Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 00:19:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038469.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_SRR5038469 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038469_1.fastq.gz SRR5038469_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 00:19:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038469.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,869,116
Mapped reads	12,114,824 / 94.14%
Unmapped reads	754,292 / 5.86%
Mapped paired reads	12,114,824 / 94.14%
Mapped reads, first in pair	6,120,674 / 47.56%
Mapped reads, second in pair	5,994,150 / 46.58%
Mapped reads, both in pair	11,969,240 / 93.01%
Mapped reads, singletons	145,584 / 1.13%
Secondary alignments	0
Supplementary alignments	204,814 / 1.59%
Read min/max/mean length	30 / 150 / 150.83
Duplicated reads (estimated)	1,751,176 / 13.61%
Duplication rate	8.85%
Clipped reads	3,289,332 / 25.56%

2.2. ACGT Content

Number/percentage of A's	496,396,178 / 28.91%
Number/percentage of C's	352,559,194 / 20.53%
Number/percentage of T's	497,063,755 / 28.94%
Number/percentage of G's	371,237,289 / 21.62%
Number/percentage of N's	35,009 / 0%

GC Percentage	42.15%

2.3. Coverage

Mean	0.5551
Standard Deviation	8.8807

2.4. Mapping Quality

Mean Mapping Quality	53.67

2.5. Insert size

Mean	78,557.26
Standard Deviation	2,693,800.16
P25/Median/P75	217 / 259 / 312

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	23,635,773
Insertions	302,903
Mapped reads with at least one insertion	2.37%
Deletions	613,430
Mapped reads with at least one deletion	4.87%
Homopolymer indels	47.62%

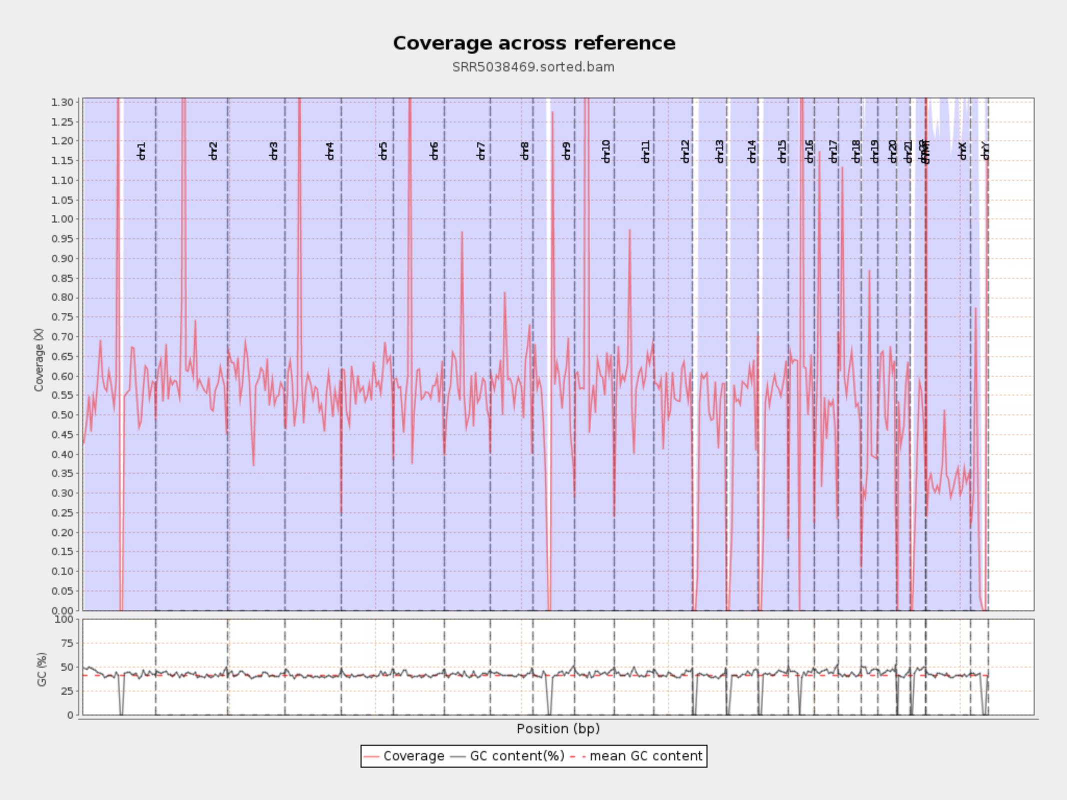
2.7. Chromosome stats

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

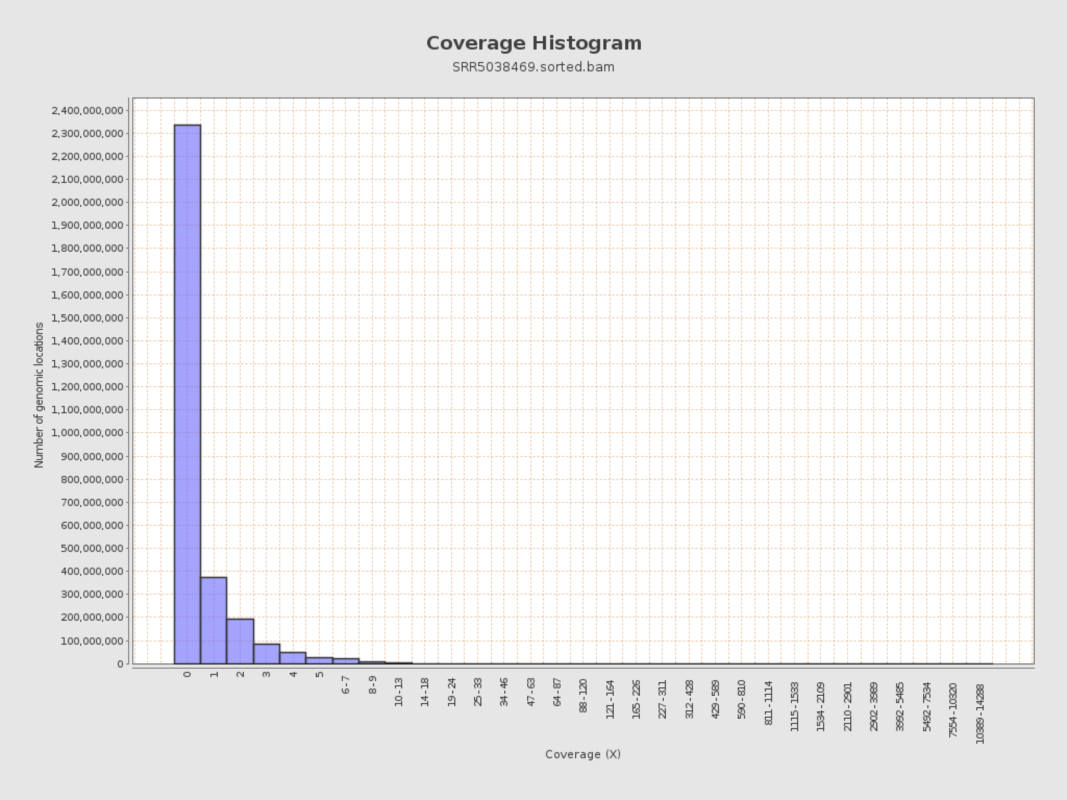
		bases	coverage	deviation
chr1	249250621	138639646	0.5562	15.0651
chr2	243199373	156818777	0.6448	9.1358
chr3	198022430	114963735	0.5806	1.3032
chr4	191154276	113289901	0.5927	6.9422
chr5	180915260	104547192	0.5779	1.3893
chr6	171115067	103720062	0.6061	12.2381
chr7	159138663	90393150	0.568	7.3774
chr8	146364022	87110468	0.5952	2.4197
chr9	141213431	74932226	0.5306	15.8288
chr10	135534747	95203251	0.7024	16.3898
chr11	135006516	81967618	0.6071	6.8818
chr12	133851895	74564776	0.5571	1.3023
chr13	115169878	51638090	0.4484	1.116
chr14	107349540	50046104	0.4662	1.2549
chr15	102531392	47417937	0.4625	1.1578
chr16	90354753	59653434	0.6602	10.0366
chr17	81195210	43828871	0.5398	10.1688
chr18	78077248	49784655	0.6376	12.9777
chr19	59128983	24657566	0.417	7.7416
chr20	63025520	36426022	0.578	2.31
chr21	48129895	22229158	0.4619	3.0042
chr22	51304566	17744921	0.3459	1.0329
chrMT	16571	5763626	347.814	245.6225
chrX	155270560	51786929	0.3335	1.9032

chrY	59373566	21367136	0.3599	8.9684

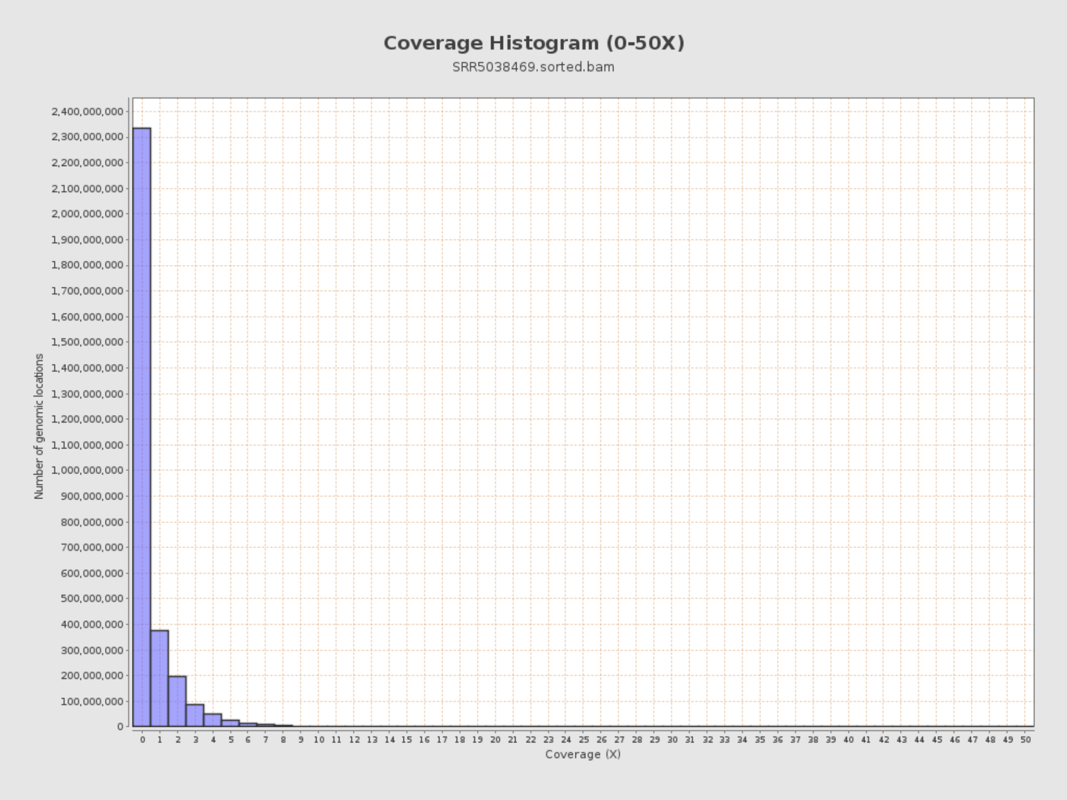
3. Results : Coverage across reference



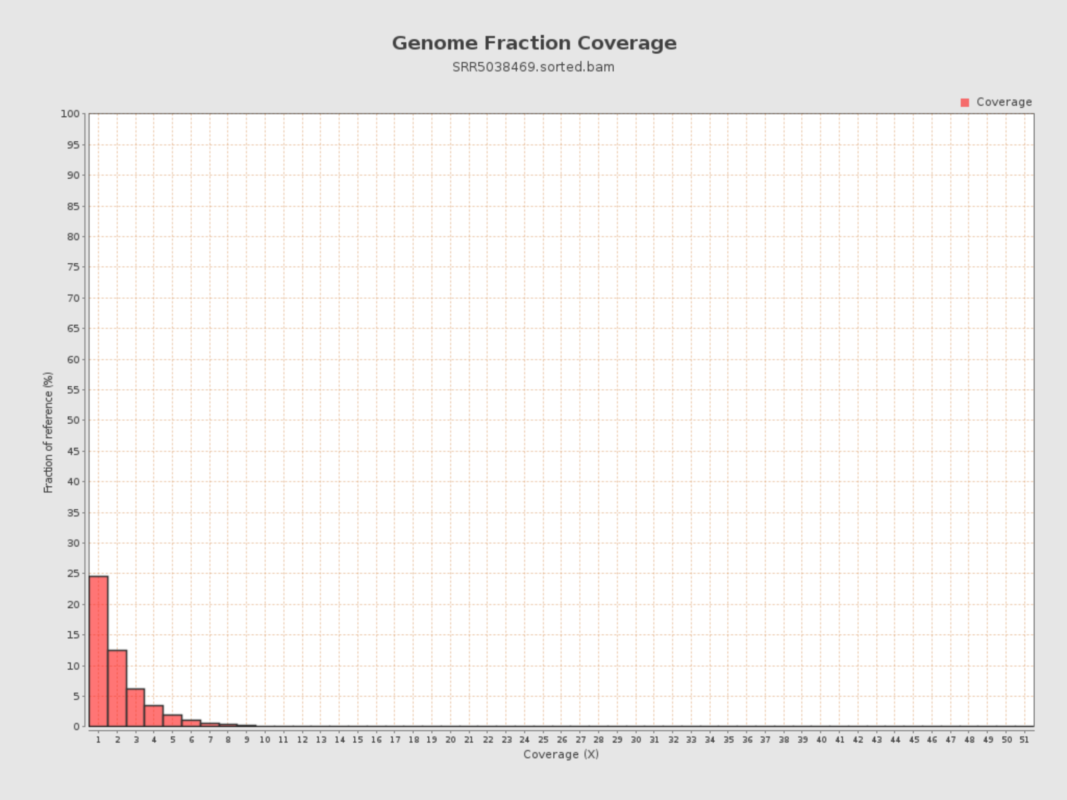
4. Results : Coverage Histogram



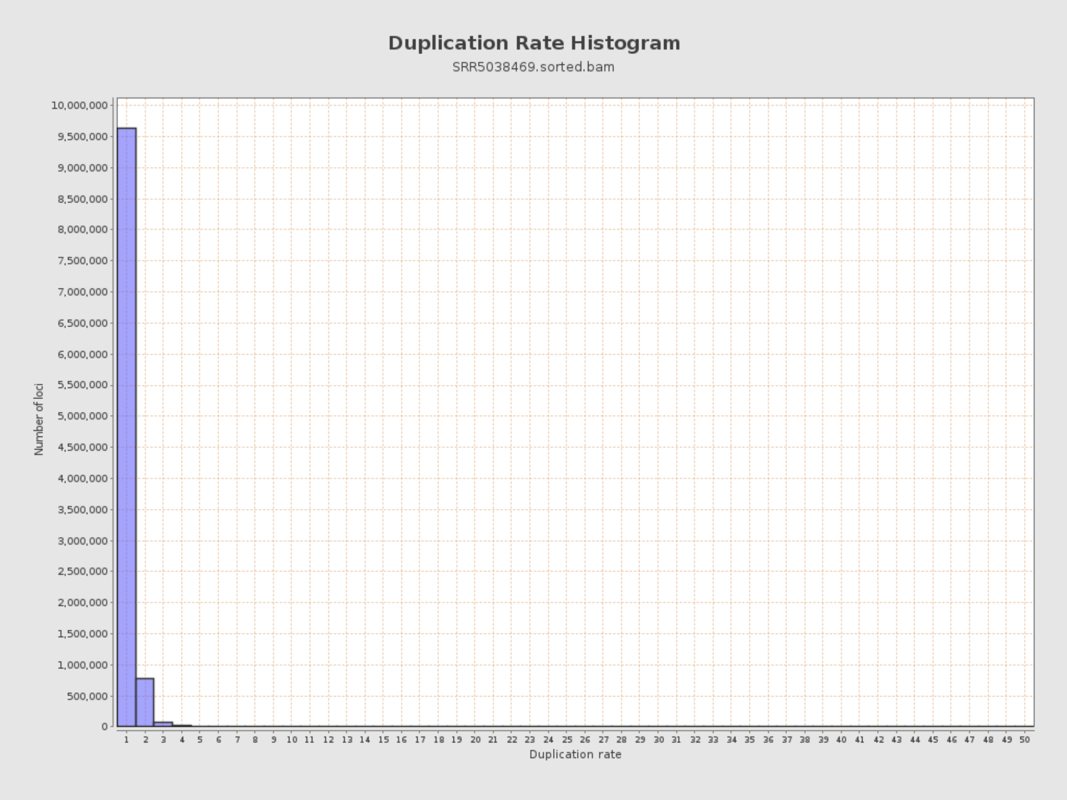
5. Results : Coverage Histogram (0-50X)



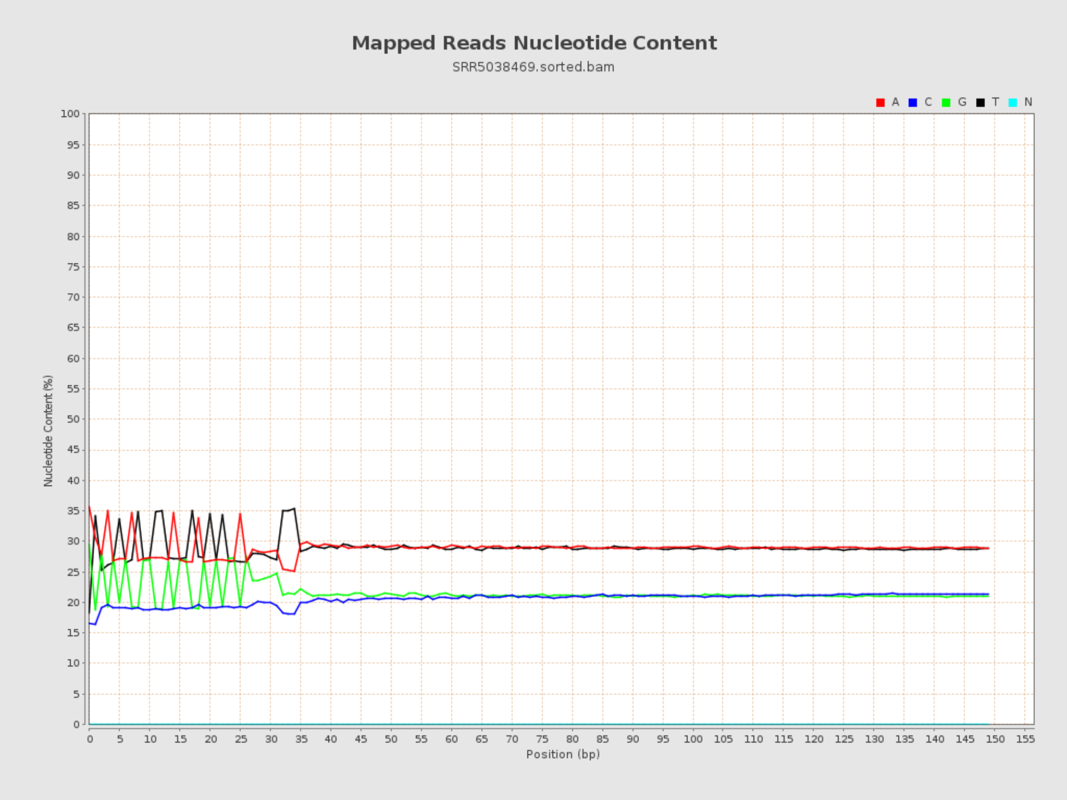
6. Results : Genome Fraction Coverage



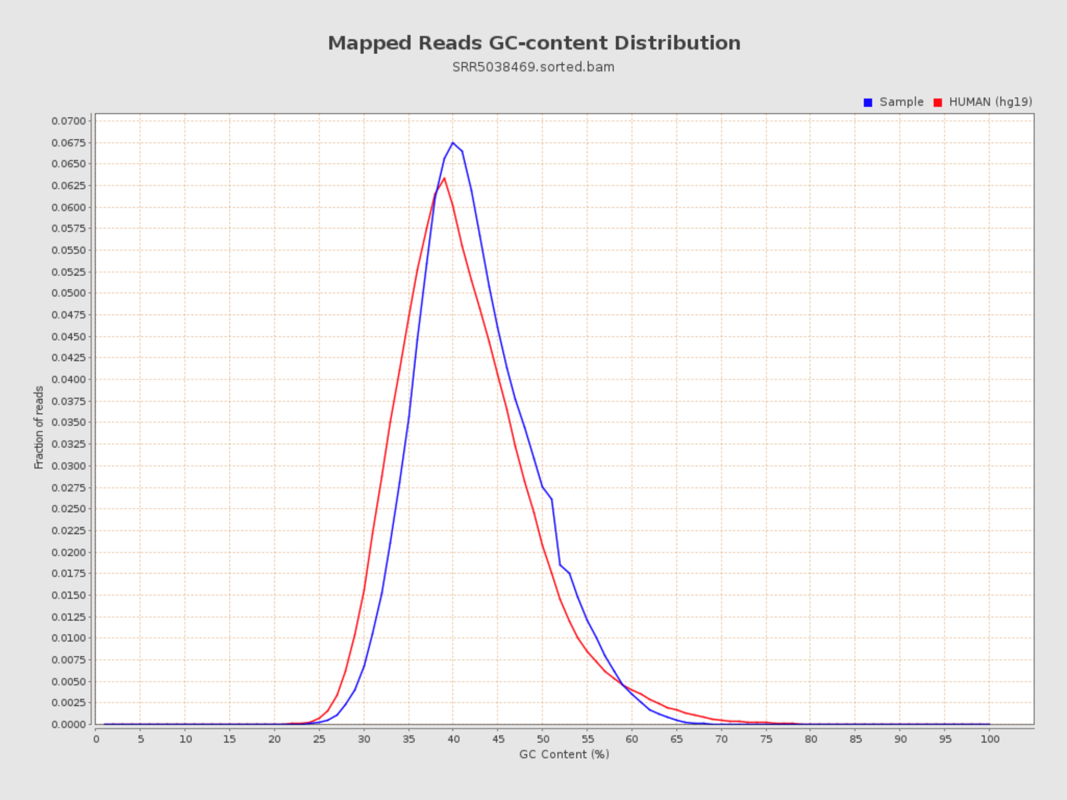
7. Results : Duplication Rate Histogram



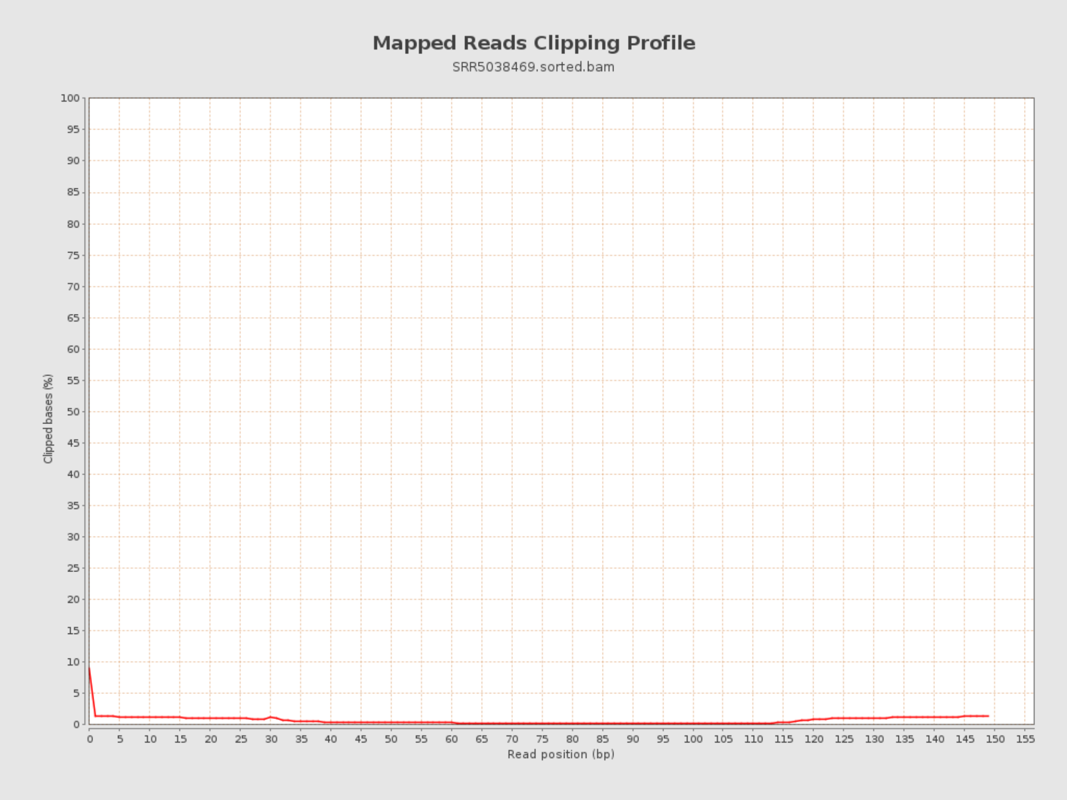
8. Results : Mapped Reads Nucleotide Content



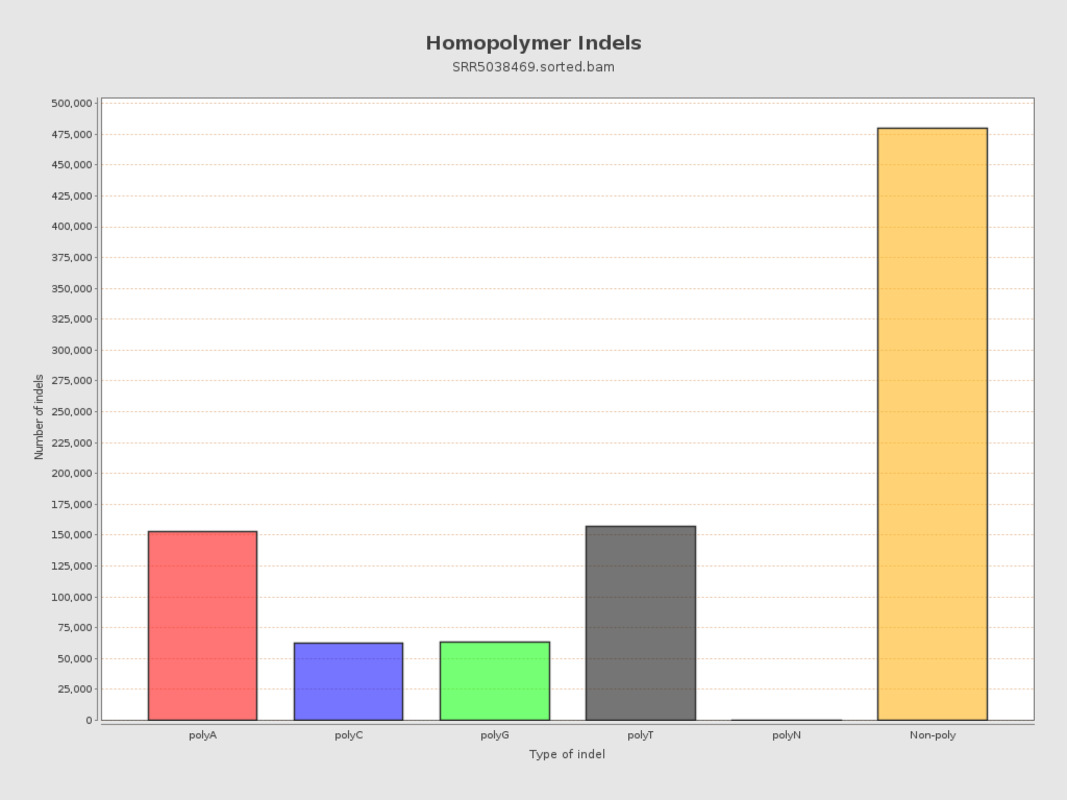
9. Results : Mapped Reads GC-content Distribution



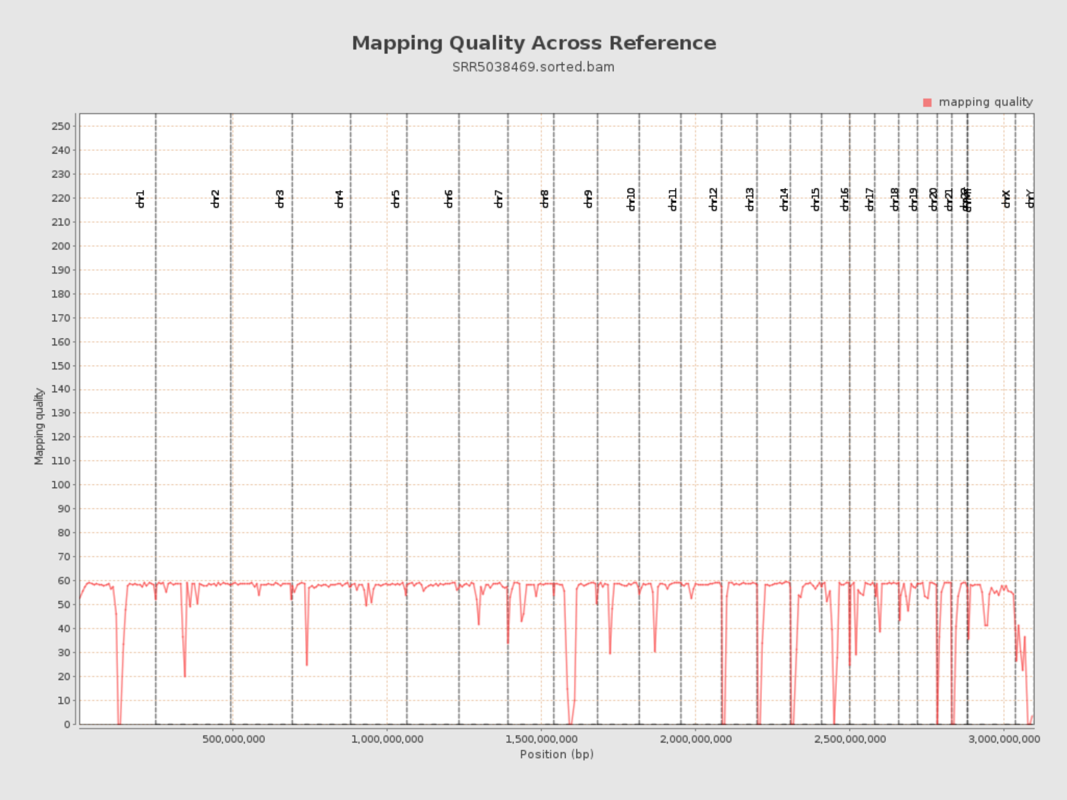
10. Results : Mapped Reads Clipping Profile



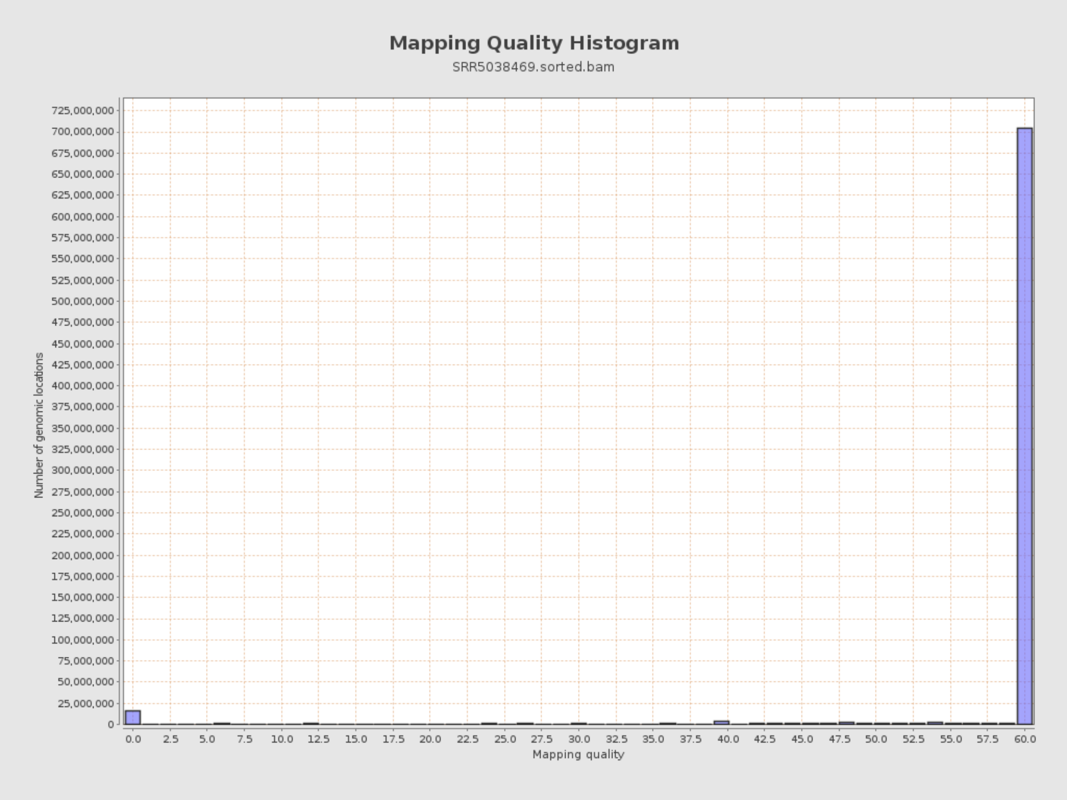
11. Results : Homopolymer Indels



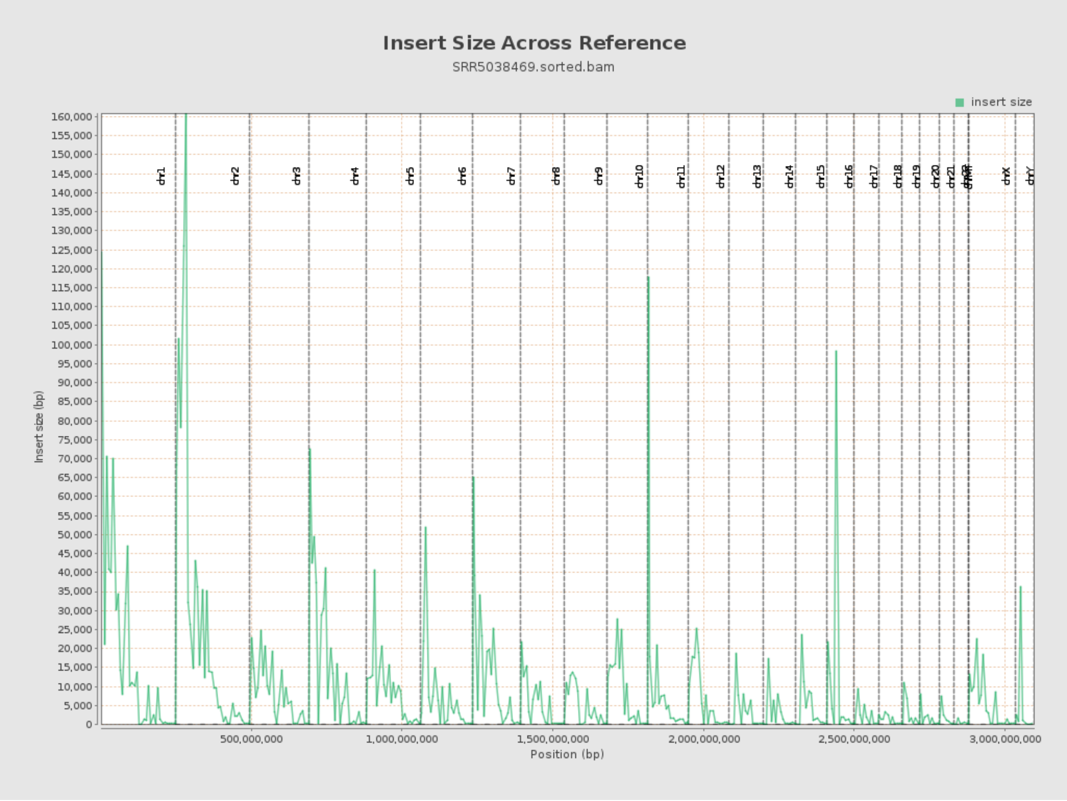
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram