Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 23:34:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777277.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_SRR1777277 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777277_1.fastq.gz SRR1777277_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 23:34:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777277.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,377,198
Mapped reads	57,712,533 / 97.2%
Unmapped reads	1,664,665 / 2.8%
Mapped paired reads	57,712,533 / 97.2%
Mapped reads, first in pair	28,857,899 / 48.6%
Mapped reads, second in pair	28,854,634 / 48.6%
Mapped reads, both in pair	57,673,764 / 97.13%
Mapped reads, singletons	38,769 / 0.07%
Secondary alignments	0
Supplementary alignments	197,487 / 0.33%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	33,448,626 / 56.33%
Duplication rate	44.87%
Clipped reads	4,124,404 / 6.95%

2.2. ACGT Content

Number/percentage of A's	1,371,374,836 / 23.92%
Number/percentage of C's	1,480,354,248 / 25.82%
Number/percentage of T's	1,374,740,375 / 23.98%
Number/percentage of G's	1,507,252,900 / 26.29%
Number/percentage of N's	213,420 / 0%

GC Percentage	52.1%

2.3. Coverage

Mean	1.8532
Standard Deviation	27.3911

2.4. Mapping Quality

Mean Mapping Quality	55.12

2.5. Insert size

Mean	96,454.3
Standard Deviation	3,205,281.85
P25/Median/P75	185 / 231 / 284

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	35,770,685
Insertions	594,767
Mapped reads with at least one insertion	1.02%
Deletions	2,305,879
Mapped reads with at least one deletion	3.91%
Homopolymer indels	55.39%

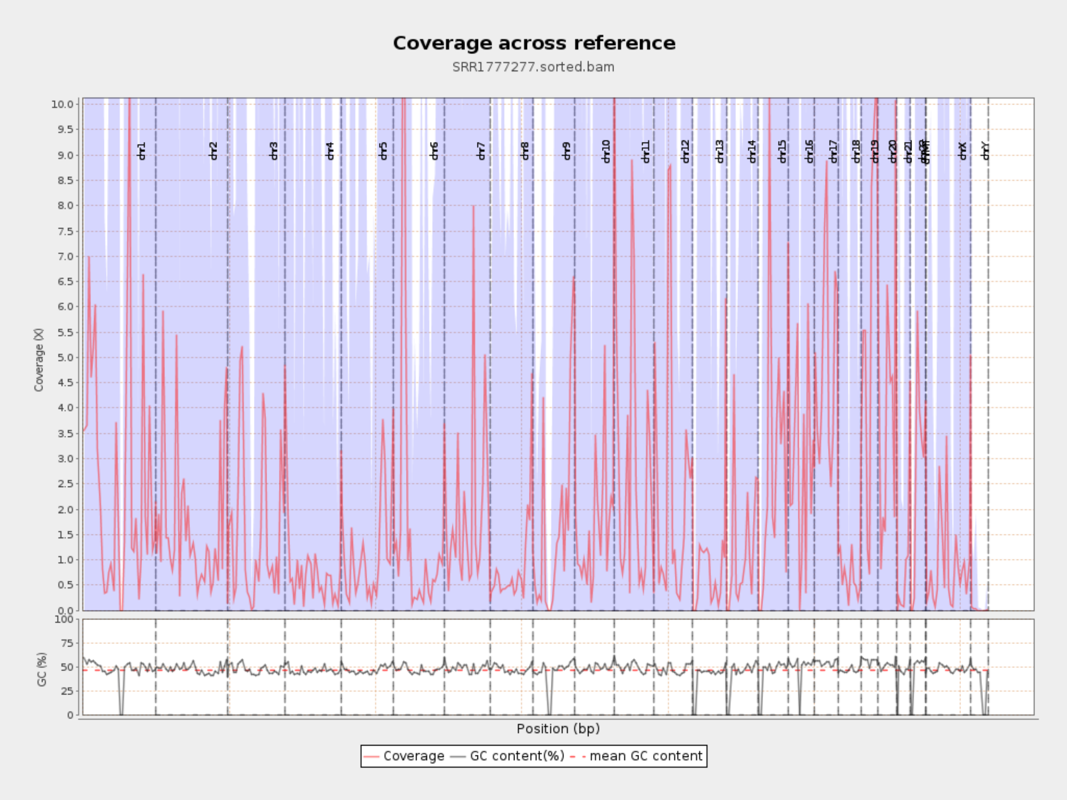
2.7. Chromosome stats

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

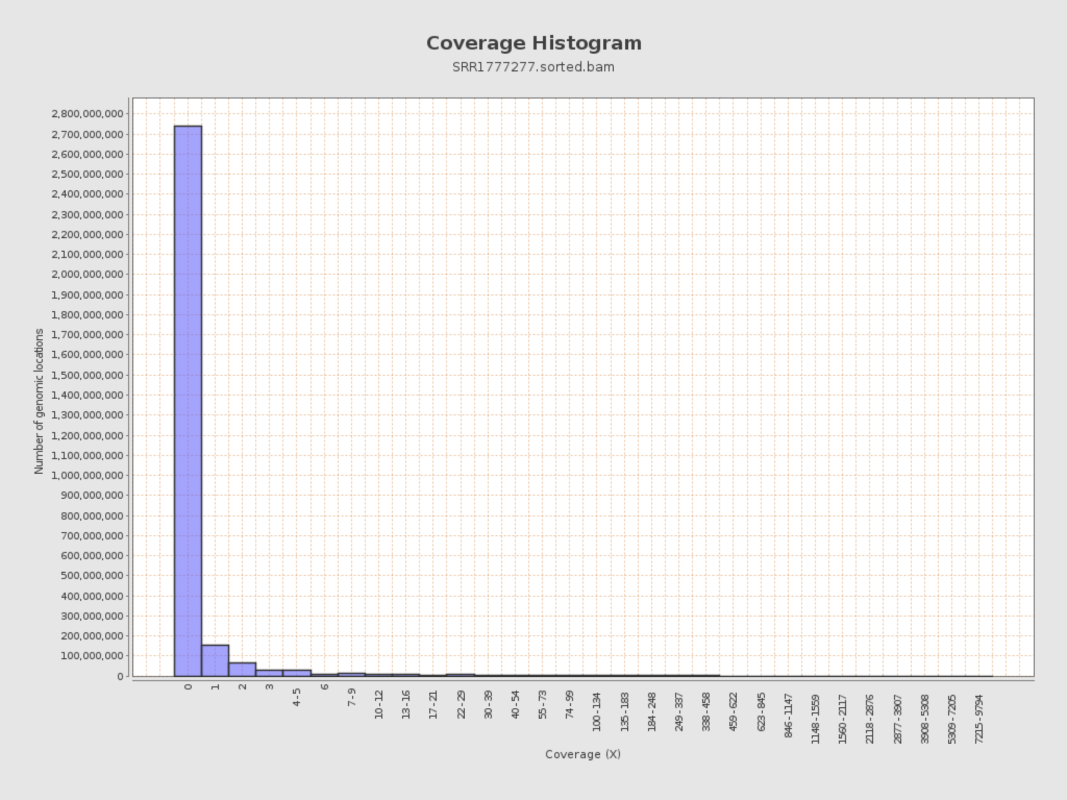
		bases	coverage	deviation
chr1	249250621	661671564	2.6546	32.5922
chr2	243199373	403047695	1.6573	24.7457
chr3	198022430	312536225	1.5783	24.944
chr4	191154276	138470834	0.7244	15.378
chr5	180915260	218448611	1.2075	18.5363
chr6	171115067	277789960	1.6234	26.8316
chr7	159138663	322257085	2.025	31.8065
chr8	146364022	130390645	0.8909	17.0035
chr9	141213431	225177385	1.5946	23.3038
chr10	135534747	220464594	1.6266	23.5209
chr11	135006516	389111640	2.8822	34.3166
chr12	133851895	334745915	2.5009	34.2041
chr13	115169878	90488328	0.7857	14.5732
chr14	107349540	126164215	1.1753	17.9836
chr15	102531392	276631106	2.698	34.4355
chr16	90354753	267954688	2.9656	34.2955
chr17	81195210	395772632	4.8743	50.0541
chr18	78077248	51368317	0.6579	11.9943
chr19	59128983	345233983	5.8387	51.2798
chr20	63025520	226886534	3.5999	43.0864
chr21	48129895	41908017	0.8707	15.1636
chr22	51304566	136402861	2.6587	30.9361
chrMT	16571	53378	3.2212	3.8064
chrX	155270560	142893895	0.9203	17.3176

chrY	59373566	985365	0.0166	0.8808

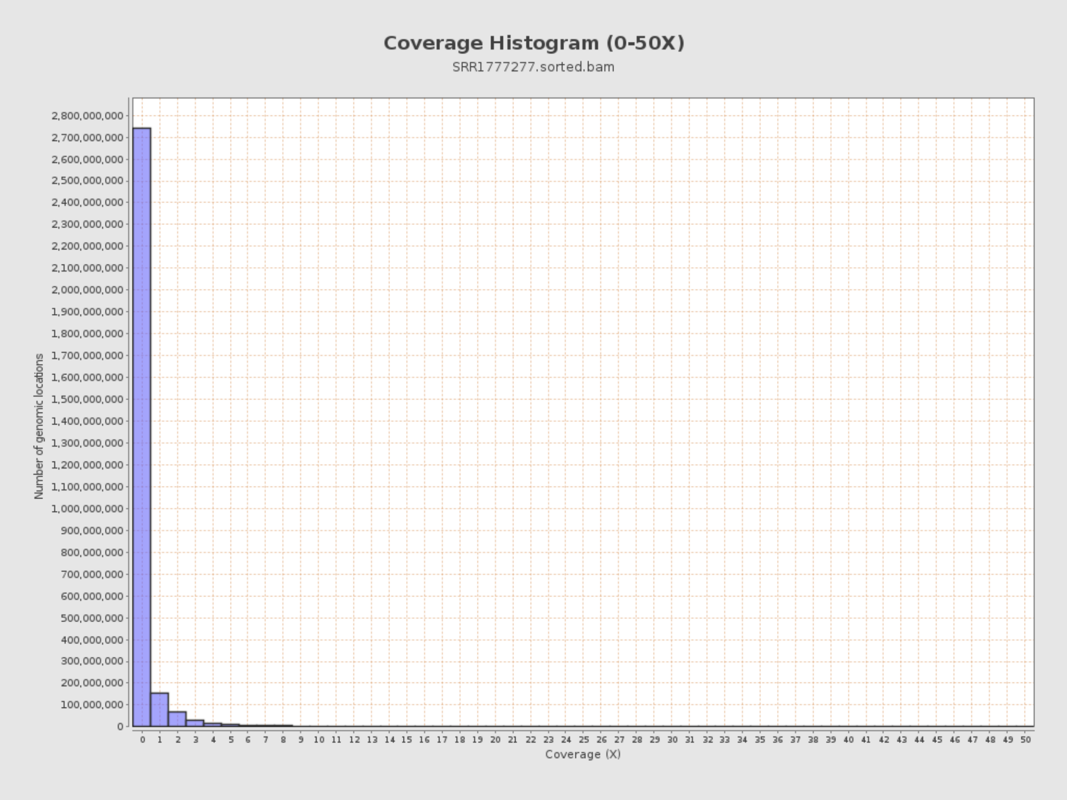
3. Results : Coverage across reference



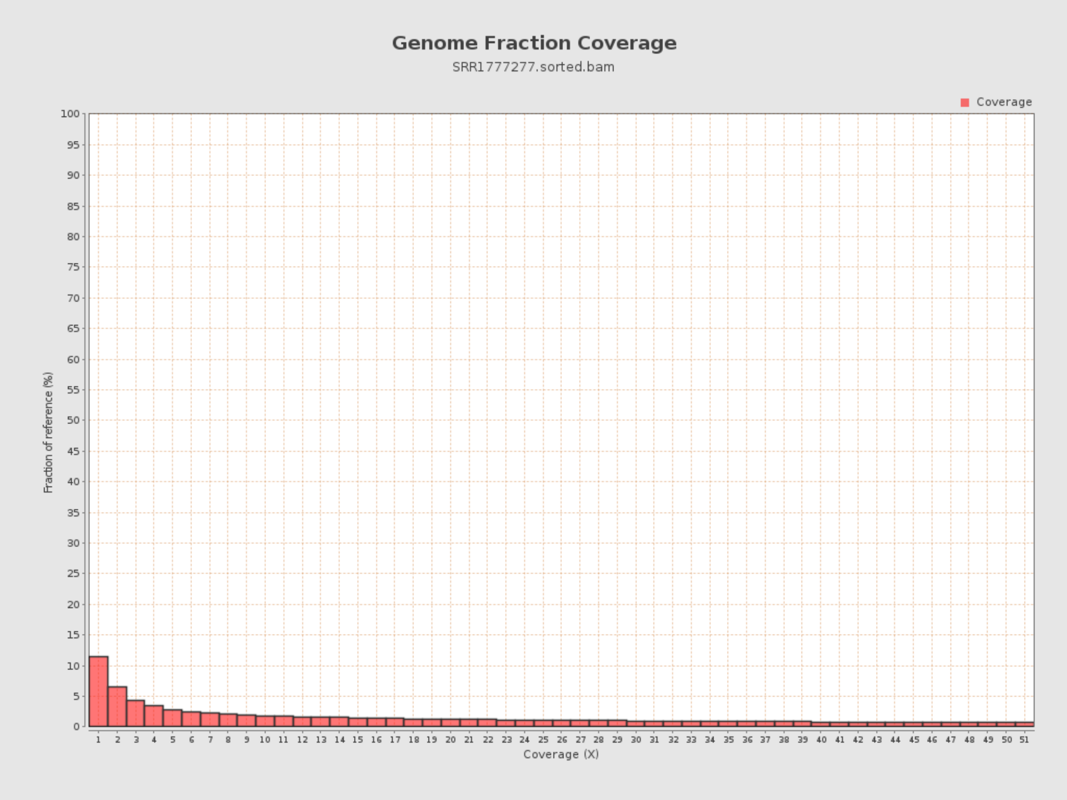
4. Results : Coverage Histogram



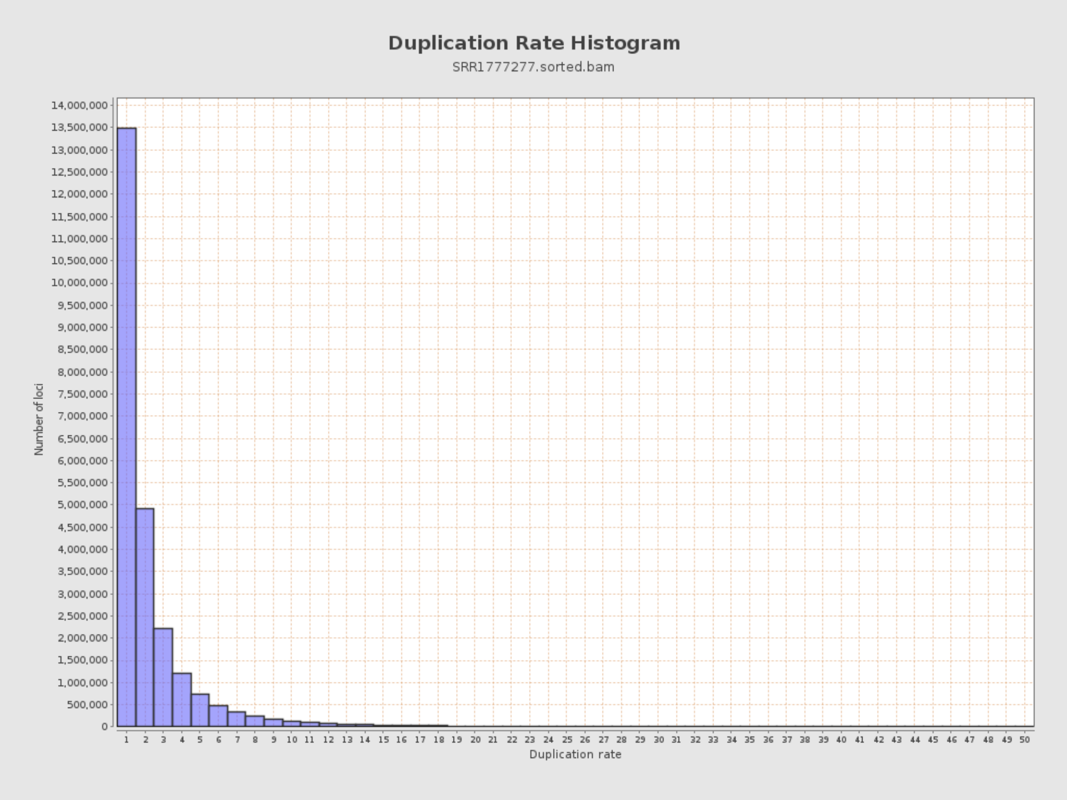
5. Results : Coverage Histogram (0-50X)



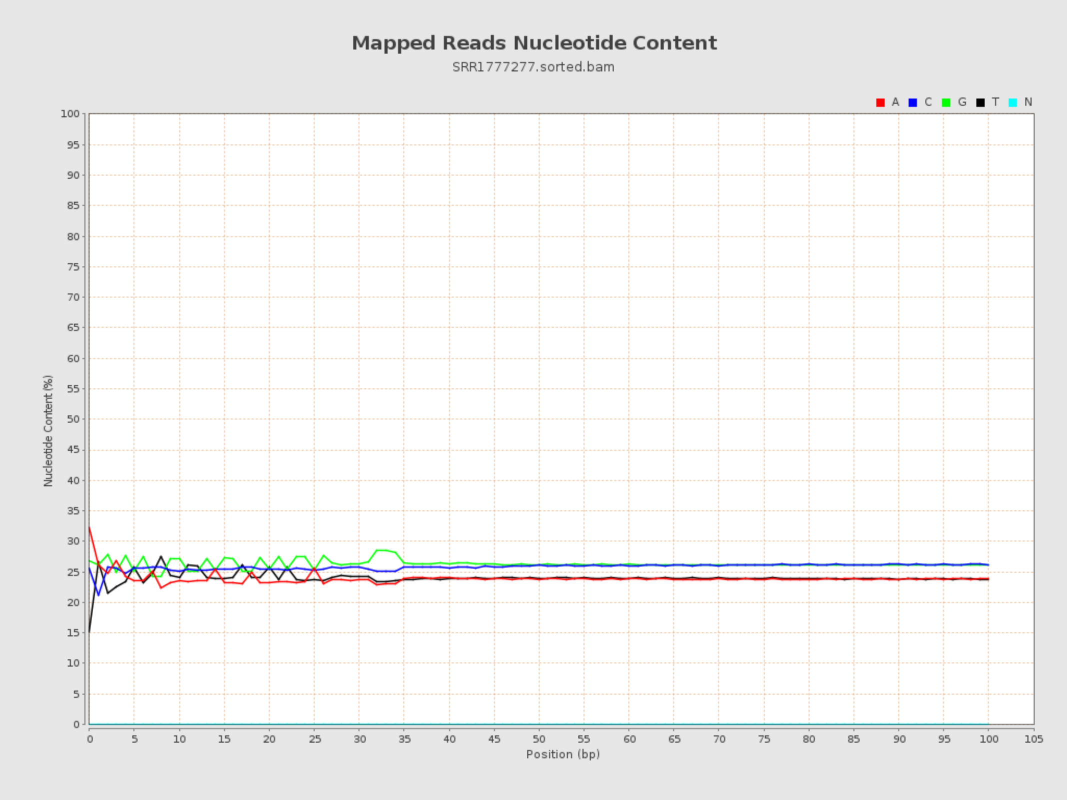
6. Results : Genome Fraction Coverage



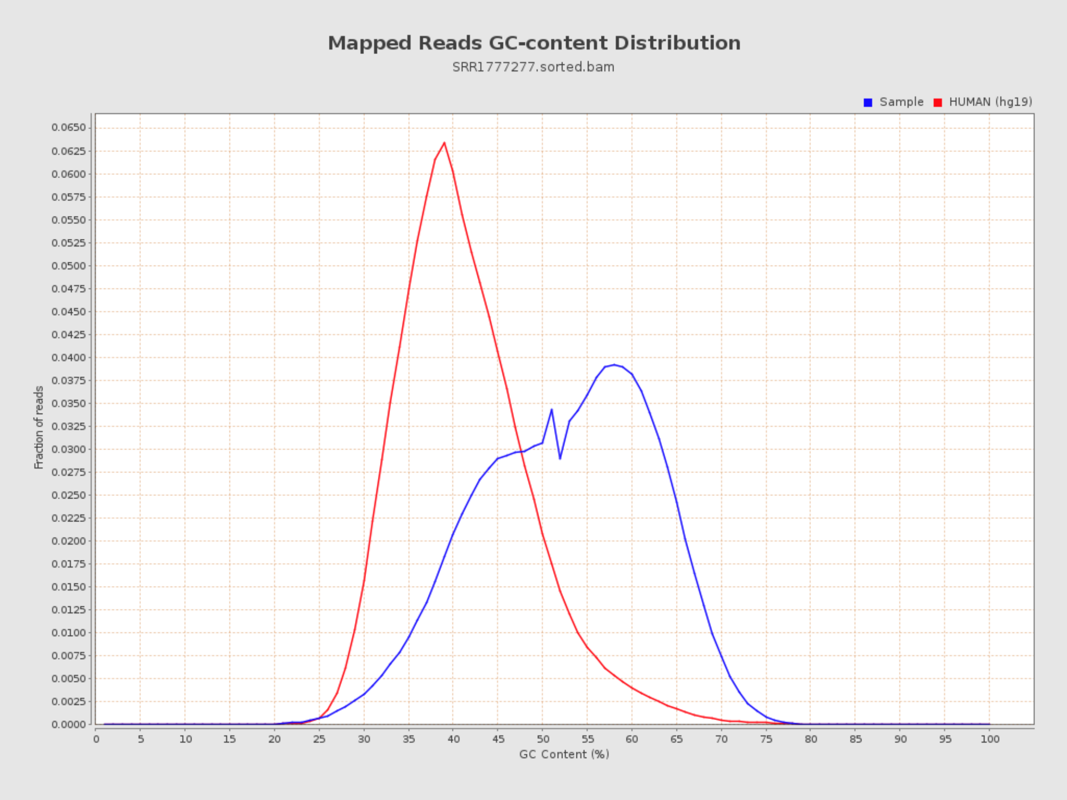
7. Results : Duplication Rate Histogram



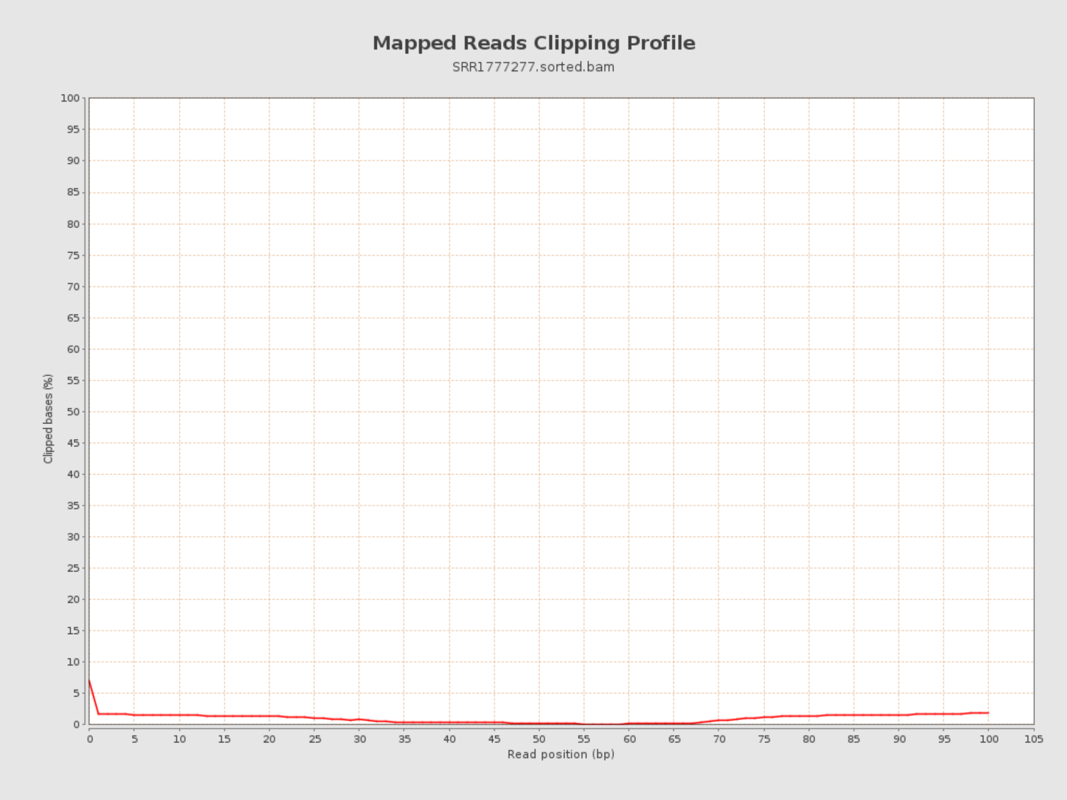
8. Results : Mapped Reads Nucleotide Content



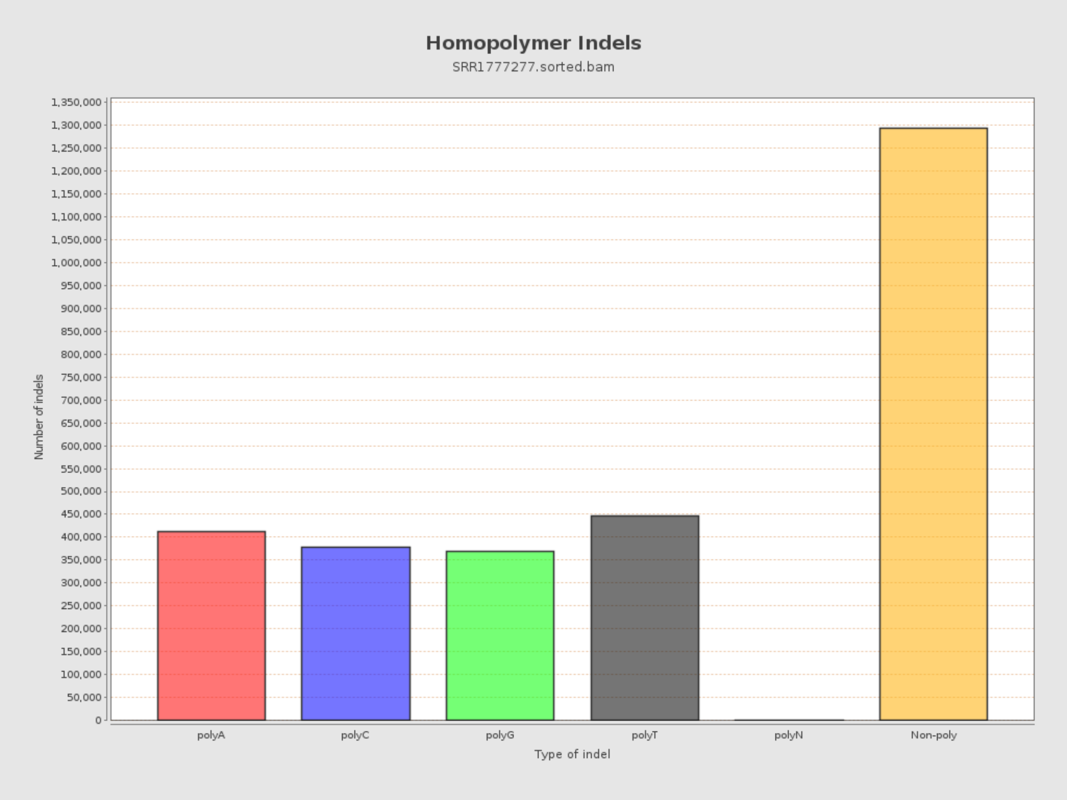
9. Results : Mapped Reads GC-content Distribution



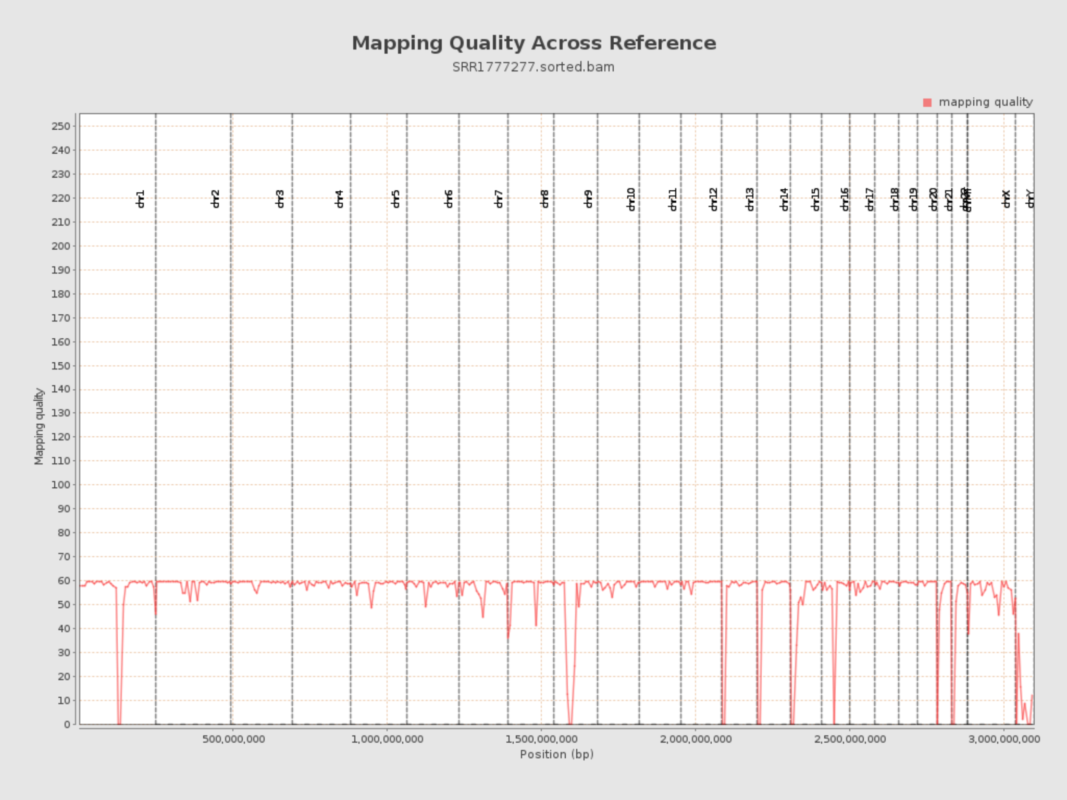
10. Results : Mapped Reads Clipping Profile



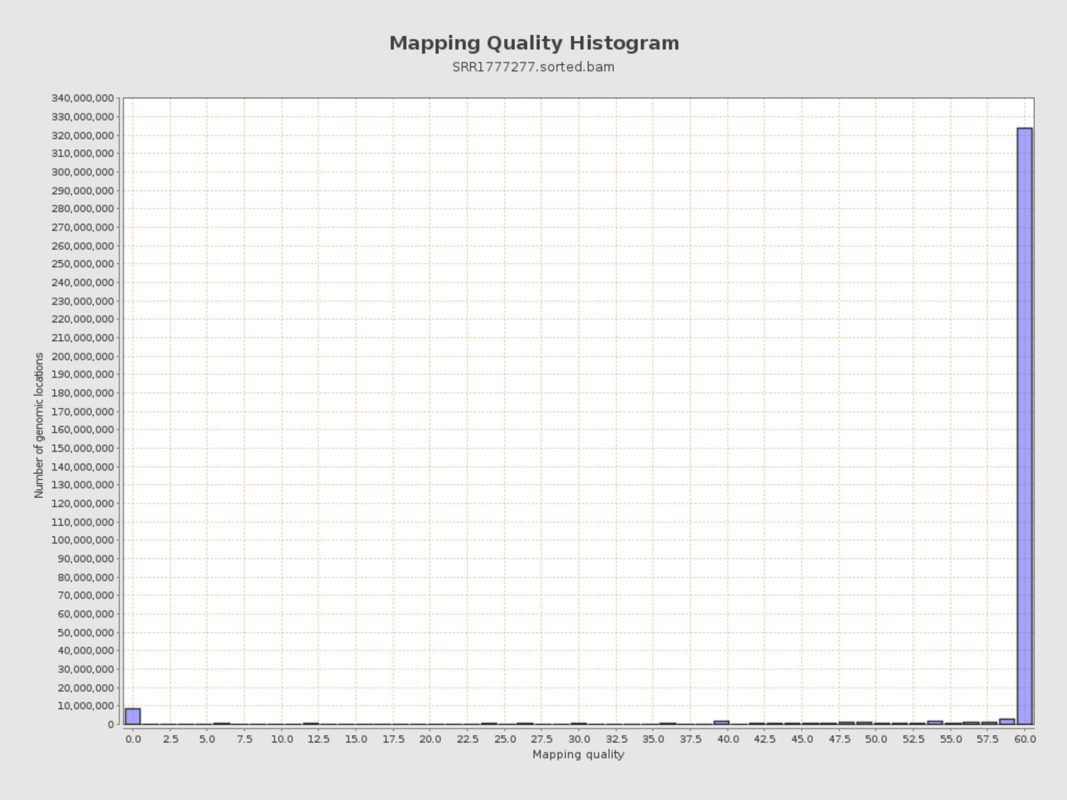
11. Results : Homopolymer Indels



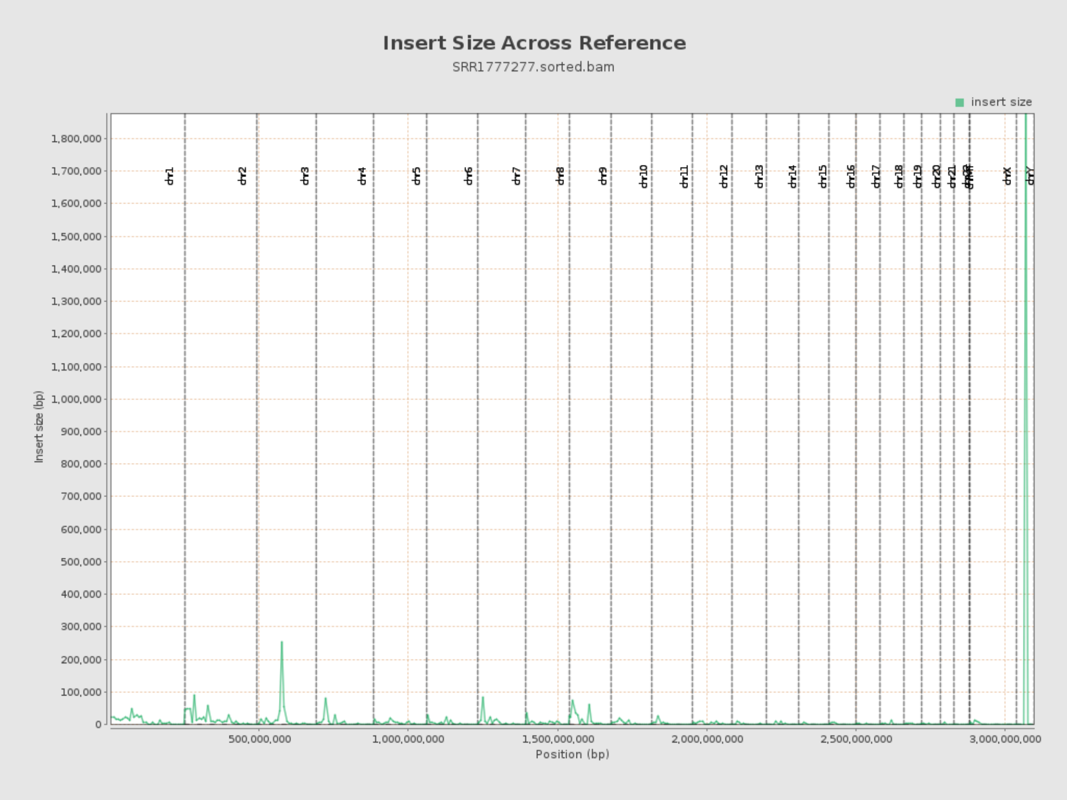
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram