Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/05 13:53:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777288.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_SRR1777288 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777288_1.fastq.gz SRR1777288_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 05 13:53:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777288.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	290,242,088
Mapped reads	283,972,727 / 97.84%
Unmapped reads	6,269,361 / 2.16%
Mapped paired reads	283,972,727 / 97.84%
Mapped reads, first in pair	142,432,378 / 49.07%
Mapped reads, second in pair	141,540,349 / 48.77%
Mapped reads, both in pair	282,481,026 / 97.33%
Mapped reads, singletons	1,491,701 / 0.51%
Secondary alignments	0
Supplementary alignments	14,336,980 / 4.94%
Read min/max/mean length	30 / 101 / 103.04
Duplicated reads (estimated)	86,025,722 / 29.64%
Duplication rate	22.9%
Clipped reads	94,437,741 / 32.54%

2.2. ACGT Content

Number/percentage of A's	7,987,802,361 / 29.25%
Number/percentage of C's	5,694,177,331 / 20.85%
Number/percentage of T's	7,821,785,284 / 28.64%
Number/percentage of G's	5,807,311,367 / 21.26%
Number/percentage of N's	1,099,244 / 0%

GC Percentage	42.11%

2.3. Coverage

Mean	8.8253
Standard Deviation	84.3095

2.4. Mapping Quality

Mean Mapping Quality	52.97

2.5. Insert size

Mean	159,733.82
Standard Deviation	3,819,657.21
P25/Median/P75	108 / 154 / 218

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	141,369,758
Insertions	6,146,738
Mapped reads with at least one insertion	2.12%
Deletions	3,370,447
Mapped reads with at least one deletion	1.15%
Homopolymer indels	46.46%

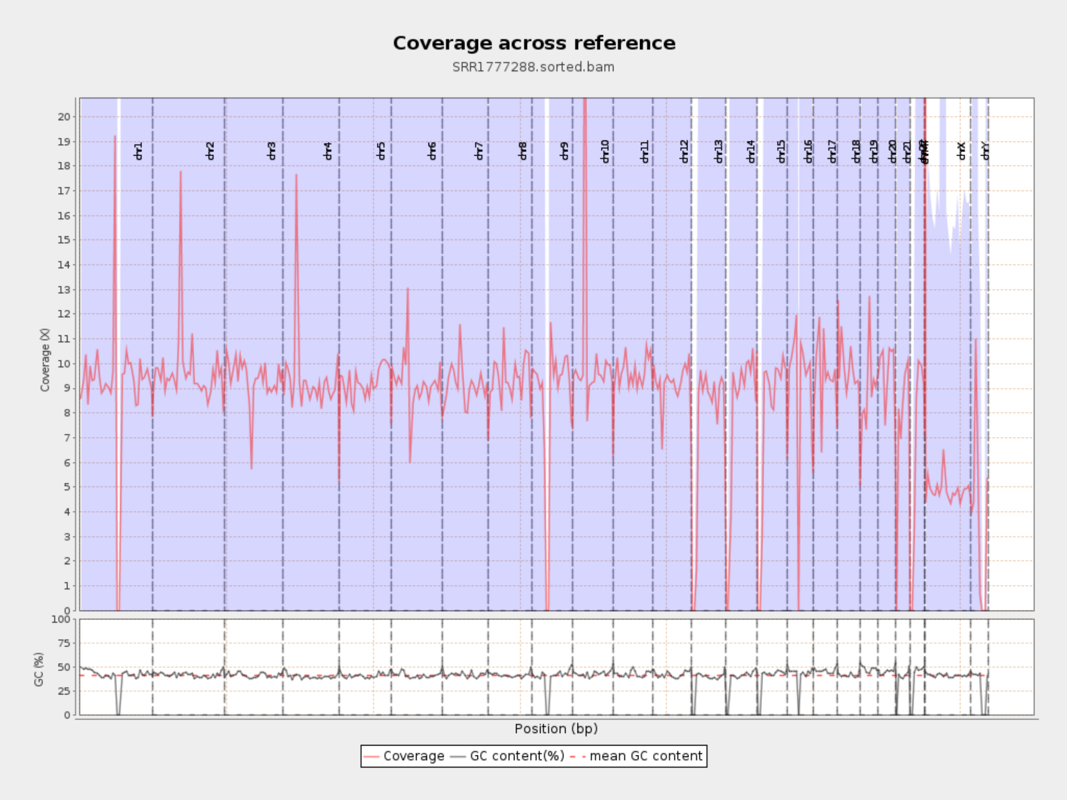
2.7. Chromosome stats

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

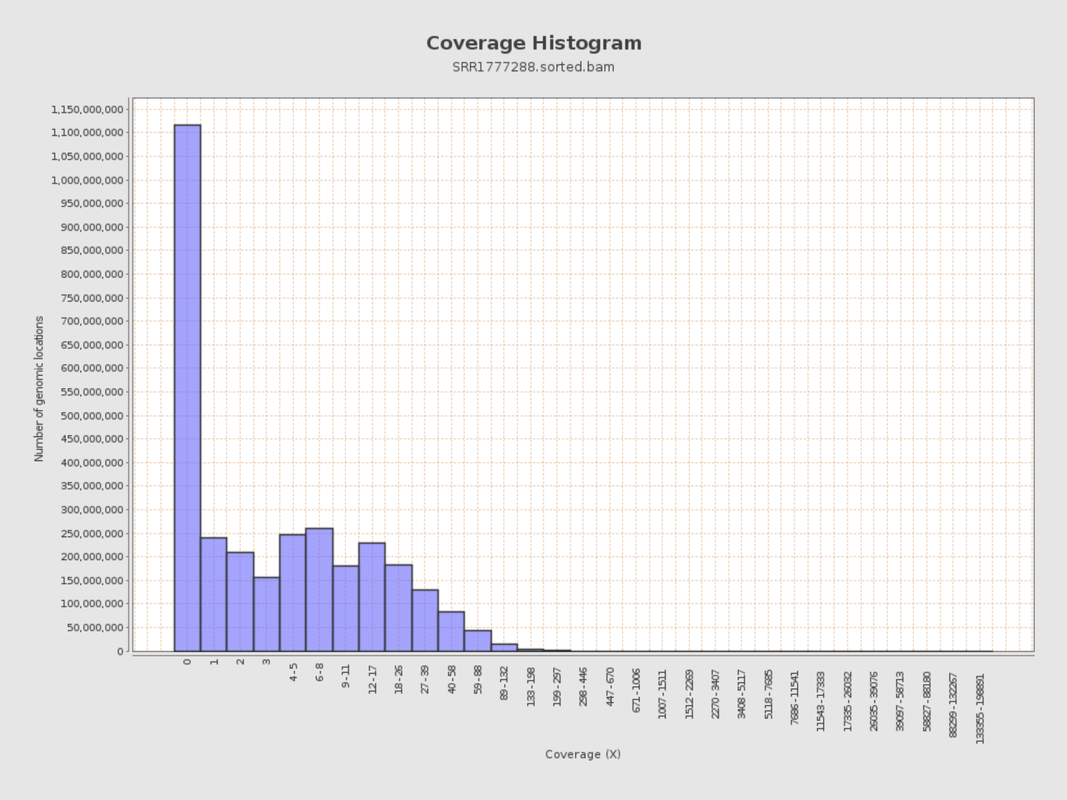
		bases	coverage	deviation
chr1	249250621	2270355398	9.1087	197.0305
chr2	243199373	2368799961	9.7402	61.3512
chr3	198022430	1853886066	9.362	24.4499
chr4	191154276	1798269866	9.4074	64.0596
chr5	180915260	1674239453	9.2543	17.5798
chr6	171115067	1583272153	9.2527	46.5435
chr7	159138663	1456851480	9.1546	72.7058
chr8	146364022	1380036319	9.4288	35.3691
chr9	141213431	1183352458	8.3799	84.9685
chr10	135534747	1441350204	10.6345	177.2508
chr11	135006516	1298651328	9.6192	45.9944
chr12	133851895	1230266007	9.1912	17.004
chr13	115169878	858931926	7.458	14.6576
chr14	107349540	845342047	7.8747	16.9261
chr15	102531392	779969467	7.6071	15.1126
chr16	90354753	806017494	8.9206	33.332
chr17	81195210	770393379	9.4882	48.9713
chr18	78077248	768265021	9.8398	112.8077
chr19	59128983	523343047	8.8509	111.7462
chr20	63025520	610578094	9.6878	23.5887
chr21	48129895	373900840	7.7686	34.2381
chr22	51304566	332233852	6.4757	15.189
chrMT	16571	121392127	7,325.5764	1,428.4629
chrX	155270560	757425286	4.8781	22.647

chrY	59373566	233430750	3.9316	63.8139

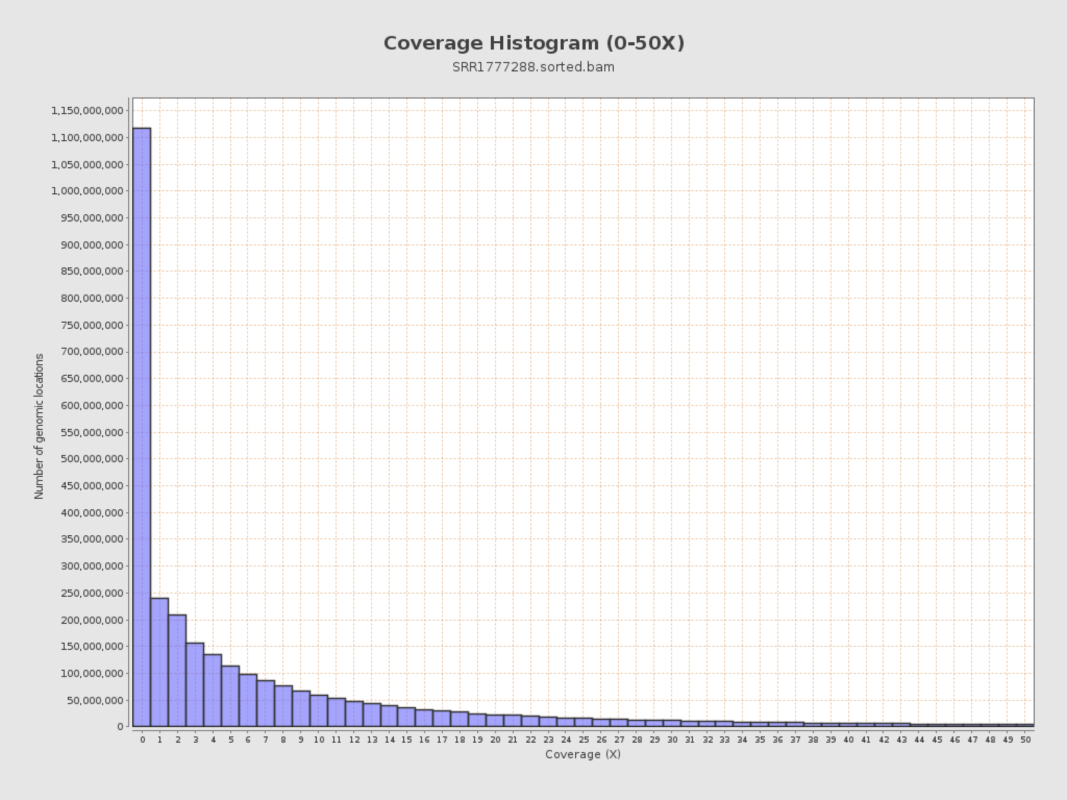
3. Results : Coverage across reference



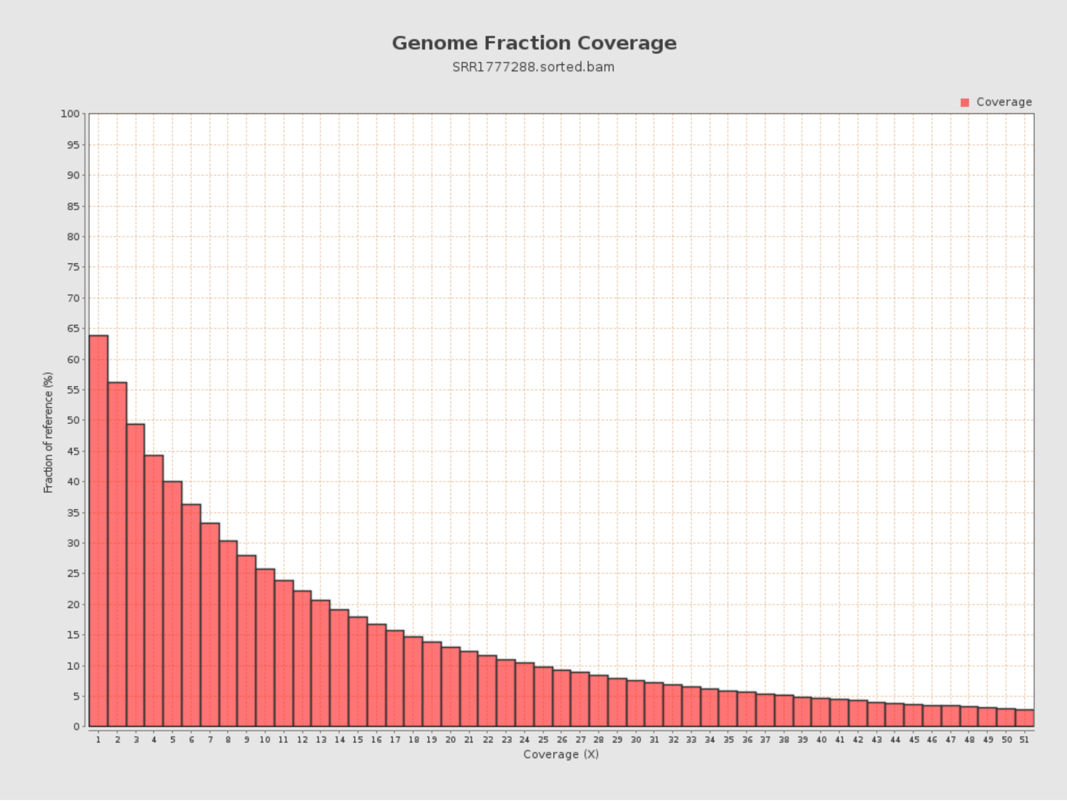
4. Results : Coverage Histogram



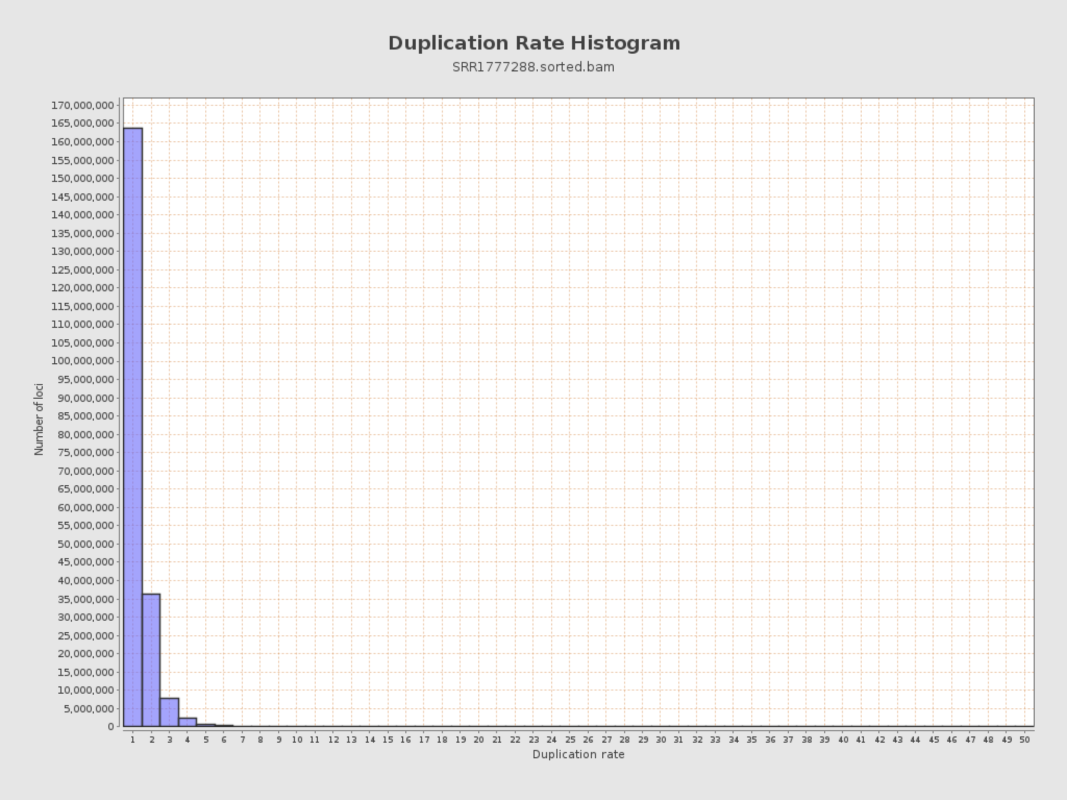
5. Results : Coverage Histogram (0-50X)



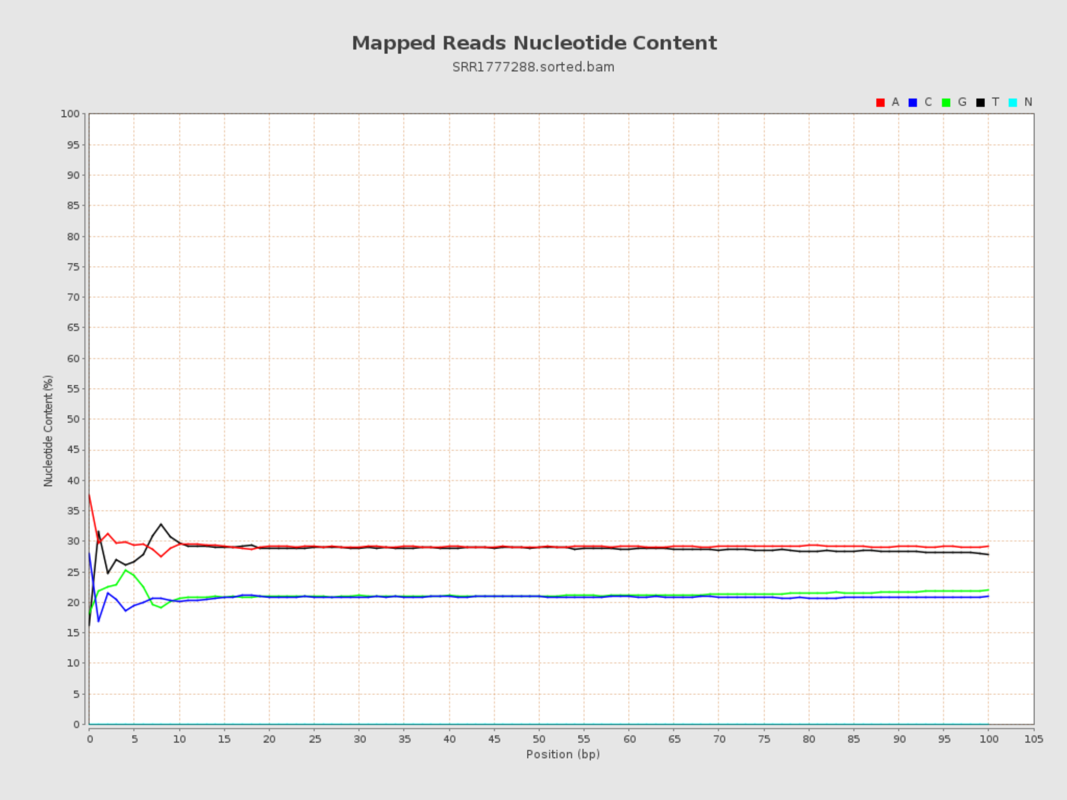
6. Results : Genome Fraction Coverage



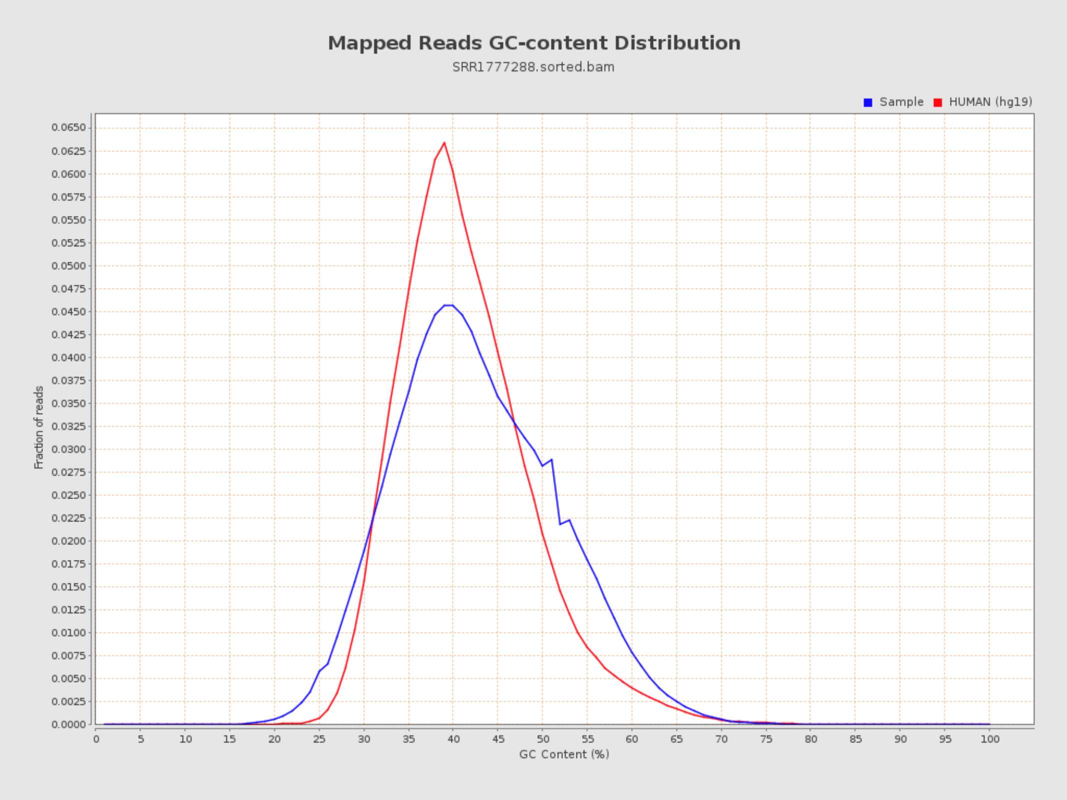
7. Results : Duplication Rate Histogram



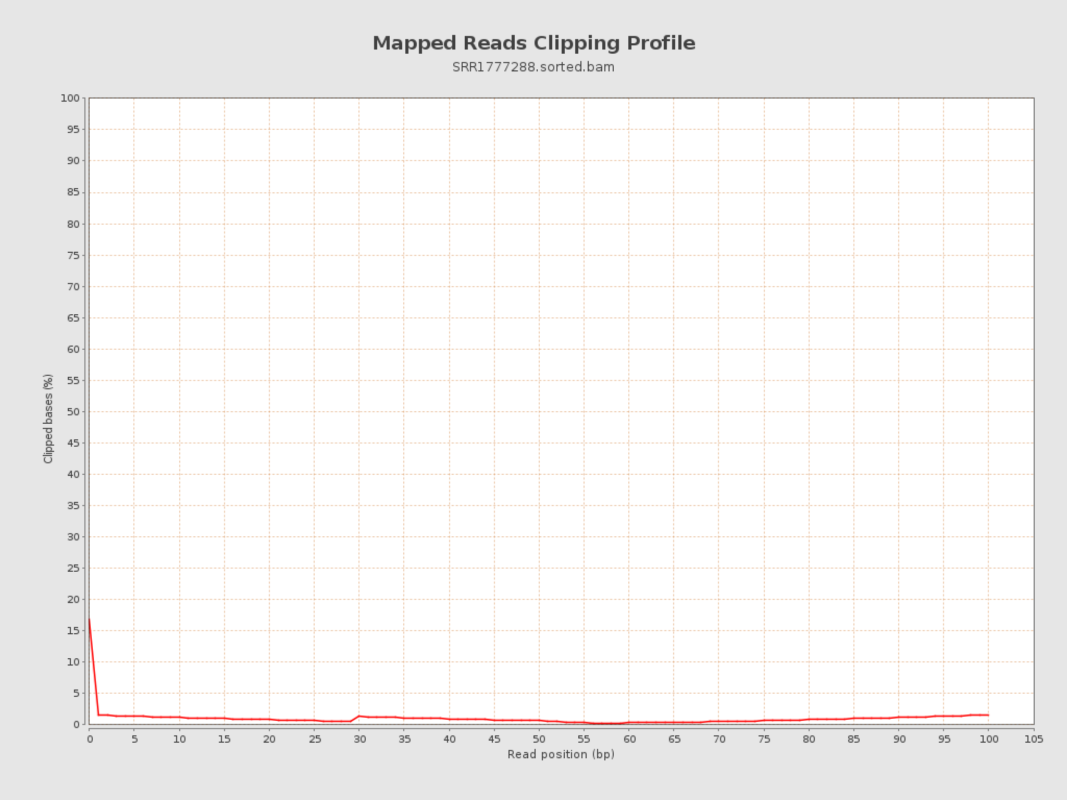
8. Results : Mapped Reads Nucleotide Content



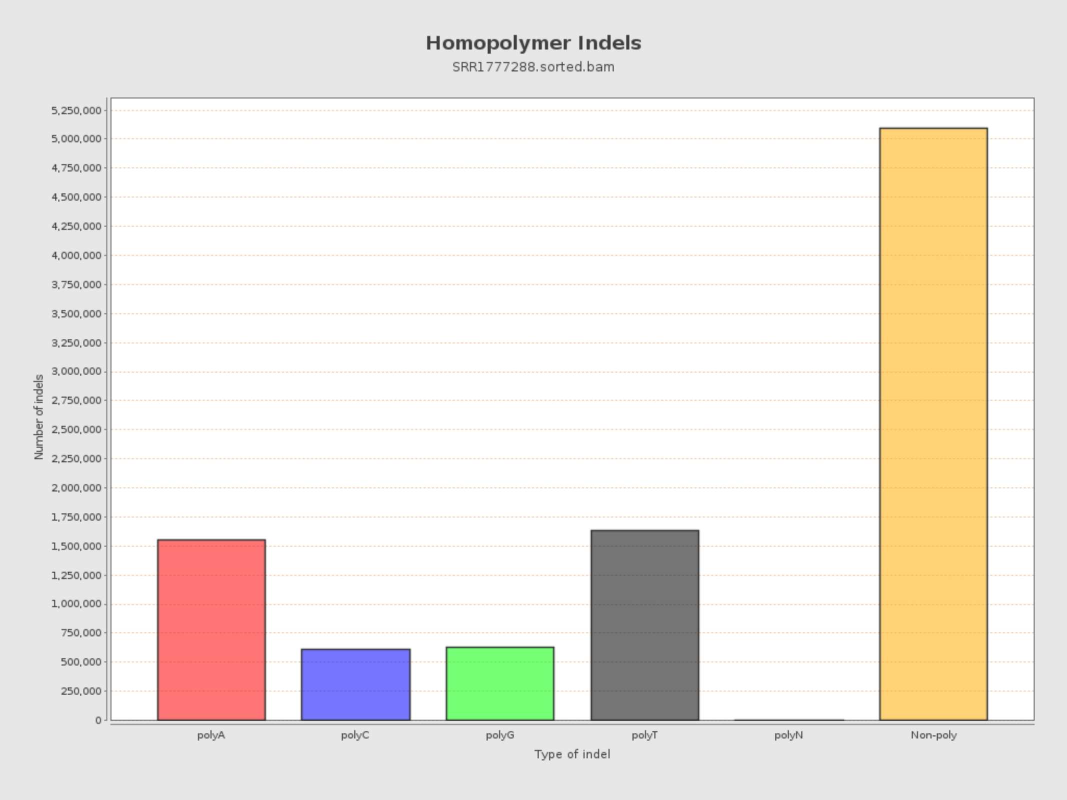
9. Results : Mapped Reads GC-content Distribution



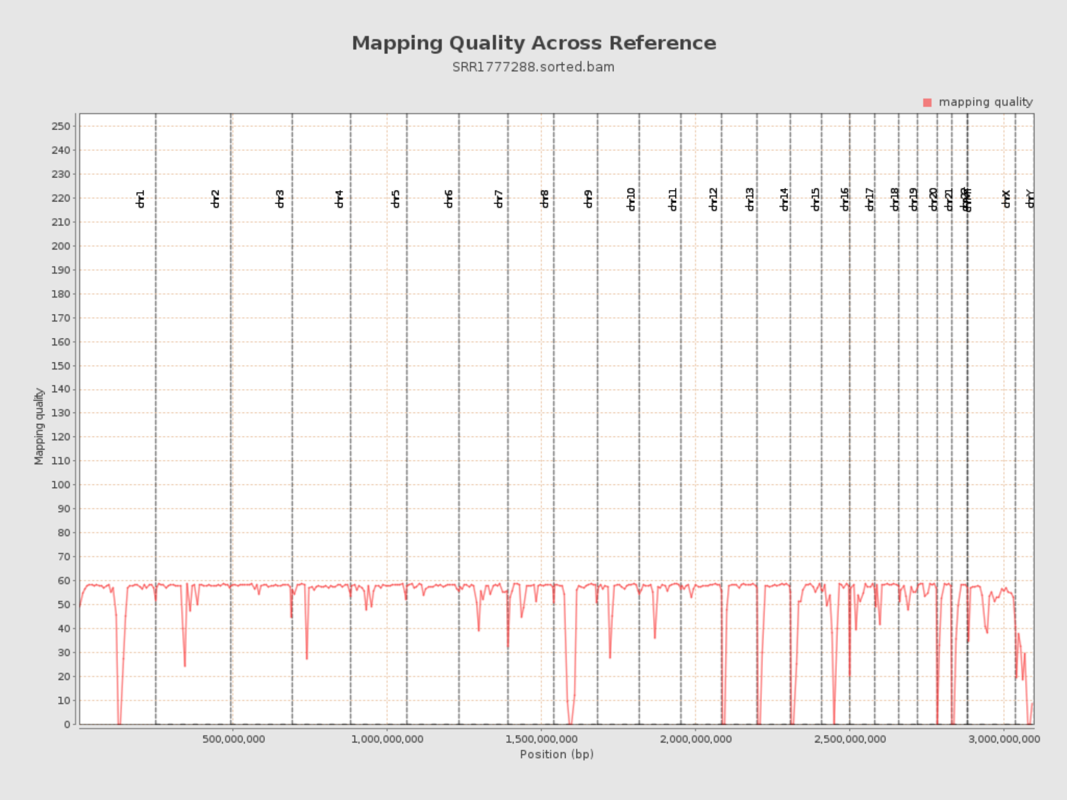
10. Results : Mapped Reads Clipping Profile



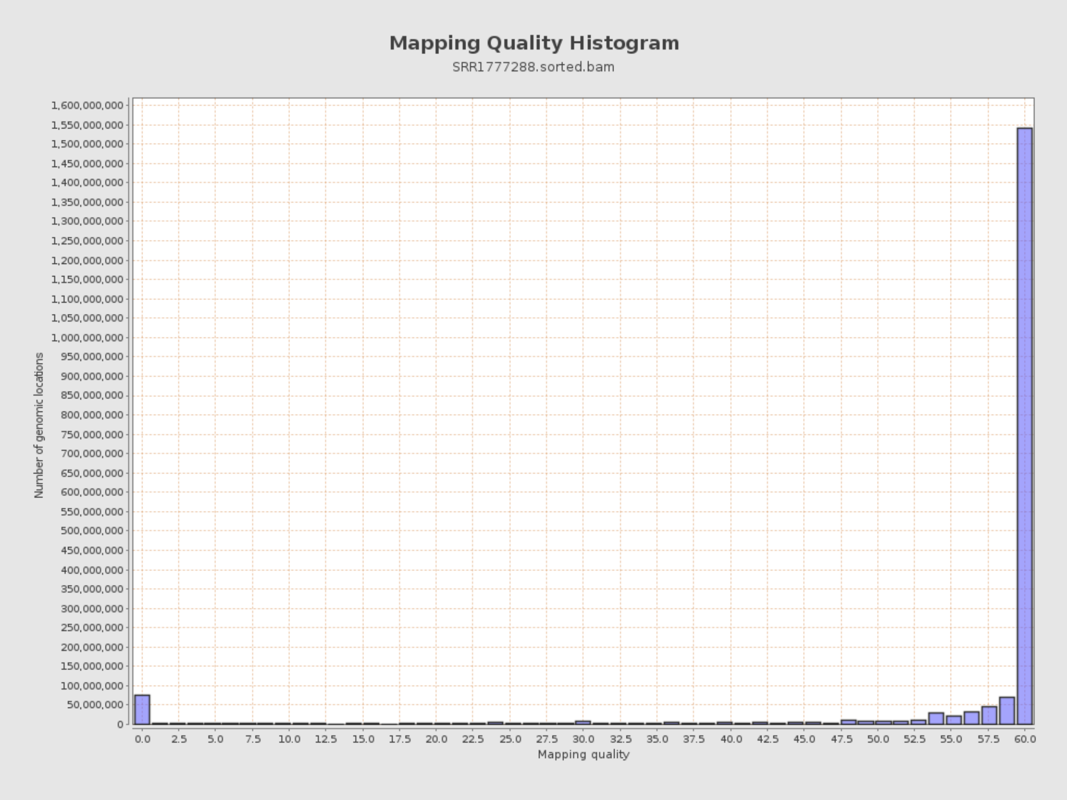
11. Results : Homopolymer Indels



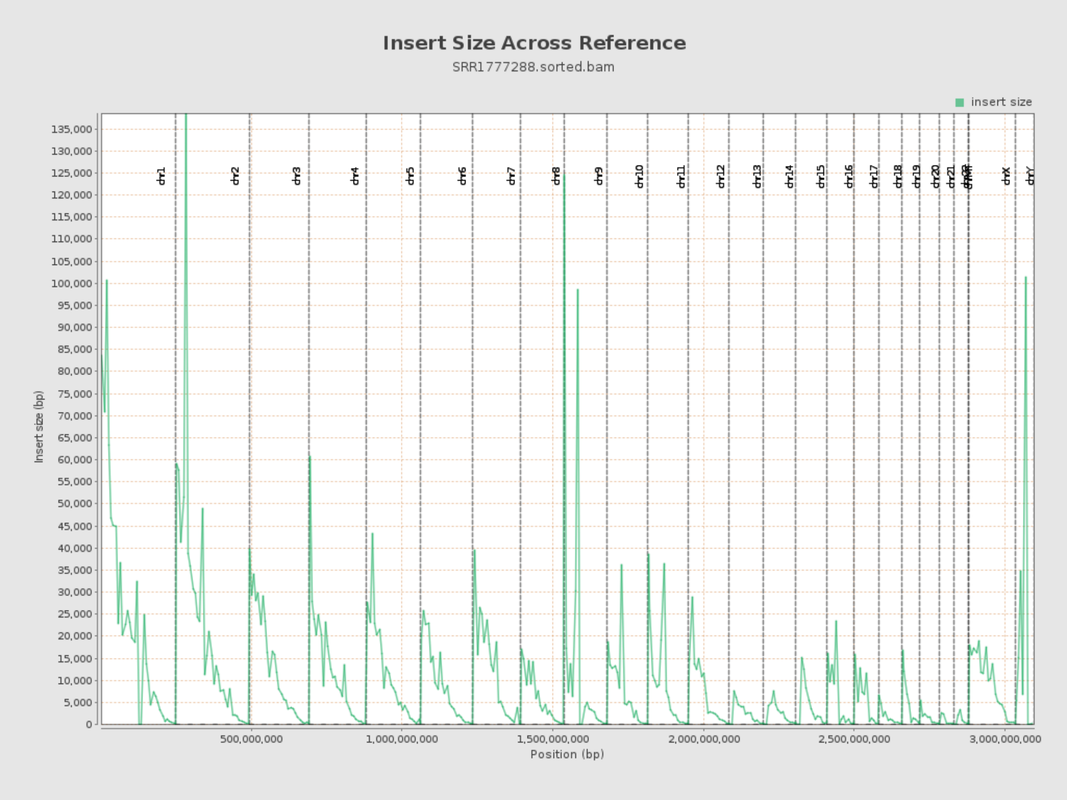
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram