Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 06:30:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618582.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_SRR618582 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618582_1.fastq.gz SRR618582_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 06:30:45 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618582.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	57,618,328
Mapped reads	55,409,245 / 96.17%
Unmapped reads	2,209,083 / 3.83%
Mapped paired reads	55,409,245 / 96.17%
Mapped reads, first in pair	28,003,694 / 48.6%
Mapped reads, second in pair	27,405,551 / 47.56%
Mapped reads, both in pair	54,258,688 / 94.17%
Mapped reads, singletons	1,150,557 / 2%
Secondary alignments	0
Supplementary alignments	219,818 / 0.38%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	12,406,147 / 21.53%
Duplication rate	19.42%
Clipped reads	12,002,700 / 20.83%

2.2. ACGT Content

Number/percentage of A's	1,425,664,391 / 27.27%
Number/percentage of C's	1,145,456,110 / 21.91%
Number/percentage of T's	1,442,013,295 / 27.58%
Number/percentage of G's	1,215,438,779 / 23.25%
Number/percentage of N's	233,600 / 0%

GC Percentage	45.15%

2.3. Coverage

Mean	1.6902
Standard Deviation	6.9783

2.4. Mapping Quality

Mean Mapping Quality	52.08

2.5. Insert size

Mean	79,812.42
Standard Deviation	2,822,522.19
P25/Median/P75	179 / 208 / 247

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	67,788,470
Insertions	962,699
Mapped reads with at least one insertion	1.71%
Deletions	2,638,490
Mapped reads with at least one deletion	4.64%
Homopolymer indels	52.43%

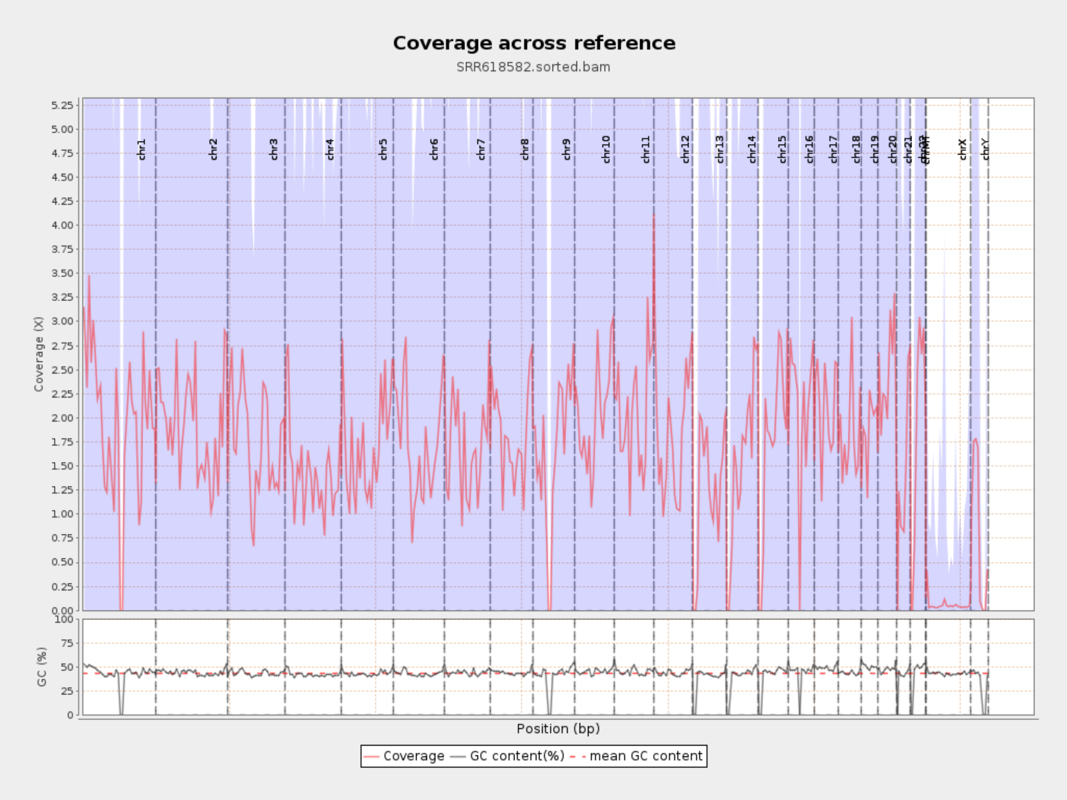
2.7. Chromosome stats

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

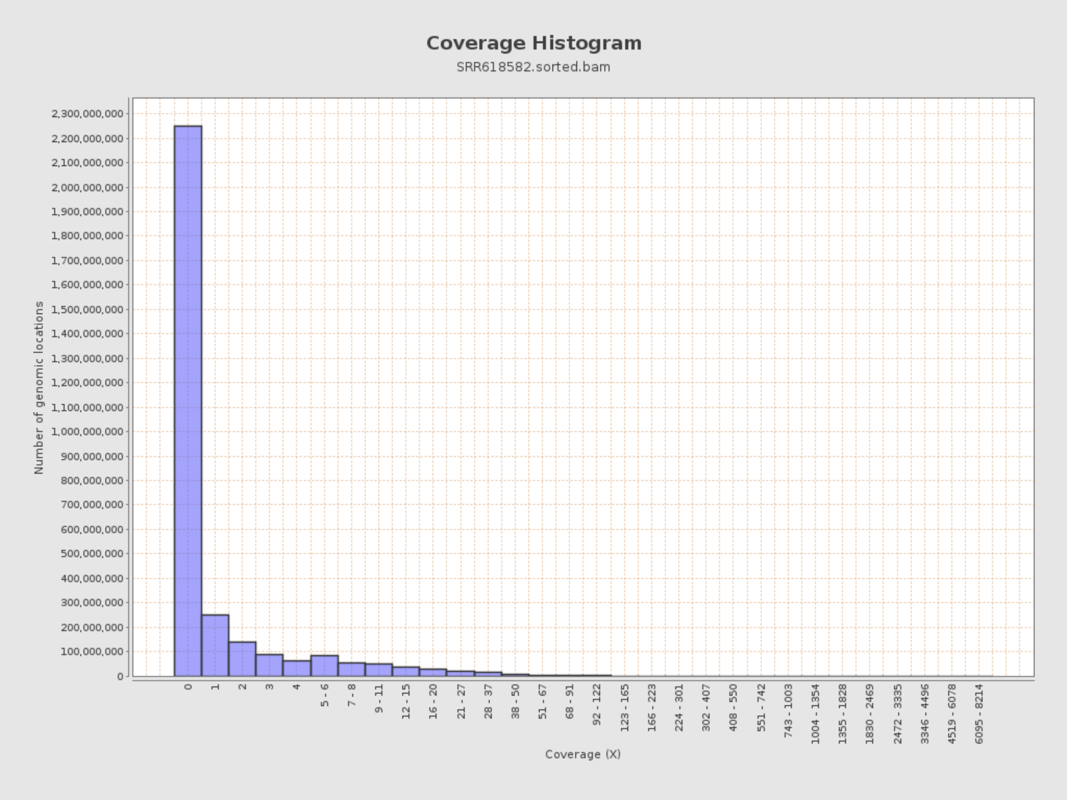
		bases	**coverage**	**deviation**
chr1	249250621	486234138	1.9508	8.0047
chr2	243199373	465935010	1.9159	8.3068
chr3	198022430	348189305	1.7583	5.7021
chr4	191154276	274066000	1.4337	5.4926
chr5	180915260	312937482	1.7297	5.7128
chr6	171115067	292196334	1.7076	5.7962
chr7	159138663	271149553	1.7039	5.7278
chr8	146364022	268741361	1.8361	6.4934
chr9	141213431	234569033	1.6611	6.7359
chr10	135534747	274653955	2.0264	6.5718
chr11	135006516	275563848	2.0411	7.1743
chr12	133851895	247278932	1.8474	6.4033
chr13	115169878	144211040	1.2522	4.6675
chr14	107349540	166205973	1.5483	5.8227
chr15	102531392	178011136	1.7362	6.4749
chr16	90354753	189150137	2.0934	15.827
chr17	81195210	171722322	2.1149	7.4455
chr18	78077248	139984038	1.7929	6.7452
chr19	59128983	111232447	1.8812	7.4626
chr20	63025520	157214038	2.4945	7.7806
chr21	48129895	68082205	1.4146	9.1042
chr22	51304566	95338267	1.8583	7.1885
chrMT	16571	2174	0.1312	0.7025
chrX	155270560	9618445	0.0619	1.5094

chrY	59373566	50137292	0.8444	6.0501

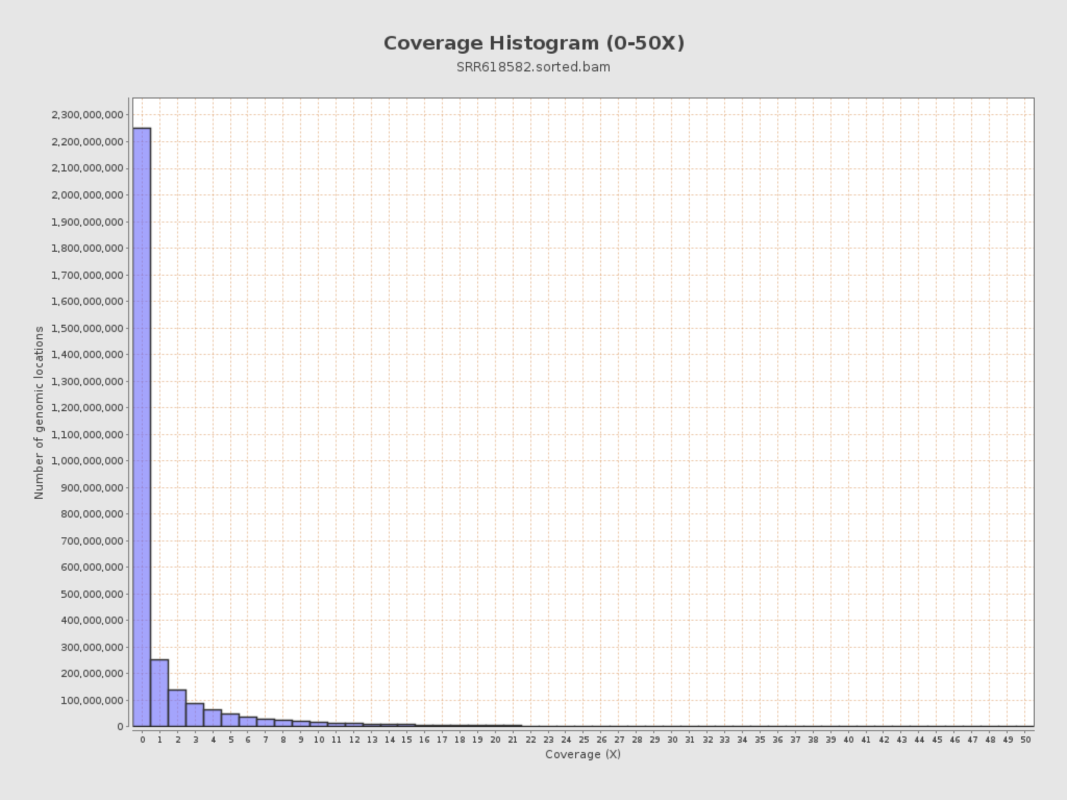
3. Results : Coverage across reference



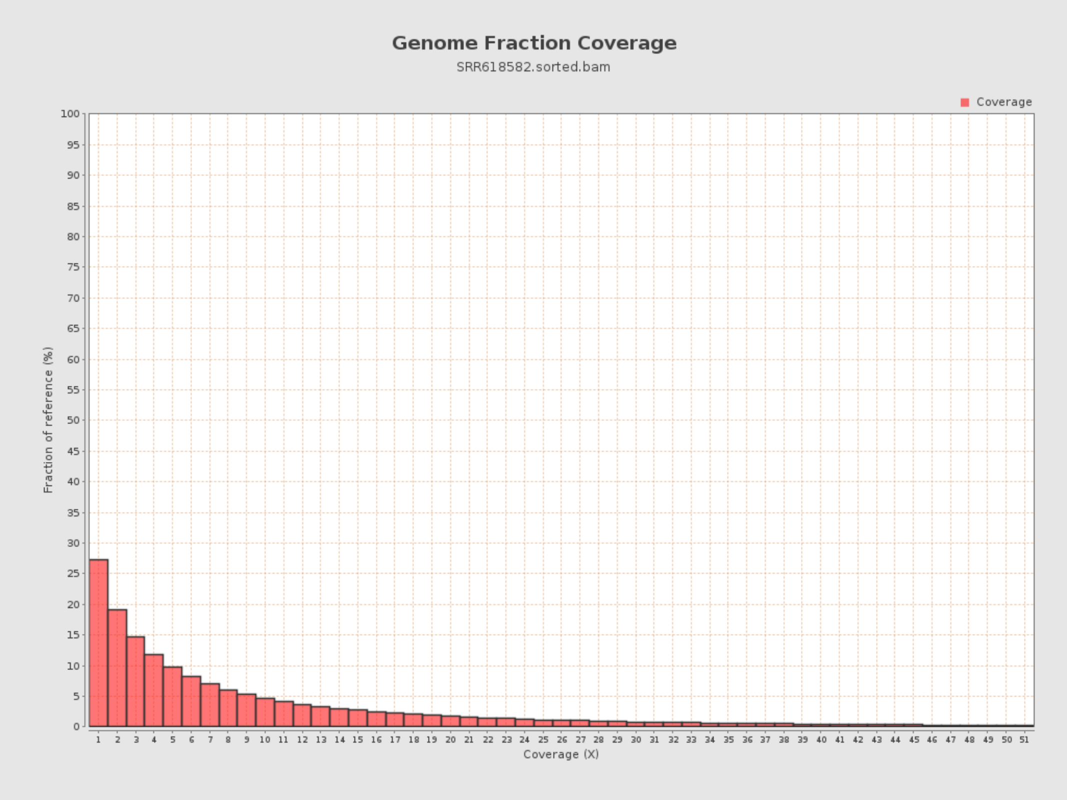
4. Results : Coverage Histogram



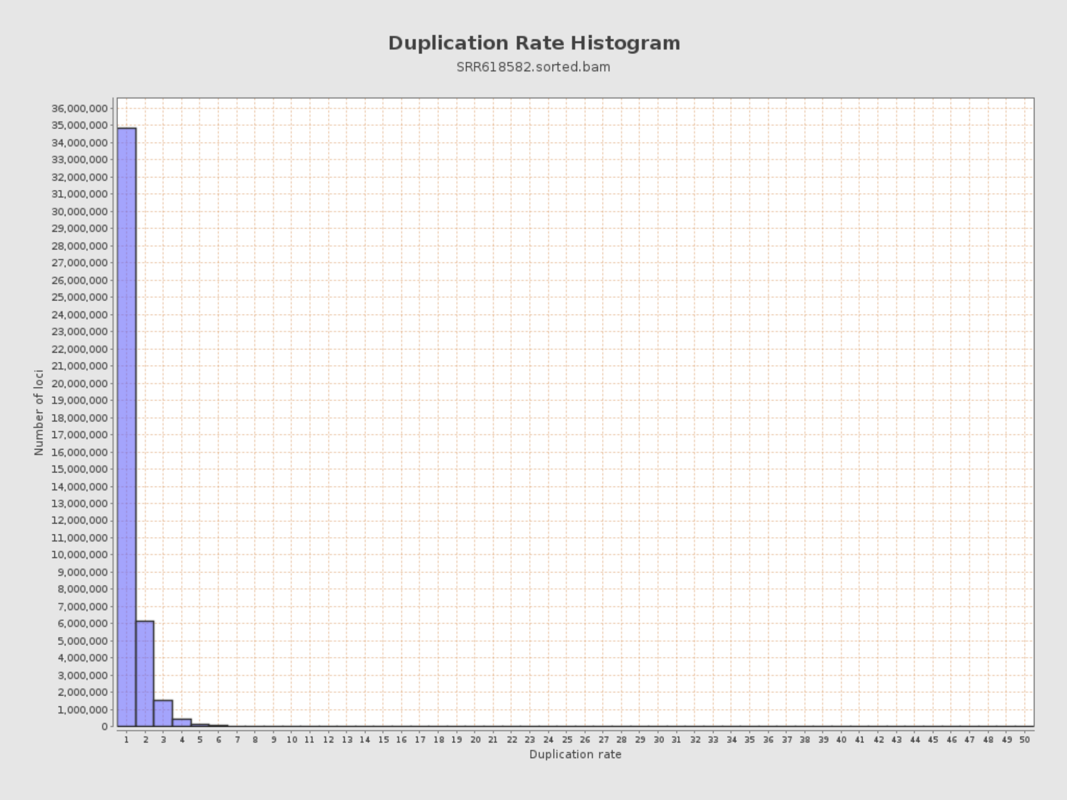
5. Results : Coverage Histogram (0-50X)



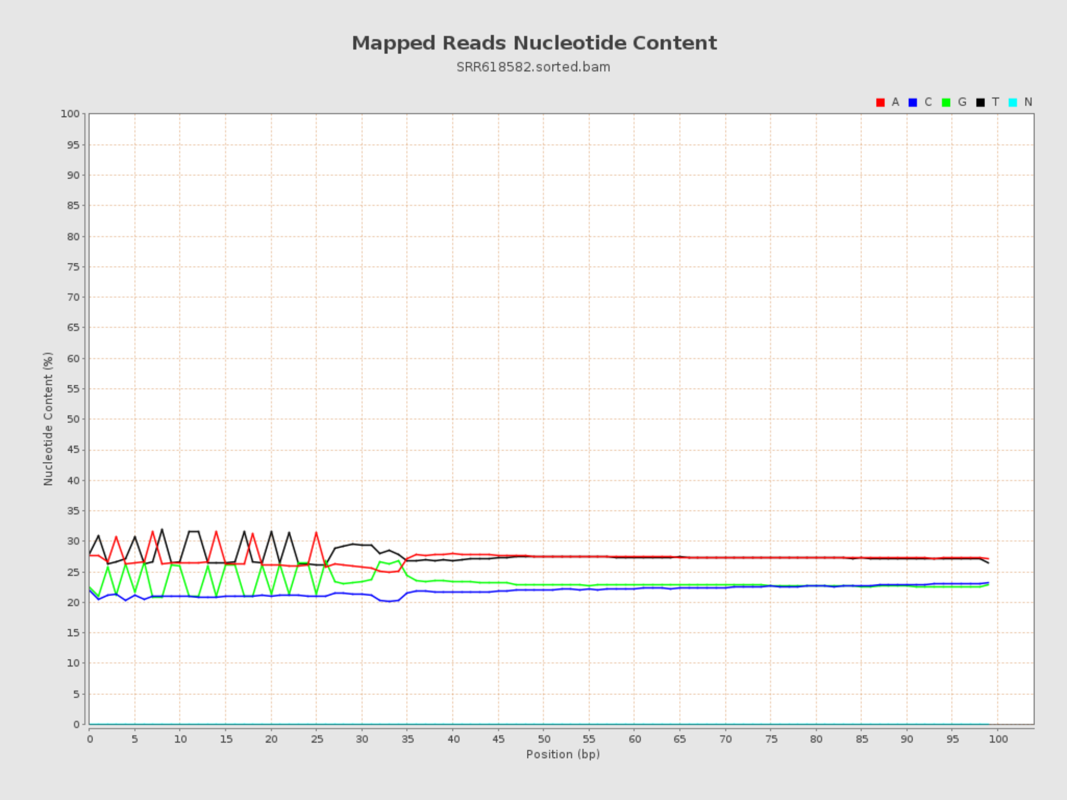
6. Results : Genome Fraction Coverage



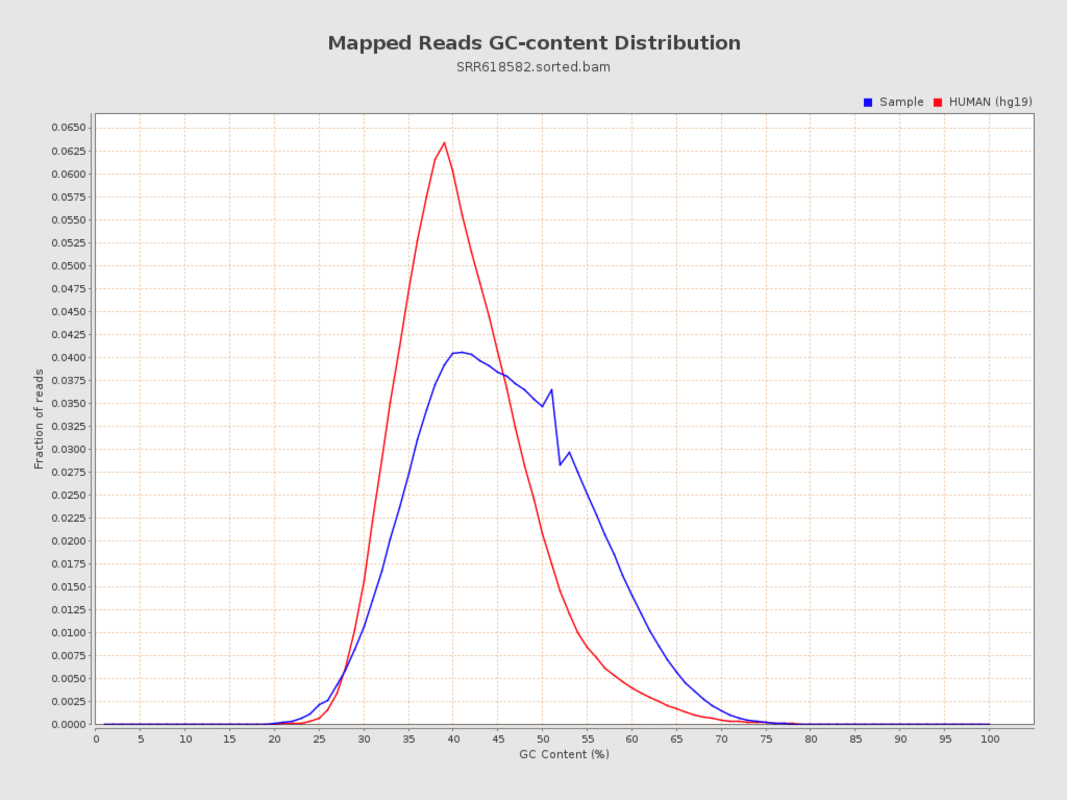
7. Results : Duplication Rate Histogram



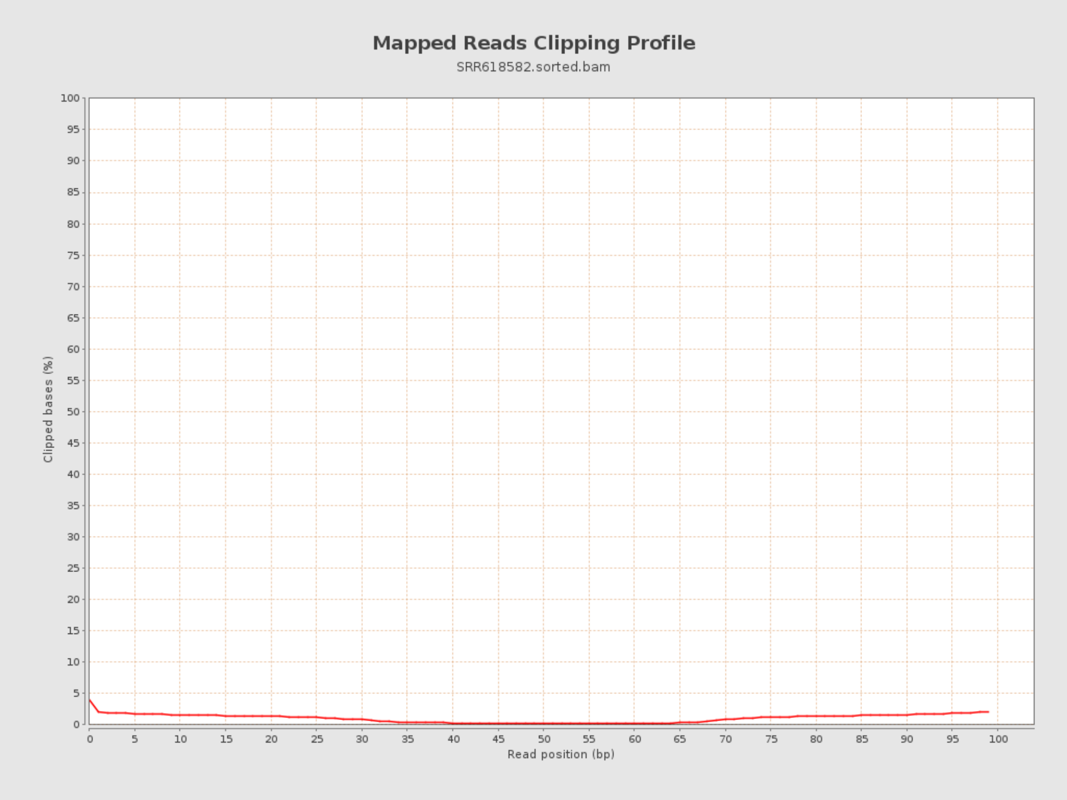
8. Results : Mapped Reads Nucleotide Content



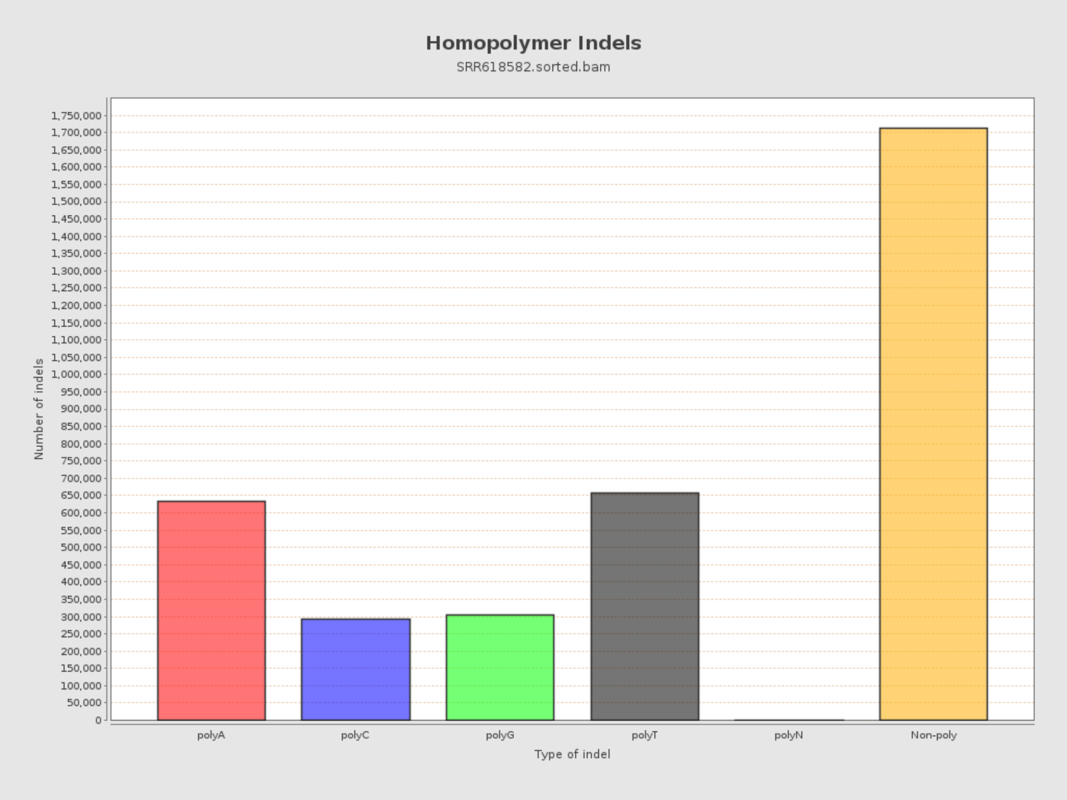
9. Results : Mapped Reads GC-content Distribution



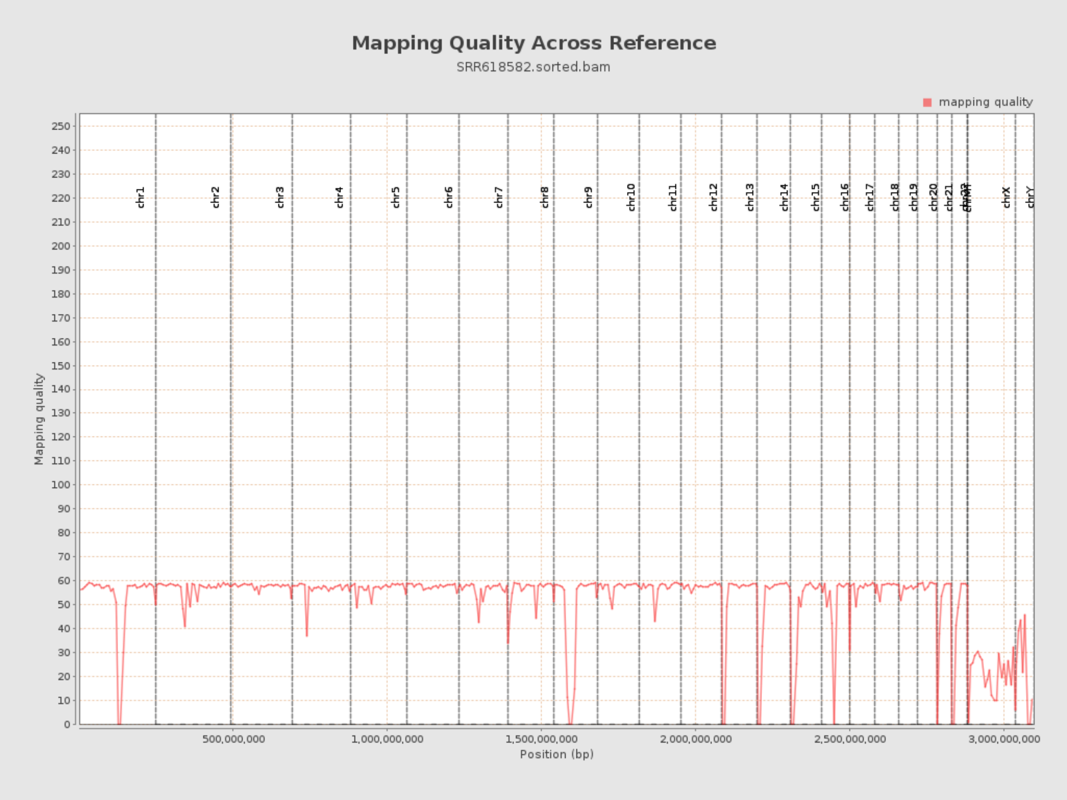
10. Results : Mapped Reads Clipping Profile



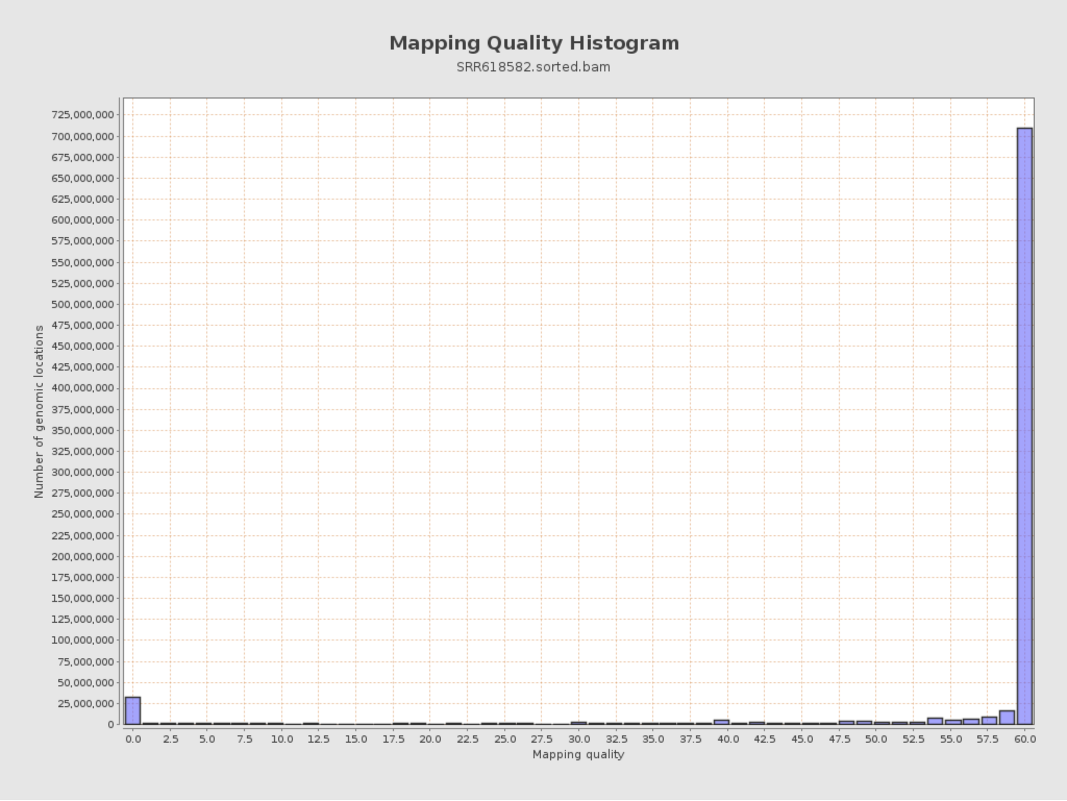
11. Results : Homopolymer Indels



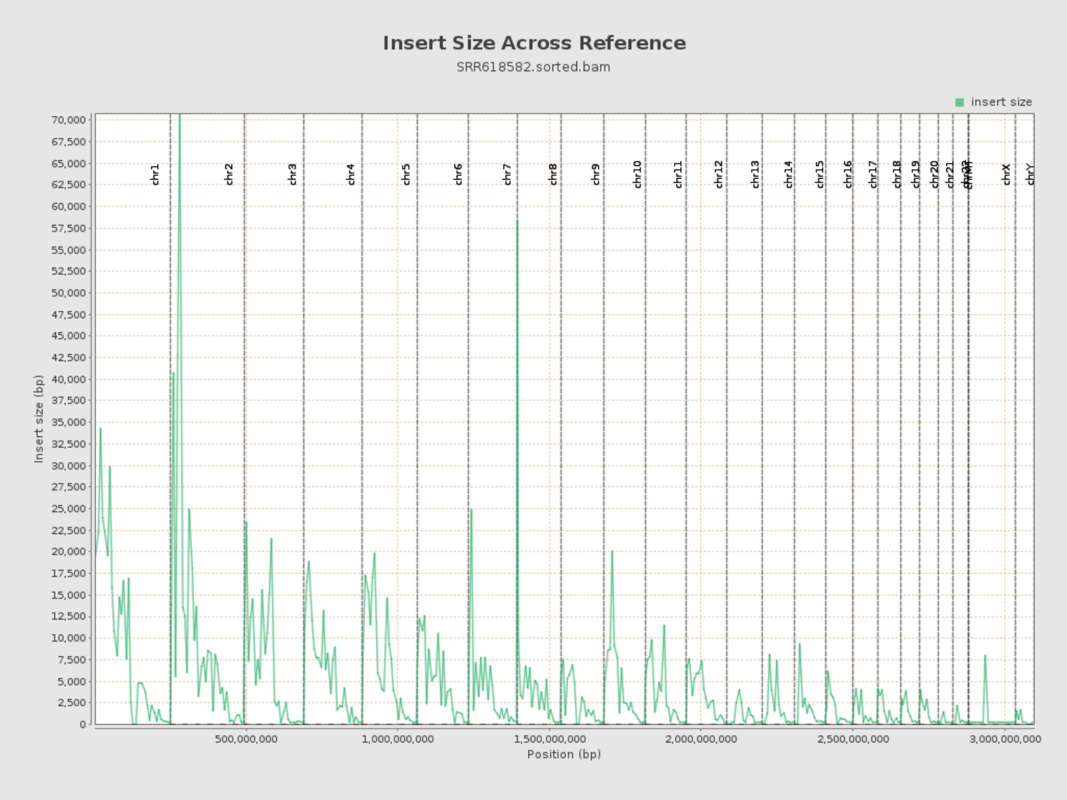
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram