Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 23:46:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779290.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_SRR1779290 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779290_1.fastq.gz SRR1779290_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 23:46:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779290.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,373,412
Mapped reads	14,952,407 / 97.26%
Unmapped reads	421,005 / 2.74%
Mapped paired reads	14,952,407 / 97.26%
Mapped reads, first in pair	7,533,746 / 49.01%
Mapped reads, second in pair	7,418,661 / 48.26%
Mapped reads, both in pair	14,819,390 / 96.4%
Mapped reads, singletons	133,017 / 0.87%
Secondary alignments	0
Supplementary alignments	36,551 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	269,481 / 1.75%
Duplication rate	1.7%
Clipped reads	479,755 / 3.12%

2.2. ACGT Content

Number/percentage of A's	364,401,376 / 30.62%
Number/percentage of C's	229,232,672 / 19.26%
Number/percentage of T's	363,330,927 / 30.53%
Number/percentage of G's	232,921,847 / 19.57%
Number/percentage of N's	224,007 / 0.02%

GC Percentage	38.83%

2.3. Coverage

Mean	0.3845
Standard Deviation	1.1367

2.4. Mapping Quality

Mean Mapping Quality	53.02

2.5. Insert size

Mean	41,740.11
Standard Deviation	1,929,229.19
P25/Median/P75	149 / 196 / 263

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	4,465,282
Insertions	82,456
Mapped reads with at least one insertion	0.55%
Deletions	102,473
Mapped reads with at least one deletion	0.68%
Homopolymer indels	46.99%

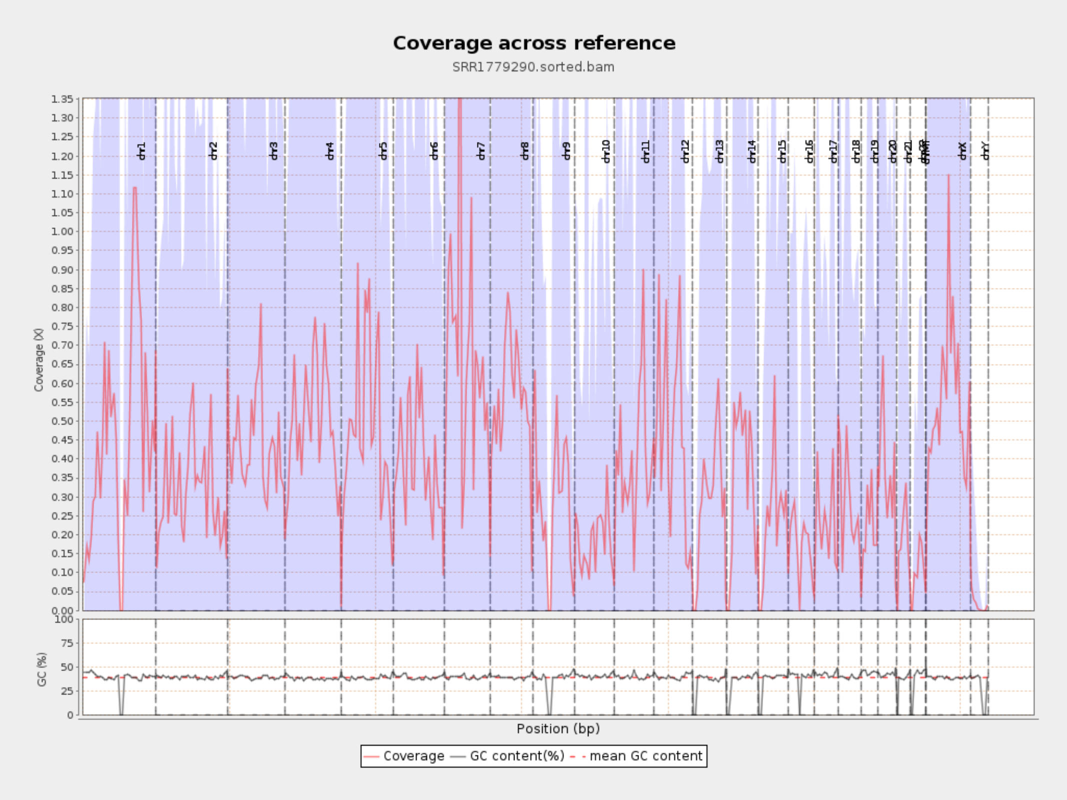
2.7. Chromosome stats

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

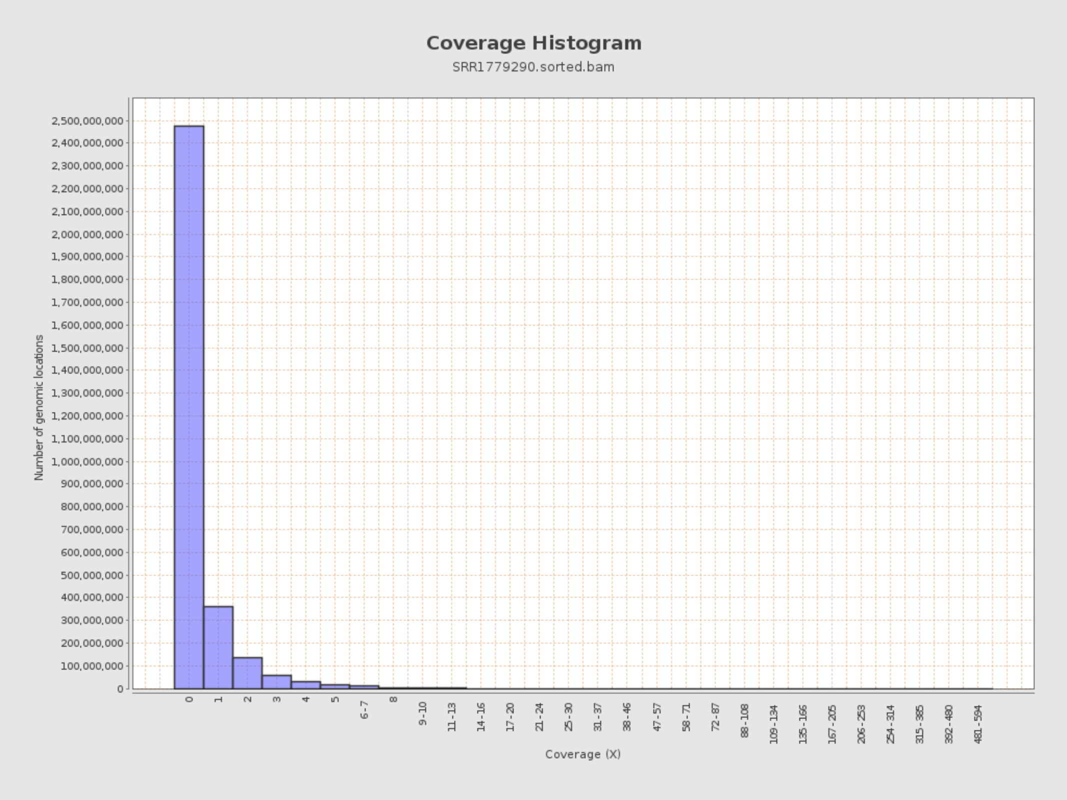
		bases	coverage	deviation
chr1	249250621	112537371	0.4515	1.3016
chr2	243199373	76891453	0.3162	0.9249
chr3	198022430	87089073	0.4398	1.0888
chr4	191154276	96057169	0.5025	1.1723
chr5	180915260	86505028	0.4782	1.1646
chr6	171115067	68126564	0.3981	1.0293
chr7	159138663	110333765	0.6933	2.1095
chr8	146364022	82141564	0.5612	1.2807
chr9	141213431	41257292	0.2922	0.8703
chr10	135534747	25207016	0.186	1.0948
chr11	135006516	54326607	0.4024	1.116
chr12	133851895	59818641	0.4469	1.1718
chr13	115169878	33556406	0.2914	0.8358
chr14	107349540	37977423	0.3538	0.9551
chr15	102531392	24321519	0.2372	0.8555
chr16	90354753	15226247	0.1685	0.6403
chr17	81195210	19144578	0.2358	0.7556
chr18	78077248	22063813	0.2826	0.8234
chr19	59128983	13253097	0.2241	0.8059
chr20	63025520	23987697	0.3806	1.0442
chr21	48129895	8727853	0.1813	0.6514
chr22	51304566	5346402	0.1042	0.4476
chrMT	16571	1016	0.0613	0.3189
chrX	155270560	85564036	0.5511	1.3484

chrY	59373566	860397	0.0145	0.1913

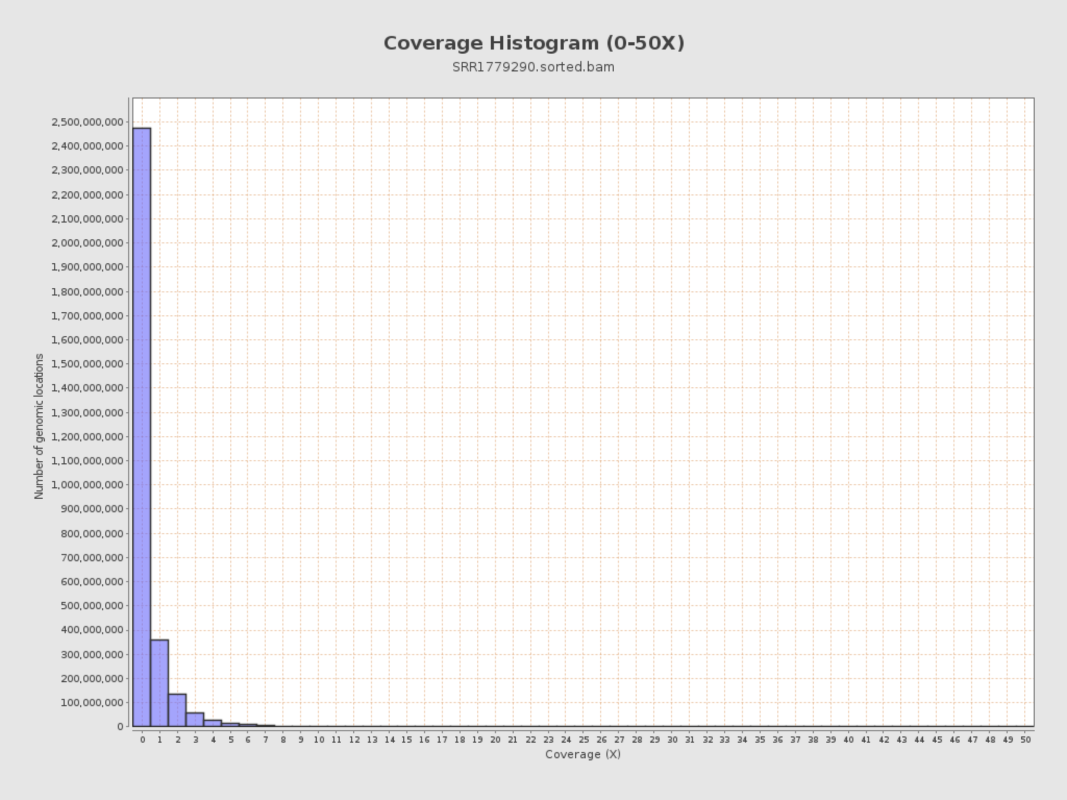
3. Results : Coverage across reference



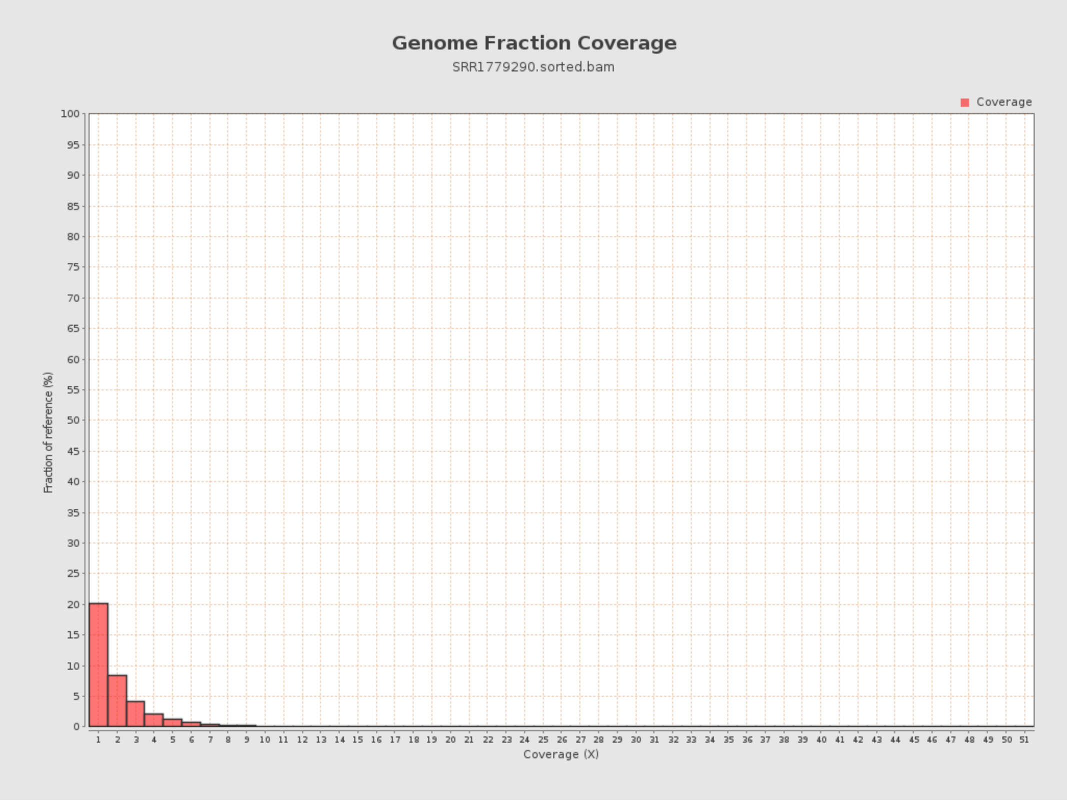
4. Results : Coverage Histogram



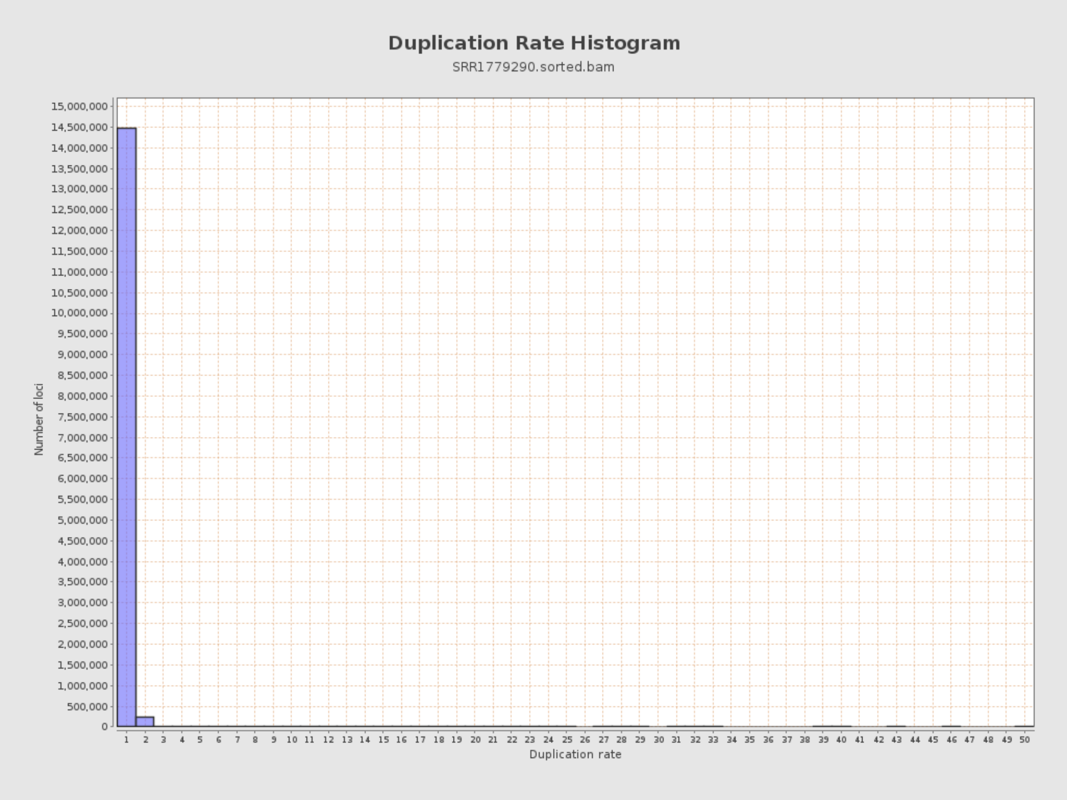
5. Results : Coverage Histogram (0-50X)



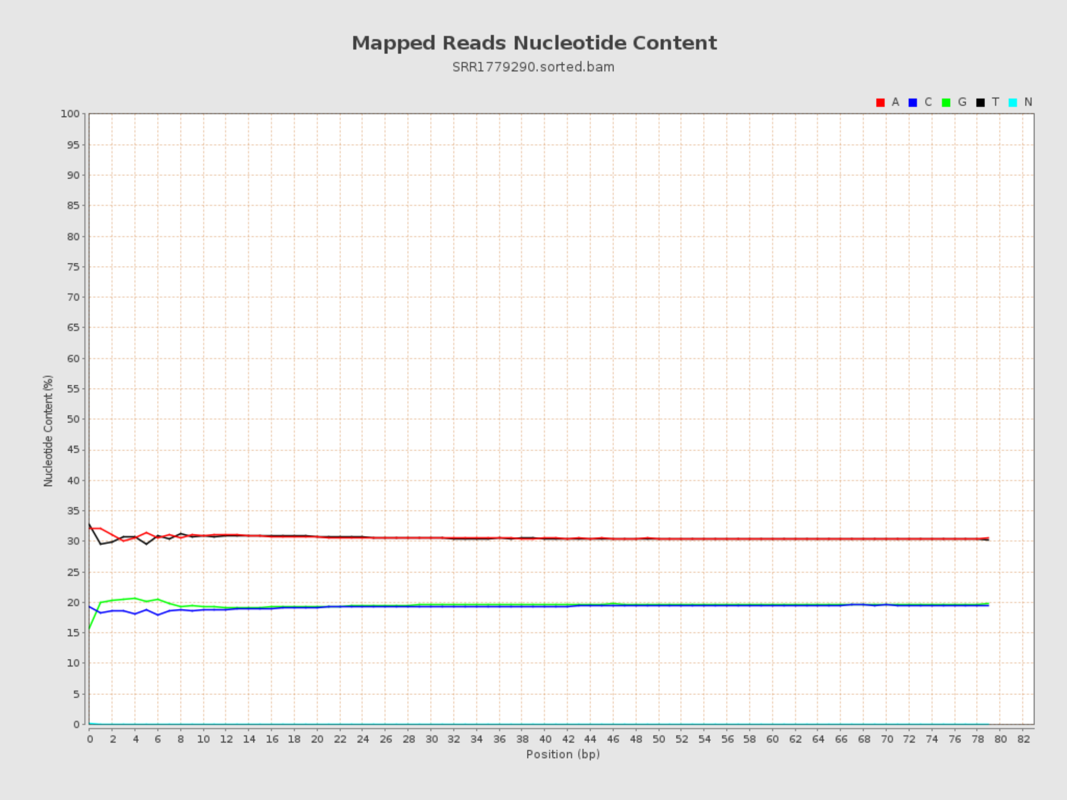
6. Results : Genome Fraction Coverage



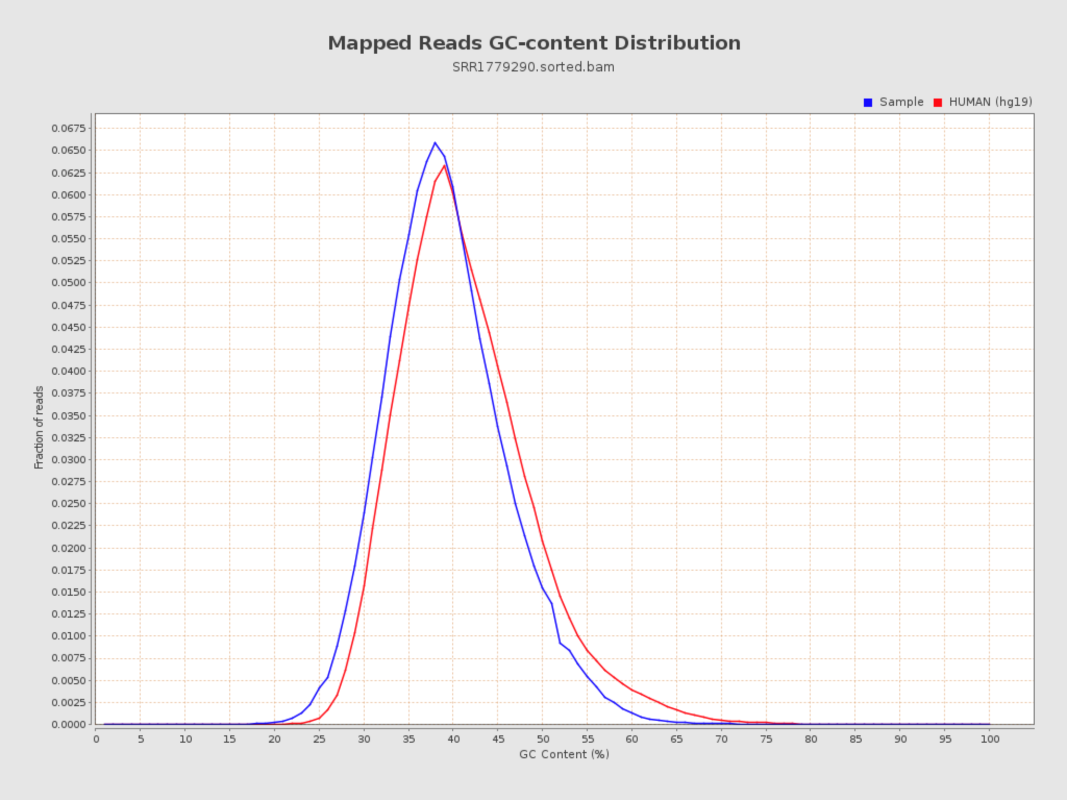
7. Results : Duplication Rate Histogram



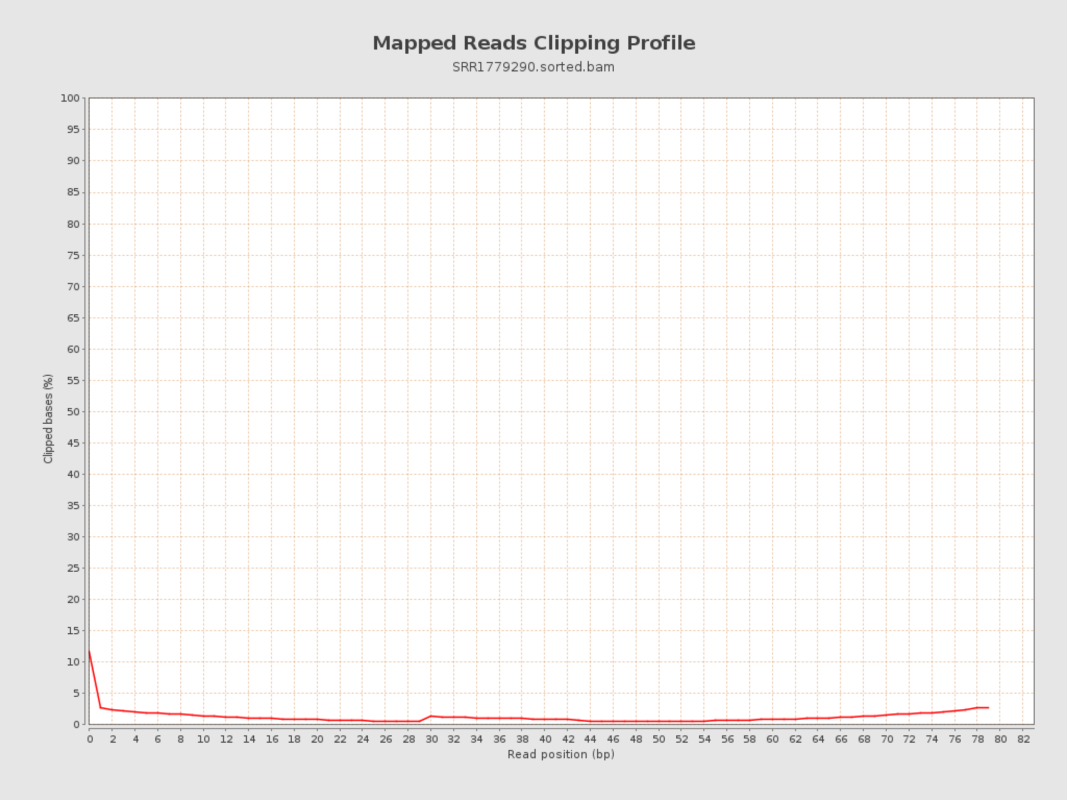
8. Results : Mapped Reads Nucleotide Content



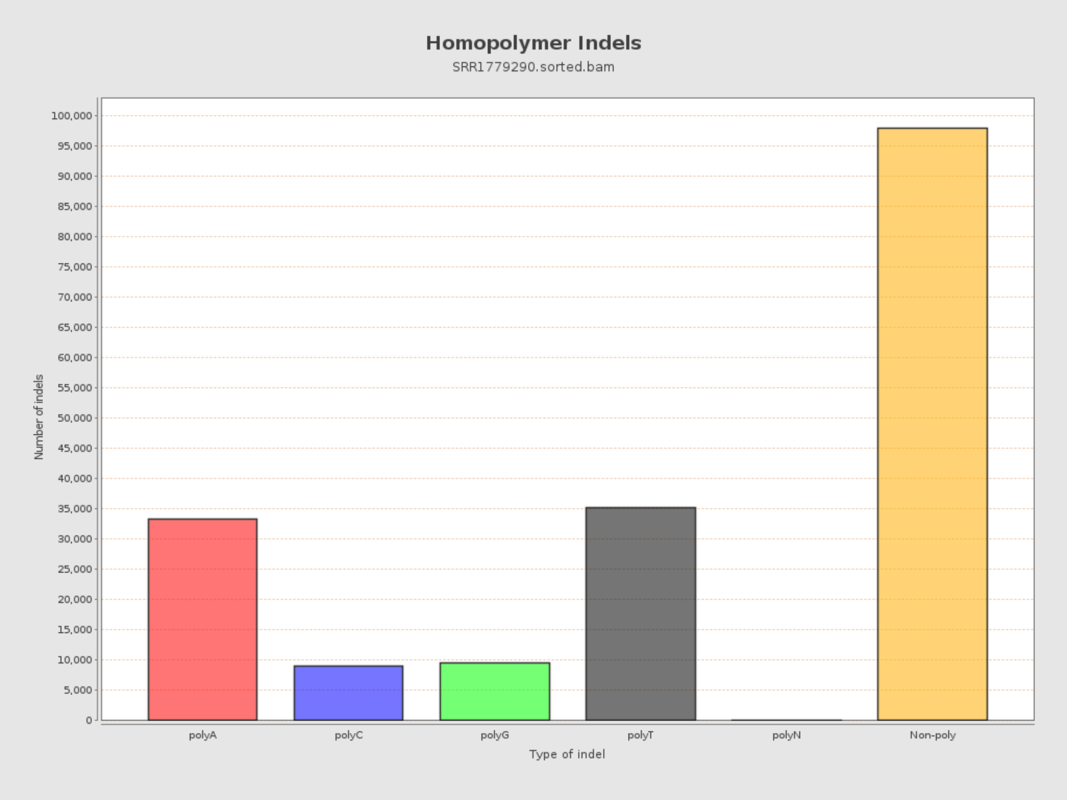
9. Results : Mapped Reads GC-content Distribution



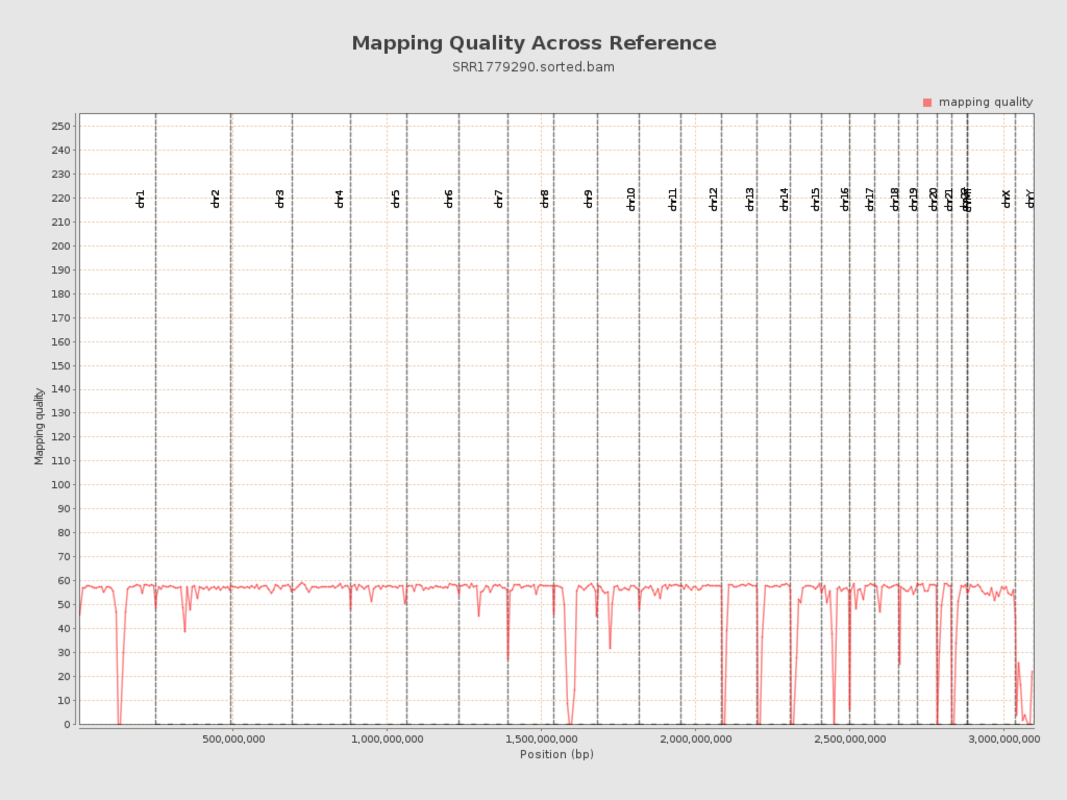
10. Results : Mapped Reads Clipping Profile



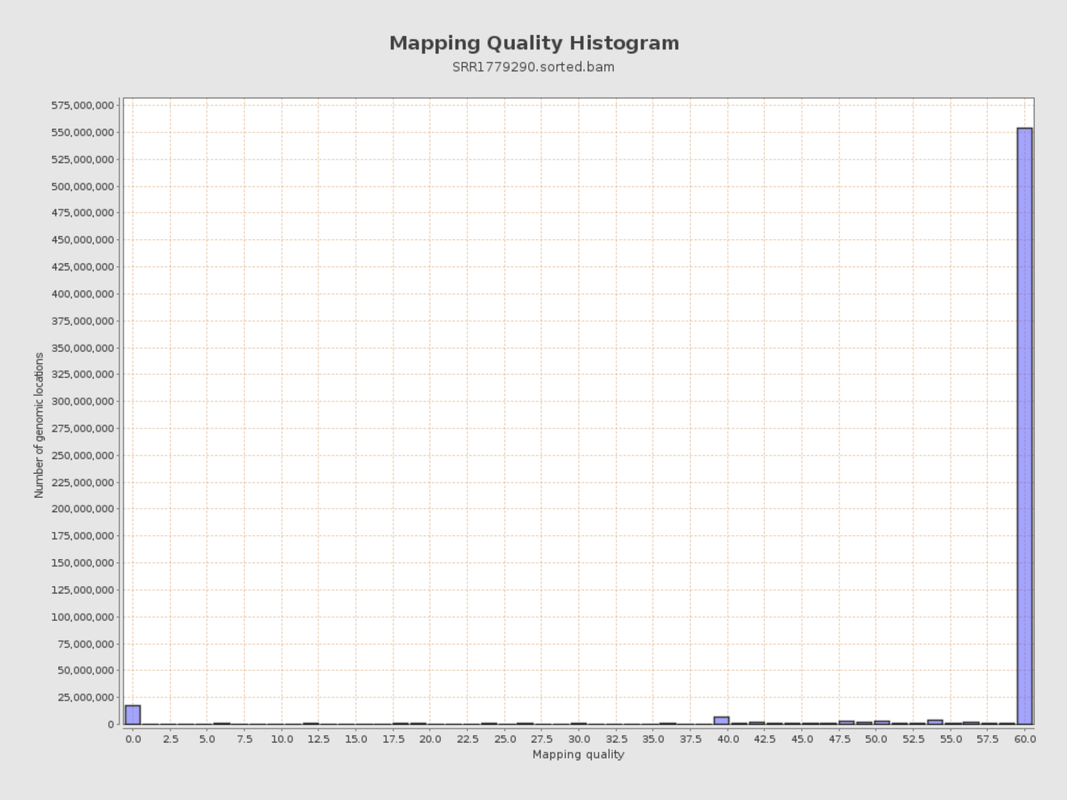
11. Results : Homopolymer Indels



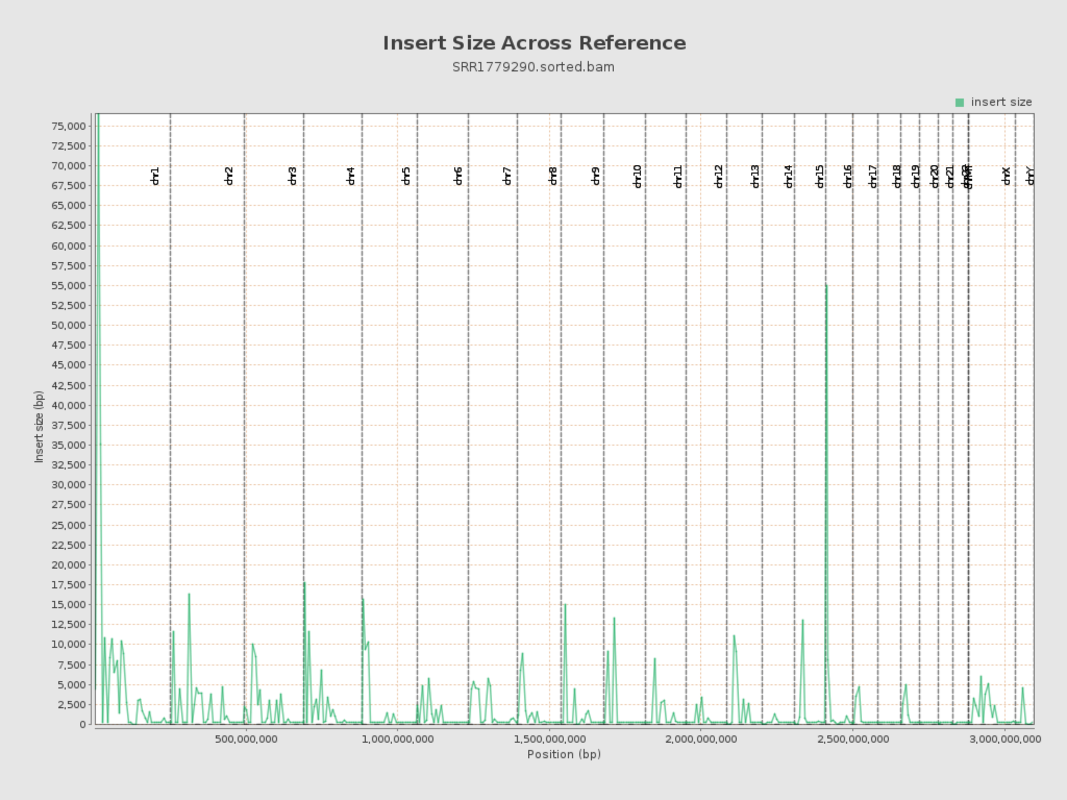
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram