Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 23:54:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038468.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_SRR5038468 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038468_1.fastq.gz SRR5038468_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 23:54:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038468.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,406,848
Mapped reads	13,803,521 / 95.81%
Unmapped reads	603,327 / 4.19%
Mapped paired reads	13,803,521 / 95.81%
Mapped reads, first in pair	6,964,652 / 48.34%
Mapped reads, second in pair	6,838,869 / 47.47%
Mapped reads, both in pair	13,654,782 / 94.78%
Mapped reads, singletons	148,739 / 1.03%
Secondary alignments	0
Supplementary alignments	265,933 / 1.85%
Read min/max/mean length	30 / 150 / 150.96
Duplicated reads (estimated)	2,315,046 / 16.07%
Duplication rate	9.54%
Clipped reads	3,009,509 / 20.89%

2.2. ACGT Content

Number/percentage of A's	586,003,041 / 29.53%
Number/percentage of C's	402,107,237 / 20.26%
Number/percentage of T's	585,053,655 / 29.48%
Number/percentage of G's	411,187,930 / 20.72%
Number/percentage of N's	43,991 / 0%

GC Percentage	40.98%

2.3. Coverage

Mean	0.6415
Standard Deviation	11.6845

2.4. Mapping Quality

Mean Mapping Quality	53.71

2.5. Insert size

Mean	78,928.36
Standard Deviation	2,638,866.42
P25/Median/P75	203 / 247 / 303

2.6. Mismatches and indels

General error rate	1.49%
Mismatches	28,434,051
Insertions	382,088
Mapped reads with at least one insertion	2.59%
Deletions	713,204
Mapped reads with at least one deletion	4.96%
Homopolymer indels	46.54%

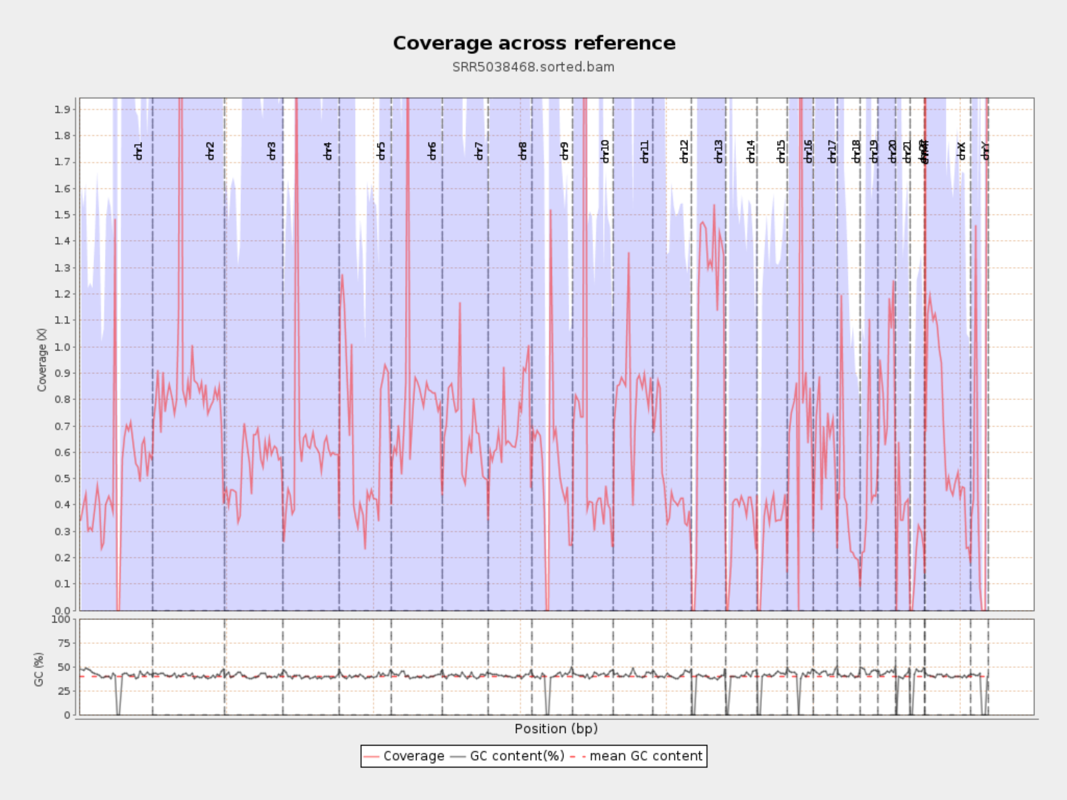
2.7. Chromosome stats

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

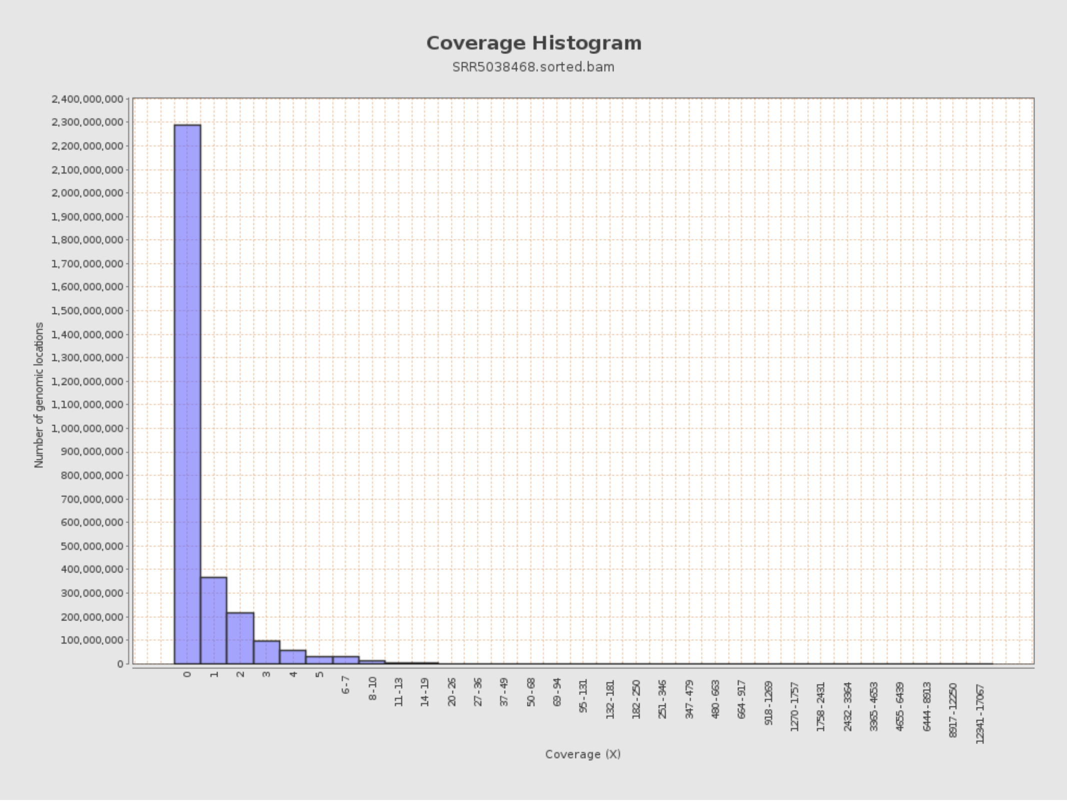
		bases	coverage	deviation
chr1	249250621	120604598	0.4839	17.7019
chr2	243199373	219458176	0.9024	15.106
chr3	198022430	109534706	0.5531	1.3476
chr4	191154276	119506606	0.6252	10.8474
chr5	180915260	117086524	0.6472	1.5679
chr6	171115067	140859775	0.8232	16.6744
chr7	159138663	107439370	0.6751	9.4092
chr8	146364022	101879178	0.6961	3.2601
chr9	141213431	73867166	0.5231	18.5577
chr10	135534747	92294852	0.681	22.1907
chr11	135006516	110420625	0.8179	8.8765
chr12	133851895	65032237	0.4859	1.2768
chr13	115169878	129335492	1.123	2.0721
chr14	107349540	35161866	0.3275	1.2088
chr15	102531392	31750428	0.3097	0.913
chr16	90354753	77709351	0.86	15.5347
chr17	81195210	49905074	0.6146	8.3155
chr18	78077248	30189690	0.3867	15.3004
chr19	59128983	25895685	0.438	9.4649
chr20	63025520	56085204	0.8899	3.6479
chr21	48129895	17540739	0.3644	5.193
chr22	51304566	9487405	0.1849	0.7928
chrMT	16571	967580	58.39	34.7637
chrX	155270560	104656260	0.674	2.6322

chrY	59373566	39211360	0.6604	18.8661

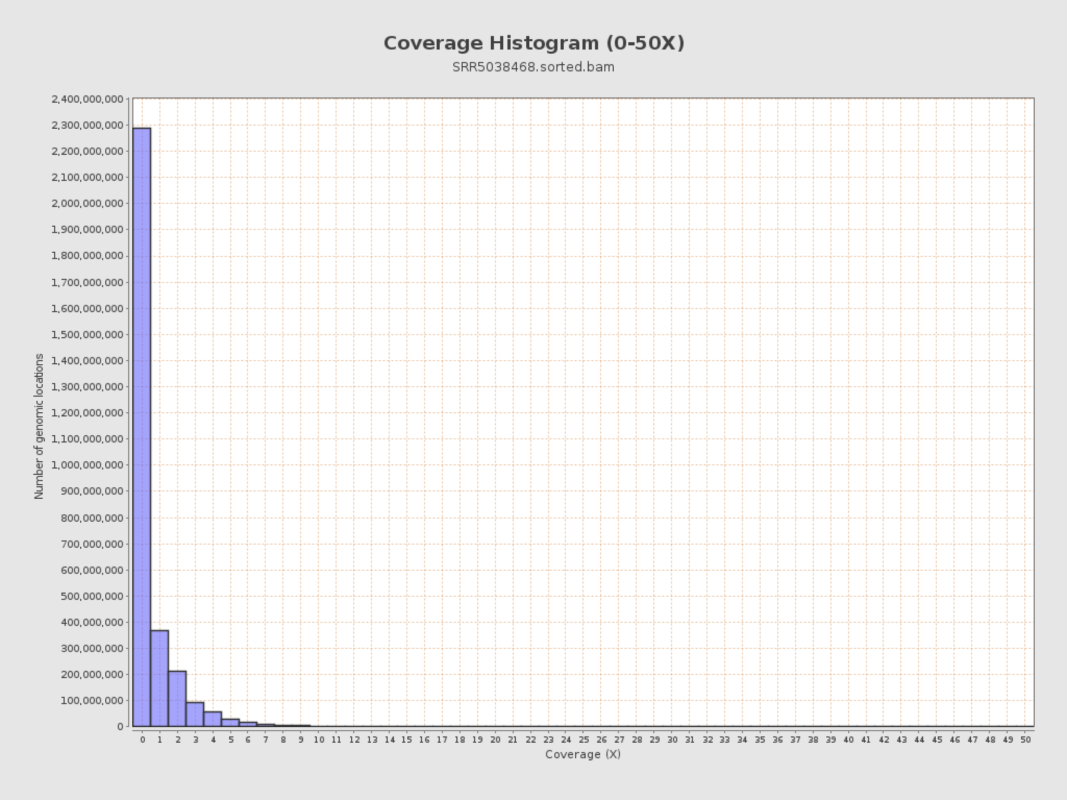
3. Results : Coverage across reference



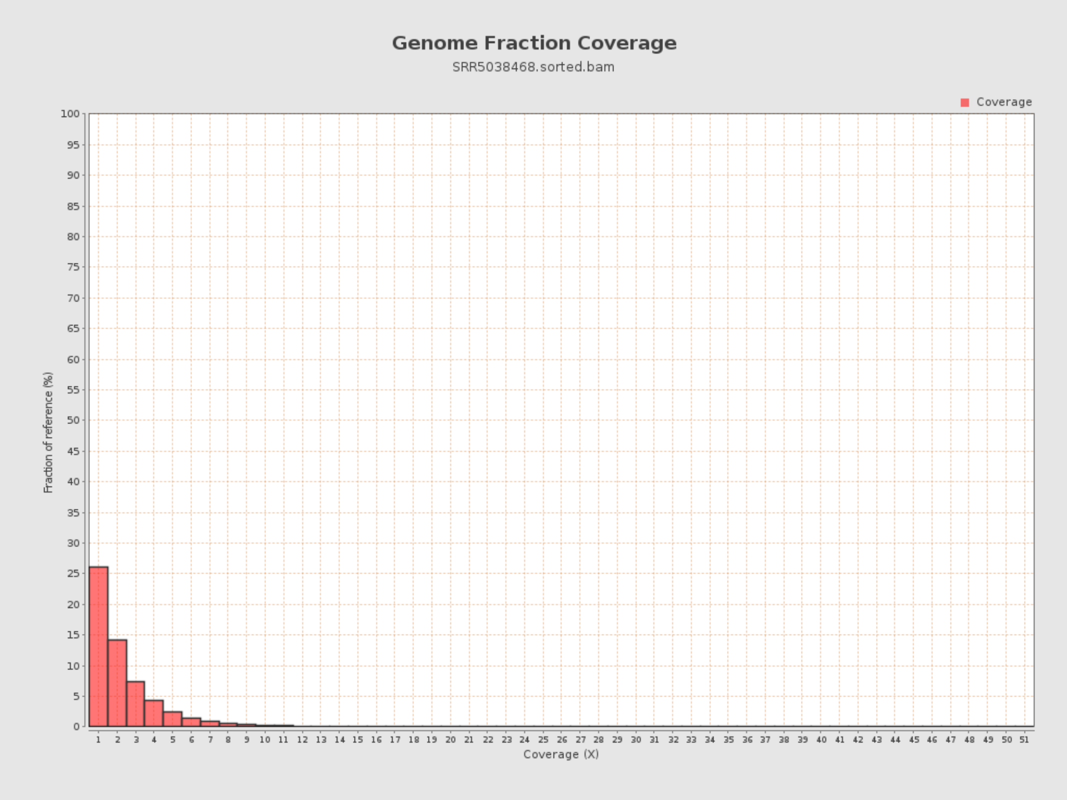
4. Results : Coverage Histogram



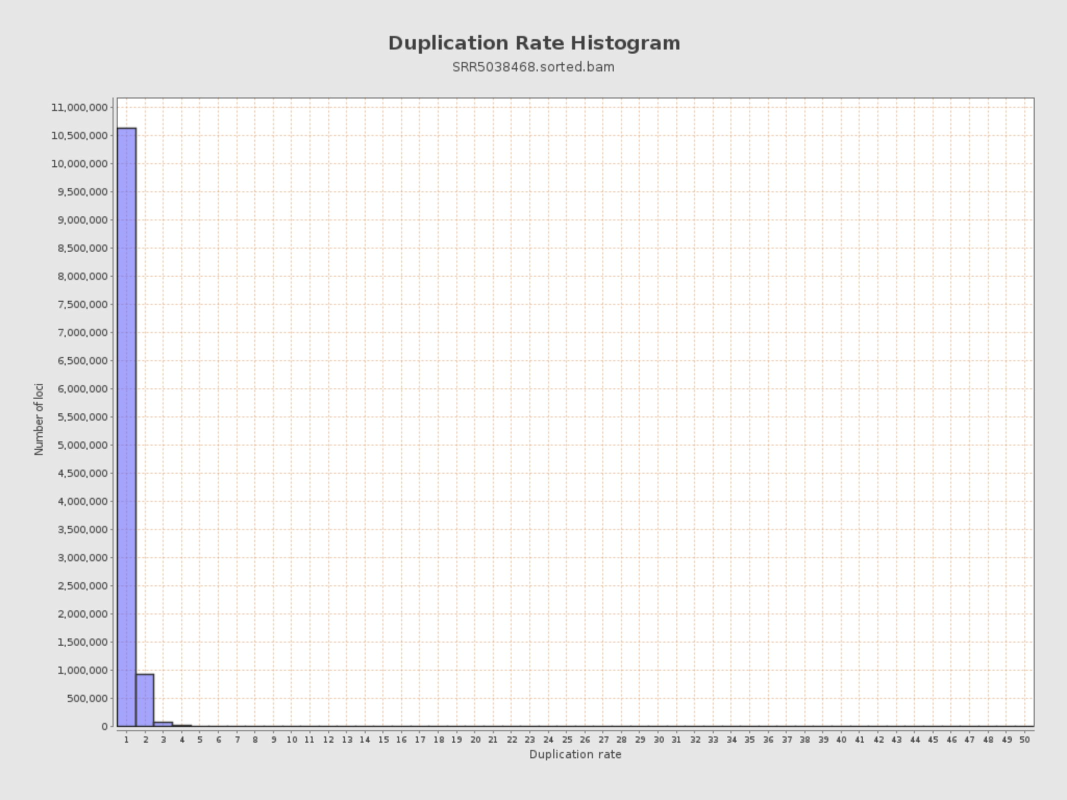
5. Results : Coverage Histogram (0-50X)



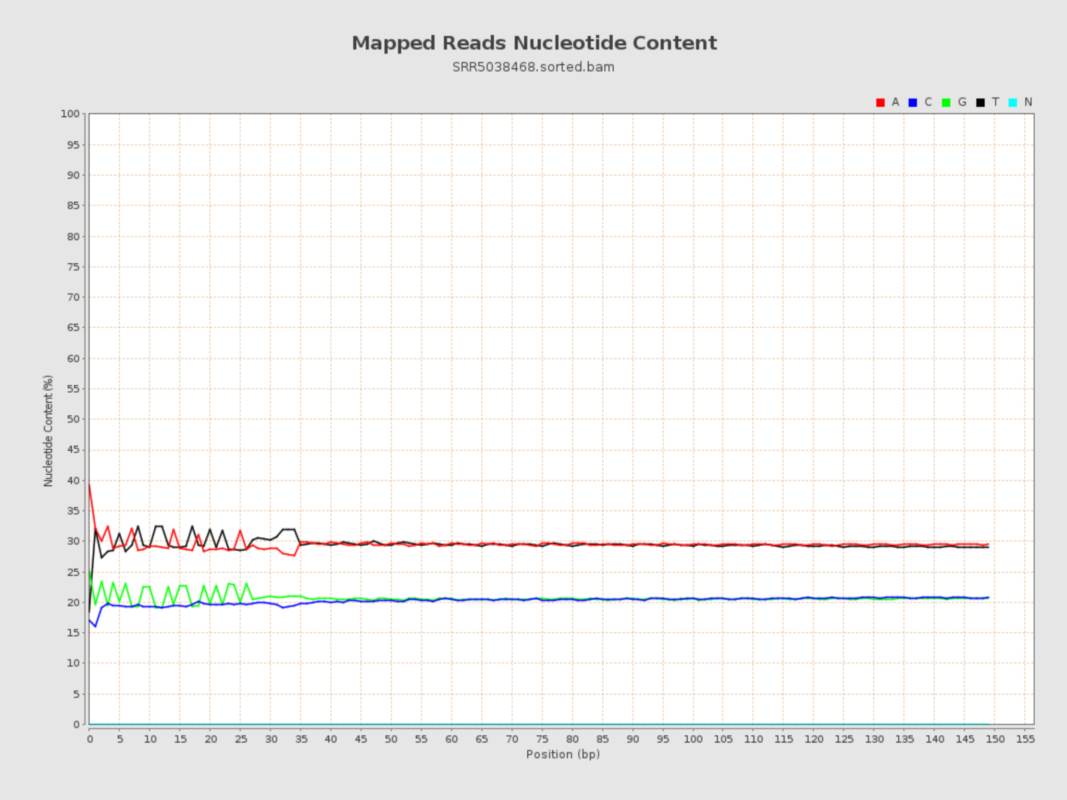
6. Results : Genome Fraction Coverage



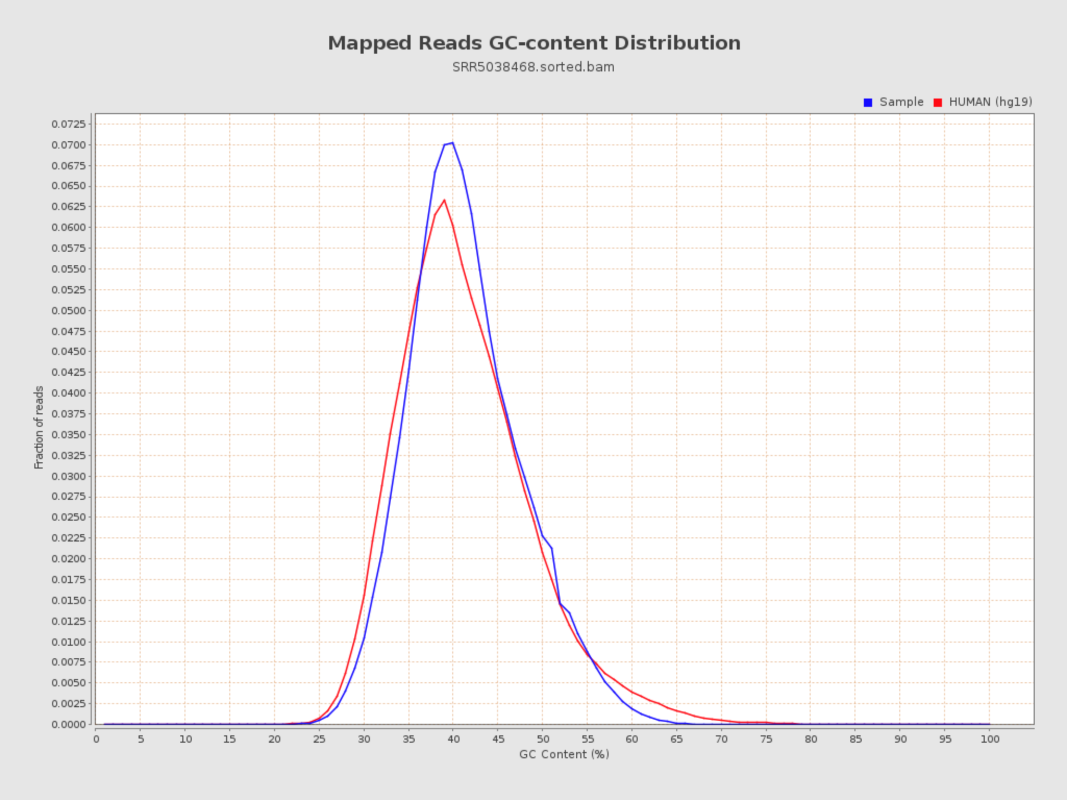
7. Results : Duplication Rate Histogram



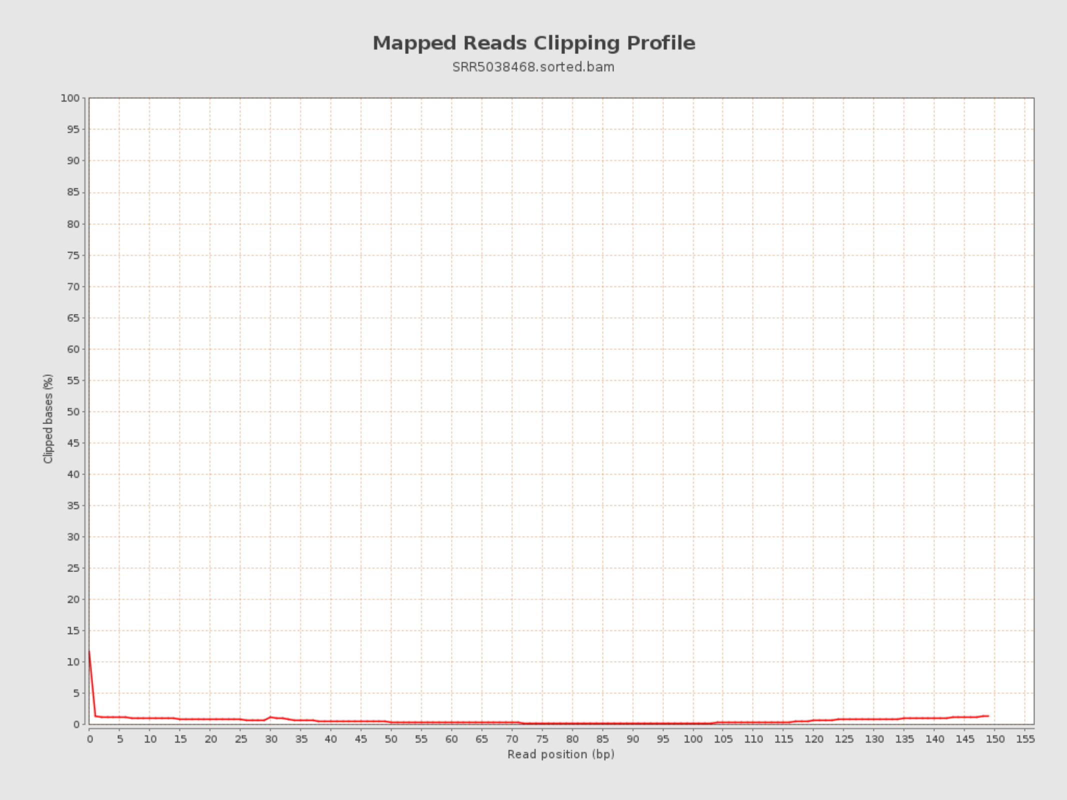
8. Results : Mapped Reads Nucleotide Content



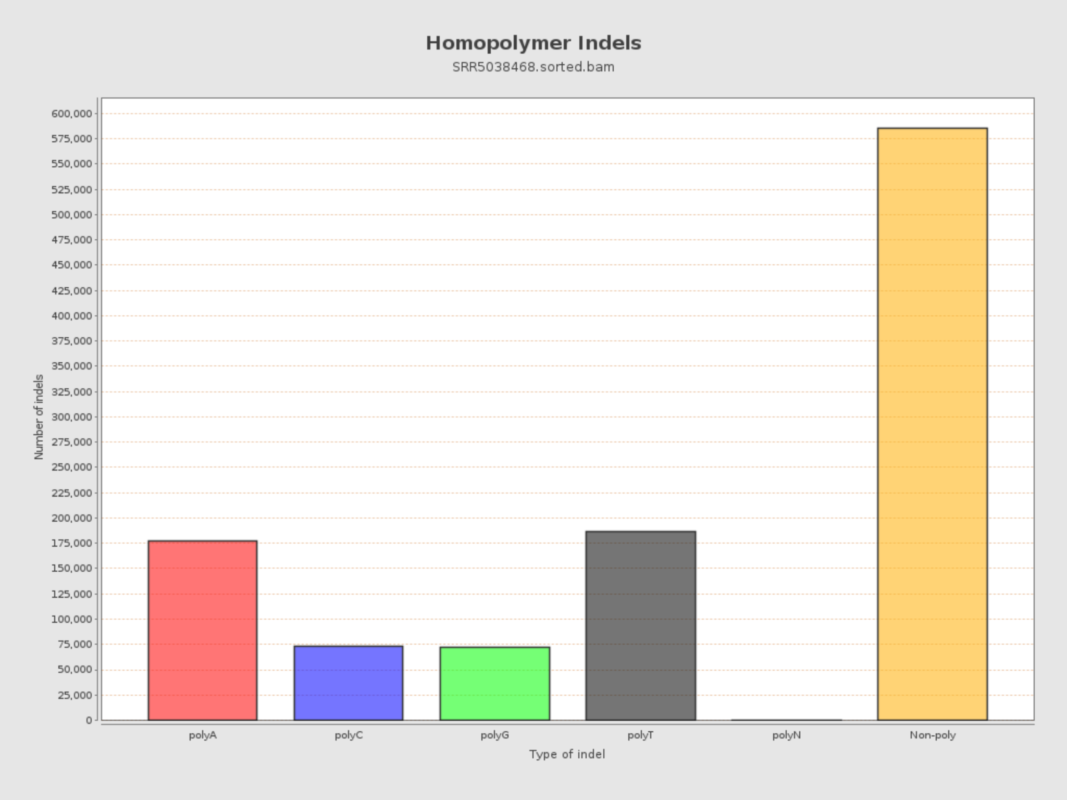
9. Results : Mapped Reads GC-content Distribution



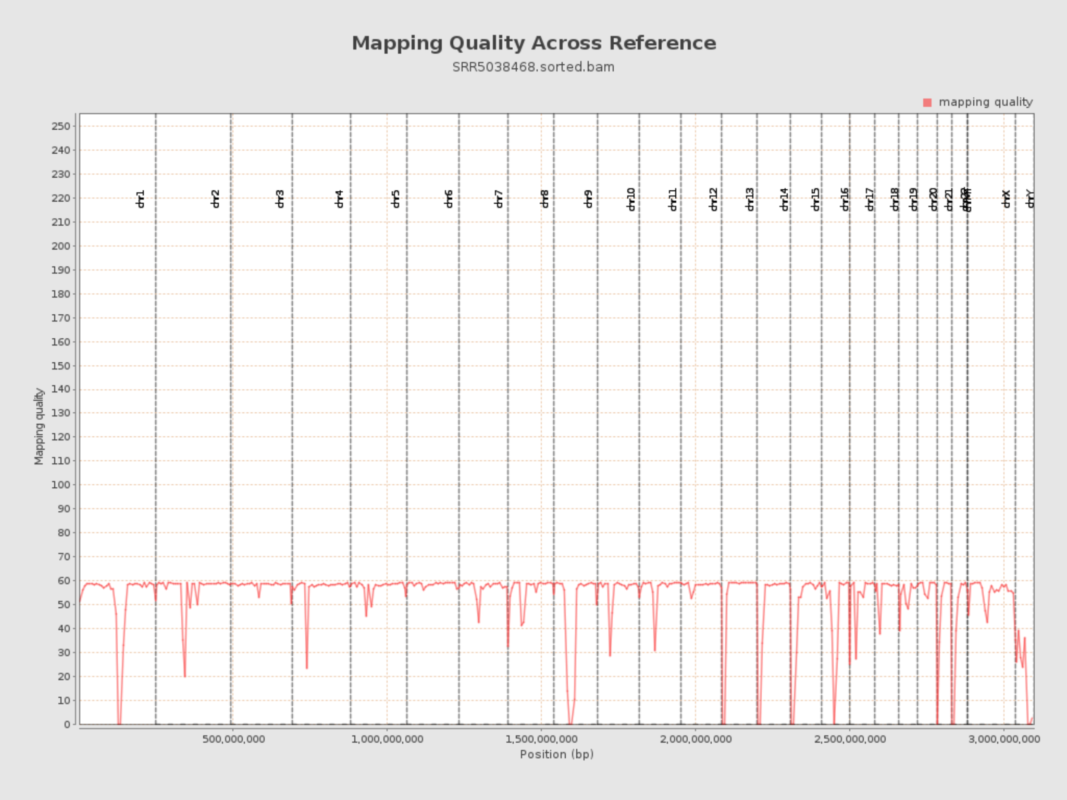
10. Results : Mapped Reads Clipping Profile



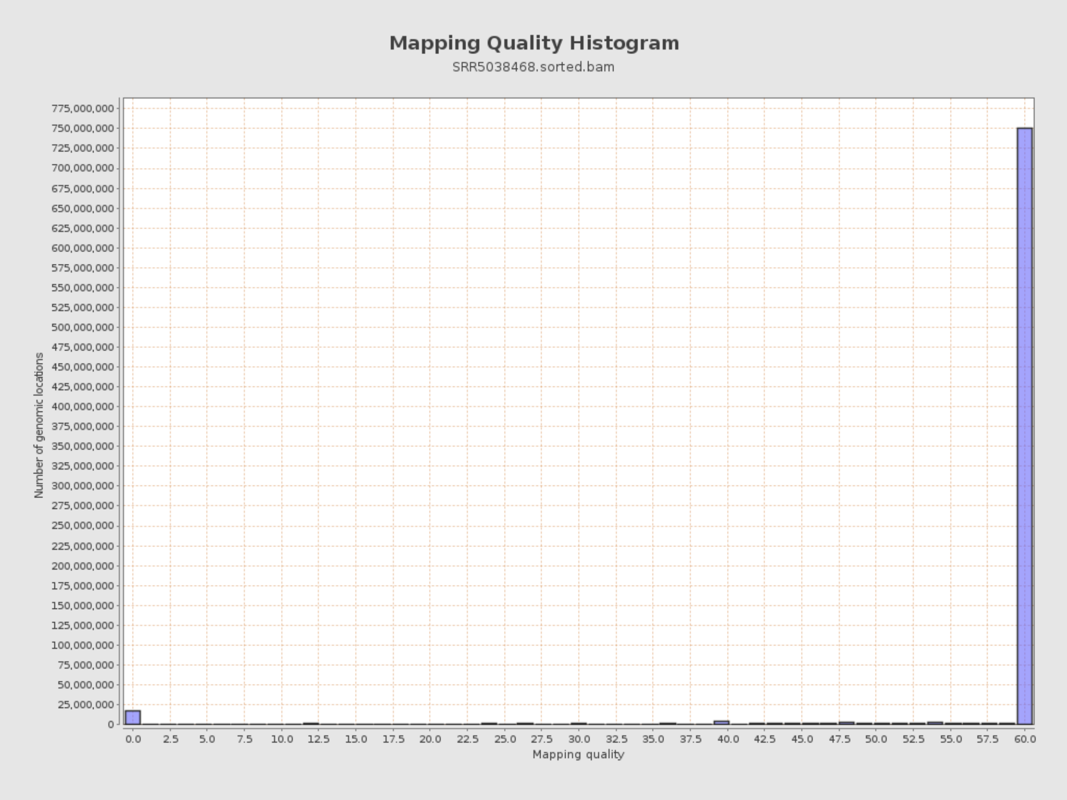
11. Results : Homopolymer Indels



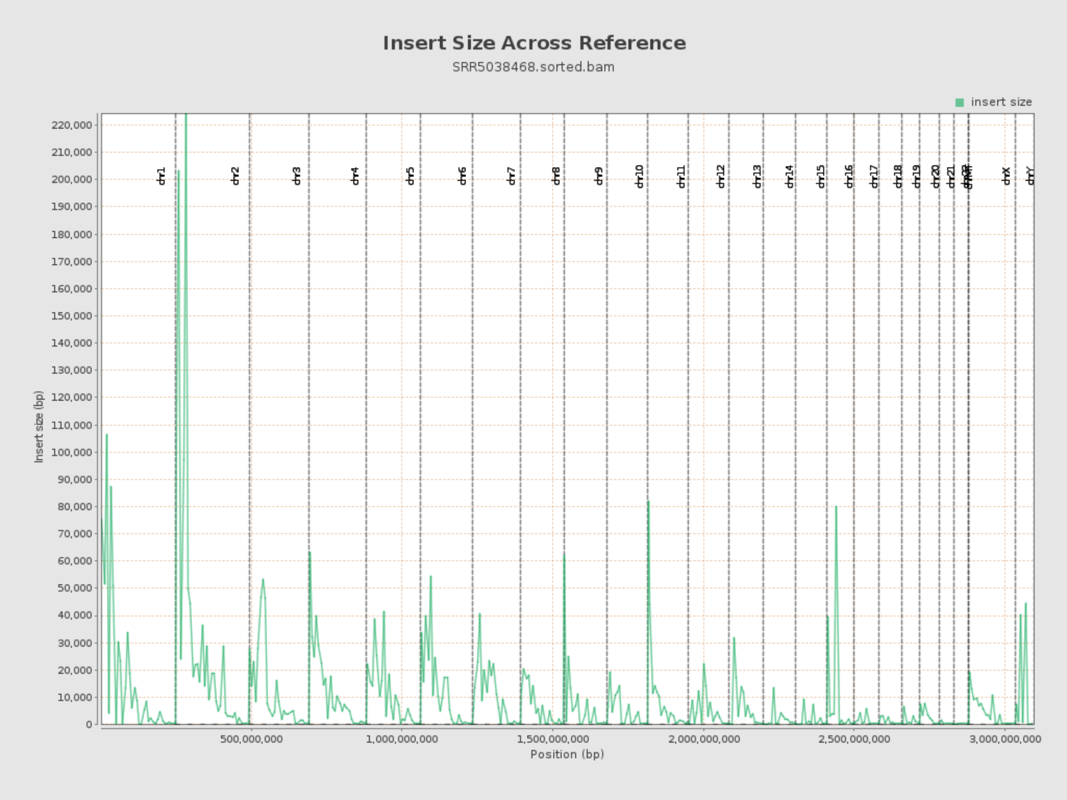
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram