Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 09:44:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472610.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_SRR3472610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472610_1.fastq.gz SRR3472610_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 09:44:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472610.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,335,212
Mapped reads	34,047,272 / 99.16%
Unmapped reads	287,940 / 0.84%
Mapped paired reads	34,047,272 / 99.16%
Mapped reads, first in pair	17,063,453 / 49.7%
Mapped reads, second in pair	16,983,819 / 49.46%
Mapped reads, both in pair	33,866,140 / 98.63%
Mapped reads, singletons	181,132 / 0.53%
Secondary alignments	0
Supplementary alignments	140,512 / 0.41%
Read min/max/mean length	30 / 101 / 99.67
Duplicated reads (estimated)	25,703,417 / 74.86%
Duplication rate	51.18%
Clipped reads	3,266,275 / 9.51%

2.2. ACGT Content

Number/percentage of A's	877,924,856 / 26.37%
Number/percentage of C's	792,867,823 / 23.82%
Number/percentage of T's	873,667,241 / 26.24%
Number/percentage of G's	784,060,444 / 23.55%
Number/percentage of N's	648,132 / 0.02%

GC Percentage	47.37%

2.3. Coverage

Mean	1.0755
Standard Deviation	43.6704

2.4. Mapping Quality

Mean Mapping Quality	54.93

2.5. Insert size

Mean	16,056.82
Standard Deviation	1,261,334.79
P25/Median/P75	137 / 191 / 260

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	19,643,475
Insertions	174,093
Mapped reads with at least one insertion	0.51%
Deletions	145,780
Mapped reads with at least one deletion	0.42%
Homopolymer indels	46.15%

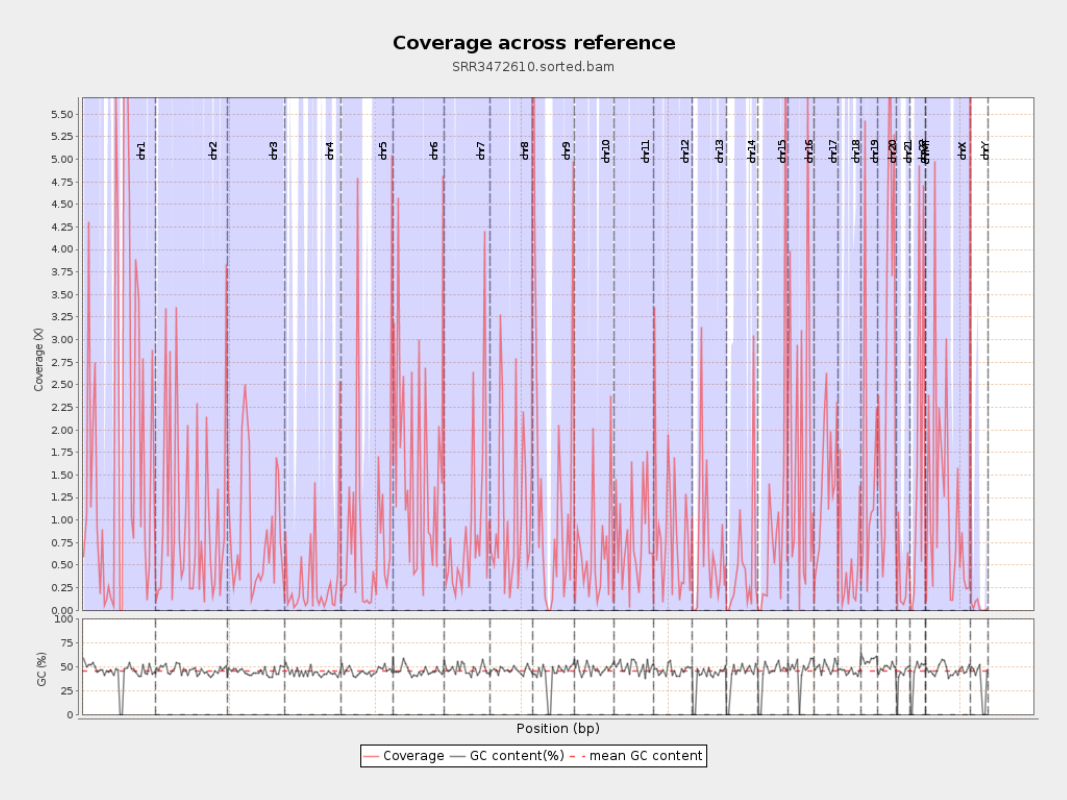
2.7. Chromosome stats

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

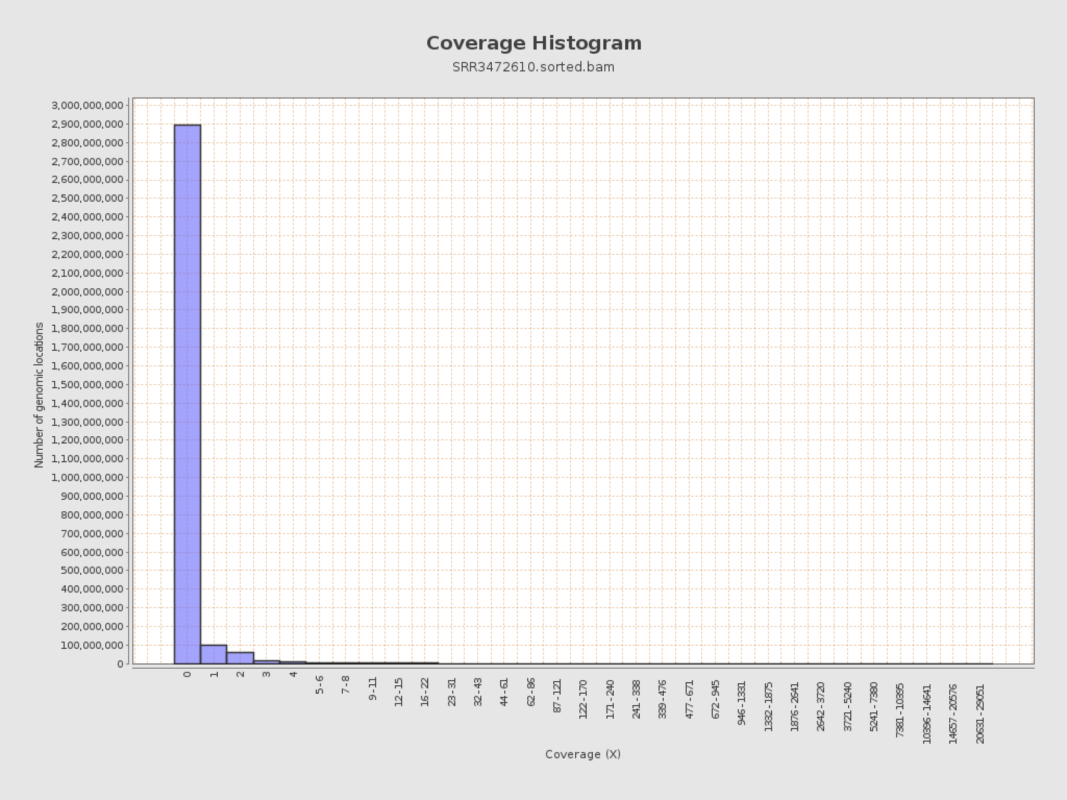
		bases	coverage	deviation
chr1	249250621	467455828	1.8754	67.6434
chr2	243199373	240765030	0.99	38.1572
chr3	198022430	172225805	0.8697	25.4673
chr4	191154276	65009828	0.3401	16.6769
chr5	180915260	170501993	0.9424	49.1082
chr6	171115067	269796920	1.5767	39.6254
chr7	159138663	142681162	0.8966	41.0696
chr8	146364022	162517156	1.1104	47.3615
chr9	141213431	171676081	1.2157	47.1261
chr10	135534747	89203100	0.6582	32.5236
chr11	135006516	108937002	0.8069	45.8014
chr12	133851895	121919016	0.9109	26.1432
chr13	115169878	80489158	0.6989	24.4958
chr14	107349540	54049442	0.5035	22.6035
chr15	102531392	110585559	1.0786	57.7018
chr16	90354753	161158397	1.7836	63.4658
chr17	81195210	113012240	1.3919	33.93
chr18	78077248	36476036	0.4672	17.0527
chr19	59128983	93952192	1.5889	41.1553
chr20	63025520	183725498	2.9151	78.4632
chr21	48129895	17677848	0.3673	22.121
chr22	51304566	92536214	1.8037	91.4426
chrMT	16571	3927	0.237	0.6185
chrX	155270560	200714345	1.2927	36.5201

chrY	59373566	2465279	0.0415	1.6061

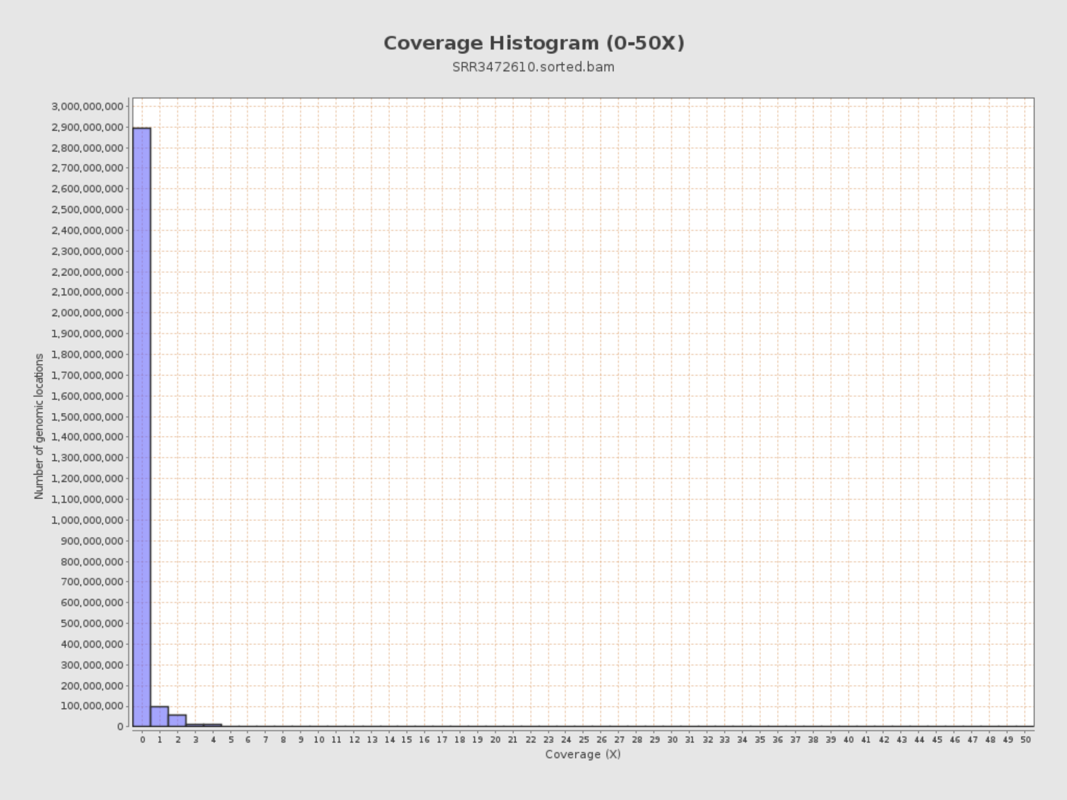
3. Results : Coverage across reference



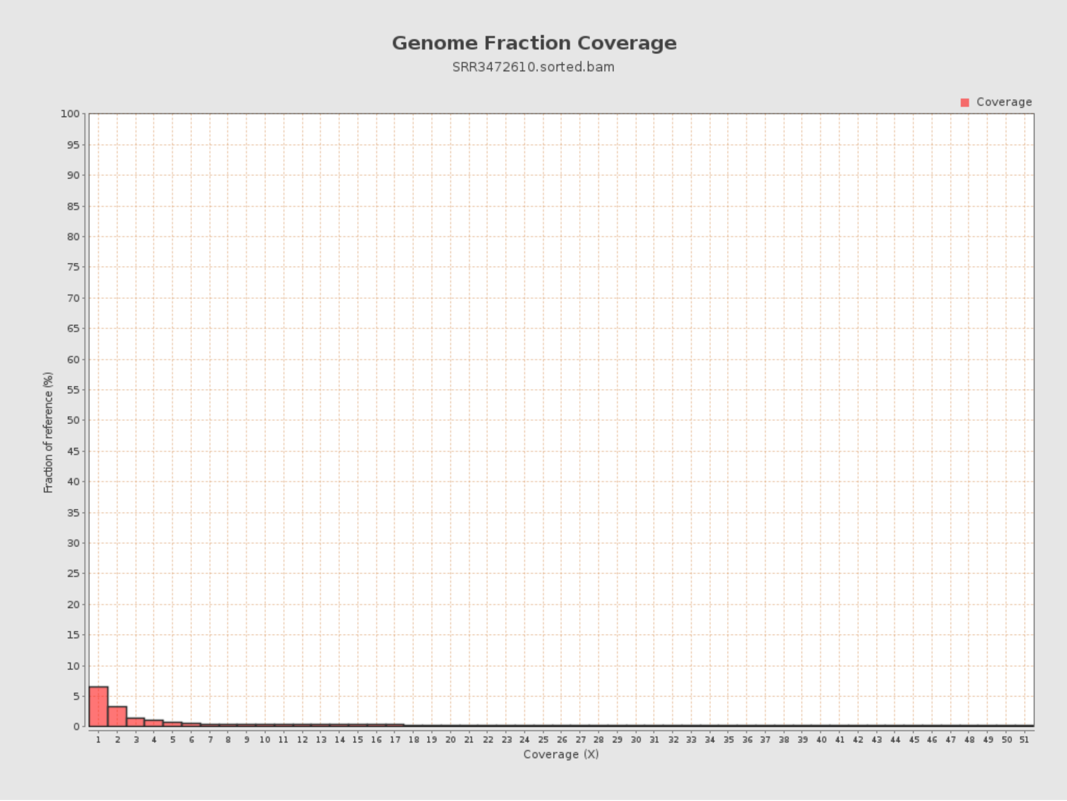
4. Results : Coverage Histogram



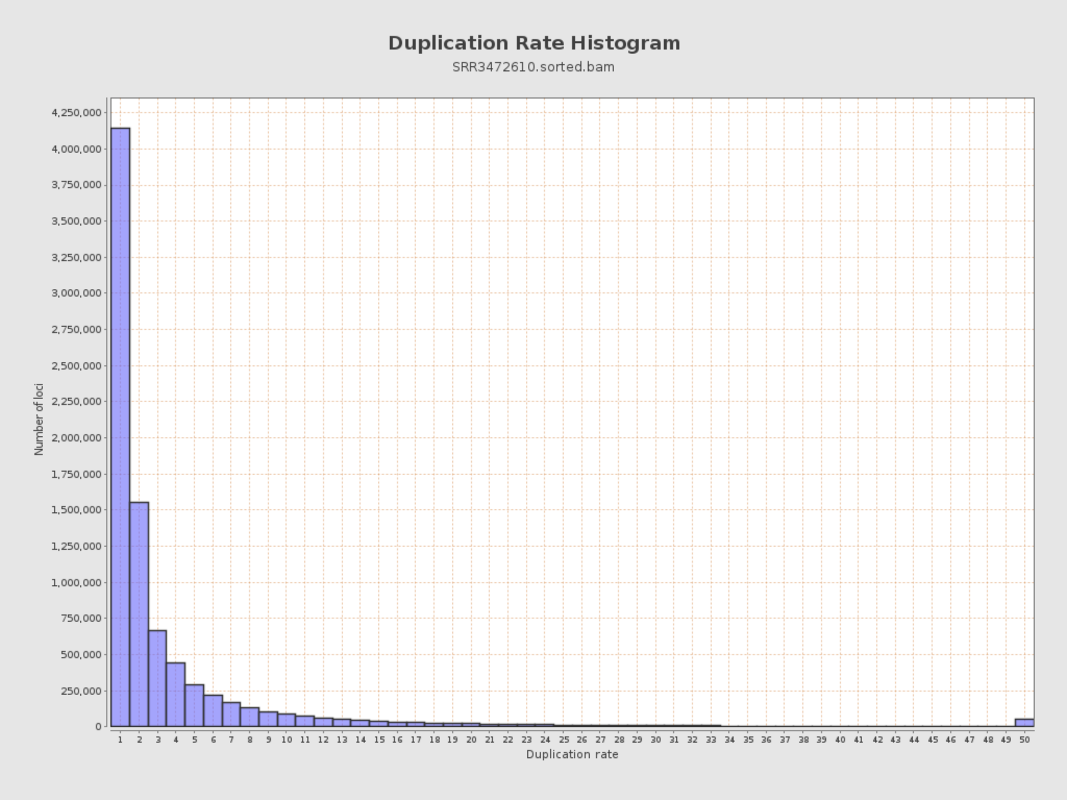
5. Results : Coverage Histogram (0-50X)



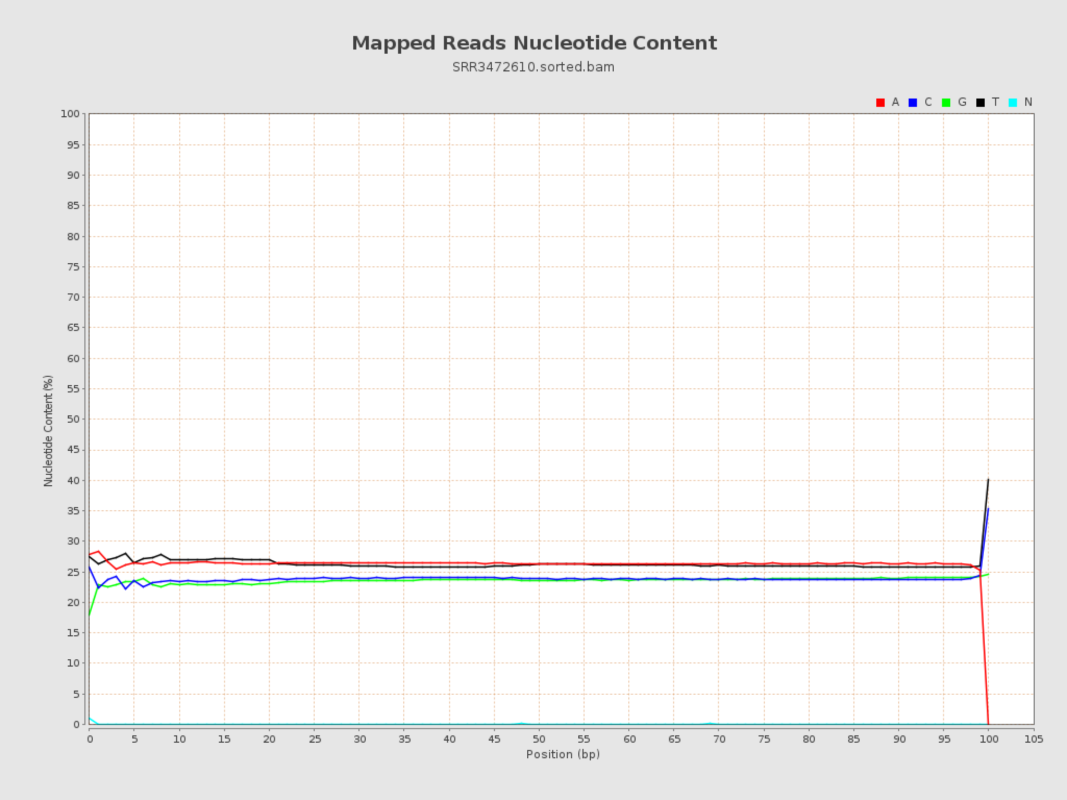
6. Results : Genome Fraction Coverage



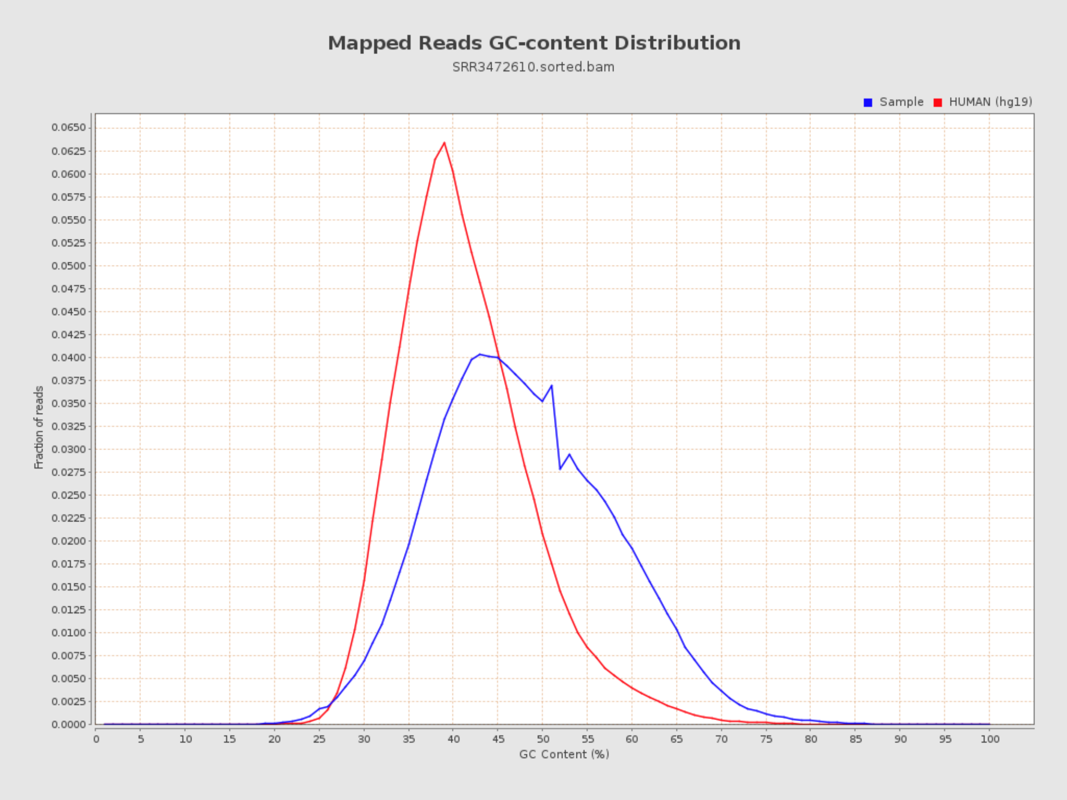
7. Results : Duplication Rate Histogram



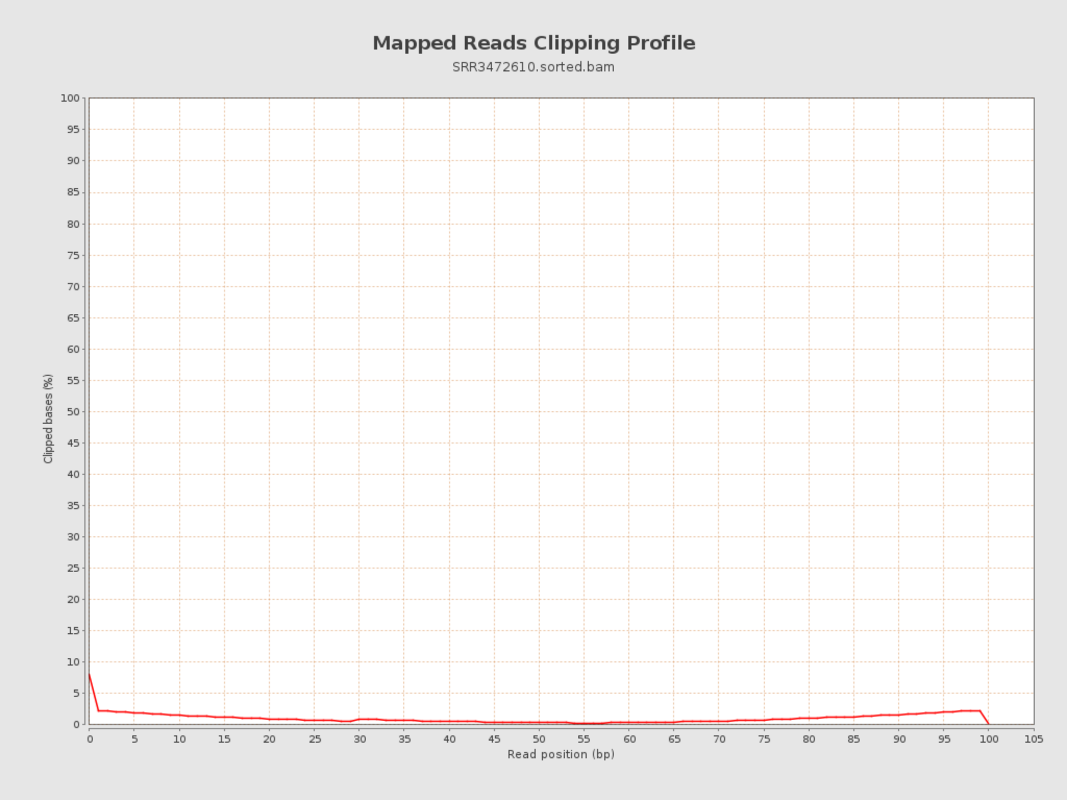
8. Results : Mapped Reads Nucleotide Content



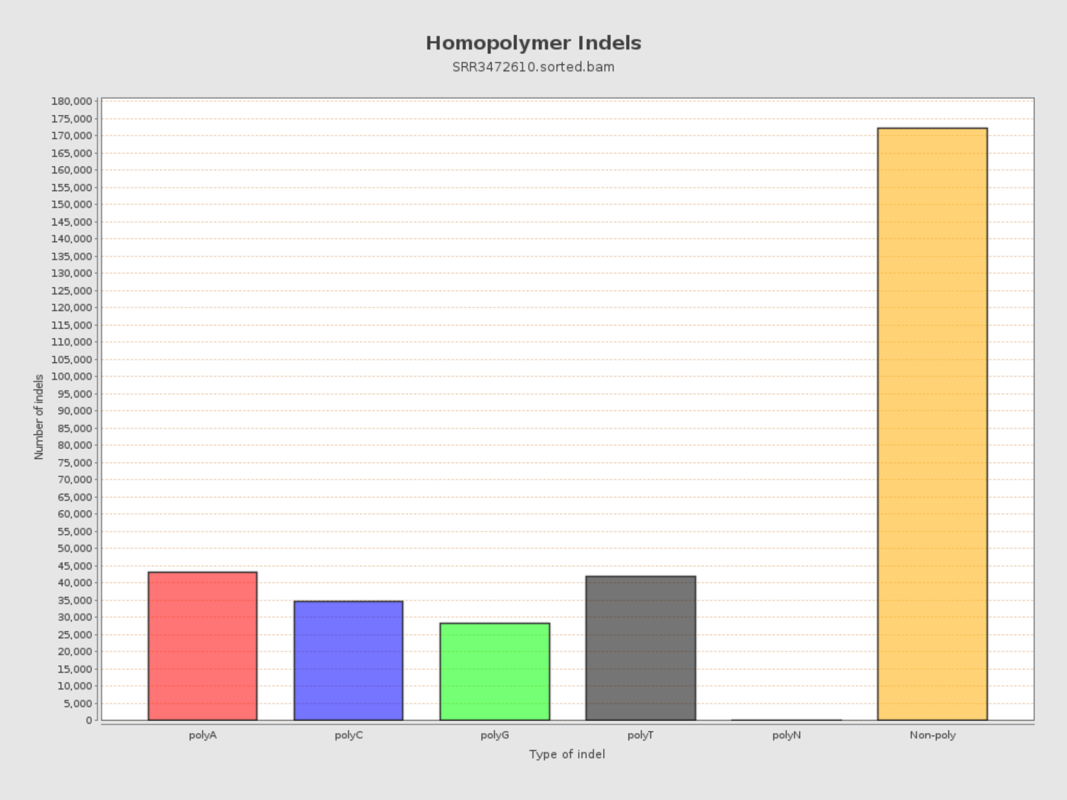
9. Results : Mapped Reads GC-content Distribution



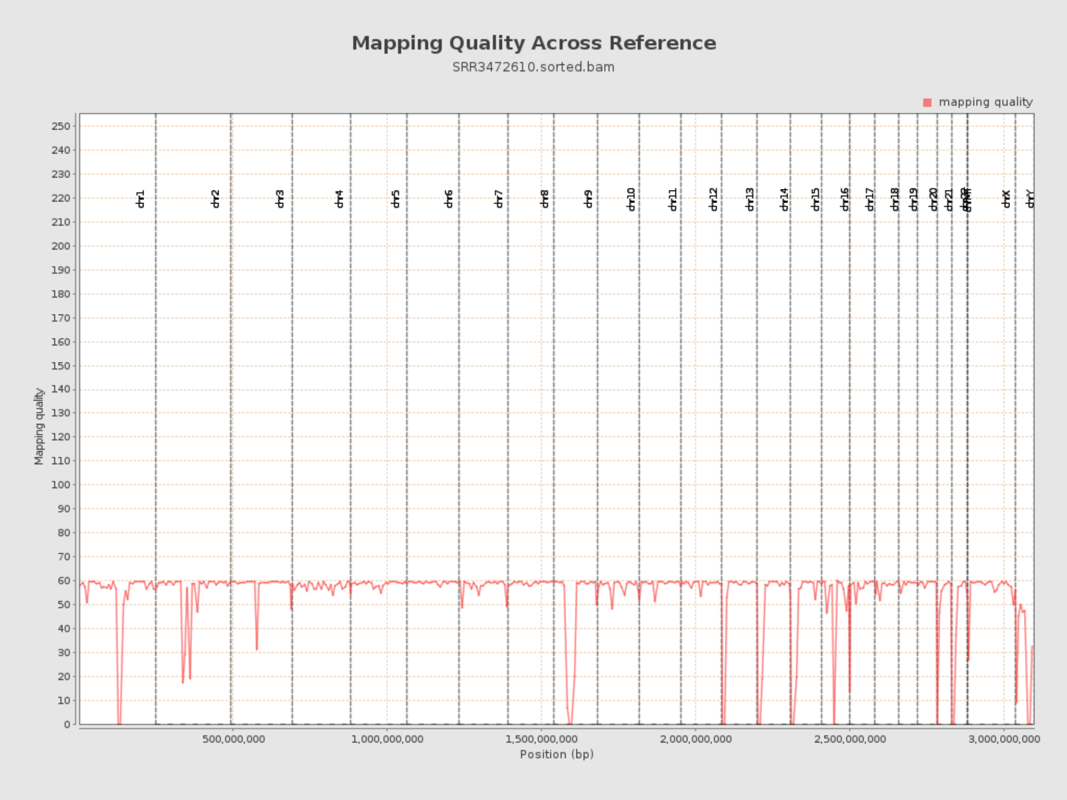
10. Results : Mapped Reads Clipping Profile



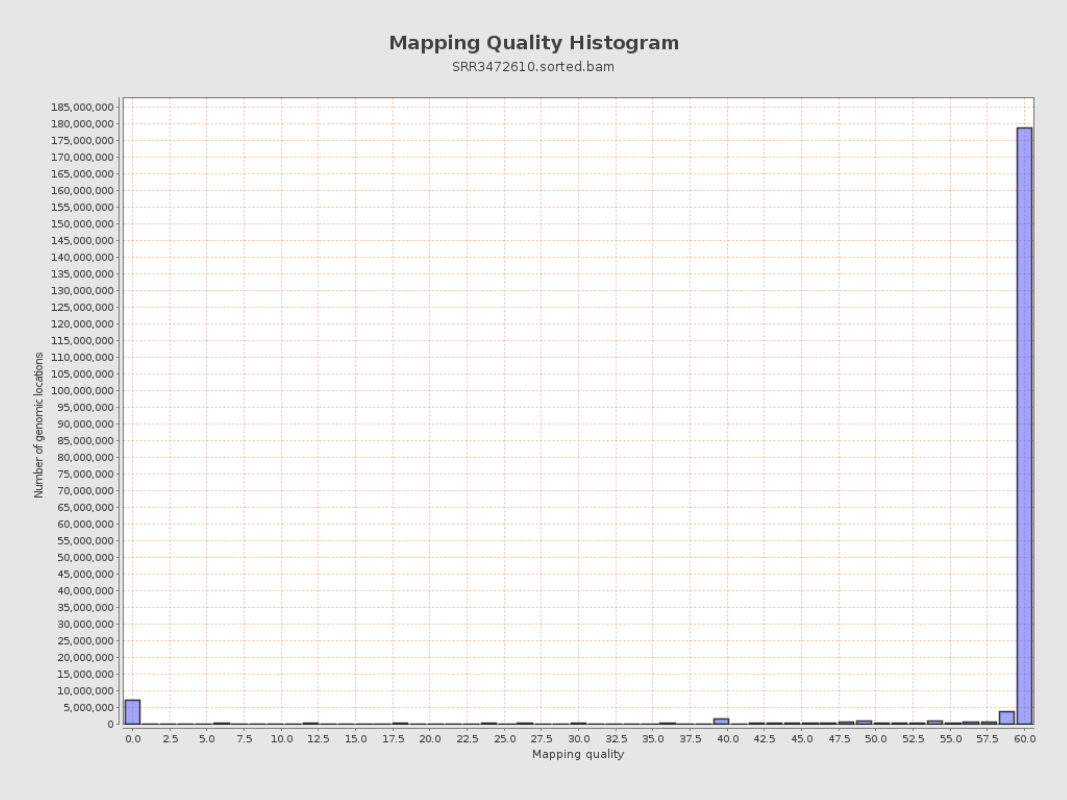
11. Results : Homopolymer Indels



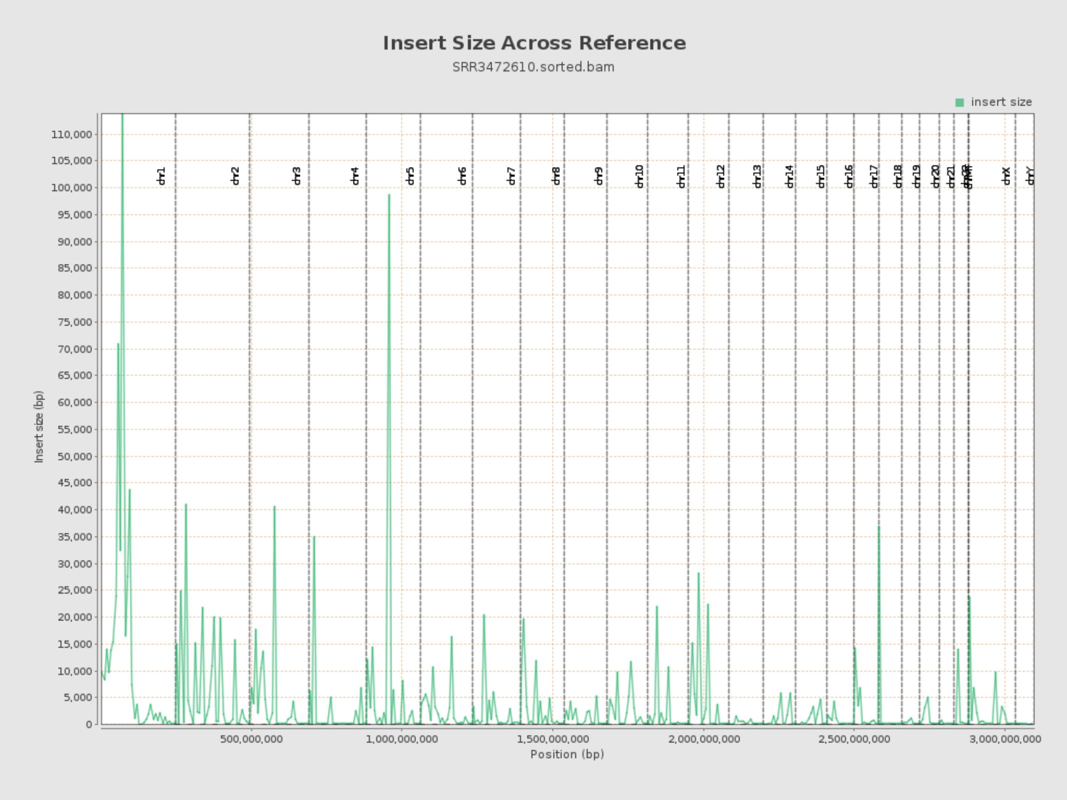
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram