Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 20:53:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038461.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_SRR5038461 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038461_1.fastq.gz SRR5038461_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 20:53:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038461.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,250,000
Mapped reads	18,058,744 / 89.18%
Unmapped reads	2,191,256 / 10.82%
Mapped paired reads	18,058,744 / 89.18%
Mapped reads, first in pair	9,188,653 / 45.38%
Mapped reads, second in pair	8,870,091 / 43.8%
Mapped reads, both in pair	17,584,570 / 86.84%
Mapped reads, singletons	474,174 / 2.34%
Secondary alignments	0
Supplementary alignments	369,174 / 1.82%
Read min/max/mean length	30 / 150 / 150.88
Duplicated reads (estimated)	4,727,851 / 23.35%
Duplication rate	18.28%
Clipped reads	10,662,665 / 52.66%

2.2. ACGT Content

Number/percentage of A's	681,827,554 / 28.99%
Number/percentage of C's	449,166,465 / 19.1%
Number/percentage of T's	700,058,060 / 29.77%
Number/percentage of G's	520,658,394 / 22.14%
Number/percentage of N's	178,985 / 0.01%

GC Percentage	41.24%

2.3. Coverage

Mean	0.7603
Standard Deviation	11.1369

2.4. Mapping Quality

Mean Mapping Quality	53.17

2.5. Insert size

Mean	85,843.83
Standard Deviation	2,792,567.77
P25/Median/P75	178 / 223 / 277

2.6. Mismatches and indels

General error rate	1.36%
Mismatches	30,733,670
Insertions	468,370
Mapped reads with at least one insertion	2.45%
Deletions	824,973
Mapped reads with at least one deletion	4.38%
Homopolymer indels	46.53%

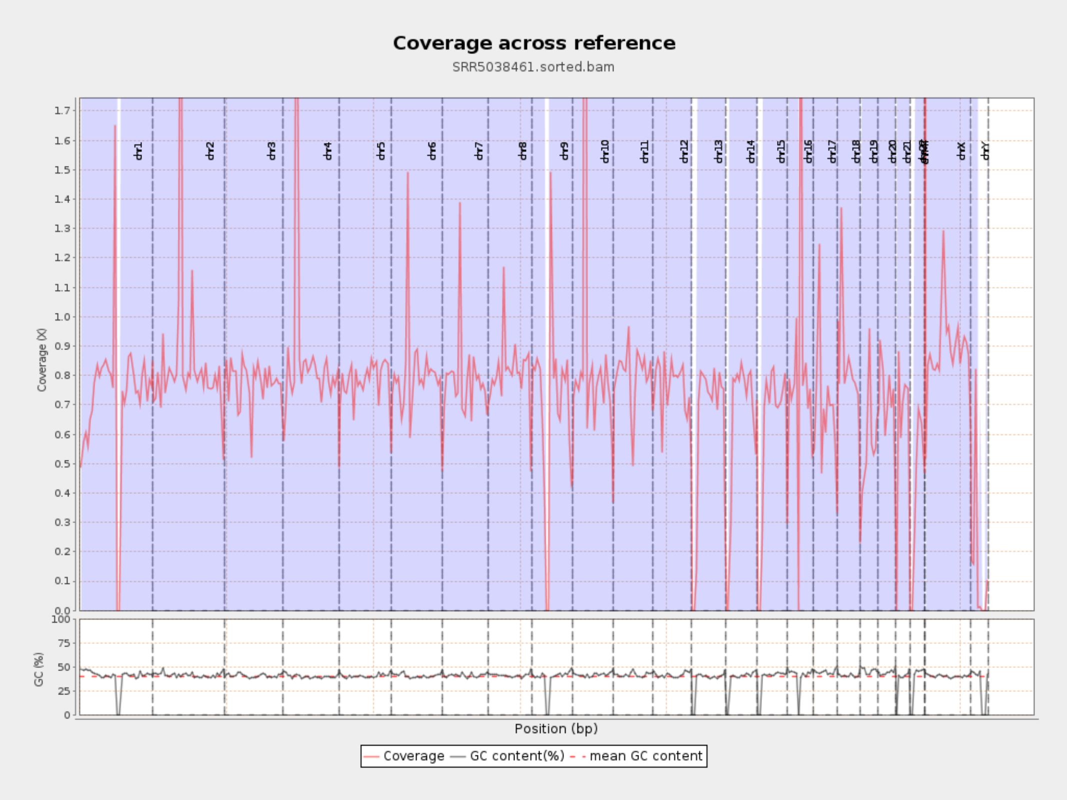
2.7. Chromosome stats

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

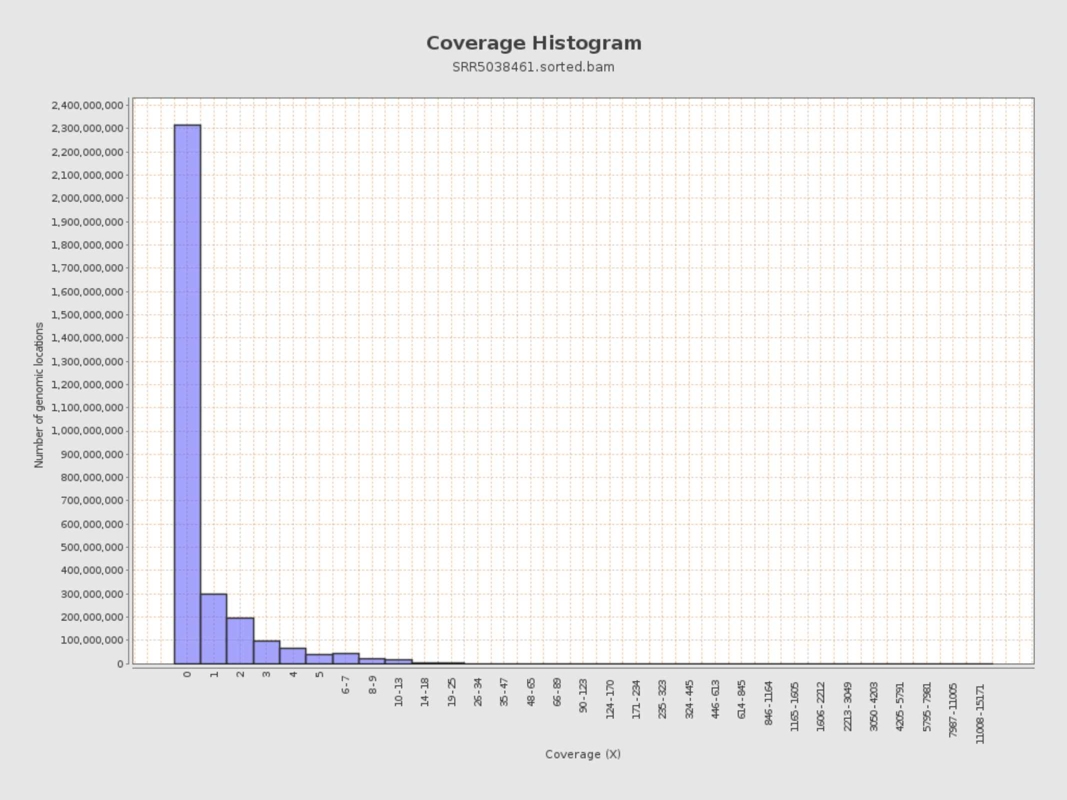
		bases	coverage	deviation
chr1	249250621	182197944	0.731	15.1162
chr2	243199373	209256178	0.8604	13.2107
chr3	198022430	153846717	0.7769	1.9791
chr4	191154276	165586035	0.8662	11.9643
chr5	180915260	141221549	0.7806	1.9819
chr6	171115067	138842852	0.8114	7.8788
chr7	159138663	124668581	0.7834	10.8021
chr8	146364022	119136486	0.814	4.1004
chr9	141213431	96277933	0.6818	16.4169
chr10	135534747	129710510	0.957	28.6365
chr11	135006516	107067267	0.7931	6.3776
chr12	133851895	102086258	0.7627	2.0278
chr13	115169878	72594638	0.6303	1.7744
chr14	107349540	67659679	0.6303	1.9679
chr15	102531392	61851296	0.6032	1.6508
chr16	90354753	74288611	0.8222	13.1626
chr17	81195210	55716646	0.6862	10.5273
chr18	78077248	66232368	0.8483	15.1854
chr19	59128983	32752051	0.5539	7.7618
chr20	63025520	45688012	0.7249	4.0358
chr21	48129895	30934356	0.6427	5.6818
chr22	51304566	20883293	0.407	1.7036
chrMT	16571	7164564	432.3556	354.6558
chrX	155270560	138527568	0.8922	3.8428

chrY	59373566	9456476	0.1593	13.7917

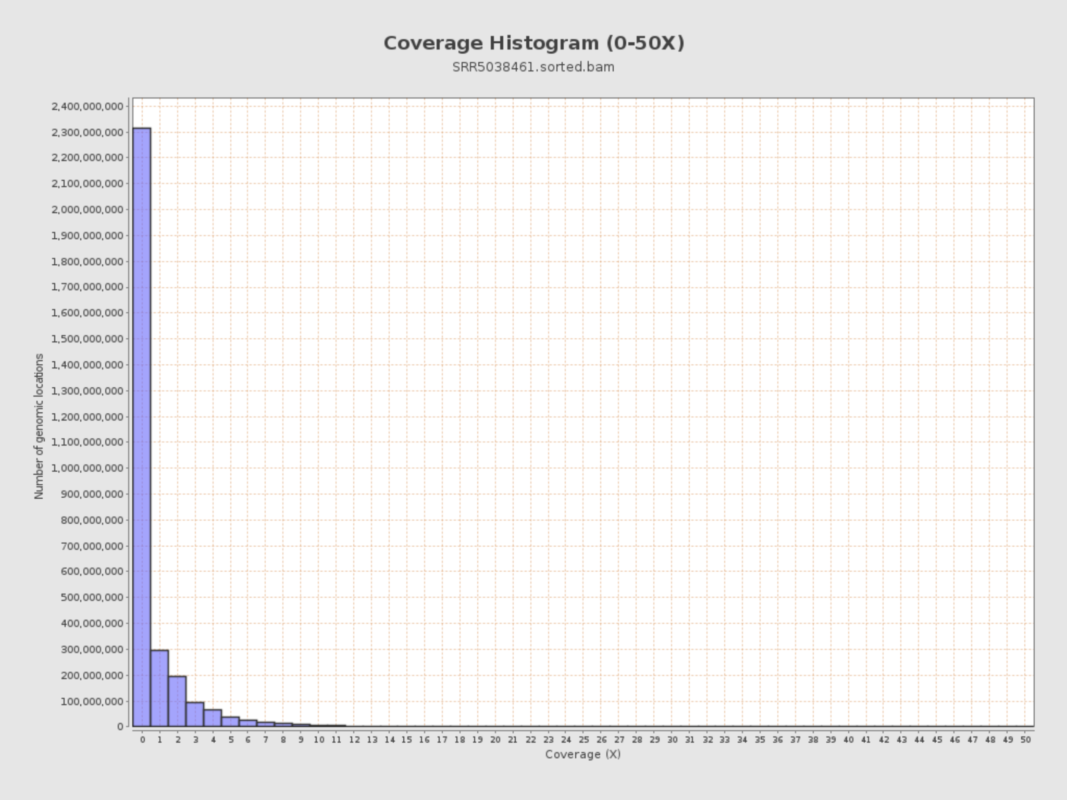
3. Results : Coverage across reference



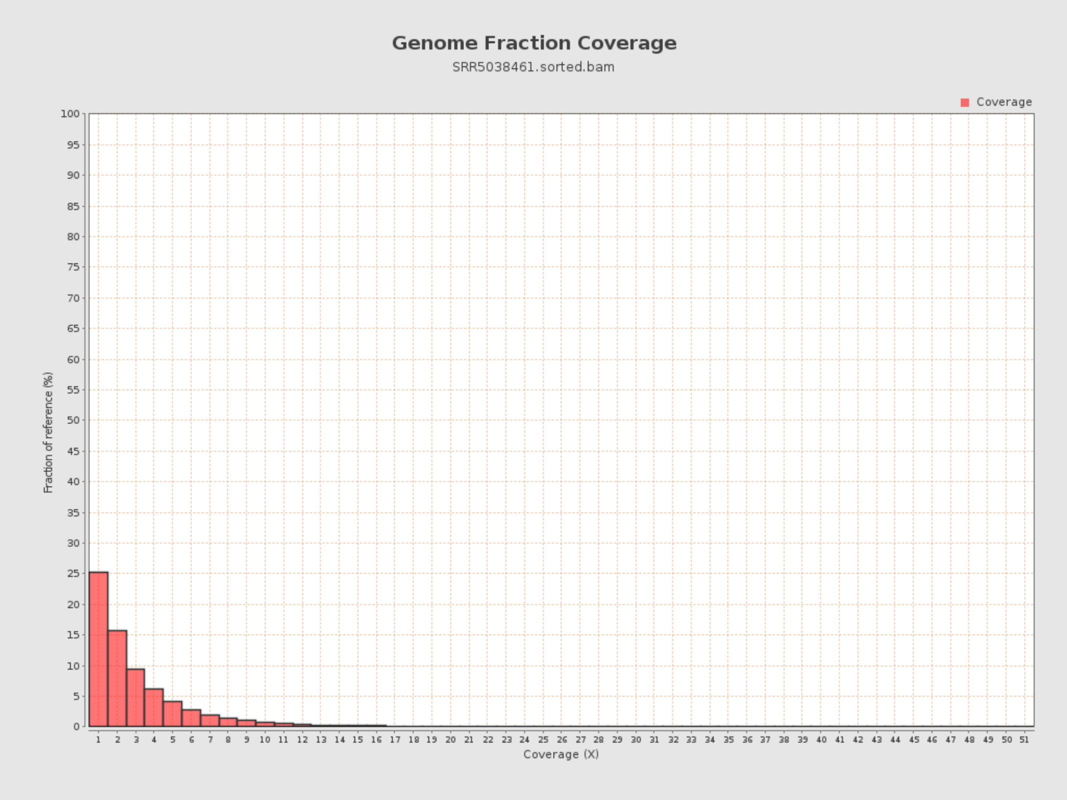
4. Results : Coverage Histogram



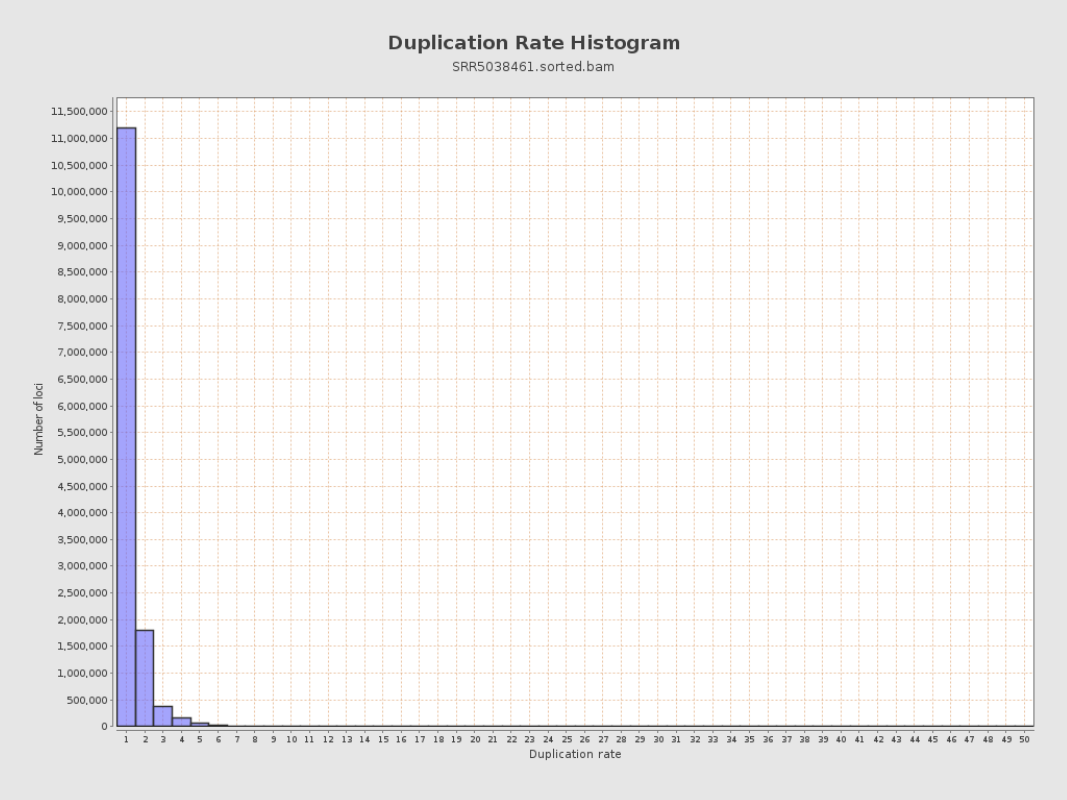
5. Results : Coverage Histogram (0-50X)



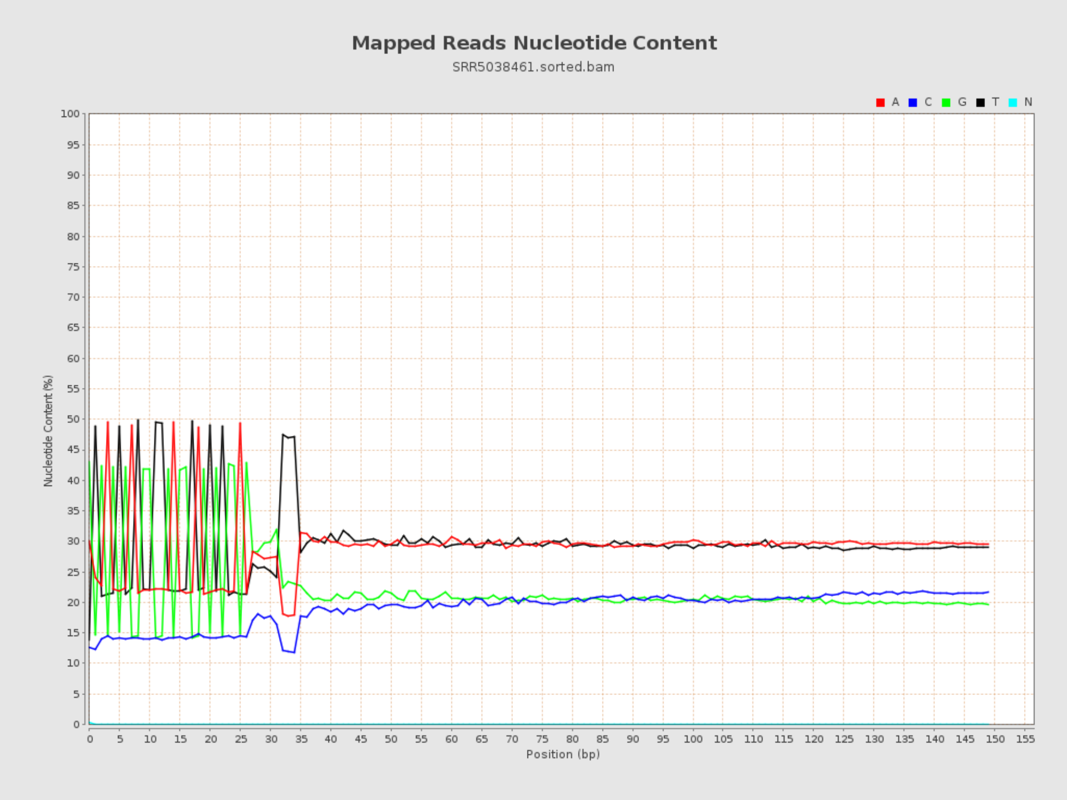
6. Results : Genome Fraction Coverage



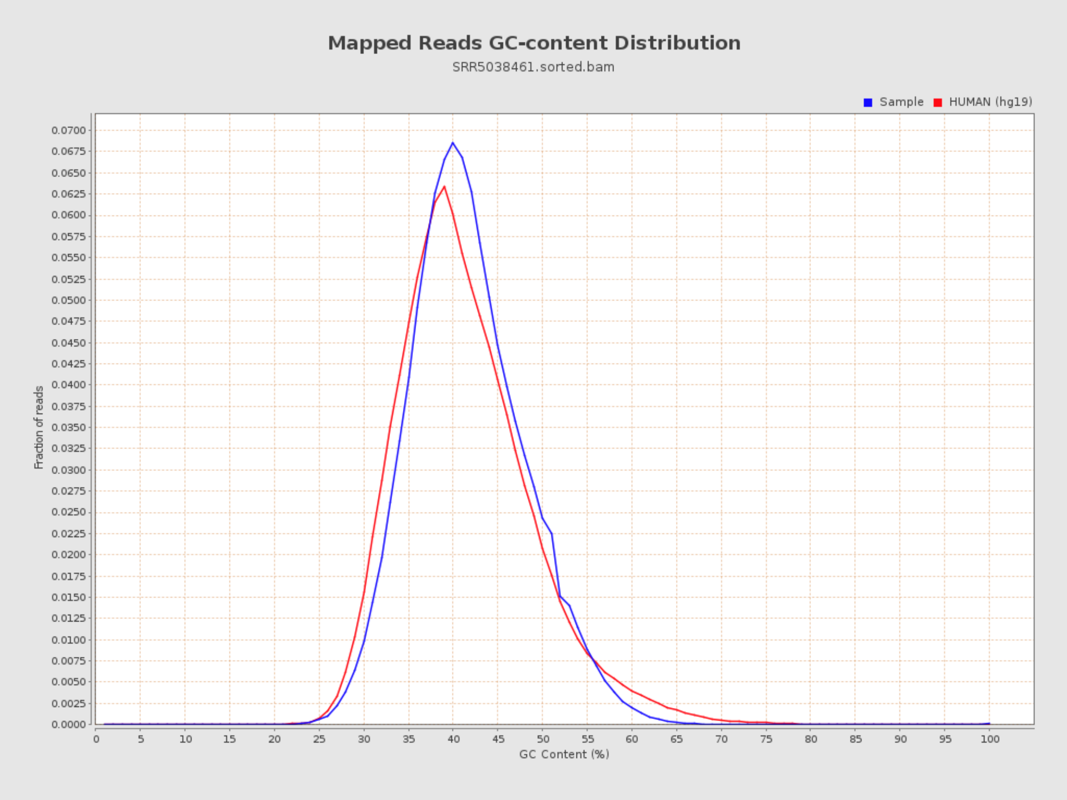
7. Results : Duplication Rate Histogram



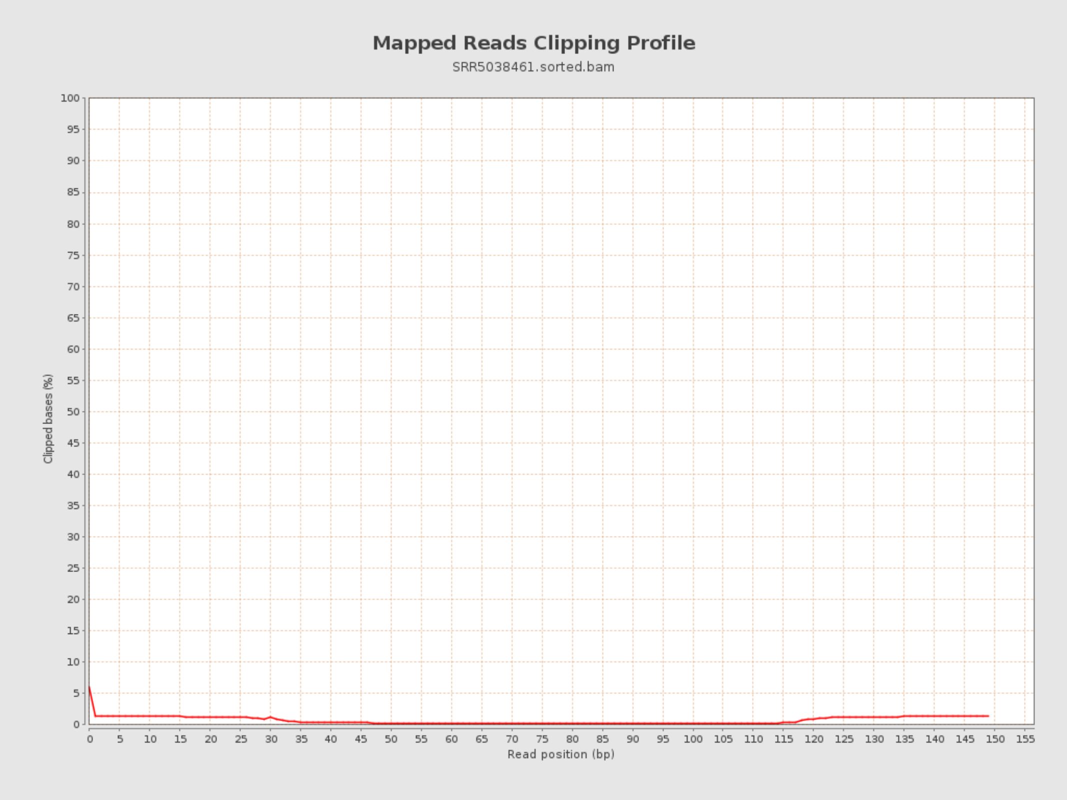
8. Results : Mapped Reads Nucleotide Content



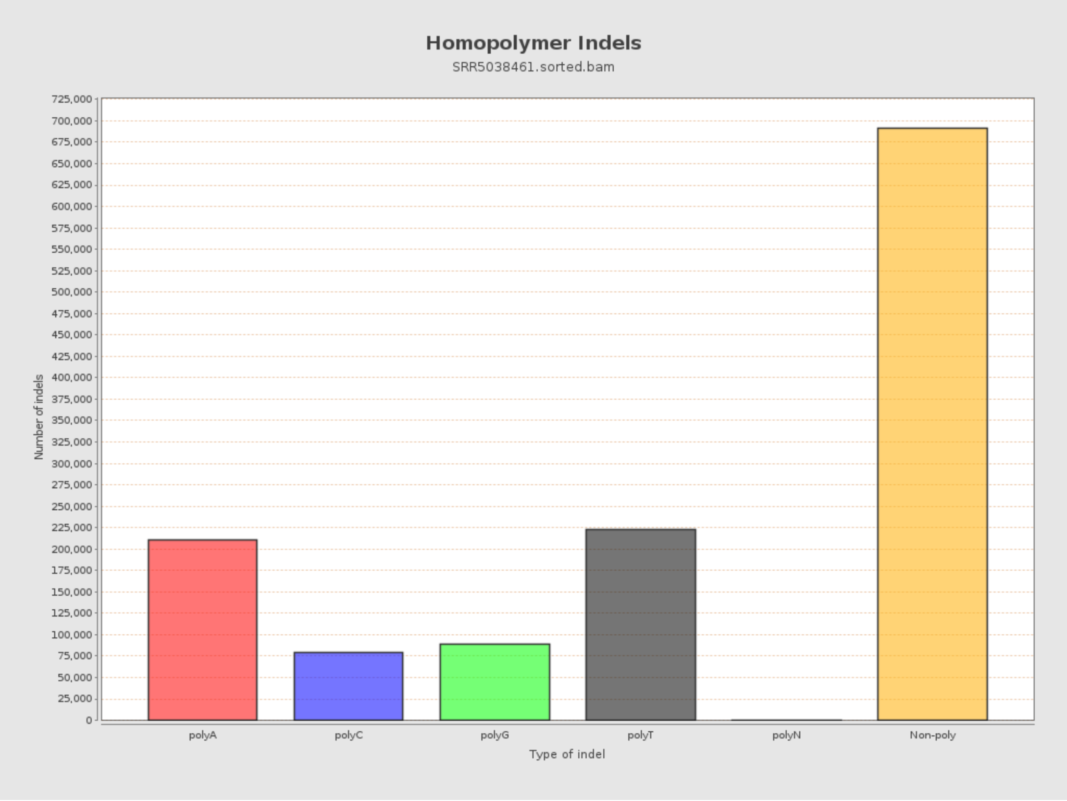
9. Results : Mapped Reads GC-content Distribution



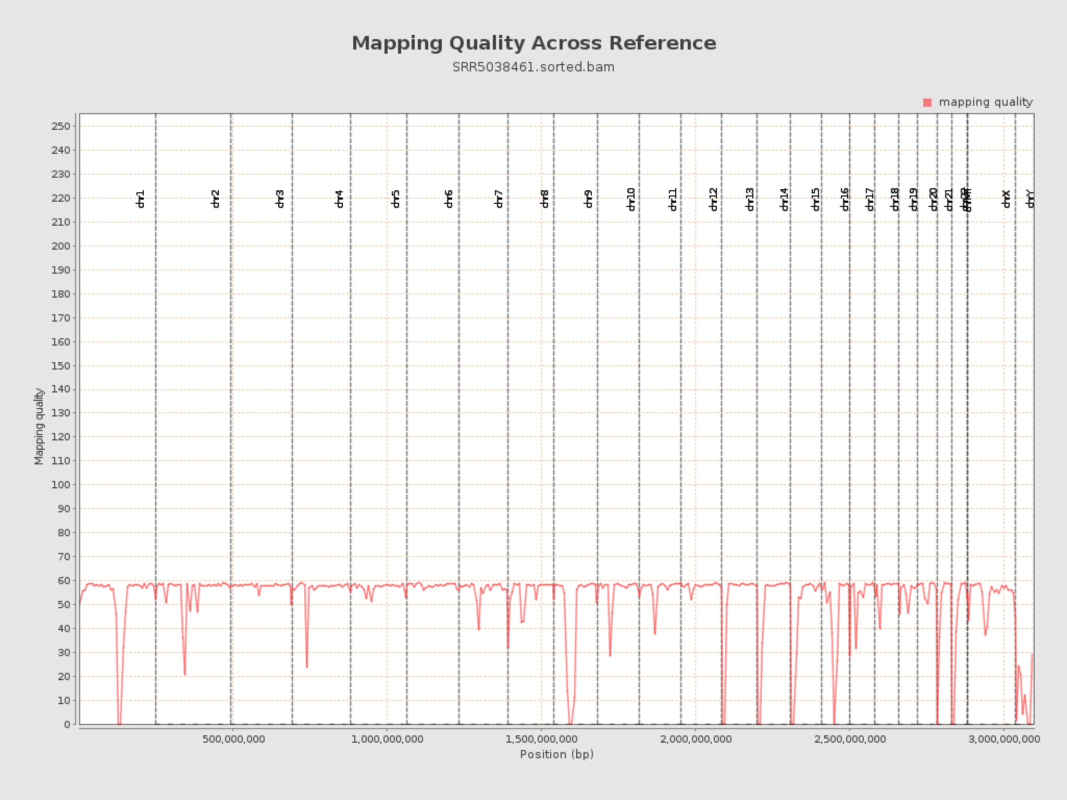
10. Results : Mapped Reads Clipping Profile



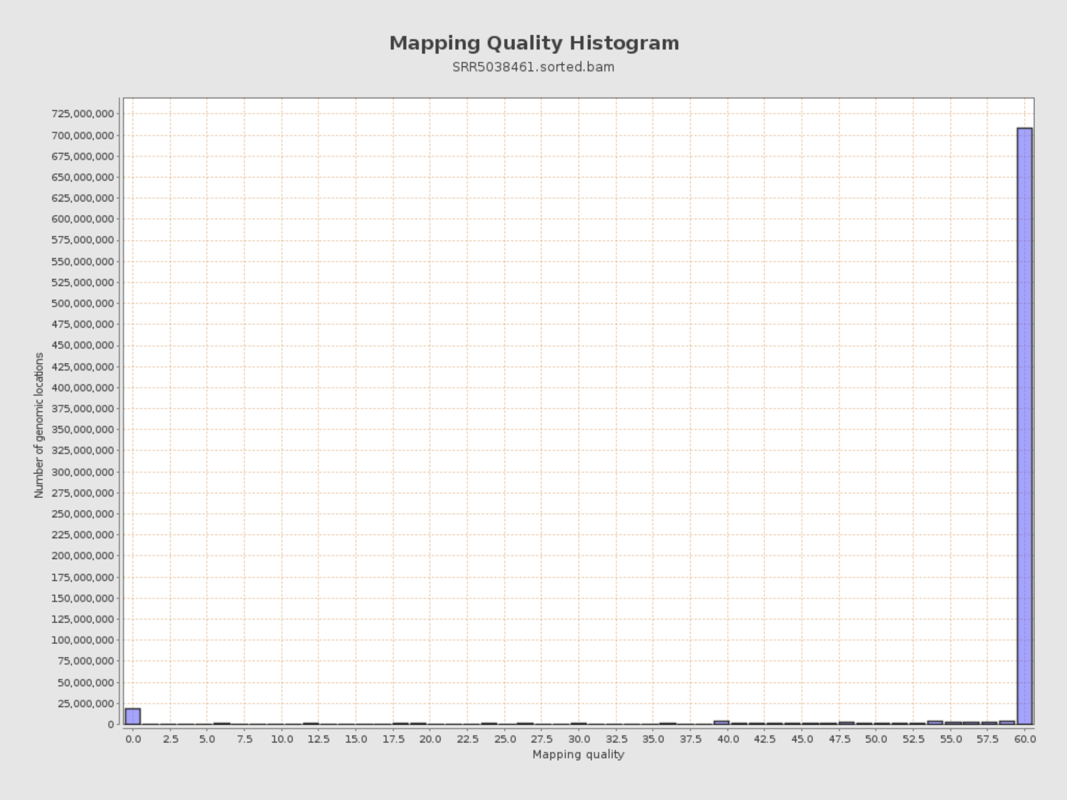
11. Results : Homopolymer Indels



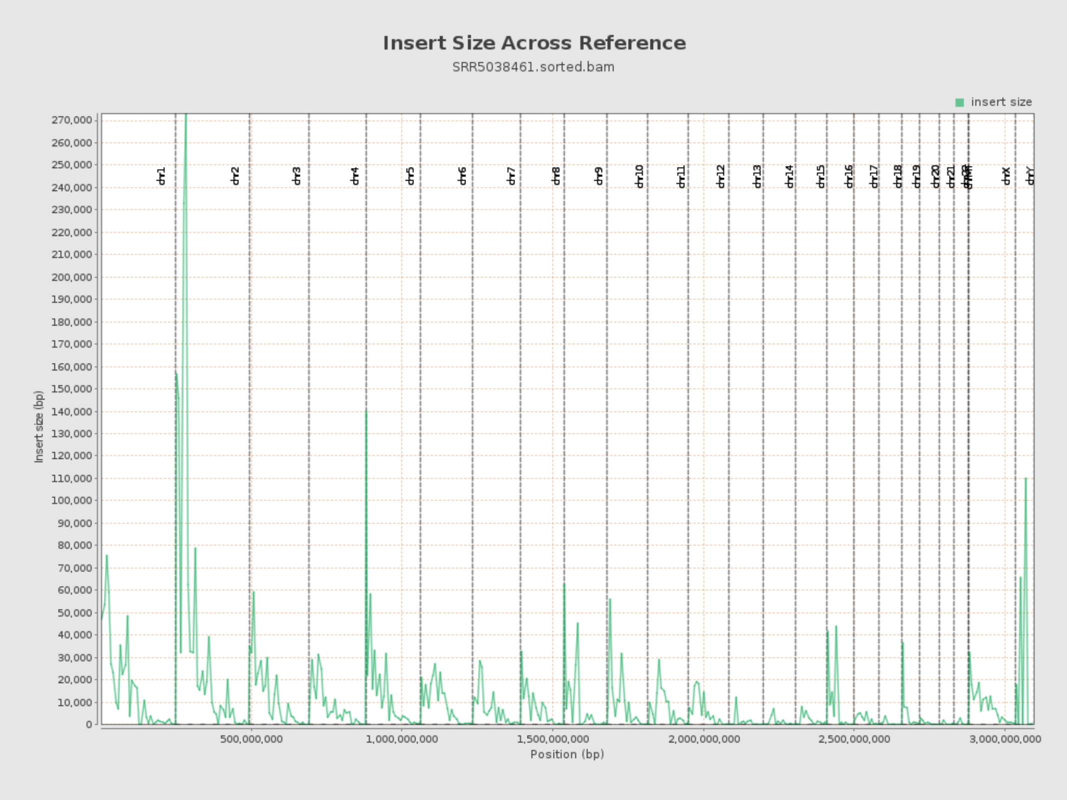
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram