Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 22:09:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038464.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_SRR5038464 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038464_1.fastq.gz SRR5038464_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 22:09:24 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038464.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,178,672
Mapped reads	18,548,637 / 96.71%
Unmapped reads	630,035 / 3.29%
Mapped paired reads	18,548,637 / 96.71%
Mapped reads, first in pair	9,340,983 / 48.71%
Mapped reads, second in pair	9,207,654 / 48.01%
Mapped reads, both in pair	18,394,202 / 95.91%
Mapped reads, singletons	154,435 / 0.81%
Secondary alignments	0
Supplementary alignments	184,767 / 0.96%
Read min/max/mean length	30 / 150 / 150.5
Duplicated reads (estimated)	1,861,644 / 9.71%
Duplication rate	7.91%
Clipped reads	1,824,558 / 9.51%

2.2. ACGT Content

Number/percentage of A's	783,785,310 / 28.69%
Number/percentage of C's	585,004,320 / 21.41%
Number/percentage of T's	778,545,360 / 28.5%
Number/percentage of G's	584,602,890 / 21.4%
Number/percentage of N's	252,486 / 0.01%

GC Percentage	42.81%

2.3. Coverage

Mean	0.8829
Standard Deviation	7.9784

2.4. Mapping Quality

Mean Mapping Quality	54.35

2.5. Insert size

Mean	100,091.13
Standard Deviation	3,186,100.55
P25/Median/P75	229 / 281 / 348

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	24,728,334
Insertions	314,008
Mapped reads with at least one insertion	1.6%
Deletions	340,213
Mapped reads with at least one deletion	1.76%
Homopolymer indels	44.58%

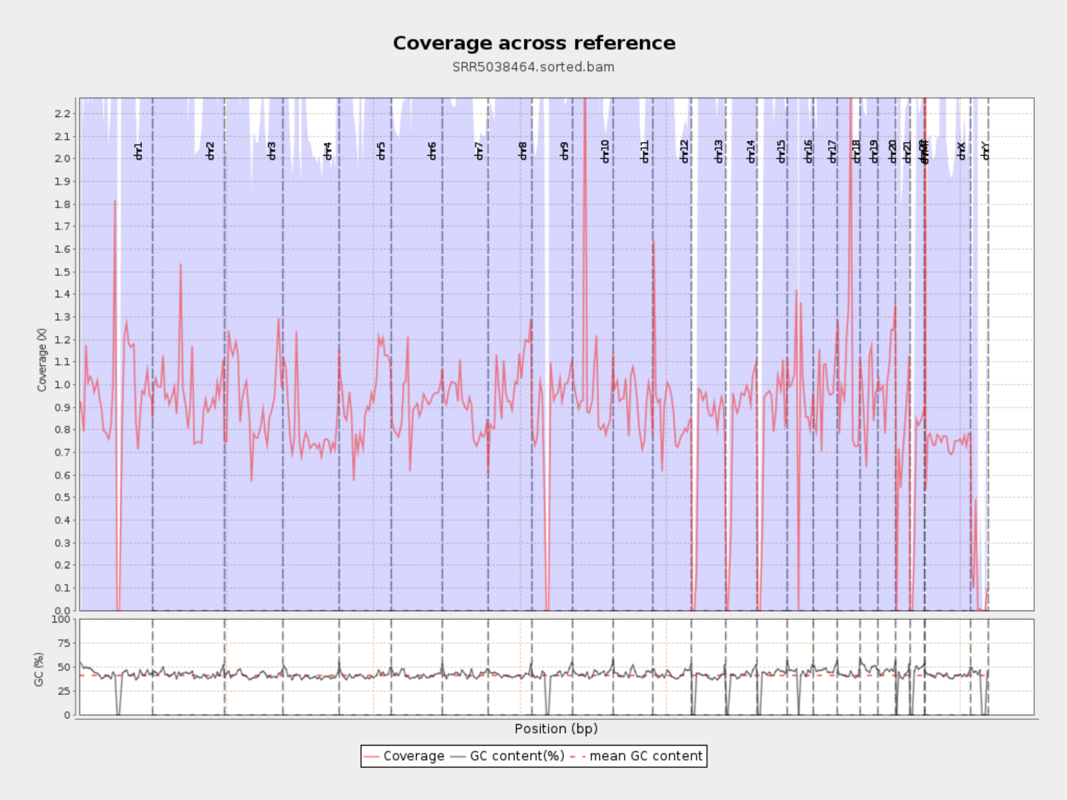
2.7. Chromosome stats

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

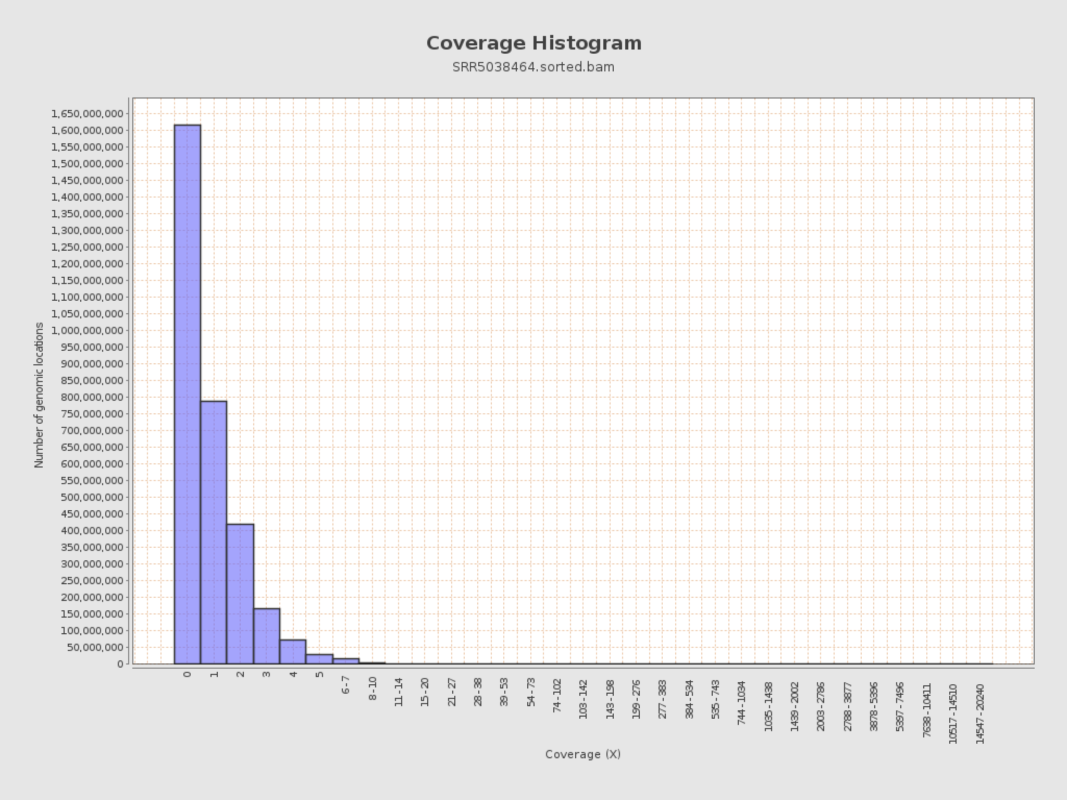
		bases	coverage	deviation
chr1	249250621	233223936	0.9357	20.4546
chr2	243199373	232150078	0.9546	7.0139
chr3	198022430	185515410	0.9368	1.2899
chr4	191154276	152046435	0.7954	4.8847
chr5	180915260	170518904	0.9425	1.2493
chr6	171115067	155628980	0.9095	3.7359
chr7	159138663	143150936	0.8995	6.5516
chr8	146364022	147859732	1.0102	4.8482
chr9	141213431	116506322	0.825	8.944
chr10	135534747	137390855	1.0137	15.7698
chr11	135006516	126219956	0.9349	3.4932
chr12	133851895	119436559	0.8923	1.4049
chr13	115169878	87530119	0.76	1.1328
chr14	107349540	85383908	0.7954	1.2085
chr15	102531392	77978619	0.7605	1.1471
chr16	90354753	85238231	0.9434	4.4211
chr17	81195210	79766966	0.9824	4.5818
chr18	78077248	84285768	1.0795	7.4145
chr19	59128983	56068795	0.9482	8.3227
chr20	63025520	66866897	1.0609	2.0351
chr21	48129895	34917299	0.7255	2.7833
chr22	51304566	30124908	0.5872	1.0372
chrMT	16571	3738602	225.6111	28.7242
chrX	155270560	115196755	0.7419	1.8138

chrY	59373566	6368219	0.1073	5.2712

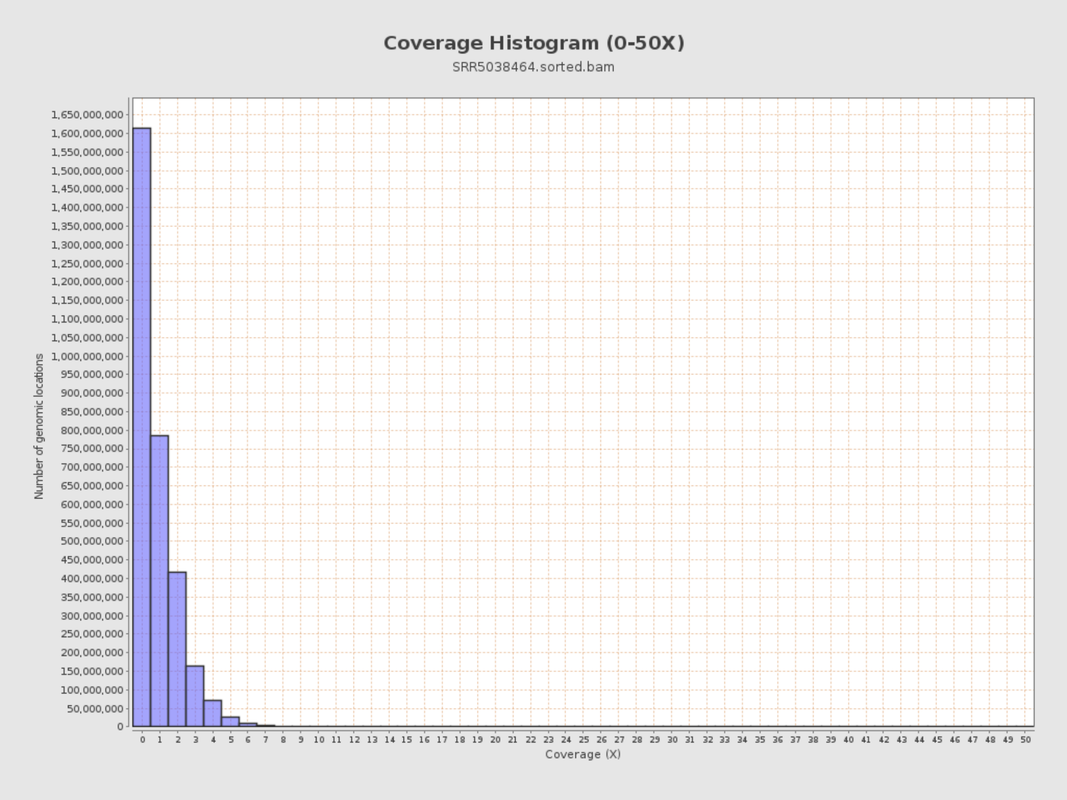
3. Results : Coverage across reference



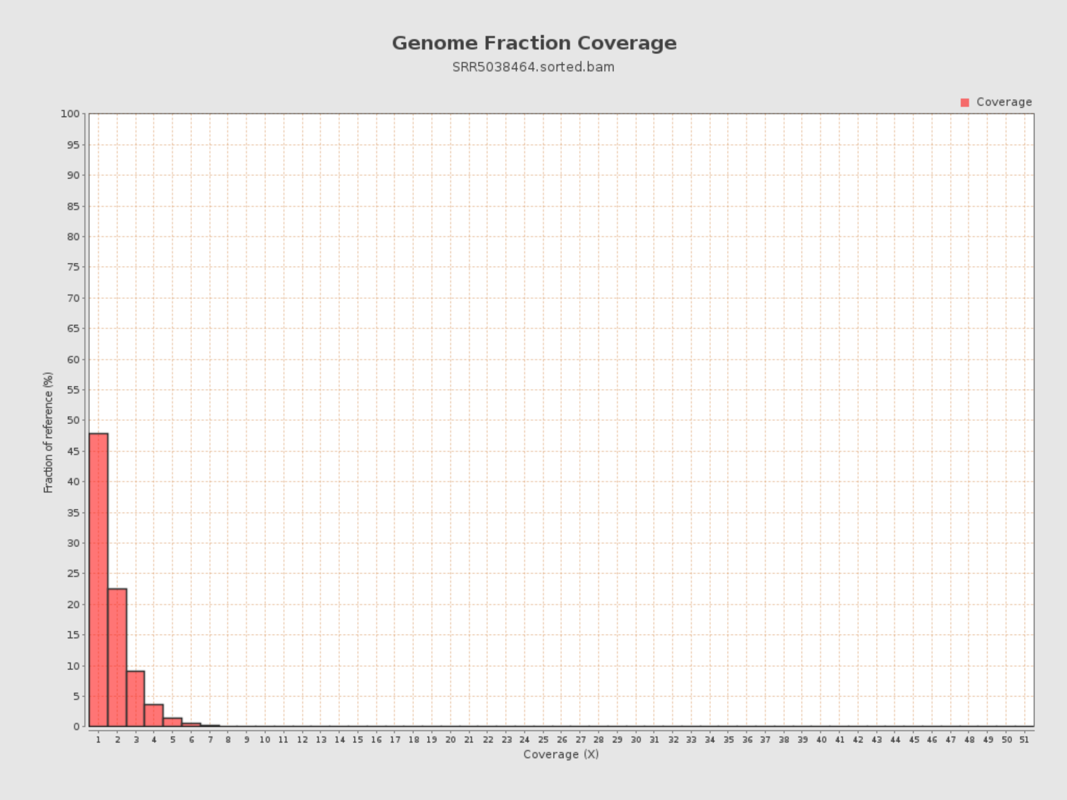
4. Results : Coverage Histogram



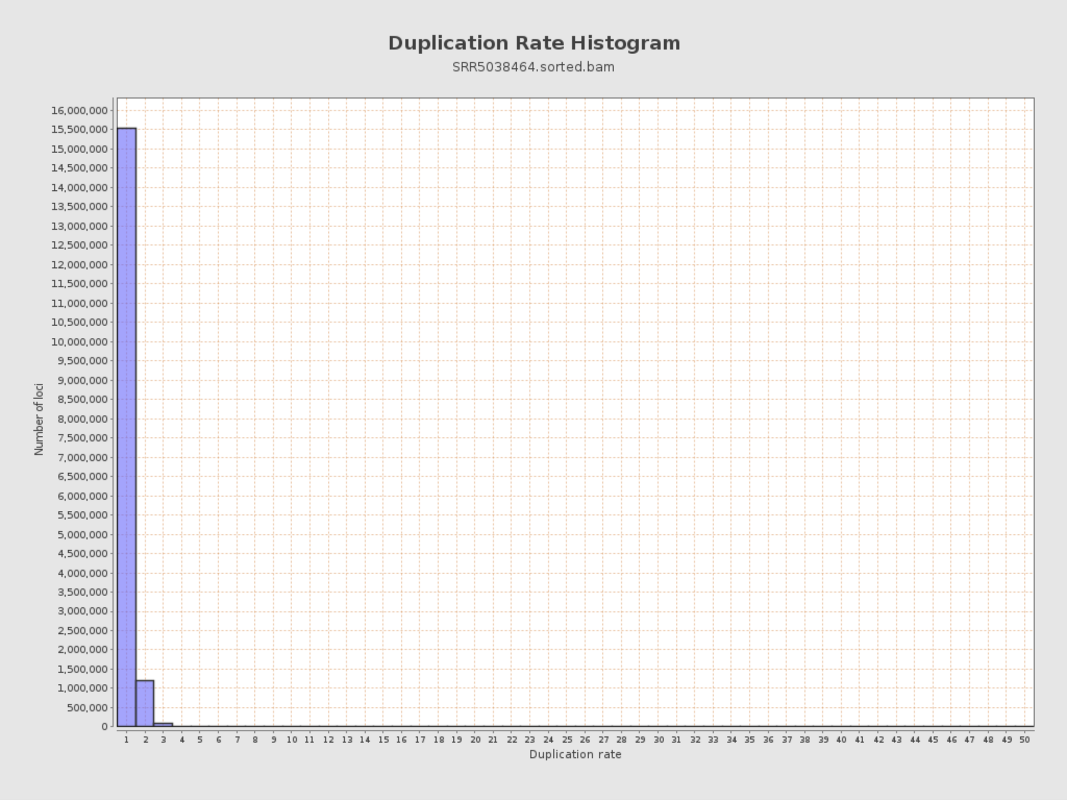
5. Results : Coverage Histogram (0-50X)



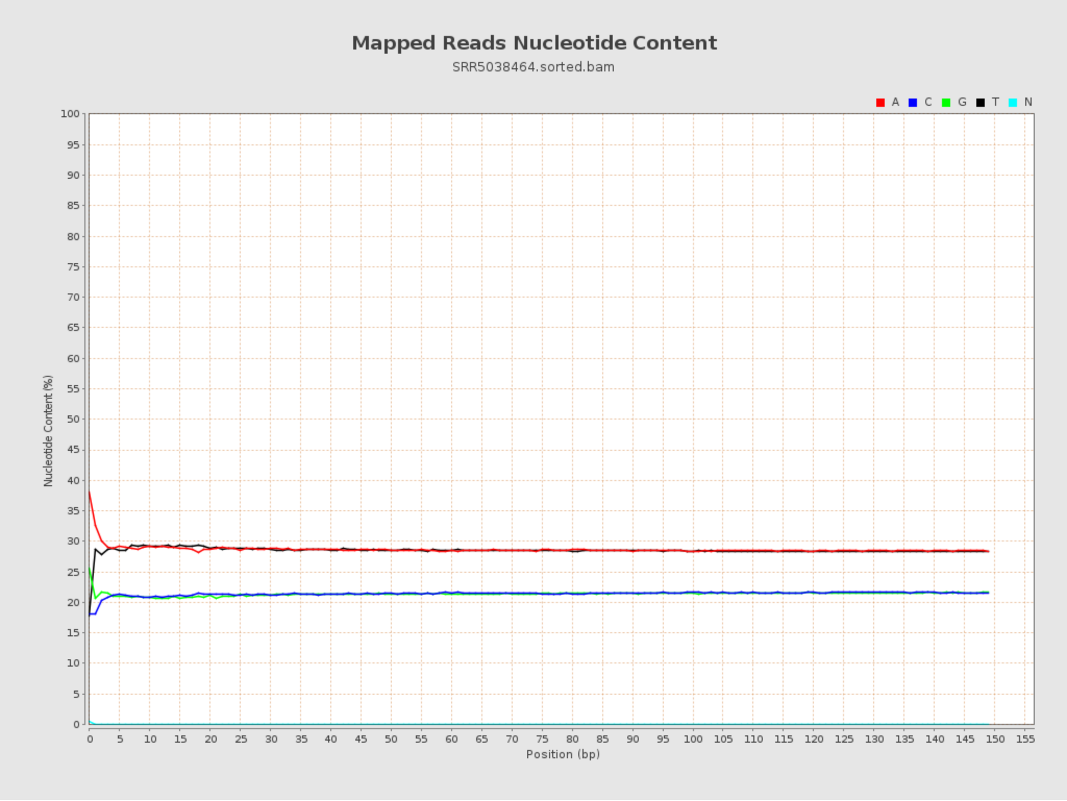
6. Results : Genome Fraction Coverage



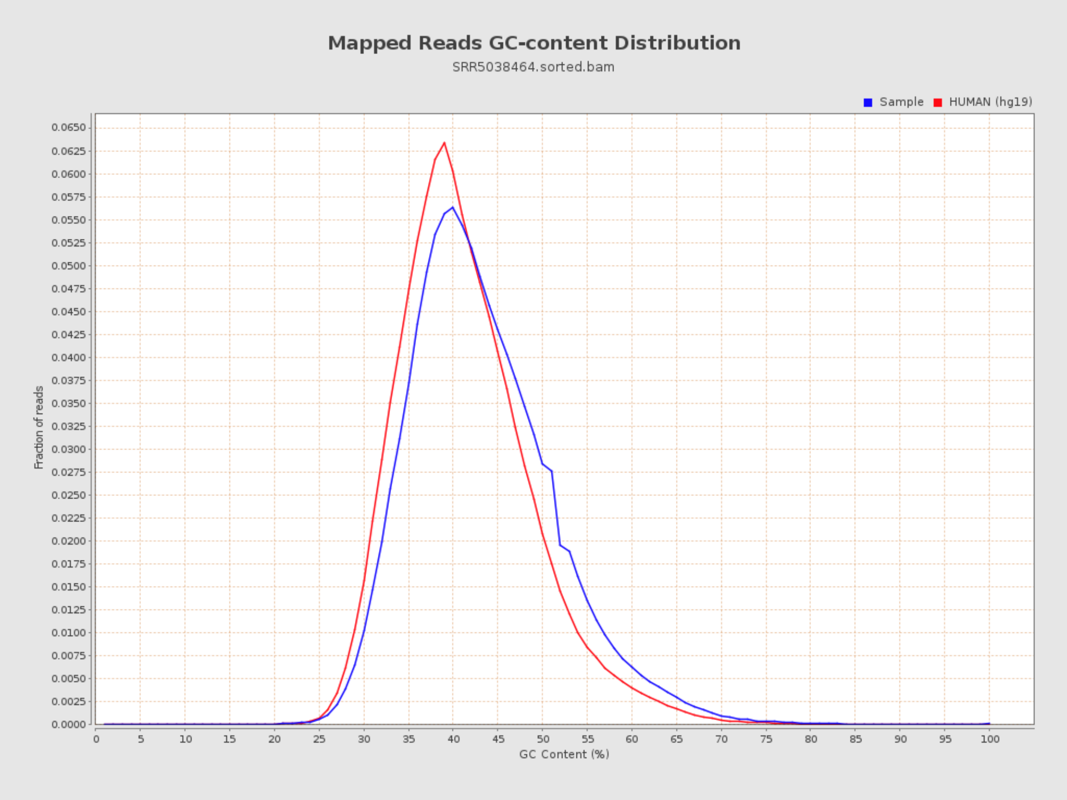
7. Results : Duplication Rate Histogram



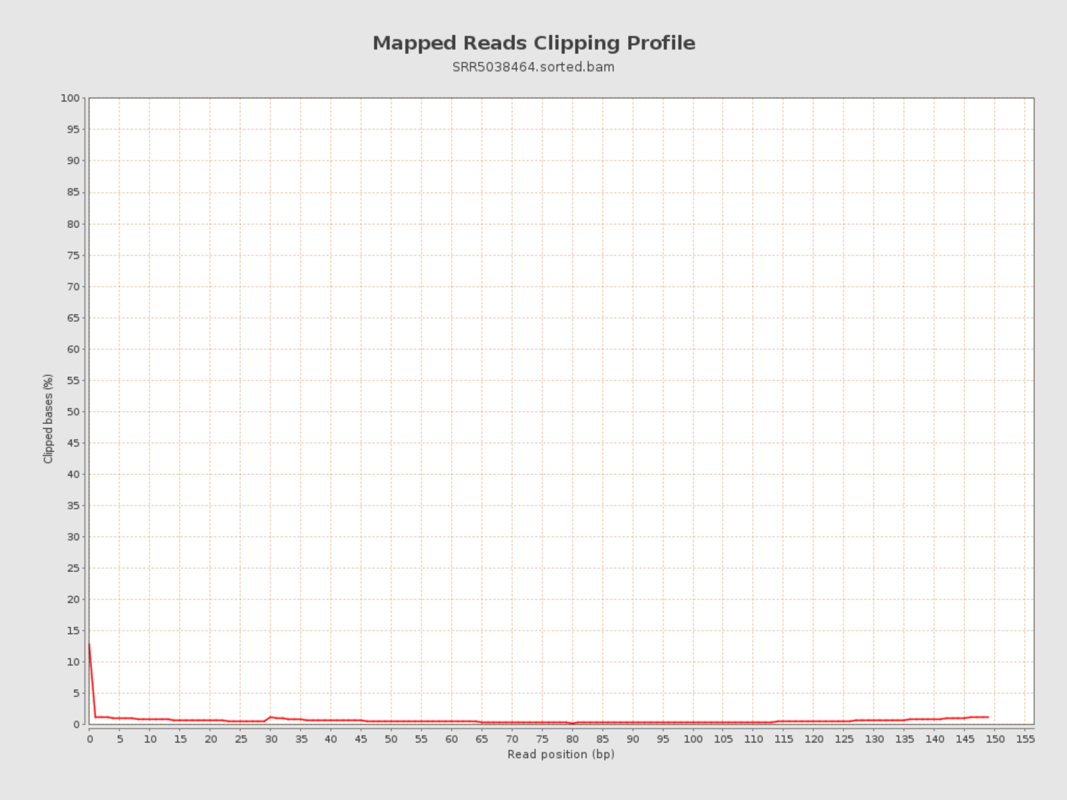
8. Results : Mapped Reads Nucleotide Content



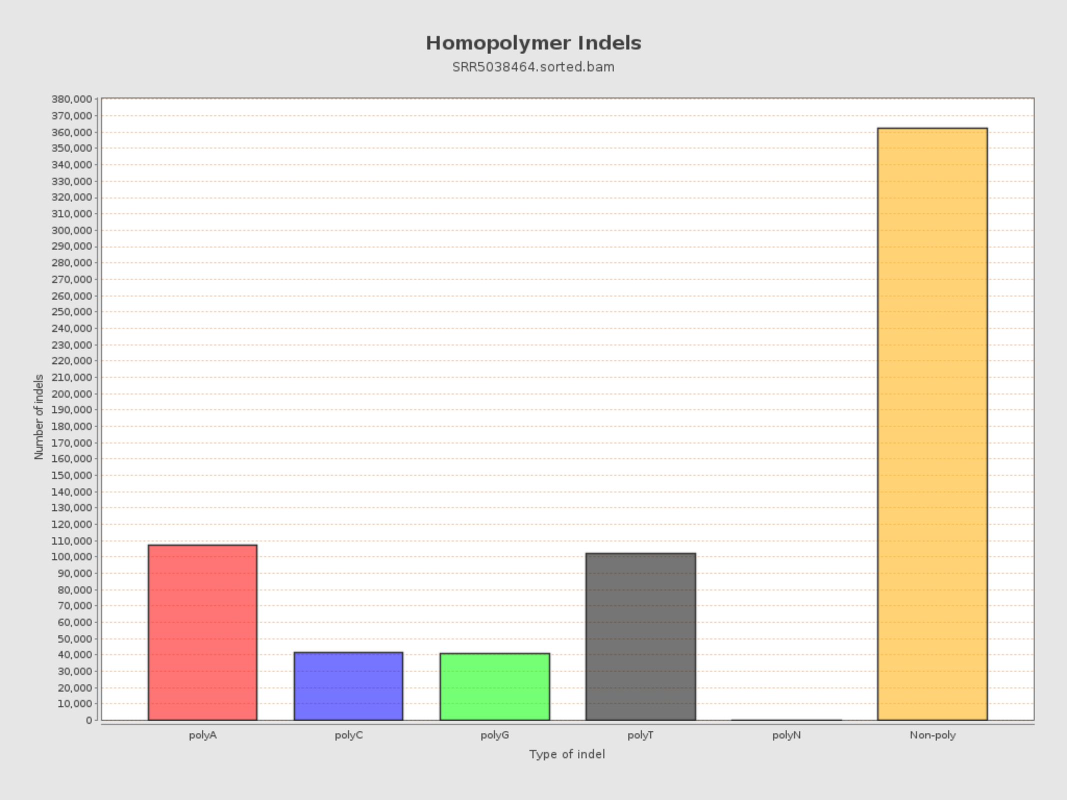
9. Results : Mapped Reads GC-content Distribution



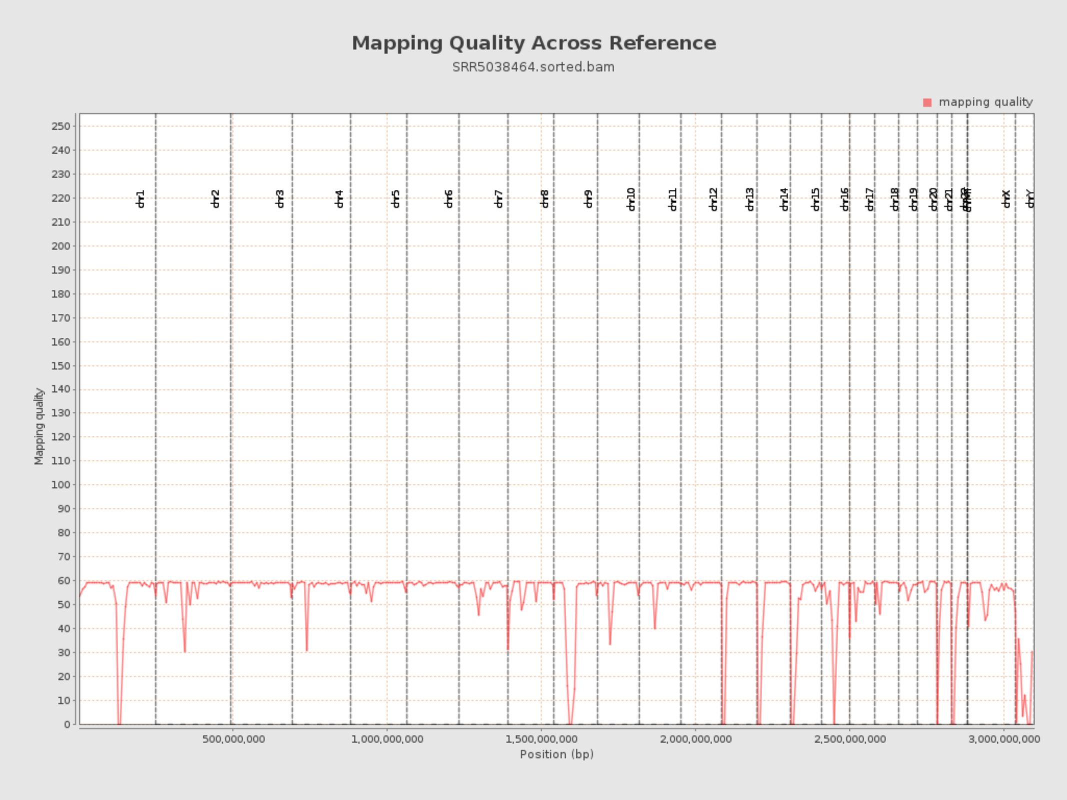
10. Results : Mapped Reads Clipping Profile



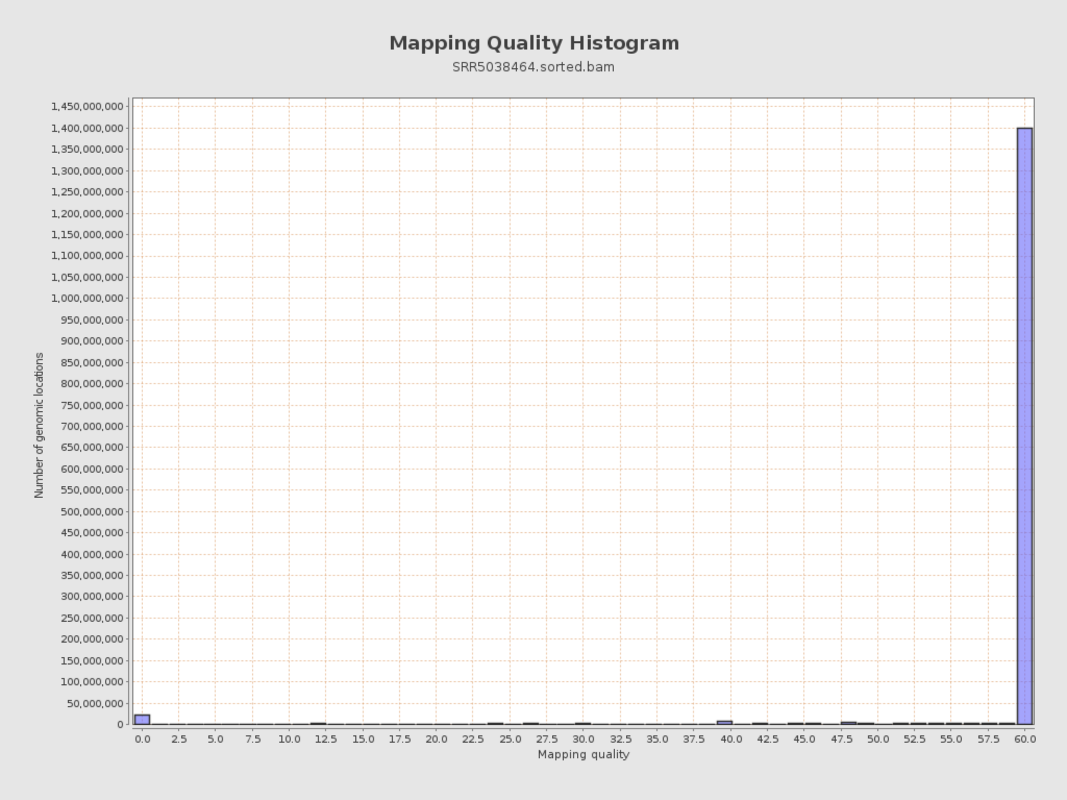
11. Results : Homopolymer Indels



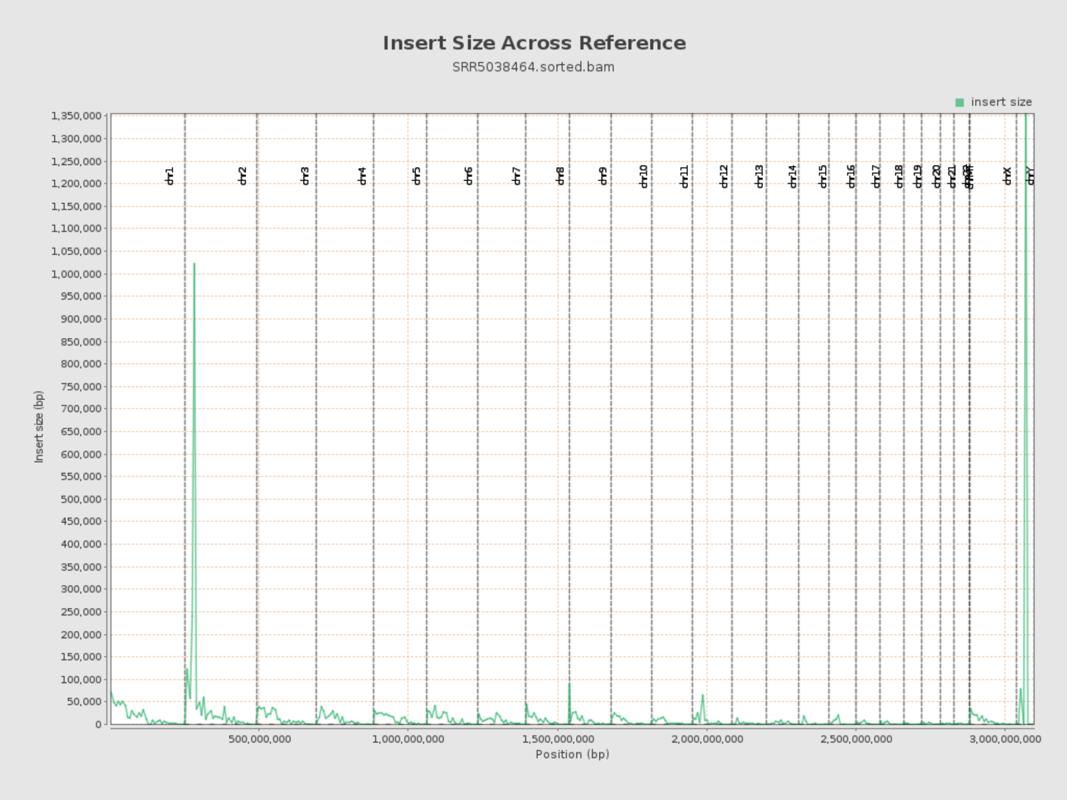
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram