Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/22 01:31:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438276.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_SRR8438276 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438276_1.fastq.gz SRR8438276_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 22 01:31:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438276.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	697,391,010
Mapped reads	695,071,512 / 99.67%
Unmapped reads	2,319,498 / 0.33%
Mapped paired reads	695,071,512 / 99.67%
Mapped reads, first in pair	347,777,449 / 49.87%
Mapped reads, second in pair	347,294,063 / 49.8%
Mapped reads, both in pair	693,425,402 / 99.43%
Mapped reads, singletons	1,646,110 / 0.24%
Secondary alignments	0
Supplementary alignments	12,284,435 / 1.76%
Read min/max/mean length	28 / 151 / 145.28
Duplicated reads (estimated)	255,278,229 / 36.6%
Duplication rate	33.89%
Clipped reads	120,365,549 / 17.26%

2.2. ACGT Content

Number/percentage of A's	30,260,849,929 / 30.24%
Number/percentage of C's	20,015,915,033 / 20%
Number/percentage of T's	28,823,027,344 / 28.8%
Number/percentage of G's	20,967,493,191 / 20.95%
Number/percentage of N's	753,277 / 0%

GC Percentage	40.96%

2.3. Coverage

Mean	32.3337
Standard Deviation	69.3751

2.4. Mapping Quality

Mean Mapping Quality	55.1

2.5. Insert size

Mean	39,845.42
Standard Deviation	1,953,270.22
P25/Median/P75	197 / 266 / 386

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	511,906,824
Insertions	12,111,454
Mapped reads with at least one insertion	1.71%
Deletions	10,826,043
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.33%

2.7. Chromosome stats

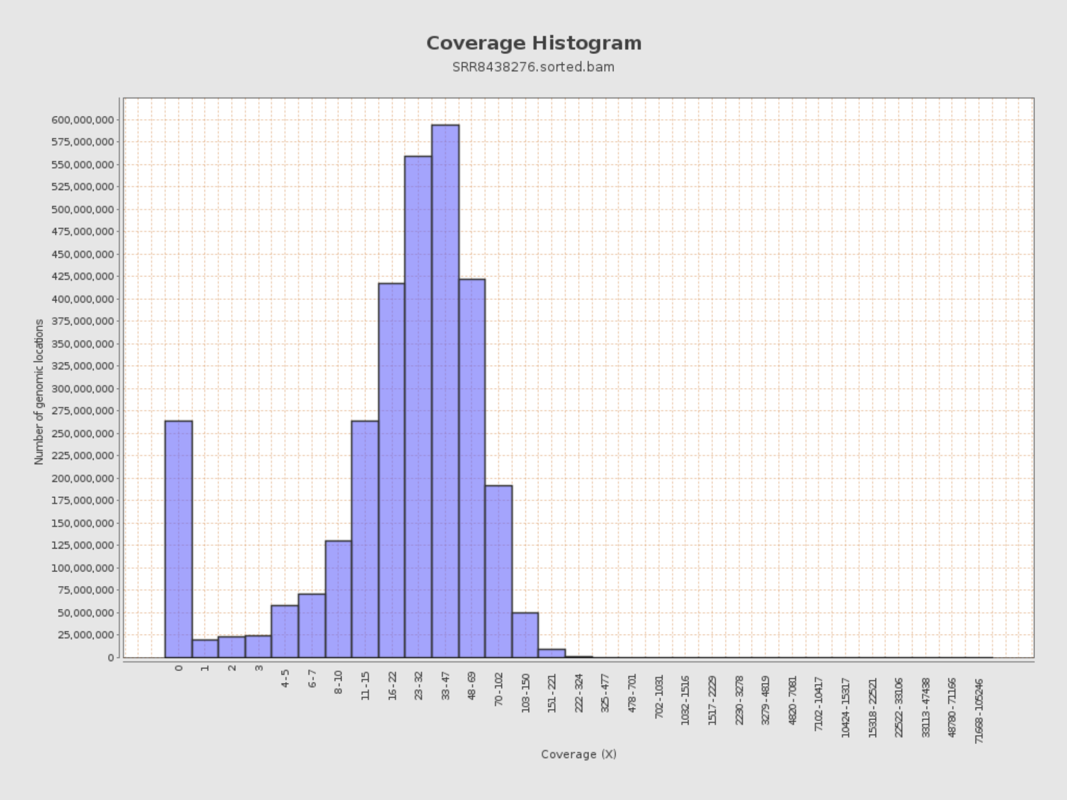
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	8204091786	32.915	29.4371
chr2	243199373	8984548958	36.9431	101.4075
chr3	198022430	7123138820	35.9714	50.7492
chr4	191154276	6844667648	35.807	25.2877
chr5	180915260	6441178706	35.6033	26.1954
chr6	171115067	6002436702	35.0784	25.9368
chr7	159138663	5472356091	34.3873	25.6689
chr8	146364022	5253568010	35.8938	26.0799
chr9	141213431	4314383666	30.5522	30.5396
chr10	135534747	4794970791	35.3782	31.0284
chr11	135006516	4706887130	34.8641	26.5794
chr12	133851895	4703894531	35.1425	25.8883
chr13	115169878	3491447168	30.3156	26.2064
chr14	107349540	3216745628	29.9652	28.0914
chr15	102531392	2937213092	28.647	28.1638
chr16	90354753	2689587098	29.767	42.8455
chr17	81195210	2375562848	29.2574	34.6153
chr18	78077248	2681572354	34.3451	26.3195
chr19	59128983	1483846732	25.0951	61.9289
chr20	63025520	2162689693	34.3145	29.2123
chr21	48129895	1276742447	26.527	37.6236
chr22	51304566	1061119197	20.6827	27.4778
chrMT	16571	373612644	22,546.1737	8,278.3811
chrX	155270560	3014861182	19.4168	17.0764

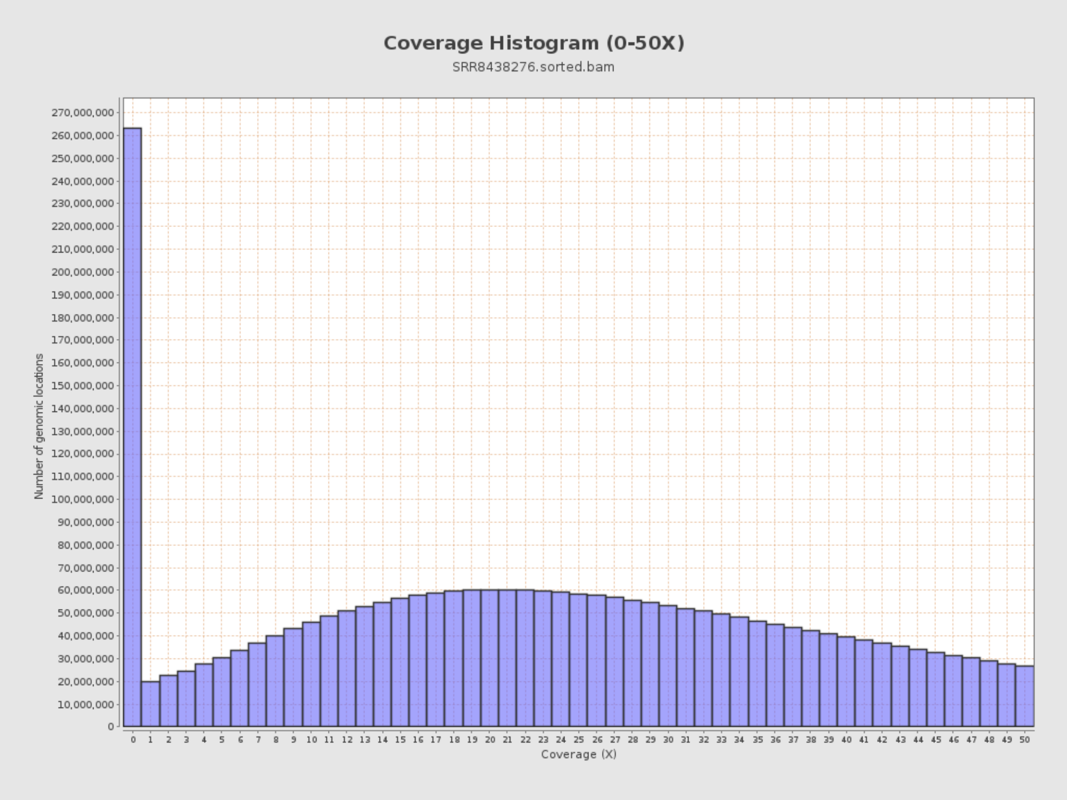
chrY	59373566	484137023	8.1541	24.0383

3. Results : Coverage across reference

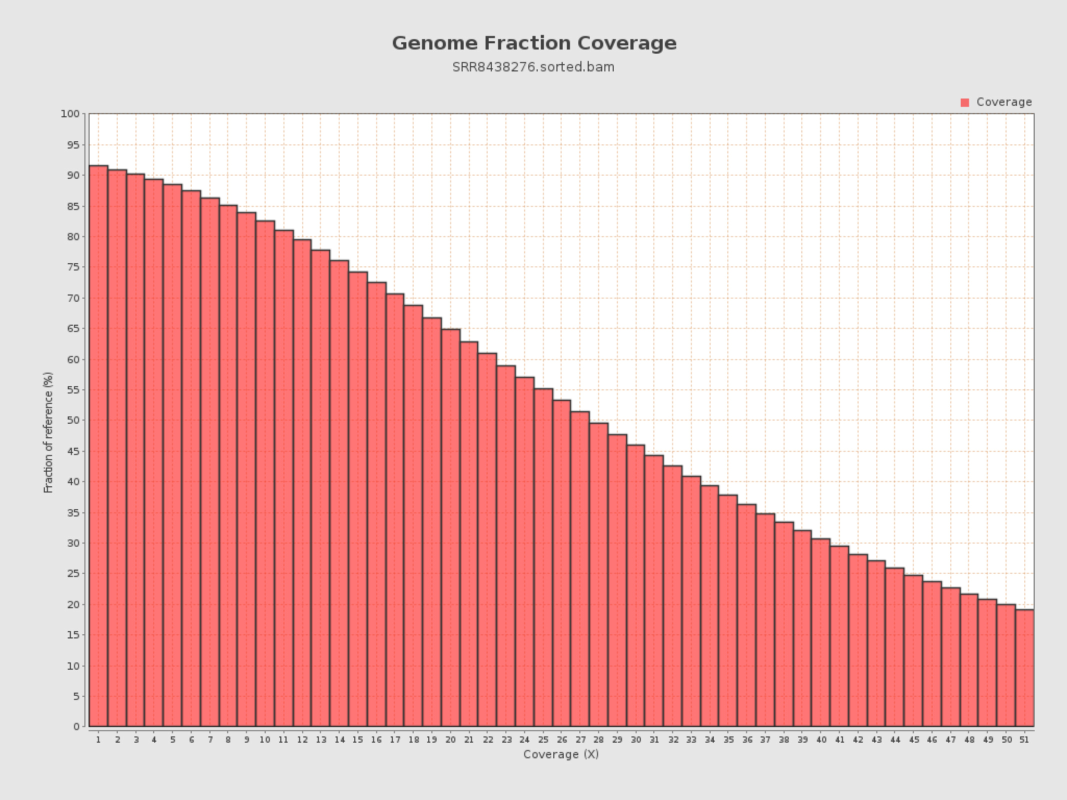
4. Results : Coverage Histogram



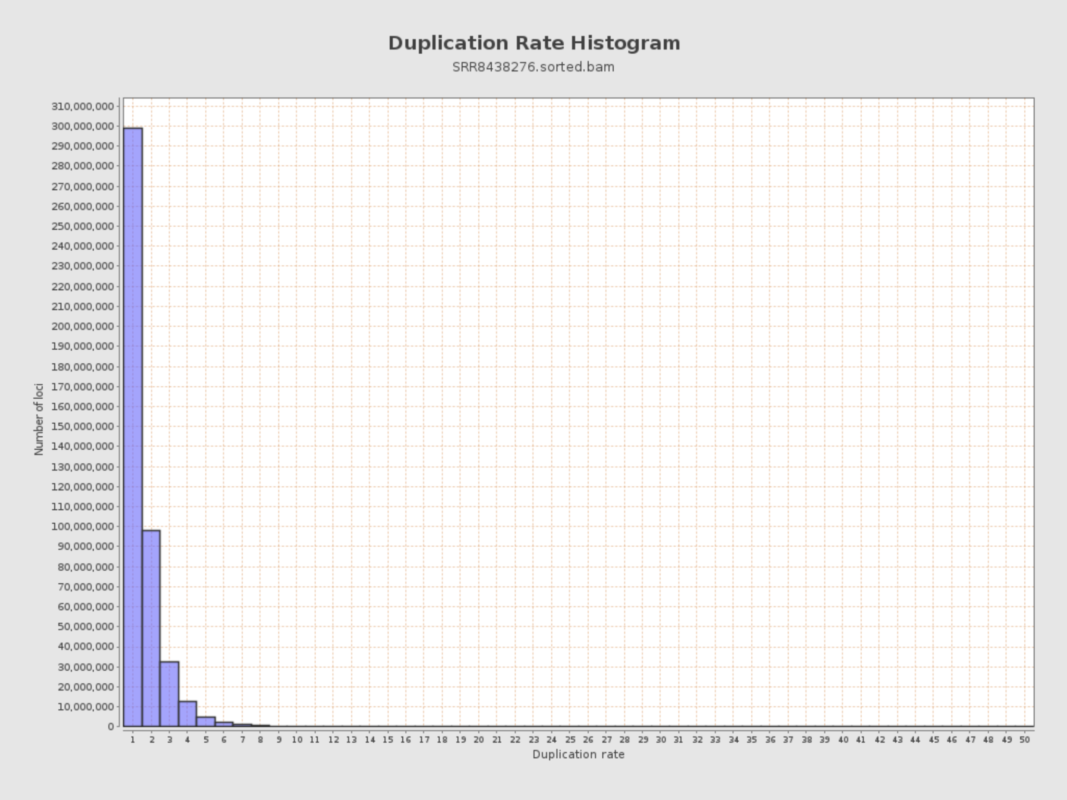
5. Results : Coverage Histogram (0-50X)



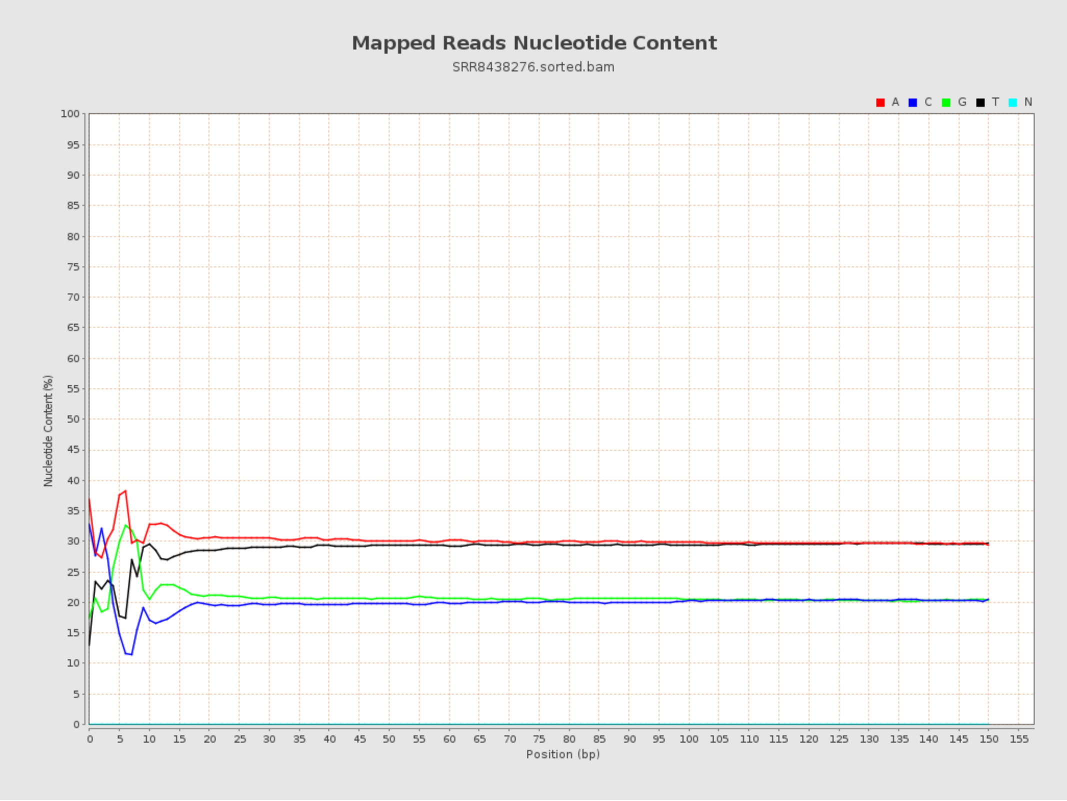
6. Results : Genome Fraction Coverage



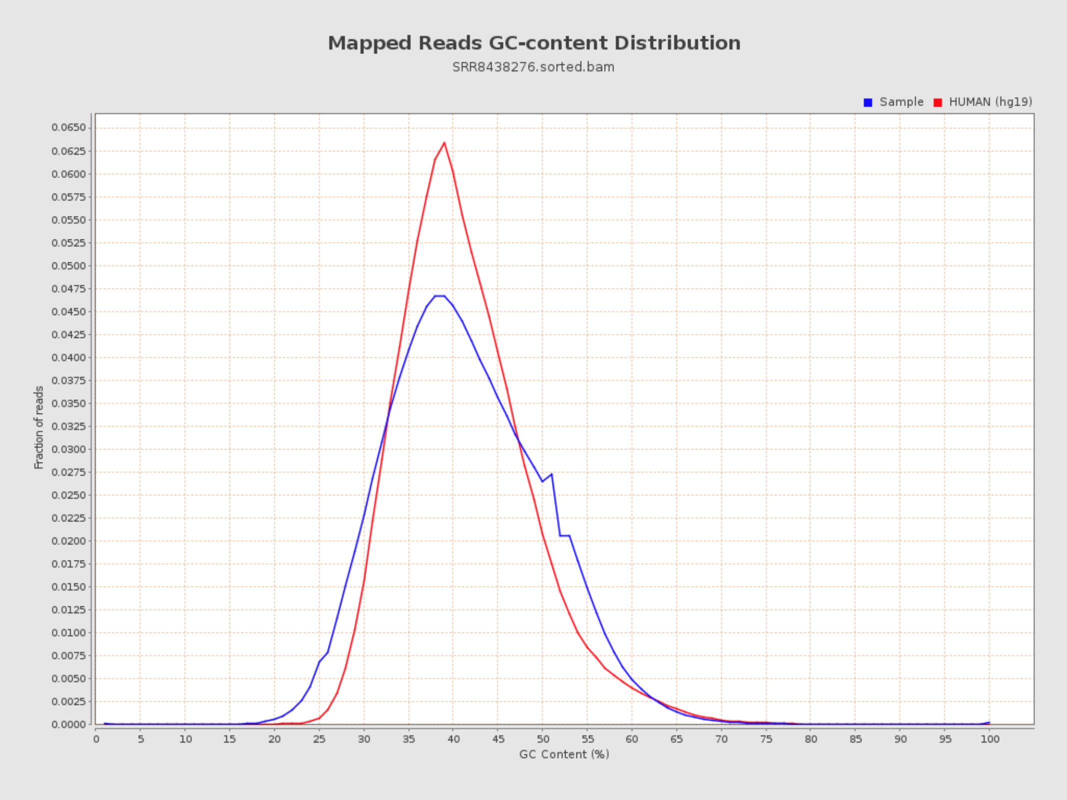
7. Results : Duplication Rate Histogram



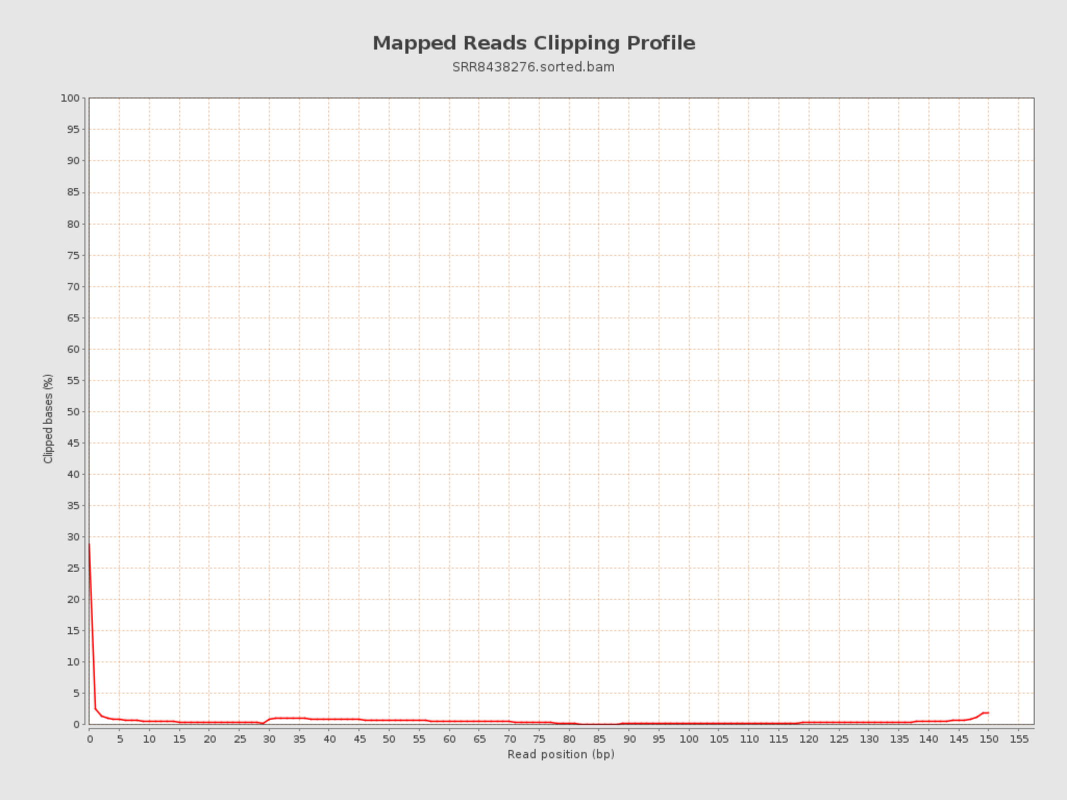
8. Results : Mapped Reads Nucleotide Content



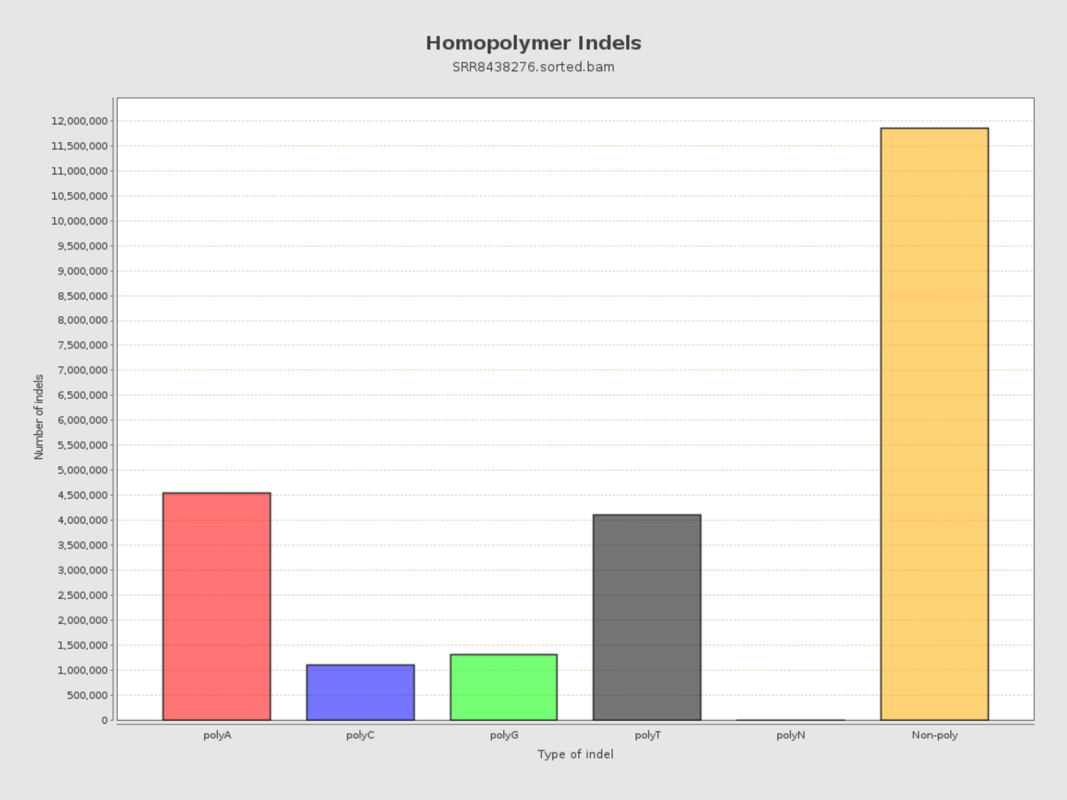
9. Results : Mapped Reads GC-content Distribution



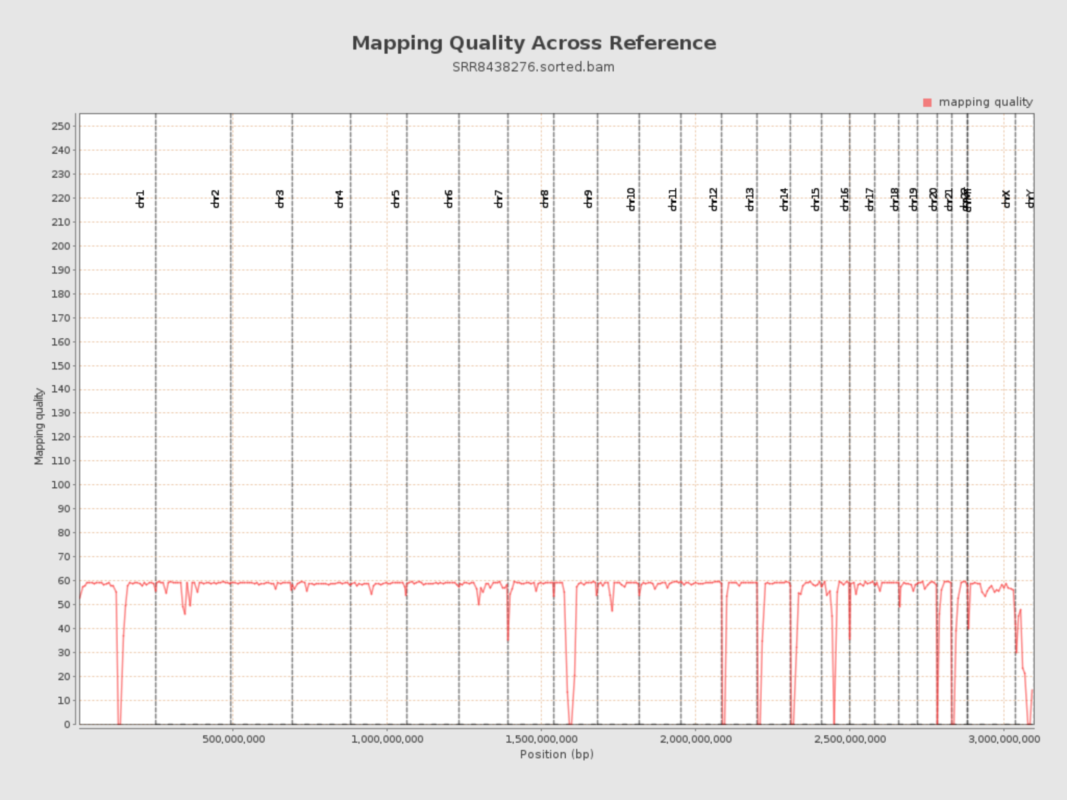
10. Results : Mapped Reads Clipping Profile



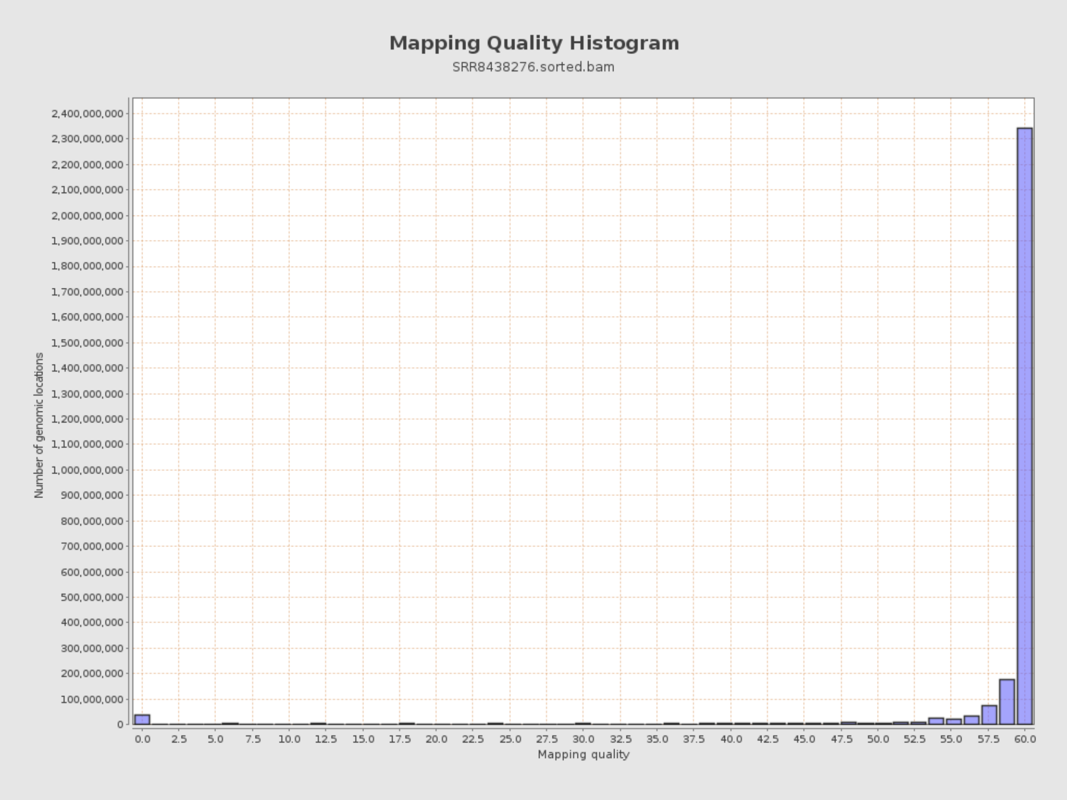
11. Results : Homopolymer Indels



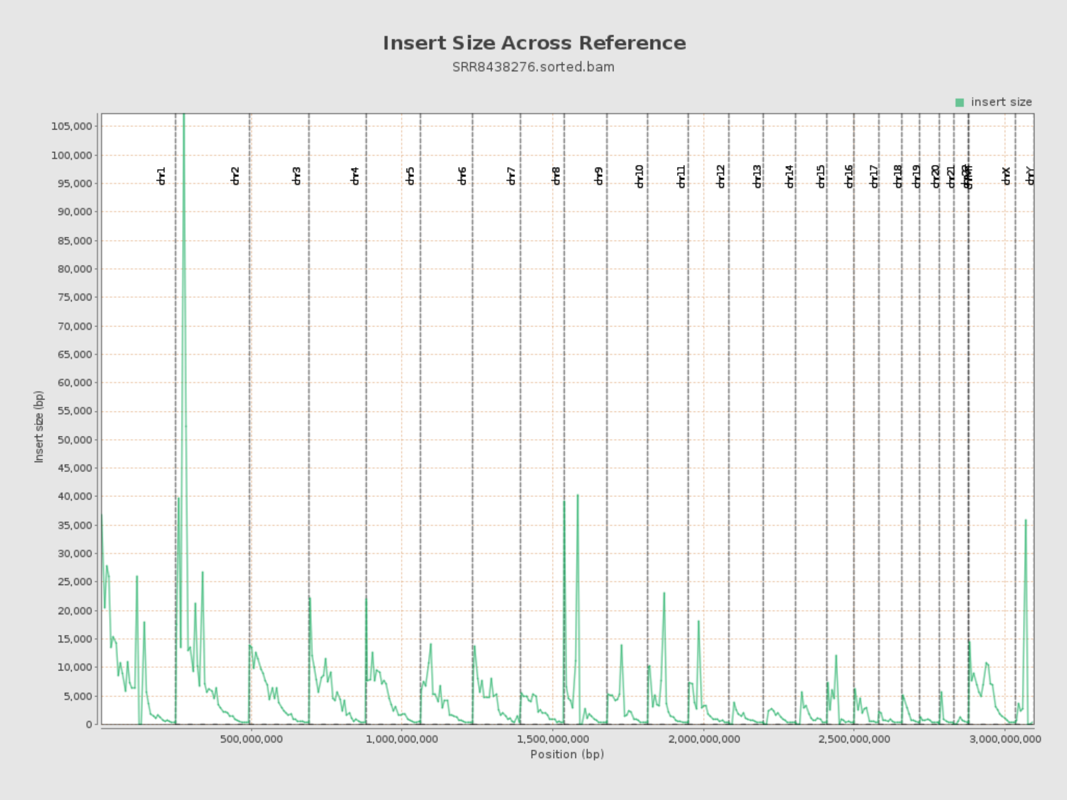
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram