Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 05:09:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777262.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_SRR1777262 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777262_1.fastq.gz SRR1777262_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 05:09:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777262.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,249,222
Mapped reads	3,151,416 / 96.99%
Unmapped reads	97,806 / 3.01%
Mapped paired reads	3,151,416 / 96.99%
Mapped reads, first in pair	1,580,916 / 48.66%
Mapped reads, second in pair	1,570,500 / 48.33%
Mapped reads, both in pair	3,132,942 / 96.42%
Mapped reads, singletons	18,474 / 0.57%
Secondary alignments	0
Supplementary alignments	53,914 / 1.66%
Read min/max/mean length	30 / 76 / 76.58
Duplicated reads (estimated)	46,290 / 1.42%
Duplication rate	1.36%
Clipped reads	378,042 / 11.63%

2.2. ACGT Content

Number/percentage of A's	70,134,590 / 29.72%
Number/percentage of C's	48,104,203 / 20.39%
Number/percentage of T's	68,659,571 / 29.1%
Number/percentage of G's	49,041,547 / 20.78%
Number/percentage of N's	13,630 / 0.01%

GC Percentage	41.17%

2.3. Coverage

Mean	0.0762
Standard Deviation	0.3539

2.4. Mapping Quality

Mean Mapping Quality	52.73

2.5. Insert size

Mean	168,728.5
Standard Deviation	3,900,762.07
P25/Median/P75	123 / 166 / 225

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	1,312,345
Insertions	45,138
Mapped reads with at least one insertion	1.42%
Deletions	21,460
Mapped reads with at least one deletion	0.67%
Homopolymer indels	49.61%

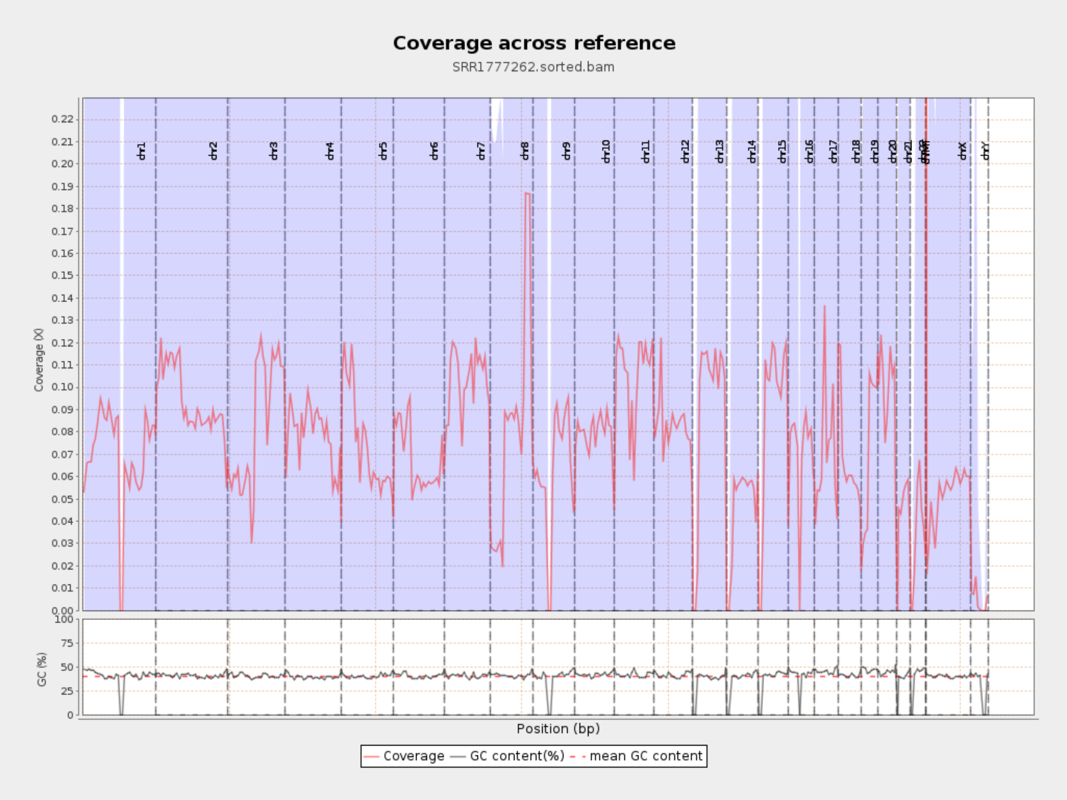
2.7. Chromosome stats

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

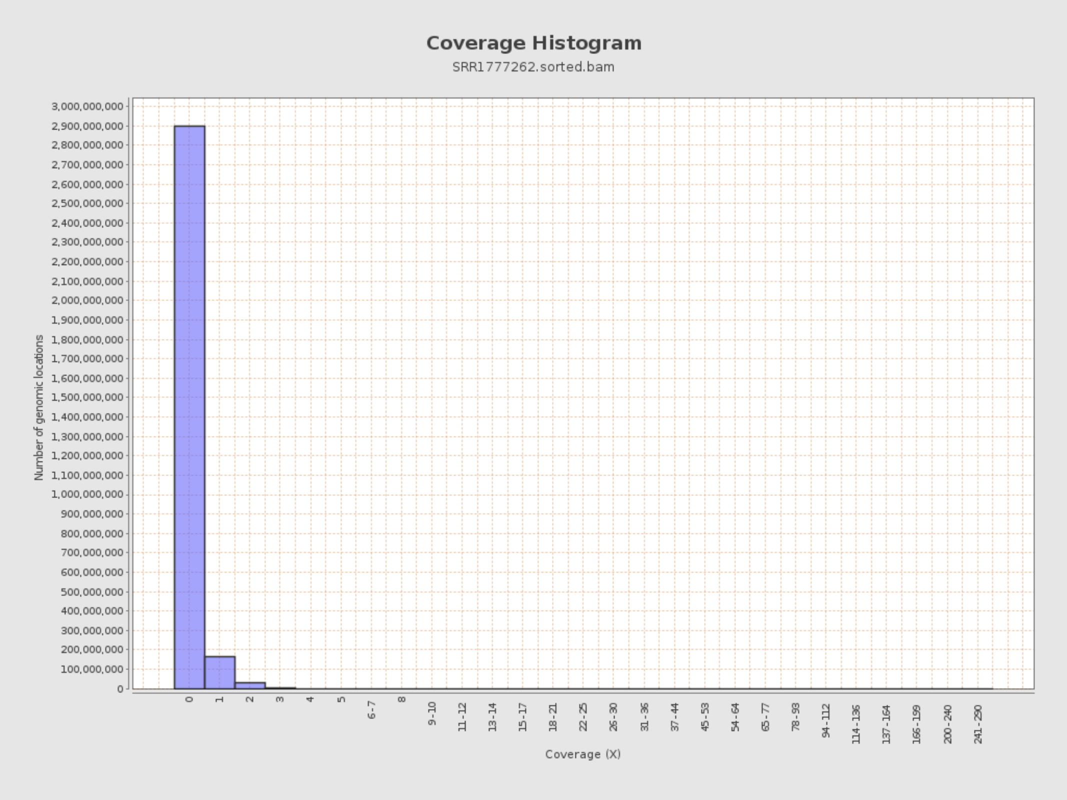
		bases	coverage	deviation
chr1	249250621	17416714	0.0699	0.4103
chr2	243199373	22875044	0.0941	0.3565
chr3	198022430	16475596	0.0832	0.3228
chr4	191154276	15179639	0.0794	0.3161
chr5	180915260	13640200	0.0754	0.3073
chr6	171115067	11613803	0.0679	0.3198
chr7	159138663	16336732	0.1027	0.3792
chr8	146364022	12178407	0.0832	0.3301
chr9	141213431	8850065	0.0627	0.3361
chr10	135534747	10869844	0.0802	0.3771
chr11	135006516	14199597	0.1052	0.372
chr12	133851895	11160054	0.0834	0.3226
chr13	115169878	10430271	0.0906	0.3385
chr14	107349540	4937645	0.046	0.2397
chr15	102531392	9052578	0.0883	0.3349
chr16	90354753	6240729	0.0691	0.3096
chr17	81195210	5723805	0.0705	0.3197
chr18	78077248	5270225	0.0675	0.3725
chr19	59128983	4243328	0.0718	0.347
chr20	63025520	6346319	0.1007	0.3568
chr21	48129895	2158267	0.0448	0.2458
chr22	51304566	1778737	0.0347	0.2087
chrMT	16571	819351	49.4449	12.0982
chrX	155270560	7915624	0.051	0.2552

chrY	59373566	282751	0.0048	0.1236

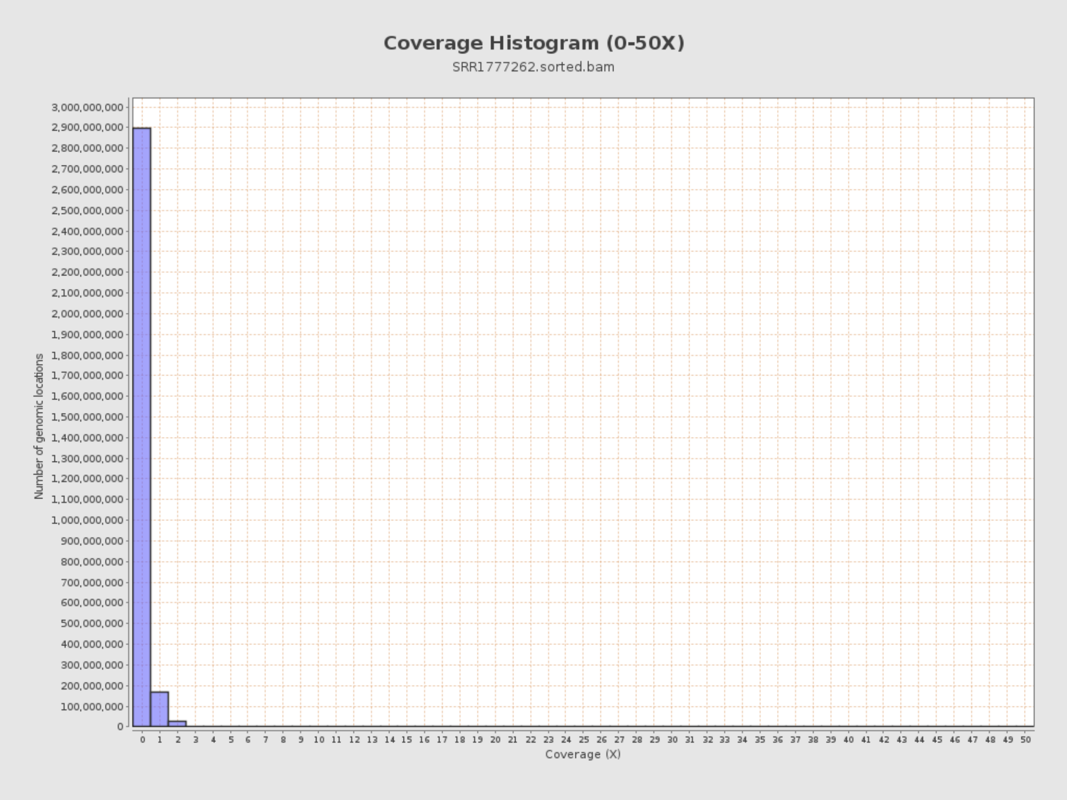
3. Results : Coverage across reference



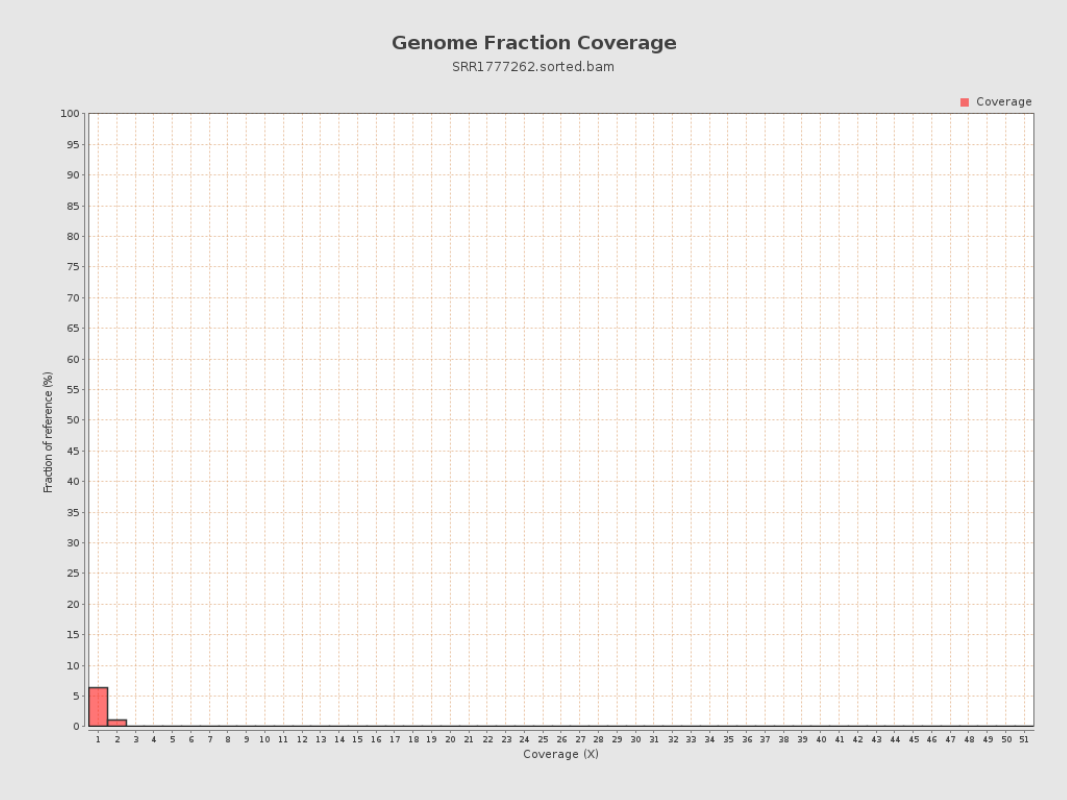
4. Results : Coverage Histogram



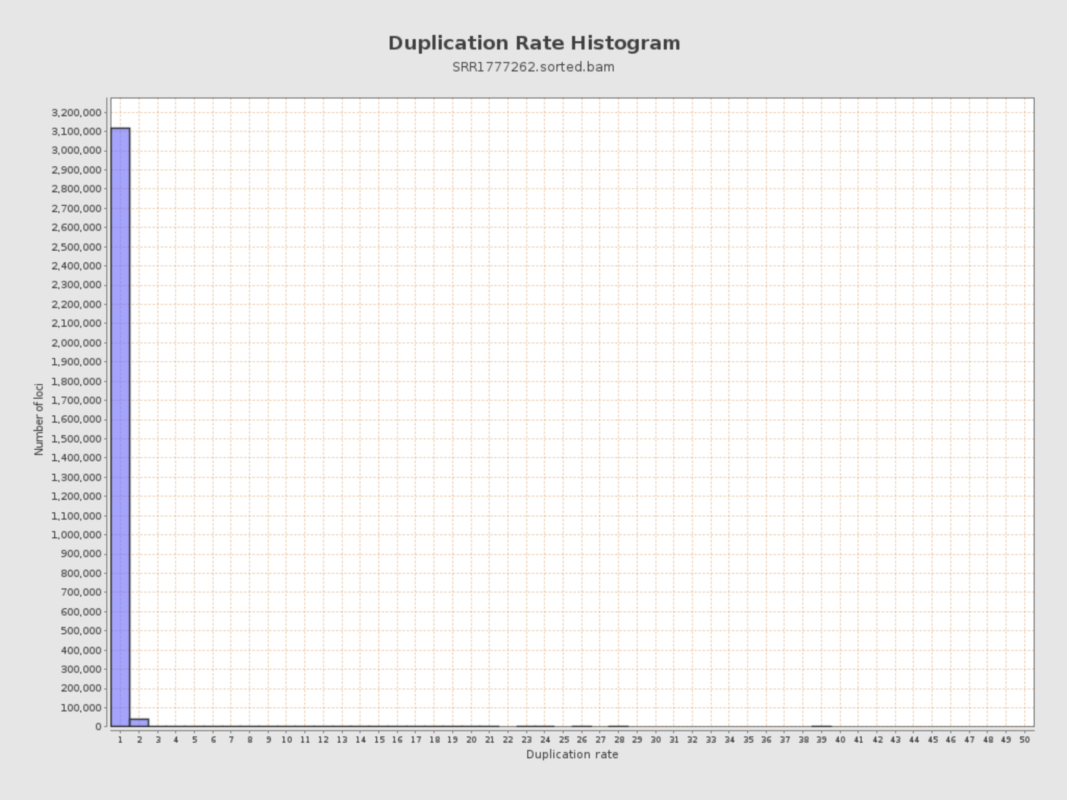
5. Results : Coverage Histogram (0-50X)



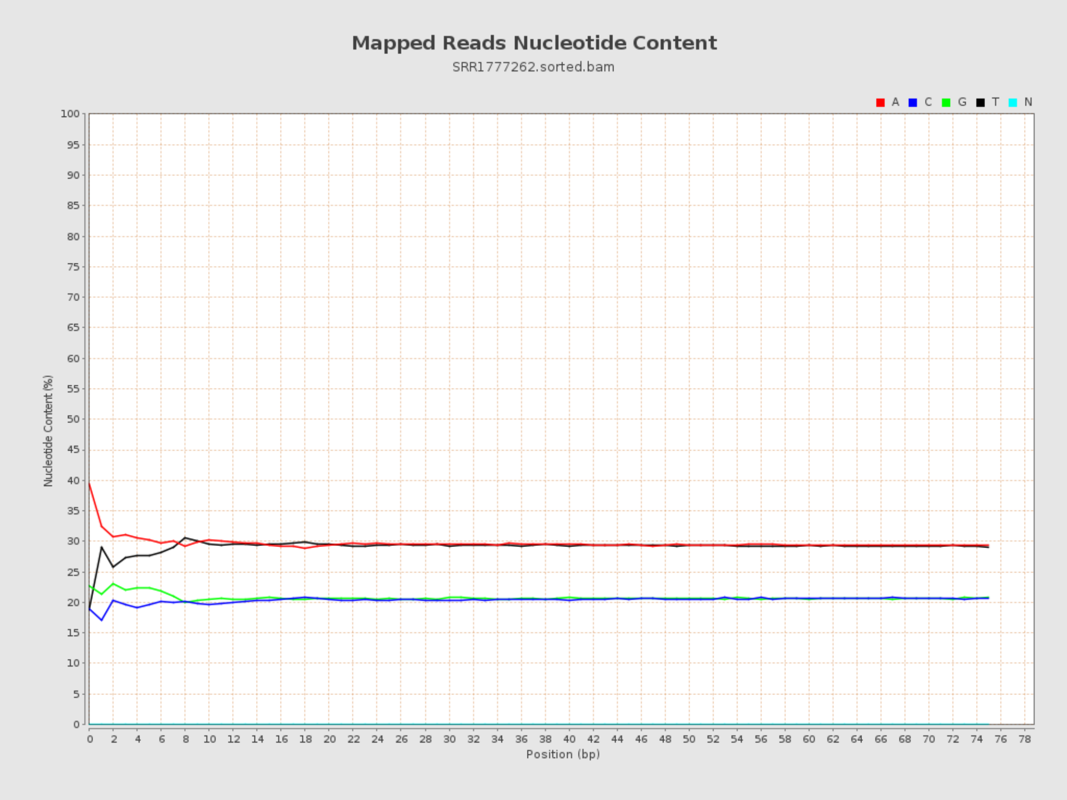
6. Results : Genome Fraction Coverage



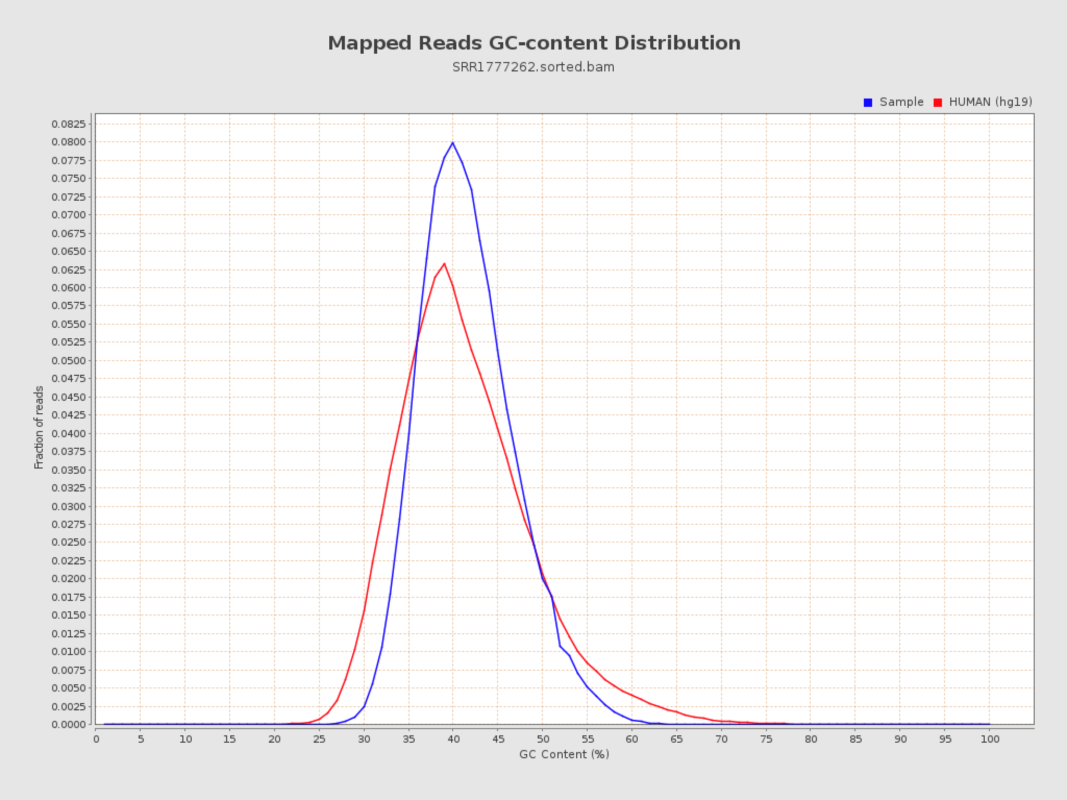
7. Results : Duplication Rate Histogram



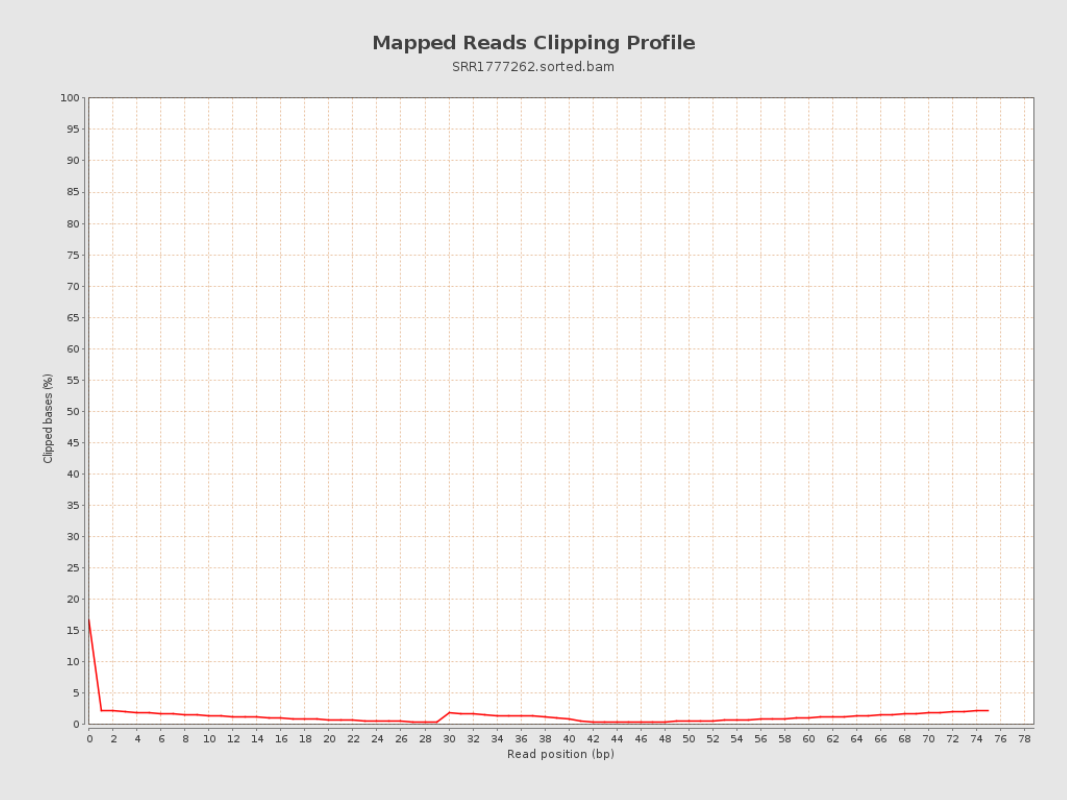
8. Results : Mapped Reads Nucleotide Content



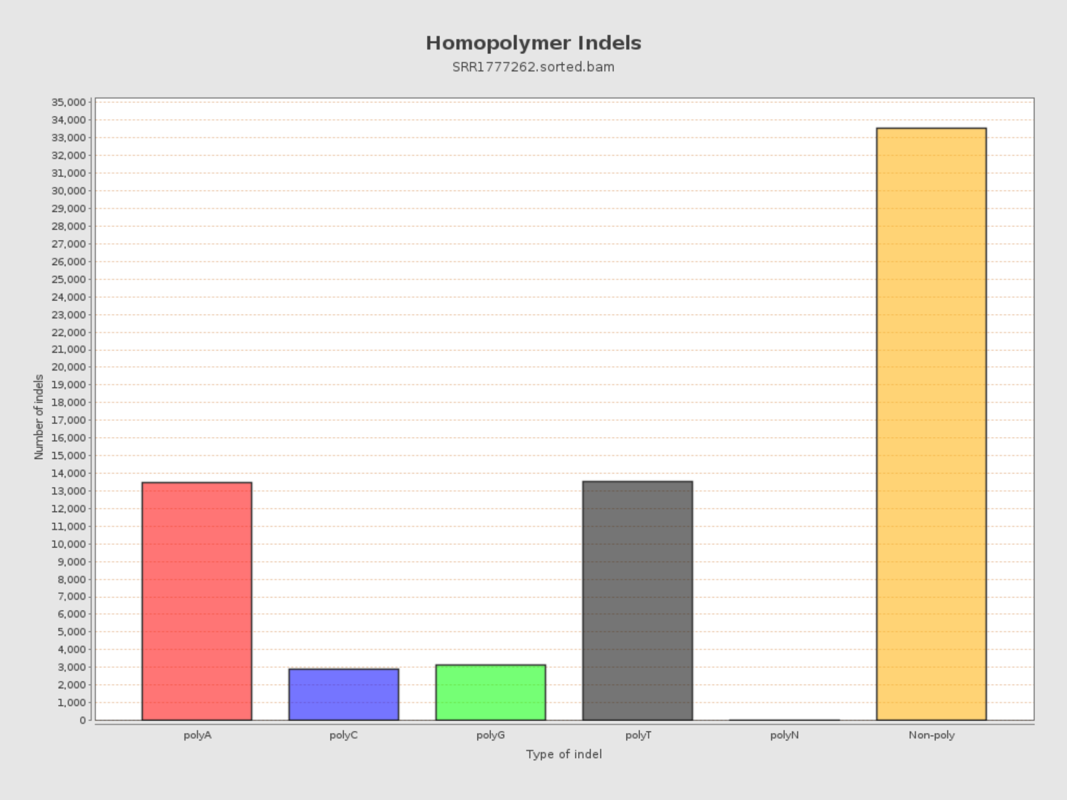
9. Results : Mapped Reads GC-content Distribution



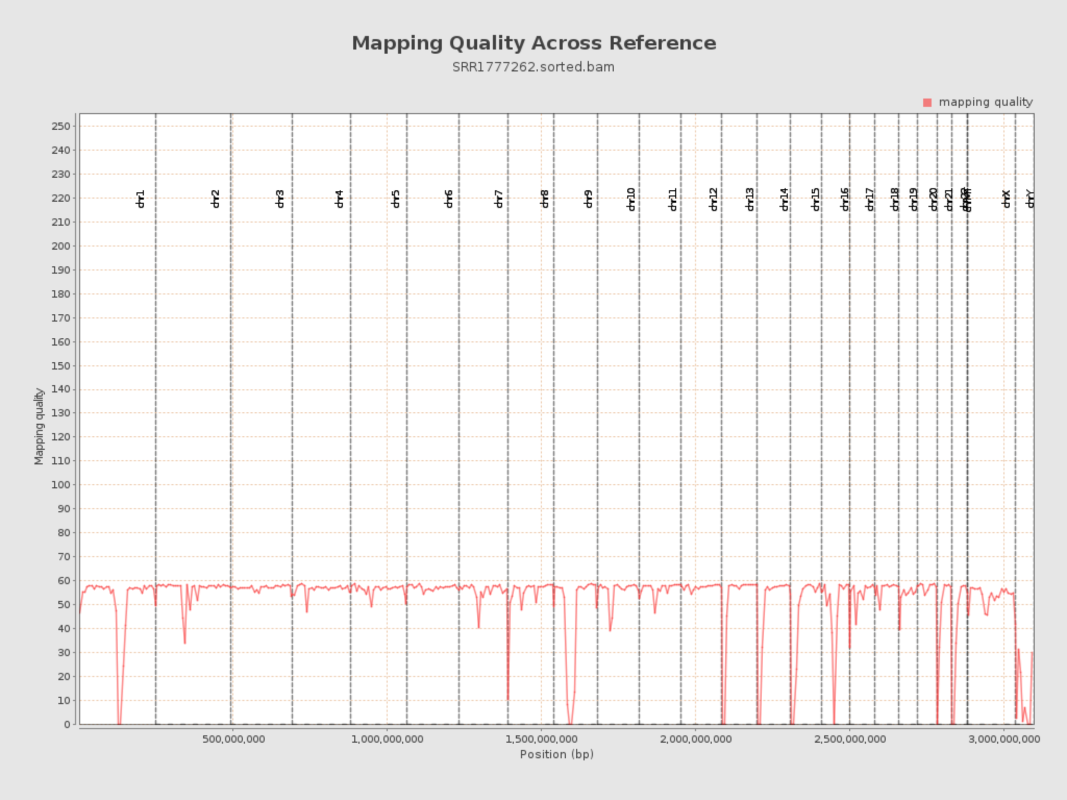
10. Results : Mapped Reads Clipping Profile



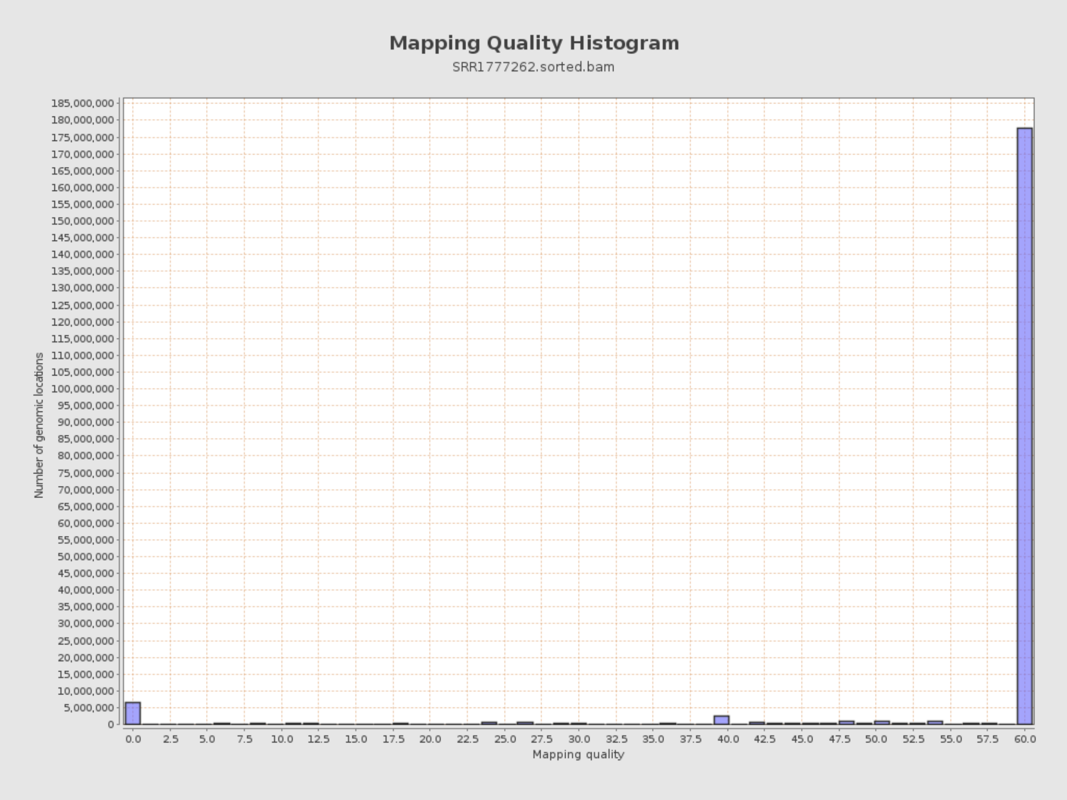
11. Results : Homopolymer Indels



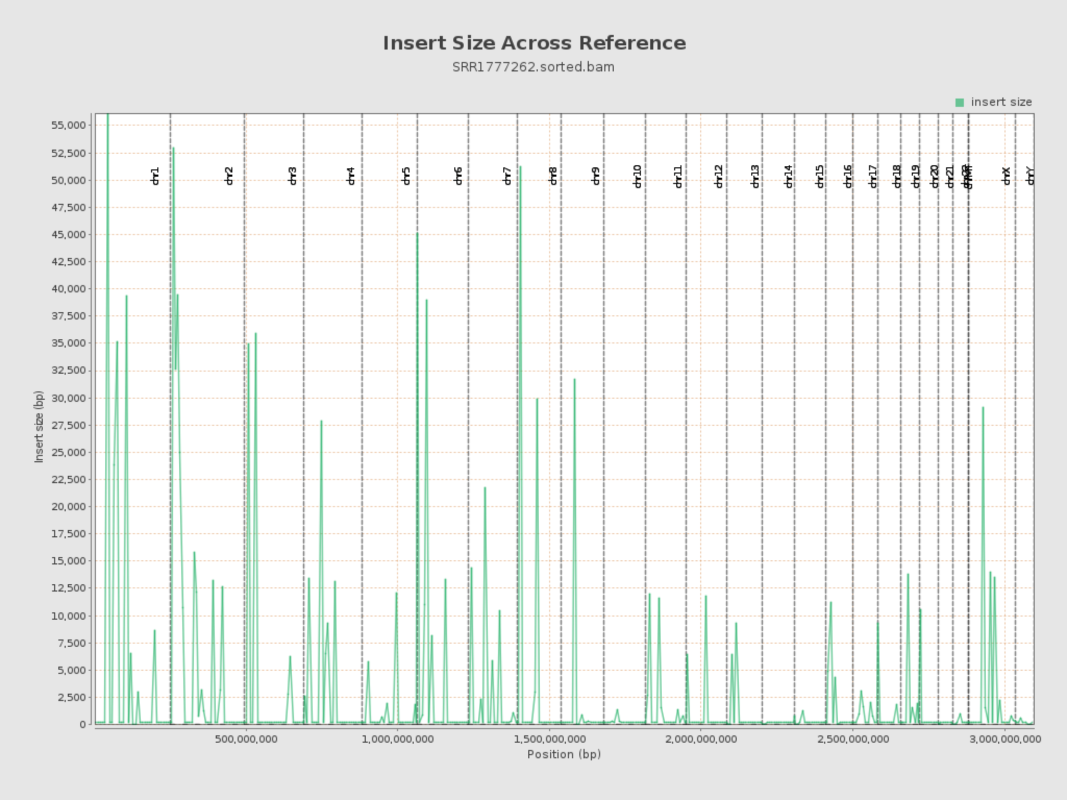
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram