Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/26 15:48:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504618.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_SRR504618 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504618_1.fastq.gz SRR504618_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 26 15:48:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504618.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	302,651,498
Mapped reads	287,251,568 / 94.91%
Unmapped reads	15,399,930 / 5.09%
Mapped paired reads	287,251,568 / 94.91%
Mapped reads, first in pair	144,090,977 / 47.61%
Mapped reads, second in pair	143,160,591 / 47.3%
Mapped reads, both in pair	282,970,128 / 93.5%
Mapped reads, singletons	4,281,440 / 1.41%
Secondary alignments	0
Supplementary alignments	3,135,834 / 1.04%
Read min/max/mean length	30 / 100 / 100.42
Duplicated reads (estimated)	85,819,244 / 28.36%
Duplication rate	18.4%
Clipped reads	42,111,948 / 13.91%

2.2. ACGT Content

Number/percentage of A's	7,376,283,622 / 26.67%
Number/percentage of C's	6,408,797,511 / 23.17%
Number/percentage of T's	7,453,723,733 / 26.95%
Number/percentage of G's	6,417,848,775 / 23.2%
Number/percentage of N's	4,685,357 / 0.02%

GC Percentage	46.37%

2.3. Coverage

Mean	8.9438
Standard Deviation	221.3076

2.4. Mapping Quality

Mean Mapping Quality	52.34

2.5. Insert size

Mean	116,331.06
Standard Deviation	3,216,948.45
P25/Median/P75	283 / 337 / 395

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	276,700,699
Insertions	8,440,075
Mapped reads with at least one insertion	2.72%
Deletions	7,863,071
Mapped reads with at least one deletion	2.55%
Homopolymer indels	34.59%

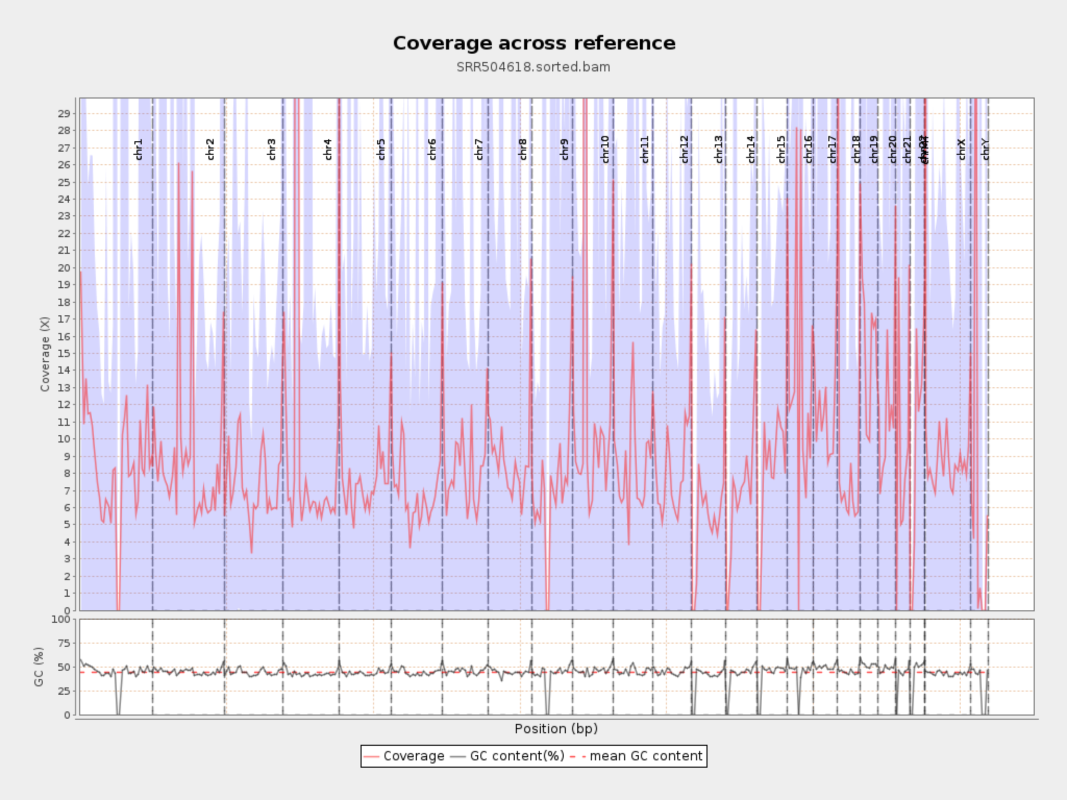
2.7. Chromosome stats

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

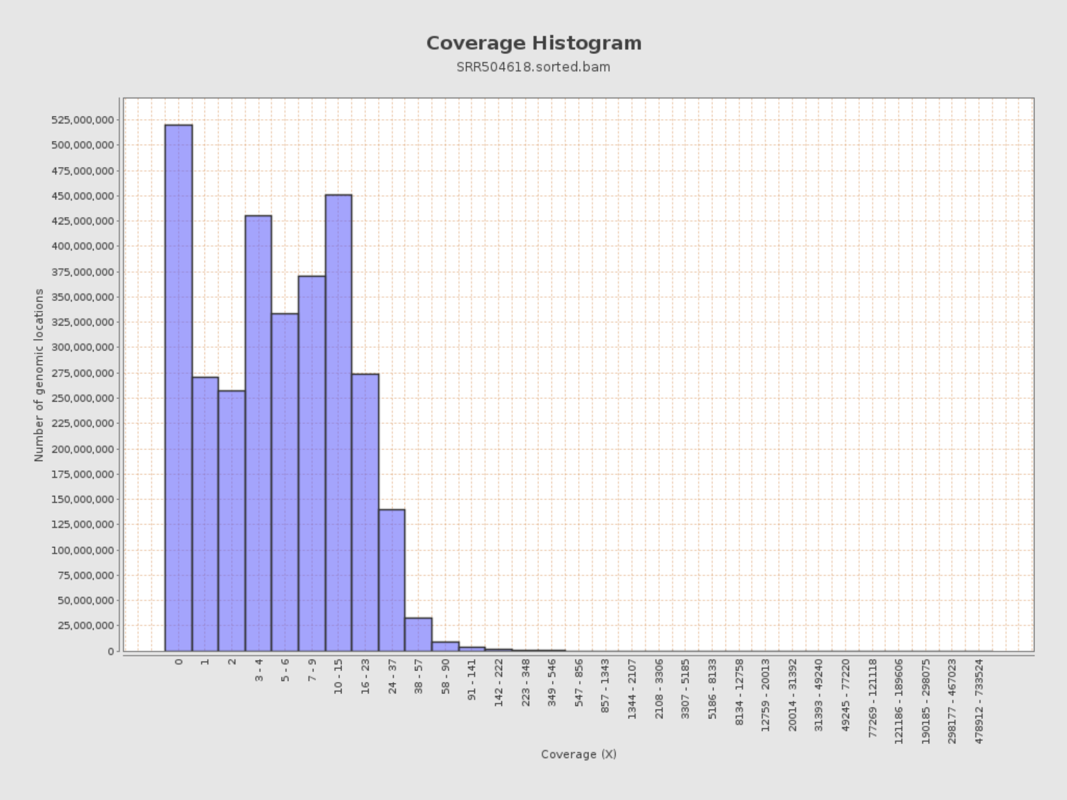
		bases	coverage	deviation
chr1	249250621	2135999103	8.5697	63.1693
chr2	243199373	2194423835	9.0231	233.553
chr3	198022430	1469328896	7.42	20.1239
chr4	191154276	2073330017	10.8464	621.8095
chr5	180915260	1432584512	7.9185	33.1462
chr6	171115067	1178657958	6.8881	30.7068
chr7	159138663	1360693163	8.5504	33.2473
chr8	146364022	1294383924	8.8436	155.1098
chr9	141213431	1010866659	7.1584	66.5296
chr10	135534747	1816276558	13.4008	471.4156
chr11	135006516	1187602671	8.7966	27.6191
chr12	133851895	1105727107	8.2608	17.0709
chr13	115169878	613282443	5.325	13.555
chr14	107349540	737654433	6.8715	29.8317
chr15	102531392	808661290	7.887	14.4439
chr16	90354753	1250615820	13.8412	180.828
chr17	81195210	957736761	11.7955	65.7044
chr18	78077248	628825551	8.0539	255.7764
chr19	59128983	937472922	15.8547	37.8987
chr20	63025520	712282722	11.3015	147.7571
chr21	48129895	462297517	9.6052	196.3529
chr22	51304566	518069568	10.0979	29.4131
chrMT	16571	10800086	651.7462	286.1037
chrX	155270560	1345842210	8.6677	19.0497

chrY	59373566	443833899	7.4753	526.0969

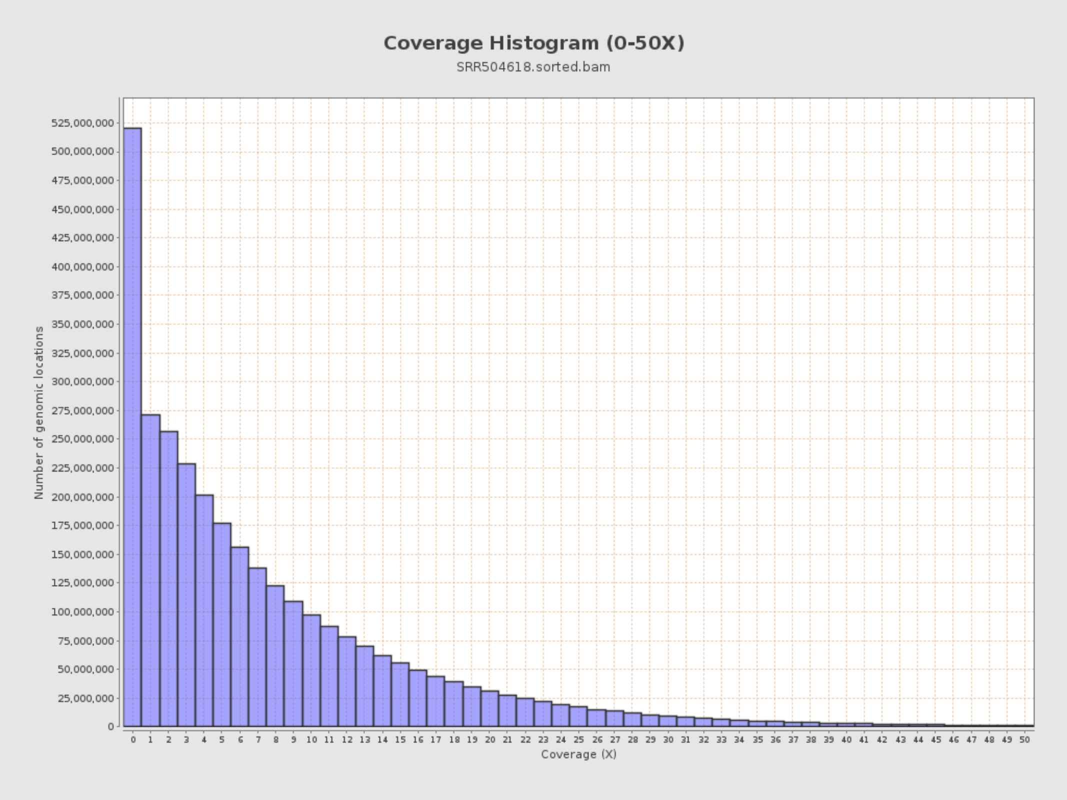
3. Results : Coverage across reference



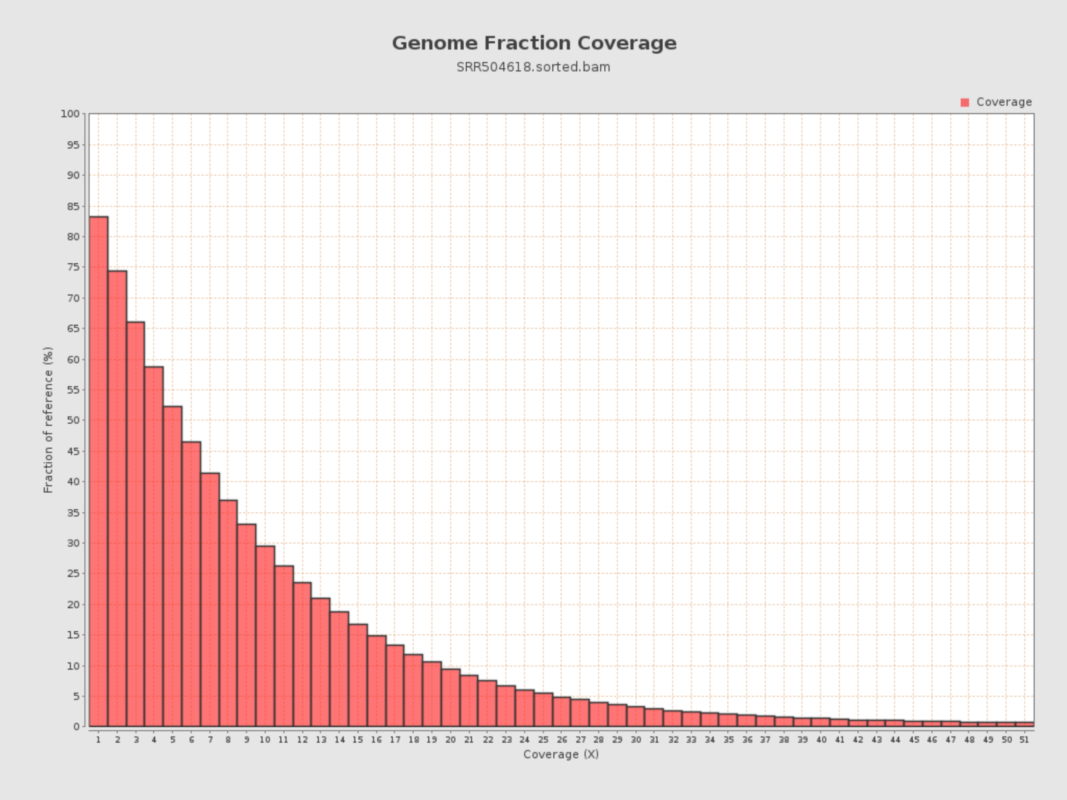
4. Results : Coverage Histogram



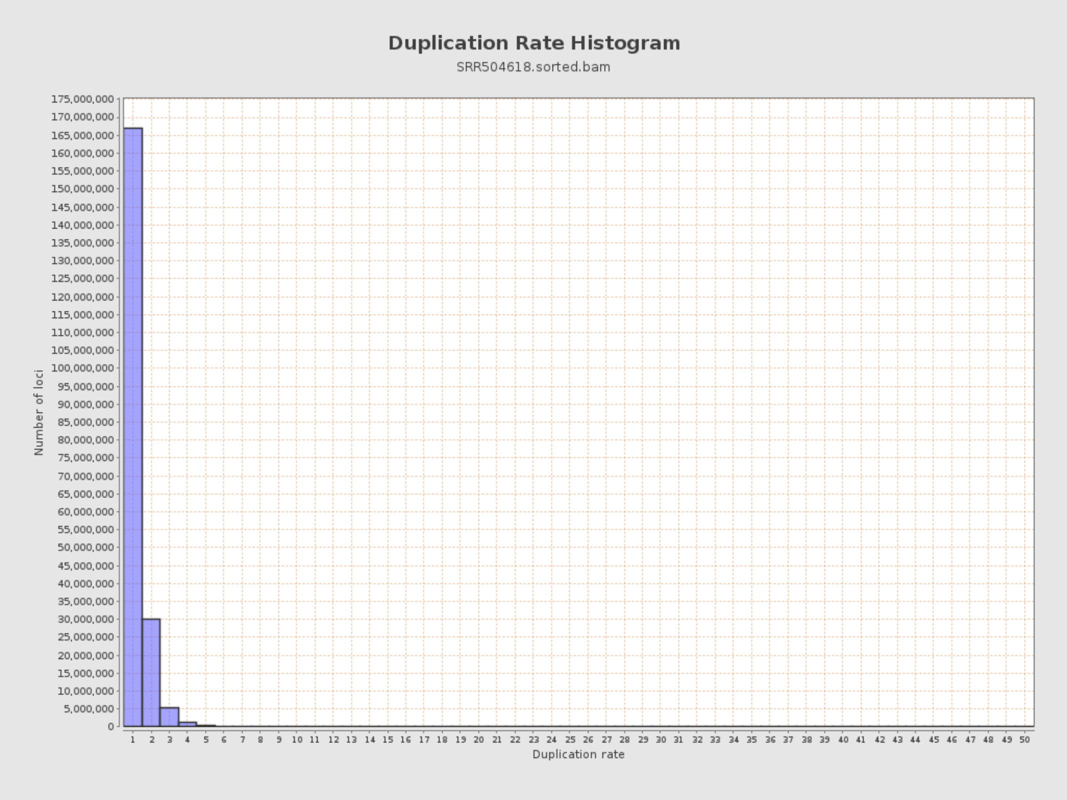
5. Results : Coverage Histogram (0-50X)



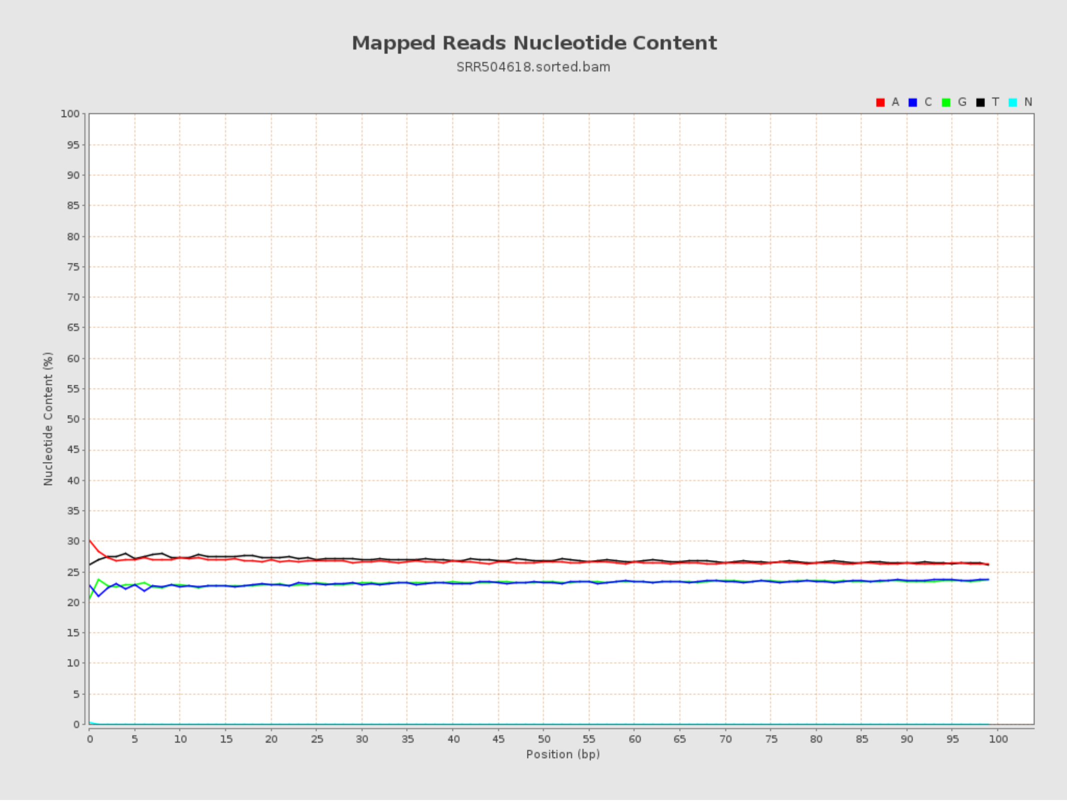
6. Results : Genome Fraction Coverage



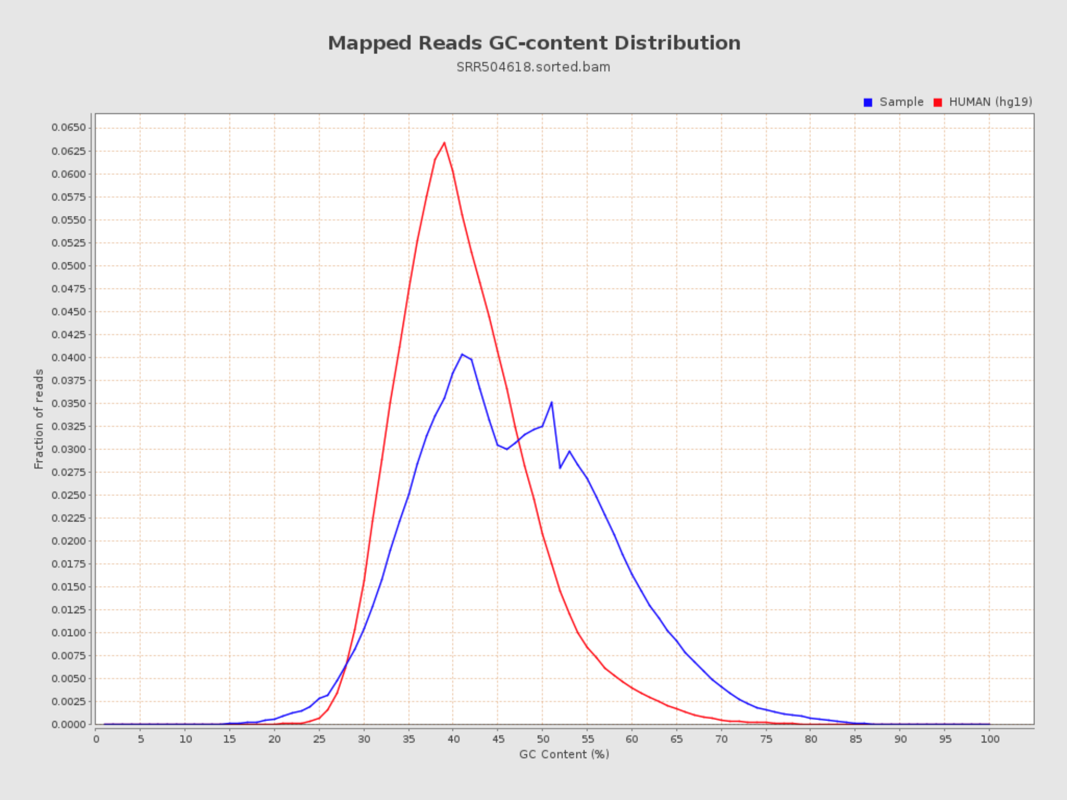
7. Results : Duplication Rate Histogram



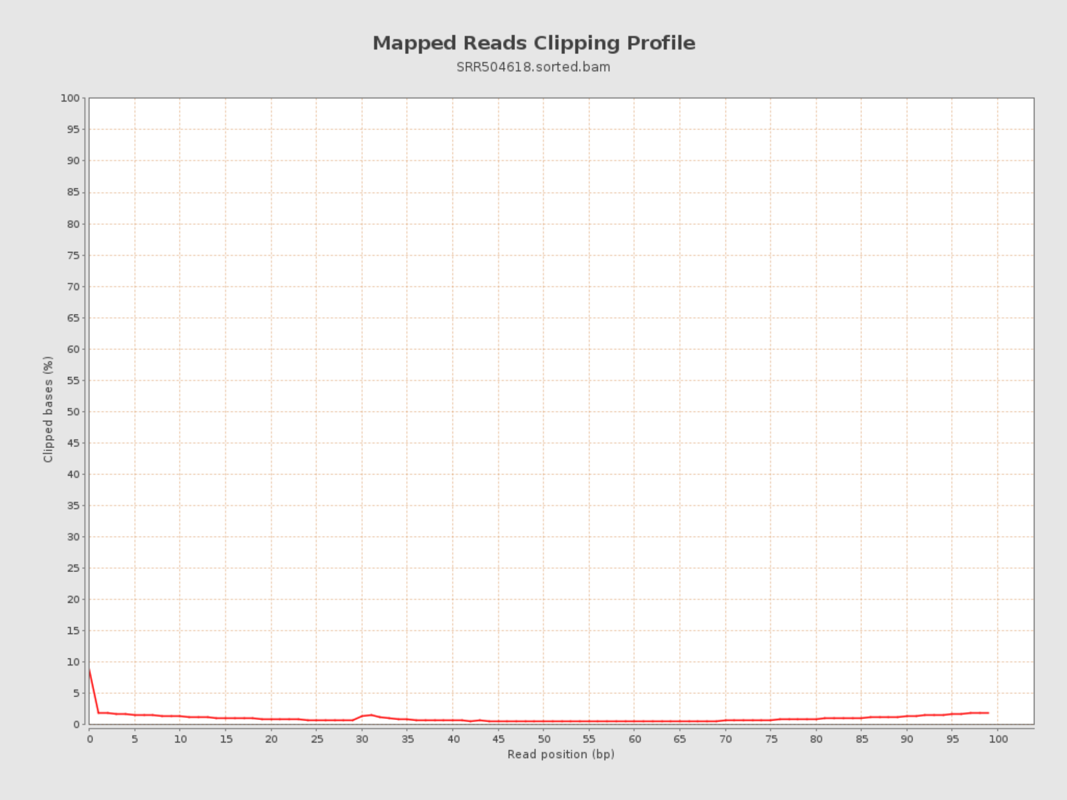
8. Results : Mapped Reads Nucleotide Content



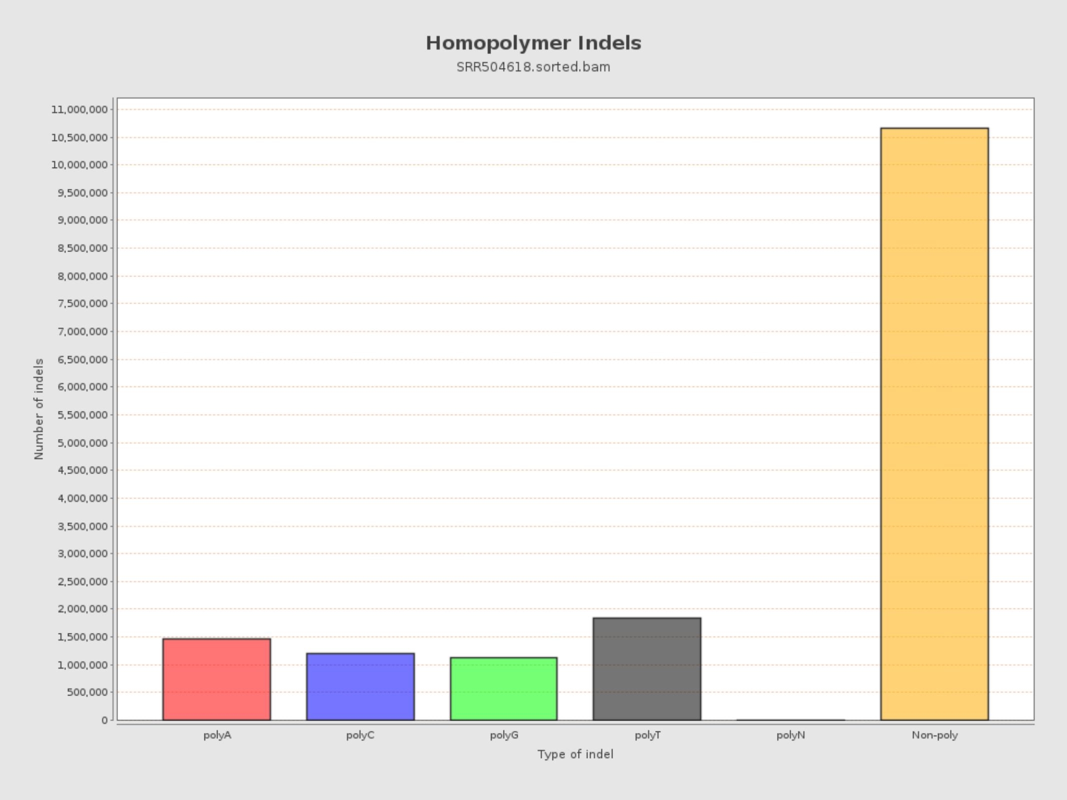
9. Results : Mapped Reads GC-content Distribution



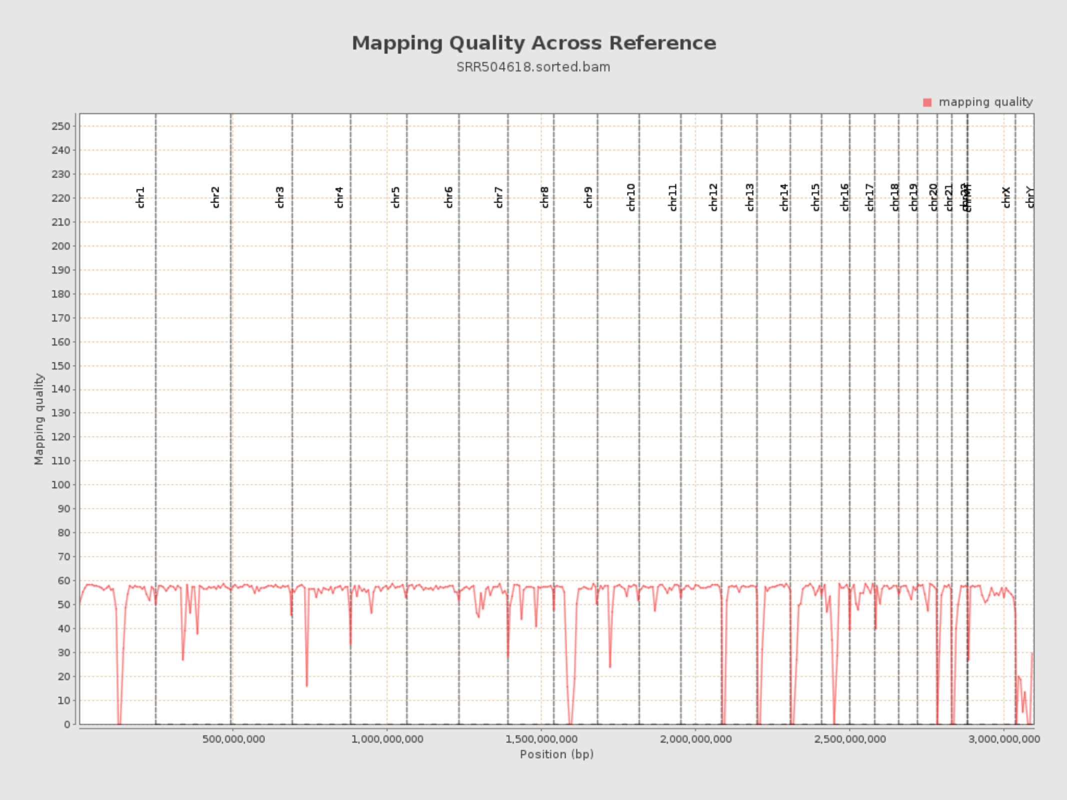
10. Results : Mapped Reads Clipping Profile



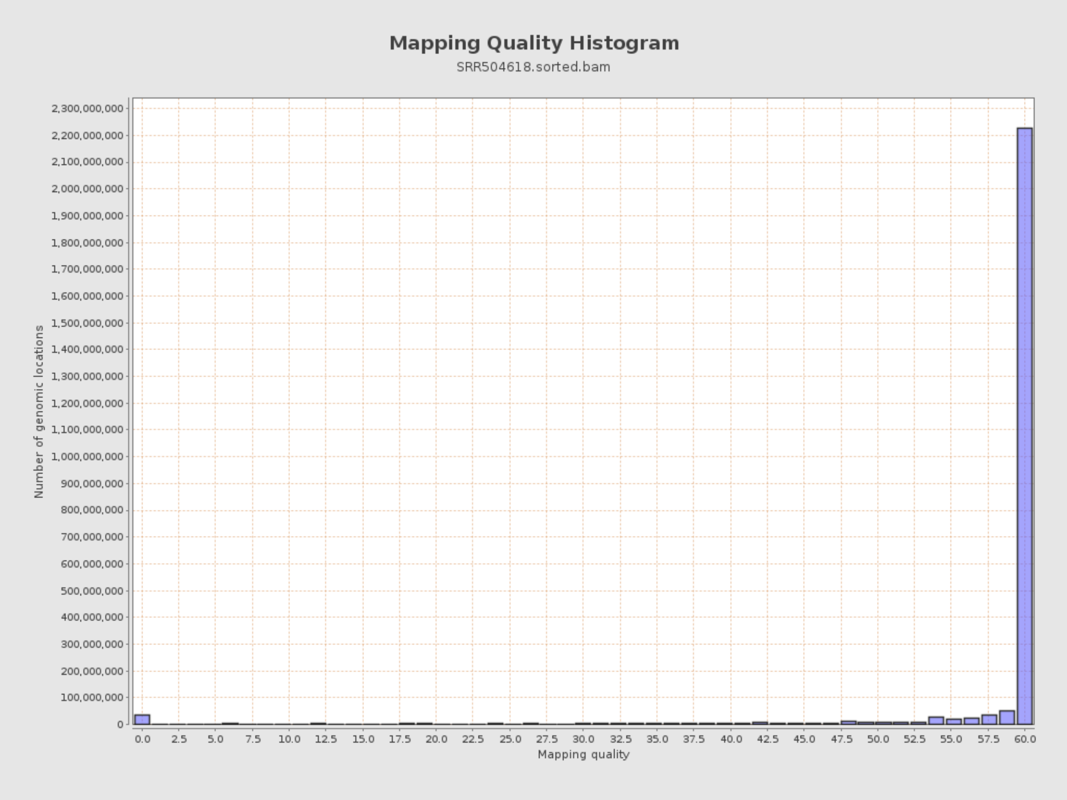
11. Results : Homopolymer Indels



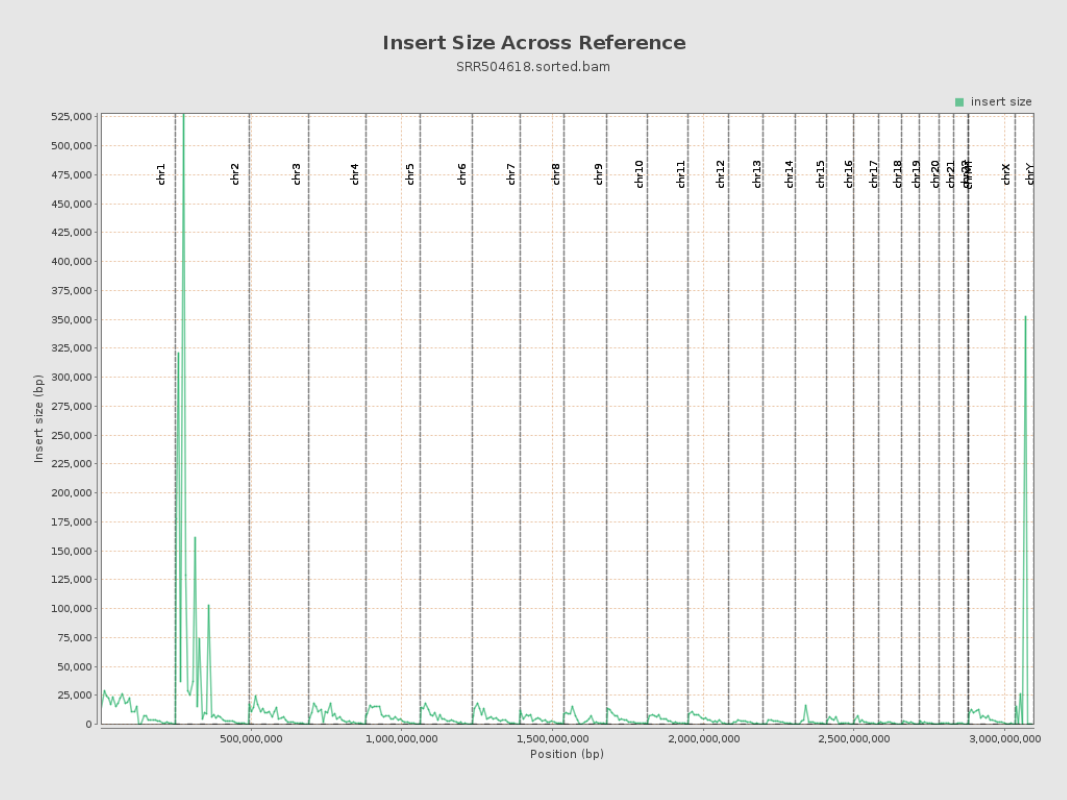
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram