Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 08:07:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779315.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_SRR1779315 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779315_1.fastq.gz SRR1779315_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 08:07:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779315.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,966,424
Mapped reads	15,108,303 / 94.63%
Unmapped reads	858,121 / 5.37%
Mapped paired reads	15,108,303 / 94.63%
Mapped reads, first in pair	7,665,626 / 48.01%
Mapped reads, second in pair	7,442,677 / 46.61%
Mapped reads, both in pair	14,859,602 / 93.07%
Mapped reads, singletons	248,701 / 1.56%
Secondary alignments	0
Supplementary alignments	36,918 / 0.23%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	465,002 / 2.91%
Duplication rate	2.88%
Clipped reads	477,774 / 2.99%

2.2. ACGT Content

Number/percentage of A's	369,714,439 / 30.75%
Number/percentage of C's	229,455,310 / 19.08%
Number/percentage of T's	369,682,087 / 30.75%
Number/percentage of G's	233,155,187 / 19.39%
Number/percentage of N's	312,703 / 0.03%

GC Percentage	38.48%

2.3. Coverage

Mean	0.3885
Standard Deviation	1.4292

2.4. Mapping Quality

Mean Mapping Quality	53.12

2.5. Insert size

Mean	41,797.28
Standard Deviation	1,935,108.5
P25/Median/P75	180 / 235 / 312

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	4,462,568
Insertions	87,915
Mapped reads with at least one insertion	0.58%
Deletions	112,185
Mapped reads with at least one deletion	0.73%
Homopolymer indels	47.14%

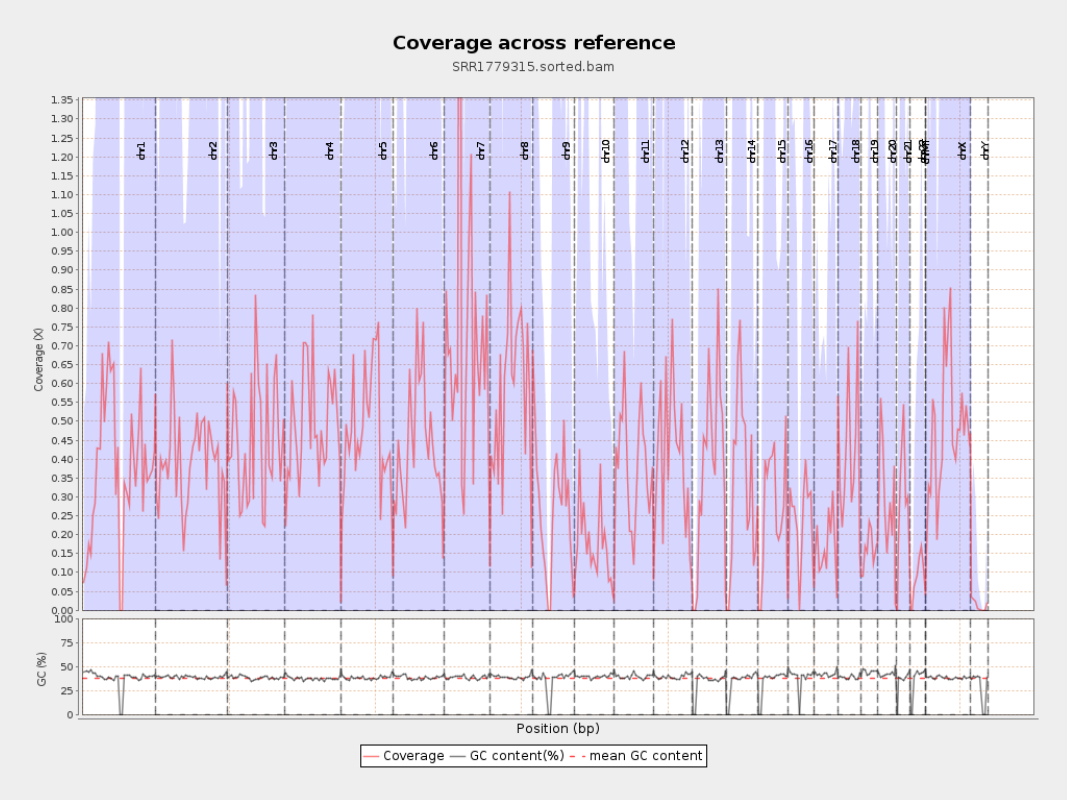
2.7. Chromosome stats

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

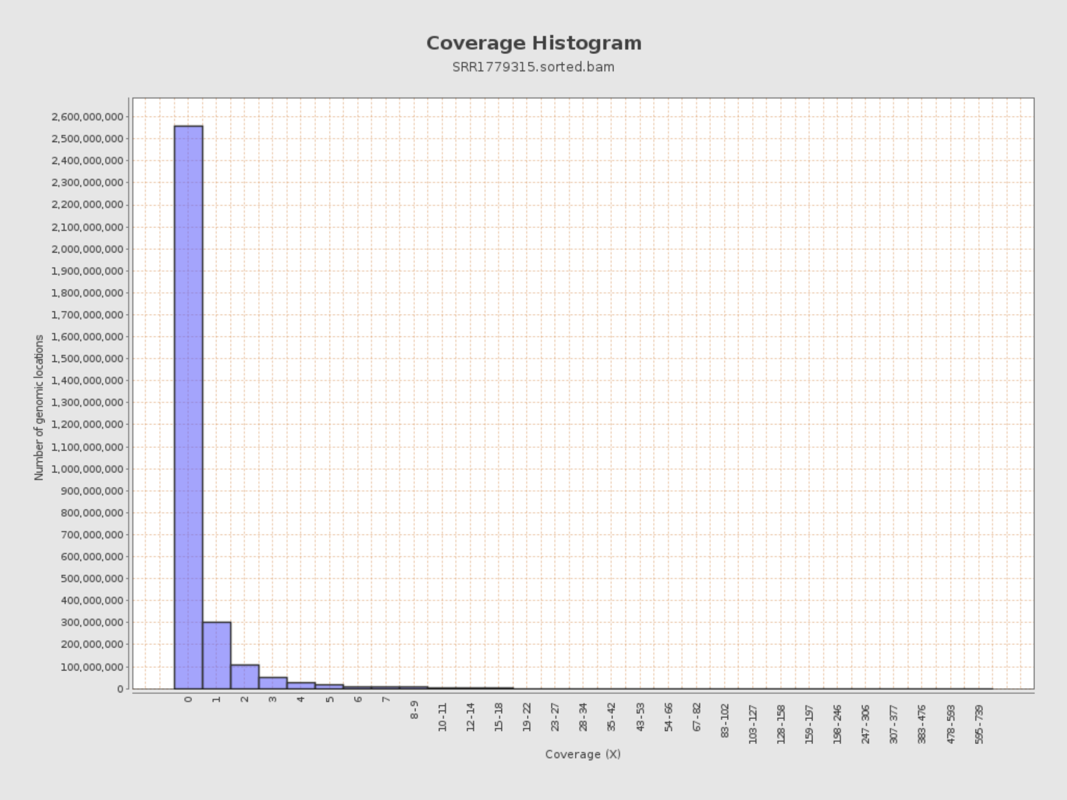
		bases	coverage	deviation
chr1	249250621	93085999	0.3735	1.434
chr2	243199373	93918261	0.3862	1.2934
chr3	198022430	89249192	0.4507	1.3944
chr4	191154276	95041011	0.4972	1.4818
chr5	180915260	84861535	0.4691	1.4817
chr6	171115067	75741089	0.4426	1.3193
chr7	159138663	118096443	0.7421	2.9191
chr8	146364022	85826804	0.5864	1.6123
chr9	141213431	36941651	0.2616	0.9491
chr10	135534747	24138467	0.1781	1.0079
chr11	135006516	51417047	0.3808	1.4003
chr12	133851895	54791629	0.4093	1.477
chr13	115169878	44390518	0.3854	1.2777
chr14	107349540	36390522	0.339	1.231
chr15	102531392	27548899	0.2687	1.0309
chr16	90354753	20817405	0.2304	0.8969
chr17	81195210	14243133	0.1754	0.7031
chr18	78077248	32513638	0.4164	1.287
chr19	59128983	9626069	0.1628	0.775
chr20	63025520	19419589	0.3081	1.0737
chr21	48129895	13438973	0.2792	1.0194
chr22	51304566	4623925	0.0901	0.5904
chrMT	16571	1082	0.0653	0.3818
chrX	155270560	75638791	0.4871	1.6064

chrY	59373566	791262	0.0133	0.1949

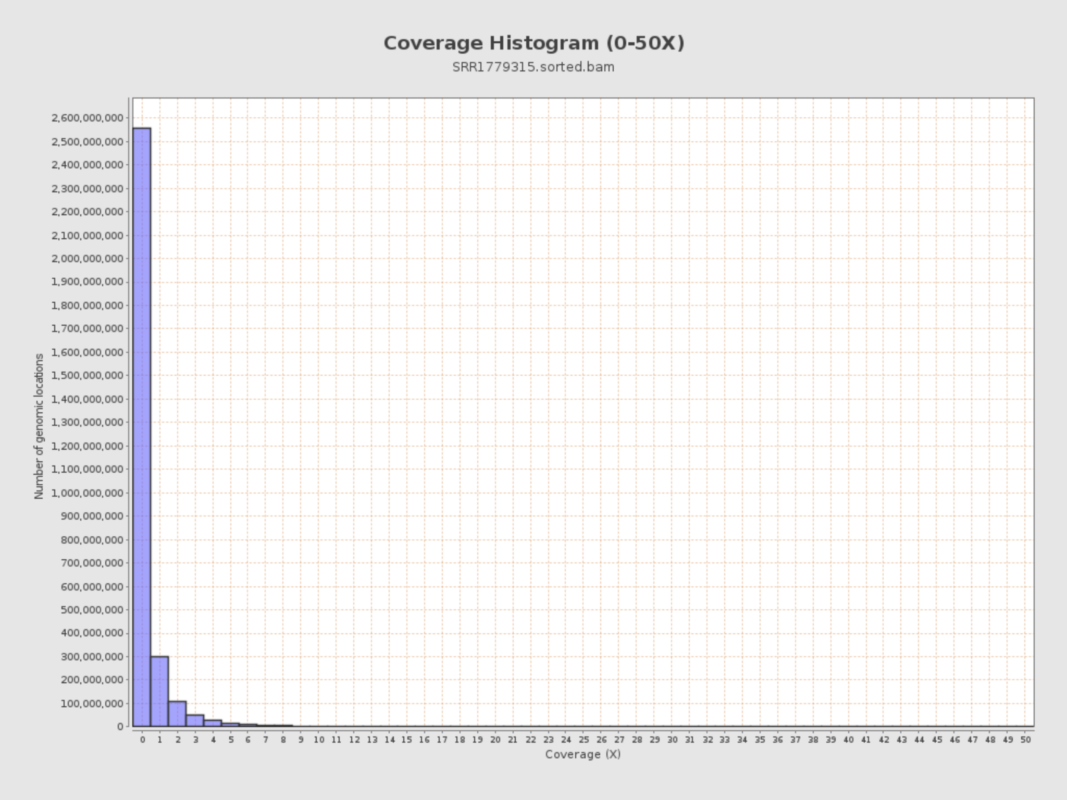
3. Results : Coverage across reference



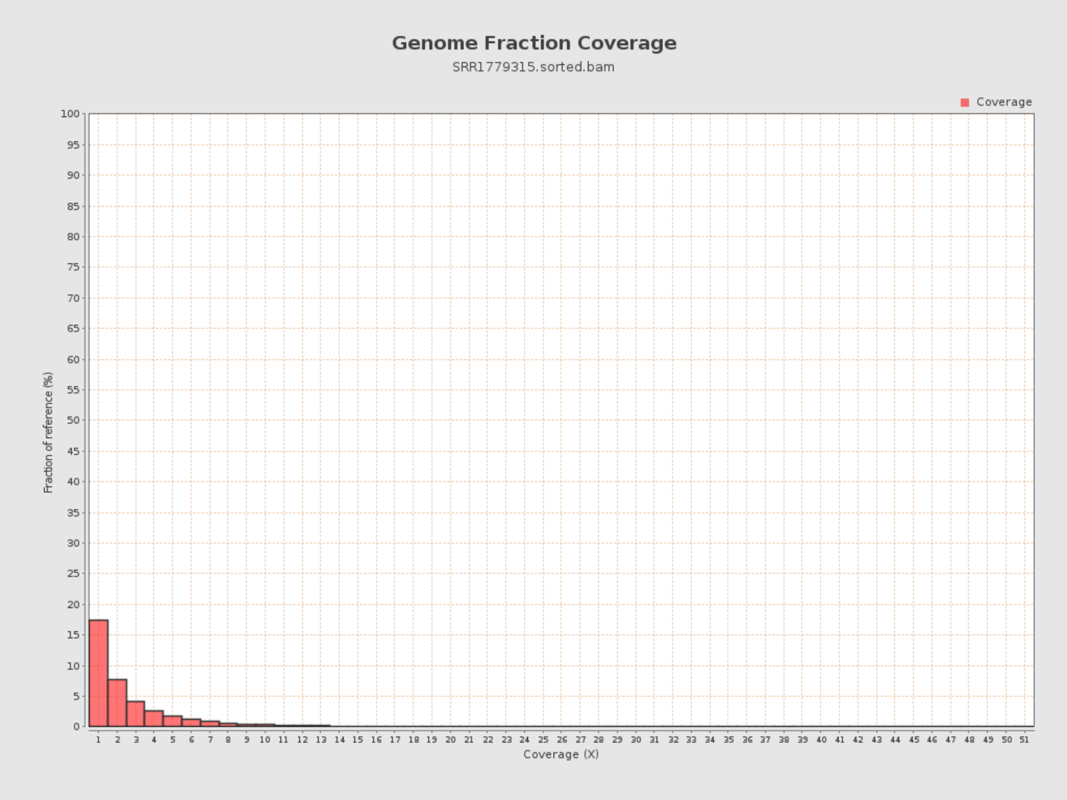
4. Results : Coverage Histogram



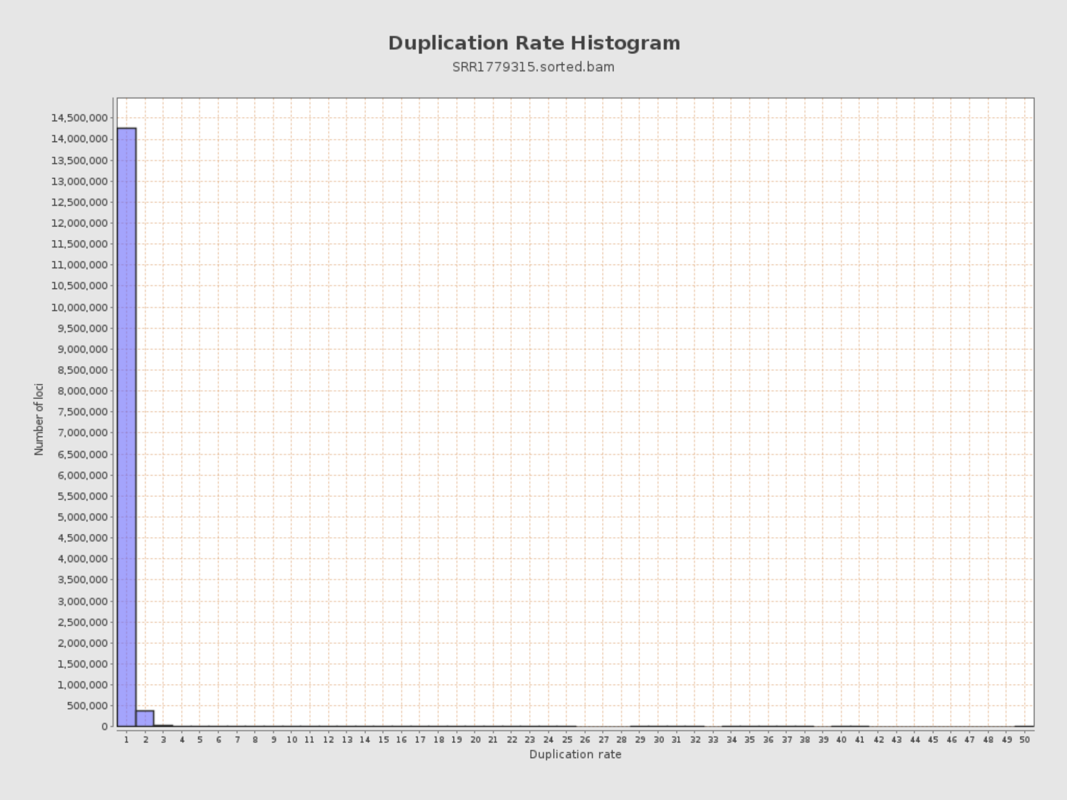
5. Results : Coverage Histogram (0-50X)



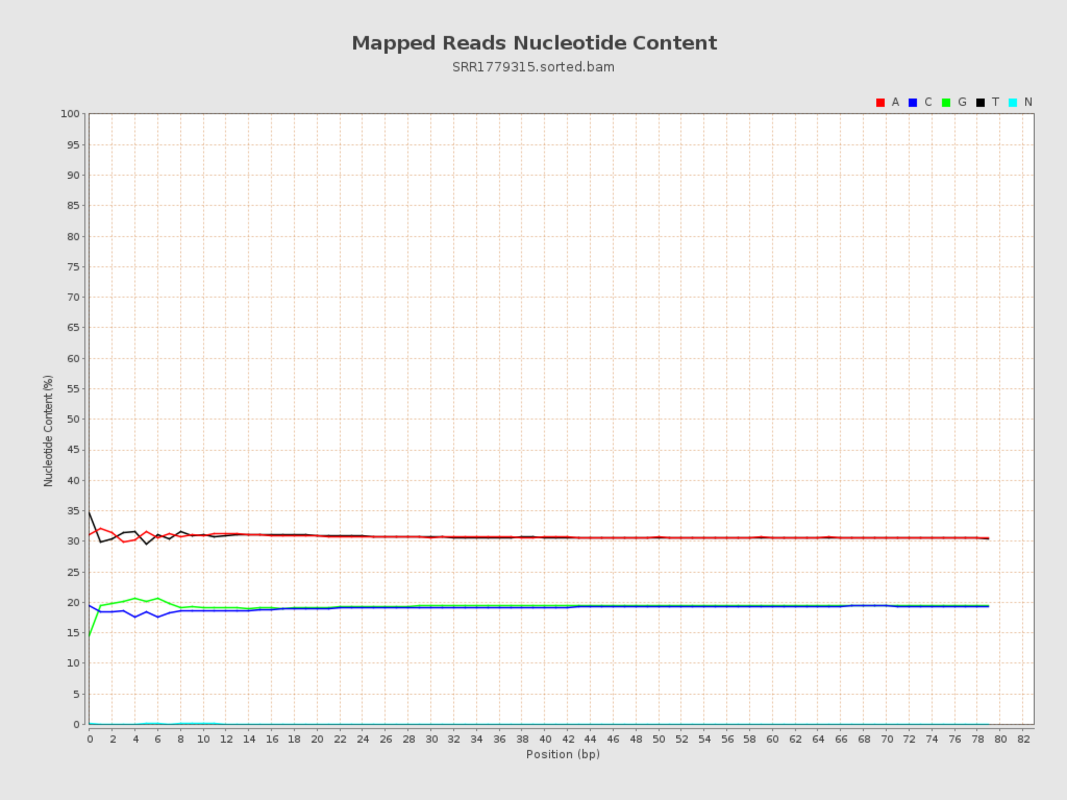
6. Results : Genome Fraction Coverage



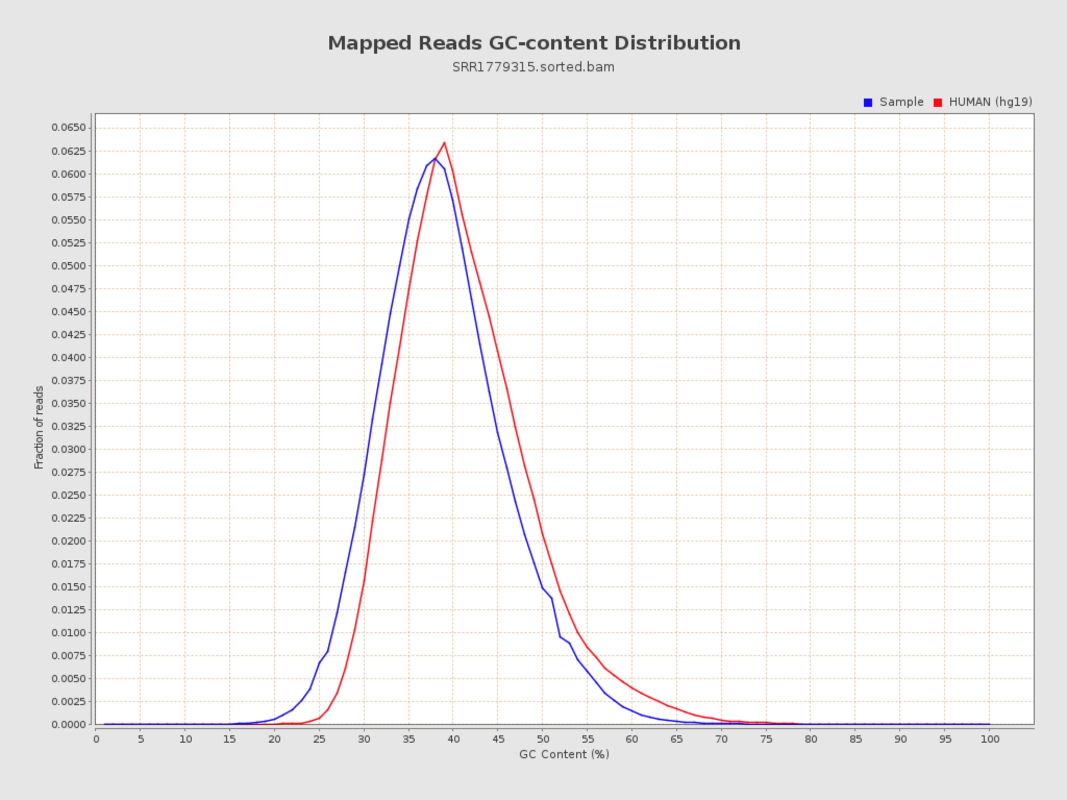
7. Results : Duplication Rate Histogram



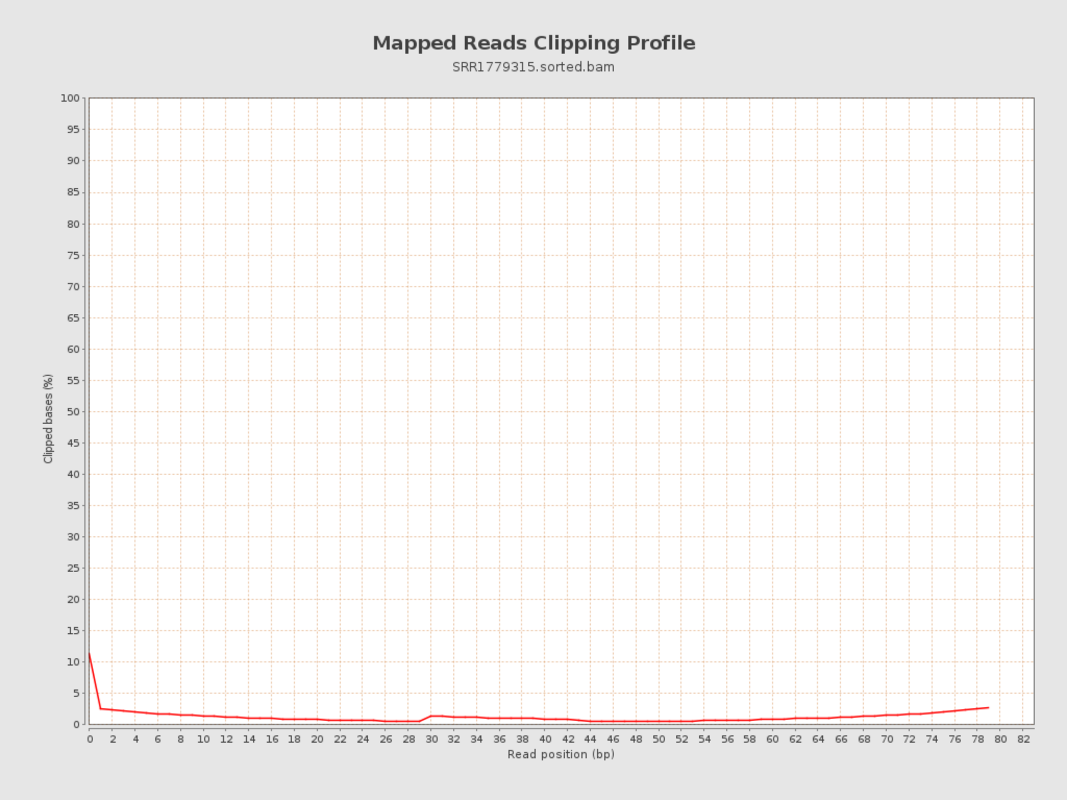
8. Results : Mapped Reads Nucleotide Content



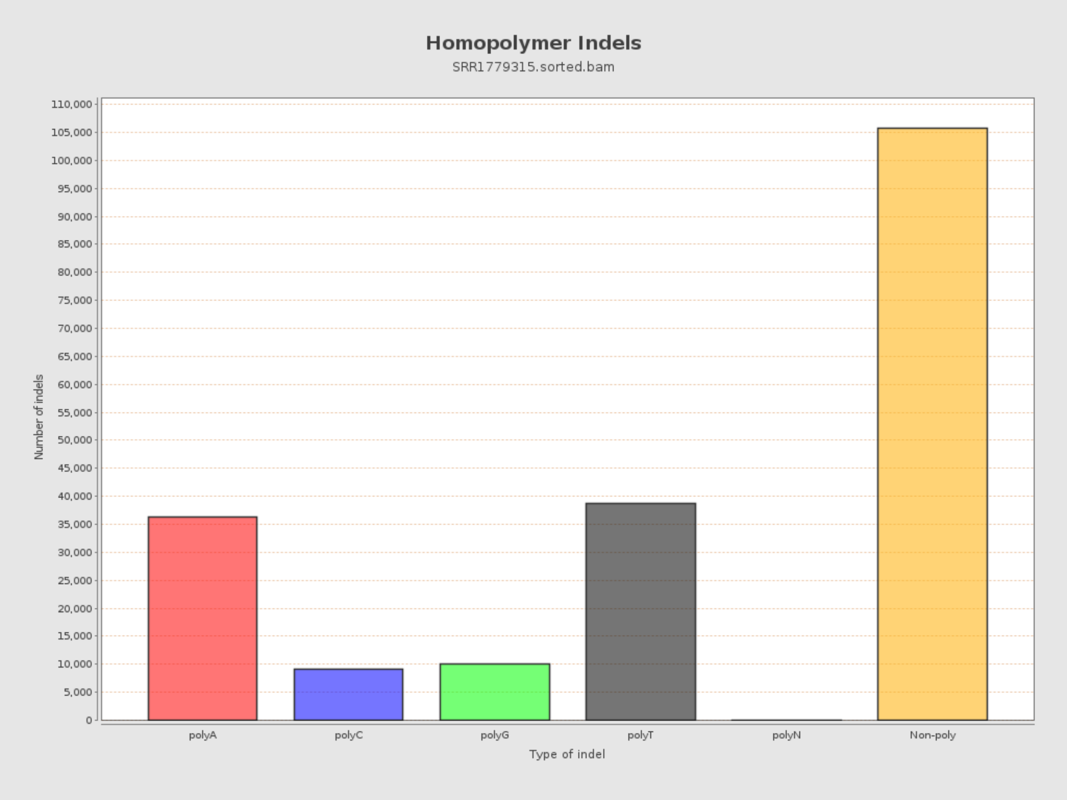
9. Results : Mapped Reads GC-content Distribution



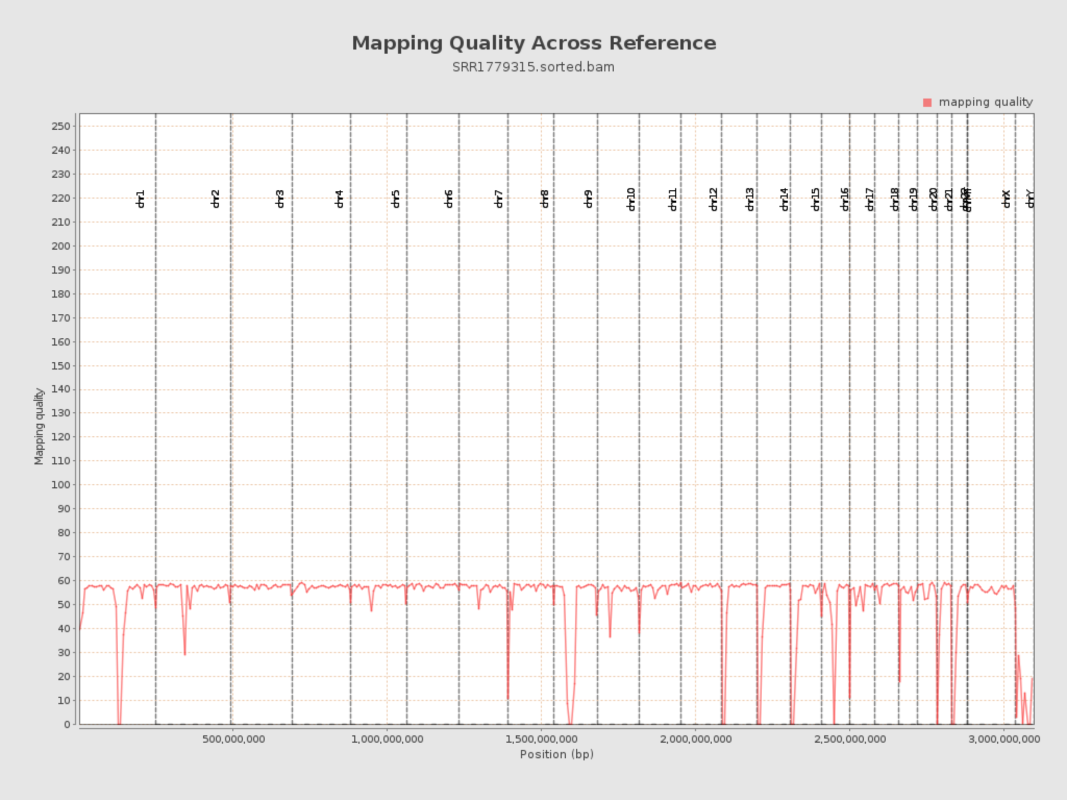
10. Results : Mapped Reads Clipping Profile



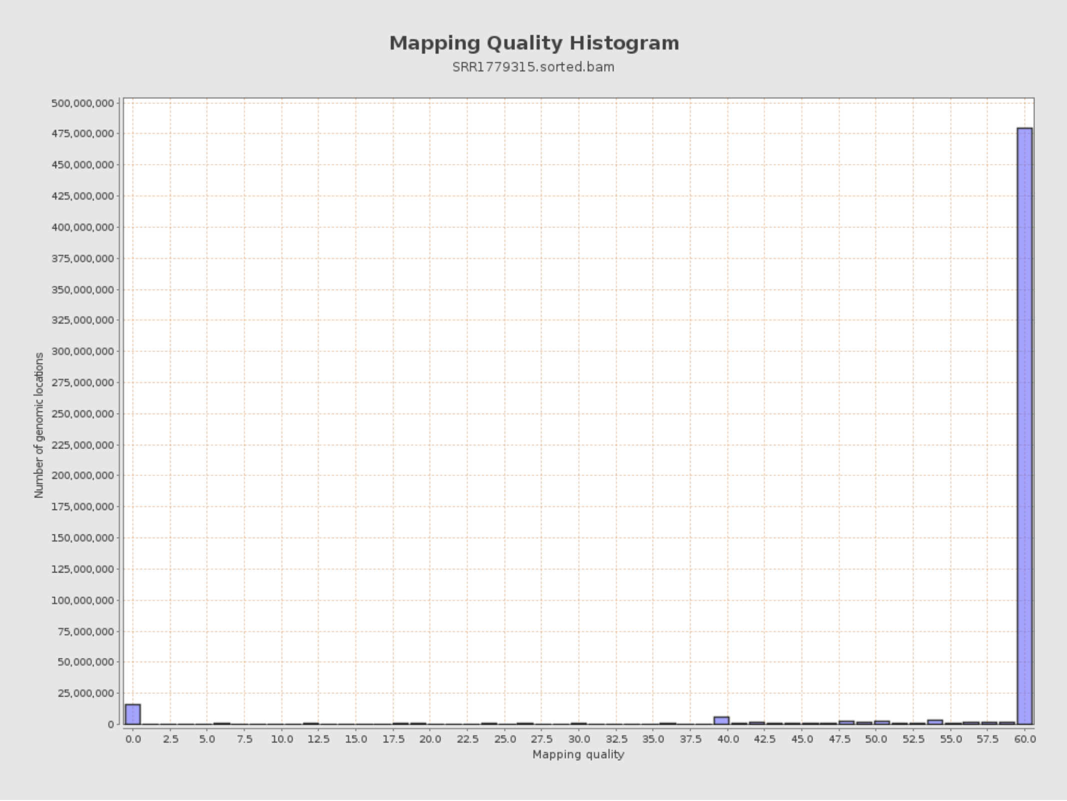
11. Results : Homopolymer Indels



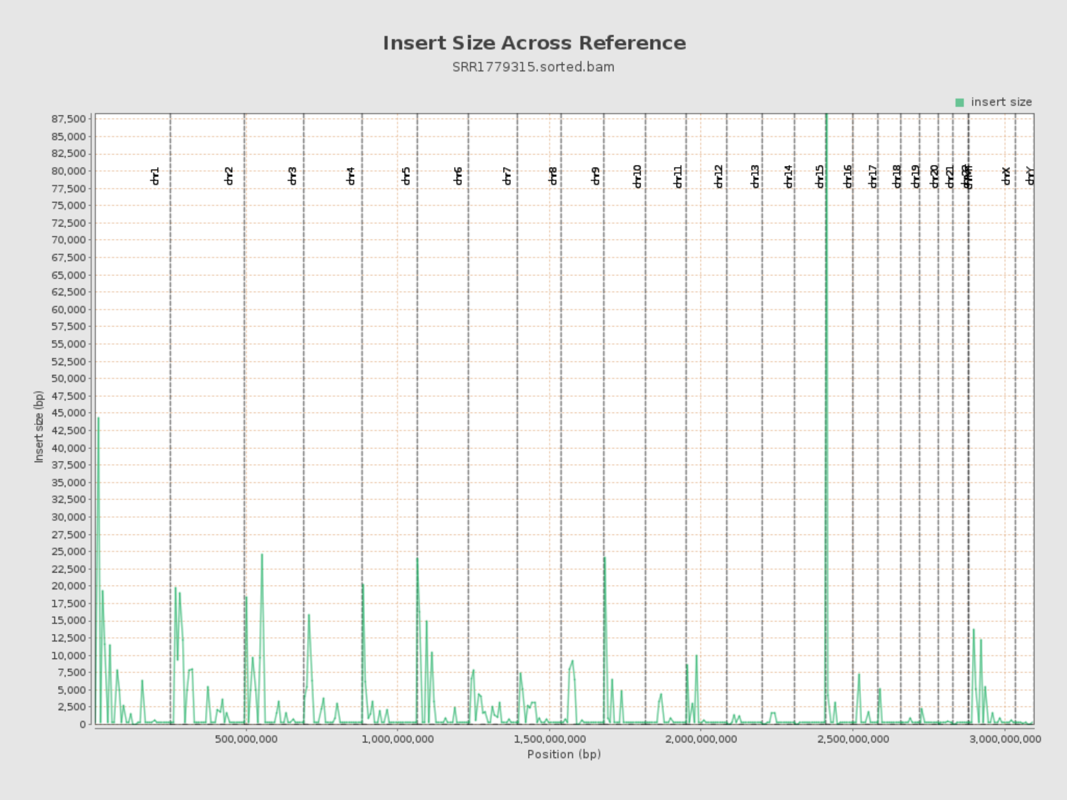
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram