Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:37:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472566.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_SRR3472566 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472566_1.fastq.gz SRR3472566_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:37:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472566.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	196,206,618
Mapped reads	193,619,052 / 98.68%
Unmapped reads	2,587,566 / 1.32%
Mapped paired reads	193,619,052 / 98.68%
Mapped reads, first in pair	97,068,486 / 49.47%
Mapped reads, second in pair	96,550,566 / 49.21%
Mapped reads, both in pair	192,918,524 / 98.32%
Mapped reads, singletons	700,528 / 0.36%
Secondary alignments	0
Supplementary alignments	107,889 / 0.05%
Read min/max/mean length	30 / 100 / 100.02
Duplicated reads (estimated)	117,926,275 / 60.1%
Duplication rate	45.69%
Clipped reads	52,658,831 / 26.84%

2.2. ACGT Content

Number/percentage of A's	4,342,128,134 / 24.39%
Number/percentage of C's	4,584,007,081 / 25.75%
Number/percentage of T's	4,448,085,093 / 24.99%
Number/percentage of G's	4,425,890,402 / 24.86%
Number/percentage of N's	2,231,992 / 0.01%

GC Percentage	50.61%

2.3. Coverage

Mean	5.7516
Standard Deviation	54.1142

2.4. Mapping Quality

Mean Mapping Quality	51.83

2.5. Insert size

Mean	5,466.45
Standard Deviation	709,547.03
P25/Median/P75	98 / 161 / 248

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	90,699,340
Insertions	1,058,643
Mapped reads with at least one insertion	0.53%
Deletions	1,311,807
Mapped reads with at least one deletion	0.66%
Homopolymer indels	40.61%

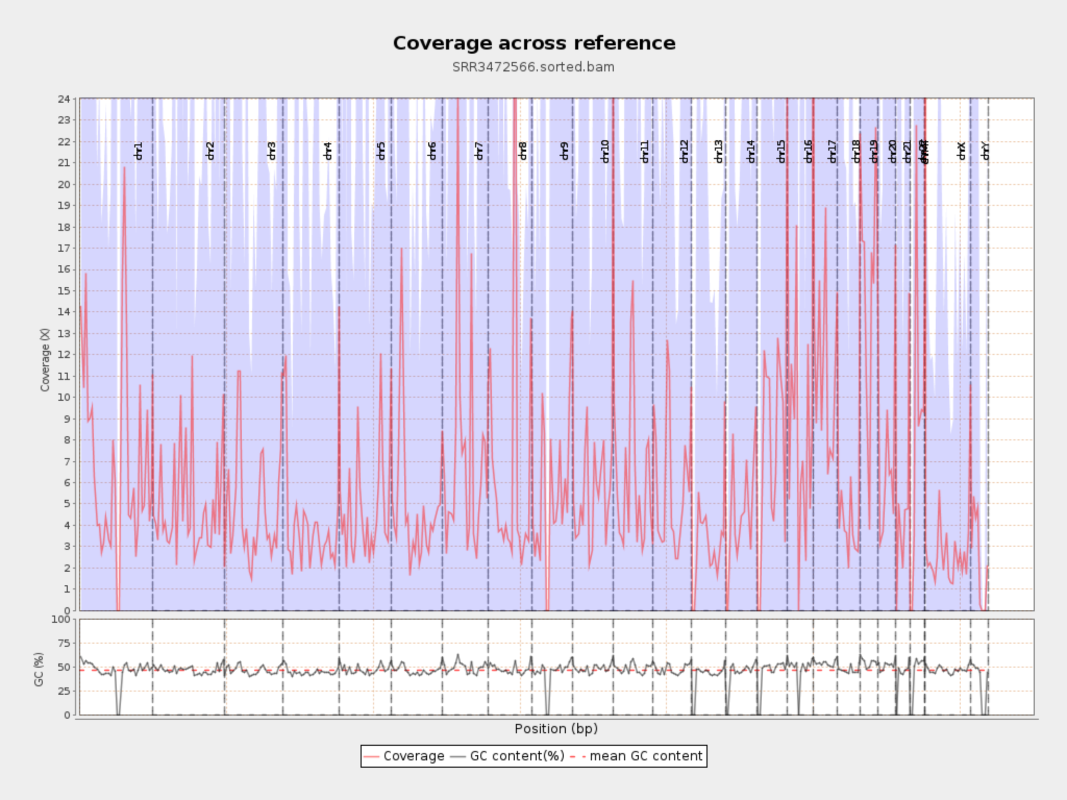
2.7. Chromosome stats

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

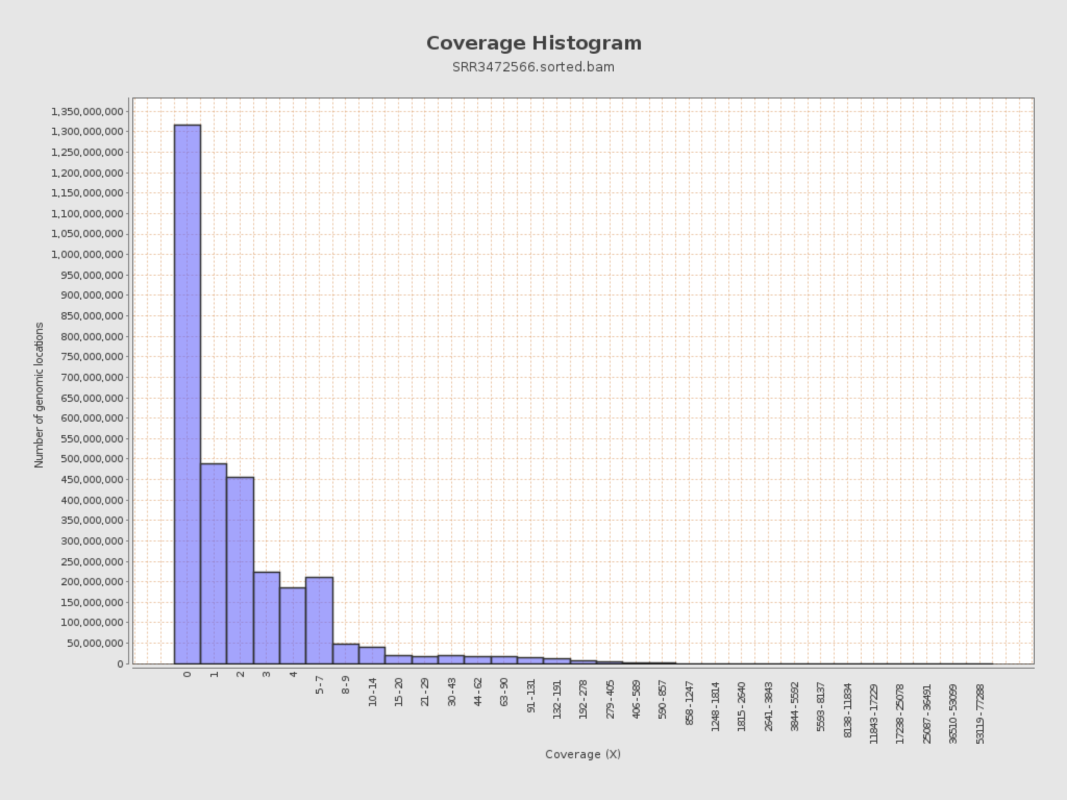
		bases	coverage	deviation
chr1	249250621	1745612599	7.0034	46.1957
chr2	243199373	1212717014	4.9865	38.9989
chr3	198022430	946752278	4.781	28.255
chr4	191154276	744780512	3.8962	30.7475
chr5	180915260	888700058	4.9122	42.7172
chr6	171115067	822501619	4.8067	26.4334
chr7	159138663	1137800971	7.1497	156.3564
chr8	146364022	941058059	6.4296	100.9973
chr9	141213431	791304008	5.6036	32.7193
chr10	135534747	733545960	5.4122	32.5598
chr11	135006516	912889572	6.7618	34.3914
chr12	133851895	774180493	5.7839	27.5758
chr13	115169878	346829838	3.0115	16.7801
chr14	107349540	482803374	4.4975	24.9732
chr15	102531392	742204467	7.2388	41.3709
chr16	90354753	791911315	8.7645	43.2307
chr17	81195210	911409782	11.2249	57.7771
chr18	78077248	311923138	3.9951	30.9659
chr19	59128983	910777539	15.4032	57.2216
chr20	63025520	412912895	6.5515	38.4391
chr21	48129895	228400357	4.7455	36.5075
chr22	51304566	449721667	8.7657	51.1526
chrMT	16571	14443455	871.6103	214.0454
chrX	155270560	404091971	2.6025	14.7529

chrY	59373566	146068662	2.4602	40.6741

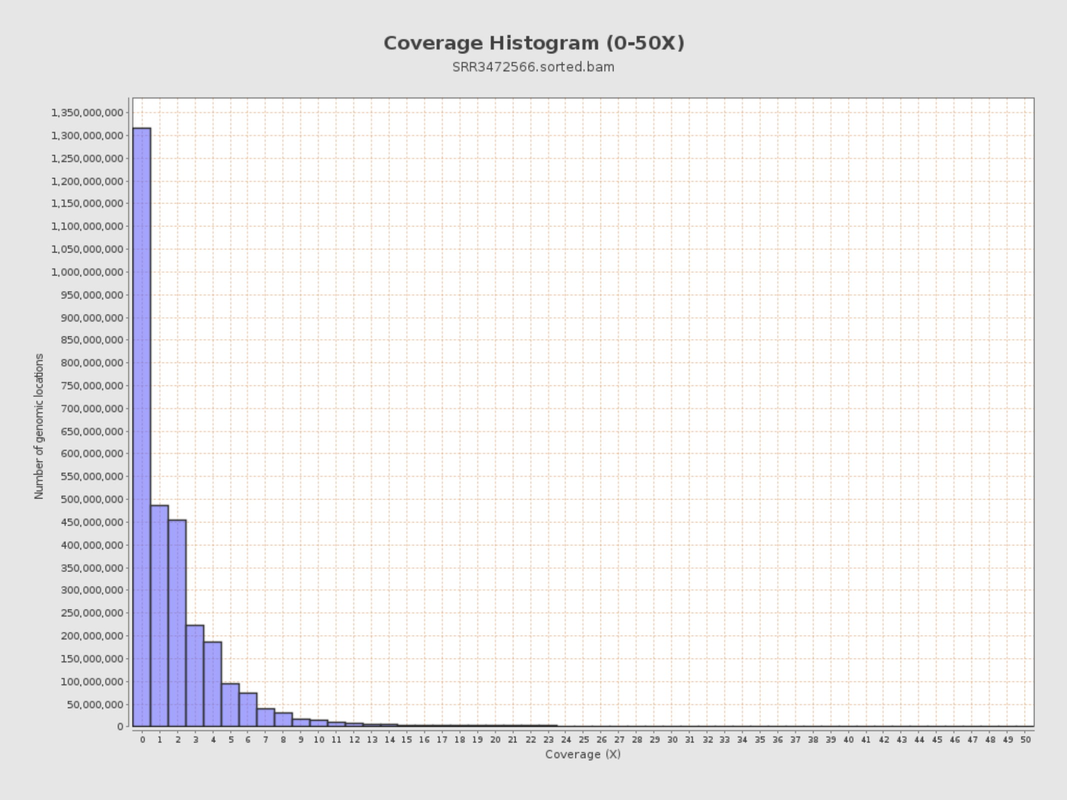
3. Results : Coverage across reference



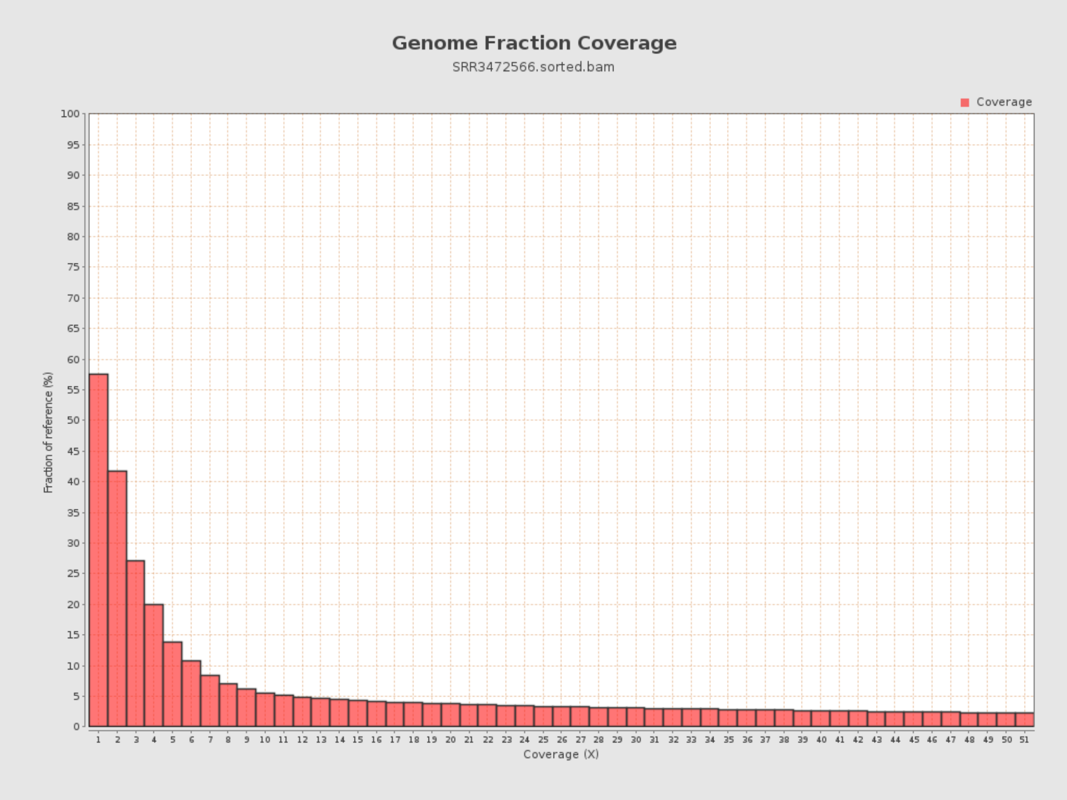
4. Results : Coverage Histogram



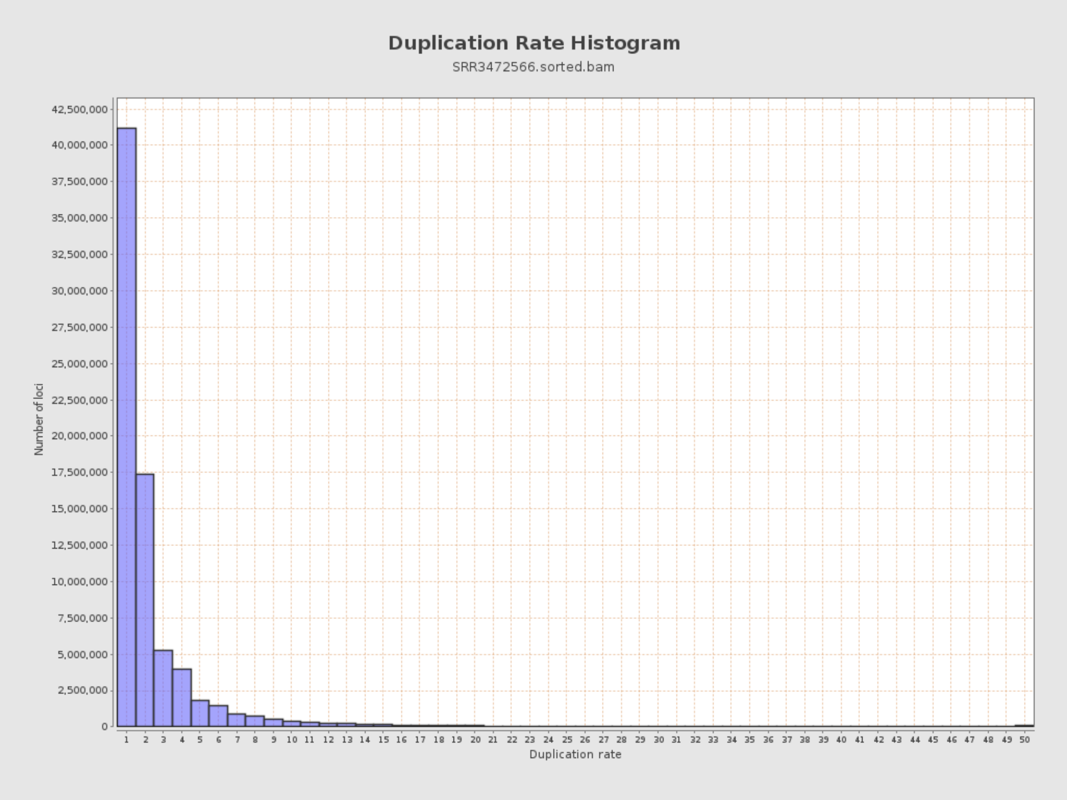
5. Results : Coverage Histogram (0-50X)



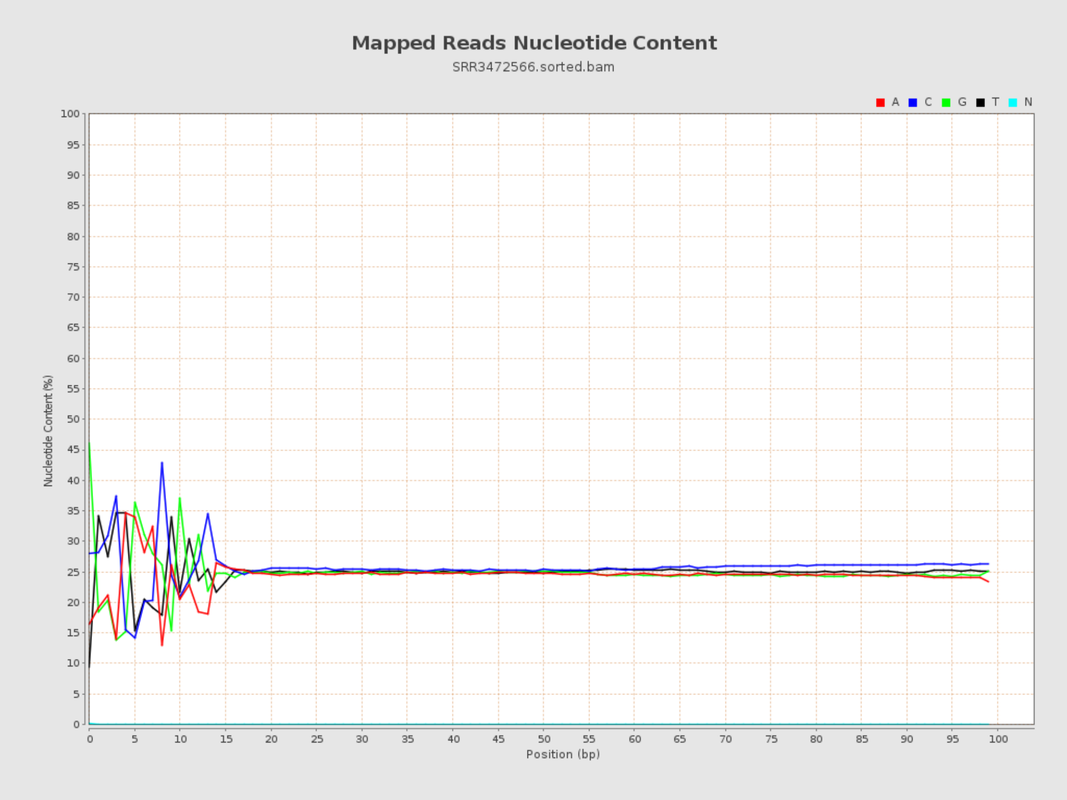
6. Results : Genome Fraction Coverage



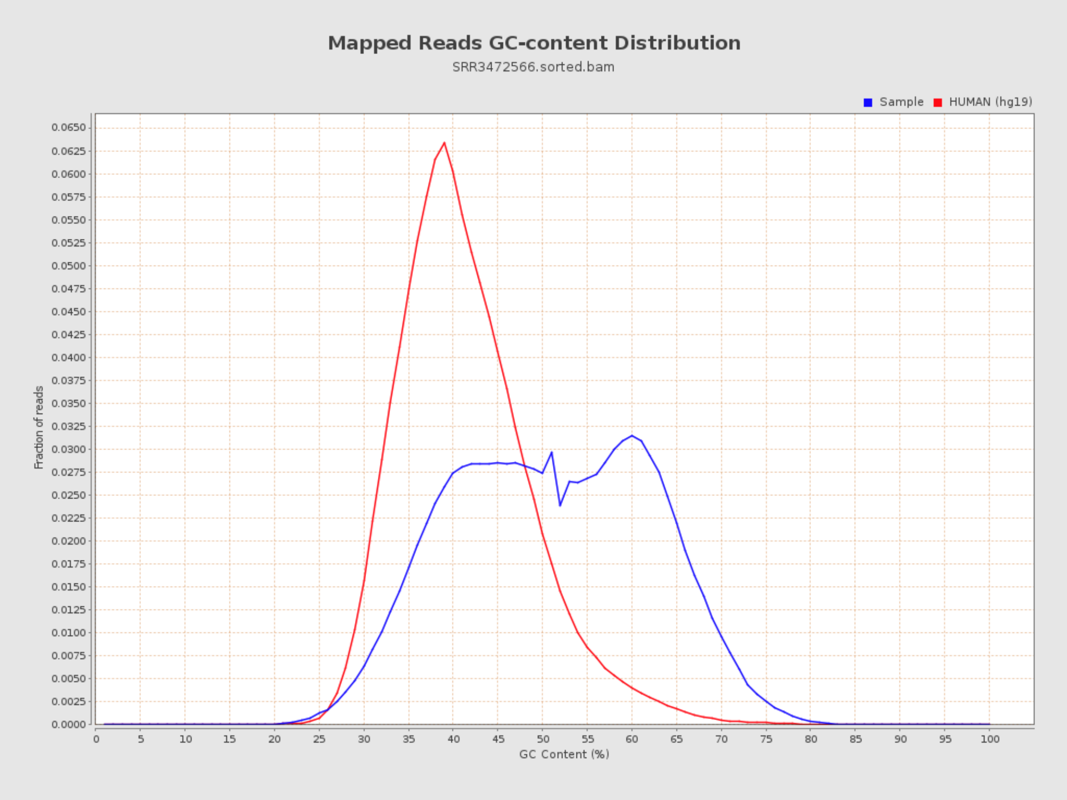
7. Results : Duplication Rate Histogram



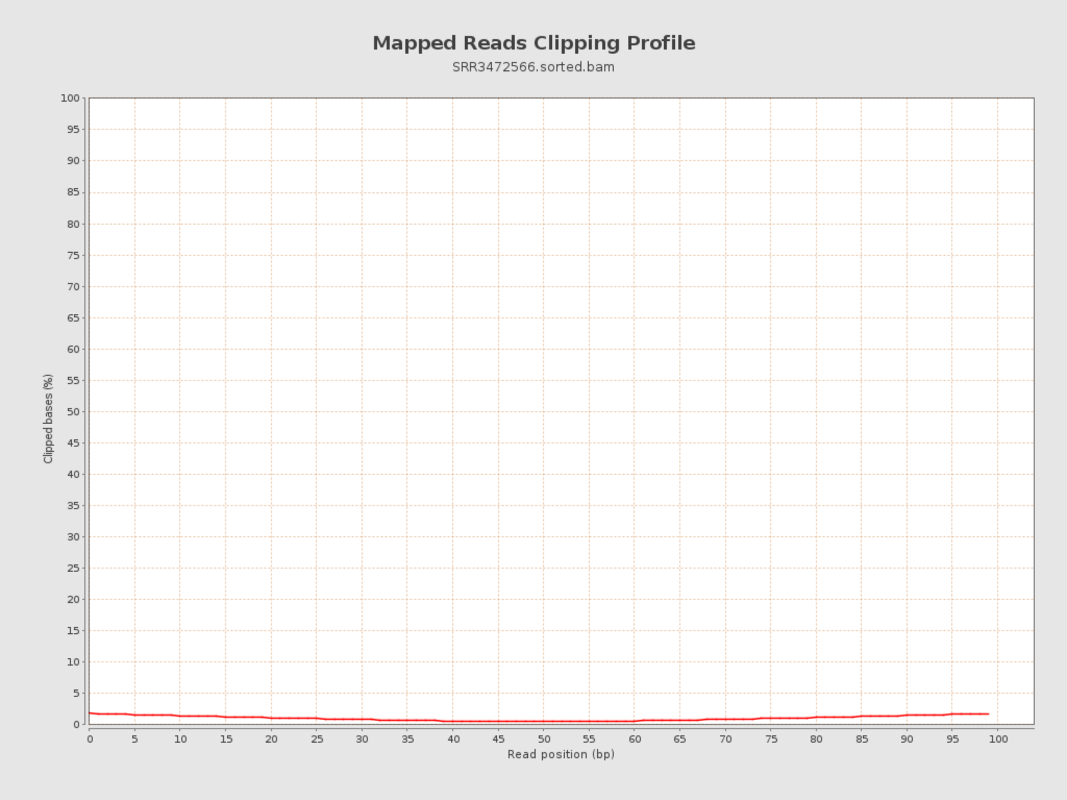
8. Results : Mapped Reads Nucleotide Content



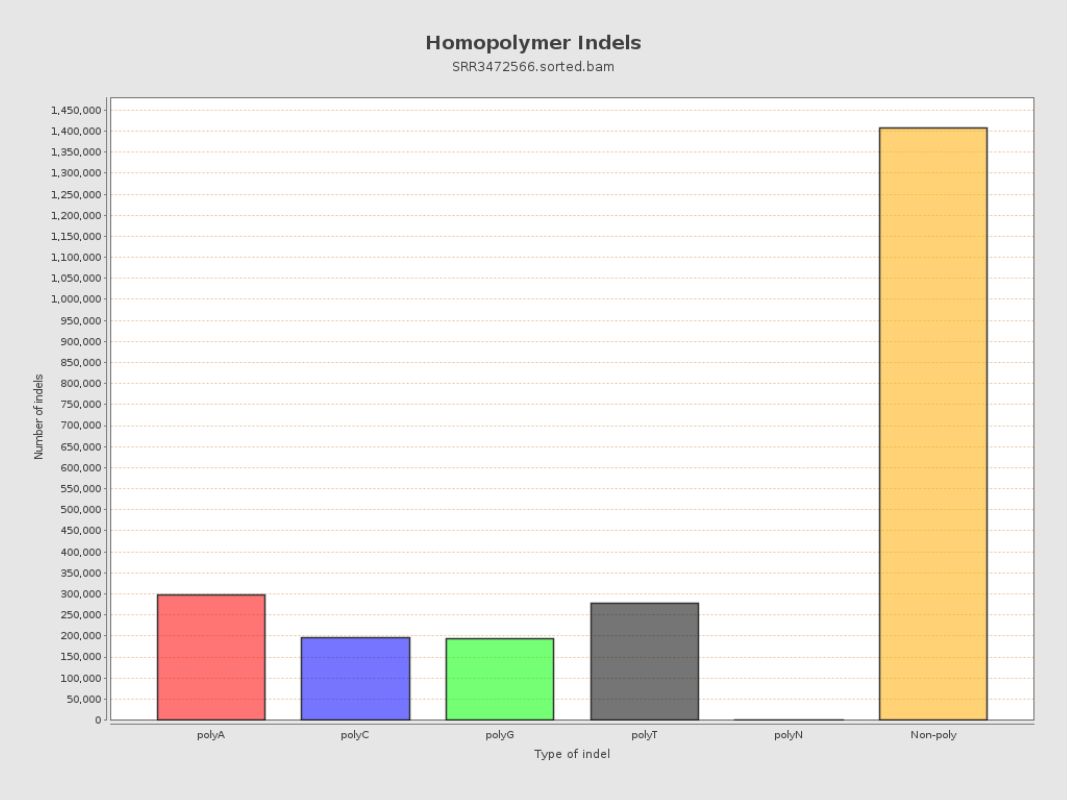
9. Results : Mapped Reads GC-content Distribution



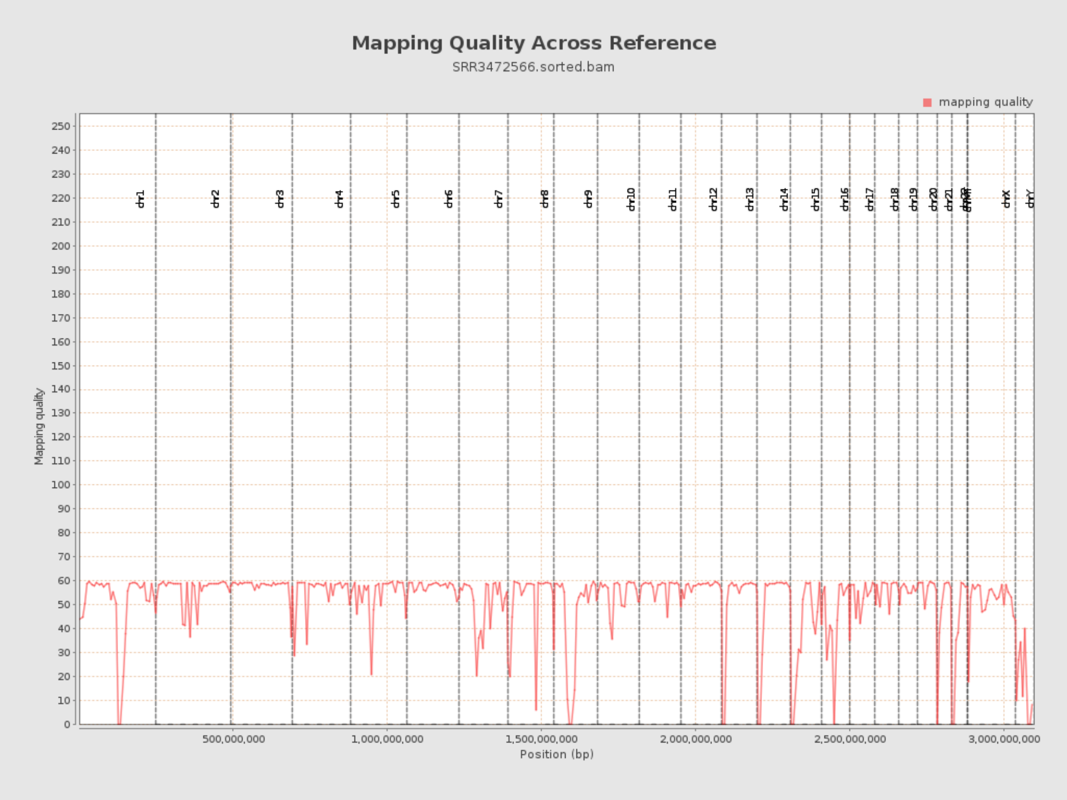
10. Results : Mapped Reads Clipping Profile



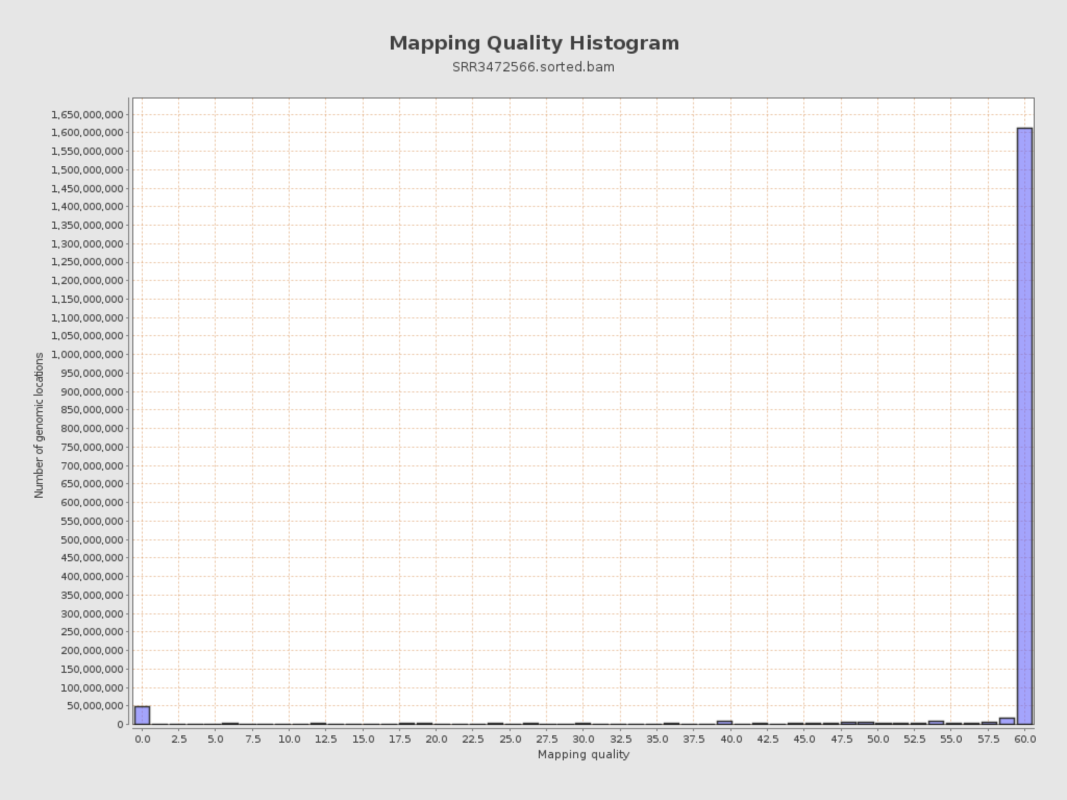
11. Results : Homopolymer Indels



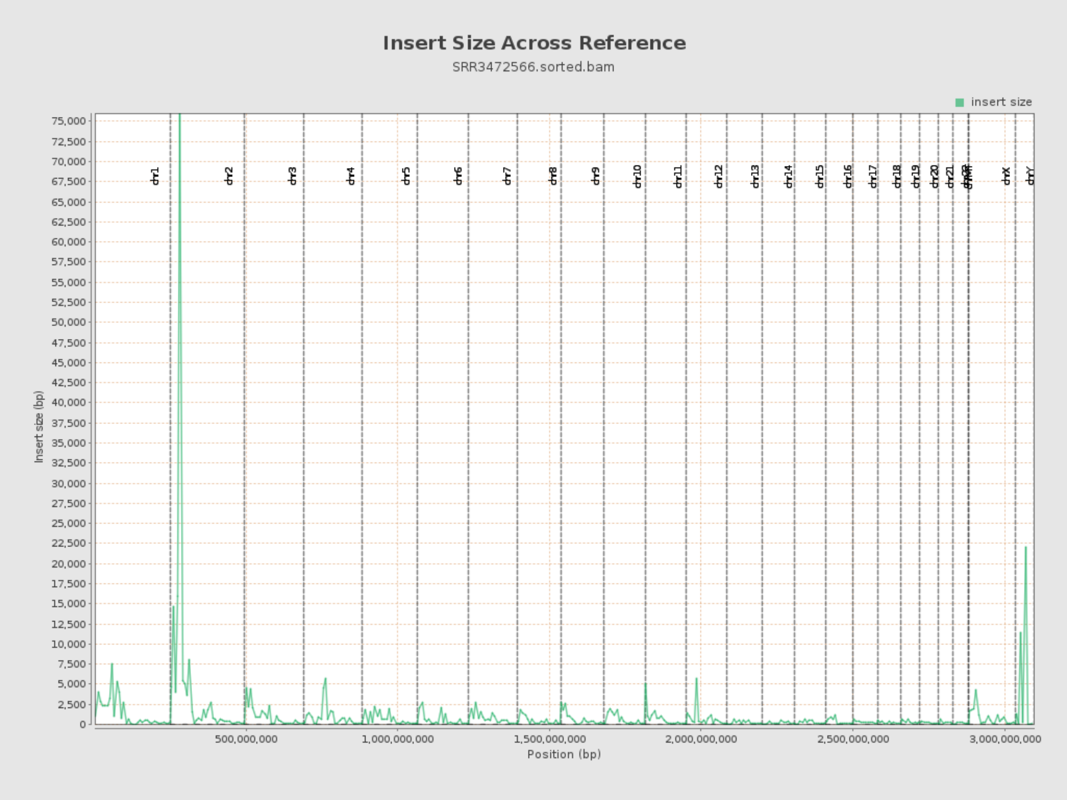
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram