Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 15:23:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438281.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_SRR8438281 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438281_1.fastq.gz SRR8438281_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 15:23:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438281.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	608,792,864
Mapped reads	606,661,749 / 99.65%
Unmapped reads	2,131,115 / 0.35%
Mapped paired reads	606,661,749 / 99.65%
Mapped reads, first in pair	303,632,693 / 49.87%
Mapped reads, second in pair	303,029,056 / 49.78%
Mapped reads, both in pair	605,112,208 / 99.4%
Mapped reads, singletons	1,549,541 / 0.25%
Secondary alignments	0
Supplementary alignments	9,795,655 / 1.61%
Read min/max/mean length	28 / 151 / 145.9
Duplicated reads (estimated)	262,101,496 / 43.05%
Duplication rate	40.82%
Clipped reads	105,993,742 / 17.41%

2.2. ACGT Content

Number/percentage of A's	26,637,758,656 / 30.35%
Number/percentage of C's	17,431,674,921 / 19.86%
Number/percentage of T's	25,310,459,584 / 28.84%
Number/percentage of G's	18,386,078,731 / 20.95%
Number/percentage of N's	655,903 / 0%

GC Percentage	40.81%

2.3. Coverage

Mean	28.3598
Standard Deviation	74.4293

2.4. Mapping Quality

Mean Mapping Quality	55

2.5. Insert size

Mean	39,218.8
Standard Deviation	1,911,358.09
P25/Median/P75	202 / 266 / 380

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	455,681,533
Insertions	11,840,504
Mapped reads with at least one insertion	1.92%
Deletions	10,453,274
Mapped reads with at least one deletion	1.69%
Homopolymer indels	48.59%

2.7. Chromosome stats

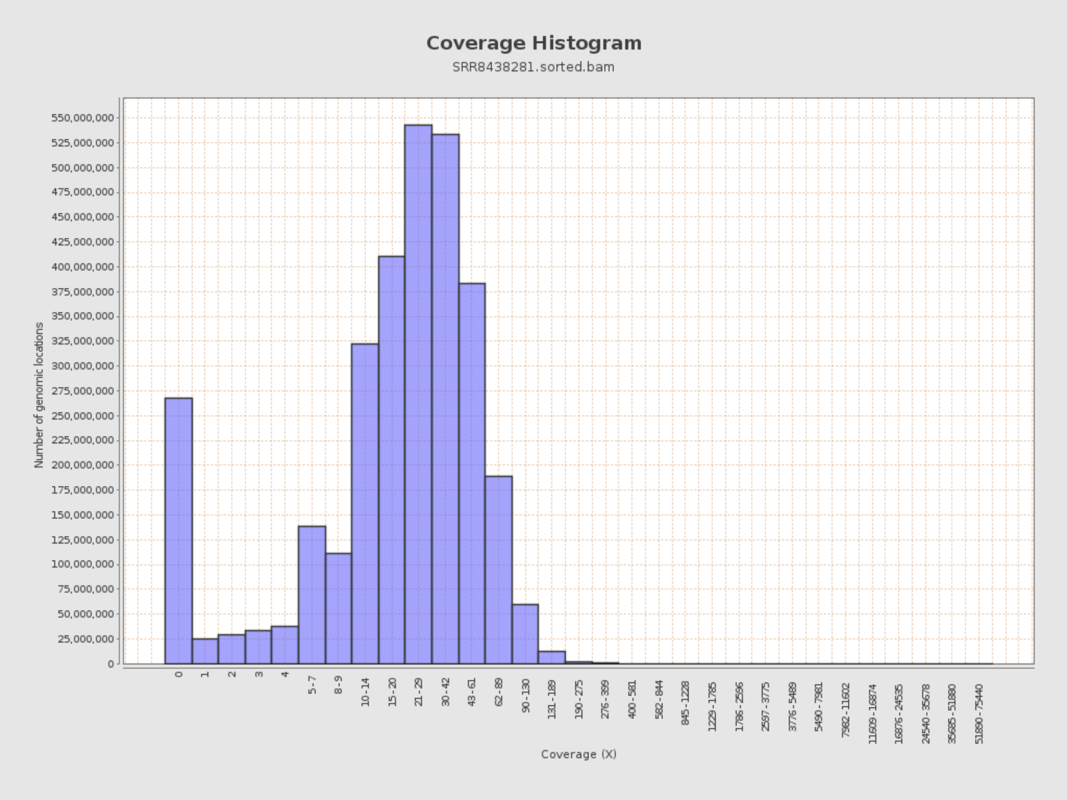
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	7161522912	28.7322	30.1787
chr2	243199373	7647901948	31.447	73.2593
chr3	198022430	6236314755	31.493	49.8766
chr4	191154276	5967768005	31.2196	23.6194
chr5	180915260	5781021048	31.9543	24.3012
chr6	171115067	5363307927	31.3433	25.7423
chr7	159138663	4717548195	29.6443	24.2082
chr8	146364022	4624370381	31.595	24.5116
chr9	141213431	3824364529	27.0822	32.5151
chr10	135534747	4100158802	30.2517	40.1677
chr11	135006516	4129612841	30.5882	25.1246
chr12	133851895	4147167791	30.9833	24.0662
chr13	115169878	3063229568	26.5975	24.3327
chr14	107349540	2828923522	26.3525	26.2934
chr15	102531392	2573262215	25.0973	25.8867
chr16	90354753	2340558136	25.9041	47.5373
chr17	81195210	2073802887	25.541	30.638
chr18	78077248	2383359077	30.5257	26.7725
chr19	59128983	1356536139	22.942	59.409
chr20	63025520	1841207551	29.2137	26.2305
chr21	48129895	1098192063	22.8173	36.51
chr22	51304566	969357274	18.8942	25.127
chrMT	16571	430383576	25,972.0944	10,650.547
chrX	155270560	2666879298	17.1757	17.1509

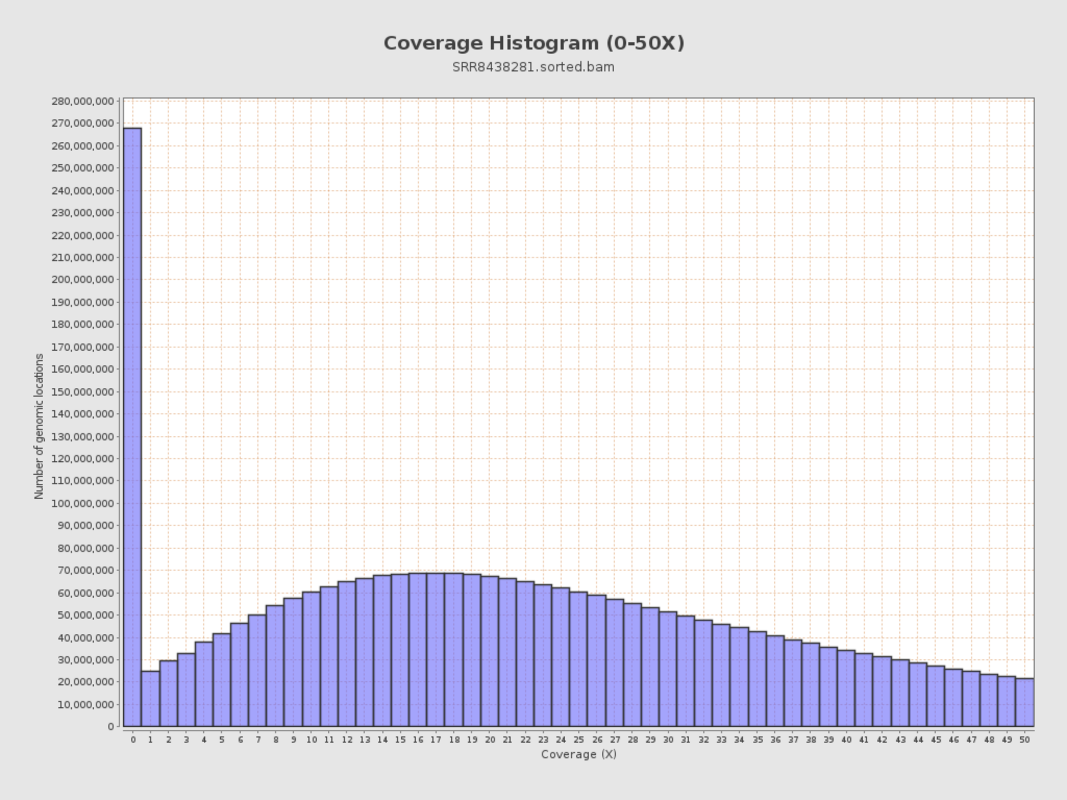
chrY	59373566	466453032	7.8562	26.9256

3. Results : Coverage across reference

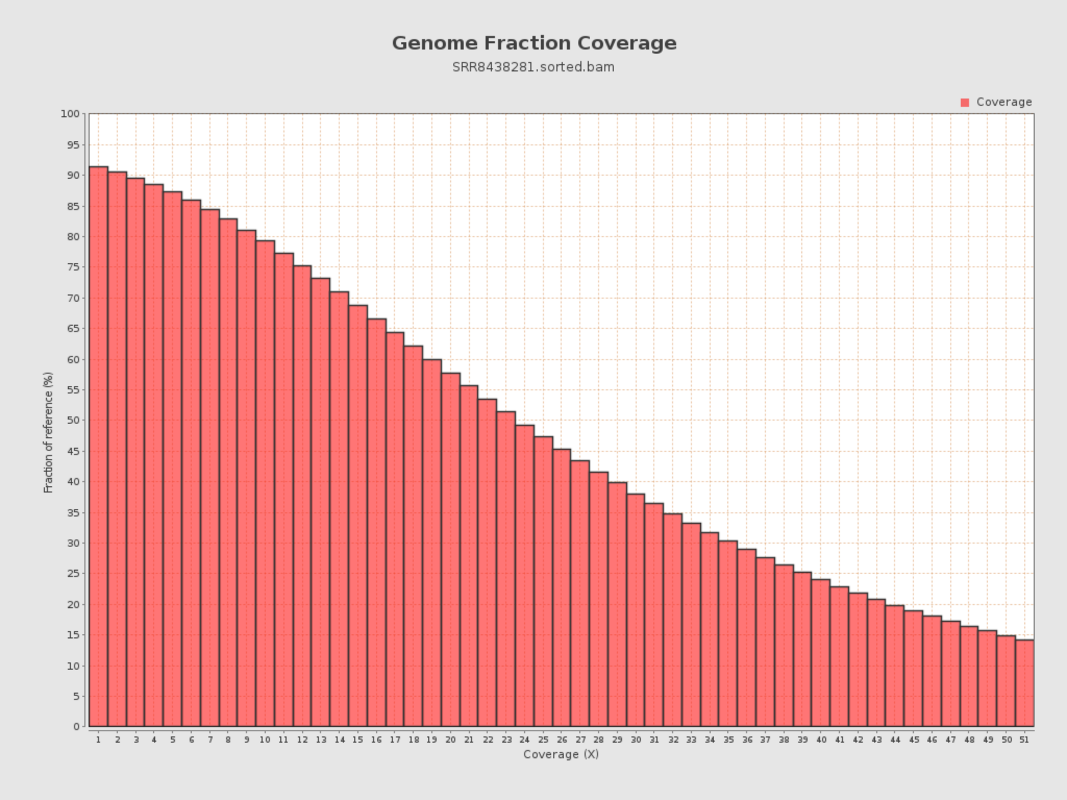
4. Results : Coverage Histogram



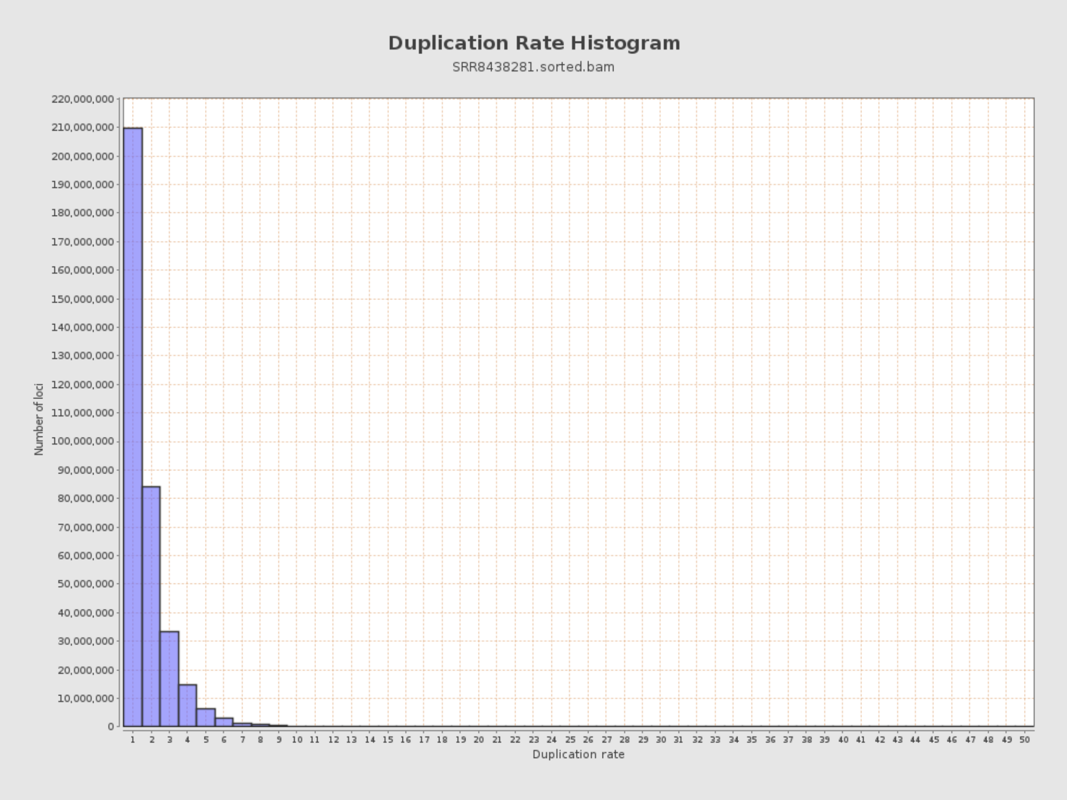
5. Results : Coverage Histogram (0-50X)



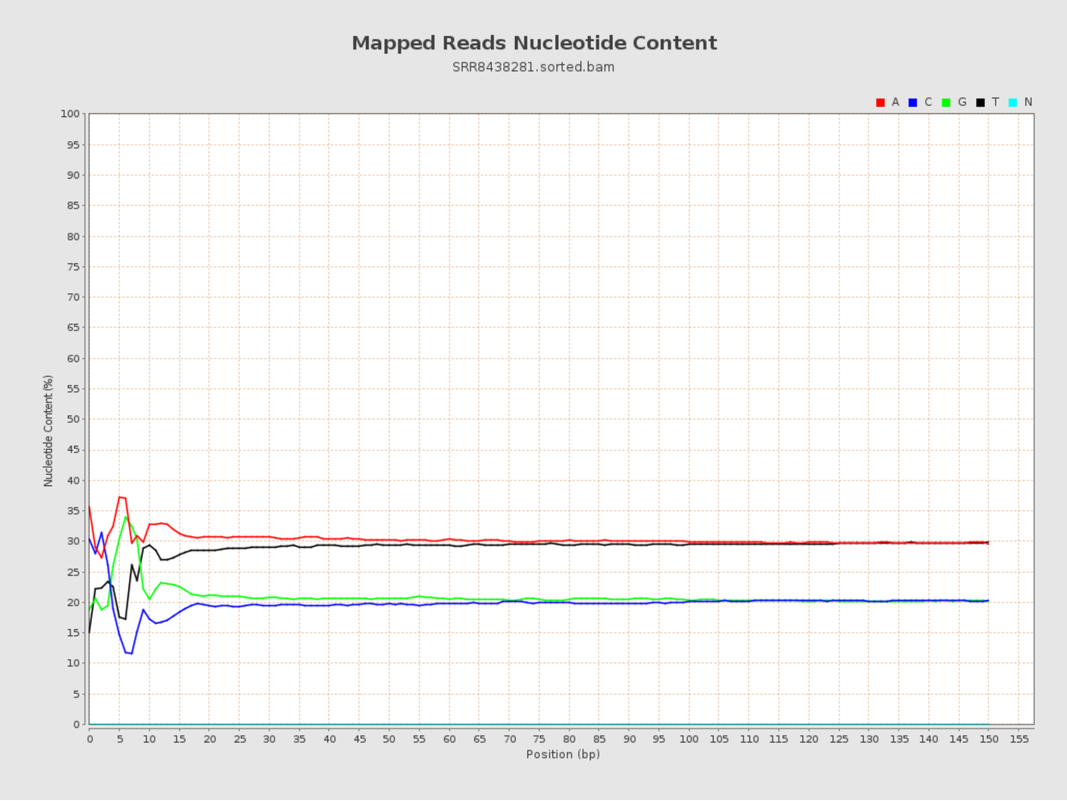
6. Results : Genome Fraction Coverage



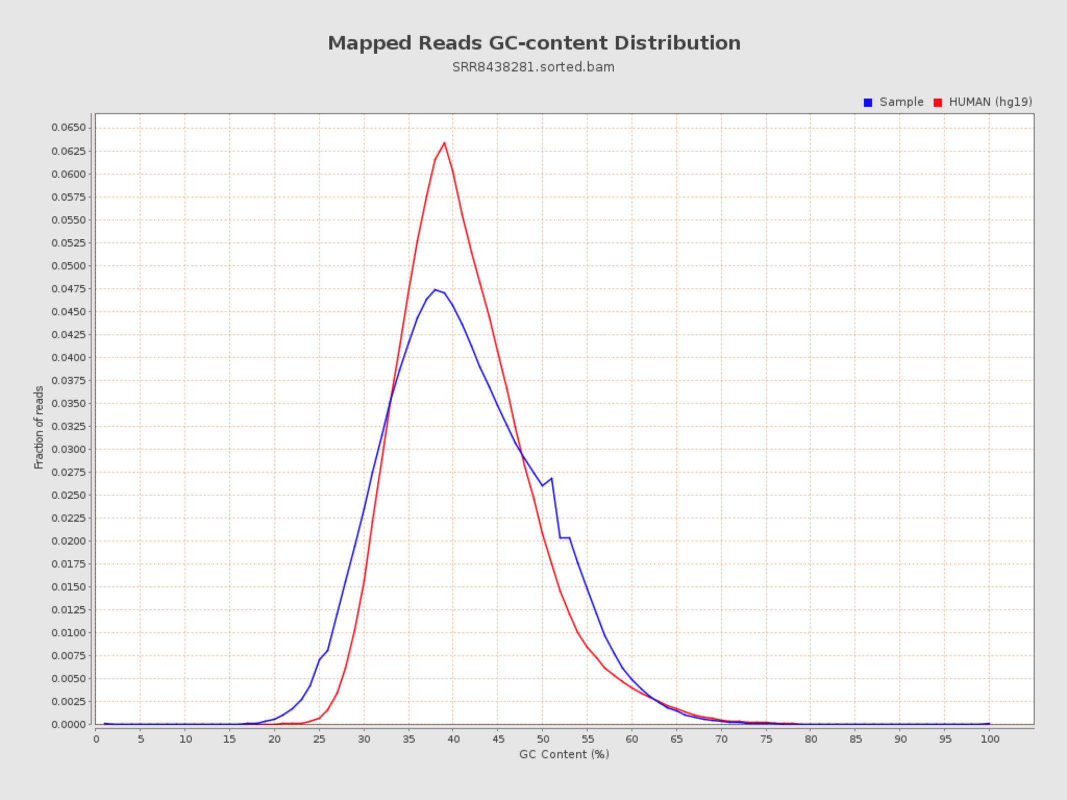
7. Results : Duplication Rate Histogram



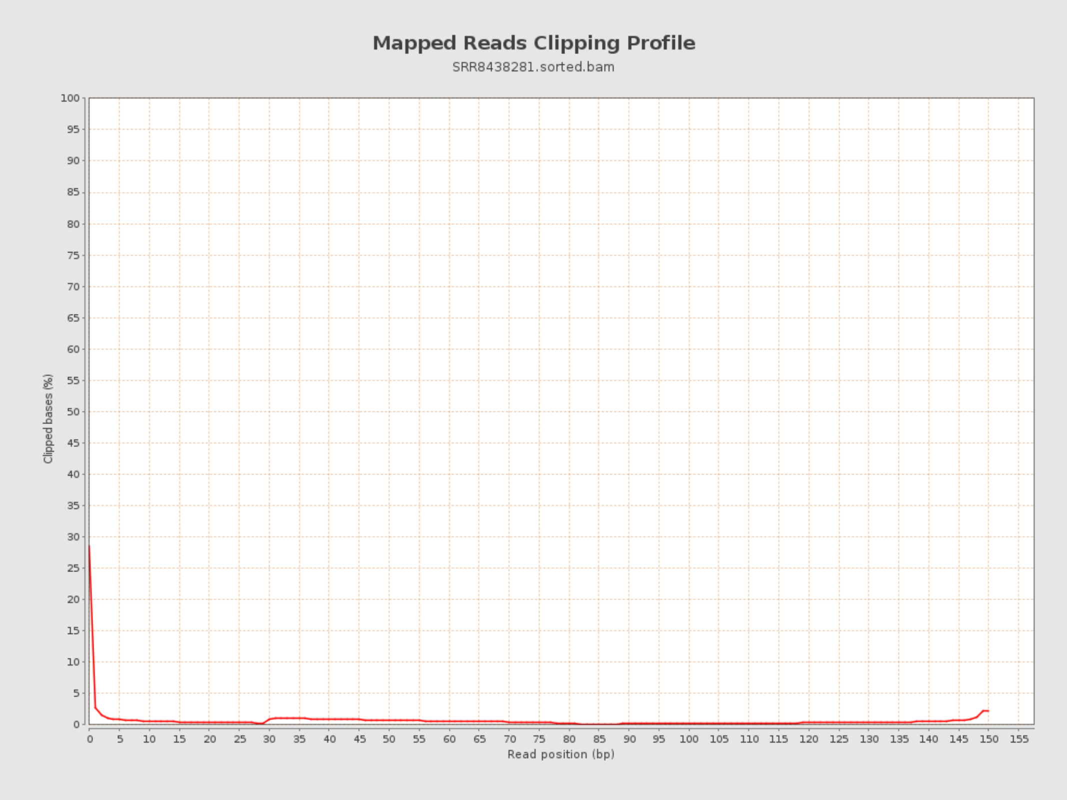
8. Results : Mapped Reads Nucleotide Content



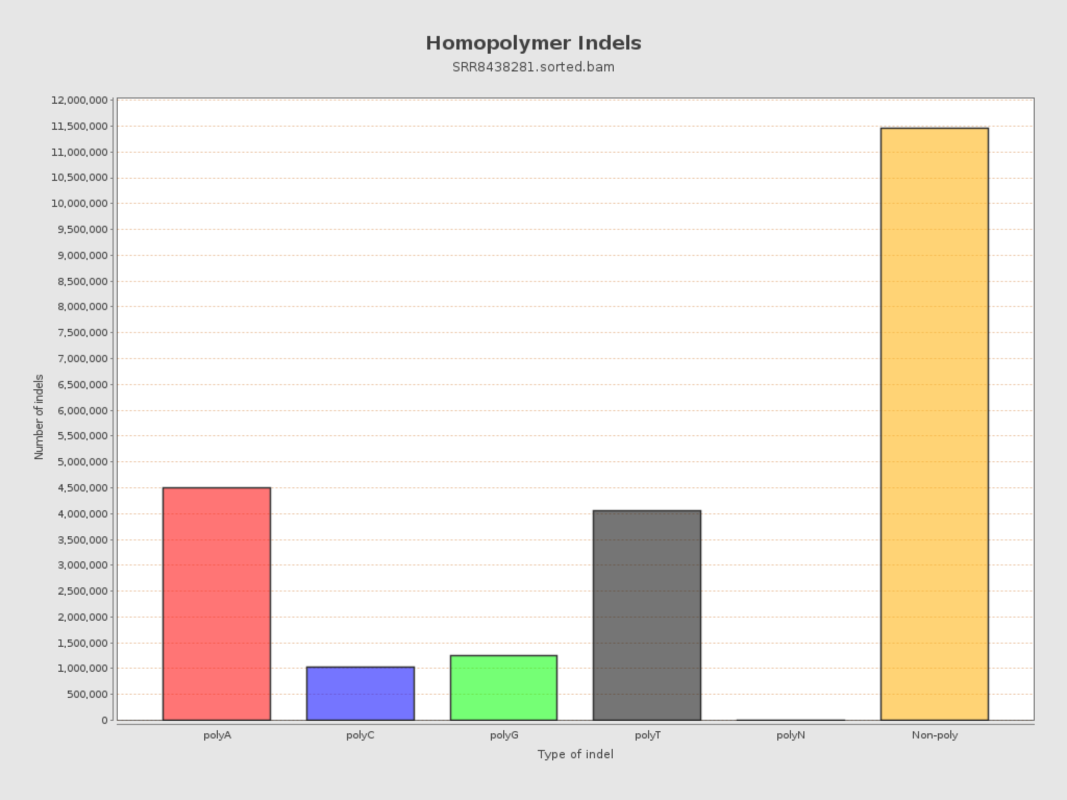
9. Results : Mapped Reads GC-content Distribution



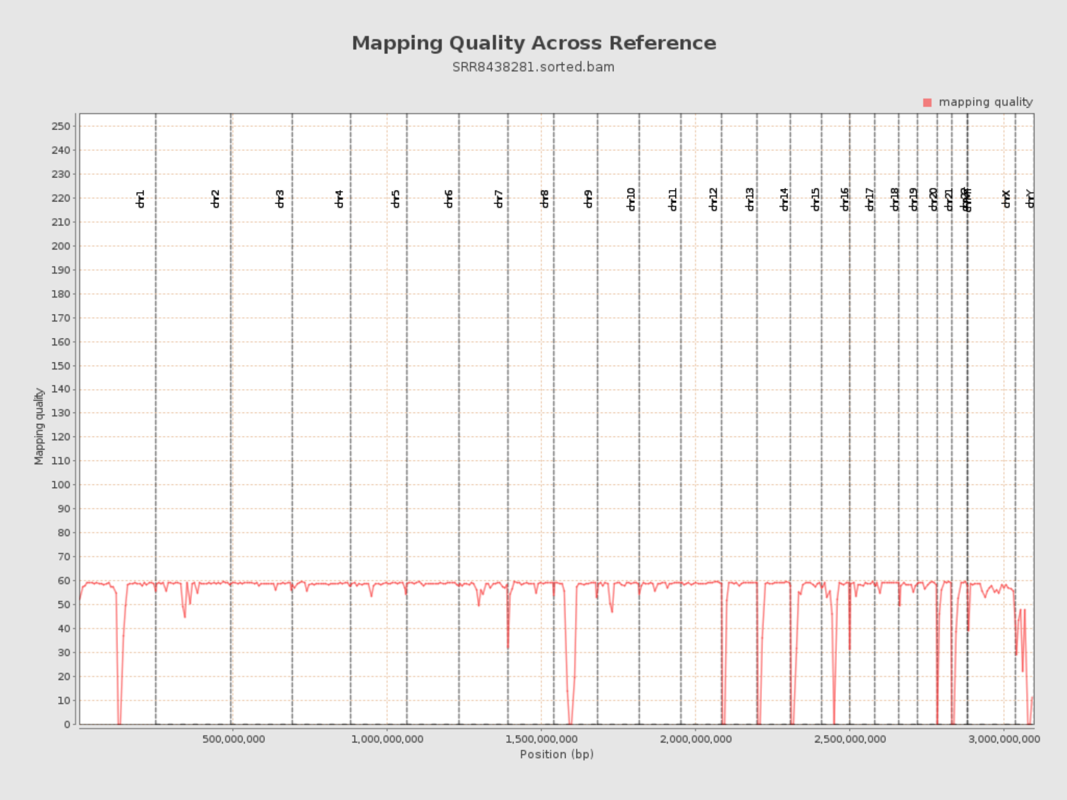
10. Results : Mapped Reads Clipping Profile



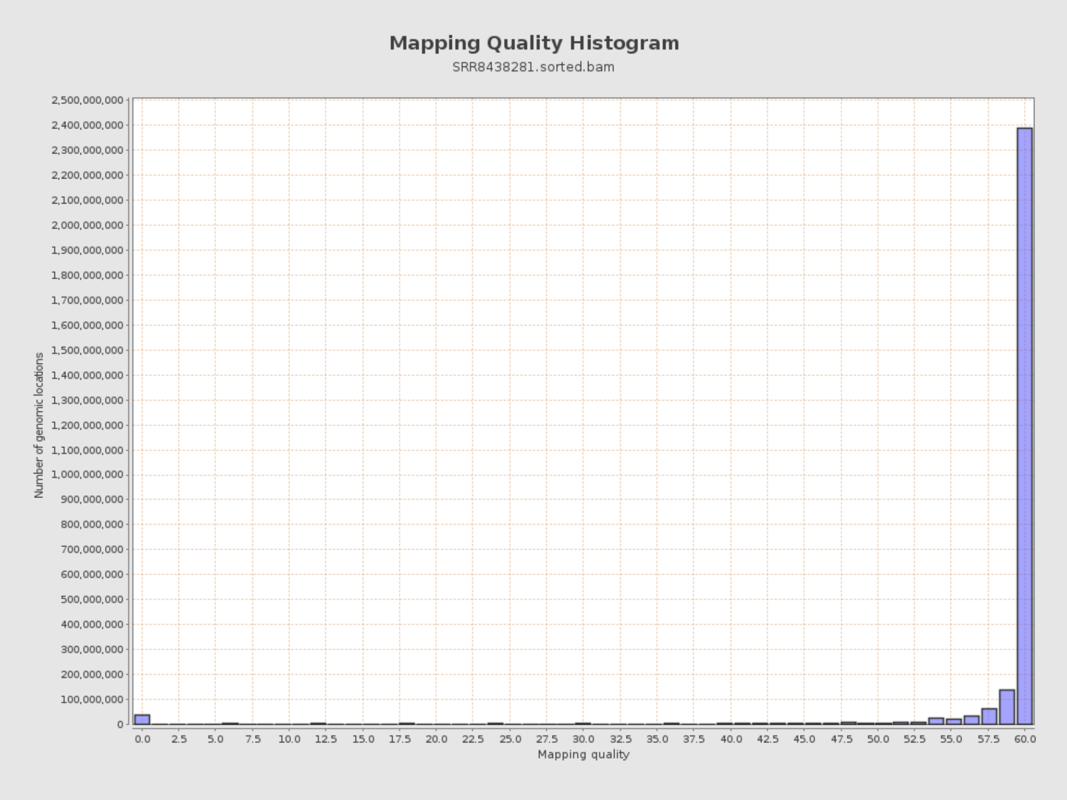
11. Results : Homopolymer Indels



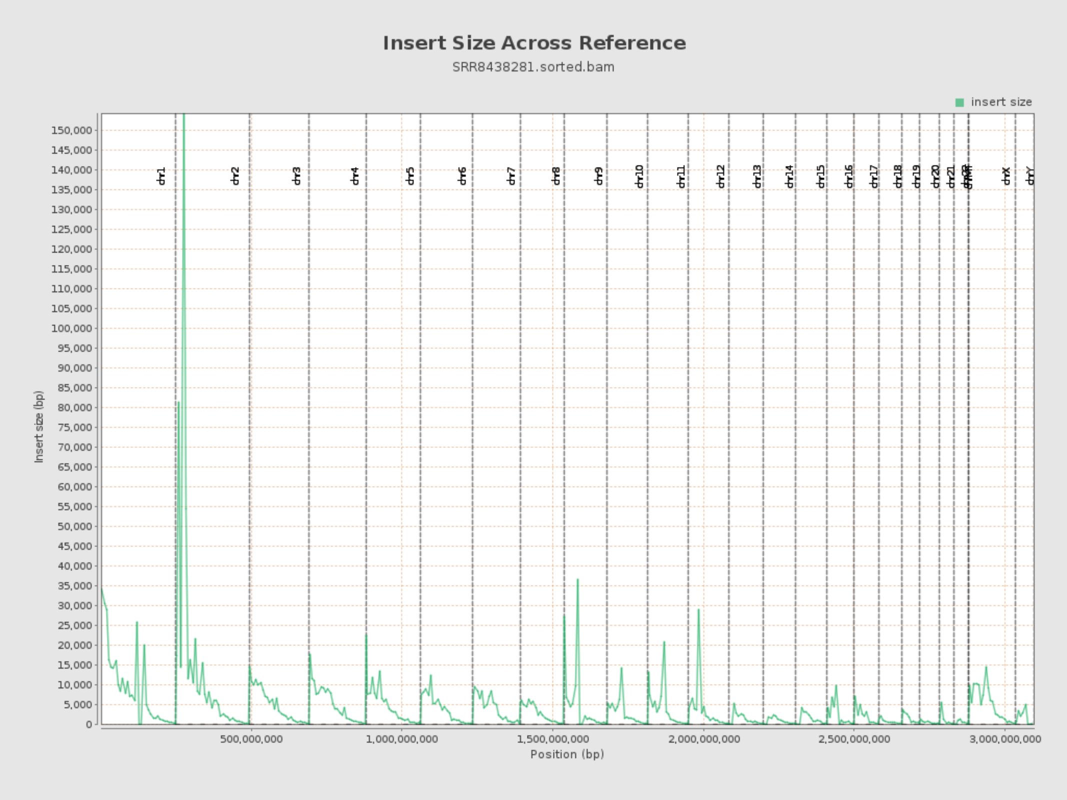
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram