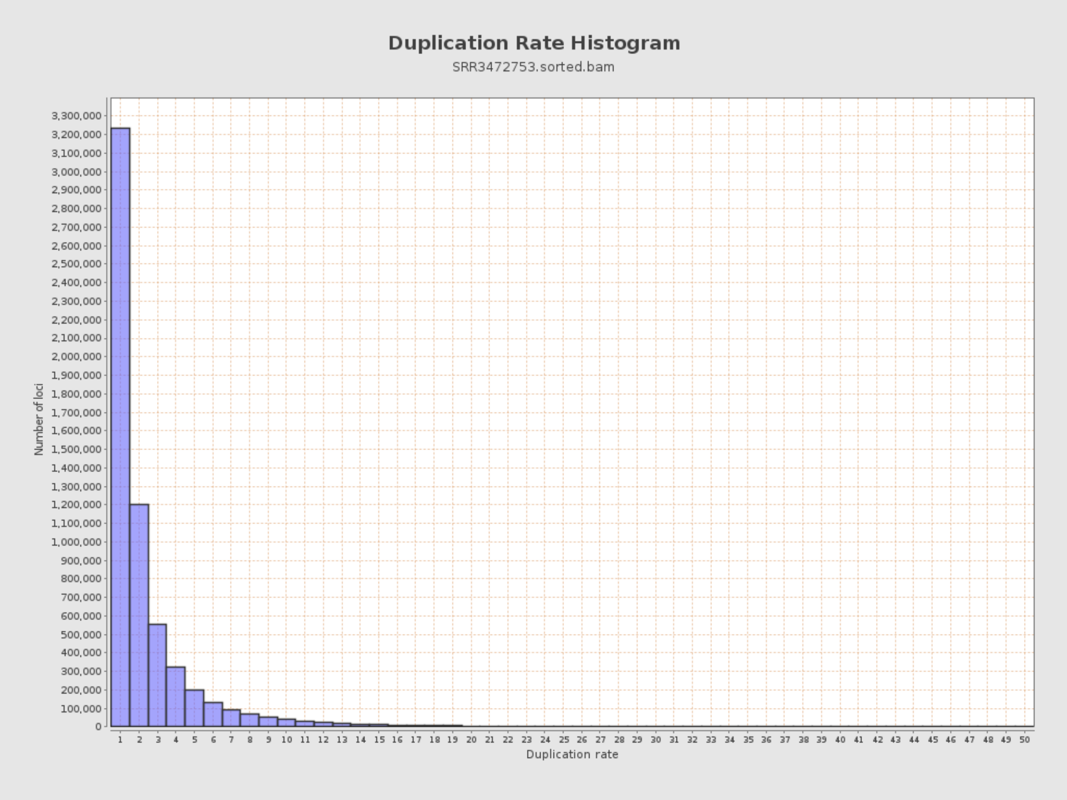
5. Results : Coverage Histogram (0-50X)



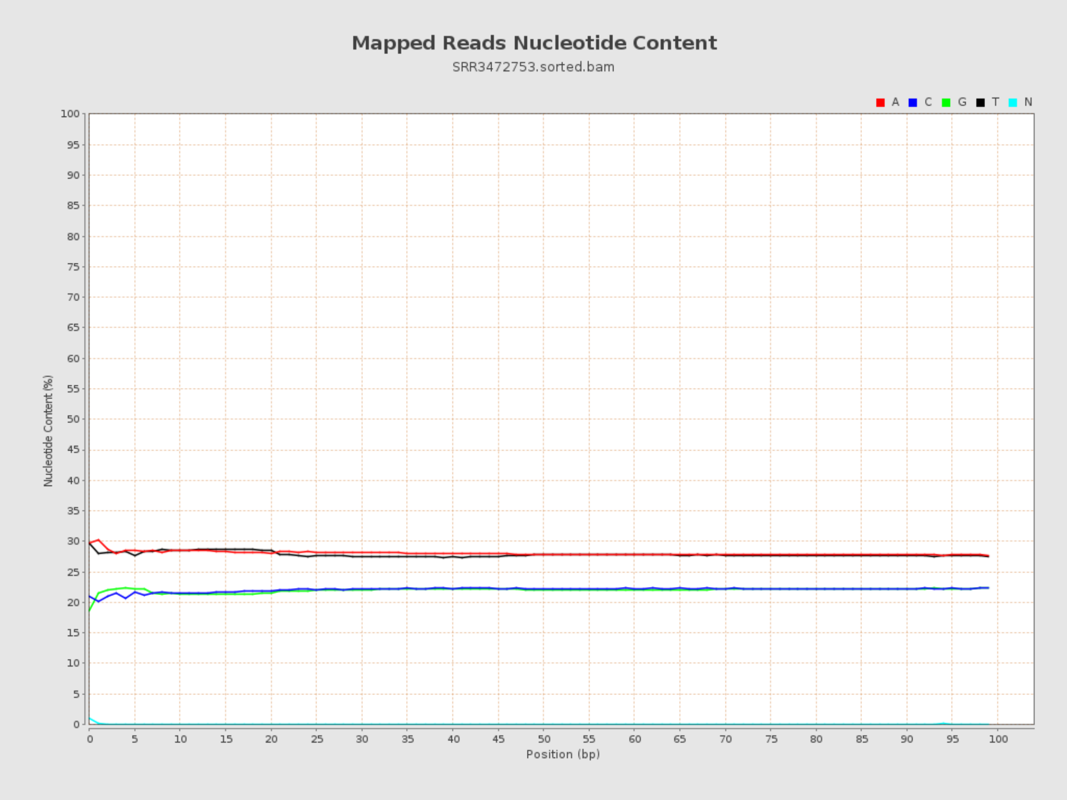
6. Results : Genome Fraction Coverage



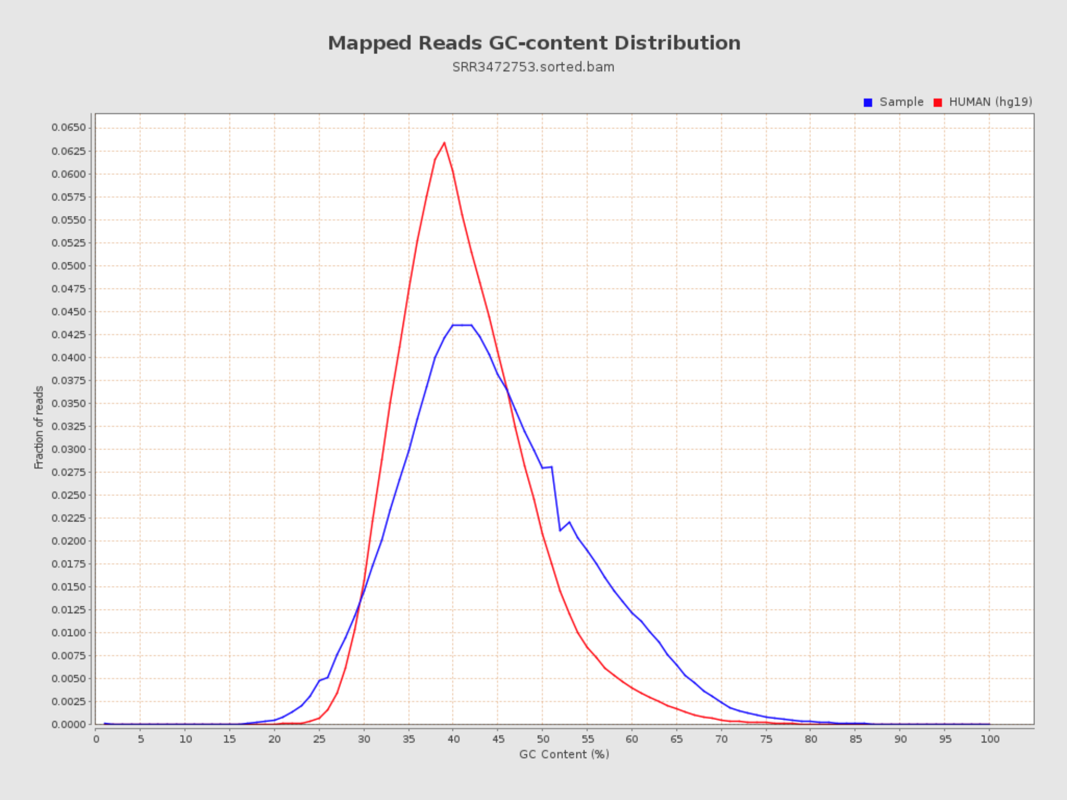
7. Results : Duplication Rate Histogram



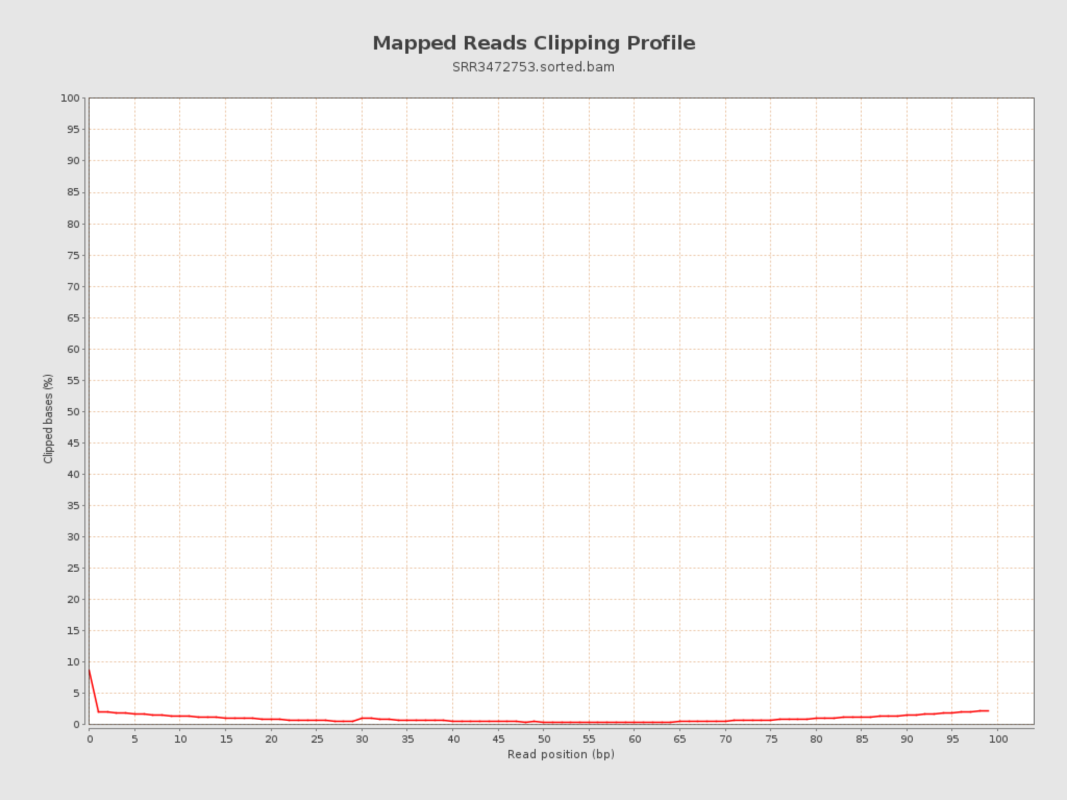
8. Results : Mapped Reads Nucleotide Content



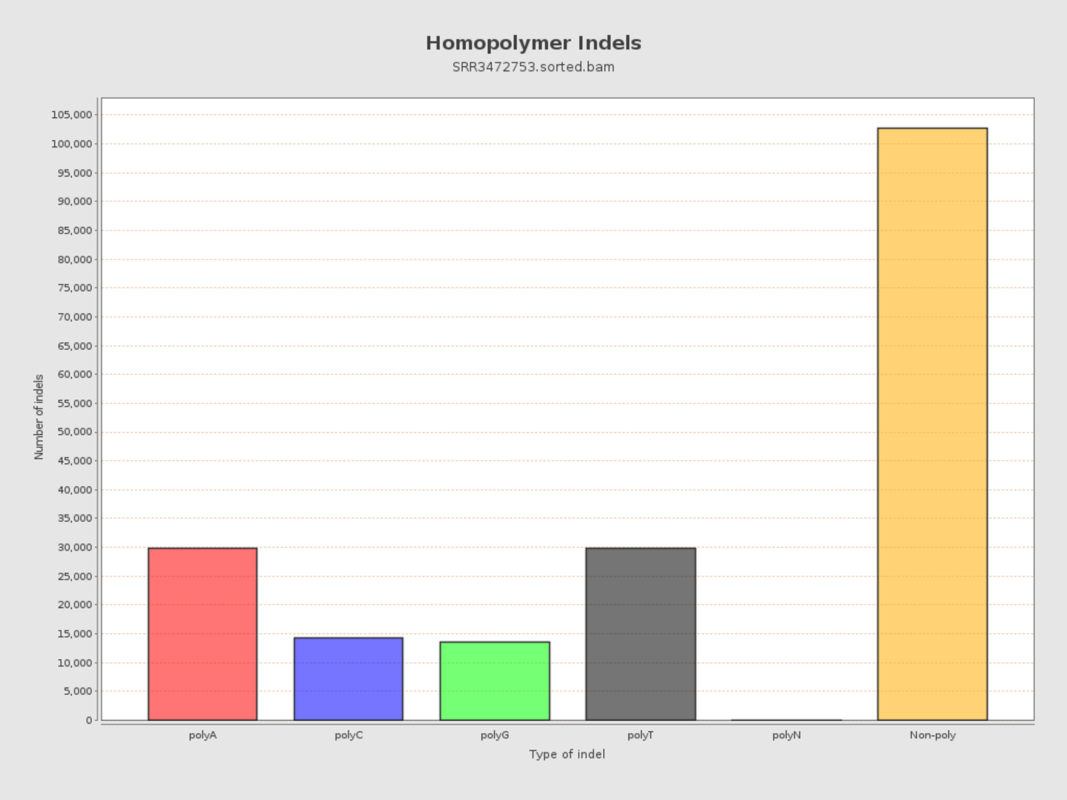
9. Results : Mapped Reads GC-content Distribution



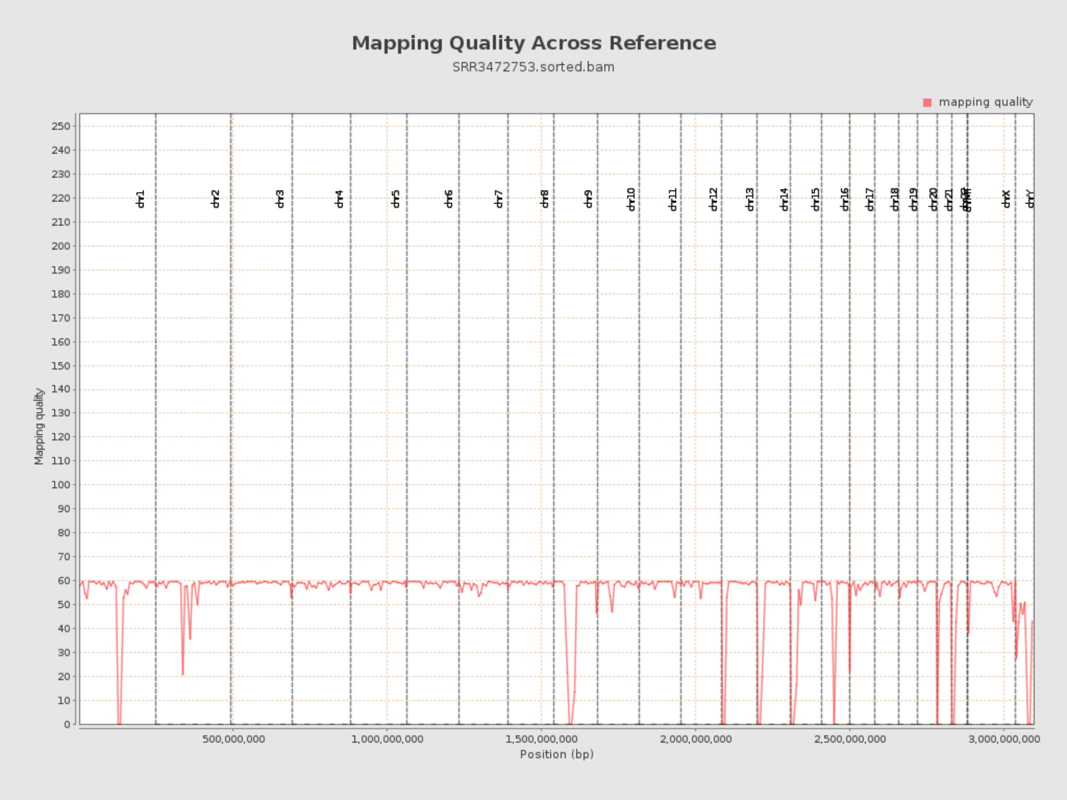
10. Results : Mapped Reads Clipping Profile



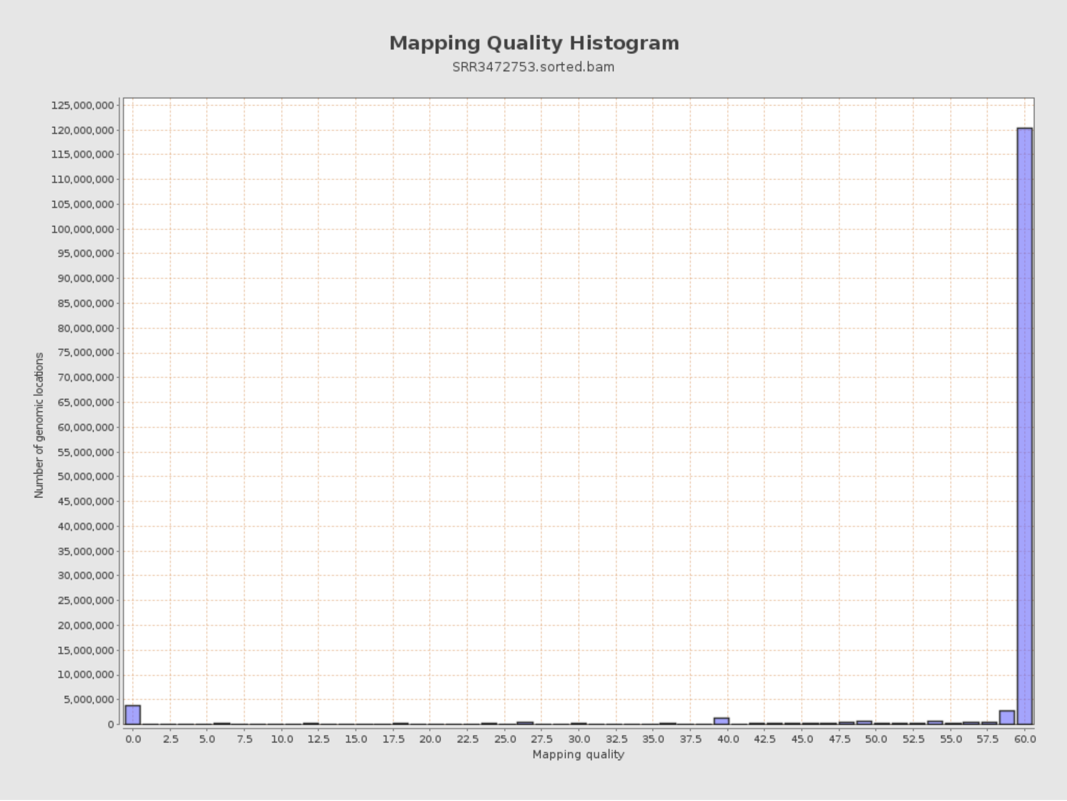
11. Results : Homopolymer Indels



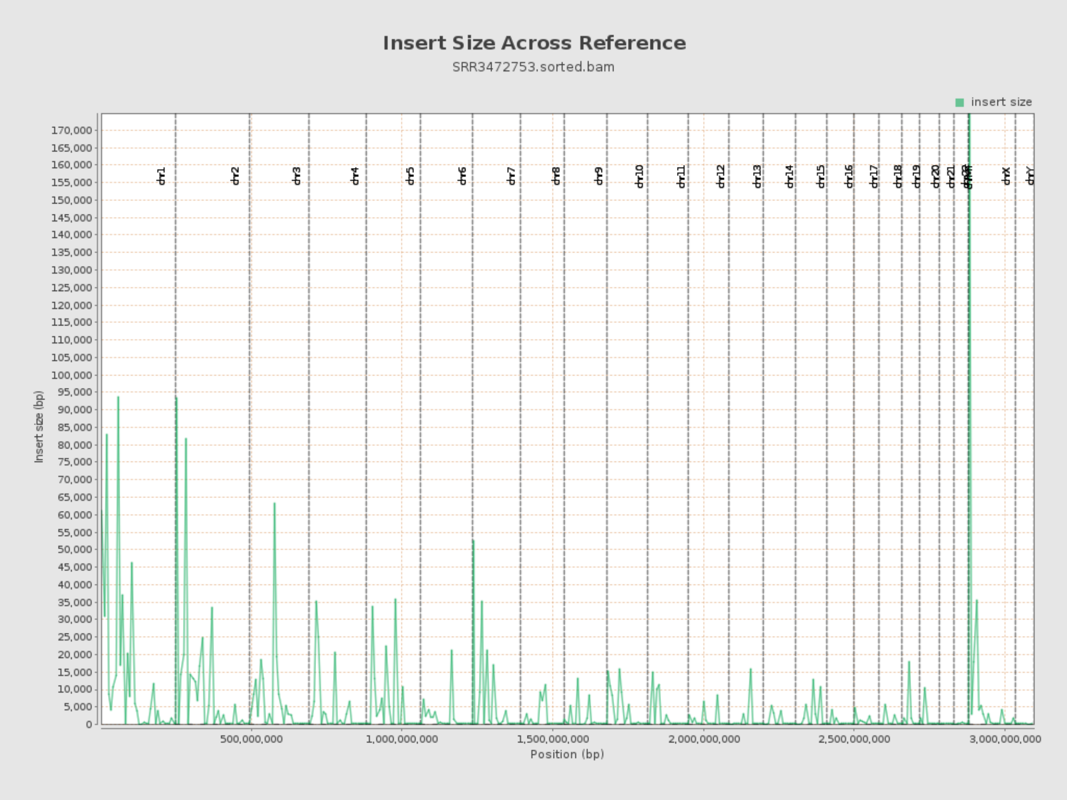
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram