Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 07:25:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779313.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_SRR1779313 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779313_1.fastq.gz SRR1779313_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 07:25:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779313.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,105,644
Mapped reads	15,862,535 / 92.73%
Unmapped reads	1,243,109 / 7.27%
Mapped paired reads	15,862,535 / 92.73%
Mapped reads, first in pair	8,014,817 / 46.85%
Mapped reads, second in pair	7,847,718 / 45.88%
Mapped reads, both in pair	15,662,502 / 91.56%
Mapped reads, singletons	200,033 / 1.17%
Secondary alignments	0
Supplementary alignments	41,764 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	361,638 / 2.11%
Duplication rate	2.09%
Clipped reads	494,511 / 2.89%

2.2. ACGT Content

Number/percentage of A's	388,999,053 / 30.81%
Number/percentage of C's	240,404,019 / 19.04%
Number/percentage of T's	388,083,099 / 30.74%
Number/percentage of G's	244,673,055 / 19.38%
Number/percentage of N's	337,148 / 0.03%

GC Percentage	38.42%

2.3. Coverage

Mean	0.4079
Standard Deviation	1.308

2.4. Mapping Quality

Mean Mapping Quality	53.09

2.5. Insert size

Mean	41,569.79
Standard Deviation	1,945,756.42
P25/Median/P75	164 / 218 / 292

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	4,404,981
Insertions	91,134
Mapped reads with at least one insertion	0.57%
Deletions	116,131
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.82%

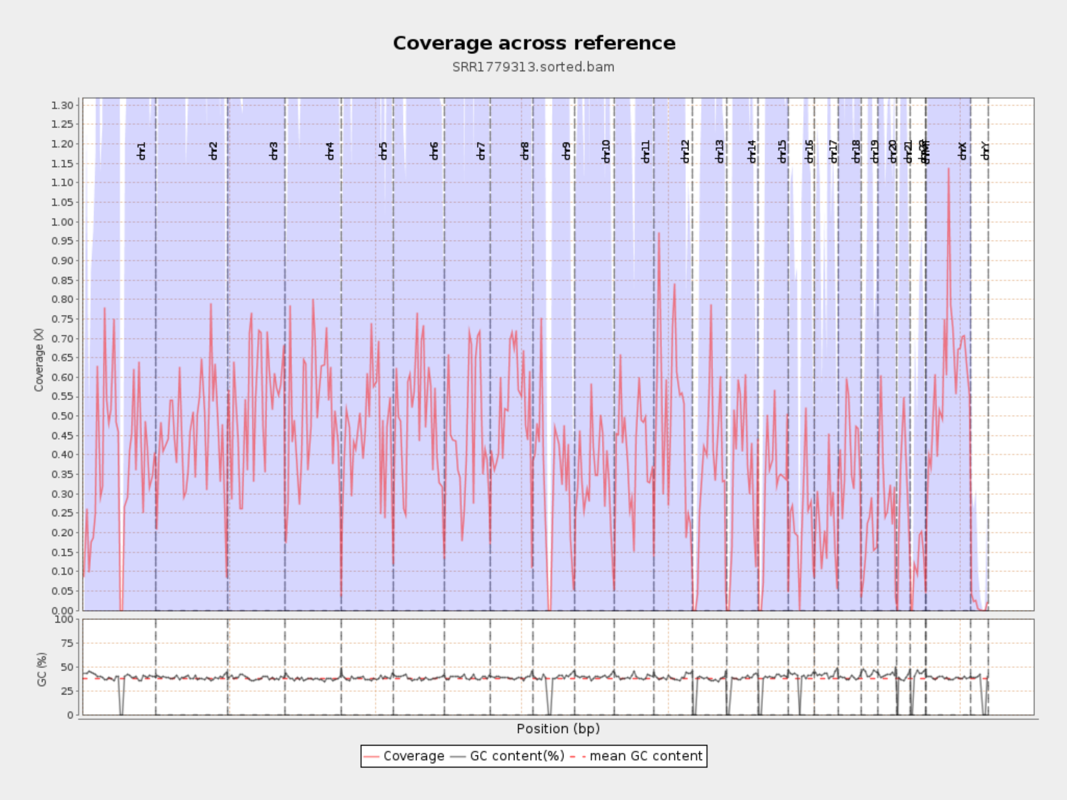
2.7. Chromosome stats

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

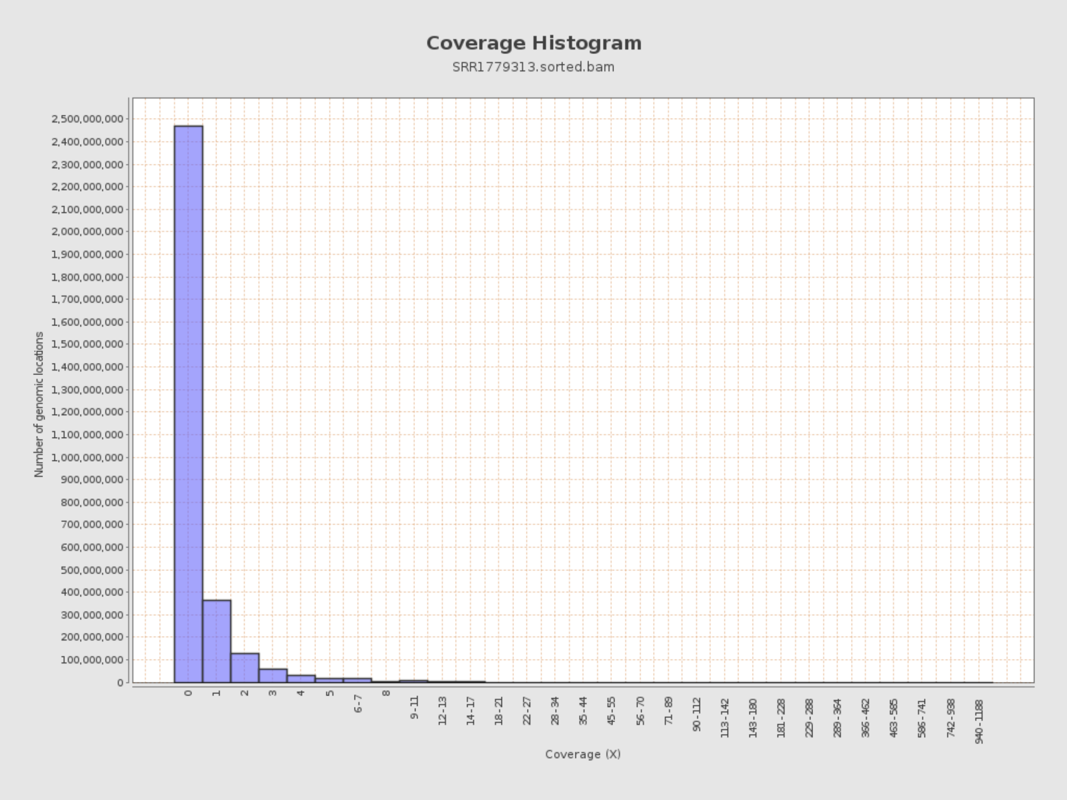
		bases	coverage	deviation
chr1	249250621	93579847	0.3754	1.4104
chr2	243199373	109772028	0.4514	1.2667
chr3	198022430	105385376	0.5322	1.4599
chr4	191154276	97082233	0.5079	1.3388
chr5	180915260	81670178	0.4514	1.3464
chr6	171115067	85219414	0.498	1.3339
chr7	159138663	71404693	0.4487	1.3187
chr8	146364022	75936299	0.5188	1.3461
chr9	141213431	47486430	0.3363	1.1167
chr10	135534747	47231370	0.3485	2.0436
chr11	135006516	55354677	0.41	1.1917
chr12	133851895	67064392	0.501	1.4481
chr13	115169878	41033016	0.3563	1.0296
chr14	107349540	36775549	0.3426	1.1496
chr15	102531392	31888306	0.311	1.0998
chr16	90354753	20543600	0.2274	0.8035
chr17	81195210	18078168	0.2227	0.8653
chr18	78077248	31748862	0.4066	1.2106
chr19	59128983	10520519	0.1779	0.9523
chr20	63025520	20523090	0.3256	1.0468
chr21	48129895	14225744	0.2956	0.9095
chr22	51304566	5941173	0.1158	0.5233
chrMT	16571	952	0.0574	0.2554
chrX	155270560	93439742	0.6018	1.6321

chrY	59373566	828762	0.014	0.1857

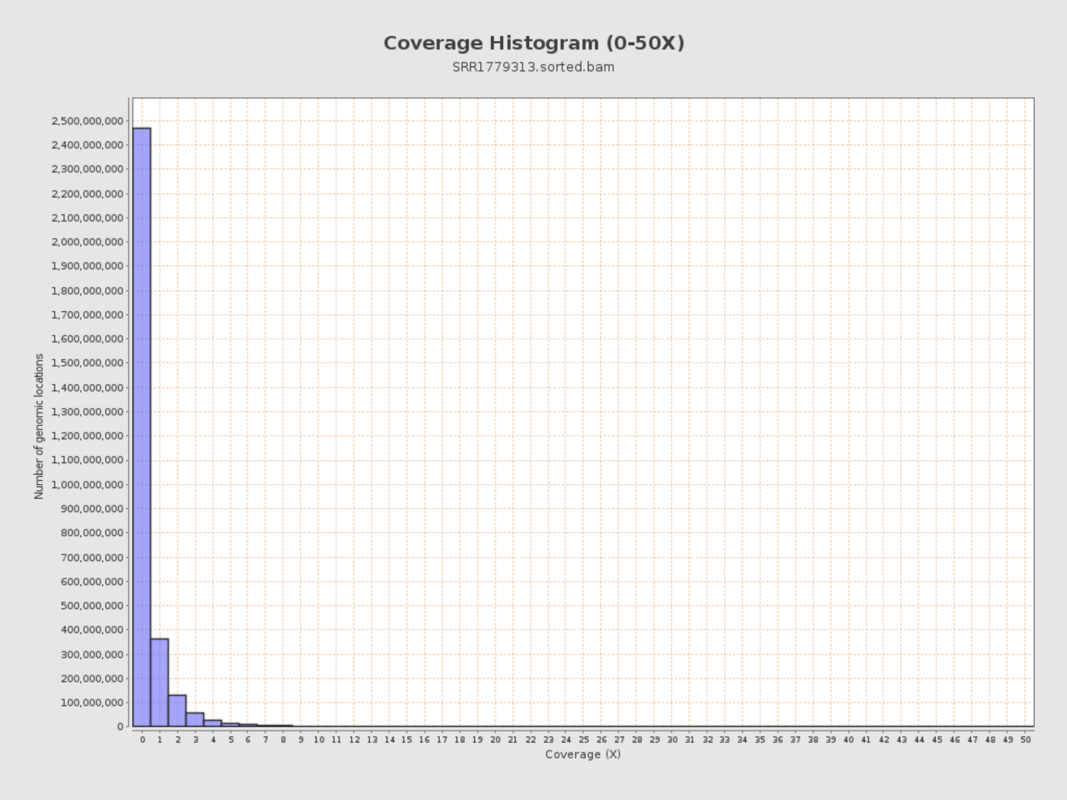
3. Results : Coverage across reference



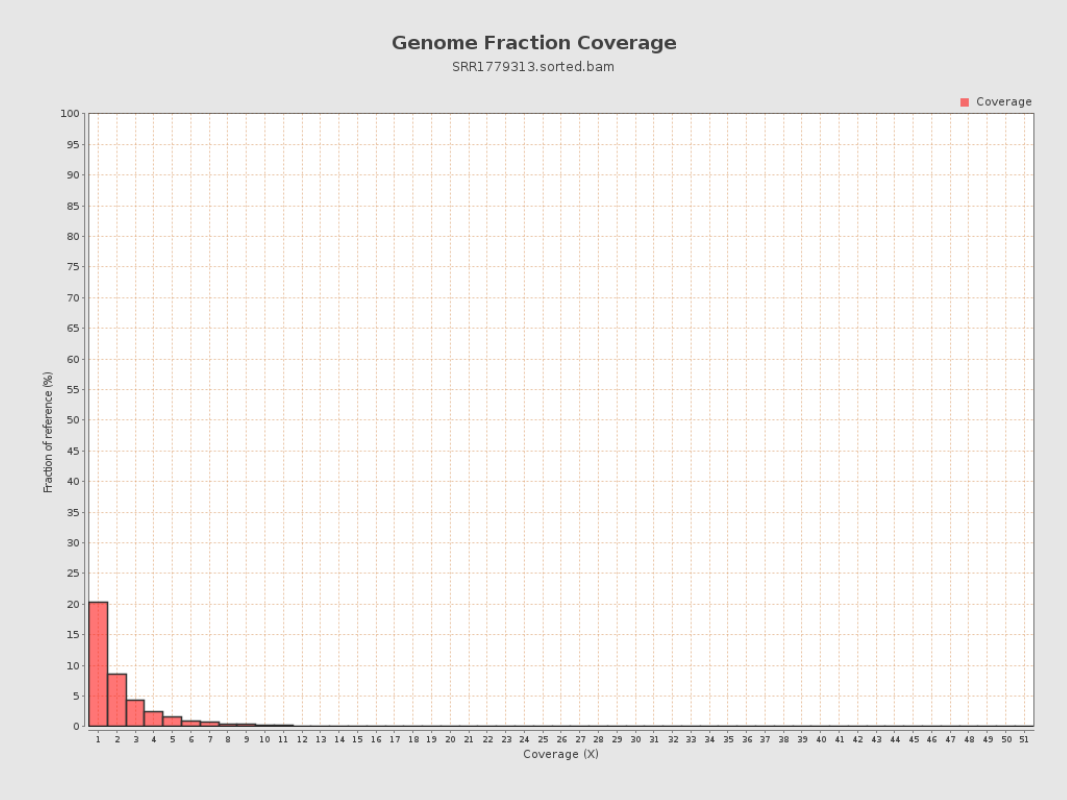
4. Results : Coverage Histogram



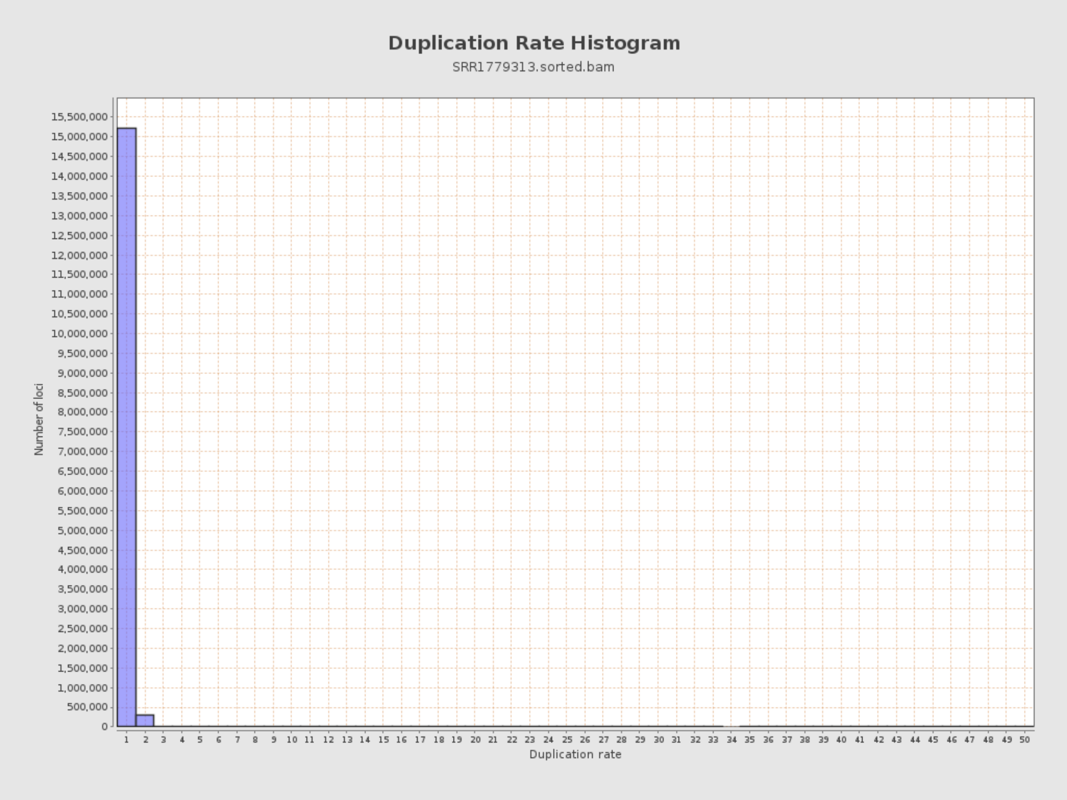
5. Results : Coverage Histogram (0-50X)



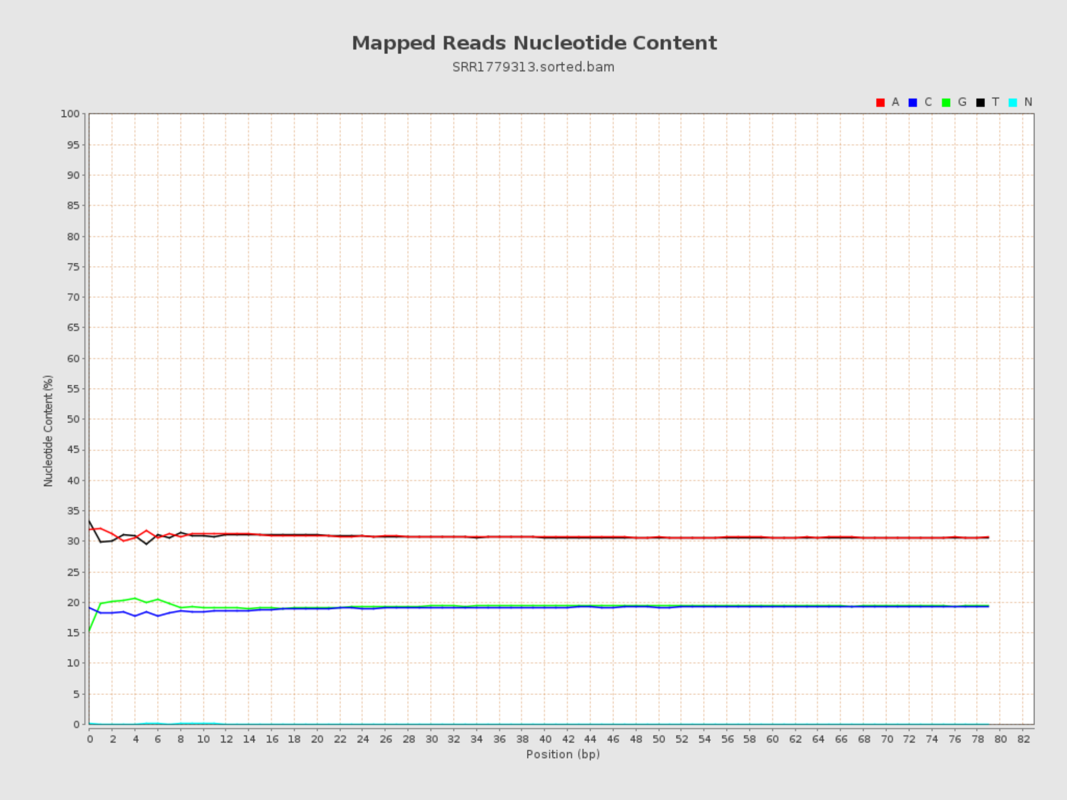
6. Results : Genome Fraction Coverage



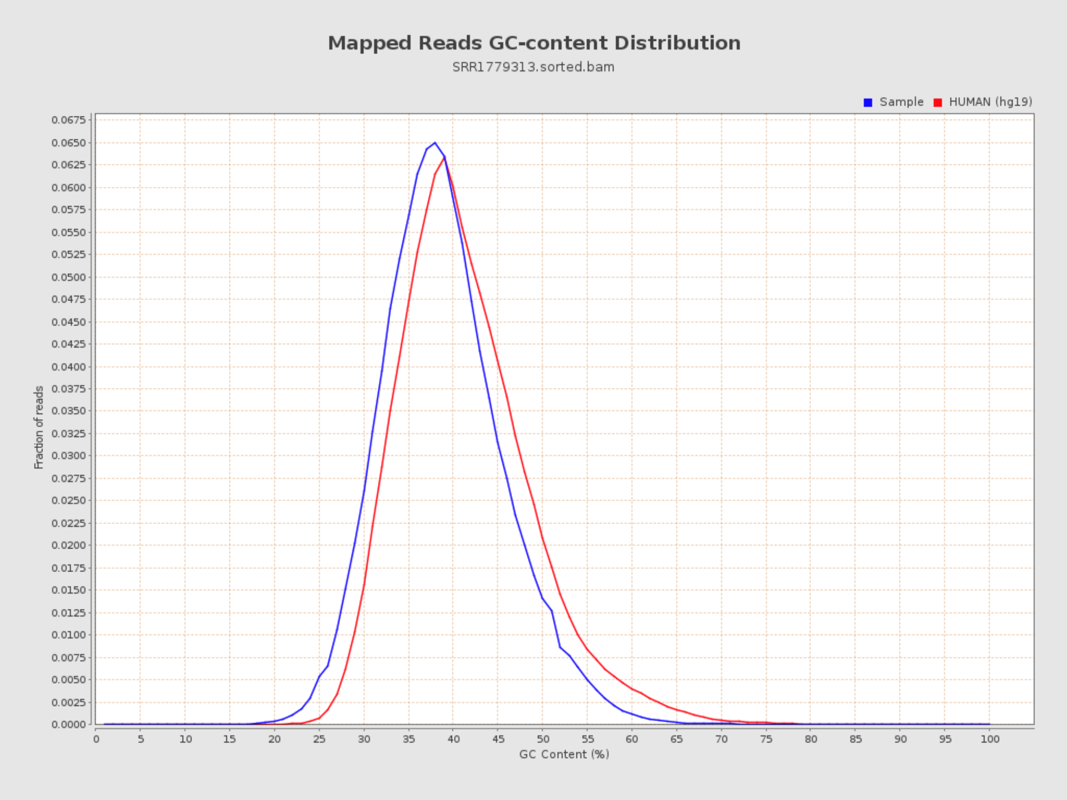
7. Results : Duplication Rate Histogram



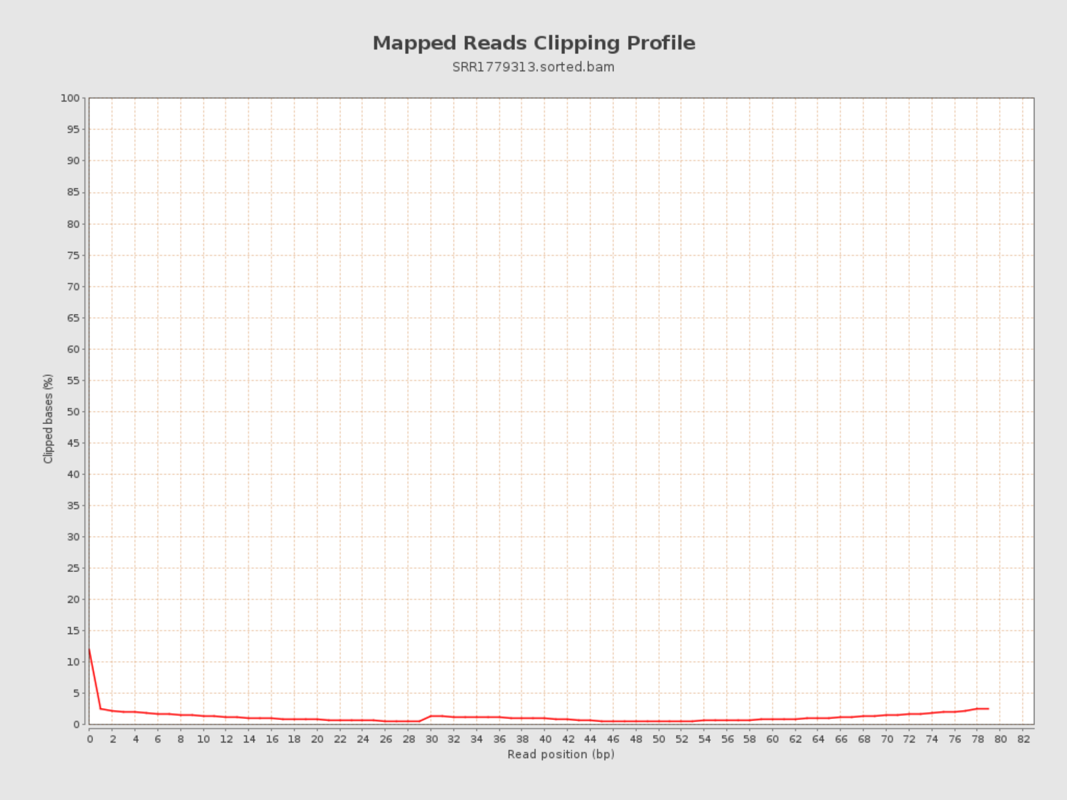
8. Results : Mapped Reads Nucleotide Content



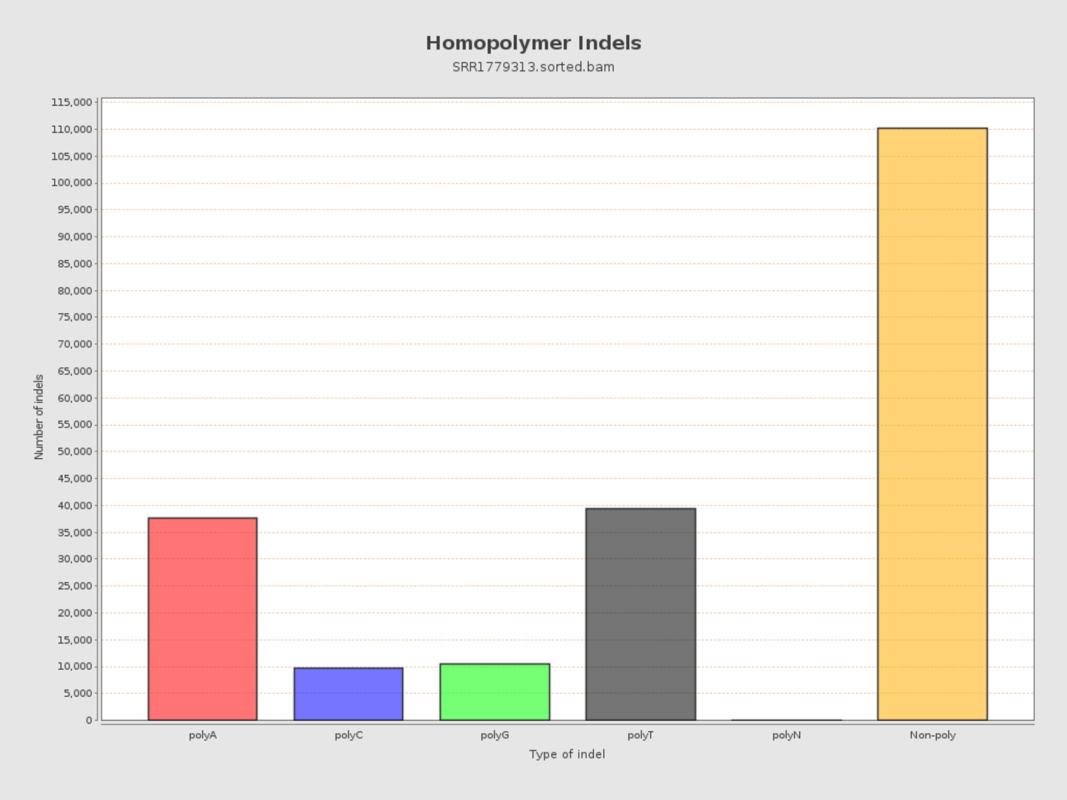
9. Results : Mapped Reads GC-content Distribution



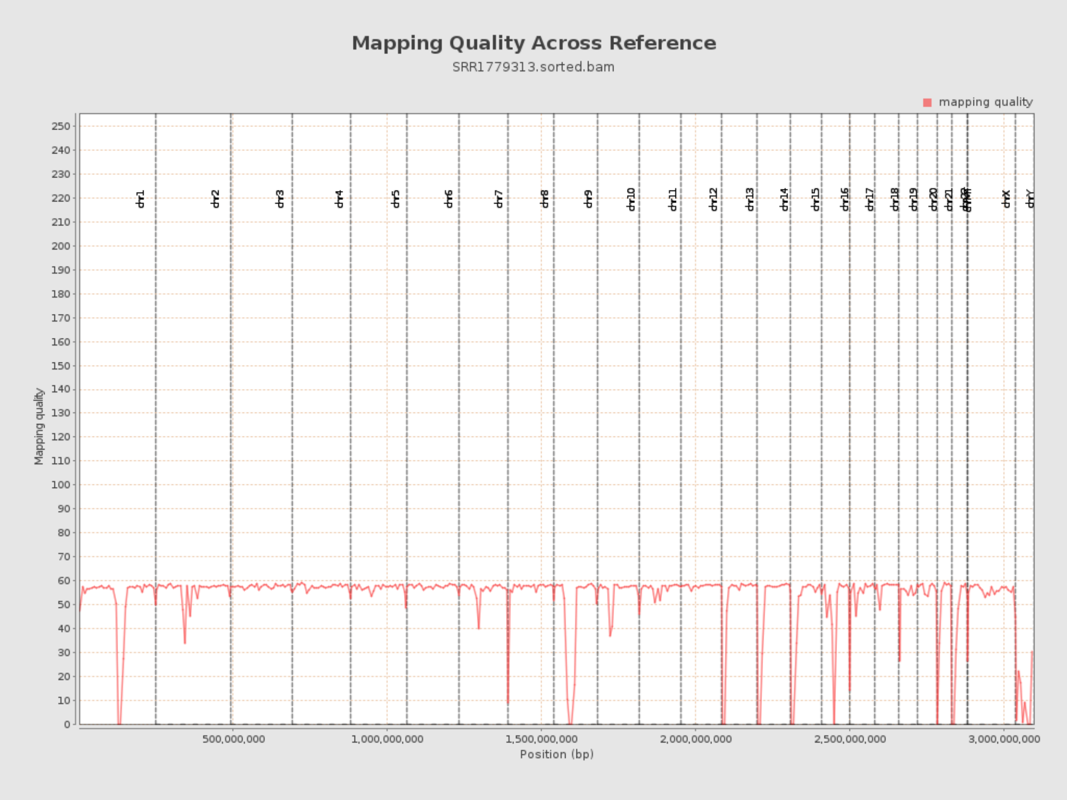
10. Results : Mapped Reads Clipping Profile



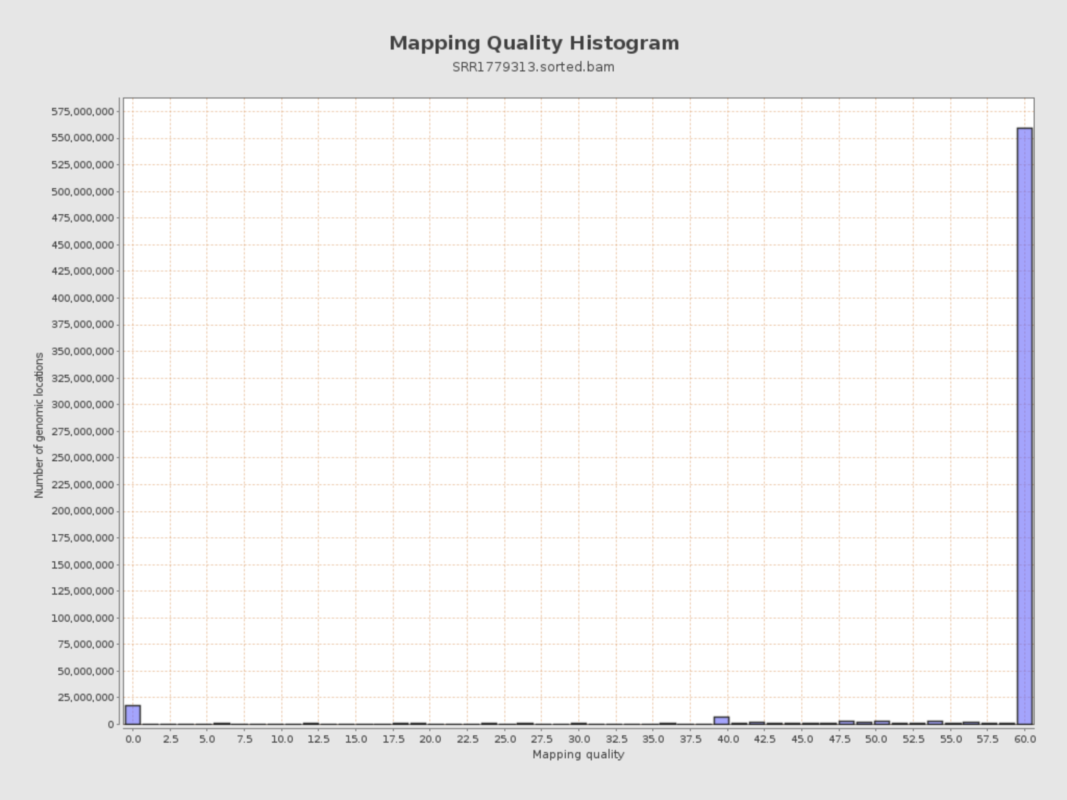
11. Results : Homopolymer Indels



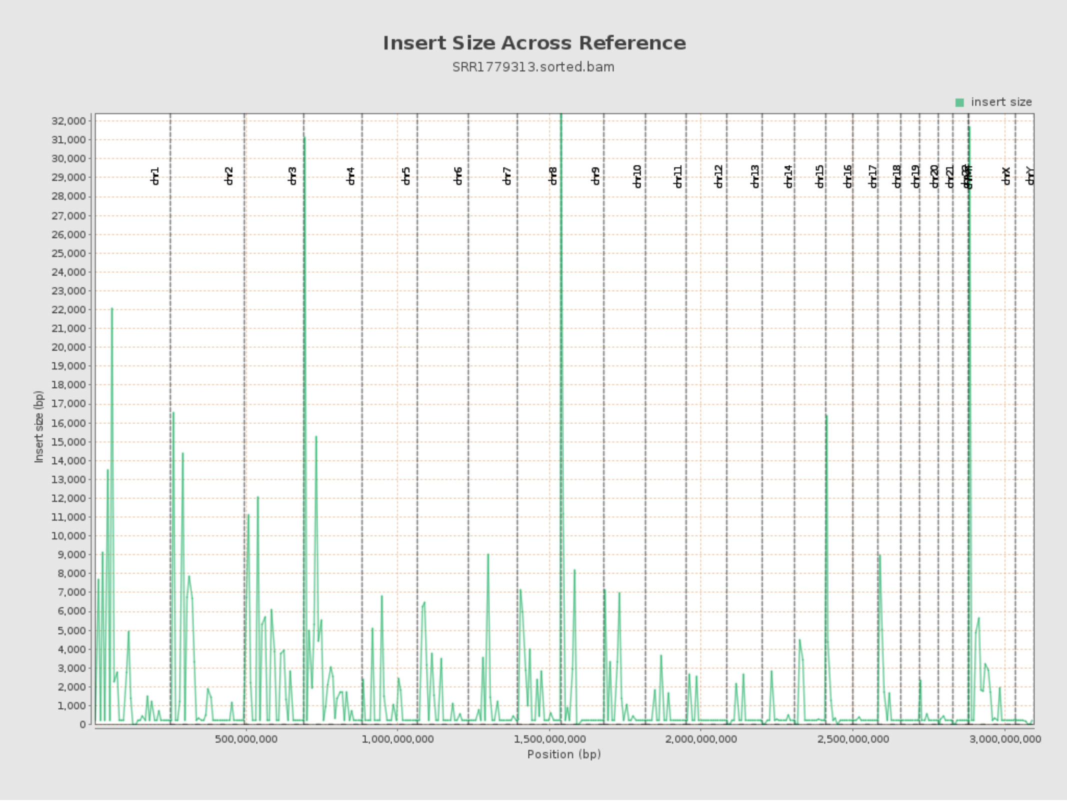
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram