Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 07:09:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777266.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_SRR1777266 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777266_1.fastq.gz SRR1777266_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 07:09:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777266.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,736,536
Mapped reads	2,644,291 / 96.63%
Unmapped reads	92,245 / 3.37%
Mapped paired reads	2,644,291 / 96.63%
Mapped reads, first in pair	1,328,505 / 48.55%
Mapped reads, second in pair	1,315,786 / 48.08%
Mapped reads, both in pair	2,624,238 / 95.9%
Mapped reads, singletons	20,053 / 0.73%
Secondary alignments	0
Supplementary alignments	42,925 / 1.57%
Read min/max/mean length	30 / 76 / 76.55
Duplicated reads (estimated)	38,702 / 1.41%
Duplication rate	1.35%
Clipped reads	309,005 / 11.29%

2.2. ACGT Content

Number/percentage of A's	58,192,704 / 29.41%
Number/percentage of C's	41,127,662 / 20.78%
Number/percentage of T's	57,142,697 / 28.87%
Number/percentage of G's	41,427,001 / 20.93%
Number/percentage of N's	10,548 / 0.01%

GC Percentage	41.72%

2.3. Coverage

Mean	0.0639
Standard Deviation	0.3257

2.4. Mapping Quality

Mean Mapping Quality	52.68

2.5. Insert size

Mean	191,610.71
Standard Deviation	4,281,779.38
P25/Median/P75	130 / 174 / 234

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	1,137,153
Insertions	41,189
Mapped reads with at least one insertion	1.54%
Deletions	17,729
Mapped reads with at least one deletion	0.66%
Homopolymer indels	49.74%

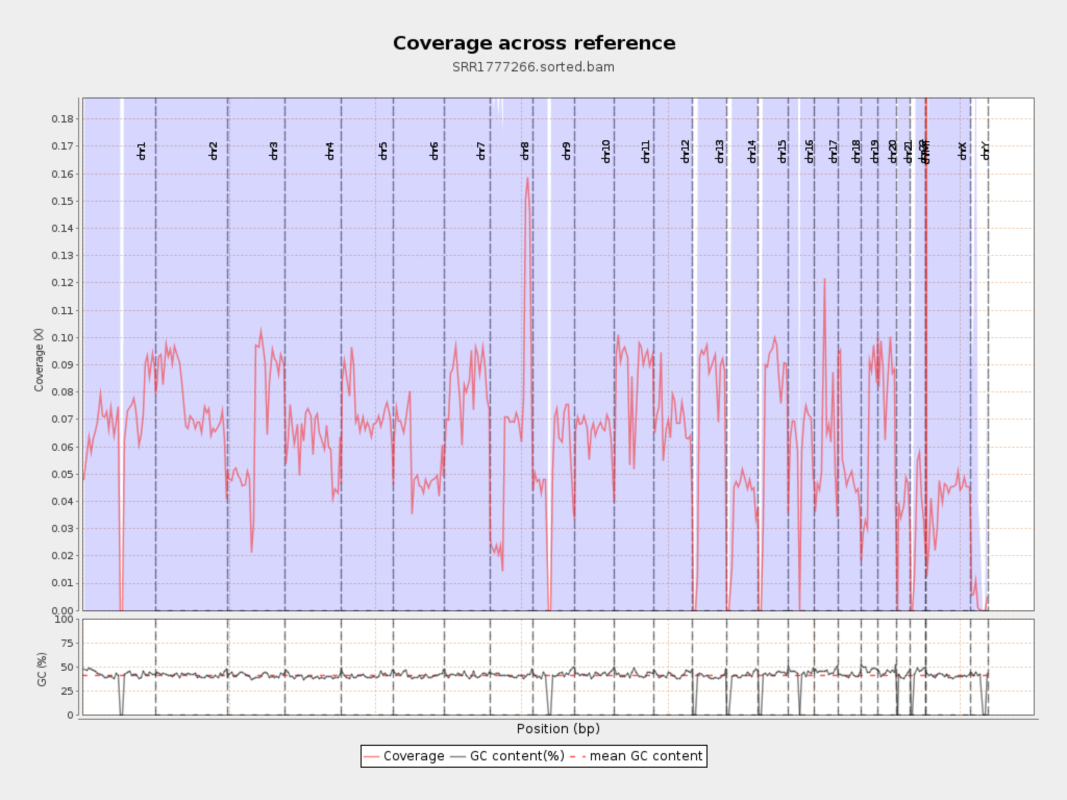
2.7. Chromosome stats

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

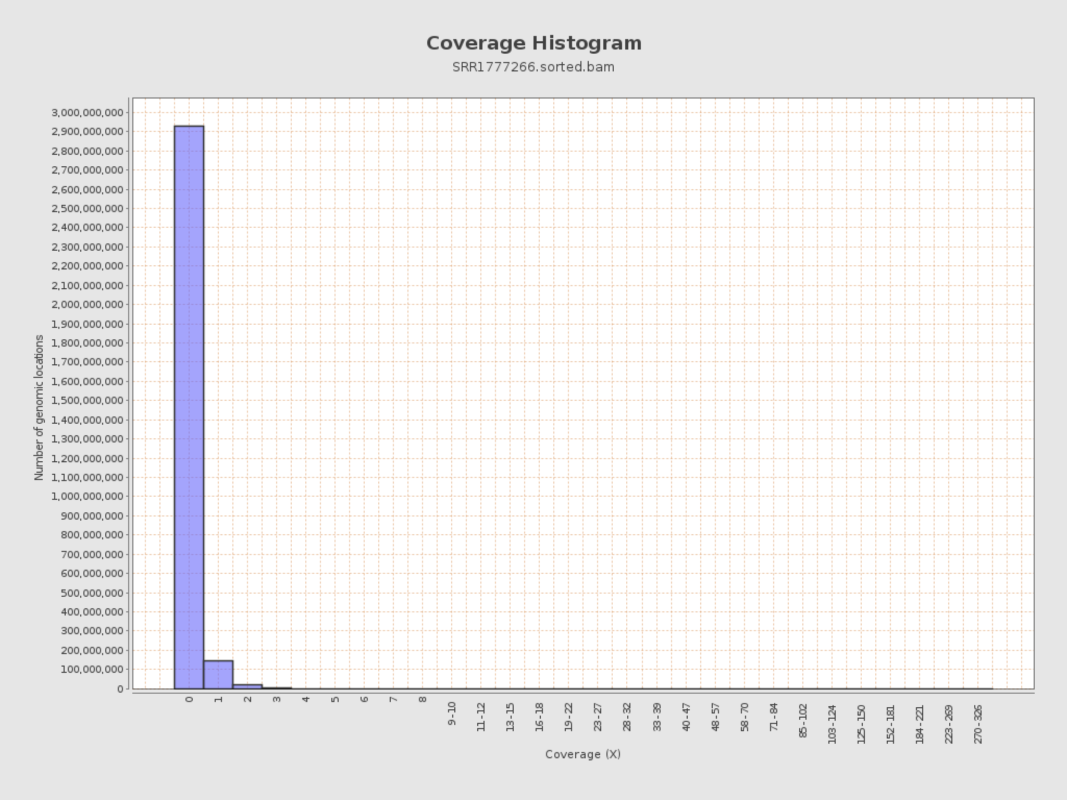
		bases	coverage	deviation
chr1	249250621	16789091	0.0674	0.437
chr2	243199373	18675588	0.0768	0.3238
chr3	198022430	13610097	0.0687	0.2925
chr4	191154276	11877956	0.0621	0.2789
chr5	180915260	13263352	0.0733	0.3015
chr6	171115067	9475934	0.0554	0.2957
chr7	159138663	13132384	0.0825	0.3435
chr8	146364022	9878544	0.0675	0.2944
chr9	141213431	7220997	0.0511	0.3236
chr10	135534747	8975244	0.0662	0.3517
chr11	135006516	11681844	0.0865	0.3375
chr12	133851895	9298499	0.0695	0.2931
chr13	115169878	8540411	0.0742	0.3042
chr14	107349540	4027114	0.0375	0.2157
chr15	102531392	7517176	0.0733	0.3032
chr16	90354753	5254968	0.0582	0.2855
chr17	81195210	5026031	0.0619	0.2949
chr18	78077248	4231500	0.0542	0.3404
chr19	59128983	3760770	0.0636	0.3376
chr20	63025520	5279831	0.0838	0.324
chr21	48129895	1748577	0.0363	0.2232
chr22	51304566	1572053	0.0306	0.1945
chrMT	16571	647137	39.0524	9.8749
chrX	155270560	6239604	0.0402	0.2257

chrY	59373566	210895	0.0036	0.0954

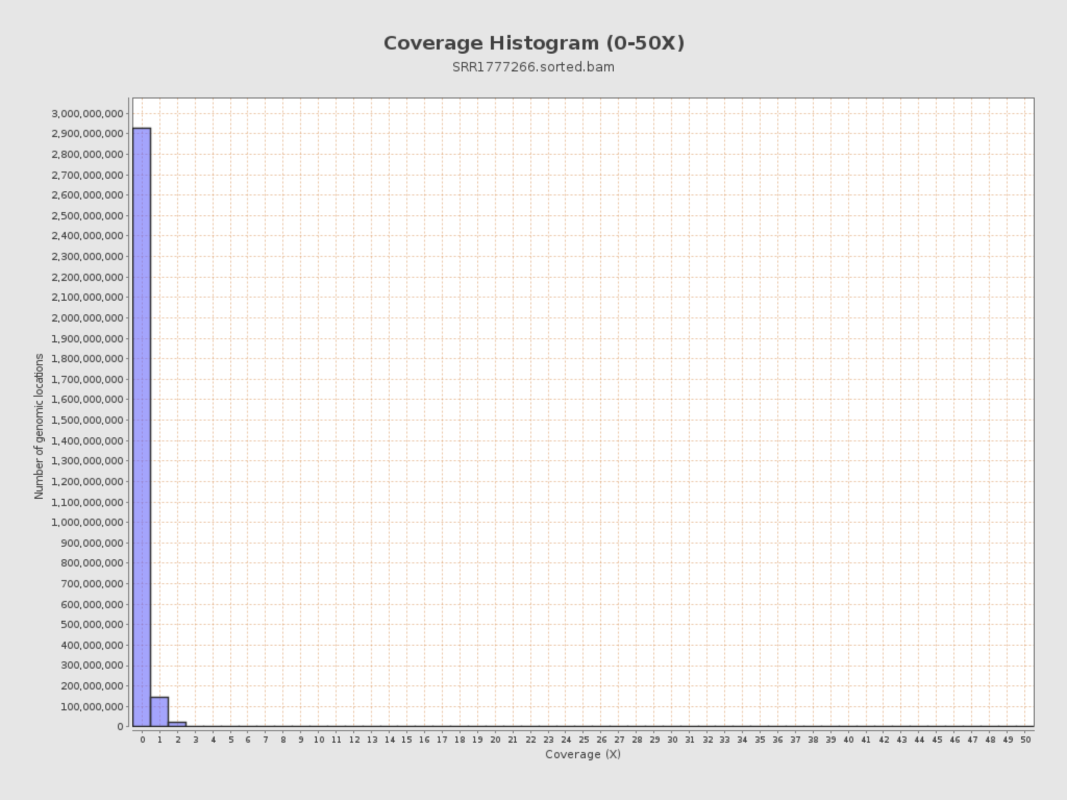
3. Results : Coverage across reference



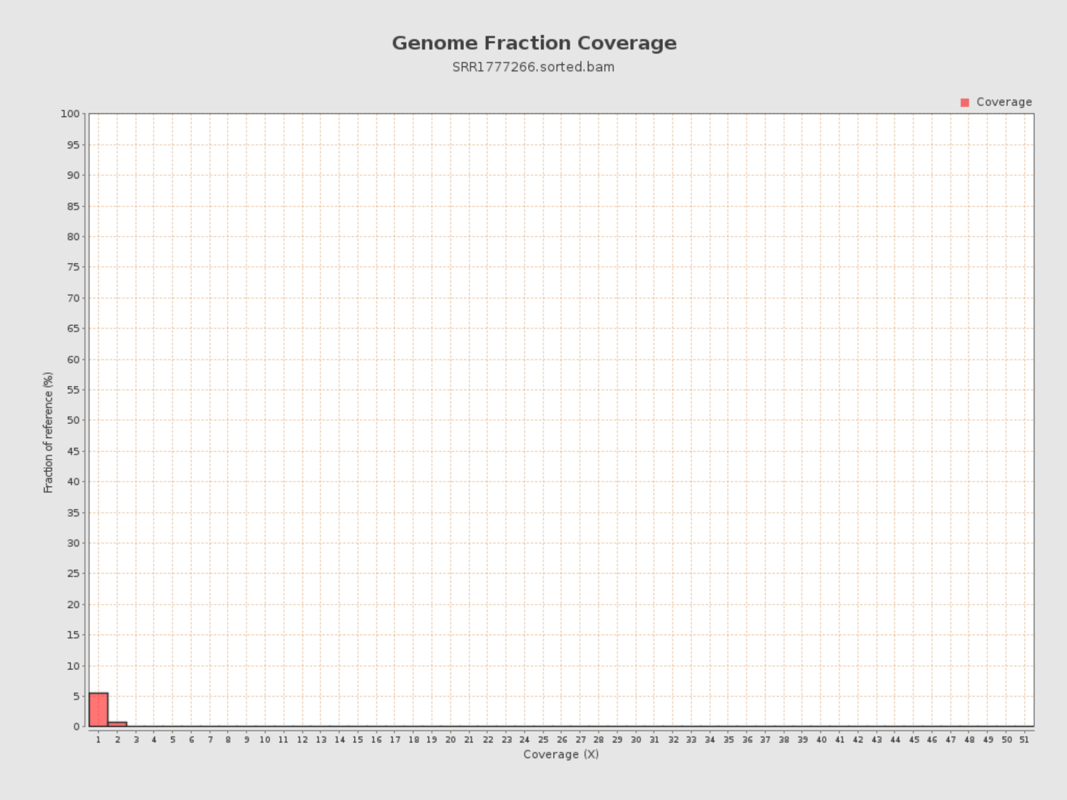
4. Results : Coverage Histogram



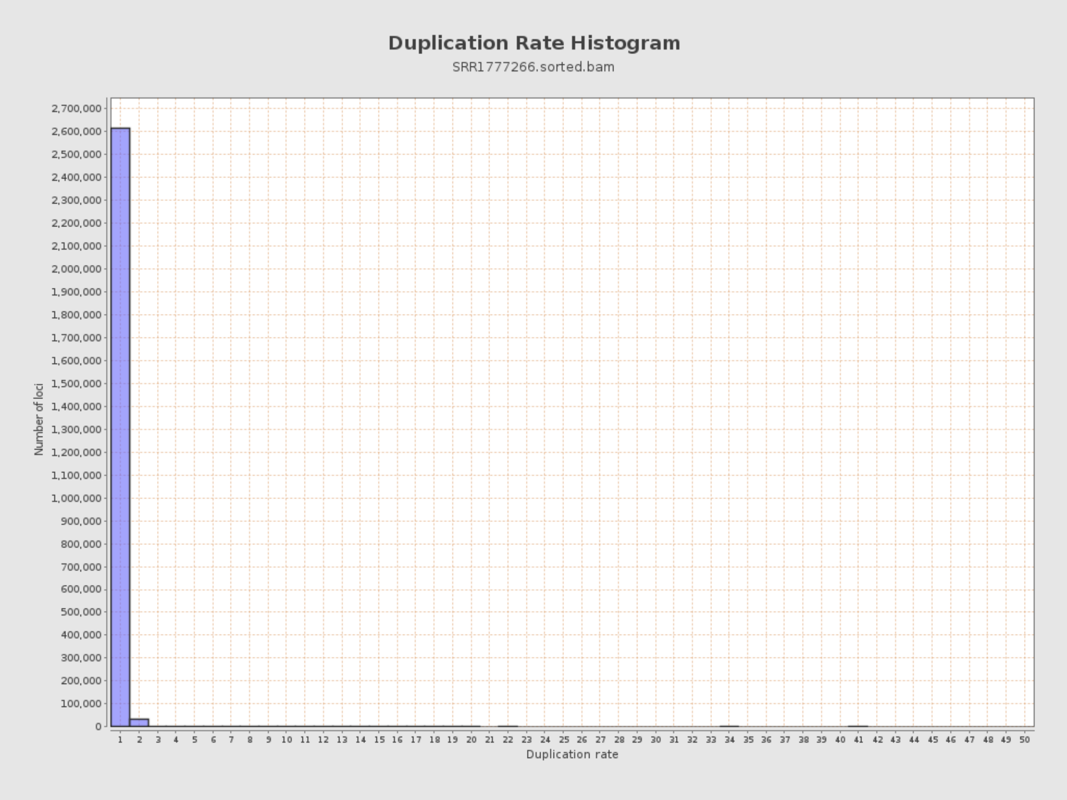
5. Results : Coverage Histogram (0-50X)



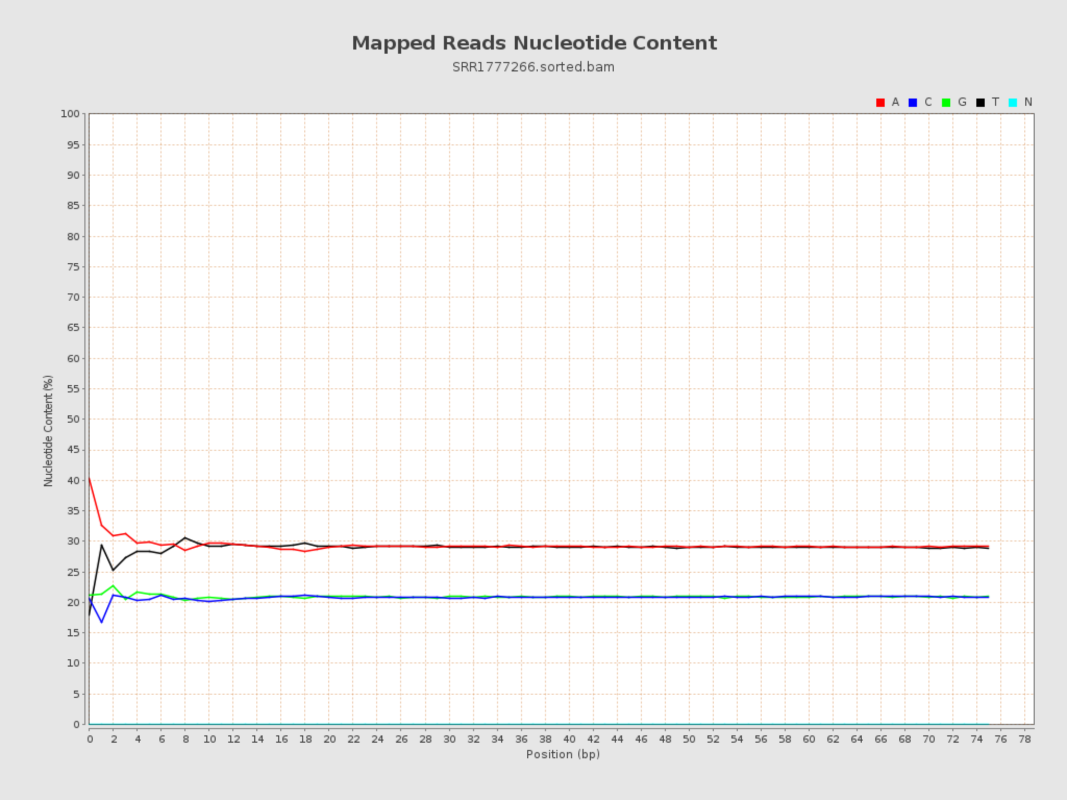
6. Results : Genome Fraction Coverage



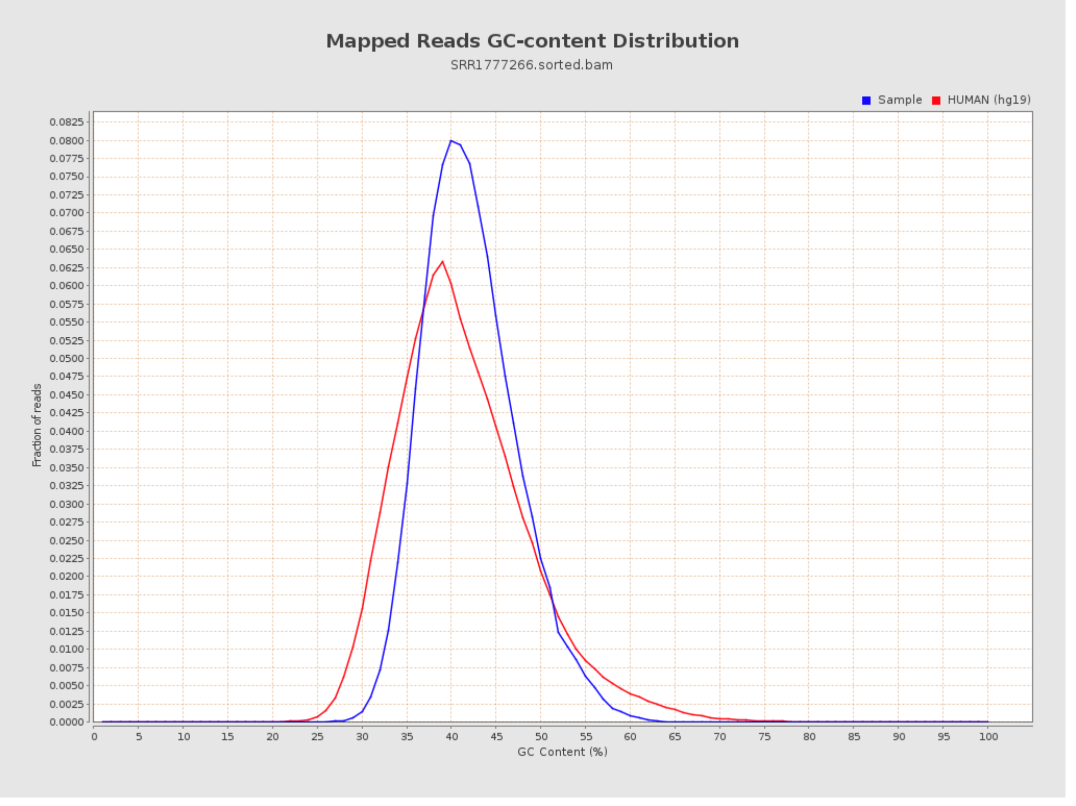
7. Results : Duplication Rate Histogram



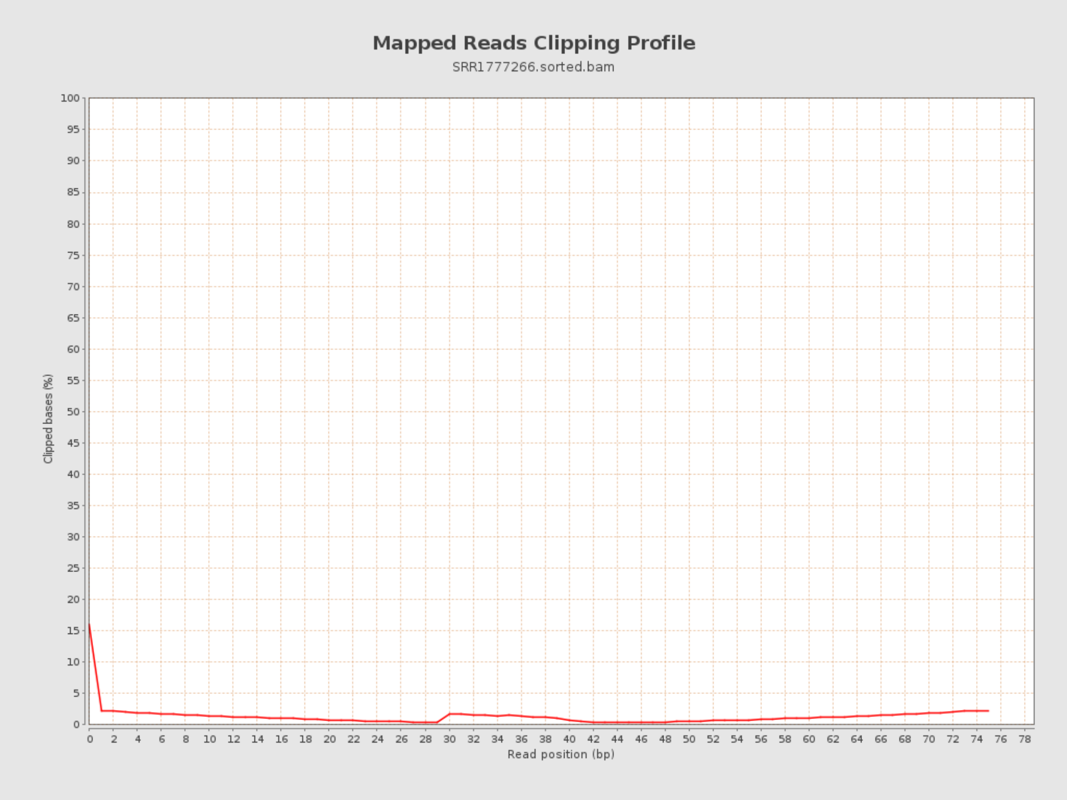
8. Results : Mapped Reads Nucleotide Content



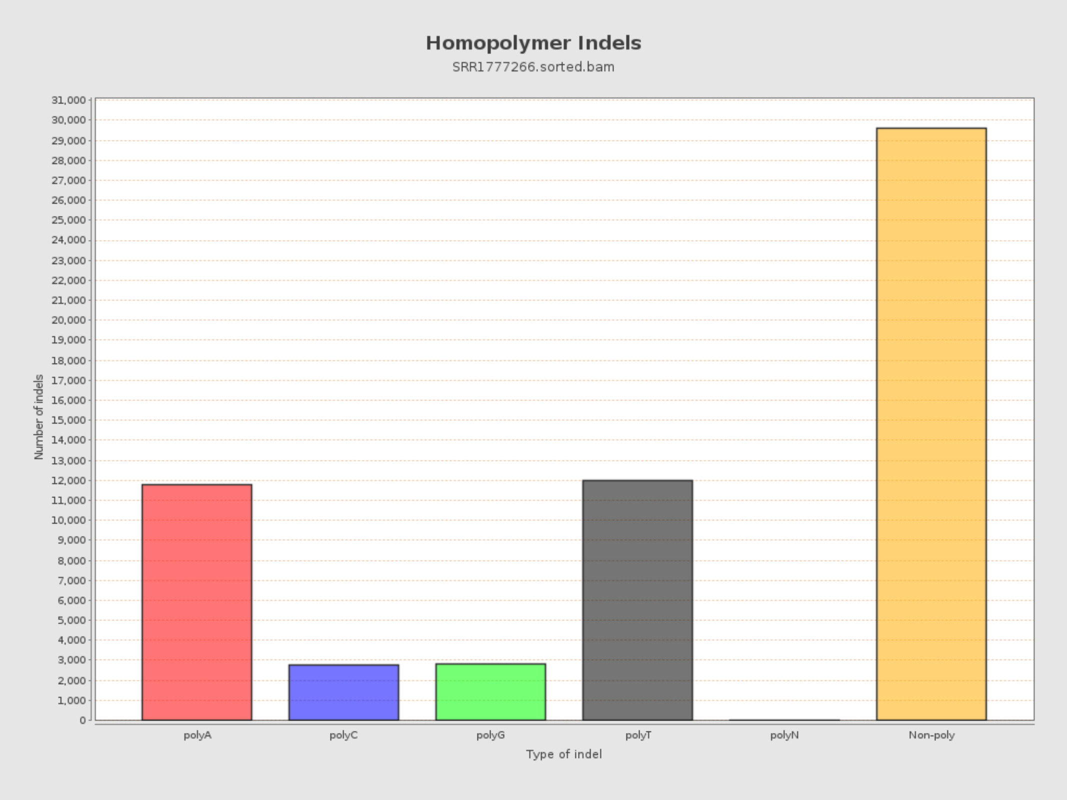
9. Results : Mapped Reads GC-content Distribution



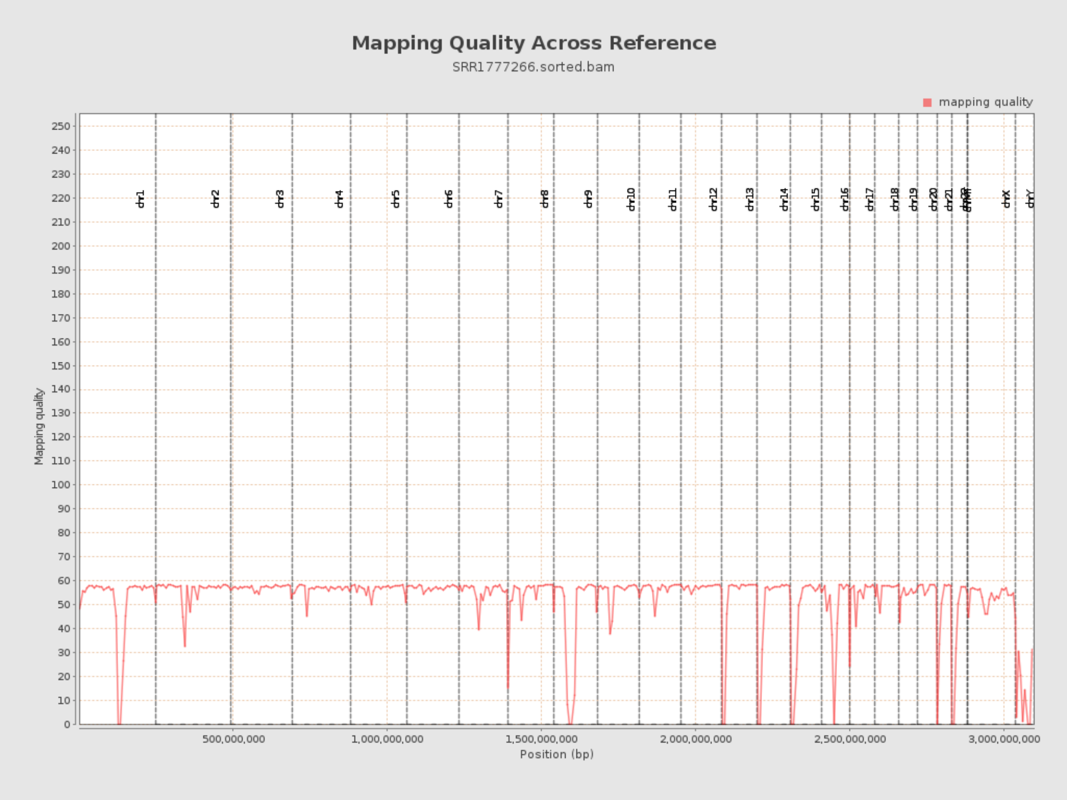
10. Results : Mapped Reads Clipping Profile



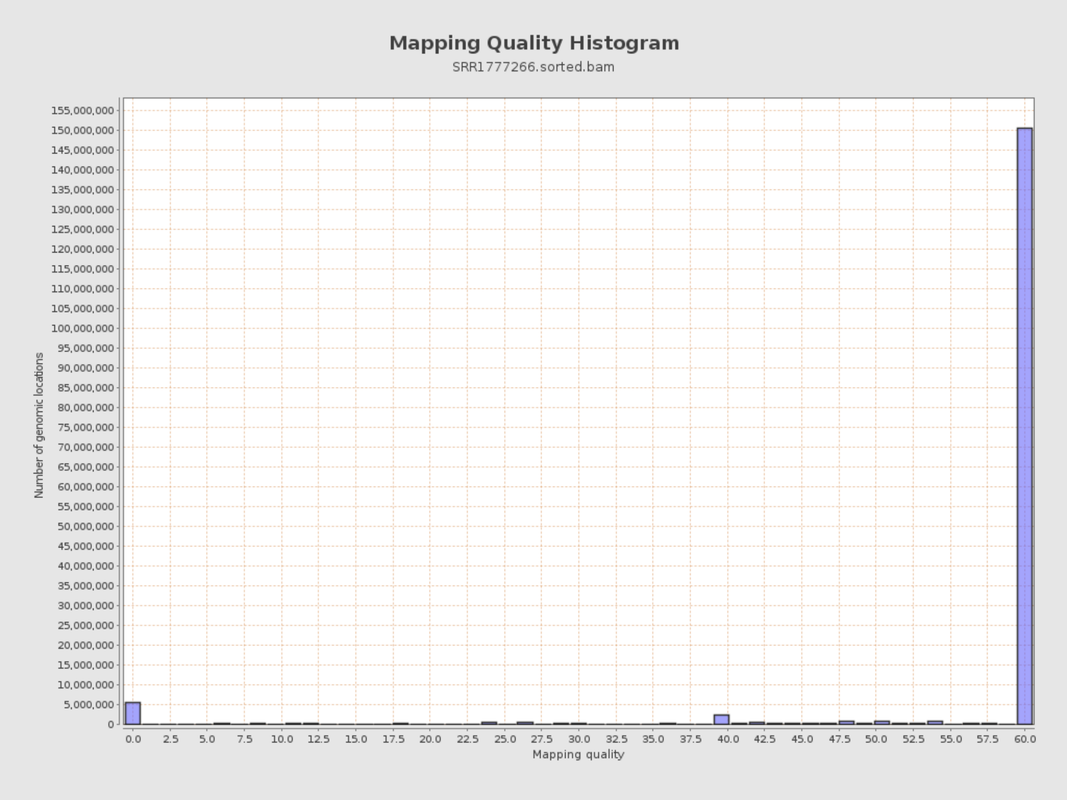
11. Results : Homopolymer Indels



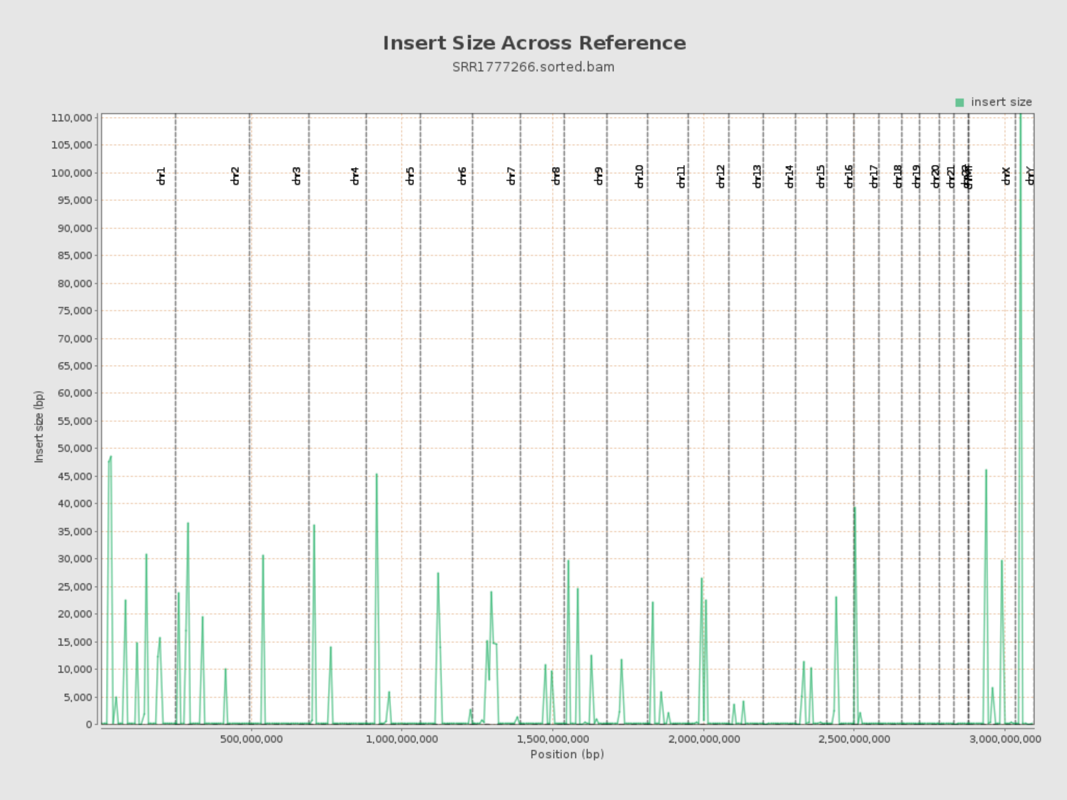
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram