Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 16:54:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779393.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_SRR1779393 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779393_1.fastq.gz SRR1779393_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 16:54:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779393.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,113,970
Mapped reads	14,403,765 / 89.39%
Unmapped reads	1,710,205 / 10.61%
Mapped paired reads	14,403,765 / 89.39%
Mapped reads, first in pair	7,245,962 / 44.97%
Mapped reads, second in pair	7,157,803 / 44.42%
Mapped reads, both in pair	14,243,074 / 88.39%
Mapped reads, singletons	160,691 / 1%
Secondary alignments	0
Supplementary alignments	128,666 / 0.8%
Read min/max/mean length	30 / 80 / 80.29
Duplicated reads (estimated)	4,939,895 / 30.66%
Duplication rate	12.94%
Clipped reads	989,165 / 6.14%

2.2. ACGT Content

Number/percentage of A's	351,692,413 / 30.81%
Number/percentage of C's	218,545,951 / 19.14%
Number/percentage of T's	346,008,195 / 30.31%
Number/percentage of G's	225,039,828 / 19.71%
Number/percentage of N's	255,071 / 0.02%

GC Percentage	38.86%

2.3. Coverage

Mean	0.3688
Standard Deviation	16.2489

2.4. Mapping Quality

Mean Mapping Quality	52.63

2.5. Insert size

Mean	113,081.56
Standard Deviation	3,127,345.55
P25/Median/P75	161 / 210 / 269

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	4,594,514
Insertions	114,465
Mapped reads with at least one insertion	0.79%
Deletions	137,792
Mapped reads with at least one deletion	0.94%
Homopolymer indels	46.5%

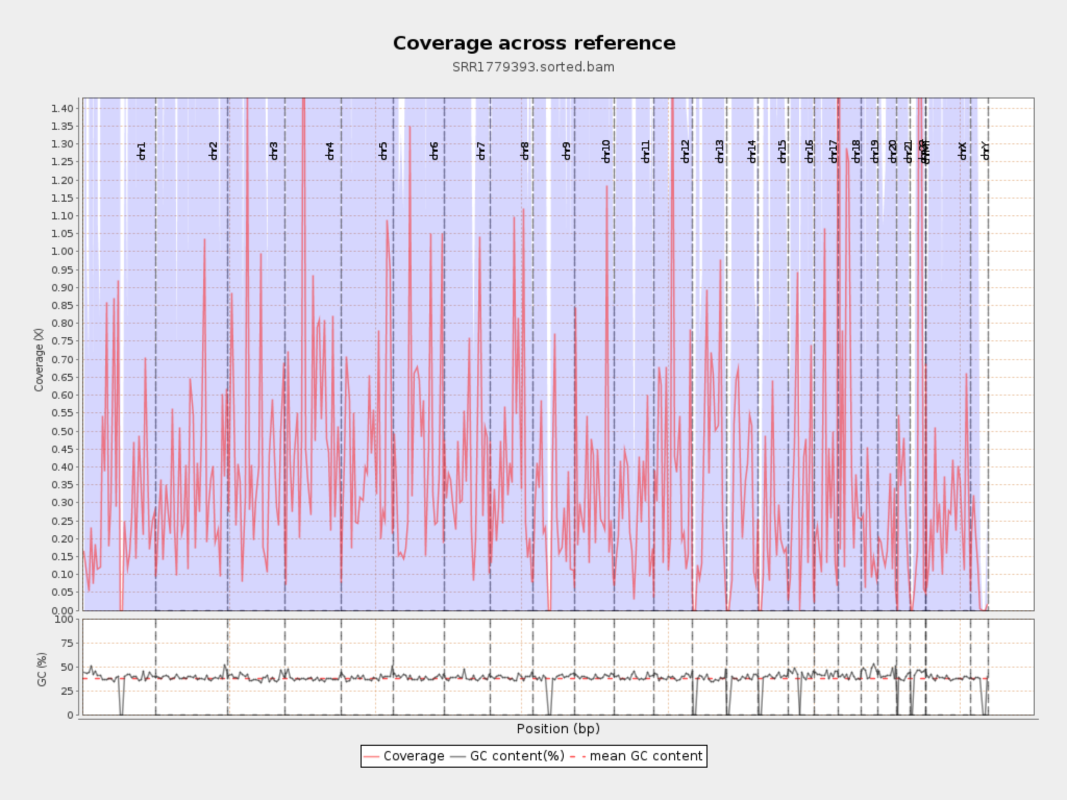
2.7. Chromosome stats

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

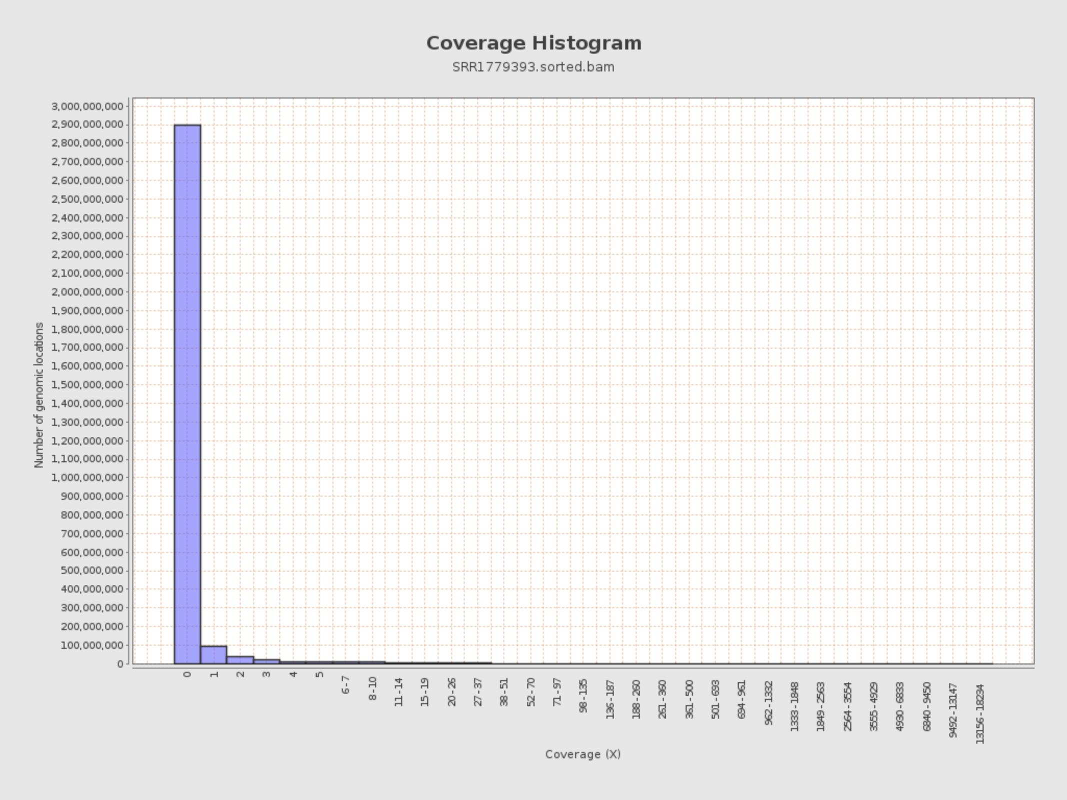
		bases	coverage	deviation
chr1	249250621	74903112	0.3005	16.6693
chr2	243199373	83749536	0.3444	8.1751
chr3	198022430	85157888	0.43	15.8616
chr4	191154276	106235314	0.5558	16.2988
chr5	180915260	80114151	0.4428	12.6678
chr6	171115067	79476605	0.4645	11.7879
chr7	159138663	62626029	0.3935	7.1893
chr8	146364022	61281354	0.4187	12.0609
chr9	141213431	38278077	0.2711	6.6792
chr10	135534747	48759791	0.3598	12.6549
chr11	135006516	36771652	0.2724	6.0902
chr12	133851895	59228169	0.4425	16.5868
chr13	115169878	45174825	0.3922	19.899
chr14	107349540	35448106	0.3302	7.4958
chr15	102531392	21422555	0.2089	7.7647
chr16	90354753	29658185	0.3282	10.8041
chr17	81195210	25285960	0.3114	35.4247
chr18	78077248	51346406	0.6576	32.3957
chr19	59128983	11761374	0.1989	7.0007
chr20	63025520	12717875	0.2018	4.8737
chr21	48129895	13809335	0.2869	3.9997
chr22	51304566	30712374	0.5986	65.0451
chrMT	16571	11376	0.6865	1.0193
chrX	155270560	41528830	0.2675	5.3252

chrY	59373566	6355141	0.107	1.8477

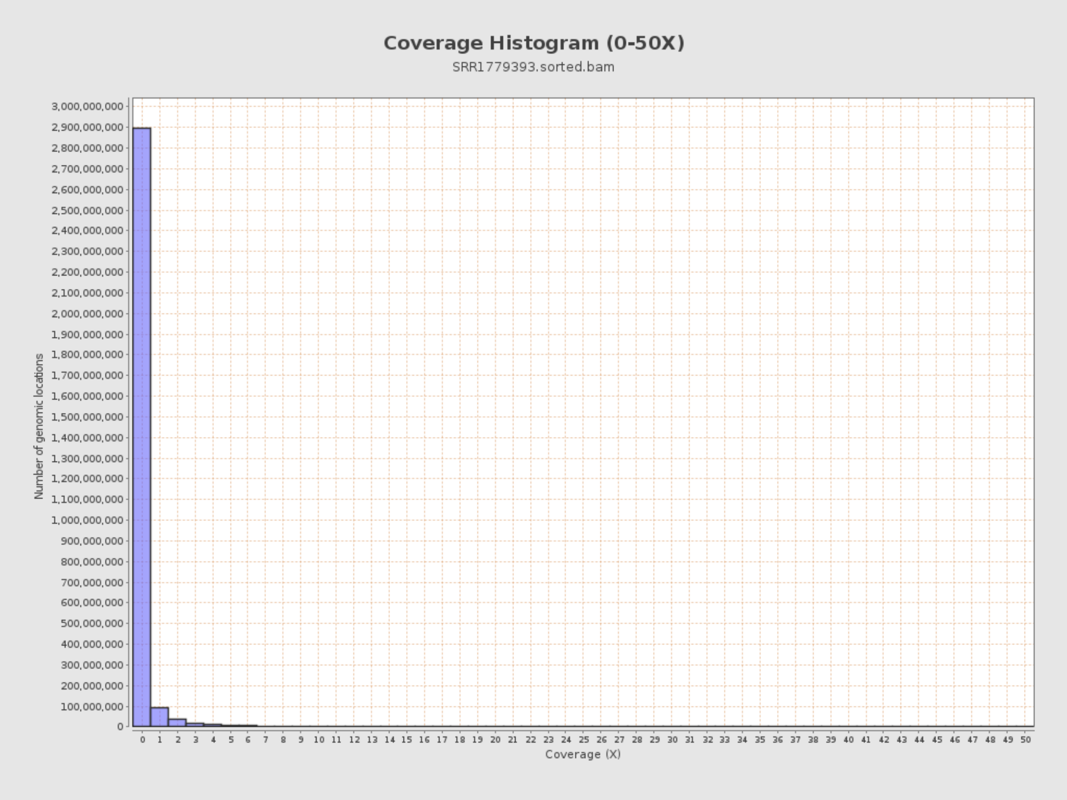
3. Results : Coverage across reference



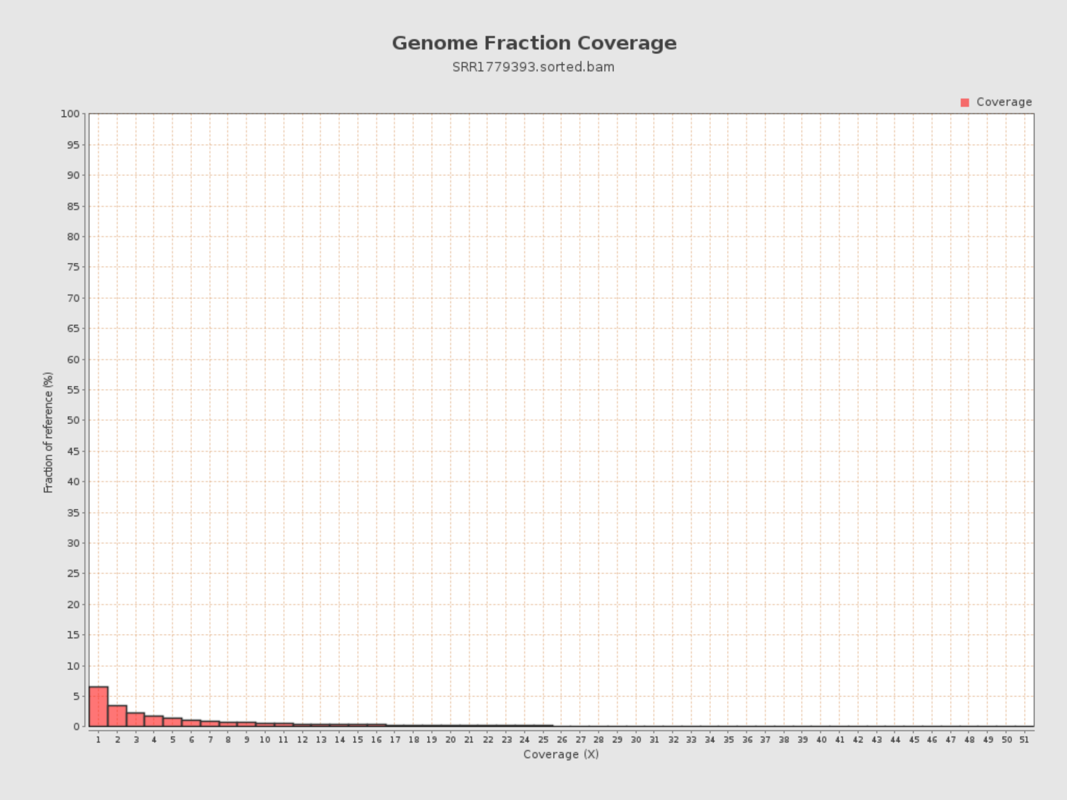
4. Results : Coverage Histogram



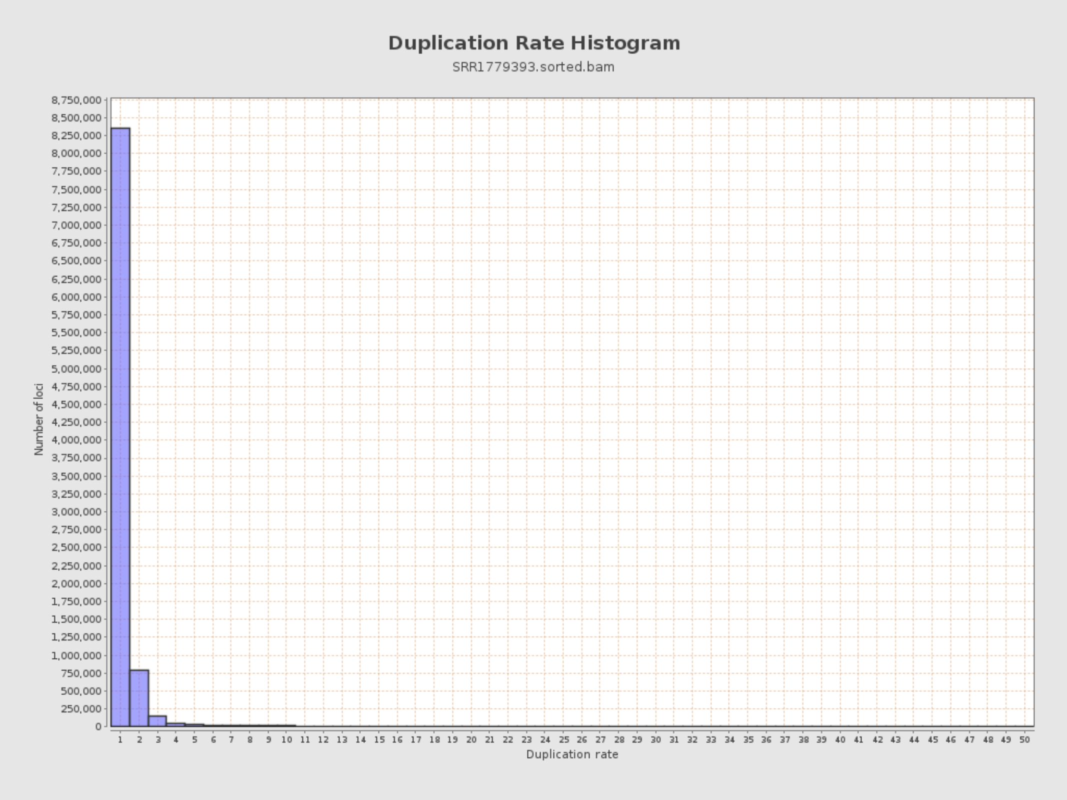
5. Results : Coverage Histogram (0-50X)



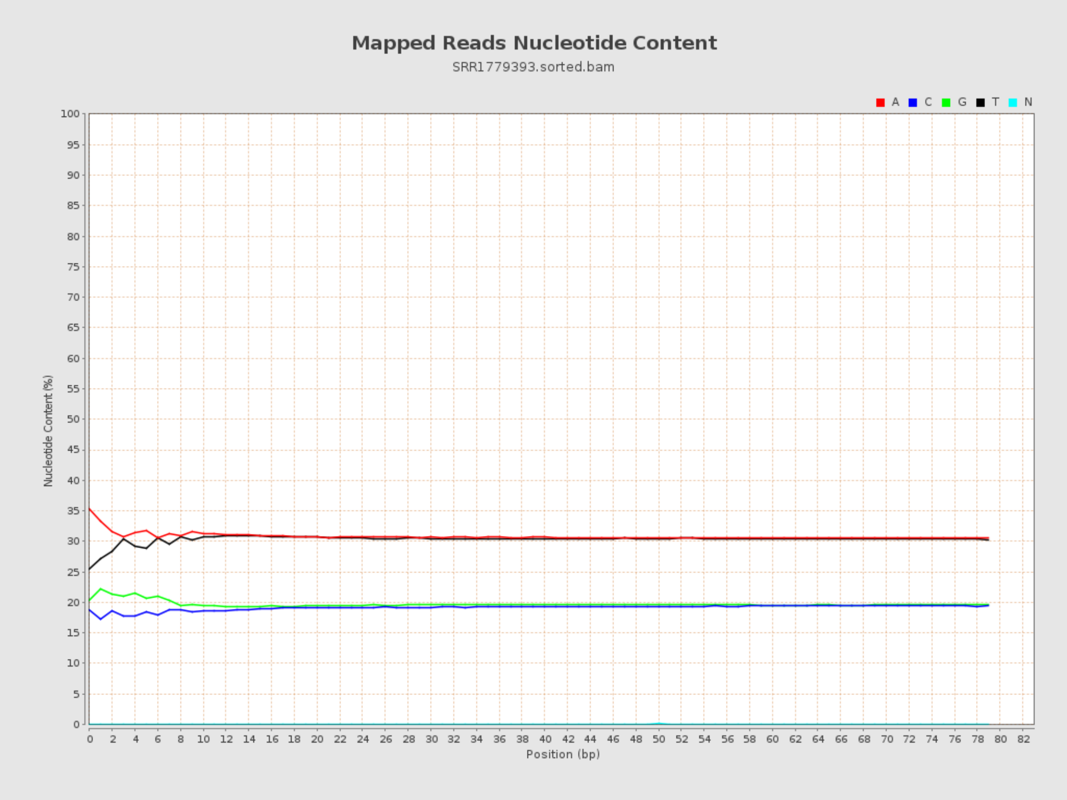
6. Results : Genome Fraction Coverage



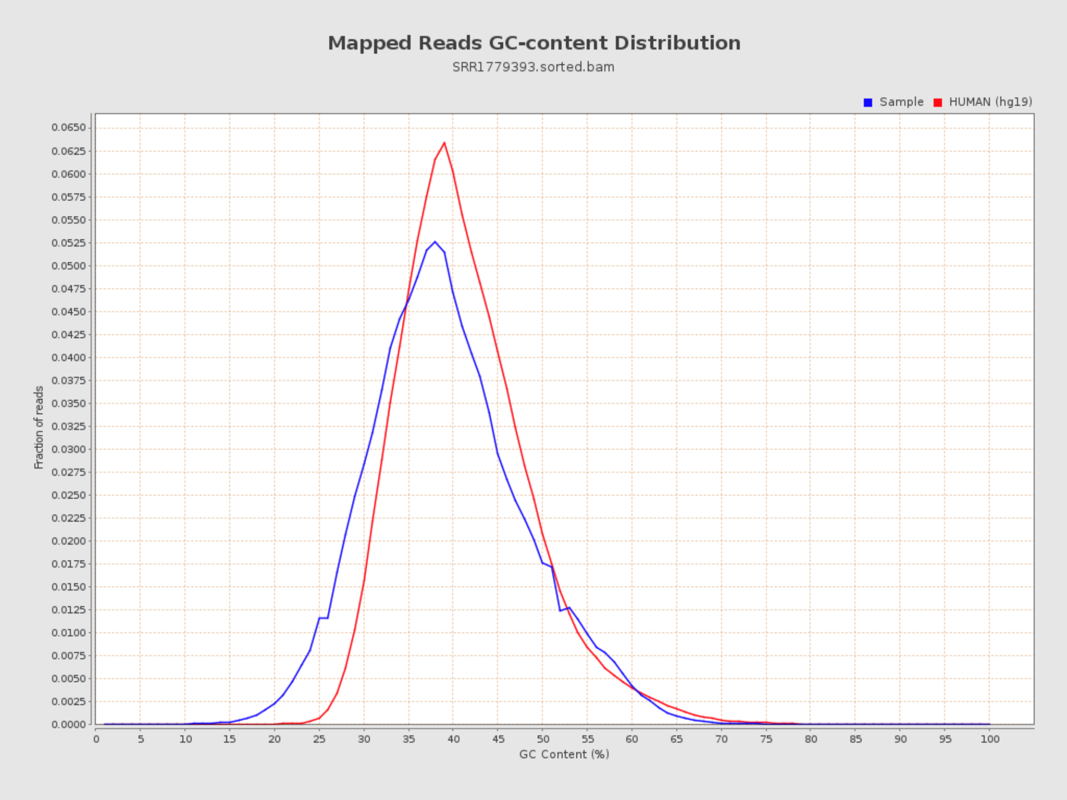
7. Results : Duplication Rate Histogram



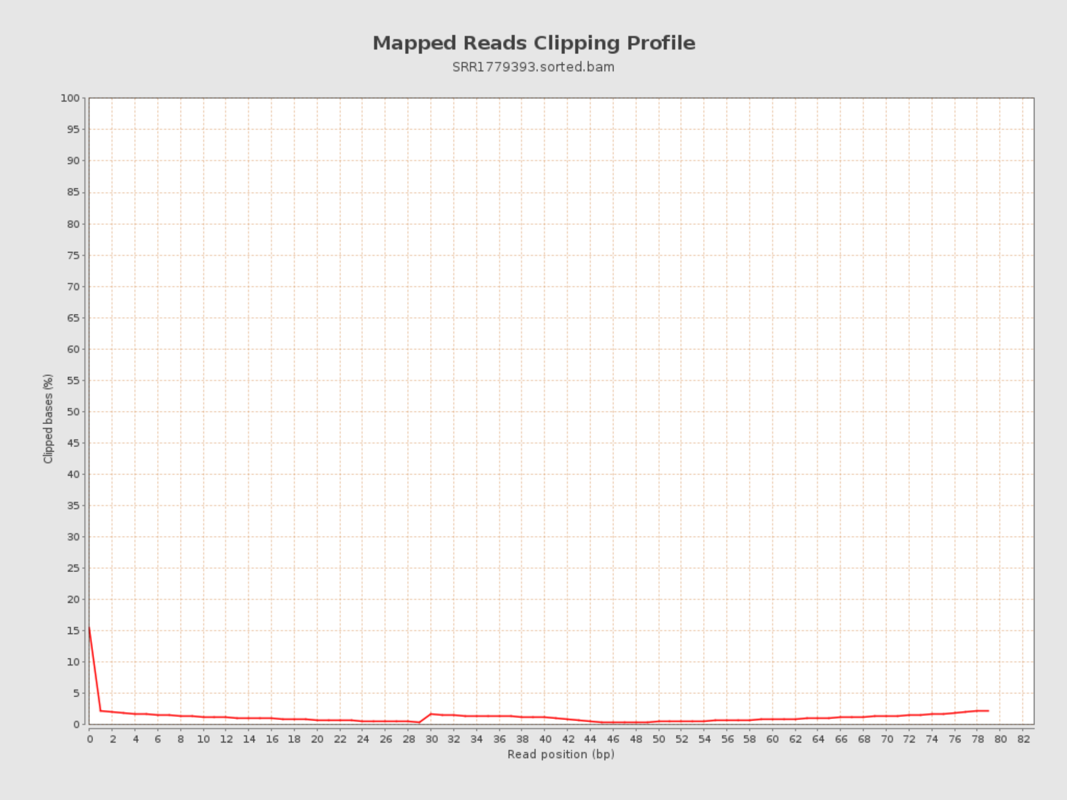
8. Results : Mapped Reads Nucleotide Content



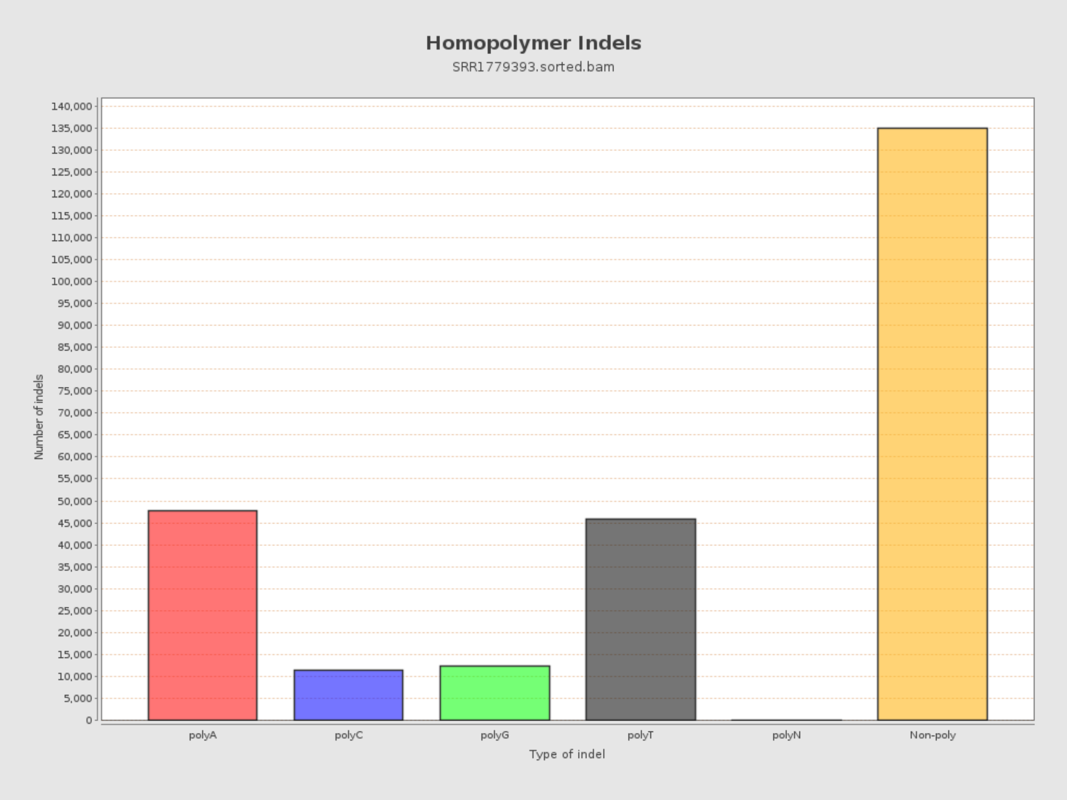
9. Results : Mapped Reads GC-content Distribution



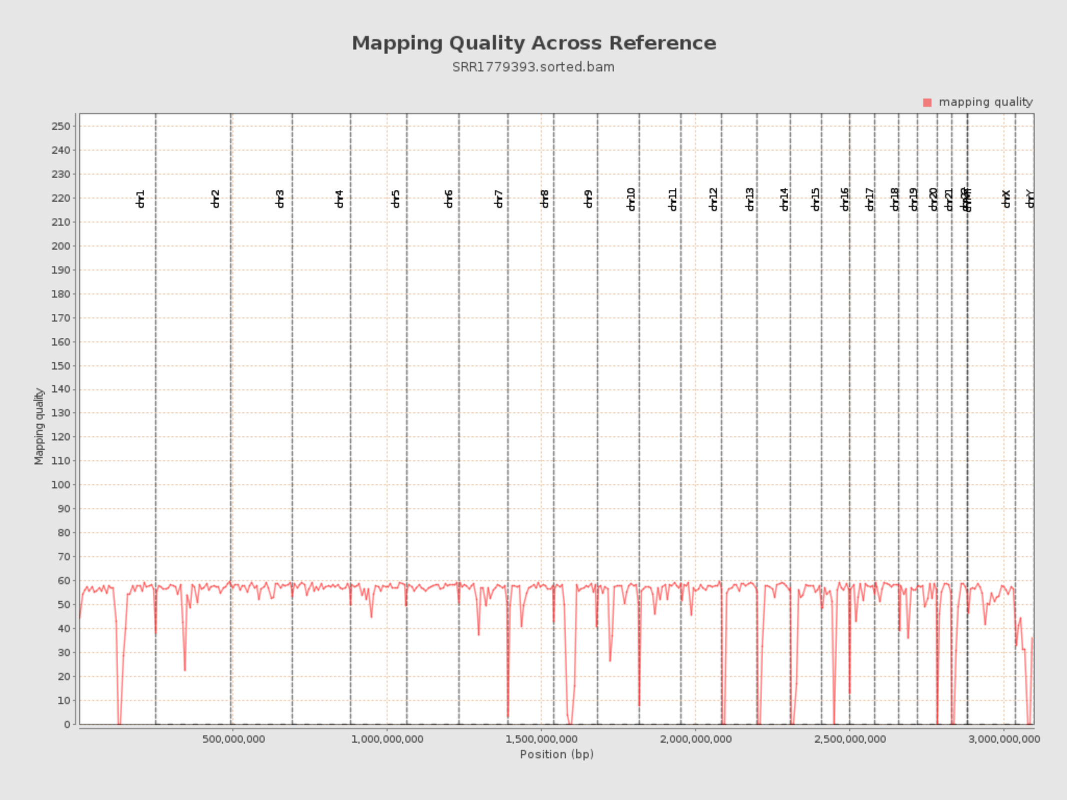
10. Results : Mapped Reads Clipping Profile



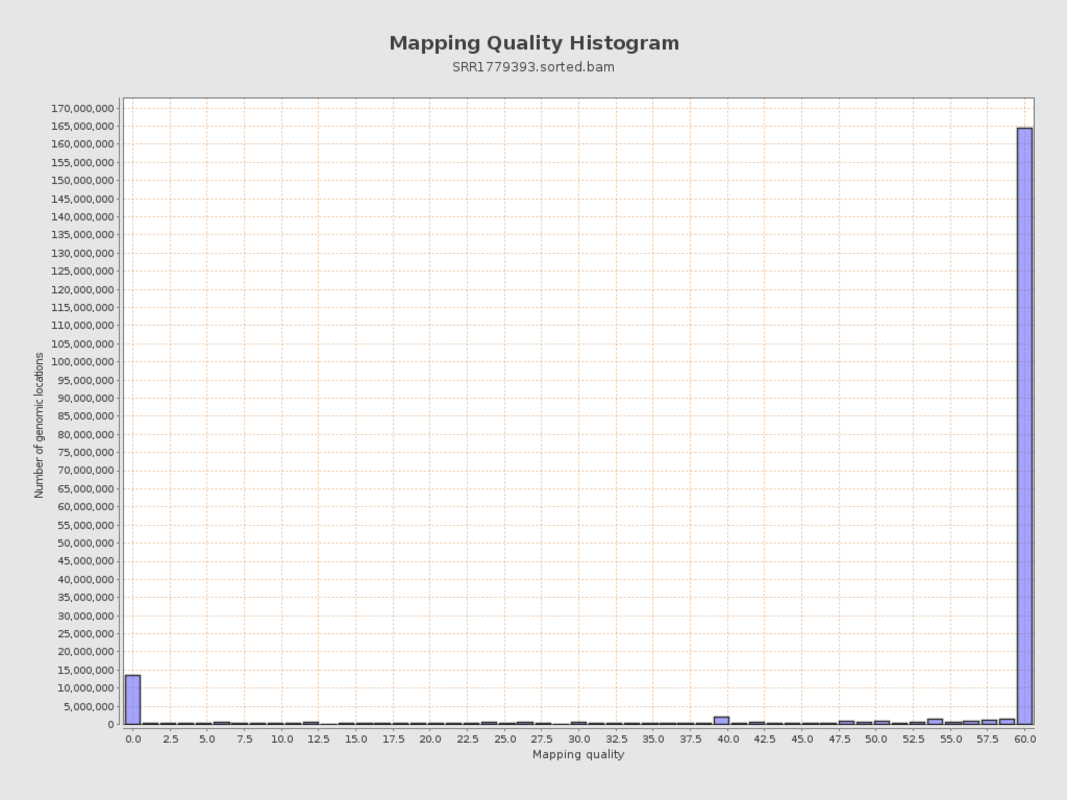
11. Results : Homopolymer Indels



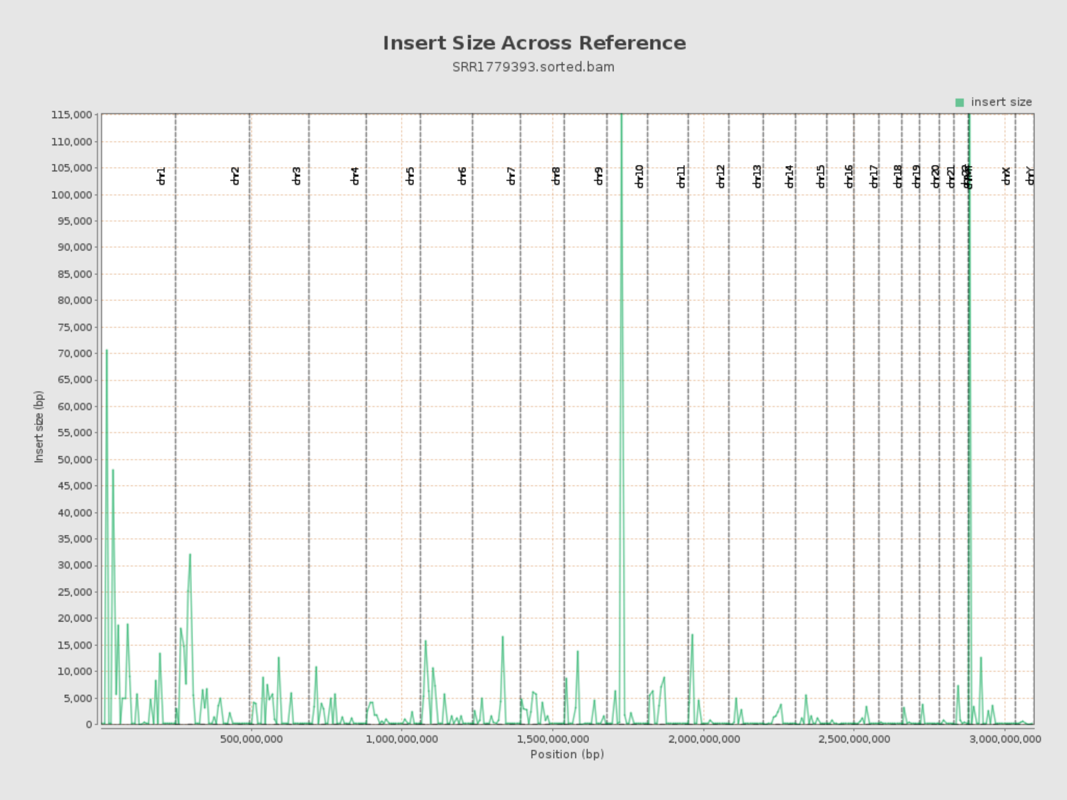
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram