Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/04 19:03:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777287.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_SRR1777287 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777287_1.fastq.gz SRR1777287_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 04 19:03:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777287.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	288,139,362
Mapped reads	282,064,577 / 97.89%
Unmapped reads	6,074,785 / 2.11%
Mapped paired reads	282,064,577 / 97.89%
Mapped reads, first in pair	141,407,643 / 49.08%
Mapped reads, second in pair	140,656,934 / 48.82%
Mapped reads, both in pair	280,724,582 / 97.43%
Mapped reads, singletons	1,339,995 / 0.47%
Secondary alignments	0
Supplementary alignments	14,278,224 / 4.96%
Read min/max/mean length	30 / 101 / 103.05
Duplicated reads (estimated)	85,265,506 / 29.59%
Duplication rate	22.85%
Clipped reads	93,384,862 / 32.41%

2.2. ACGT Content

Number/percentage of A's	7,932,554,981 / 29.23%
Number/percentage of C's	5,660,620,657 / 20.86%
Number/percentage of T's	7,769,668,395 / 28.63%
Number/percentage of G's	5,774,613,223 / 21.28%
Number/percentage of N's	1,717,344 / 0.01%

GC Percentage	42.14%

2.3. Coverage

Mean	8.7695
Standard Deviation	83.4087

2.4. Mapping Quality

Mean Mapping Quality	52.98

2.5. Insert size

Mean	159,437.72
Standard Deviation	3,819,175.74
P25/Median/P75	108 / 154 / 218

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	134,540,855
Insertions	6,146,924
Mapped reads with at least one insertion	2.13%
Deletions	3,376,707
Mapped reads with at least one deletion	1.16%
Homopolymer indels	46.41%

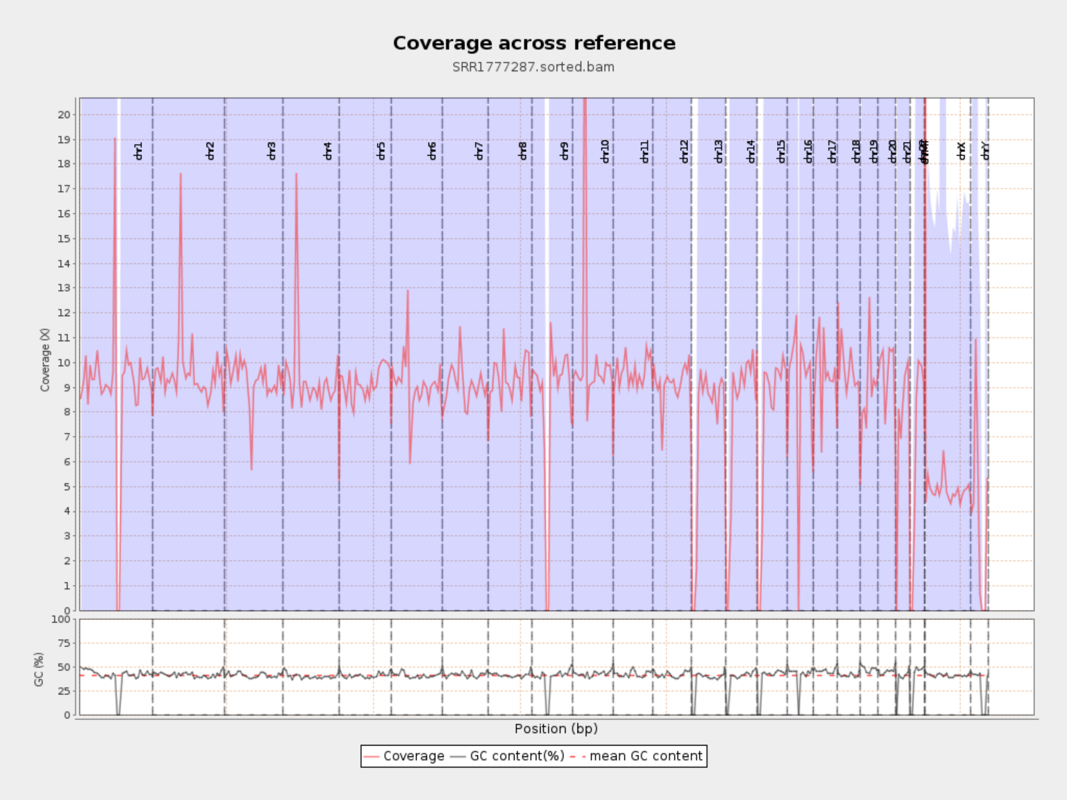
2.7. Chromosome stats

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

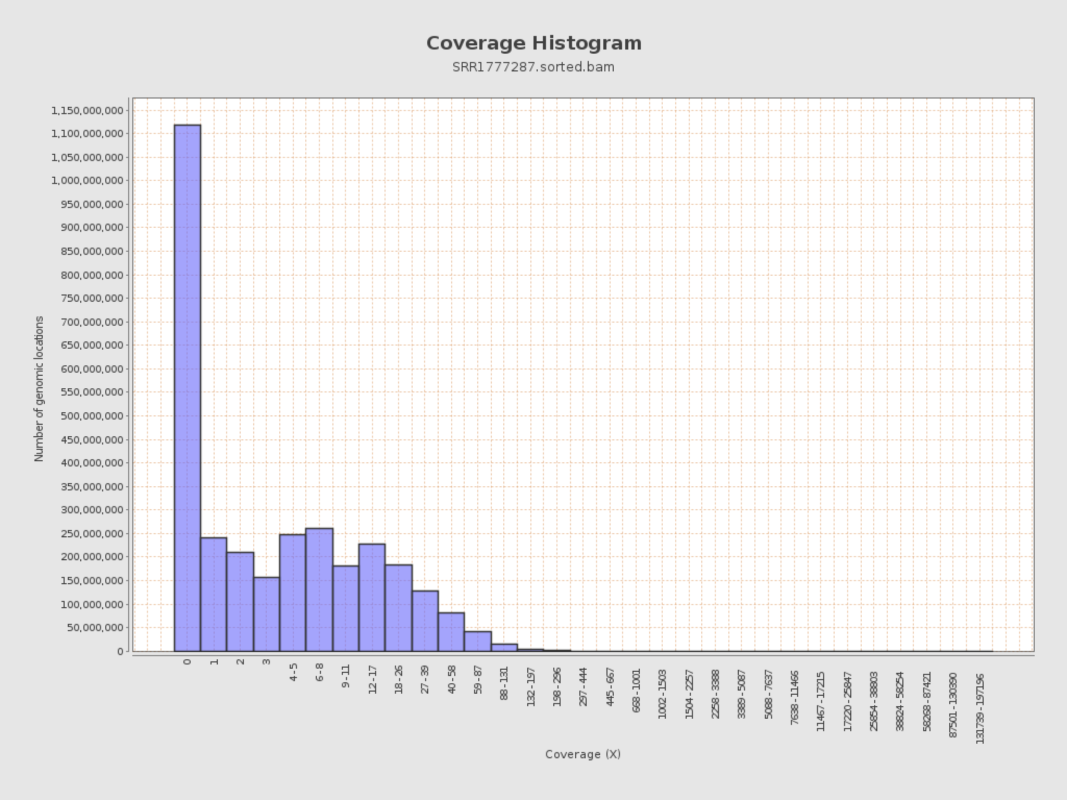
		bases	coverage	deviation
chr1	249250621	2256697970	9.0539	194.8229
chr2	243199373	2351998132	9.6711	60.8815
chr3	198022430	1840729735	9.2956	24.1425
chr4	191154276	1785739093	9.3419	63.934
chr5	180915260	1660967517	9.1809	17.454
chr6	171115067	1571428367	9.1835	46.1889
chr7	159138663	1447856407	9.0981	71.6099
chr8	146364022	1371108007	9.3678	34.9757
chr9	141213431	1176143822	8.3288	84.047
chr10	135534747	1431354367	10.5608	175.1176
chr11	135006516	1290677276	9.5601	45.6665
chr12	133851895	1222427276	9.1327	16.9431
chr13	115169878	853591526	7.4116	14.5848
chr14	107349540	840150281	7.8263	16.8469
chr15	102531392	775677256	7.5653	15.0043
chr16	90354753	802019499	8.8763	33.0892
chr17	81195210	768589353	9.4659	48.0939
chr18	78077248	762389310	9.7646	111.4017
chr19	59128983	522121474	8.8302	109.8778
chr20	63025520	608089897	9.6483	23.528
chr21	48129895	370858159	7.7054	34.2015
chr22	51304566	331847599	6.4682	15.1151
chrMT	16571	121016322	7,302.898	1,428.8999
chrX	155270560	752455058	4.8461	22.2566

chrY	59373566	231671625	3.9019	63.6512

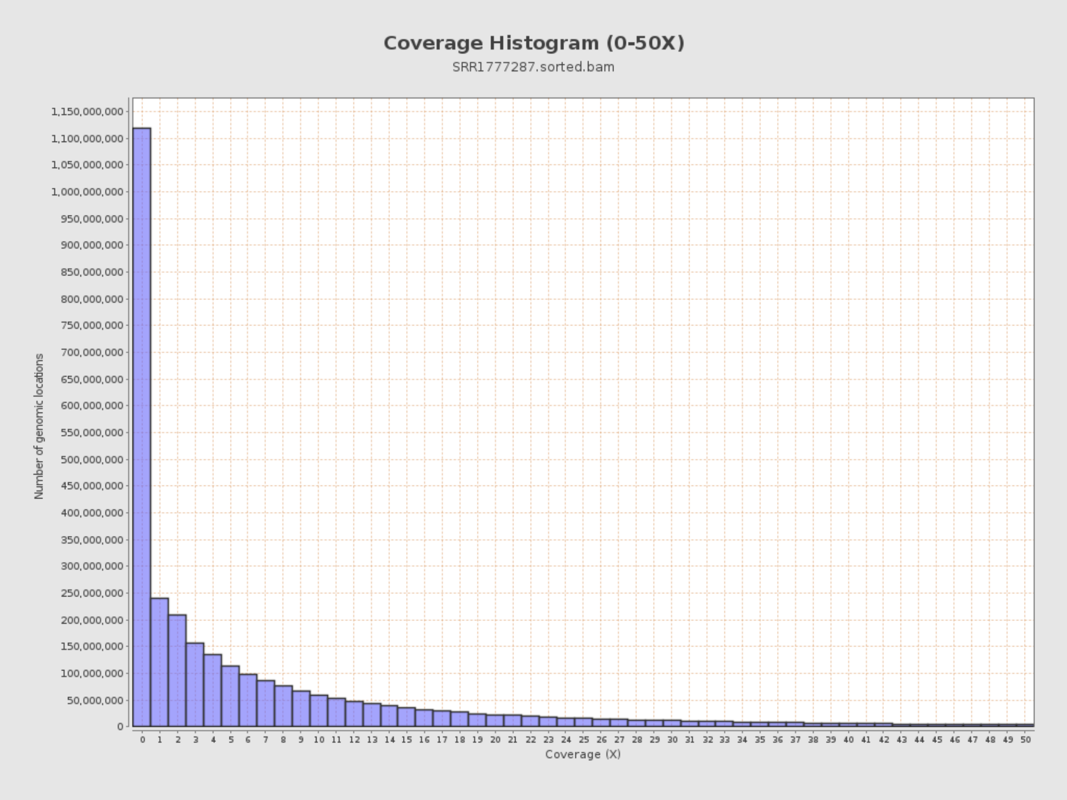
3. Results : Coverage across reference



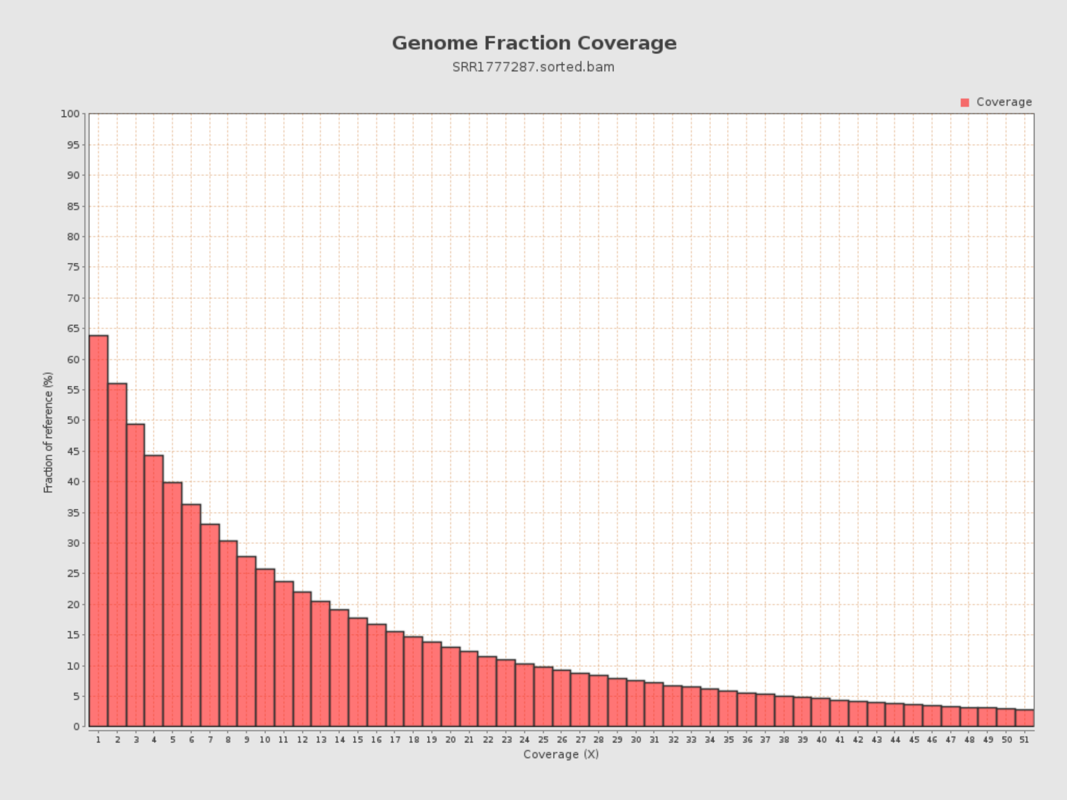
4. Results : Coverage Histogram



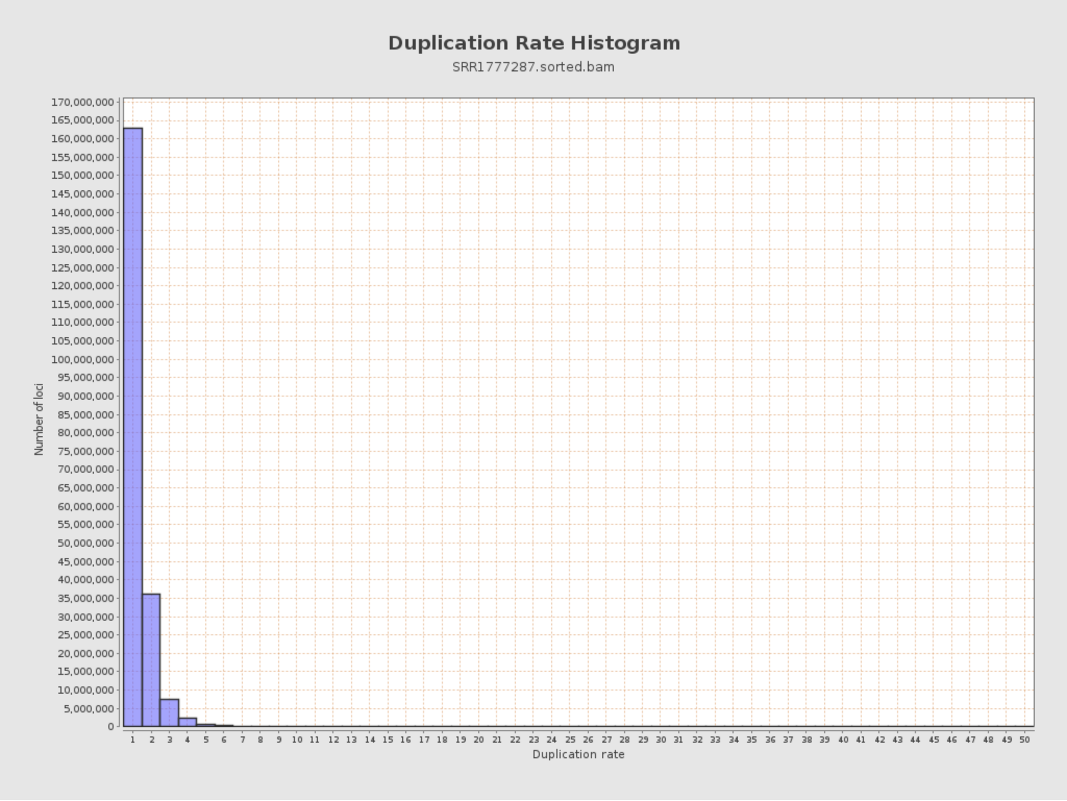
5. Results : Coverage Histogram (0-50X)



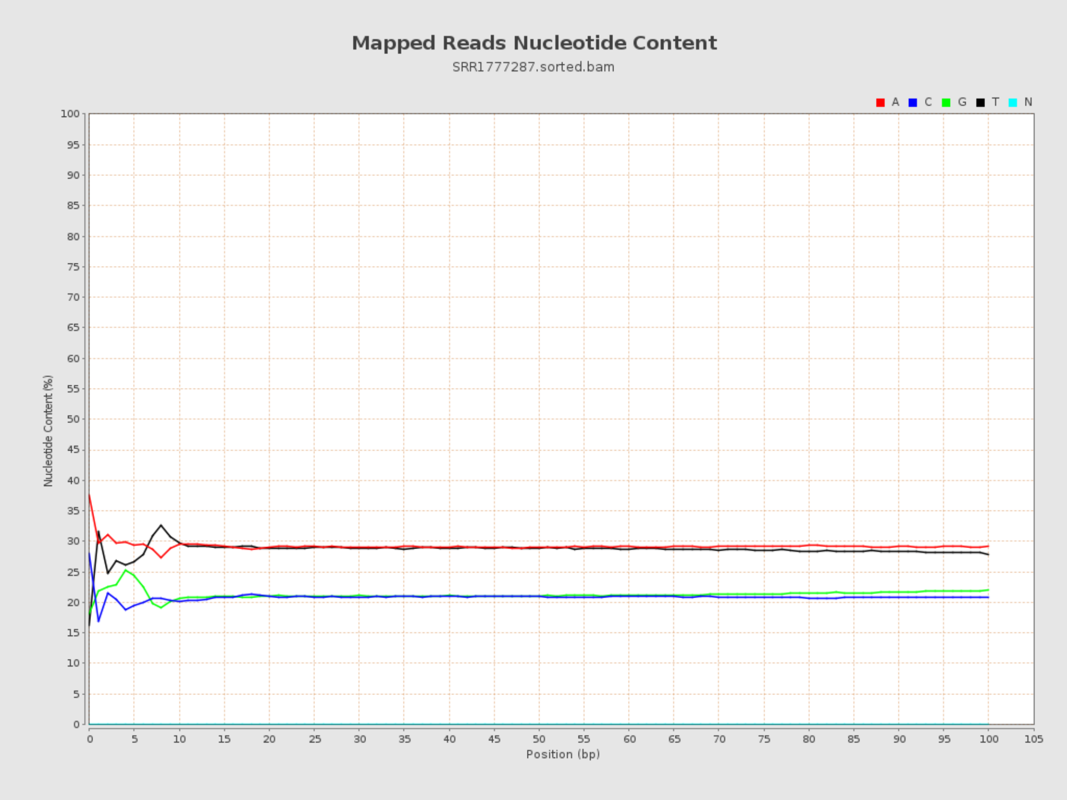
6. Results : Genome Fraction Coverage



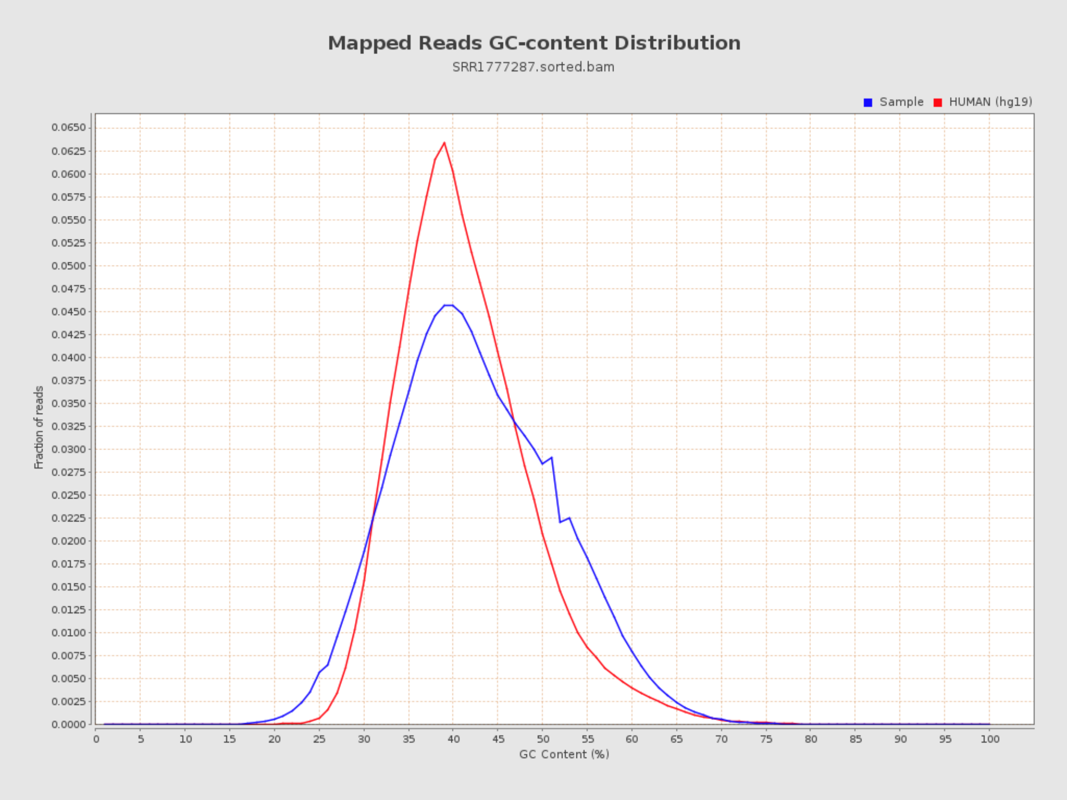
7. Results : Duplication Rate Histogram



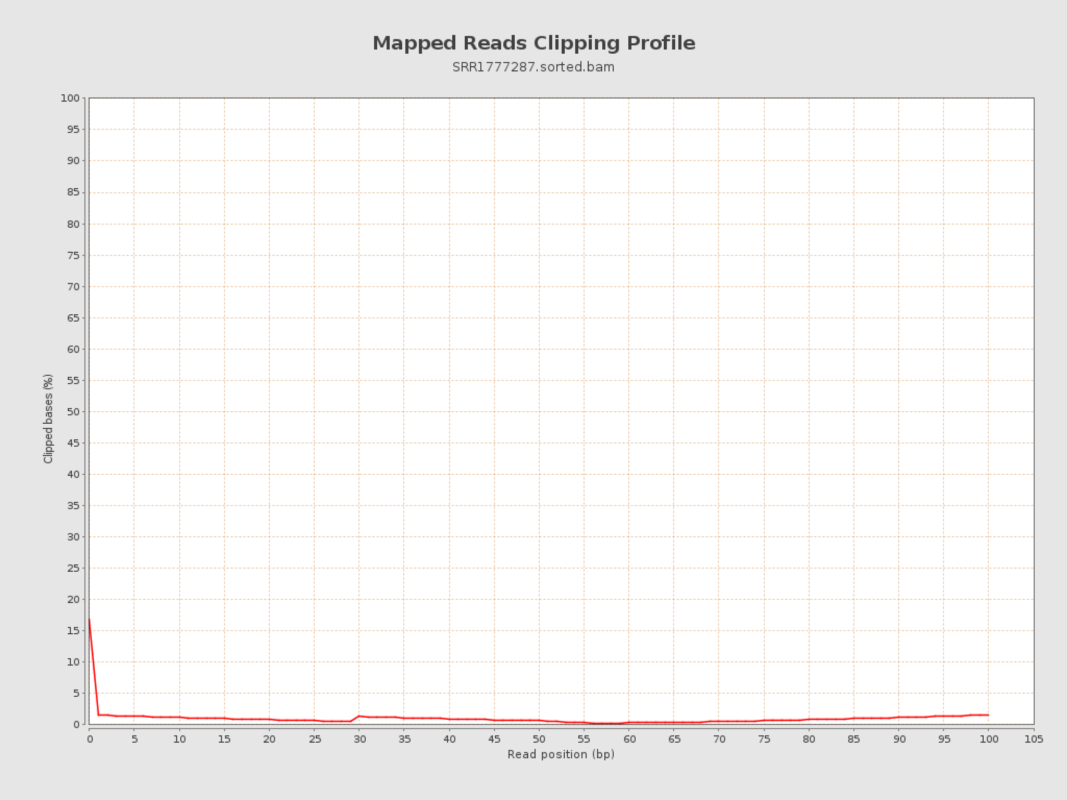
8. Results : Mapped Reads Nucleotide Content



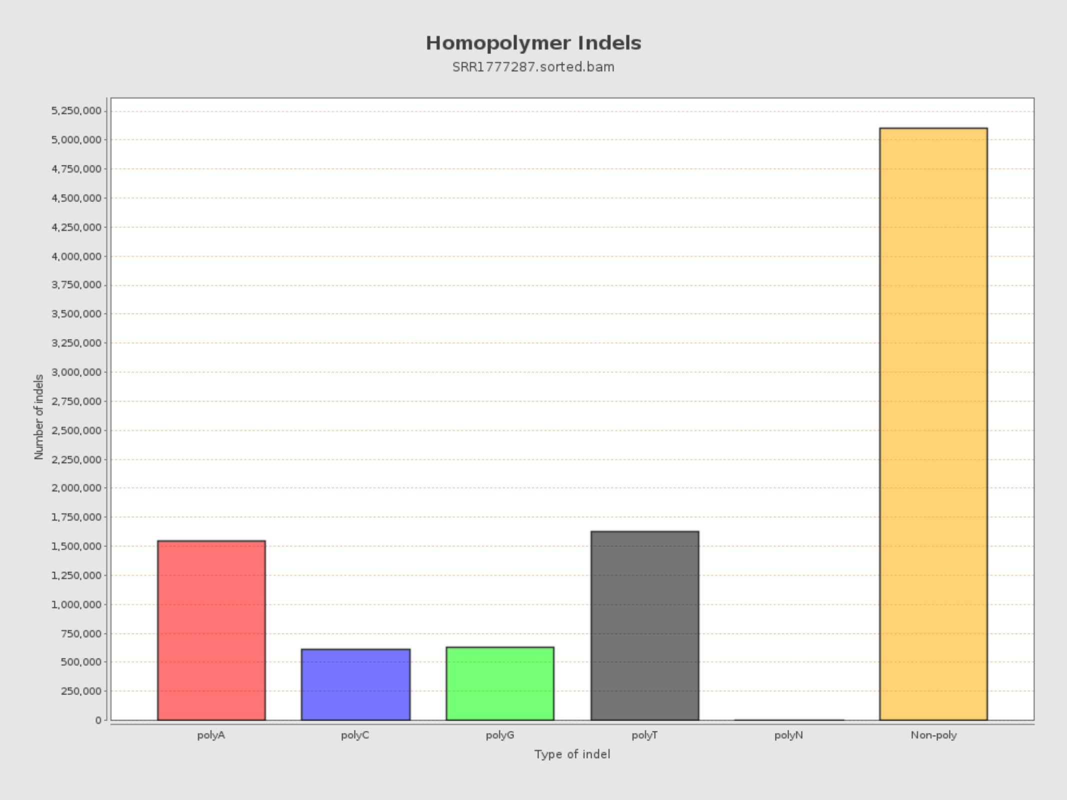
9. Results : Mapped Reads GC-content Distribution



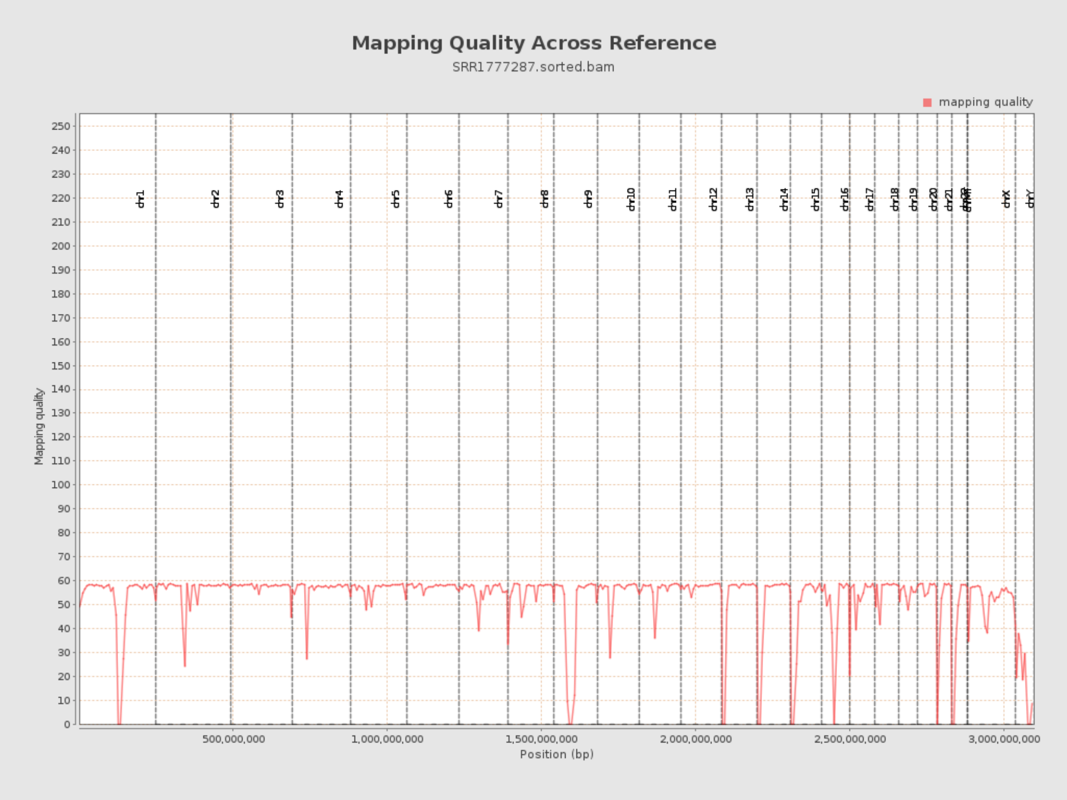
10. Results : Mapped Reads Clipping Profile



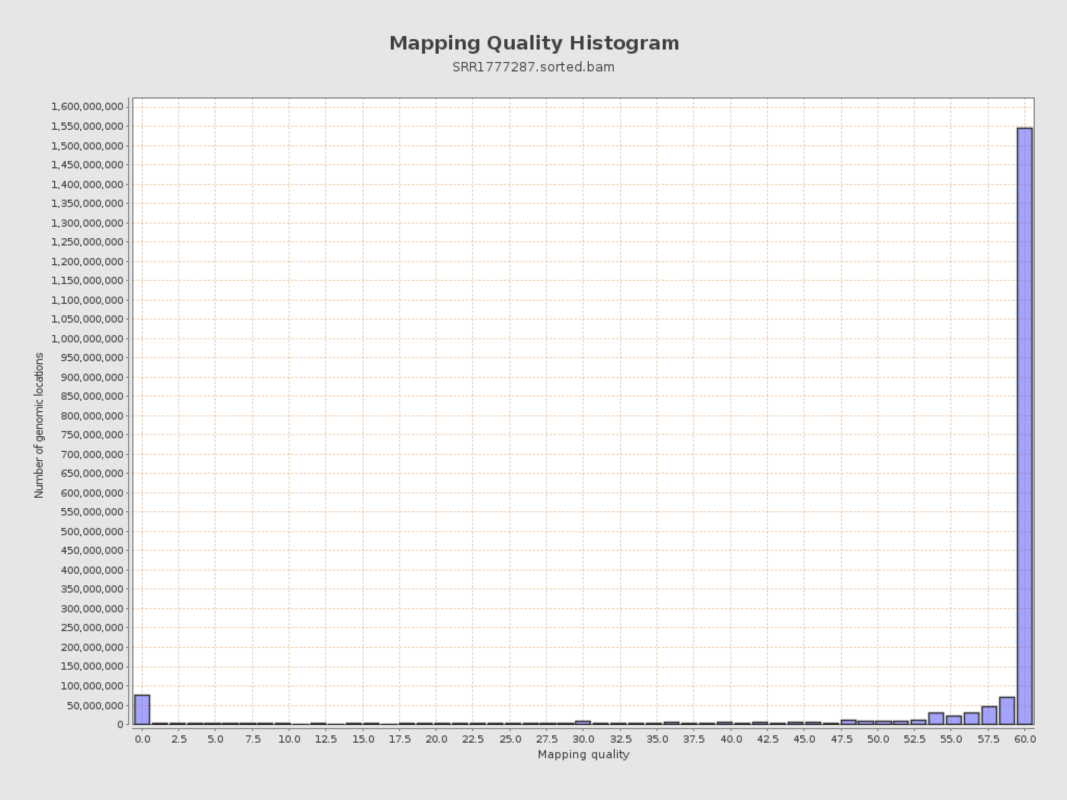
11. Results : Homopolymer Indels



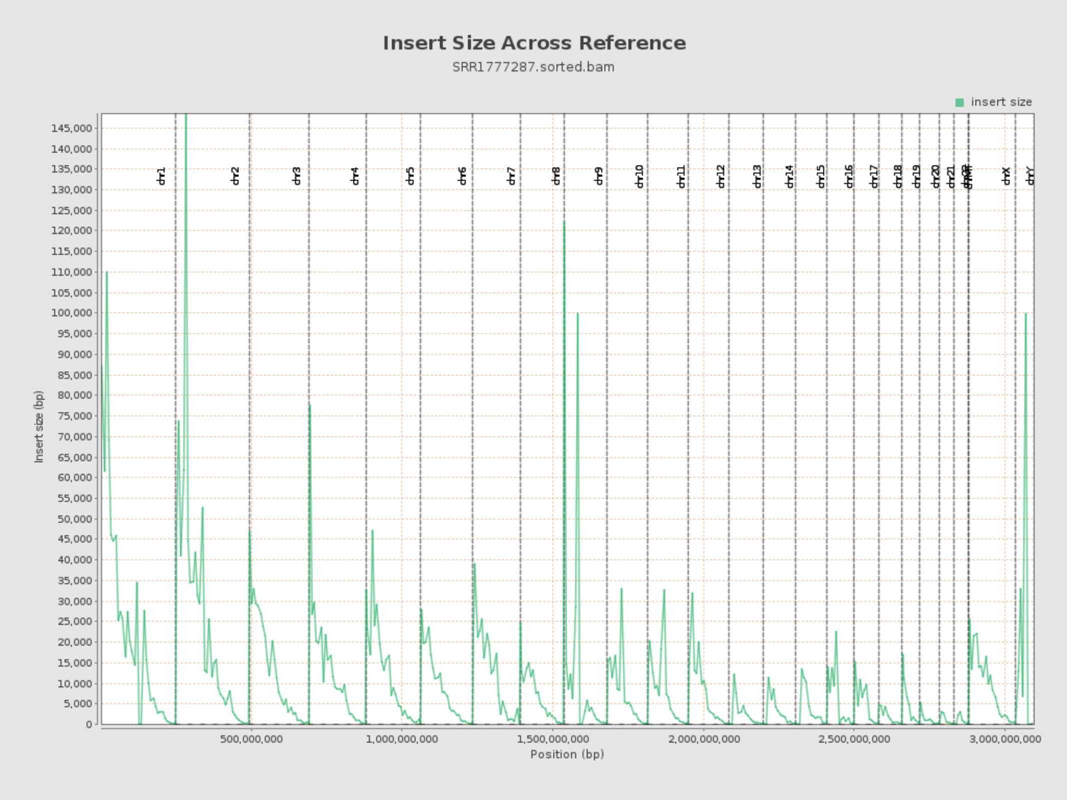
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram