Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/07 04:53:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960918.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_SRR960918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960918_1.fastq.gz SRR960918_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Jan 07 04:53:00 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	230,533,412
Mapped reads	225,638,750 / 97.88%
Unmapped reads	4,894,662 / 2.12%
Mapped paired reads	225,638,750 / 97.88%
Mapped reads, first in pair	113,352,705 / 49.17%
Mapped reads, second in pair	112,286,045 / 48.71%
Mapped reads, both in pair	223,586,492 / 96.99%
Mapped reads, singletons	2,052,258 / 0.89%
Secondary alignments	0
Supplementary alignments	465,635 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	38,528,179 / 16.71%
Duplication rate	12.3%
Clipped reads	39,667,722 / 17.21%

2.2. ACGT Content

Number/percentage of A's	6,750,173,722 / 30.65%
Number/percentage of C's	4,269,609,852 / 19.39%
Number/percentage of T's	6,746,439,736 / 30.64%
Number/percentage of G's	4,250,847,081 / 19.3%
Number/percentage of N's	2,962,030 / 0.01%

GC Percentage	38.69%

2.3. Coverage

Mean	7.1152
Standard Deviation	105.6654

2.4. Mapping Quality

Mean Mapping Quality	53.57

2.5. Insert size

Mean	18,977.32
Standard Deviation	1,278,539.84
P25/Median/P75	155 / 183 / 213

2.6. Mismatches and indels

General error rate	1.45%
Mismatches	313,846,396
Insertions	2,634,953
Mapped reads with at least one insertion	1.14%
Deletions	2,950,017
Mapped reads with at least one deletion	1.27%
Homopolymer indels	40.43%

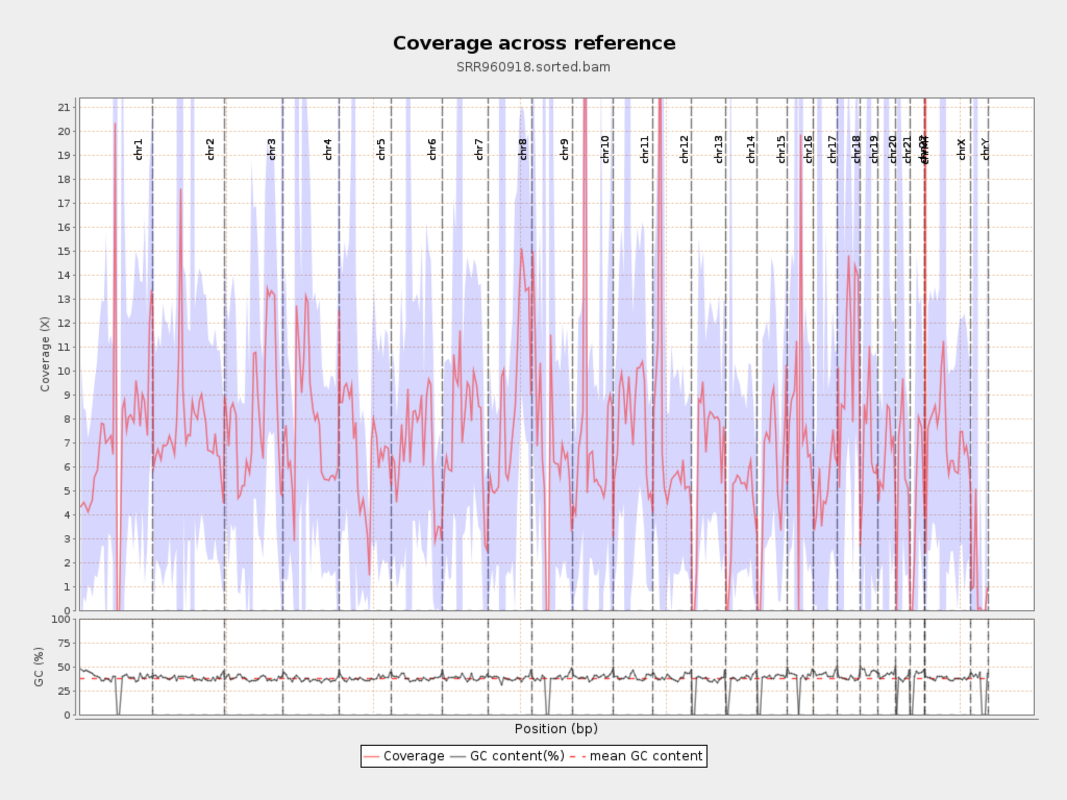
2.7. Chromosome stats

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

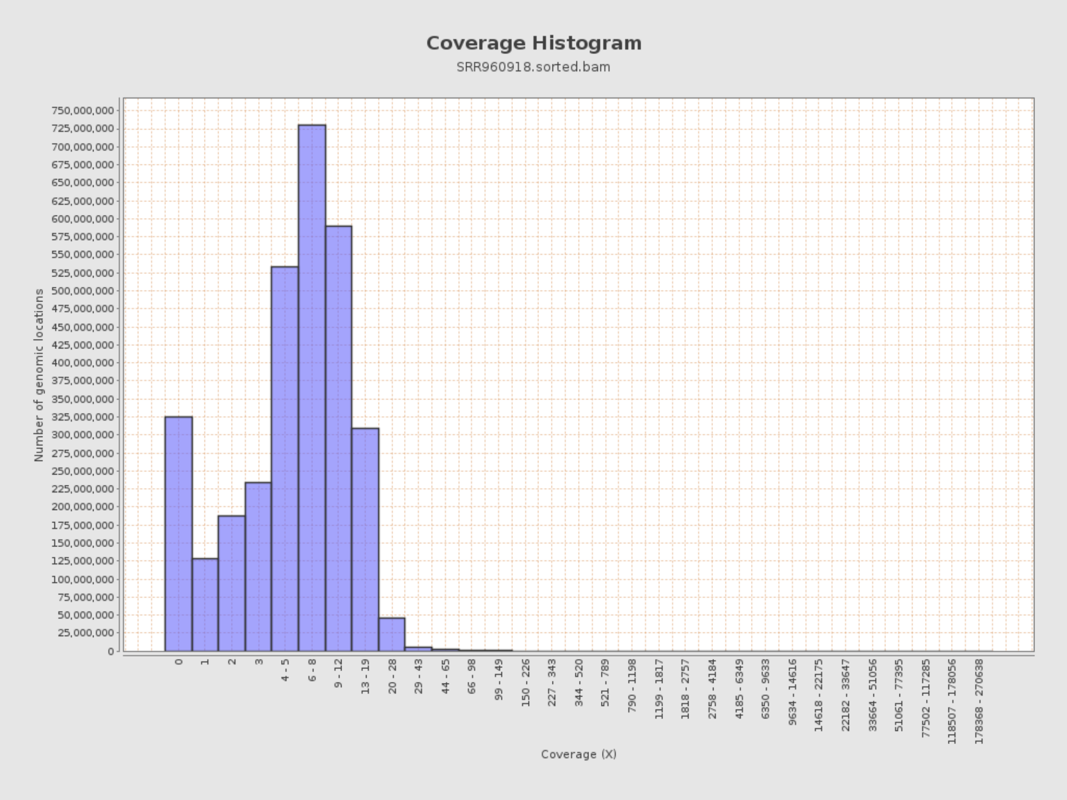
		bases	**coverage**	**deviation**
chr1	249250621	1829412160	7.3396	279.69
chr2	243199373	1855103239	7.6279	56.1759
chr3	198022430	1640086856	8.2823	9.618
chr4	191154276	1457060597	7.6224	57.237
chr5	180915260	1197839673	6.621	9.4918
chr6	171115067	1160147634	6.7799	27.6187
chr7	159138663	1211700183	7.6141	69.1514
chr8	146364022	1293599284	8.8382	137.4015
chr9	141213431	939398275	6.6523	99.3812
chr10	135534747	1048743616	7.7378	202.5294
chr11	135006516	1073725340	7.9531	44.2537
chr12	133851895	996145805	7.4421	11.7868
chr13	115169878	761957652	6.6159	4.9389
chr14	107349540	468304970	4.3624	7.4311
chr15	102531392	591546272	5.7694	5.2324
chr16	90354753	721638897	7.9867	86.9036
chr17	81195210	417411664	5.1408	26.1565
chr18	78077248	846211147	10.8381	102.1879
chr19	59128983	404202498	6.8359	117.6141
chr20	63025520	412153865	6.5395	18.8652
chr21	48129895	293569132	6.0995	22.8311
chr22	51304566	225295336	4.3913	5.8065
chrMT	16571	4937759	297.9759	59.8241
chrX	155270560	1115995900	7.1874	29.7694

chrY	59373566	60242216	1.0146	53.2687

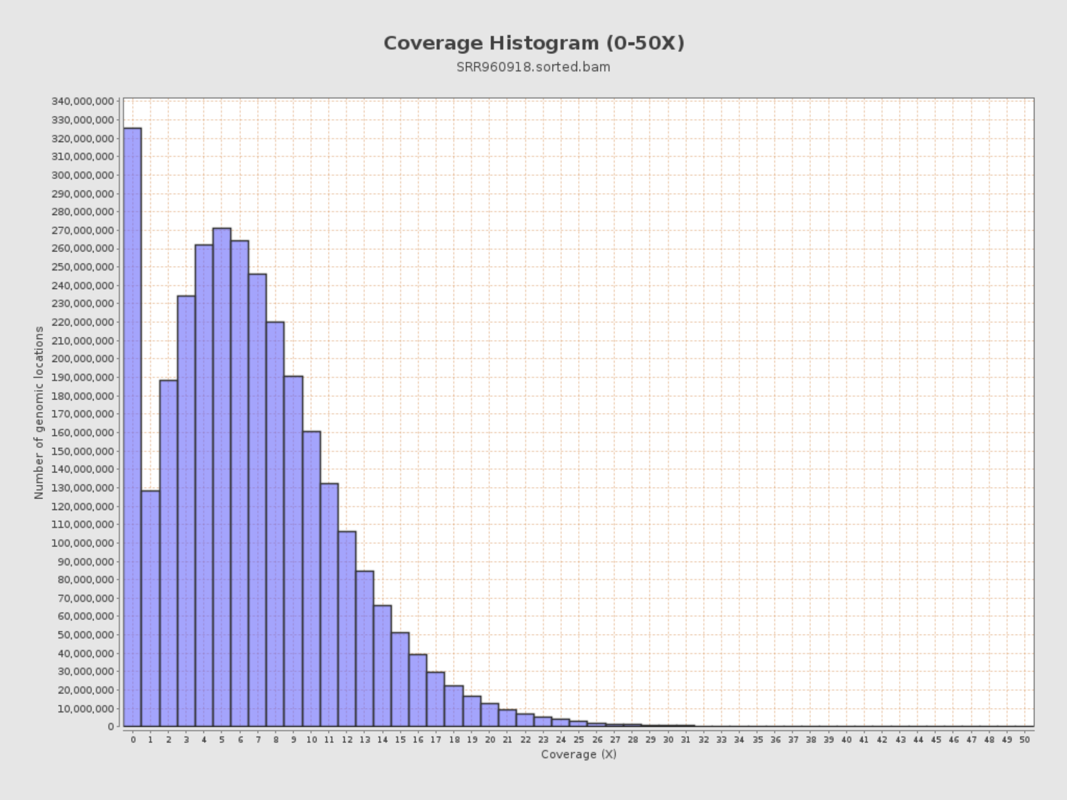
3. Results : Coverage across reference



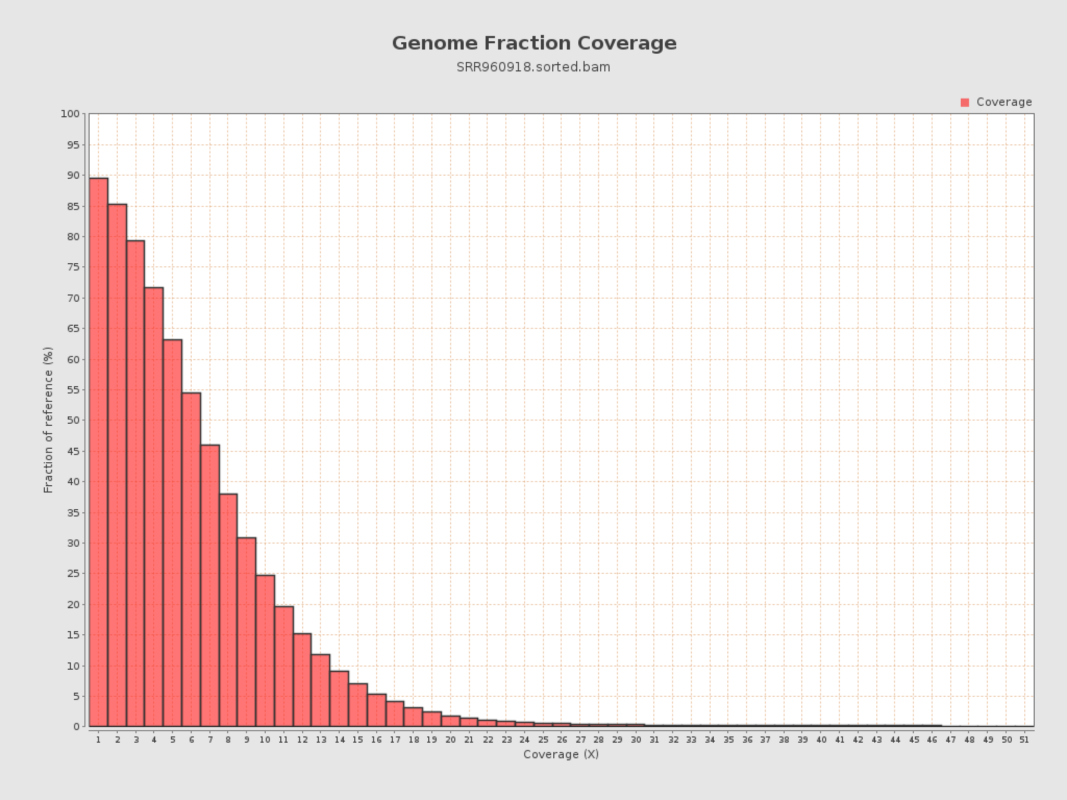
4. Results : Coverage Histogram



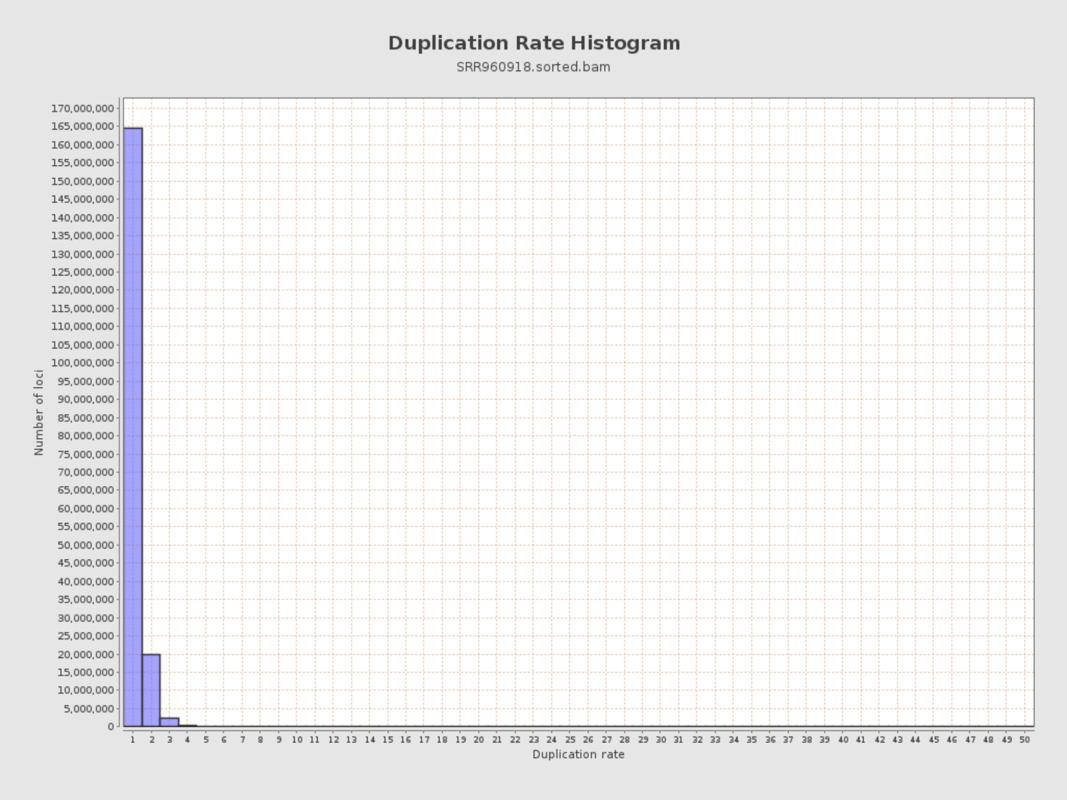
5. Results : Coverage Histogram (0-50X)



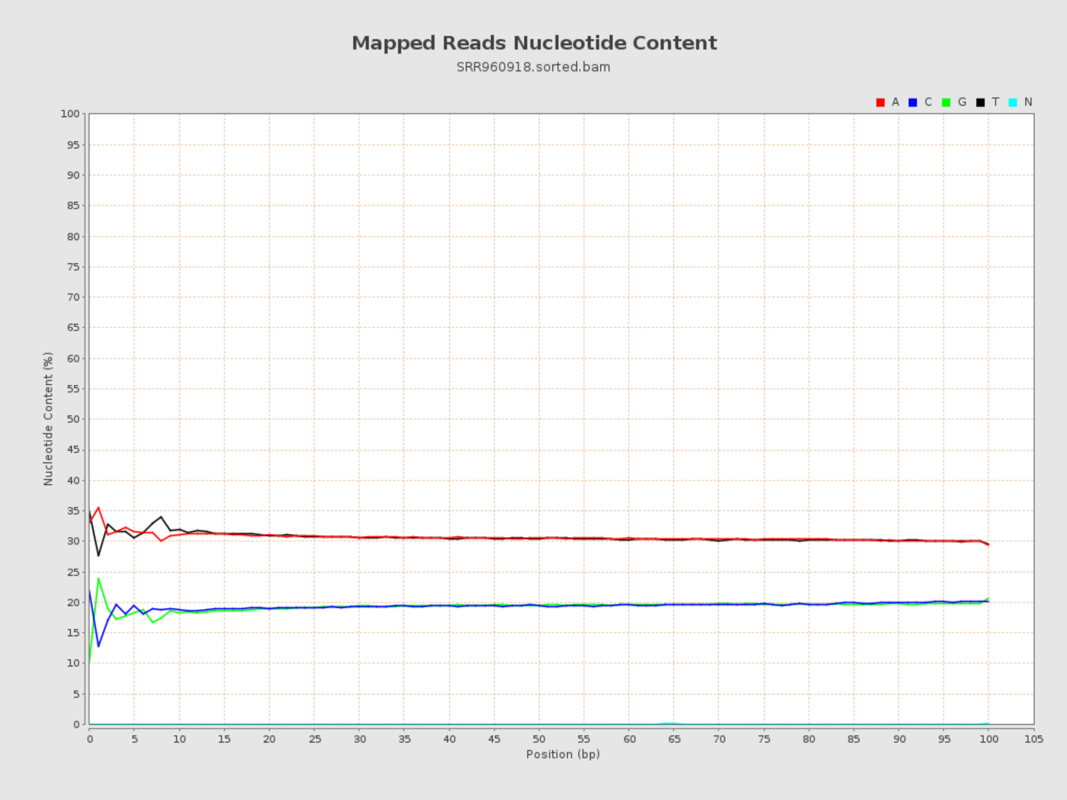
6. Results : Genome Fraction Coverage



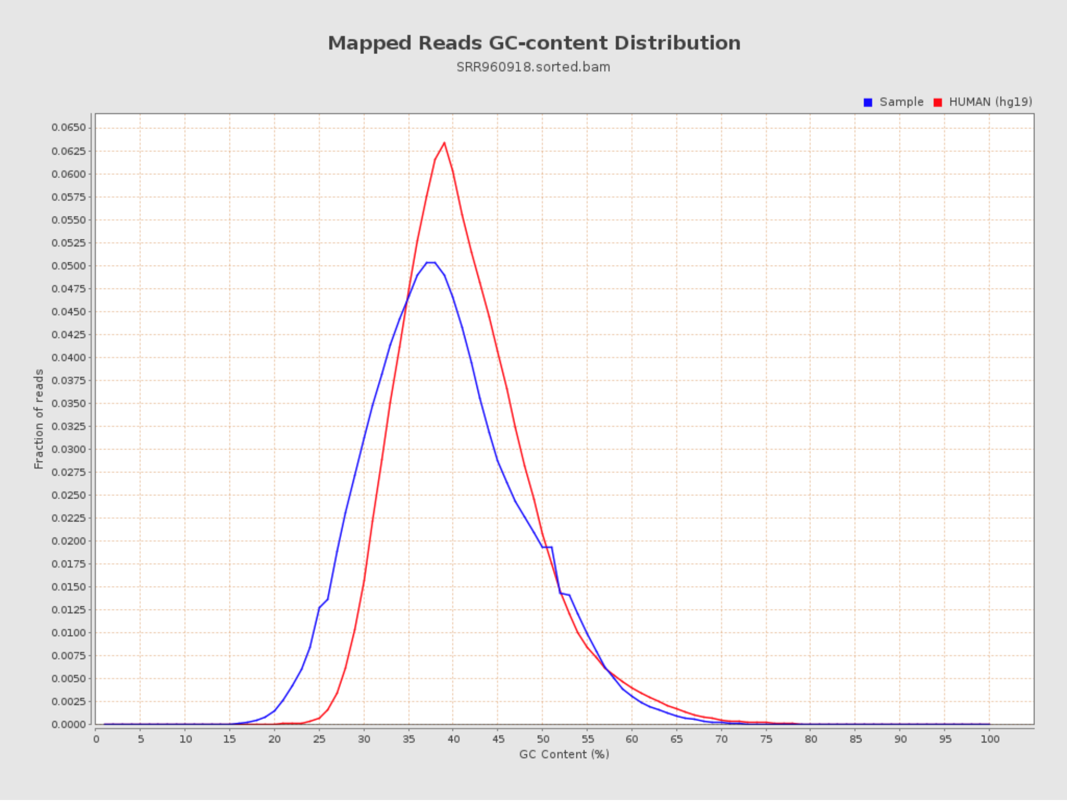
7. Results : Duplication Rate Histogram



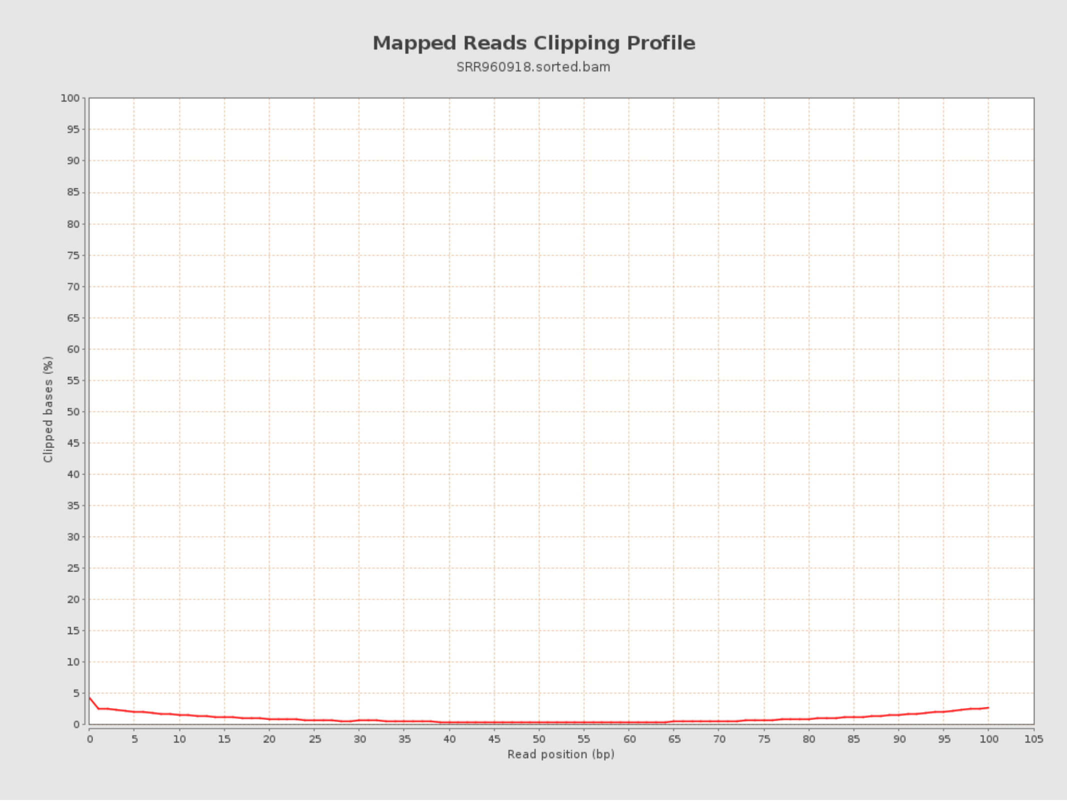
8. Results : Mapped Reads Nucleotide Content



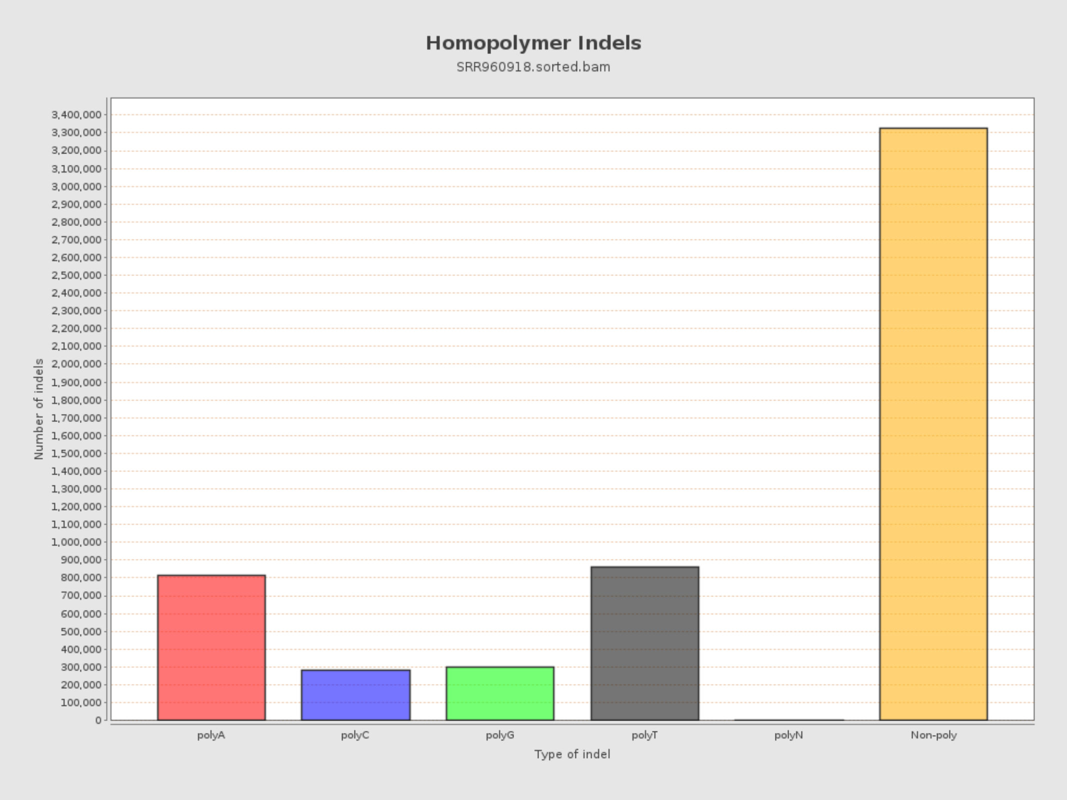
9. Results : Mapped Reads GC-content Distribution



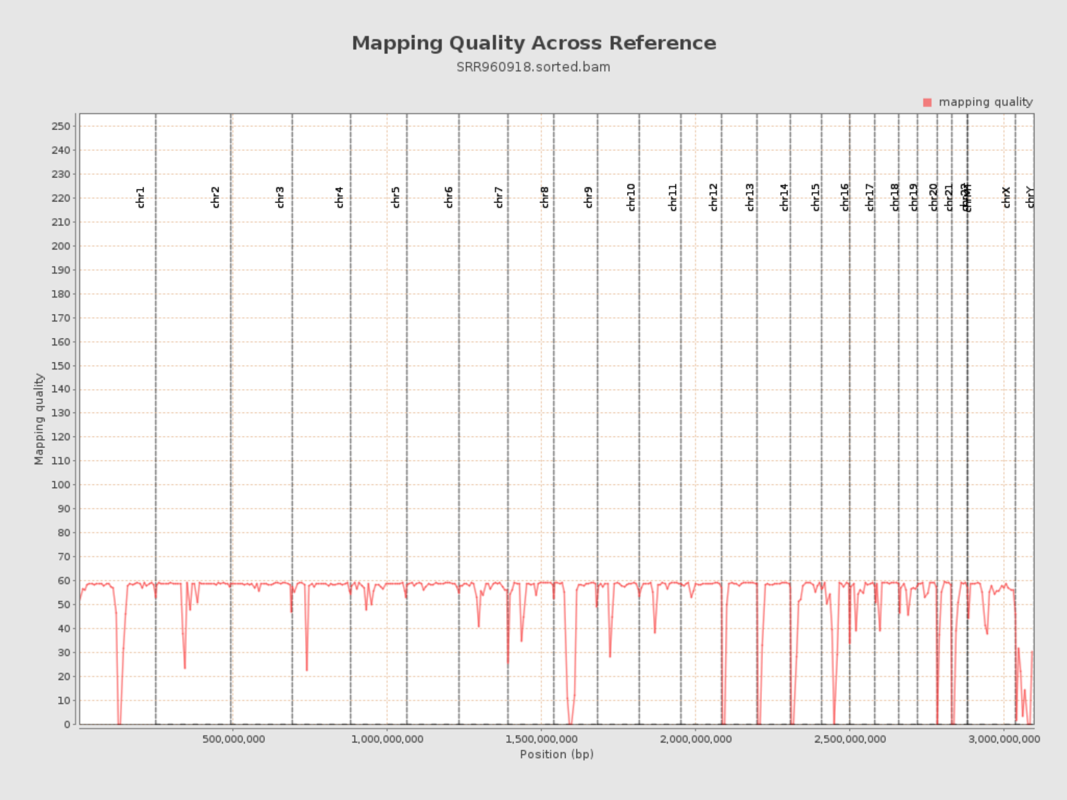
10. Results : Mapped Reads Clipping Profile



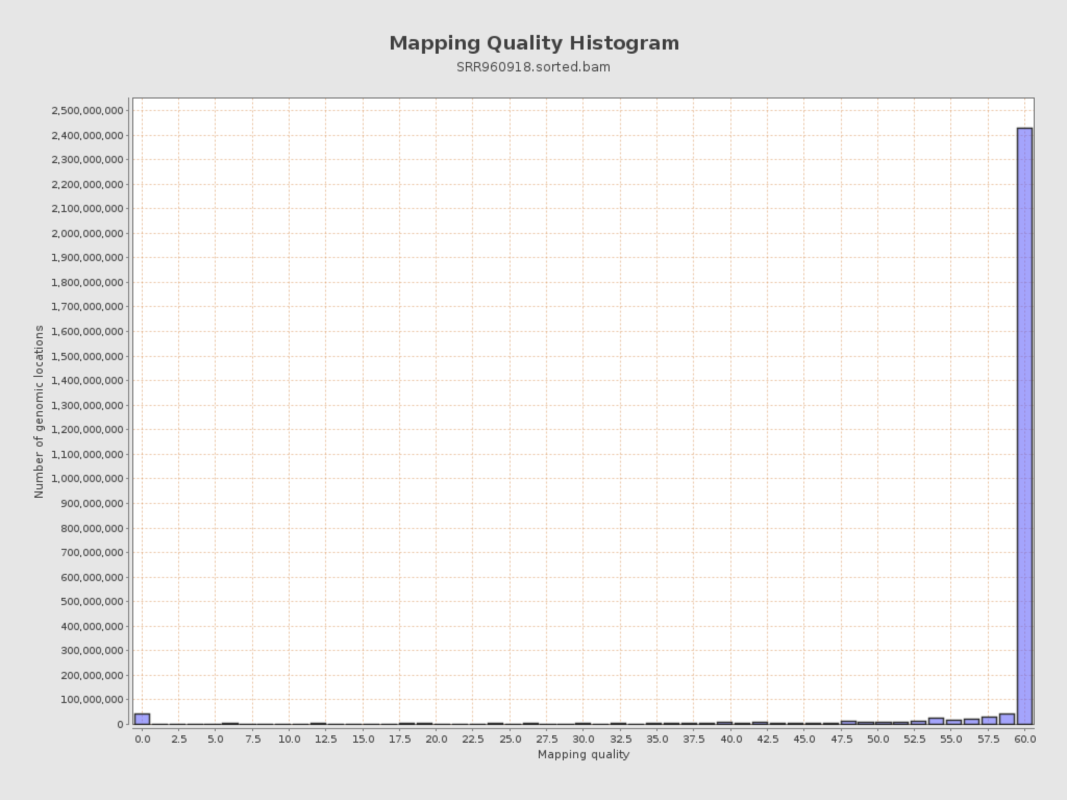
11. Results : Homopolymer Indels



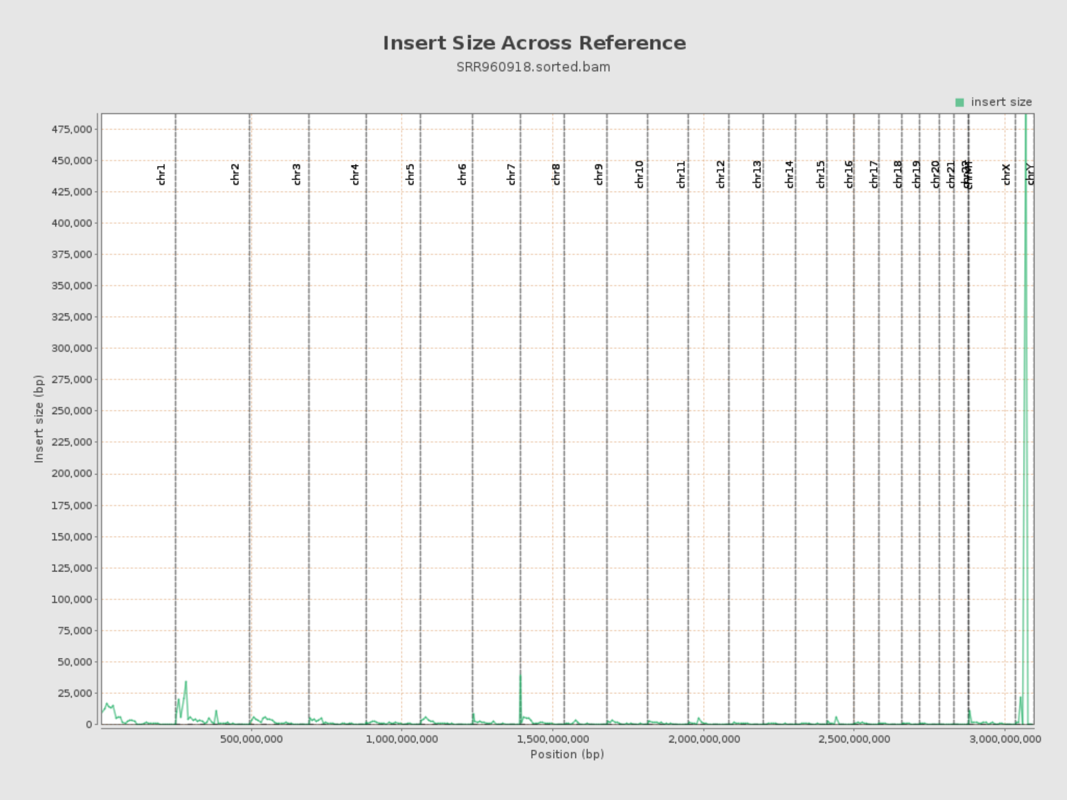
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram