Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 07:19:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438267.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_SRR8438267 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438267_1.fastq.gz SRR8438267_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 07:19:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438267.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	773,454,946
Mapped reads	771,000,221 / 99.68%
Unmapped reads	2,454,725 / 0.32%
Mapped paired reads	771,000,221 / 99.68%
Mapped reads, first in pair	385,621,342 / 49.86%
Mapped reads, second in pair	385,378,879 / 49.83%
Mapped reads, both in pair	769,260,312 / 99.46%
Mapped reads, singletons	1,739,909 / 0.22%
Secondary alignments	0
Supplementary alignments	13,257,529 / 1.71%
Read min/max/mean length	28 / 151 / 145.8
Duplicated reads (estimated)	382,860,649 / 49.5%
Duplication rate	46.7%
Clipped reads	140,696,521 / 18.19%

2.2. ACGT Content

Number/percentage of A's	33,723,182,714 / 30.28%
Number/percentage of C's	22,226,887,112 / 19.96%
Number/percentage of T's	32,205,450,063 / 28.92%
Number/percentage of G's	23,208,110,001 / 20.84%
Number/percentage of N's	682,824 / 0%

GC Percentage	40.8%

2.3. Coverage

Mean	35.9839
Standard Deviation	63.5809

2.4. Mapping Quality

Mean Mapping Quality	55.05

2.5. Insert size

Mean	41,055.5
Standard Deviation	1,951,214.85
P25/Median/P75	187 / 241 / 320

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	561,573,008
Insertions	13,981,249
Mapped reads with at least one insertion	1.79%
Deletions	12,415,359
Mapped reads with at least one deletion	1.58%
Homopolymer indels	48.51%

2.7. Chromosome stats

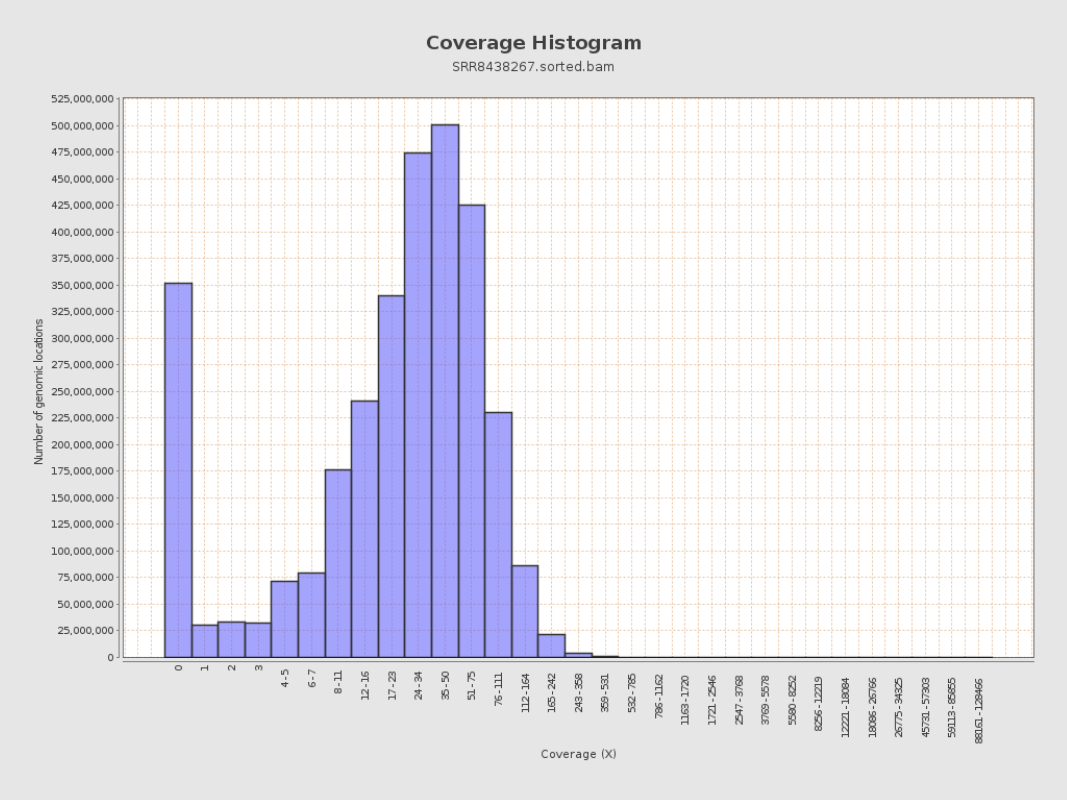
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	**coverage**	**deviation**
chr1	249250621	9151111348	36.7145	37.0047
chr2	243199373	10151697139	41.7423	122.8747
chr3	198022430	8210939845	41.4647	48.5192
chr4	191154276	7457438027	39.0127	33.1227
chr5	180915260	7489816318	41.3996	35.4352
chr6	171115067	7044783788	41.1699	35.9535
chr7	159138663	6168167273	38.7597	35.1885
chr8	146364022	5534171548	37.811	33.8293
chr9	141213431	4525759364	32.0491	37.1532
chr10	135534747	5824718939	42.9758	44.5997
chr11	135006516	5877385798	43.5341	37.8049
chr12	133851895	5793679601	43.2843	36.4236
chr13	115169878	3412450057	29.6297	31.3508
chr14	107349540	3206284639	29.8677	33.4658
chr15	102531392	3041667087	29.6657	35.3653
chr16	90354753	2462701238	27.2559	43.7822
chr17	81195210	2797790467	34.4576	38.0862
chr18	78077248	3038038362	38.9107	35.7571
chr19	59128983	1790432839	30.2801	58.1412
chr20	63025520	2004365995	31.8025	35.2893
chr21	48129895	1567614173	32.5705	39.6419
chr22	51304566	1157356547	22.5585	31.2526
chrMT	16571	261120483	15,757.6781	6,178.0757
chrX	155270560	2962996402	19.0828	23.0359

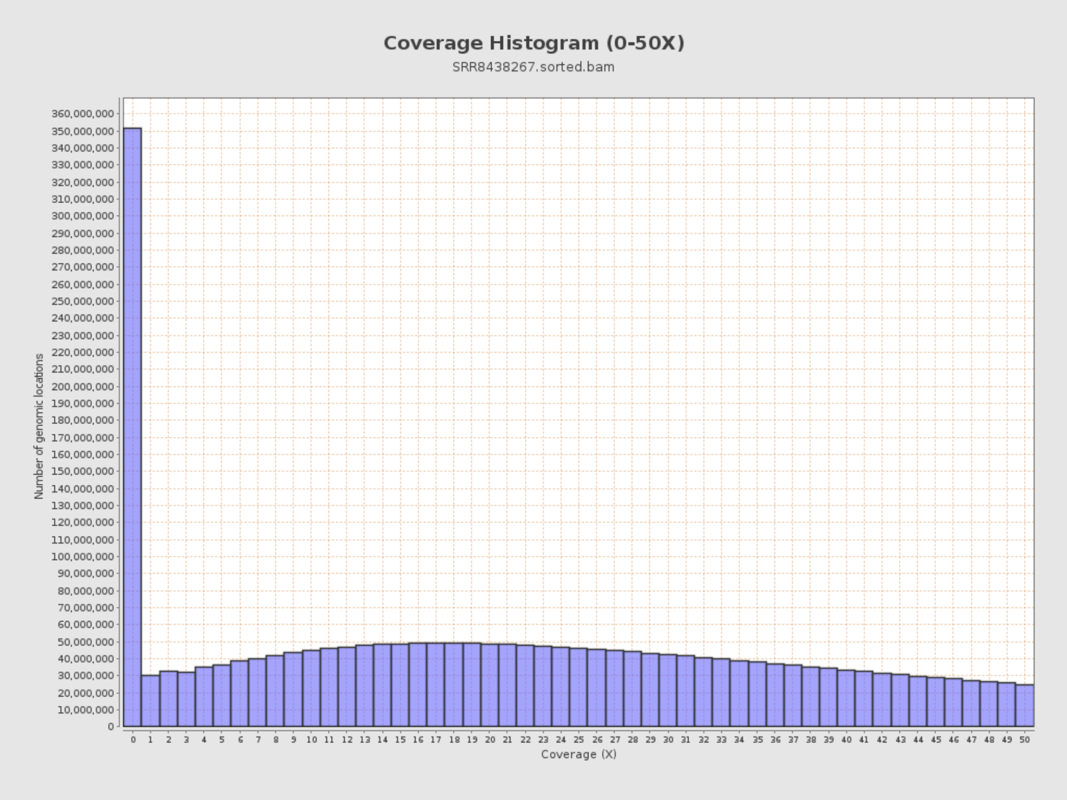
chrY	59373566	462532386	7.7902	24.2049

3. Results : Coverage across reference

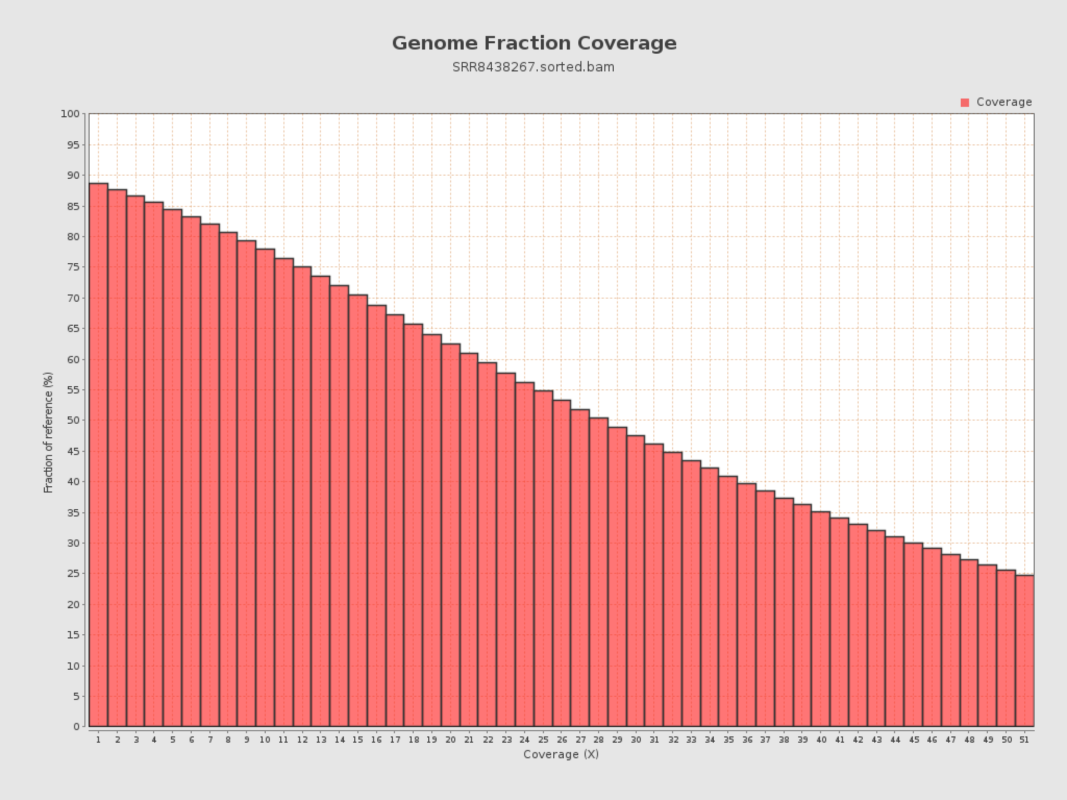
4. Results : Coverage Histogram



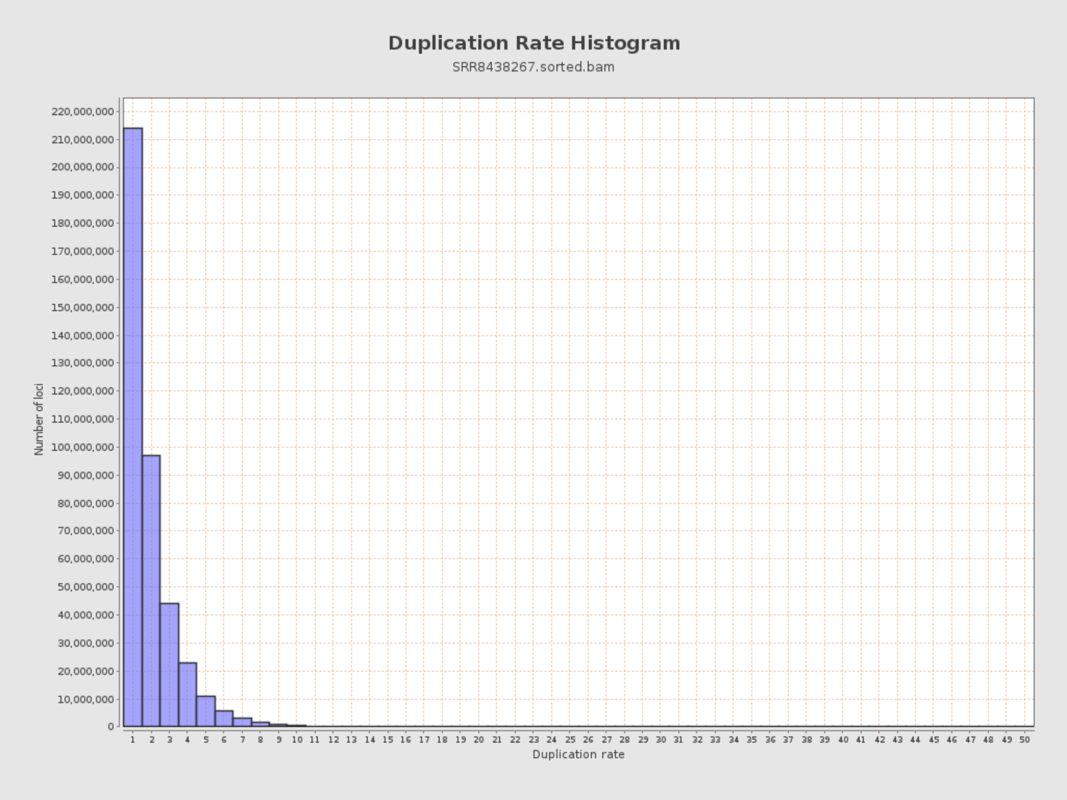
5. Results : Coverage Histogram (0-50X)



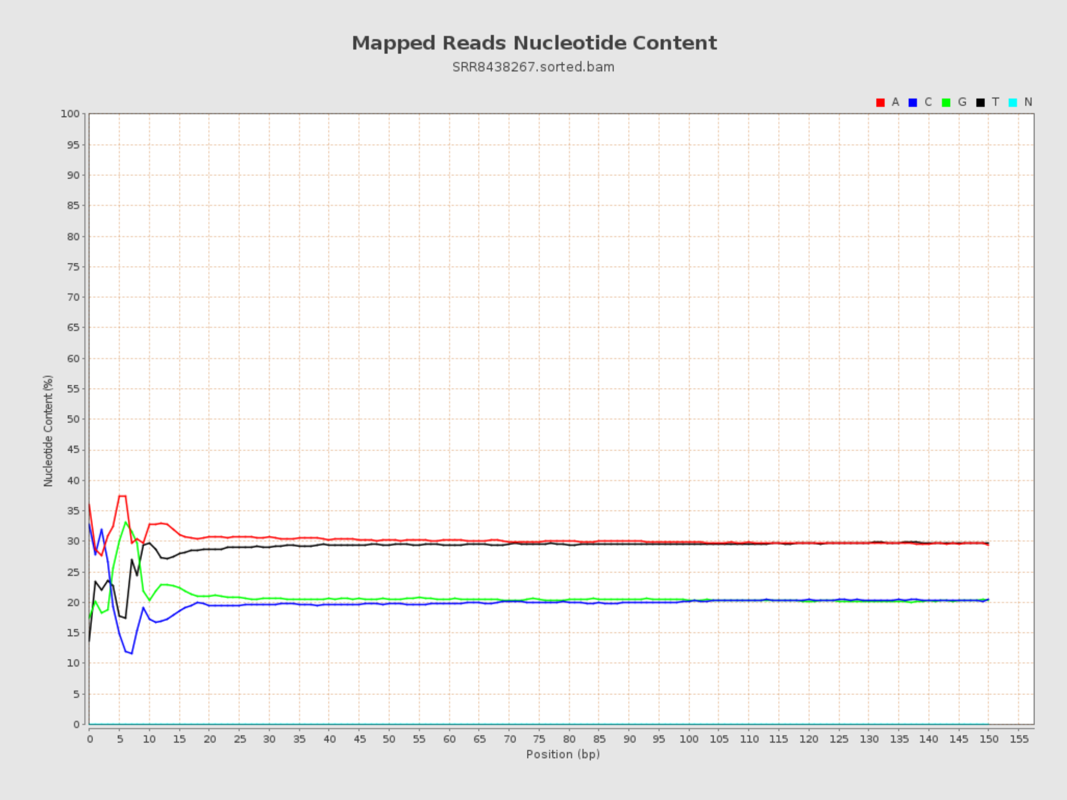
6. Results : Genome Fraction Coverage



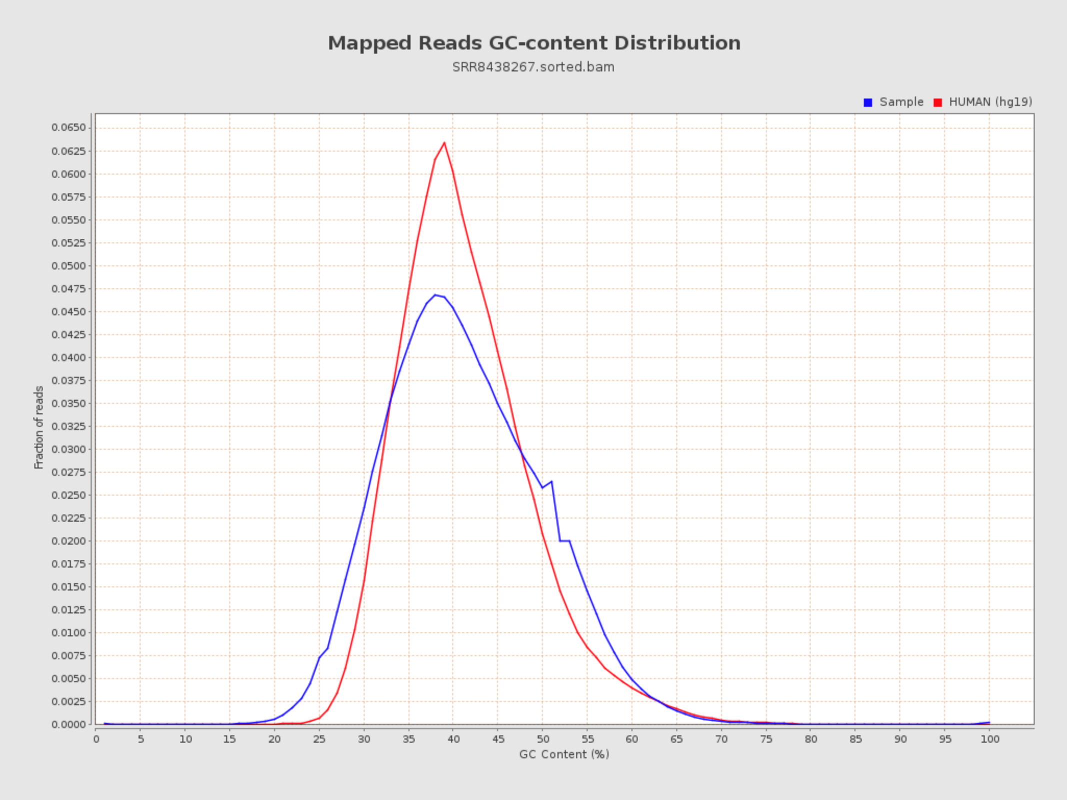
7. Results : Duplication Rate Histogram



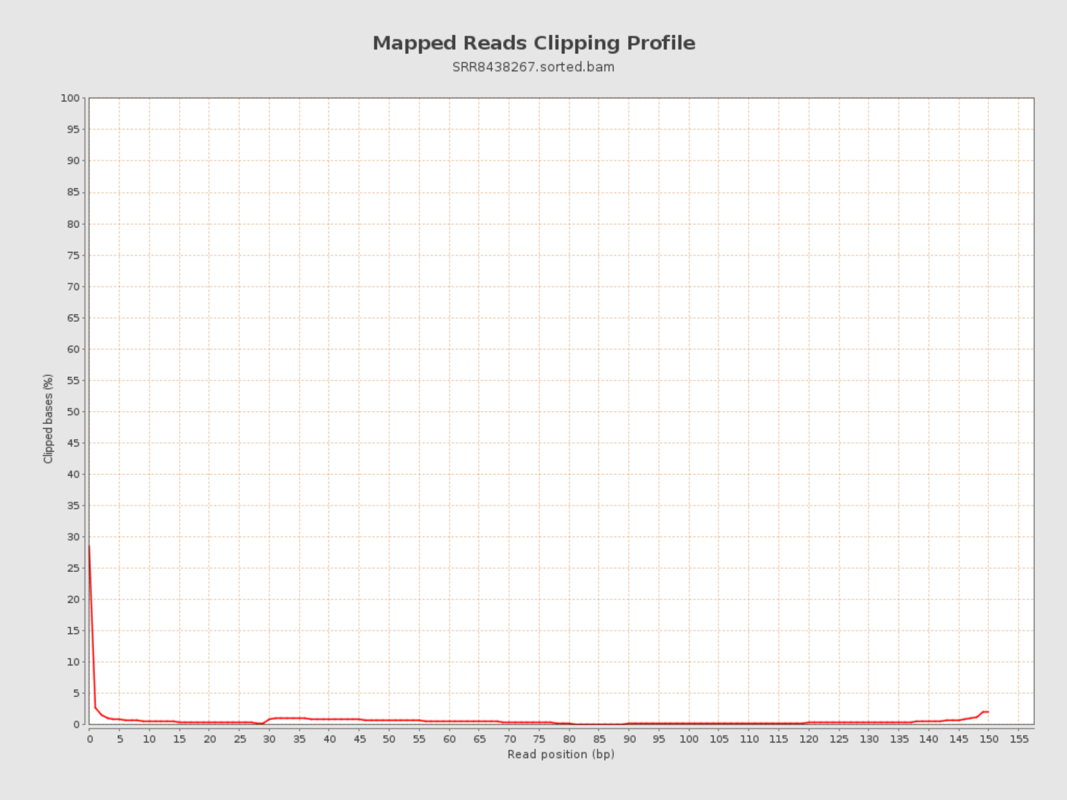
8. Results : Mapped Reads Nucleotide Content



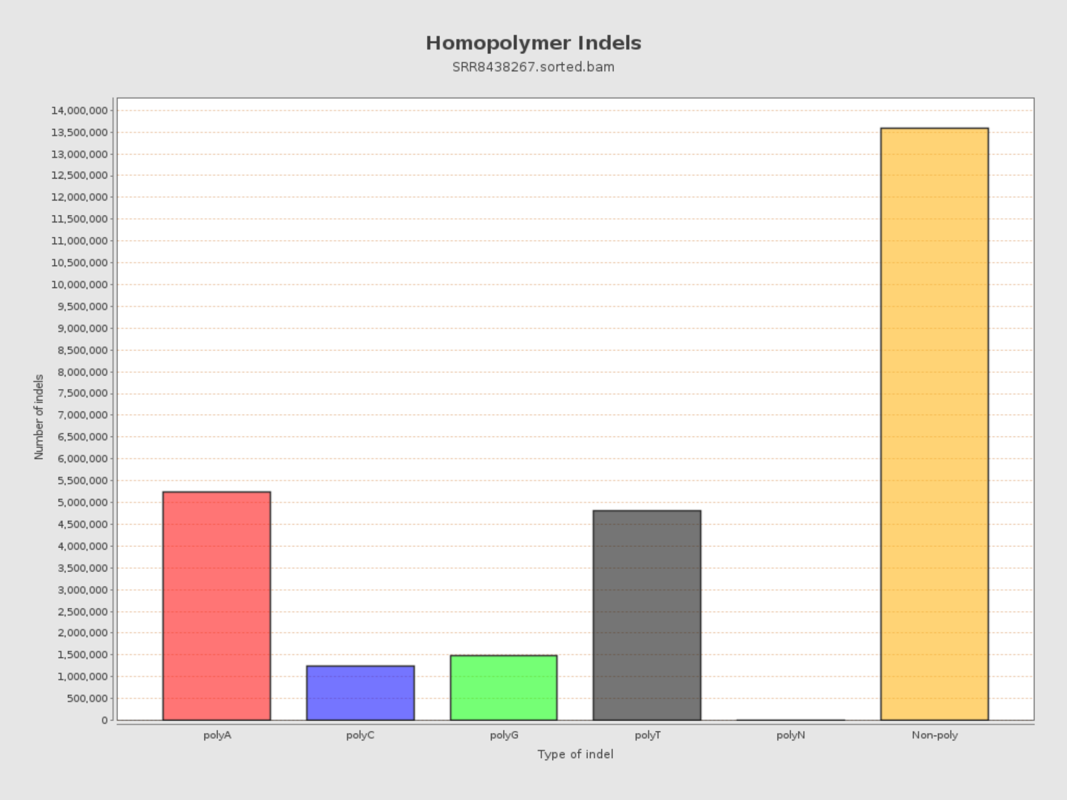
9. Results : Mapped Reads GC-content Distribution



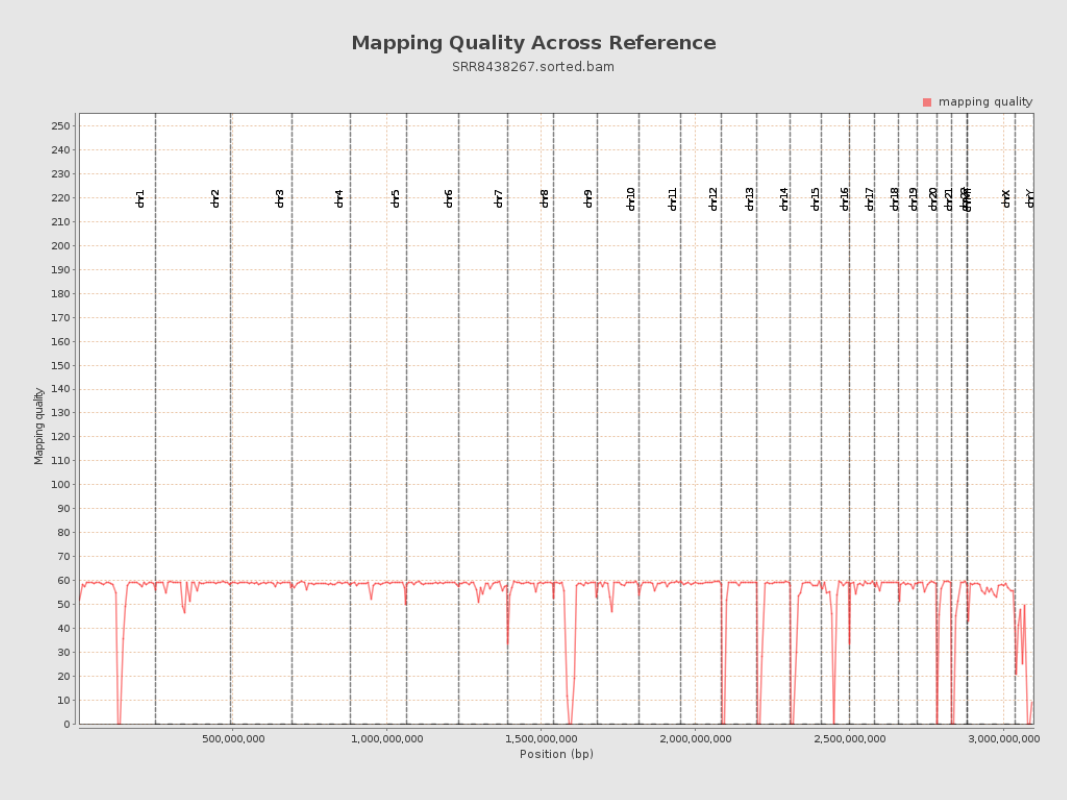
10. Results : Mapped Reads Clipping Profile



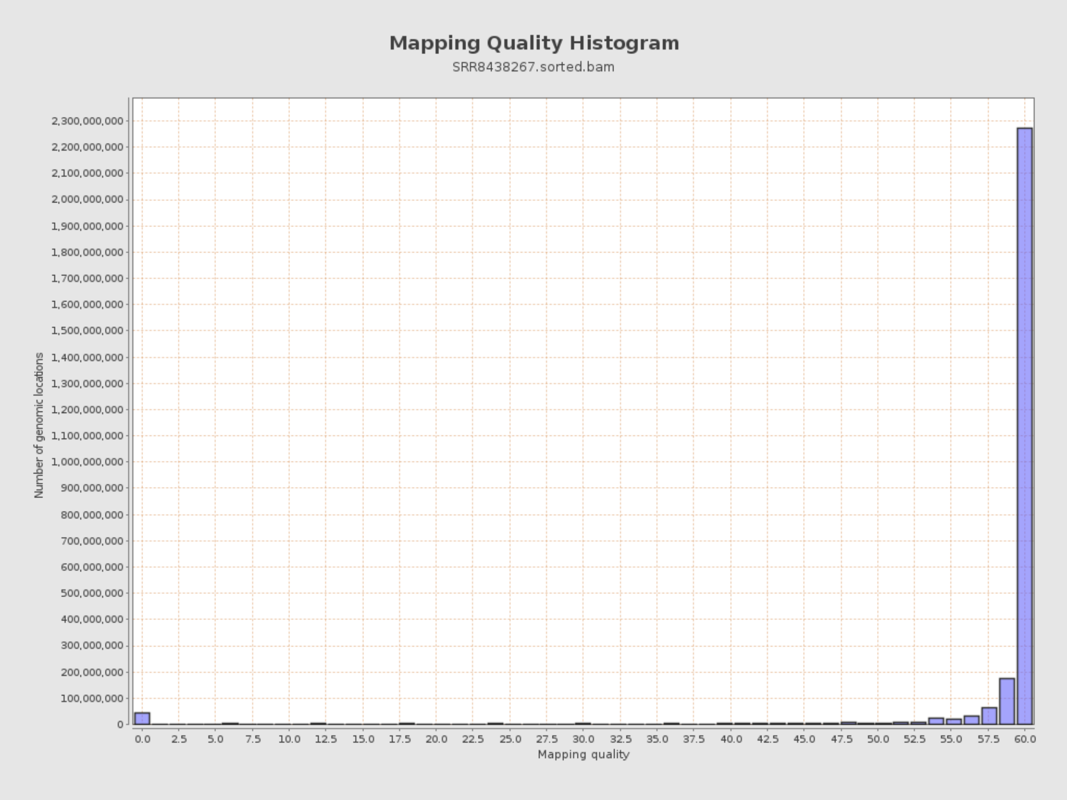
11. Results : Homopolymer Indels



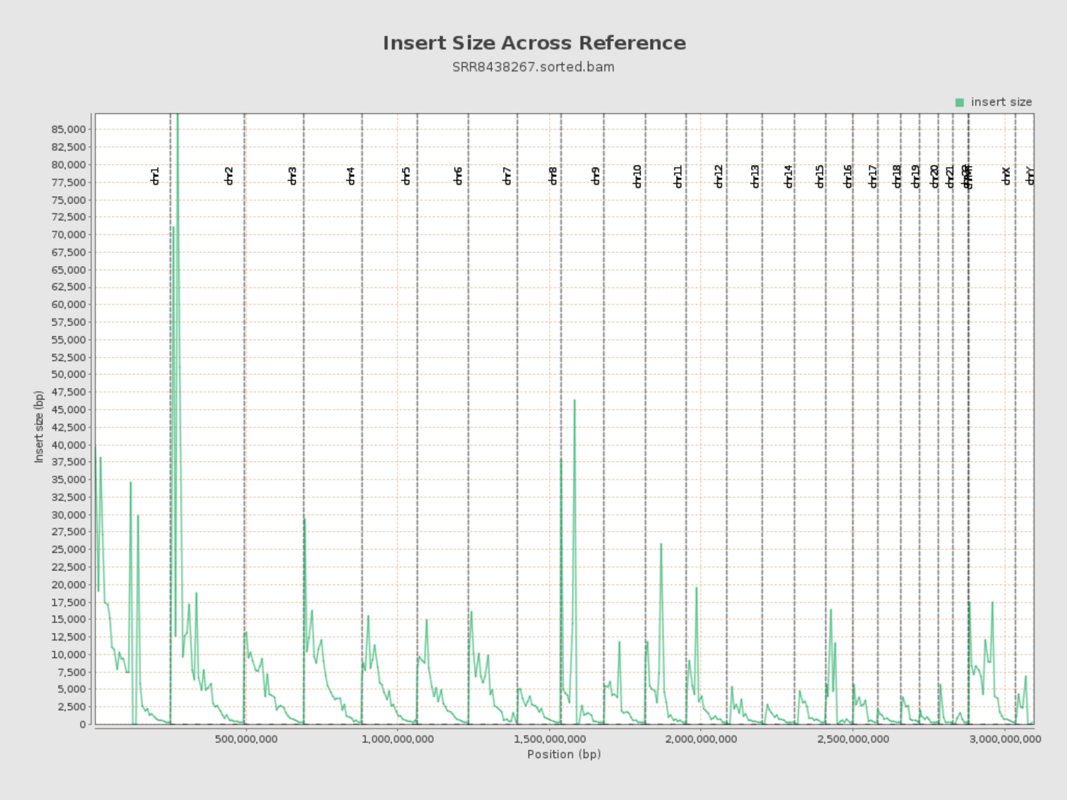
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram