Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:13:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472487.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_SRR3472487 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472487_1.fastq.gz SRR3472487_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:13:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472487.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,672,406
Mapped reads	19,353,746 / 98.38%
Unmapped reads	318,660 / 1.62%
Mapped paired reads	19,353,746 / 98.38%
Mapped reads, first in pair	9,724,122 / 49.43%
Mapped reads, second in pair	9,629,624 / 48.95%
Mapped reads, both in pair	19,200,628 / 97.6%
Mapped reads, singletons	153,118 / 0.78%
Secondary alignments	0
Supplementary alignments	92,833 / 0.47%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	12,933,396 / 65.74%
Duplication rate	45.48%
Clipped reads	1,636,626 / 8.32%

2.2. ACGT Content

Number/percentage of A's	524,067,665 / 27.52%
Number/percentage of C's	431,174,114 / 22.64%
Number/percentage of T's	520,287,223 / 27.32%
Number/percentage of G's	428,695,800 / 22.51%
Number/percentage of N's	293,343 / 0.02%

GC Percentage	45.15%

2.3. Coverage

Mean	0.6153
Standard Deviation	26.0078

2.4. Mapping Quality

Mean Mapping Quality	55.09

2.5. Insert size

Mean	34,521.32
Standard Deviation	1,813,586.55
P25/Median/P75	172 / 241 / 326

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	12,087,613
Insertions	110,068
Mapped reads with at least one insertion	0.56%
Deletions	106,608
Mapped reads with at least one deletion	0.55%
Homopolymer indels	42.08%

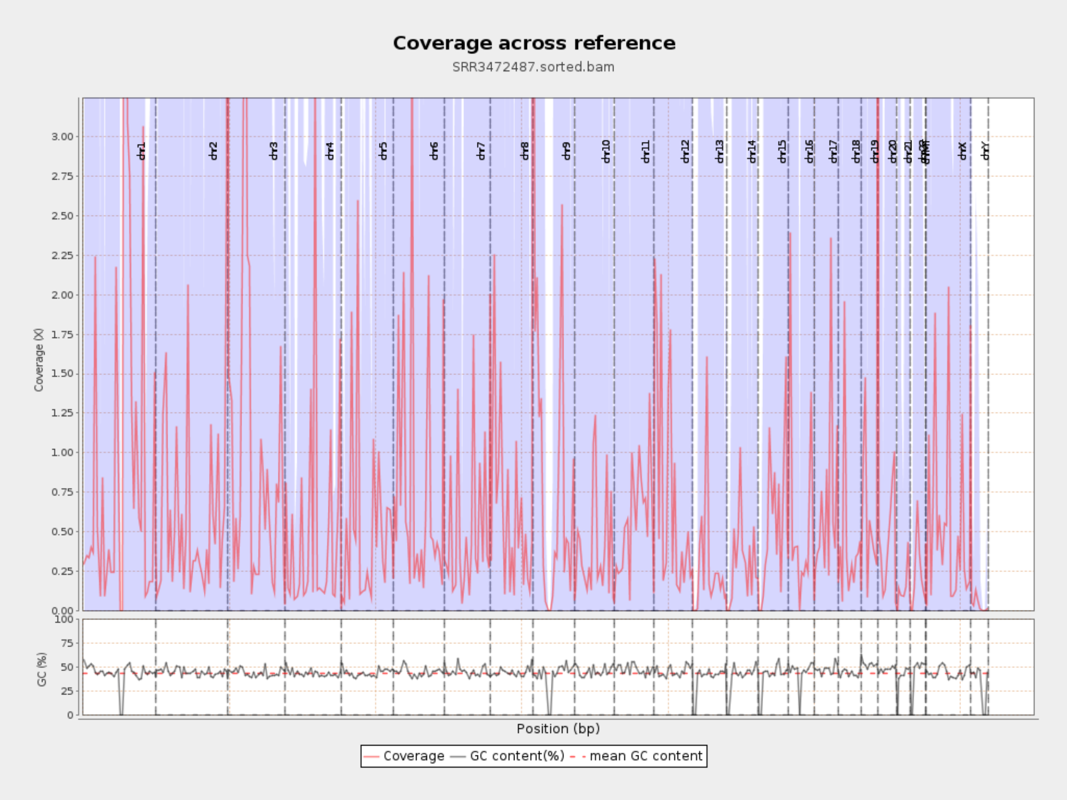
2.7. Chromosome stats

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

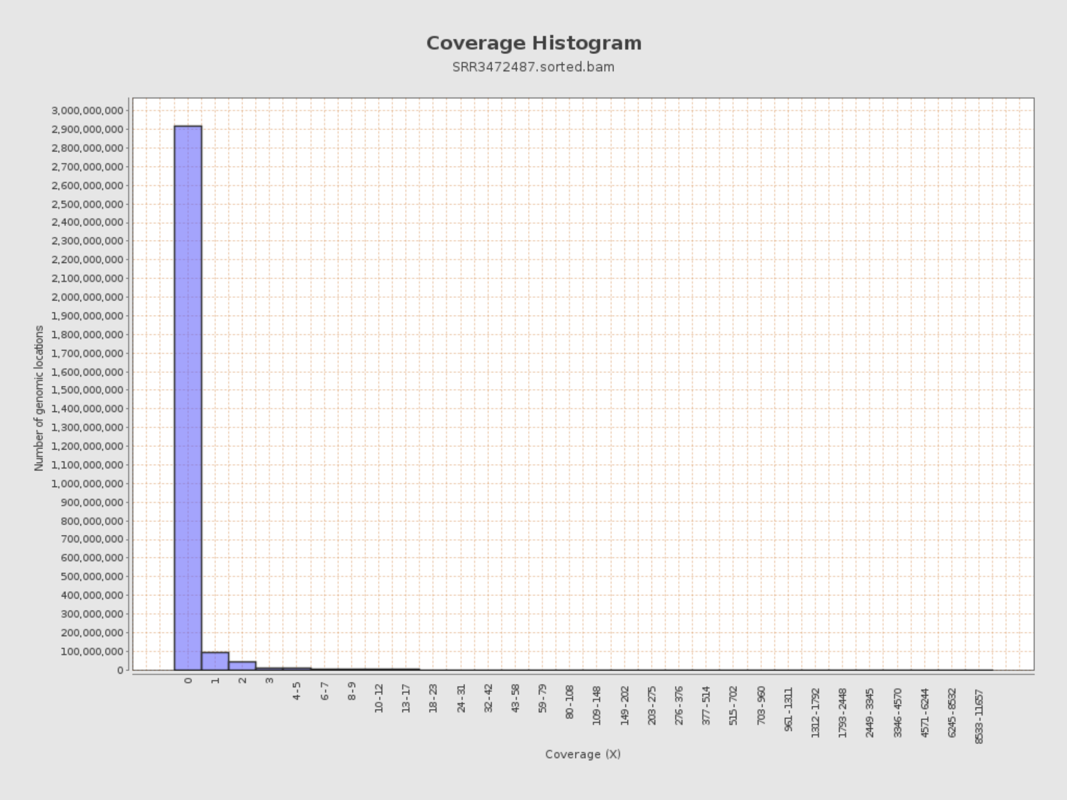
		bases	coverage	deviation
chr1	249250621	247377866	0.9925	43.367
chr2	243199373	140488893	0.5777	24.839
chr3	198022430	214325080	1.0823	27.9395
chr4	191154276	99863117	0.5224	38.5302
chr5	180915260	96973052	0.536	20.5087
chr6	171115067	135584893	0.7924	25.6591
chr7	159138663	78947580	0.4961	20.5287
chr8	146364022	89925282	0.6144	24.2598
chr9	141213431	109952848	0.7786	28.6801
chr10	135534747	56941810	0.4201	17.5619
chr11	135006516	78114415	0.5786	21.7996
chr12	133851895	103100113	0.7703	29.1102
chr13	115169878	31640569	0.2747	11.7556
chr14	107349540	34272773	0.3193	10.7506
chr15	102531392	58072597	0.5664	20.8839
chr16	90354753	50248086	0.5561	14.5929
chr17	81195210	54948108	0.6767	21.3004
chr18	78077248	34128115	0.4371	28.7504
chr19	59128983	49061561	0.8297	36.1216
chr20	63025520	29029859	0.4606	19.4258
chr21	48129895	7403640	0.1538	5.6251
chr22	51304566	11773120	0.2295	6.7487
chrMT	16571	7037	0.4247	1.2515
chrX	155270560	90398941	0.5822	19.7492

chrY	59373566	2167769	0.0365	1.1975

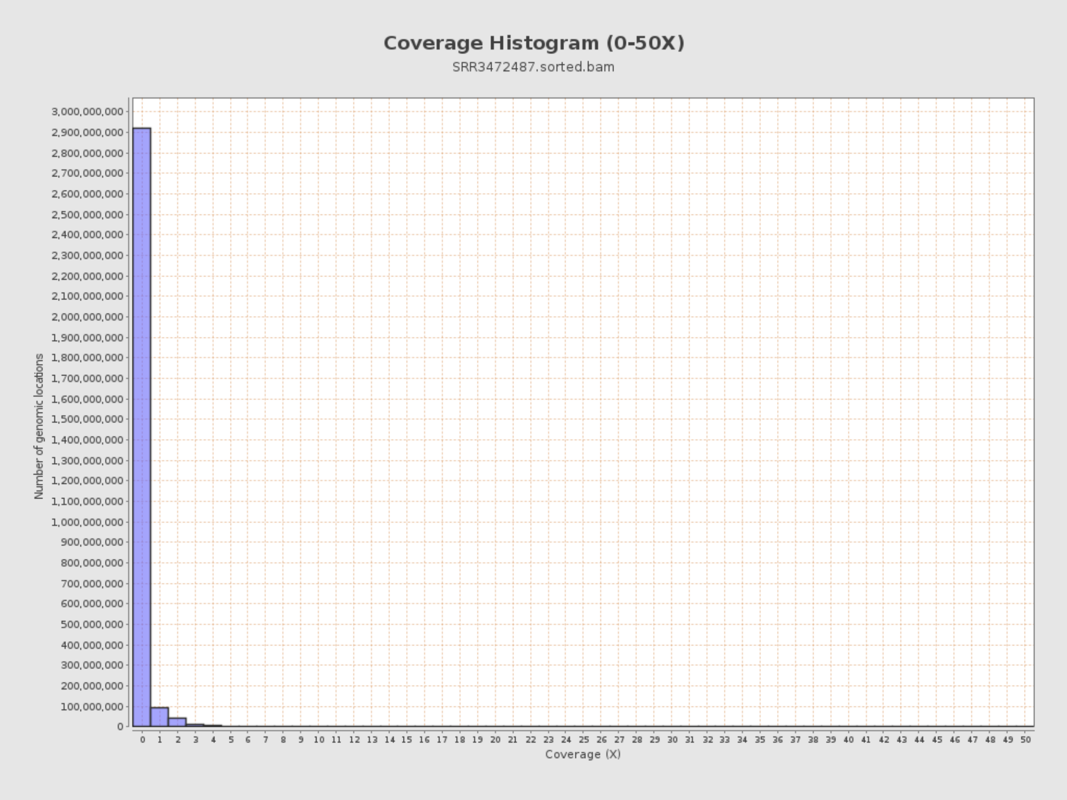
3. Results : Coverage across reference



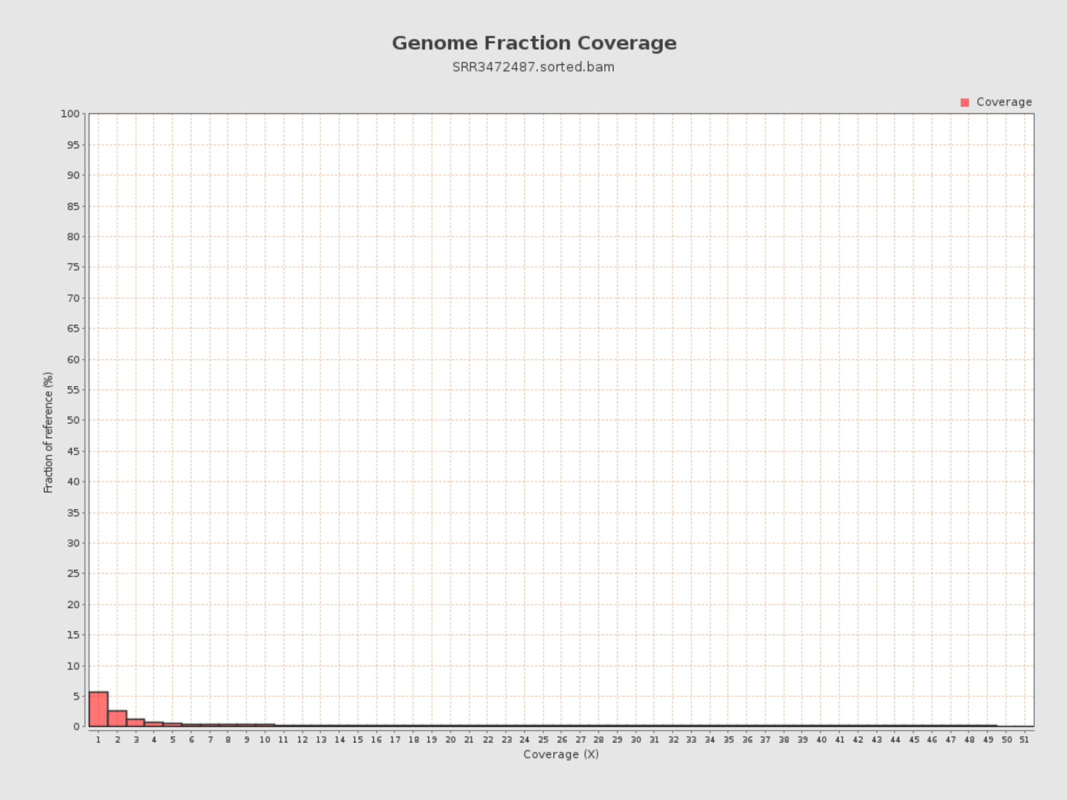
4. Results : Coverage Histogram



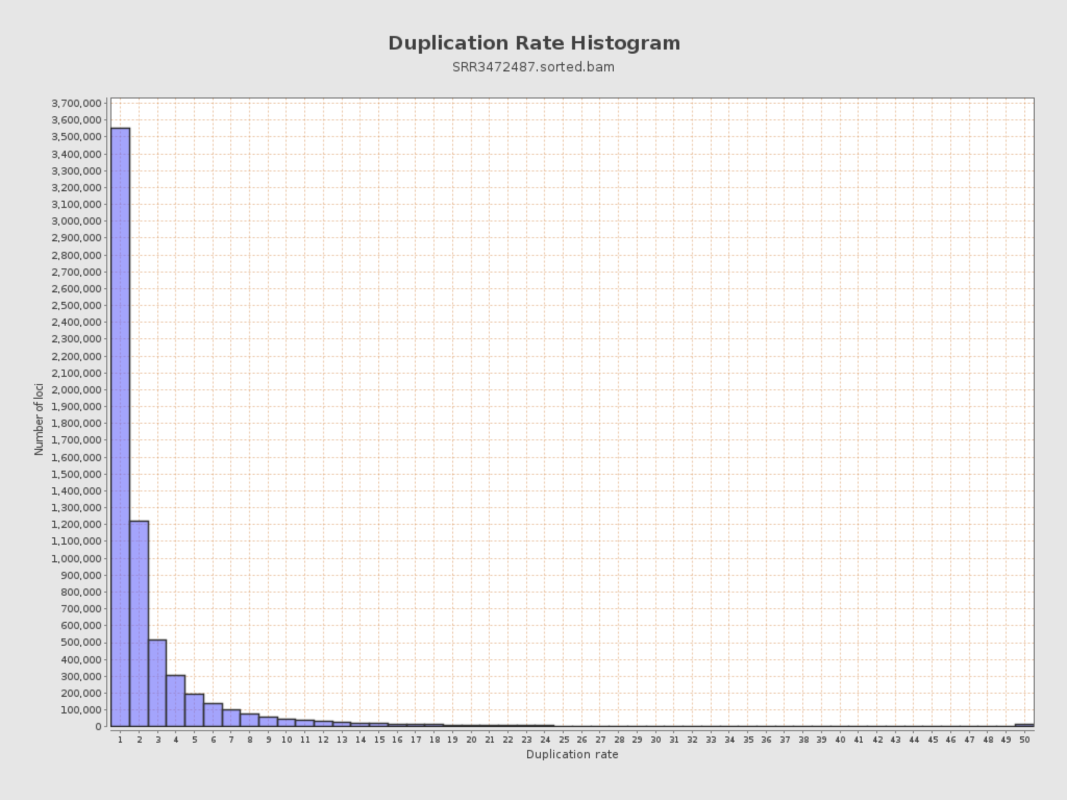
5. Results : Coverage Histogram (0-50X)



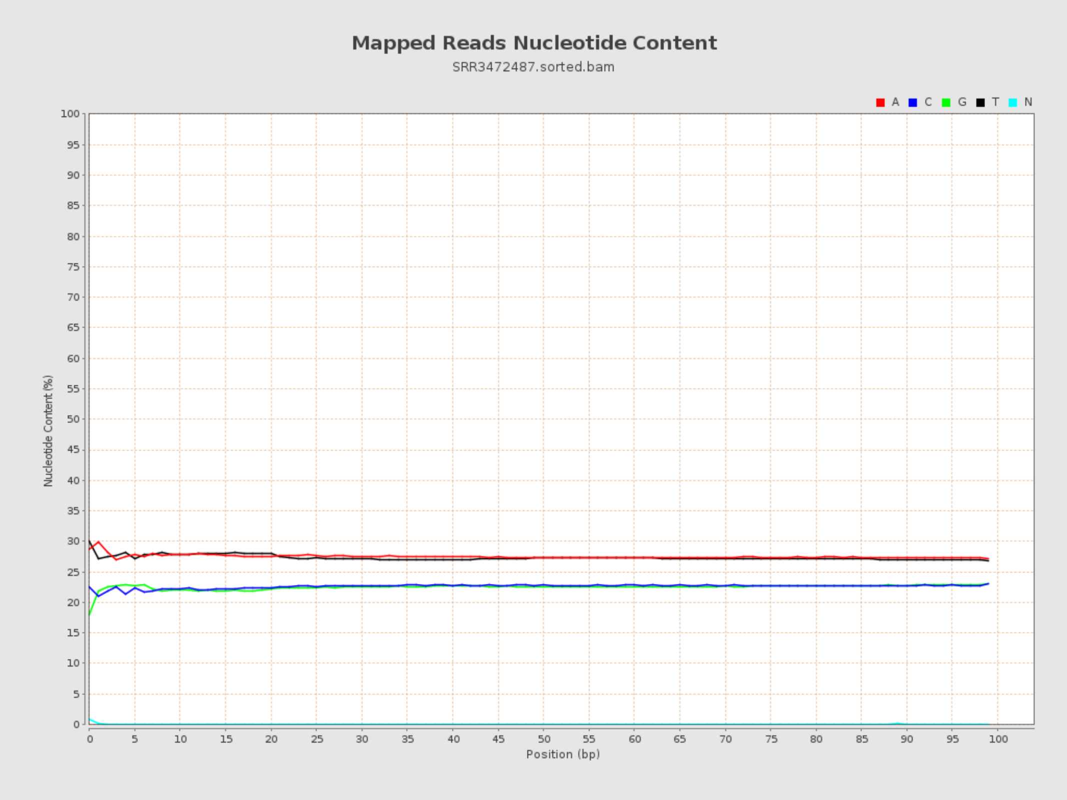
6. Results : Genome Fraction Coverage



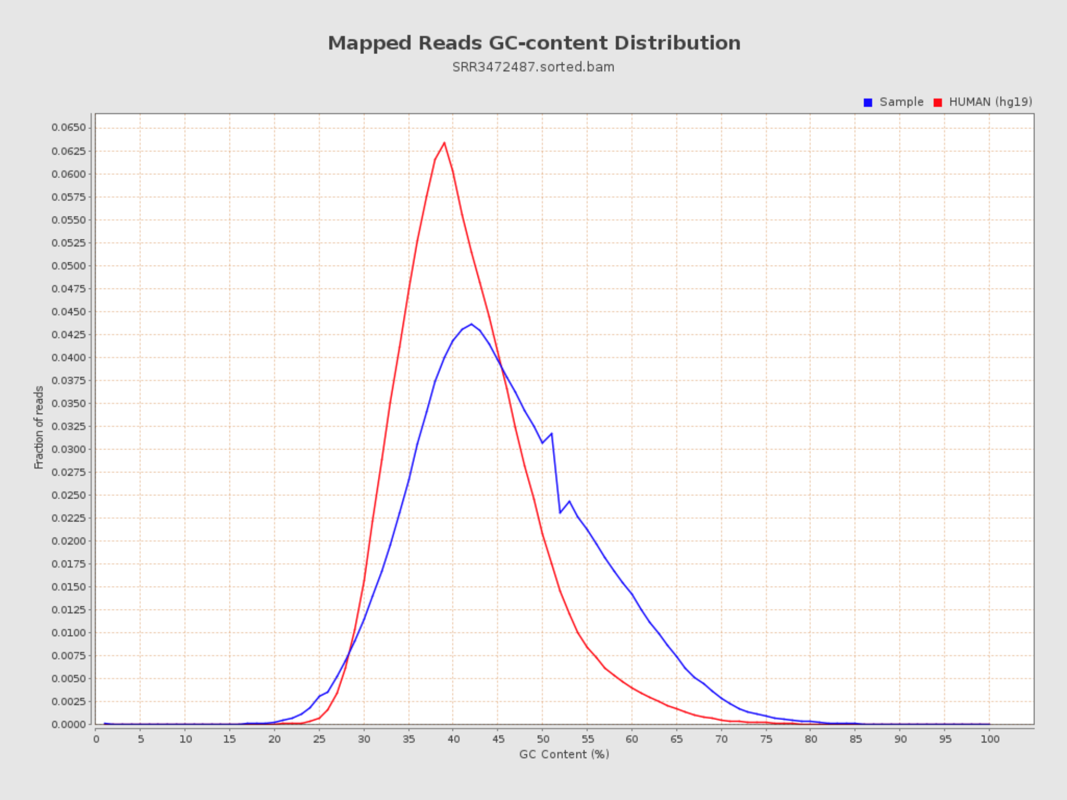
7. Results : Duplication Rate Histogram



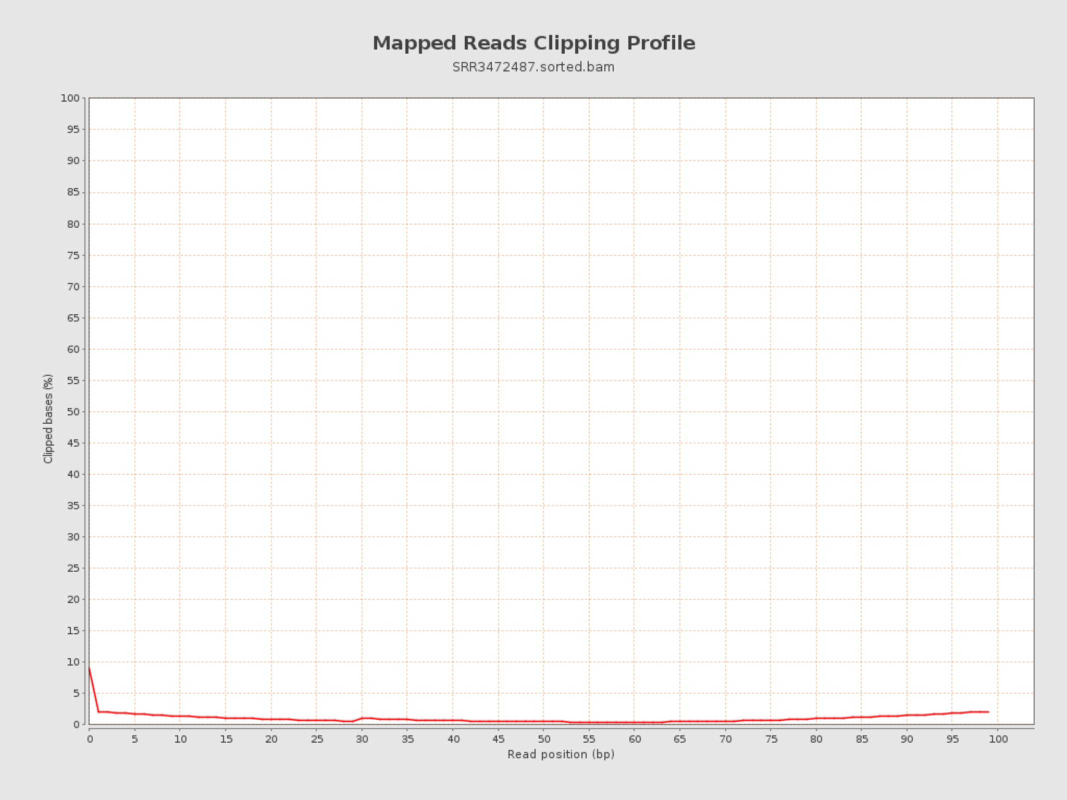
8. Results : Mapped Reads Nucleotide Content



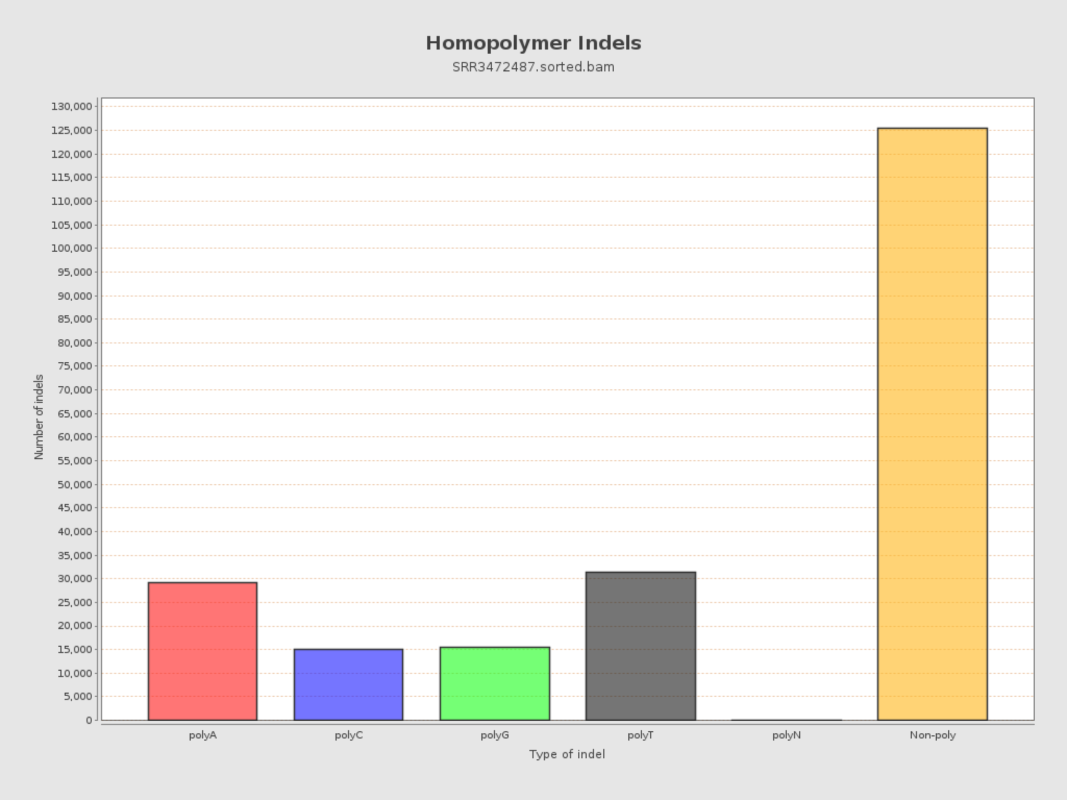
9. Results : Mapped Reads GC-content Distribution



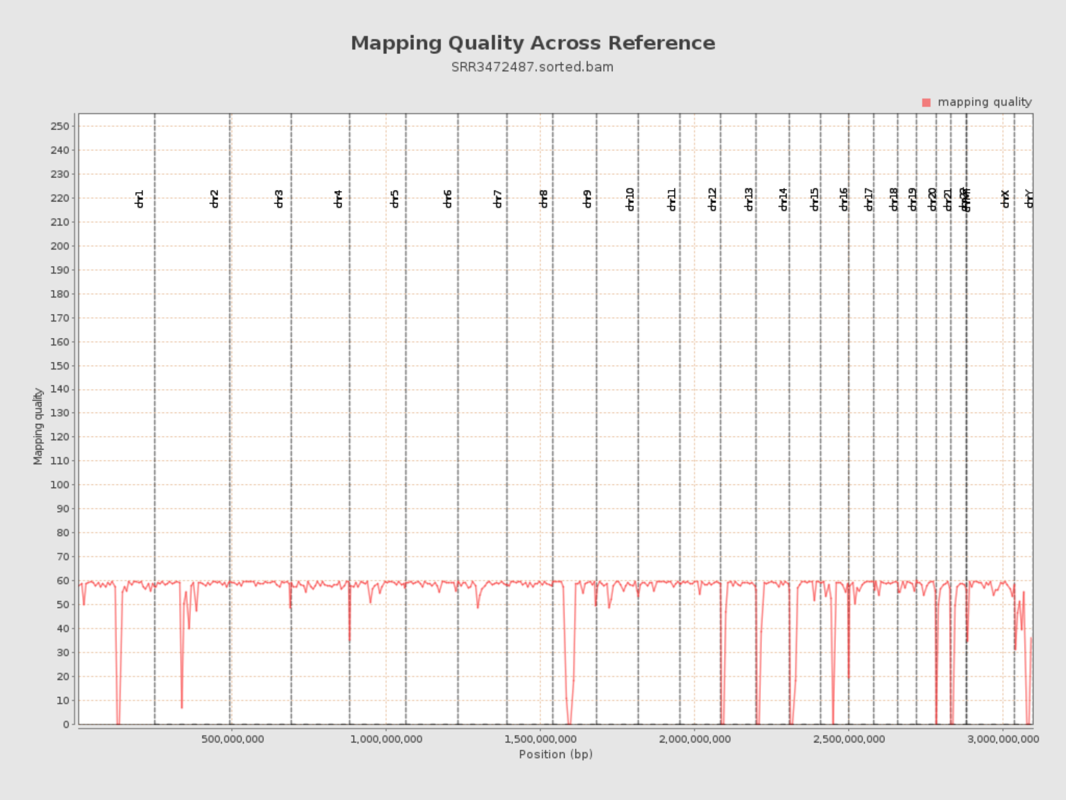
10. Results : Mapped Reads Clipping Profile



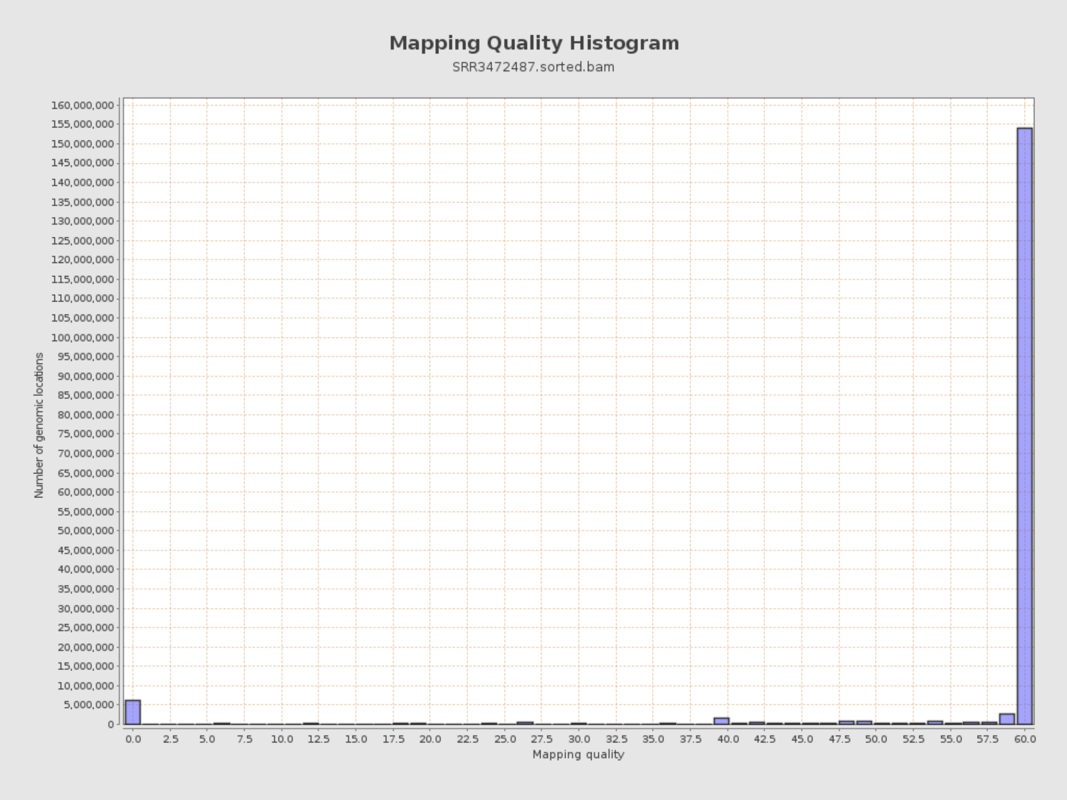
11. Results : Homopolymer Indels



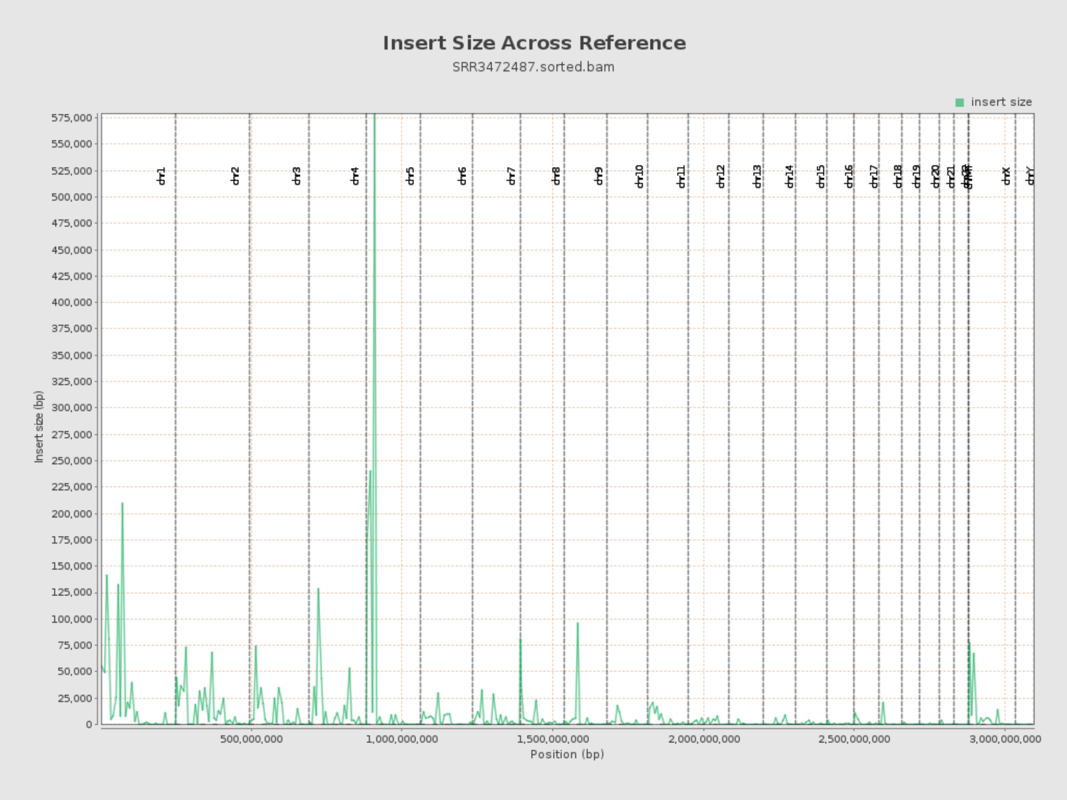
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram