Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/04 02:49:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777284.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_SRR1777284 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777284_1.fastq.gz SRR1777284_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 04 02:49:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777284.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	138,993,724
Mapped reads	137,145,857 / 98.67%
Unmapped reads	1,847,867 / 1.33%
Mapped paired reads	137,145,857 / 98.67%
Mapped reads, first in pair	68,753,946 / 49.47%
Mapped reads, second in pair	68,391,911 / 49.21%
Mapped reads, both in pair	136,488,978 / 98.2%
Mapped reads, singletons	656,879 / 0.47%
Secondary alignments	0
Supplementary alignments	548,330 / 0.39%
Read min/max/mean length	30 / 101 / 101.16
Duplicated reads (estimated)	16,956,661 / 12.2%
Duplication rate	8.06%
Clipped reads	23,442,836 / 16.87%

2.2. ACGT Content

Number/percentage of A's	3,878,933,872 / 29.09%
Number/percentage of C's	2,788,730,972 / 20.92%
Number/percentage of T's	3,829,527,191 / 28.72%
Number/percentage of G's	2,834,499,079 / 21.26%
Number/percentage of N's	502,967 / 0%

GC Percentage	42.18%

2.3. Coverage

Mean	4.308
Standard Deviation	52.6393

2.4. Mapping Quality

Mean Mapping Quality	53.56

2.5. Insert size

Mean	115,315.18
Standard Deviation	3,318,099.24
P25/Median/P75	124 / 169 / 226

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	67,369,269
Insertions	1,388,921
Mapped reads with at least one insertion	0.98%
Deletions	1,783,624
Mapped reads with at least one deletion	1.27%
Homopolymer indels	43.51%

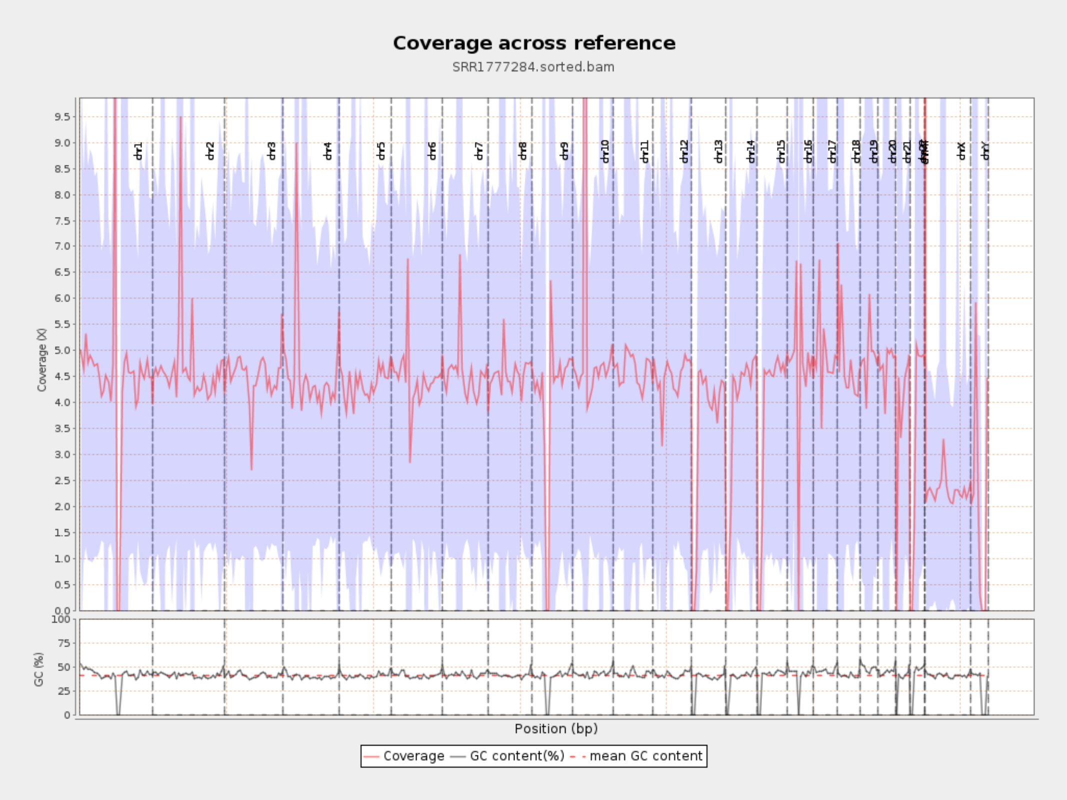
2.7. Chromosome stats

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

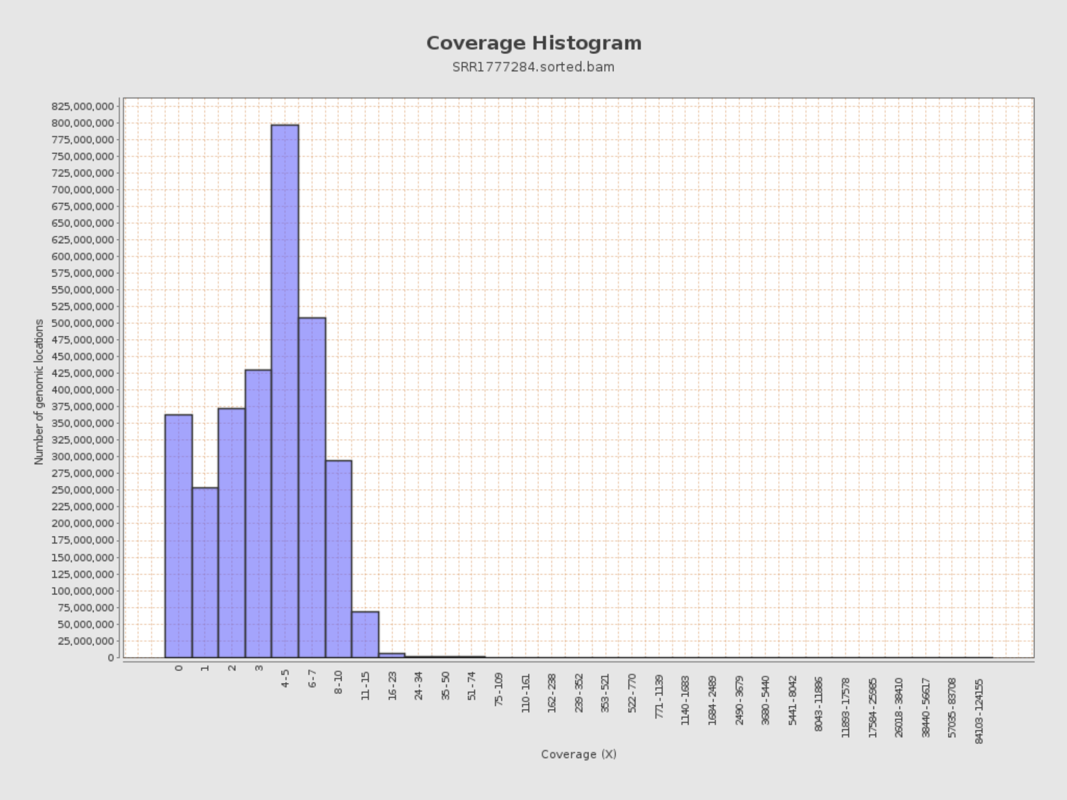
		bases	coverage	deviation
chr1	249250621	1115489469	4.4754	123.8226
chr2	243199373	1143148437	4.7005	32.5436
chr3	198022430	887265286	4.4806	11.186
chr4	191154276	860820006	4.5033	34.6018
chr5	180915260	791772132	4.3765	4.9766
chr6	171115067	763321149	4.4609	27.5738
chr7	159138663	728123188	4.5754	44.6274
chr8	146364022	666833479	4.556	16.011
chr9	141213431	573904039	4.0641	48.3246
chr10	135534747	738828283	5.4512	137.3313
chr11	135006516	625793351	4.6353	28.4789
chr12	133851895	599824822	4.4813	4.6238
chr13	115169878	406985602	3.5338	3.0507
chr14	107349540	404162262	3.7649	5.0121
chr15	102531392	385389216	3.7587	3.29
chr16	90354753	424721776	4.7006	22.4396
chr17	81195210	396635404	4.885	28.8268
chr18	78077248	368239672	4.7164	60.7418
chr19	59128983	290013417	4.9048	57.5398
chr20	63025520	298915825	4.7428	9.5655
chr21	48129895	186351582	3.8718	16.0116
chr22	51304566	175052333	3.412	6.8518
chrMT	16571	14831073	895.0017	92.2026
chrX	155270560	358828877	2.311	12.9983

chrY	59373566	131054717	2.2073	39.9188

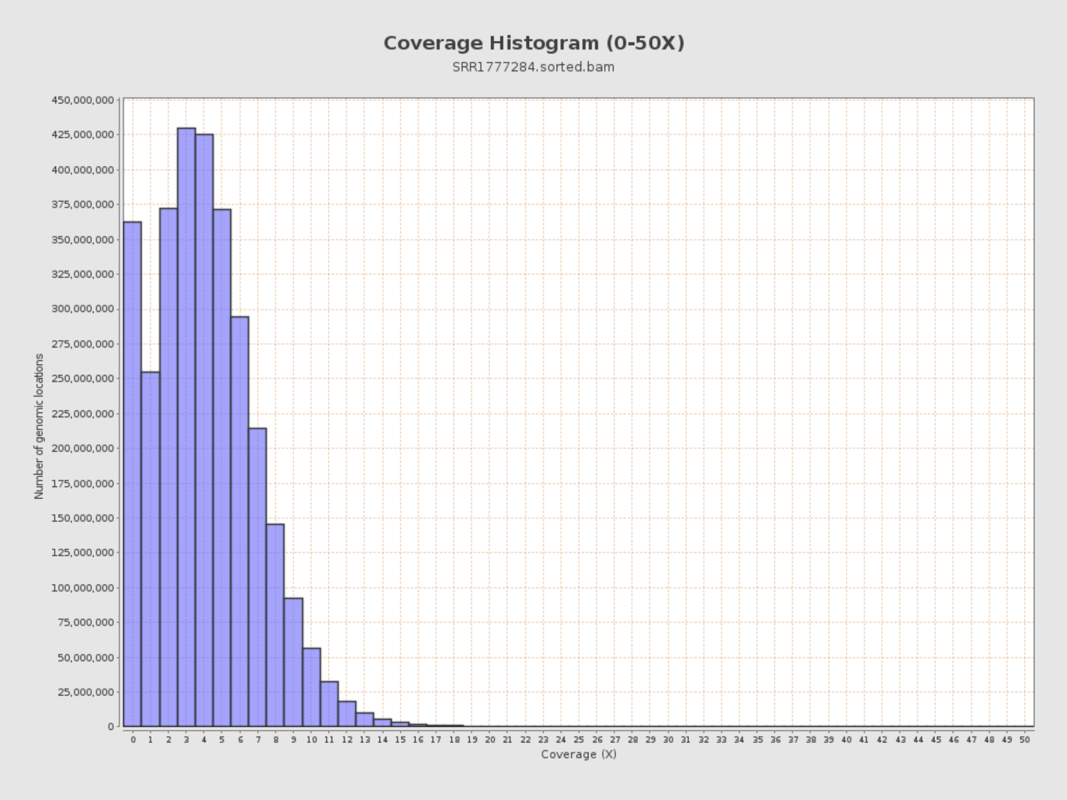
3. Results : Coverage across reference



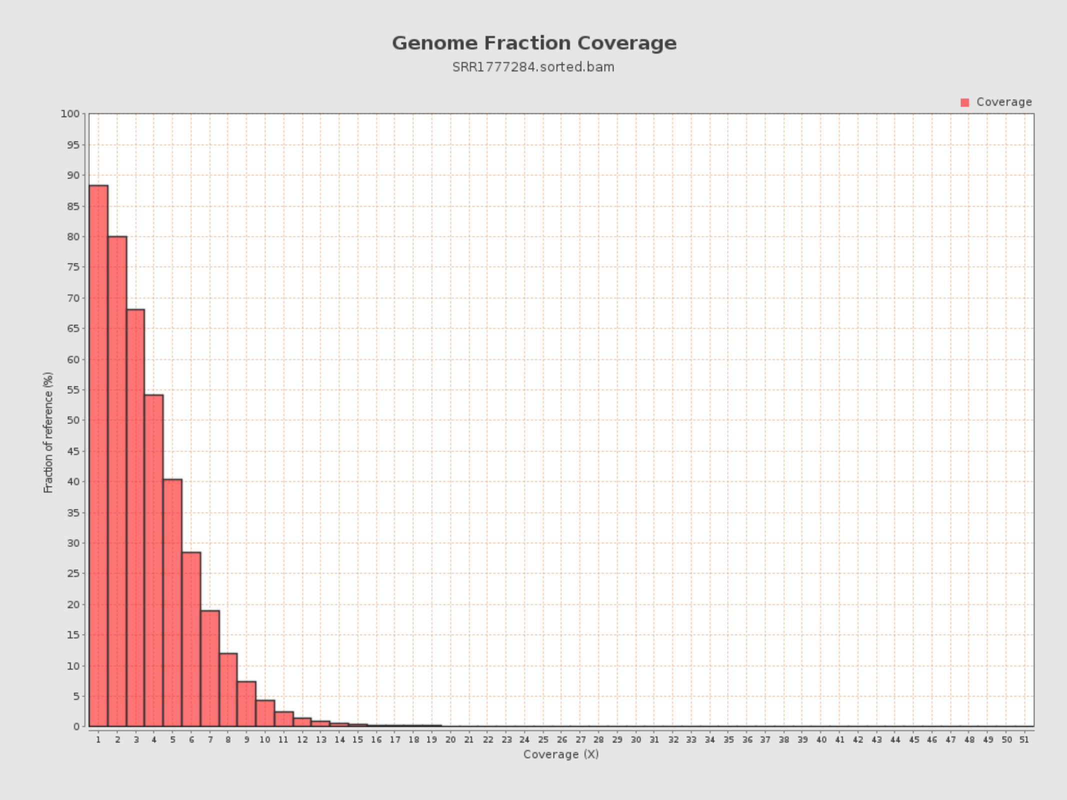
4. Results : Coverage Histogram



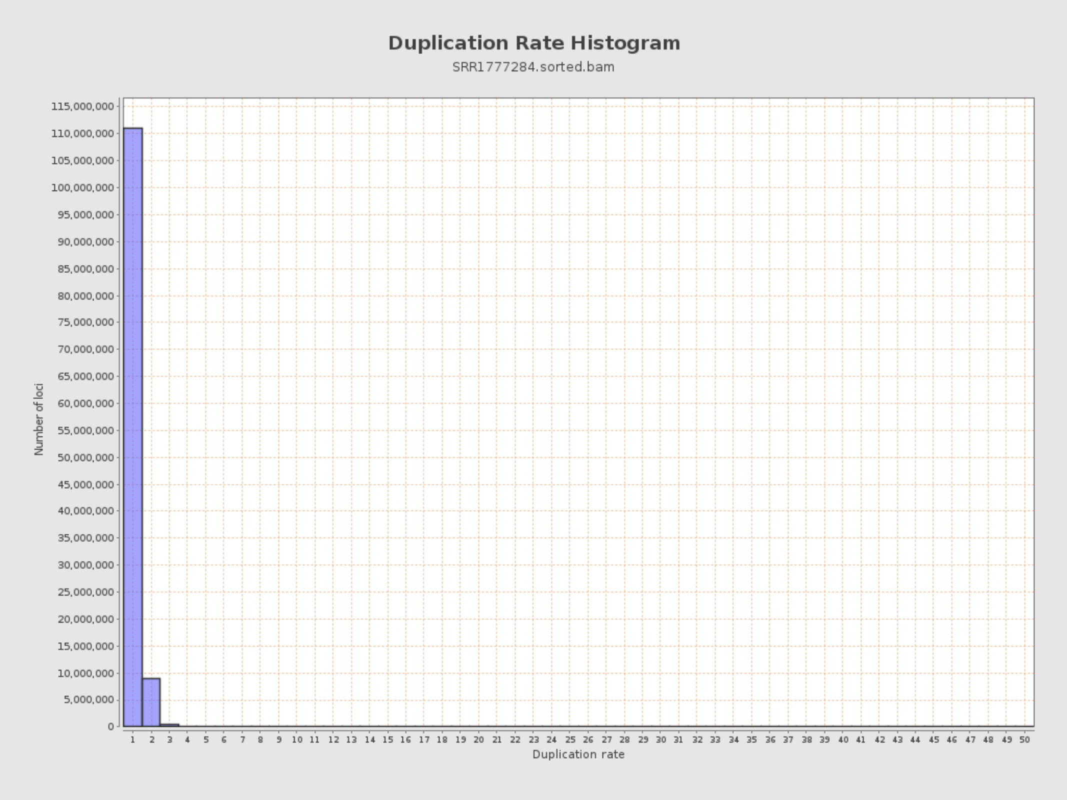
5. Results : Coverage Histogram (0-50X)



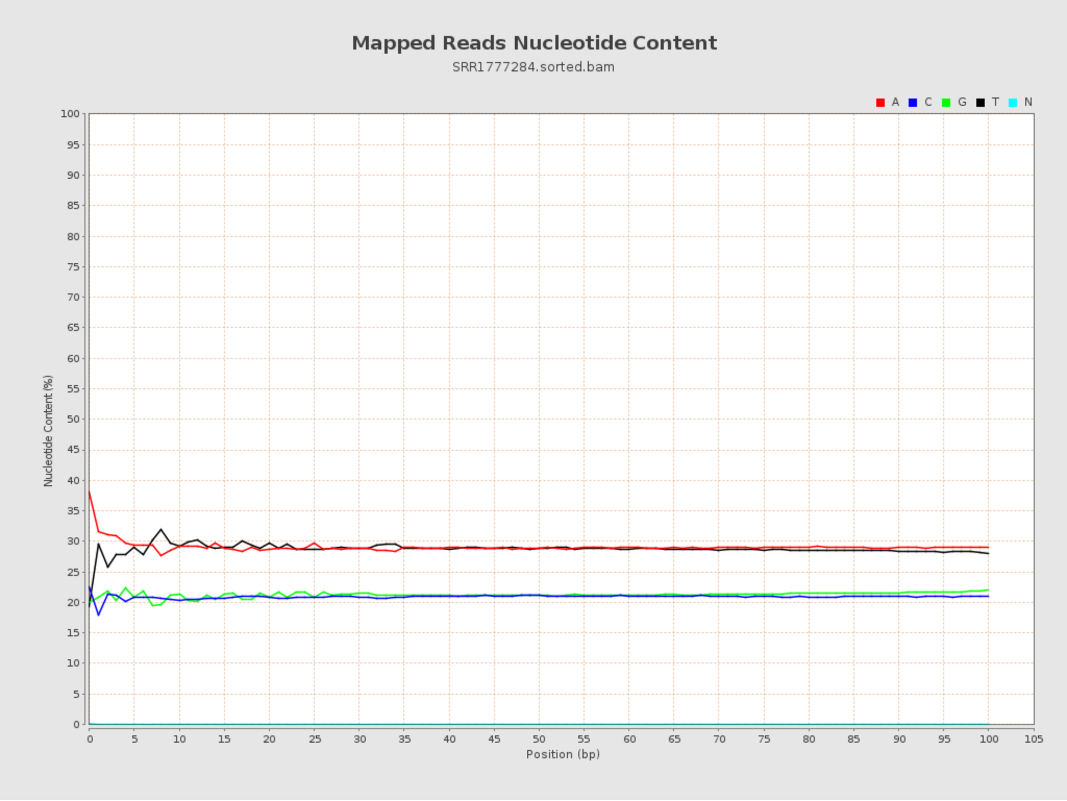
6. Results : Genome Fraction Coverage



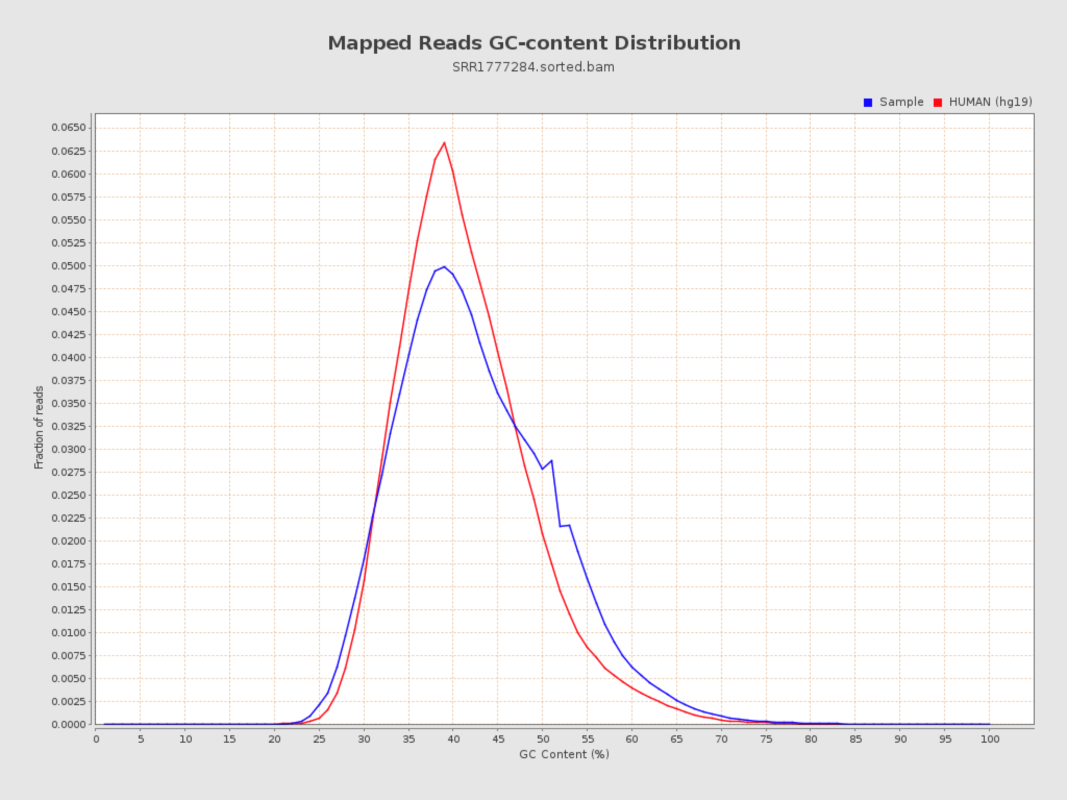
7. Results : Duplication Rate Histogram



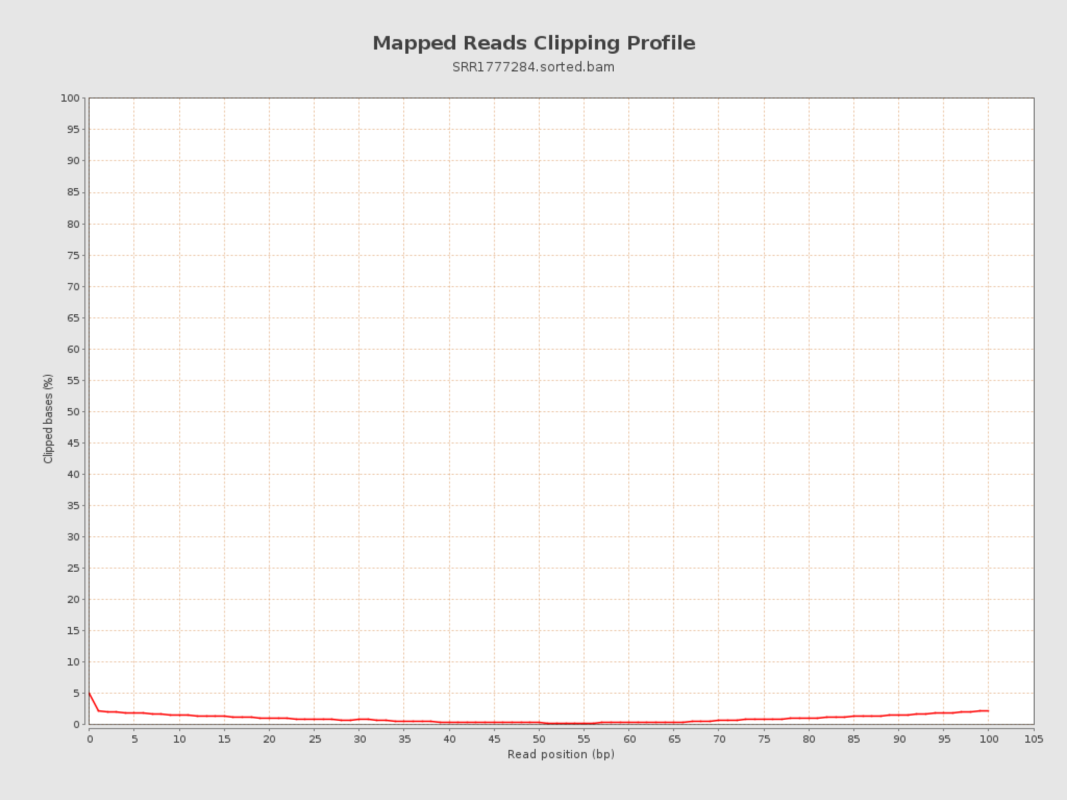
8. Results : Mapped Reads Nucleotide Content



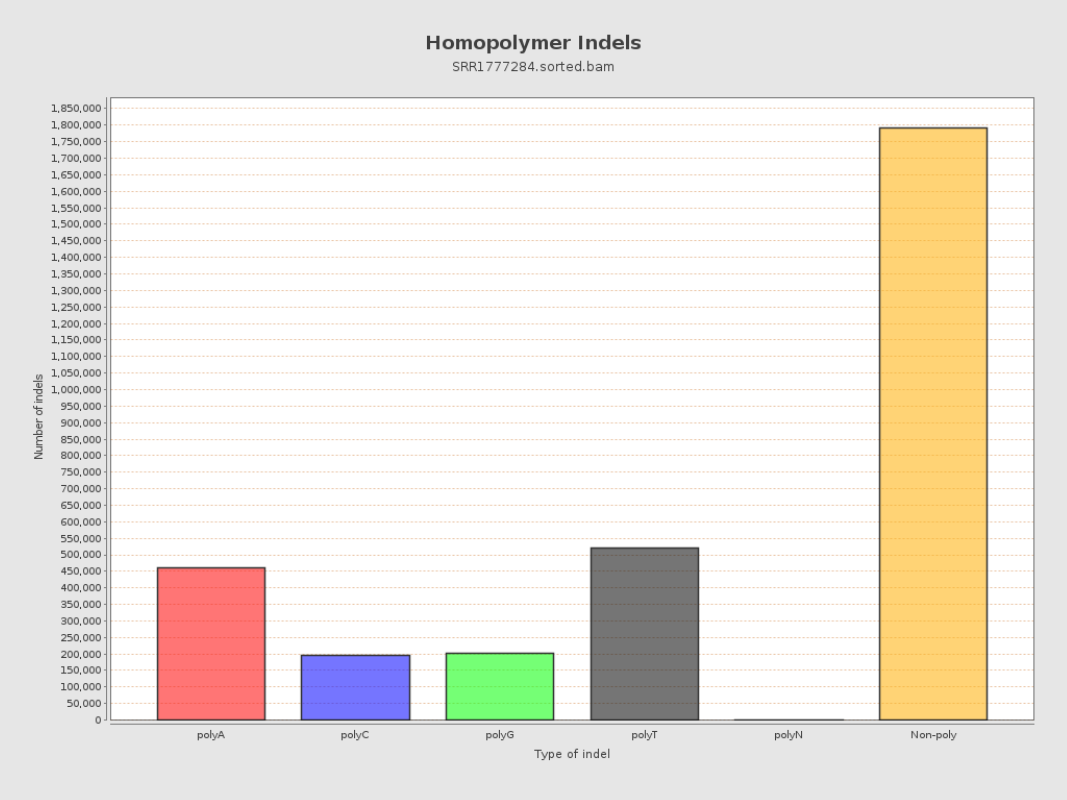
9. Results : Mapped Reads GC-content Distribution



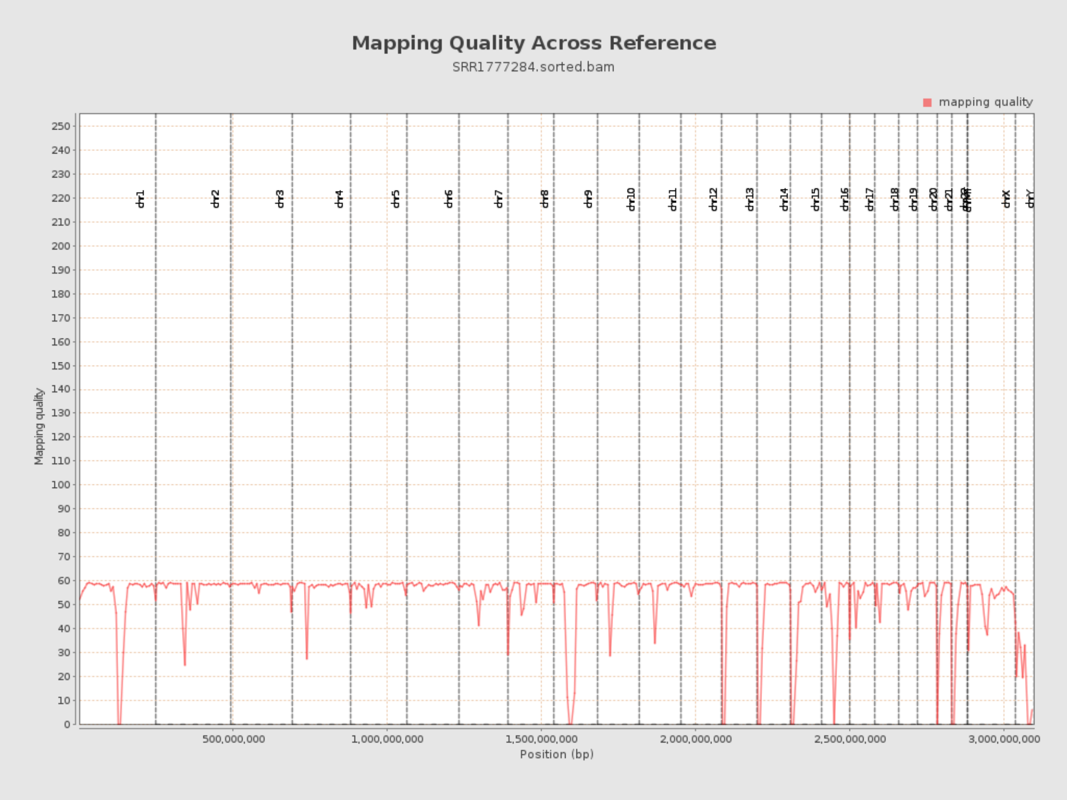
10. Results : Mapped Reads Clipping Profile



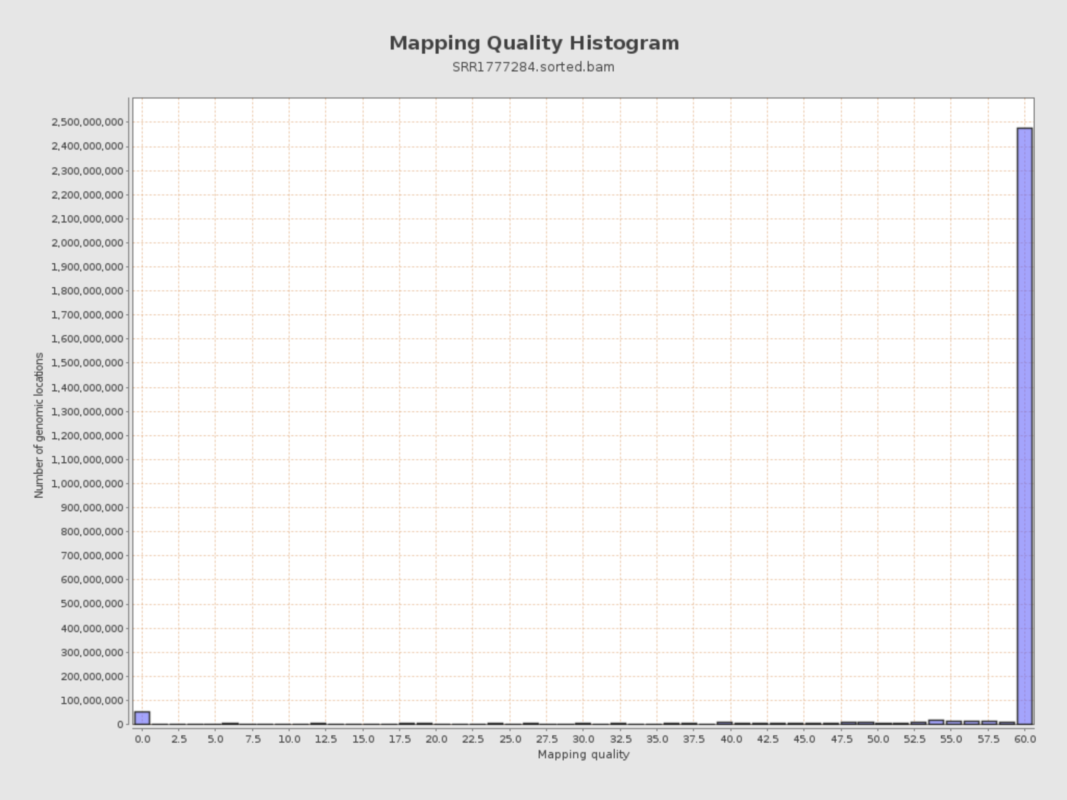
11. Results : Homopolymer Indels



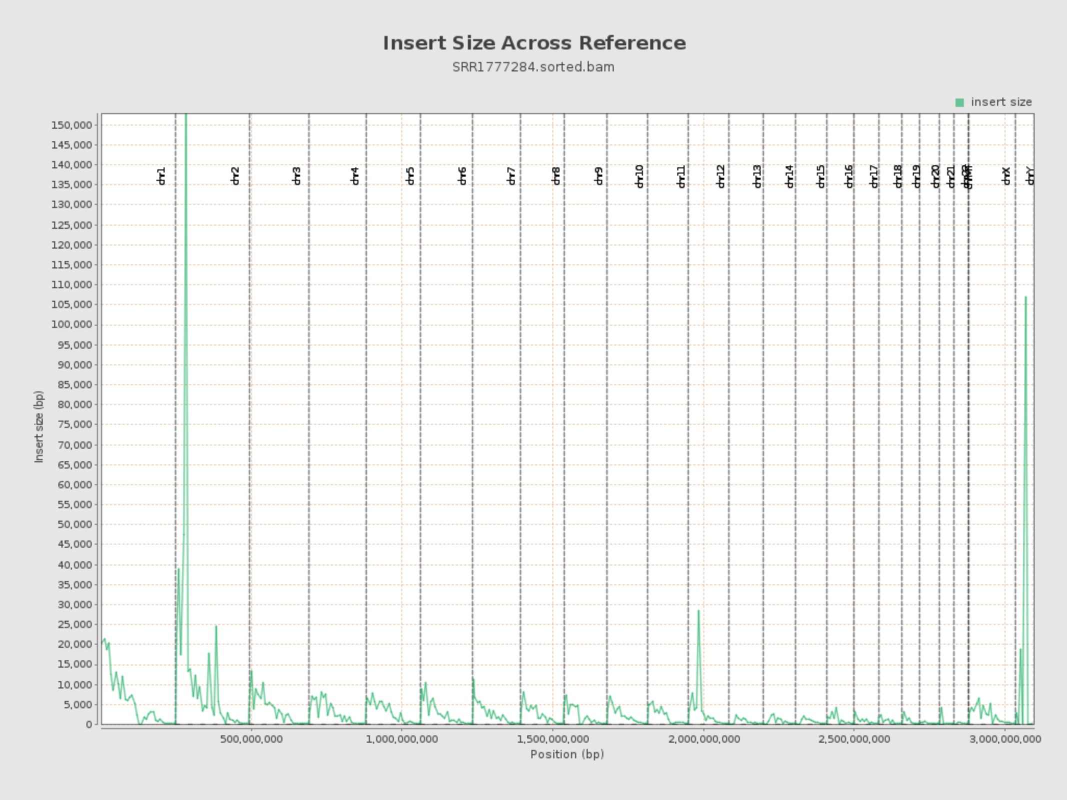
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram