Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 03:19:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777253.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_SRR1777253 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777253_1.fastq.gz SRR1777253_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 03:19:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777253.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,193,444
Mapped reads	11,525,424 / 94.52%
Unmapped reads	668,020 / 5.48%
Mapped paired reads	11,525,424 / 94.52%
Mapped reads, first in pair	5,800,532 / 47.57%
Mapped reads, second in pair	5,724,892 / 46.95%
Mapped reads, both in pair	11,242,756 / 92.2%
Mapped reads, singletons	282,668 / 2.32%
Secondary alignments	0
Supplementary alignments	1,659,455 / 13.61%
Read min/max/mean length	30 / 101 / 106.32
Duplicated reads (estimated)	6,486,972 / 53.2%
Duplication rate	6.5%
Clipped reads	7,578,051 / 62.15%

2.2. ACGT Content

Number/percentage of A's	292,731,731 / 29.47%
Number/percentage of C's	205,135,977 / 20.65%
Number/percentage of T's	286,579,594 / 28.85%
Number/percentage of G's	208,721,970 / 21.02%
Number/percentage of N's	17,323 / 0%

GC Percentage	41.67%

2.3. Coverage

Mean	0.3219
Standard Deviation	141.047

2.4. Mapping Quality

Mean Mapping Quality	52.45

2.5. Insert size

Mean	1,031,151.17
Standard Deviation	4,817,912.16
P25/Median/P75	96 / 162 / 276

2.6. Mismatches and indels

General error rate	1.46%
Mismatches	12,004,355
Insertions	870,762
Mapped reads with at least one insertion	6.88%
Deletions	984,066
Mapped reads with at least one deletion	7.37%
Homopolymer indels	23.29%

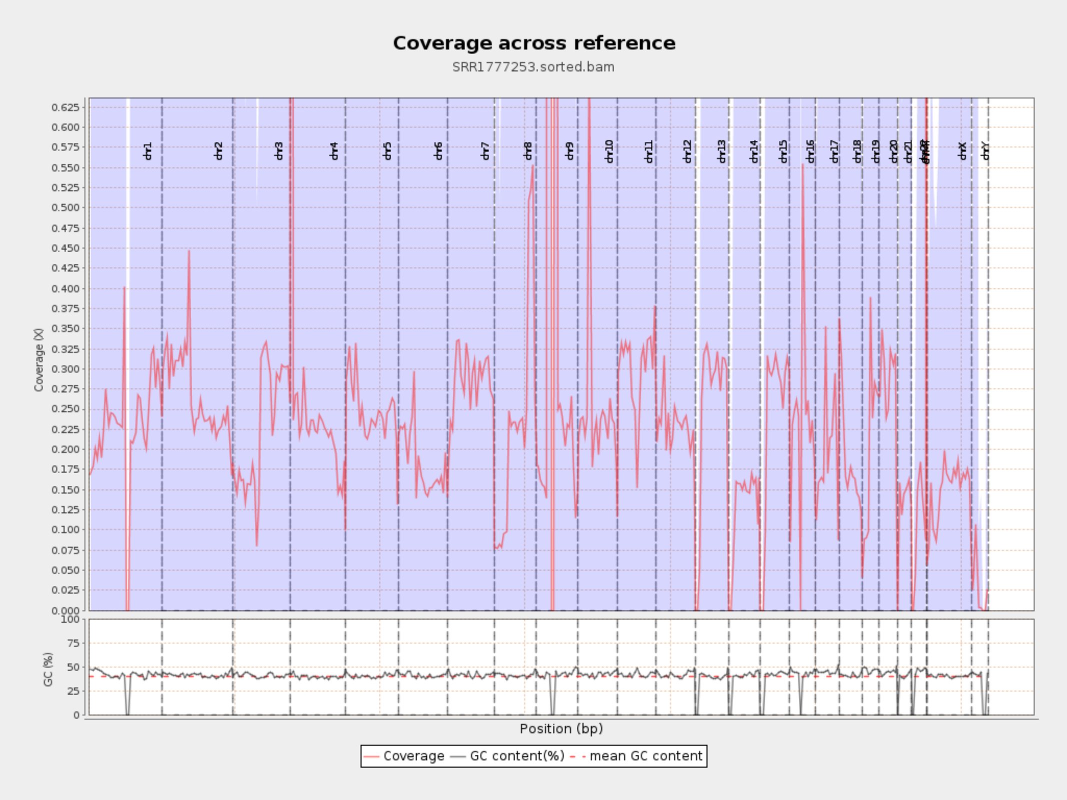
2.7. Chromosome stats

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

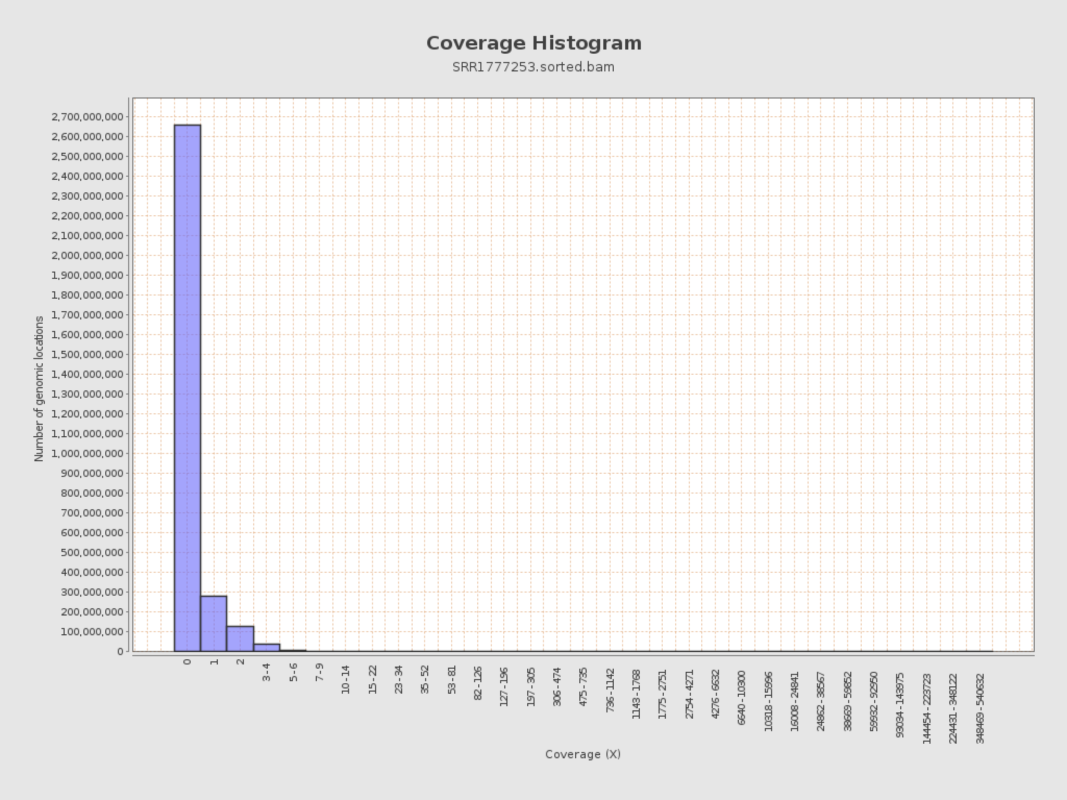
		bases	coverage	deviation
chr1	249250621	56667497	0.2274	3.8749
chr2	243199373	65704753	0.2702	1.8273
chr3	198022430	44675195	0.2256	0.8661
chr4	191154276	73993698	0.3871	96.2435
chr5	180915260	45099914	0.2493	0.8056
chr6	171115067	31521082	0.1842	3.3192
chr7	159138663	45603751	0.2866	2.771
chr8	146364022	34190442	0.2336	1.3168
chr9	141213431	306133618	2.1679	650.7543
chr10	135534747	34353508	0.2535	4.2848
chr11	135006516	40191170	0.2977	1.9827
chr12	133851895	30624011	0.2288	0.7931
chr13	115169878	28635369	0.2486	0.714
chr14	107349540	13553803	0.1263	1.1206
chr15	102531392	24532459	0.2393	0.6786
chr16	90354753	21143886	0.234	2.5205
chr17	81195210	15948850	0.1964	1.1131
chr18	78077248	14837255	0.19	2.1458
chr19	59128983	11953382	0.2022	2.2172
chr20	63025520	18117836	0.2875	0.9443
chr21	48129895	6369169	0.1323	2.9177
chr22	51304566	4992503	0.0973	0.6417
chrMT	16571	3273336	197.534	39.6234
chrX	155270560	22955737	0.1478	0.6934

chrY	59373566	1532245	0.0258	1.2865

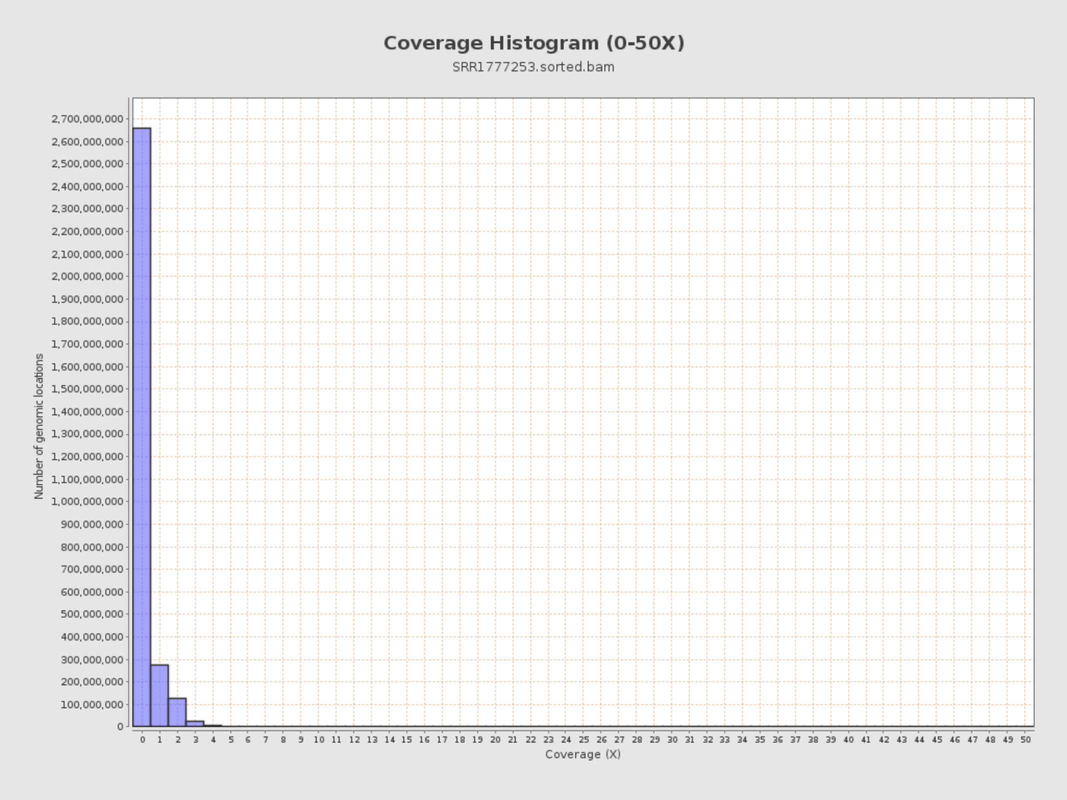
3. Results : Coverage across reference



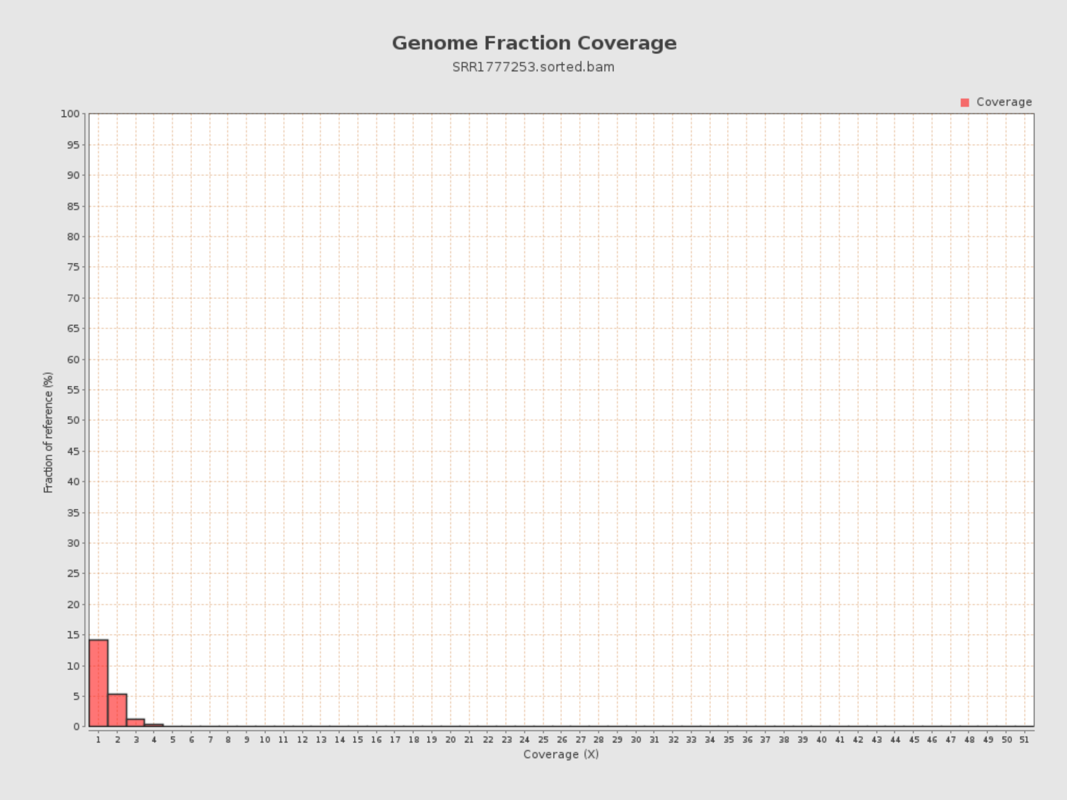
4. Results : Coverage Histogram



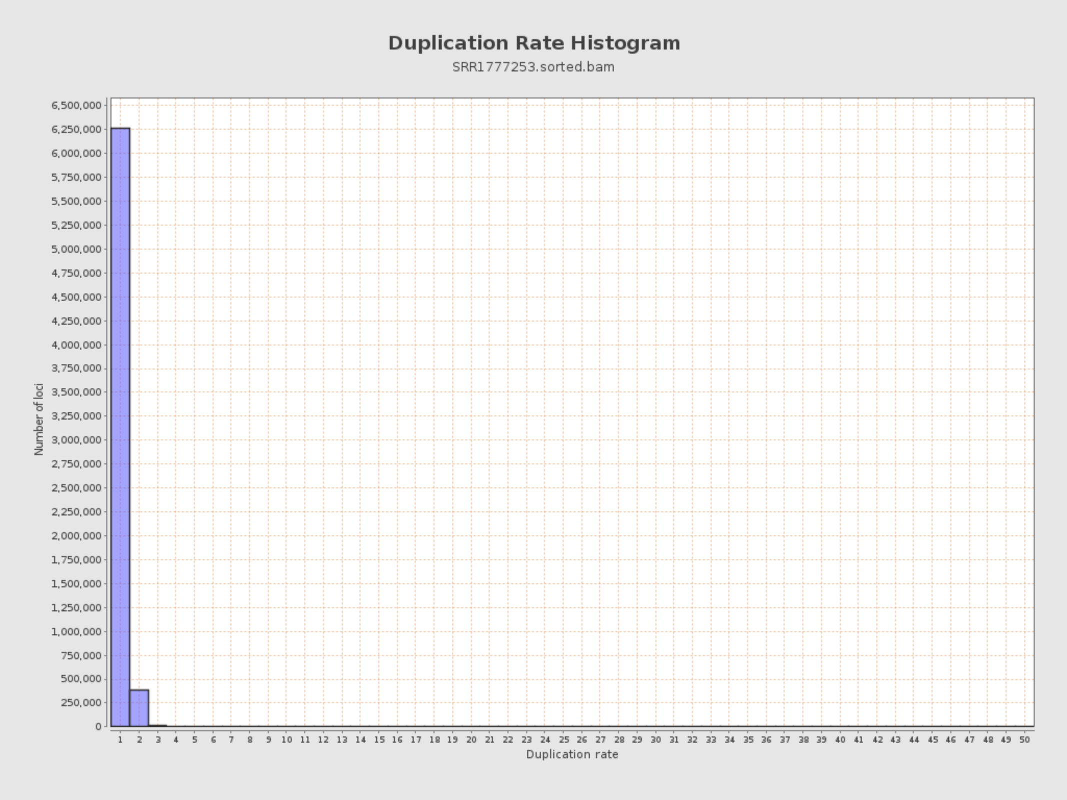
5. Results : Coverage Histogram (0-50X)



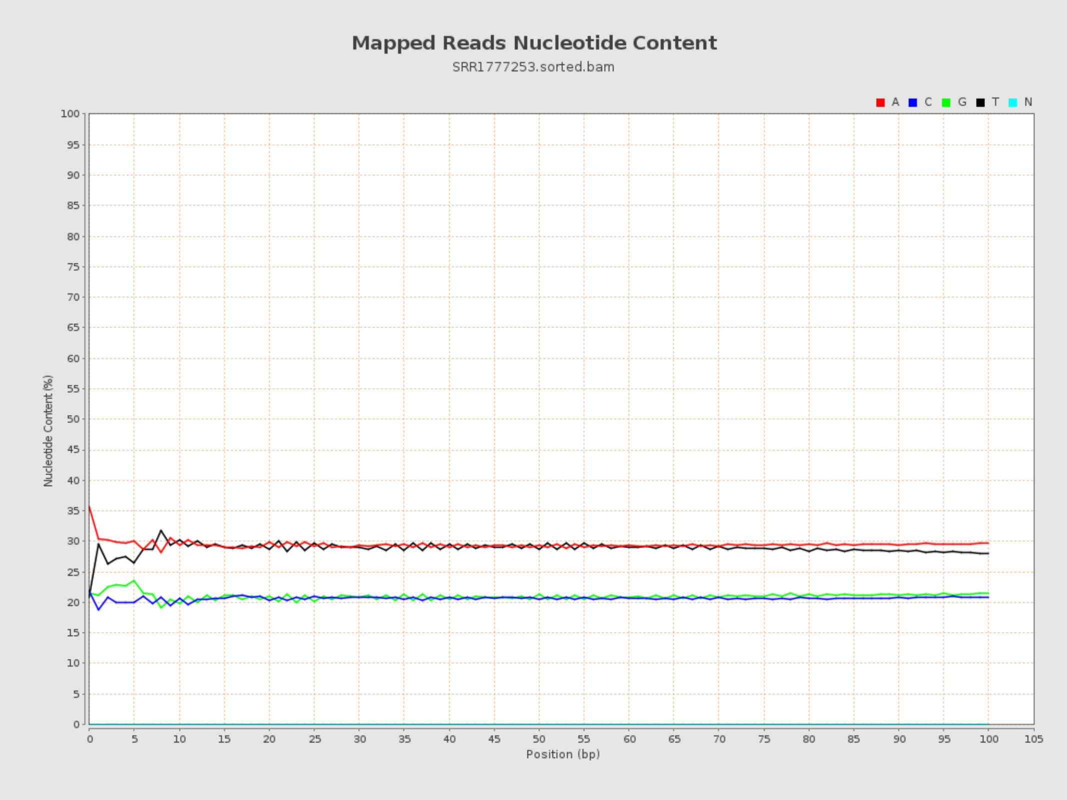
6. Results : Genome Fraction Coverage



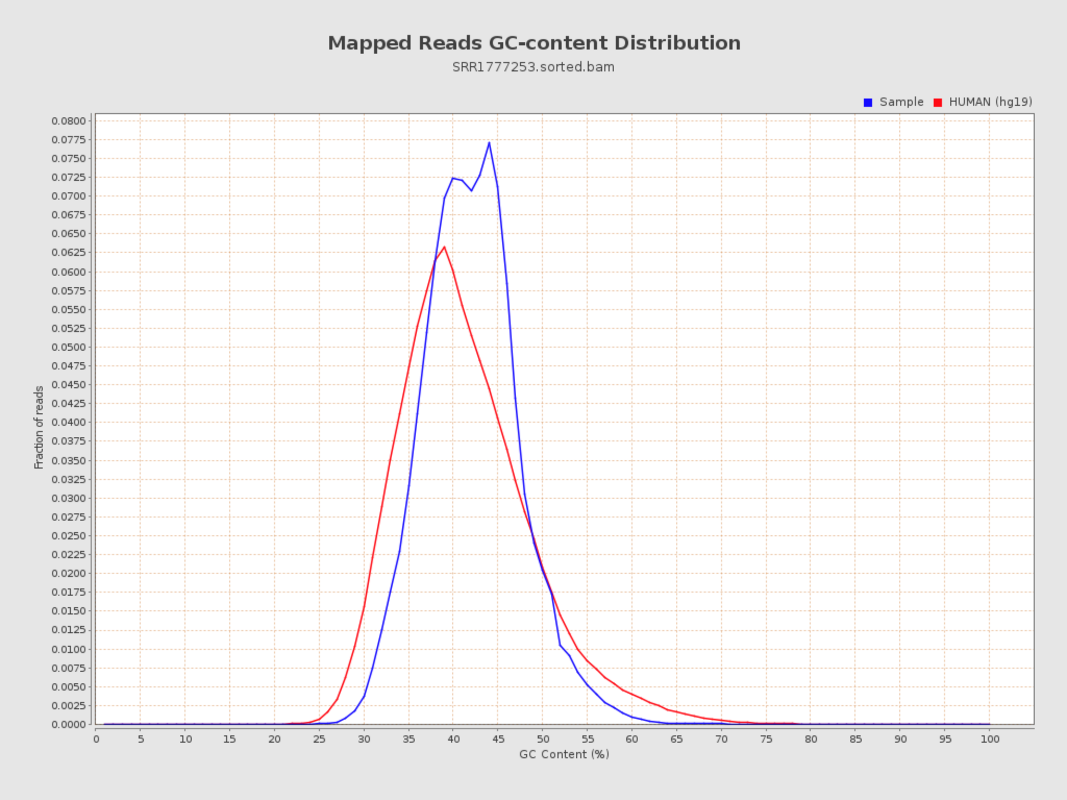
7. Results : Duplication Rate Histogram



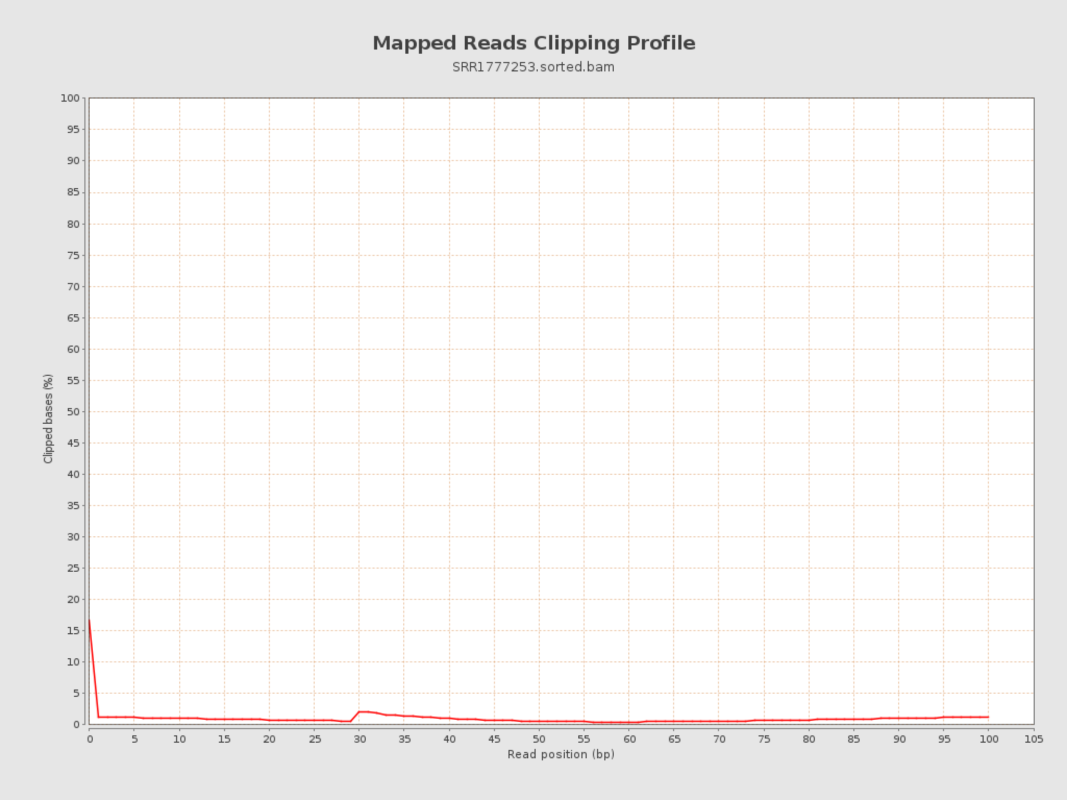
8. Results : Mapped Reads Nucleotide Content



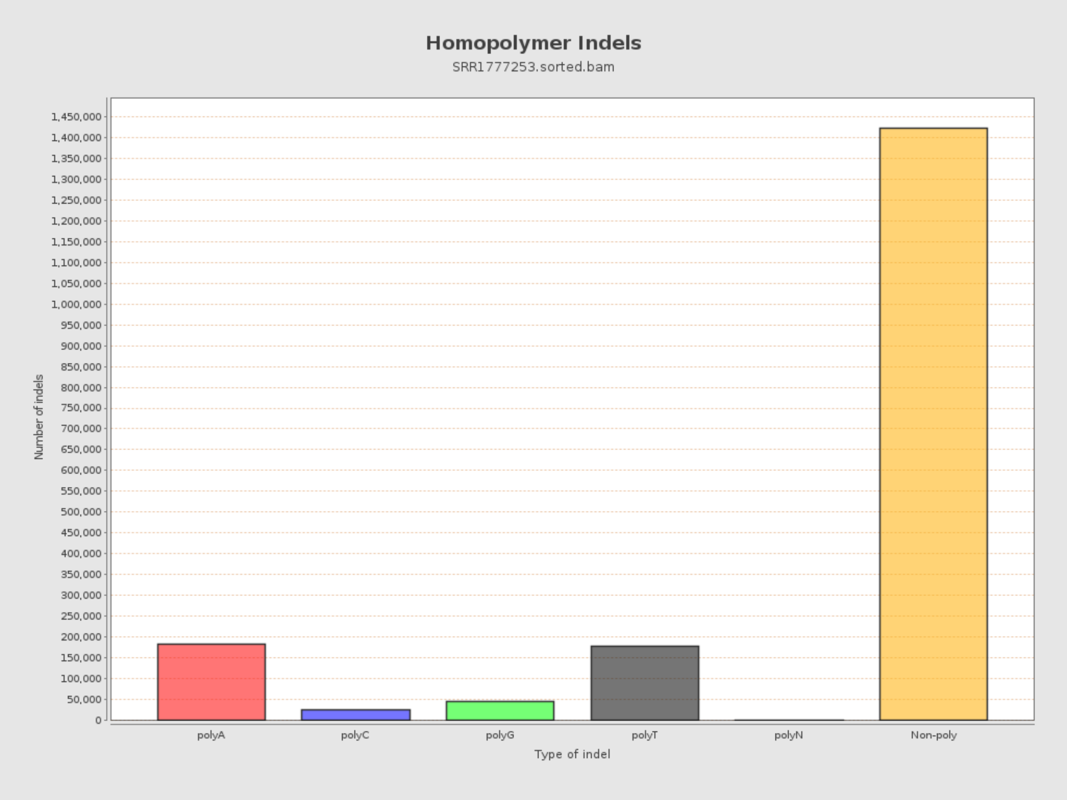
9. Results : Mapped Reads GC-content Distribution



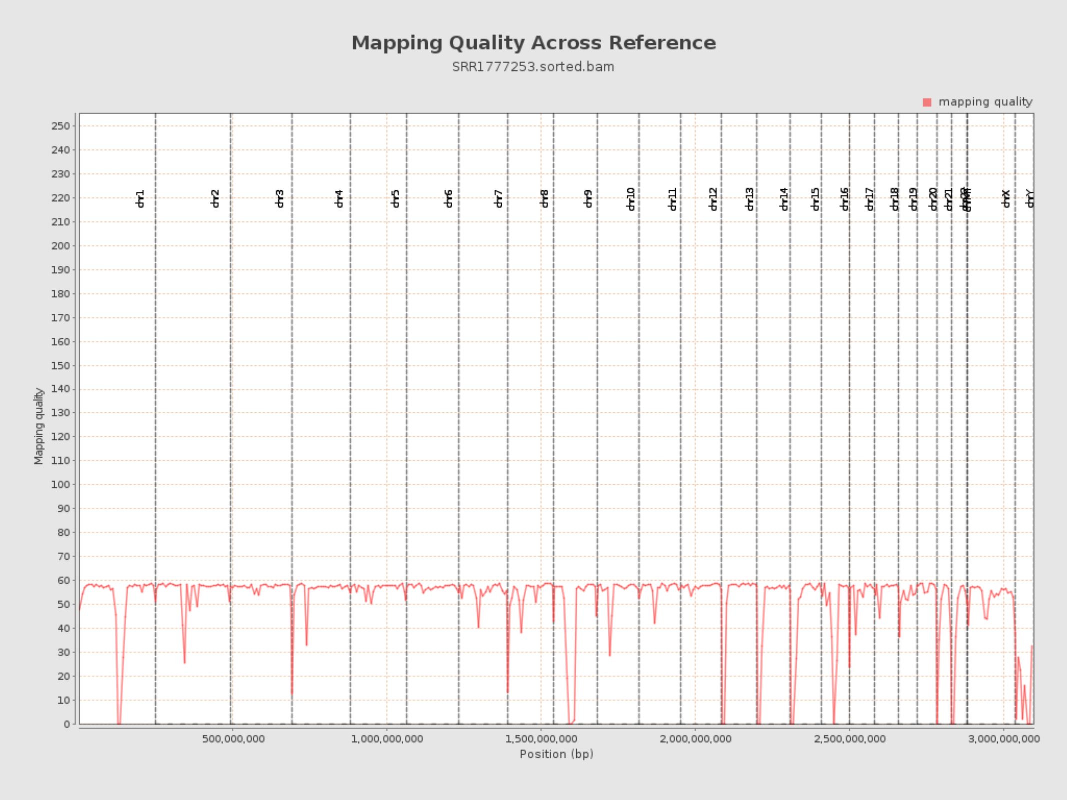
10. Results : Mapped Reads Clipping Profile



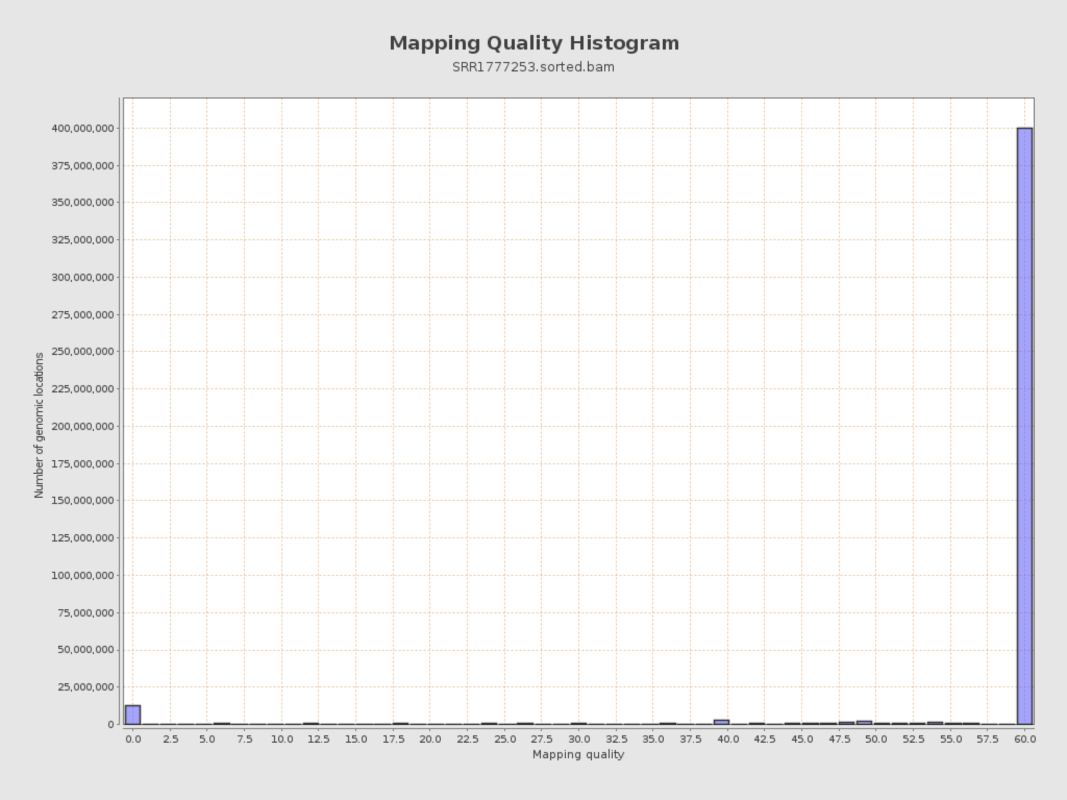
11. Results : Homopolymer Indels



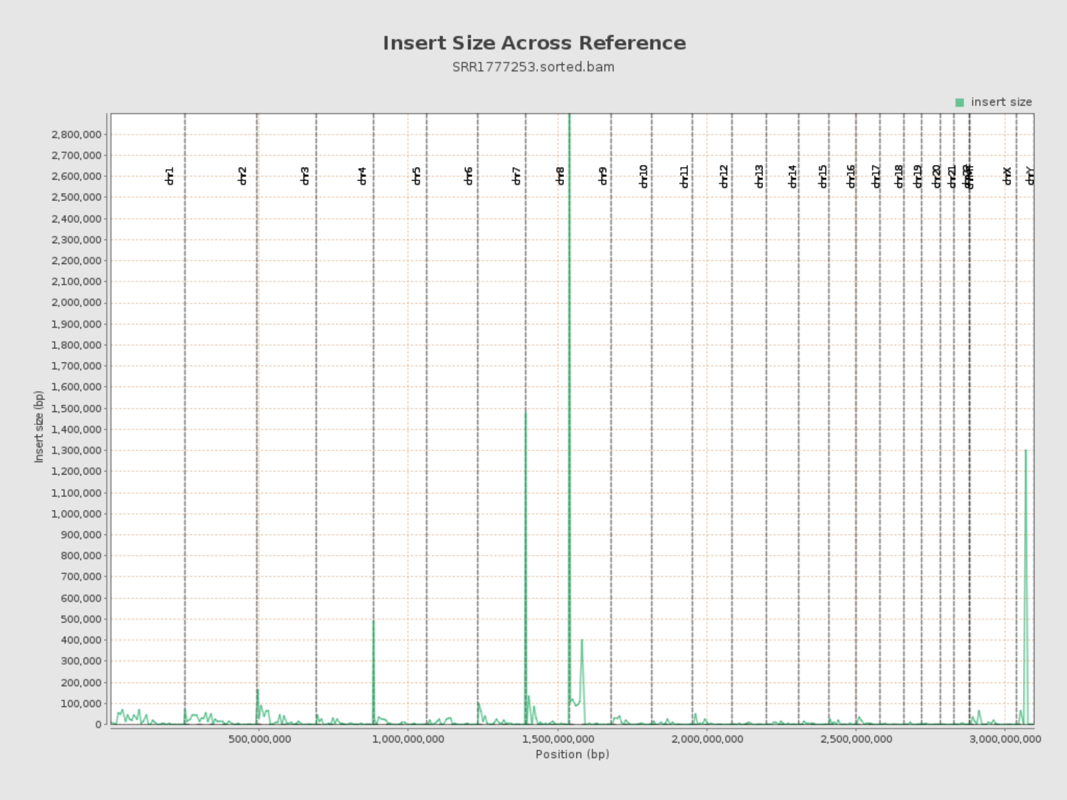
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram