Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/25 05:24:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781822.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_SRR1781822 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781822_1.fastq.gz SRR1781822_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 25 05:24:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781822.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	386,387,256
Mapped reads	366,552,220 / 94.87%
Unmapped reads	19,835,036 / 5.13%
Mapped paired reads	366,552,220 / 94.87%
Mapped reads, first in pair	188,197,058 / 48.71%
Mapped reads, second in pair	178,355,162 / 46.16%
Mapped reads, both in pair	354,670,002 / 91.79%
Mapped reads, singletons	11,882,218 / 3.08%
Secondary alignments	0
Supplementary alignments	1,344,452 / 0.35%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	42,062,171 / 10.89%
Duplication rate	11.04%
Clipped reads	30,471,128 / 7.89%

2.2. ACGT Content

Number/percentage of A's	10,408,371,866 / 29.29%
Number/percentage of C's	7,285,179,098 / 20.5%
Number/percentage of T's	10,363,669,559 / 29.16%
Number/percentage of G's	7,383,248,836 / 20.77%
Number/percentage of N's	99,360,012 / 0.28%

GC Percentage	41.27%

2.3. Coverage

Mean	11.4827
Standard Deviation	13.357

2.4. Mapping Quality

Mean Mapping Quality	53.7

2.5. Insert size

Mean	44,804.76
Standard Deviation	2,057,358.87
P25/Median/P75	169 / 207 / 250

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	216,660,384
Insertions	3,204,490
Mapped reads with at least one insertion	0.86%
Deletions	3,167,660
Mapped reads with at least one deletion	0.85%
Homopolymer indels	45.7%

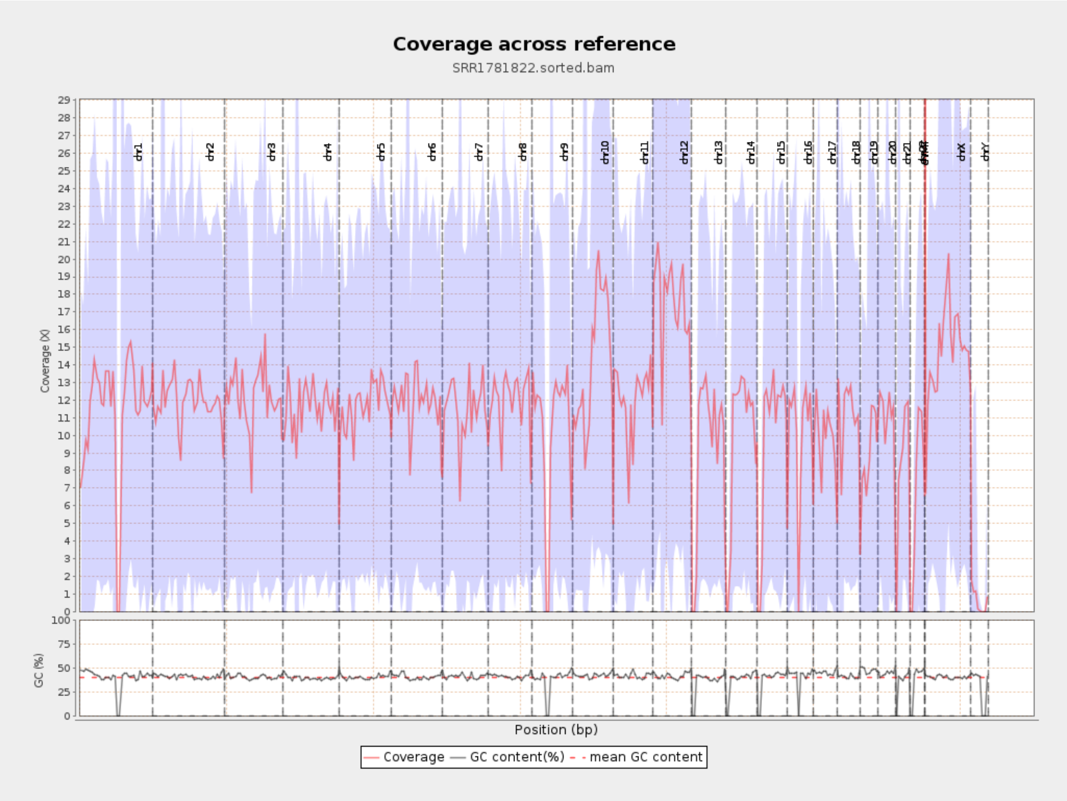
2.7. Chromosome stats

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

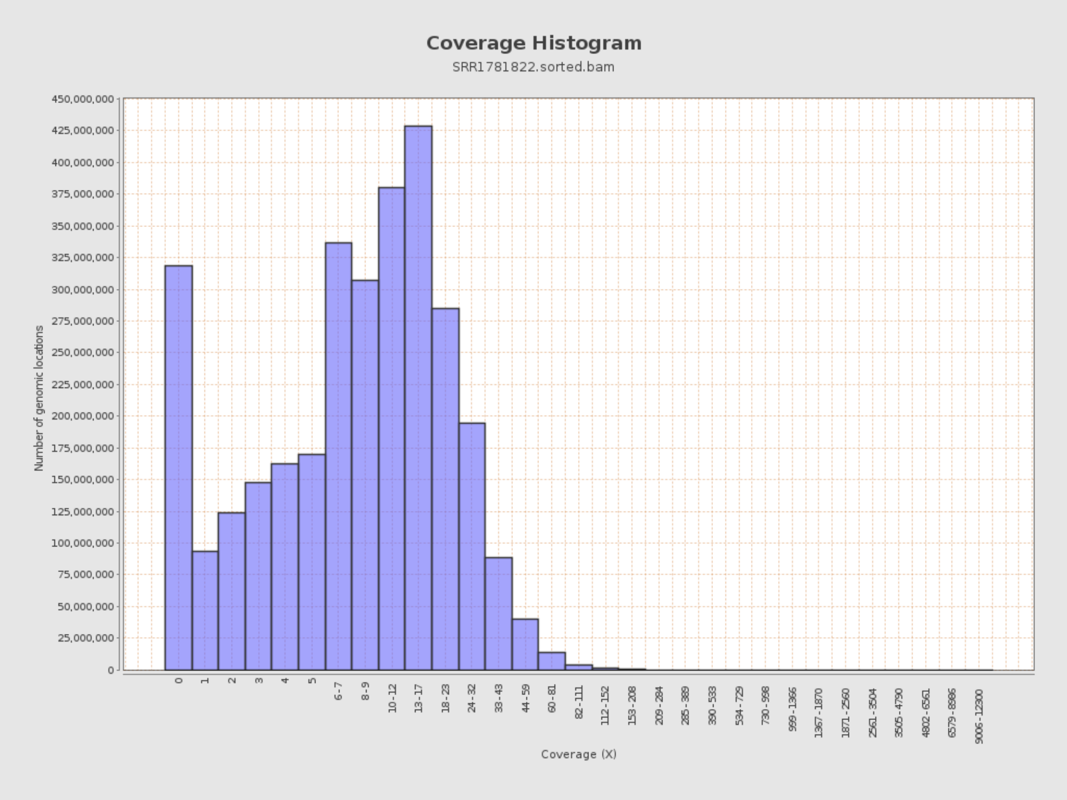
		bases	coverage	deviation
chr1	249250621	2845174970	11.4149	17.7598
chr2	243199373	2904604053	11.9433	14.7073
chr3	198022430	2419359891	12.2176	10.7894
chr4	191154276	2231091364	11.6717	11.7886
chr5	180915260	2113664008	11.6832	9.9208
chr6	171115067	2058290639	12.0287	11.6181
chr7	159138663	1819974966	11.4364	12.0336
chr8	146364022	1760890897	12.0309	11.1205
chr9	141213431	1431452162	10.1368	13.4203
chr10	135534747	1949319302	14.3824	20.0695
chr11	135006516	1612454260	11.9435	11.2104
chr12	133851895	2360218688	17.6331	15.7043
chr13	115169878	1086967614	9.438	9.7023
chr14	107349540	1055809474	9.8352	10.6636
chr15	102531392	1002150792	9.7741	10.7229
chr16	90354753	884356165	9.7876	11.0786
chr17	81195210	793034030	9.767	11.5158
chr18	78077248	883614122	11.3172	13.7031
chr19	59128983	535384393	9.0545	13.4059
chr20	63025520	696097285	11.0447	12.5513
chr21	48129895	417788486	8.6804	16.8033
chr22	51304566	349736822	6.8169	9.9053
chrMT	16571	2028602	122.4188	35.0904
chrX	155270560	2299396468	14.809	13.2648

chrY	59373566	34146062	0.5751	6.3175

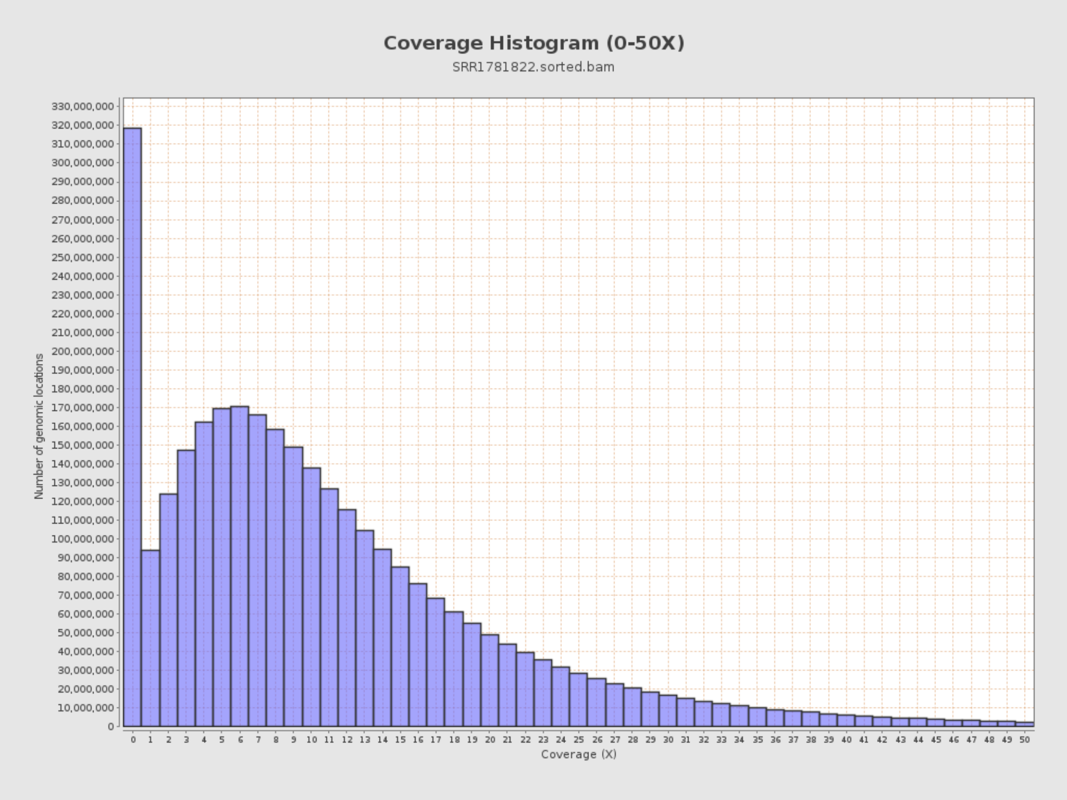
3. Results : Coverage across reference



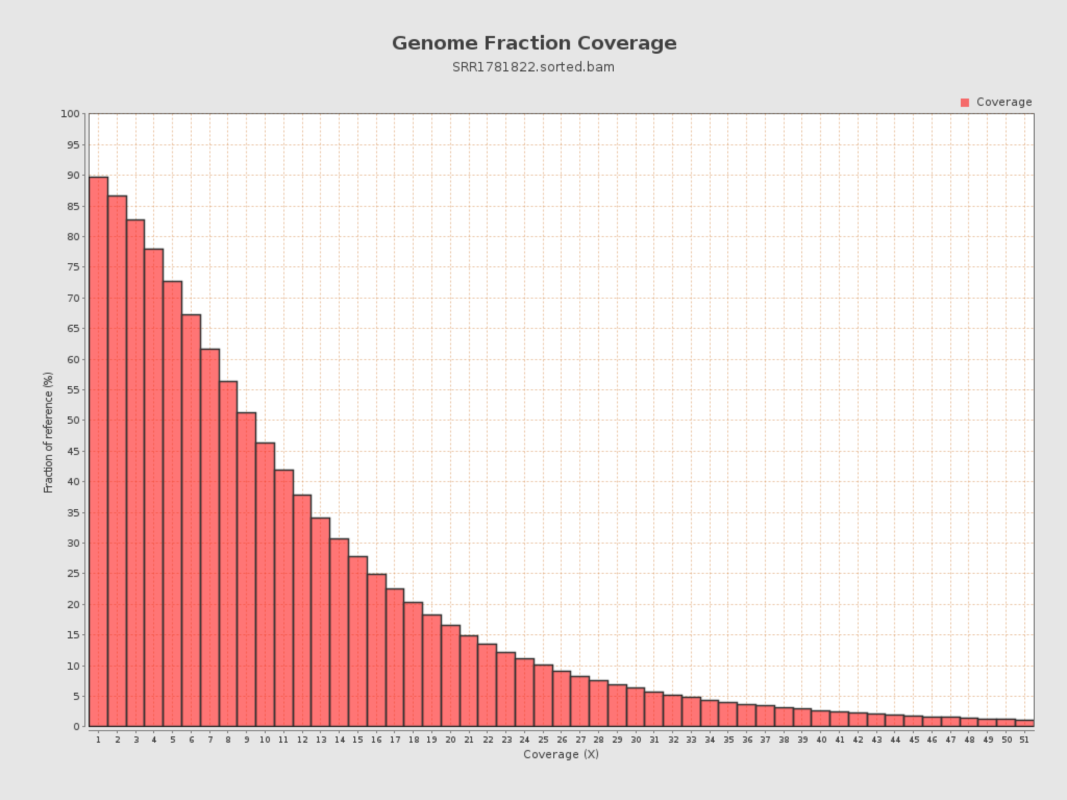
4. Results : Coverage Histogram



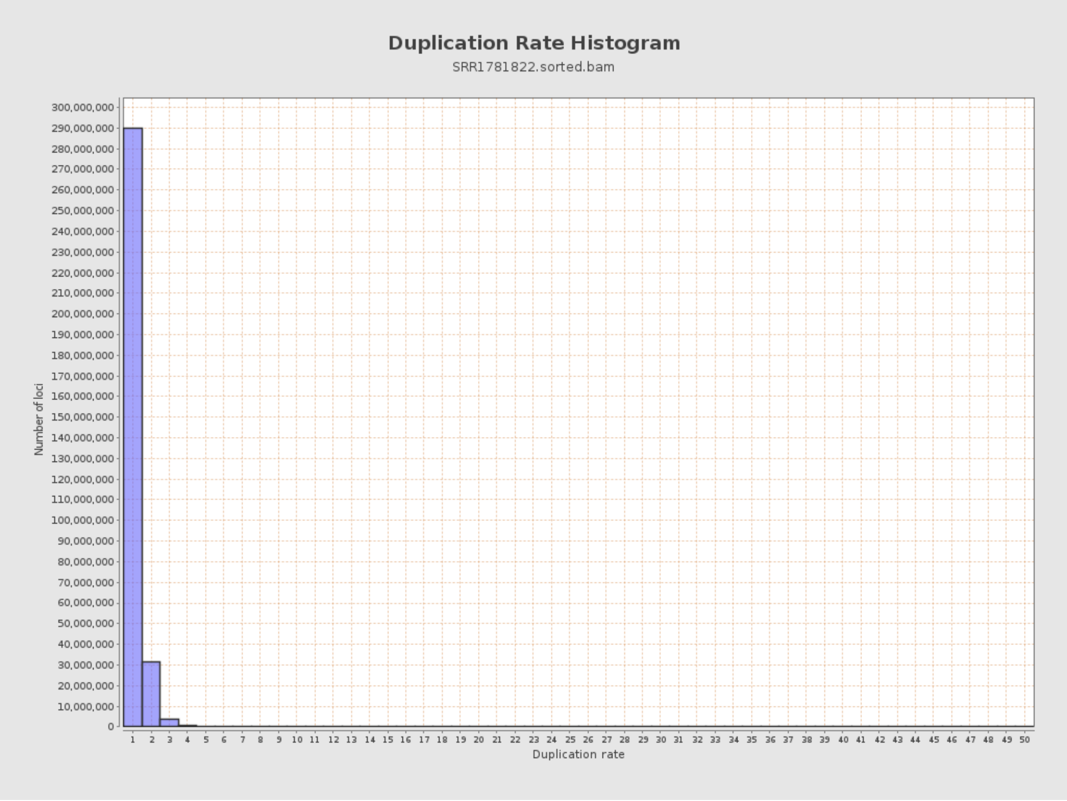
5. Results : Coverage Histogram (0-50X)



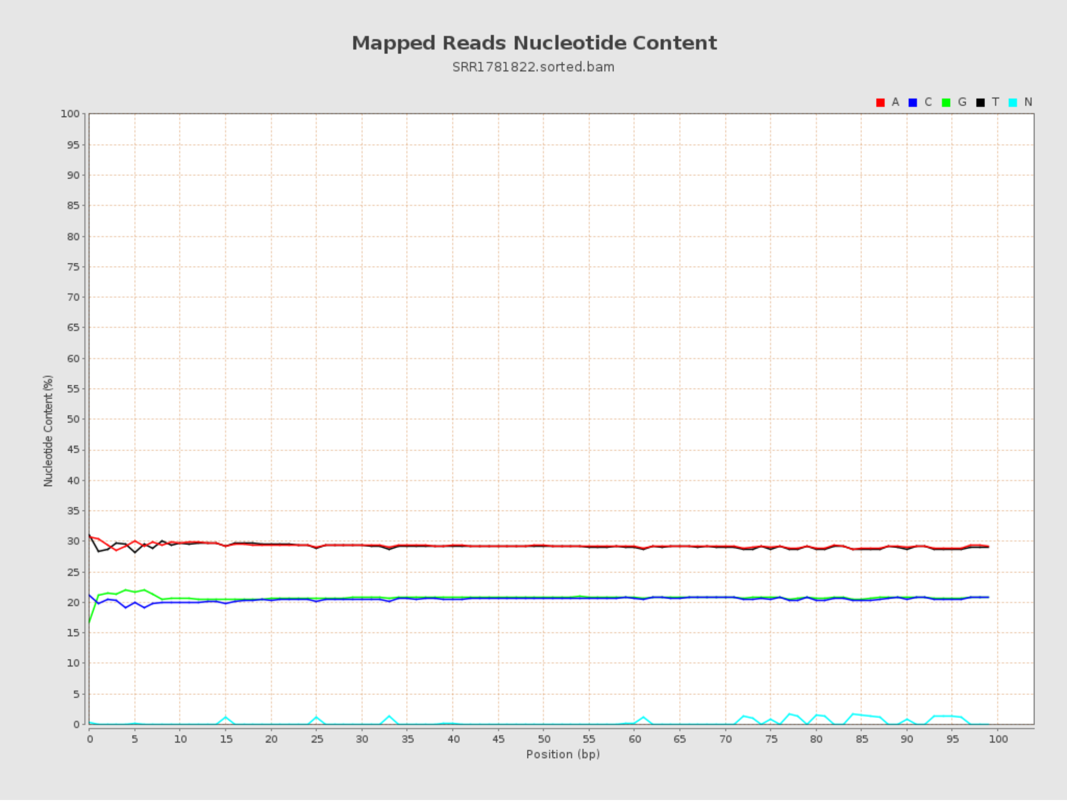
6. Results : Genome Fraction Coverage



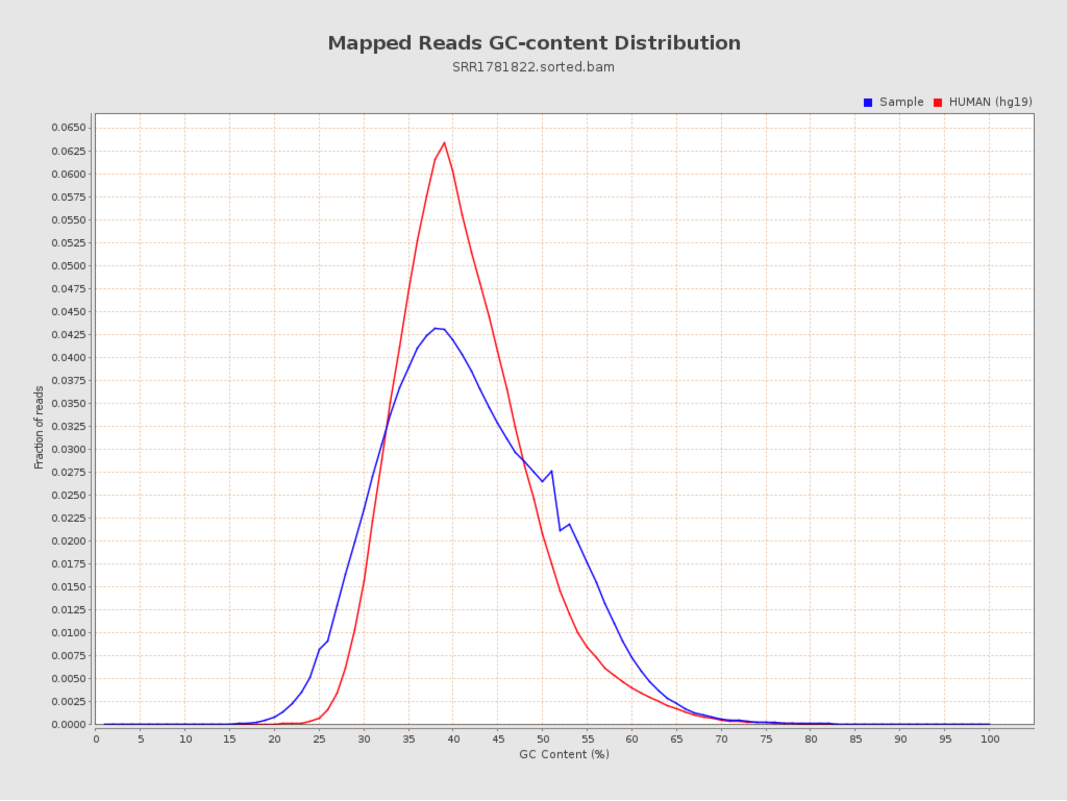
7. Results : Duplication Rate Histogram



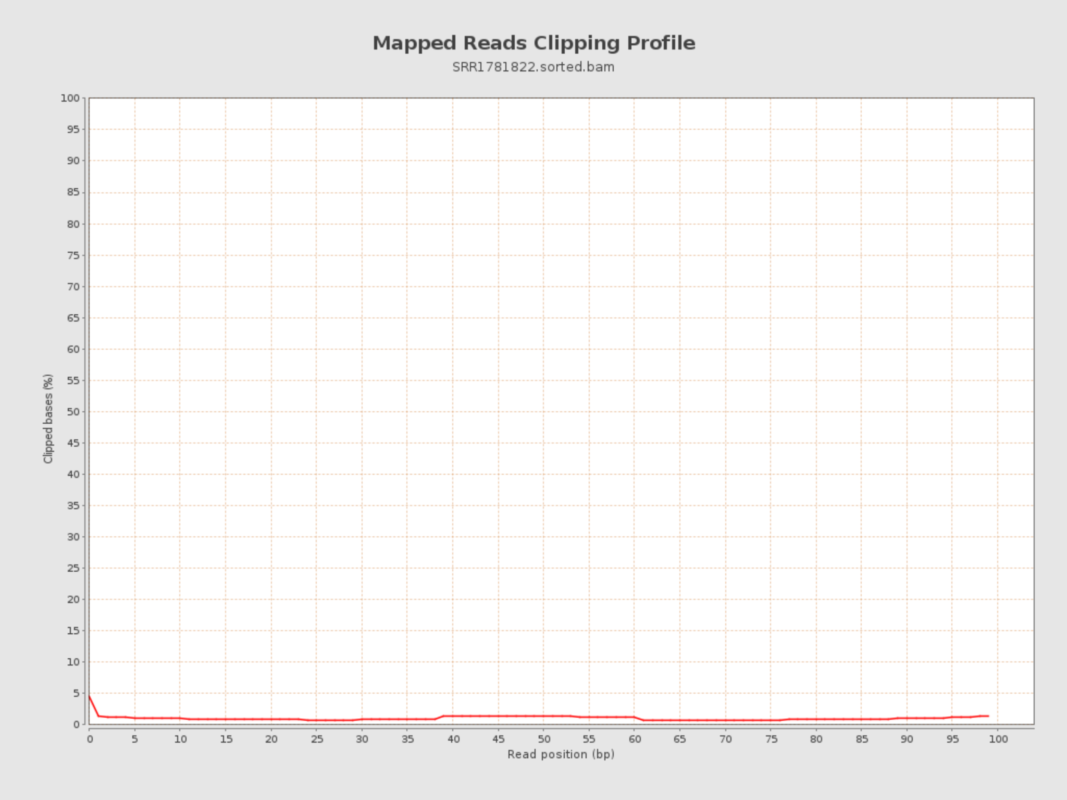
8. Results : Mapped Reads Nucleotide Content



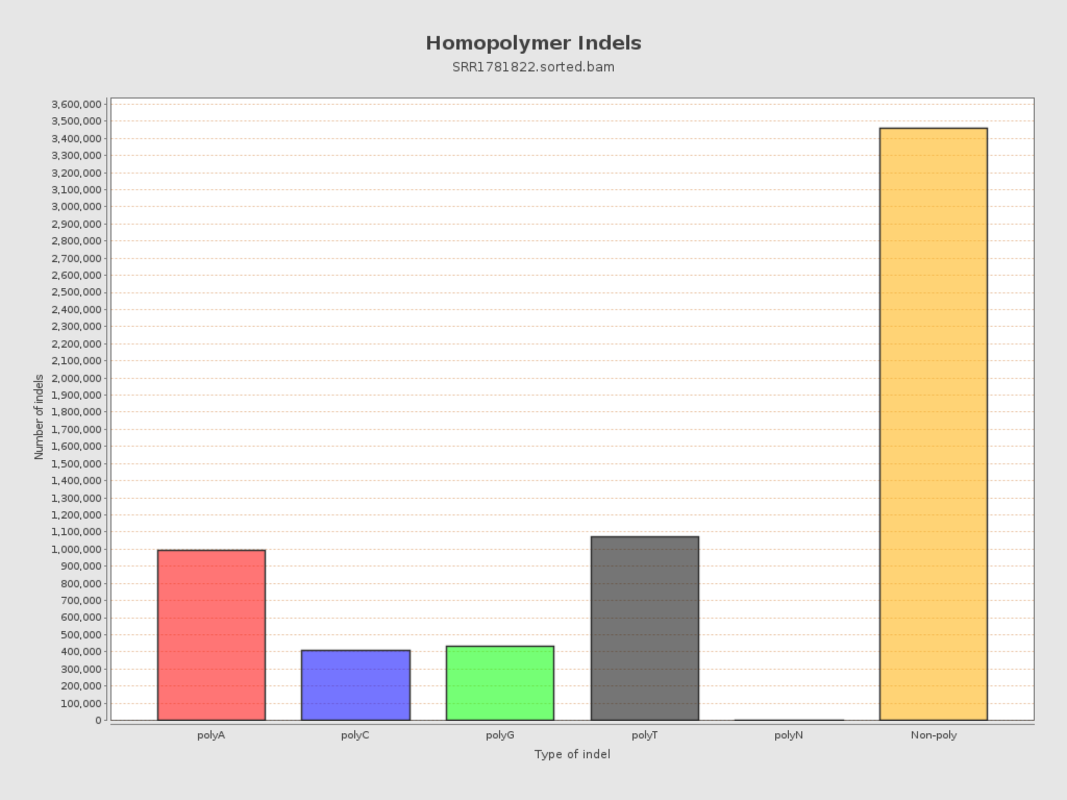
9. Results : Mapped Reads GC-content Distribution



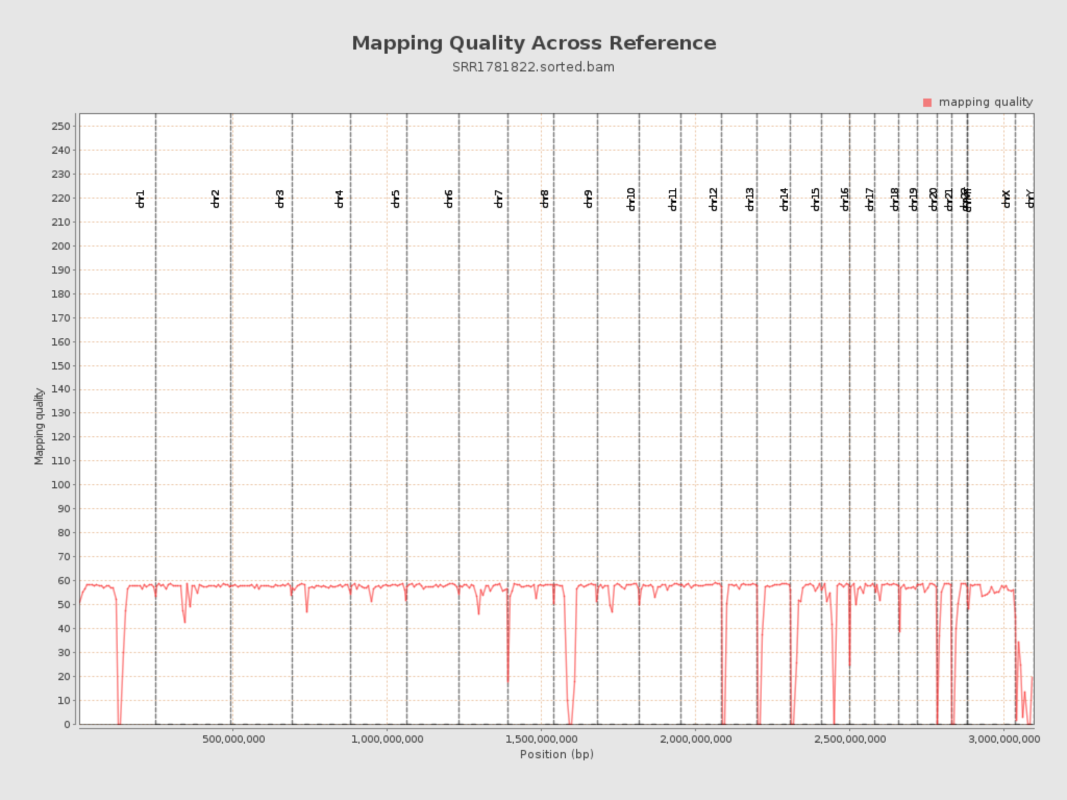
10. Results : Mapped Reads Clipping Profile



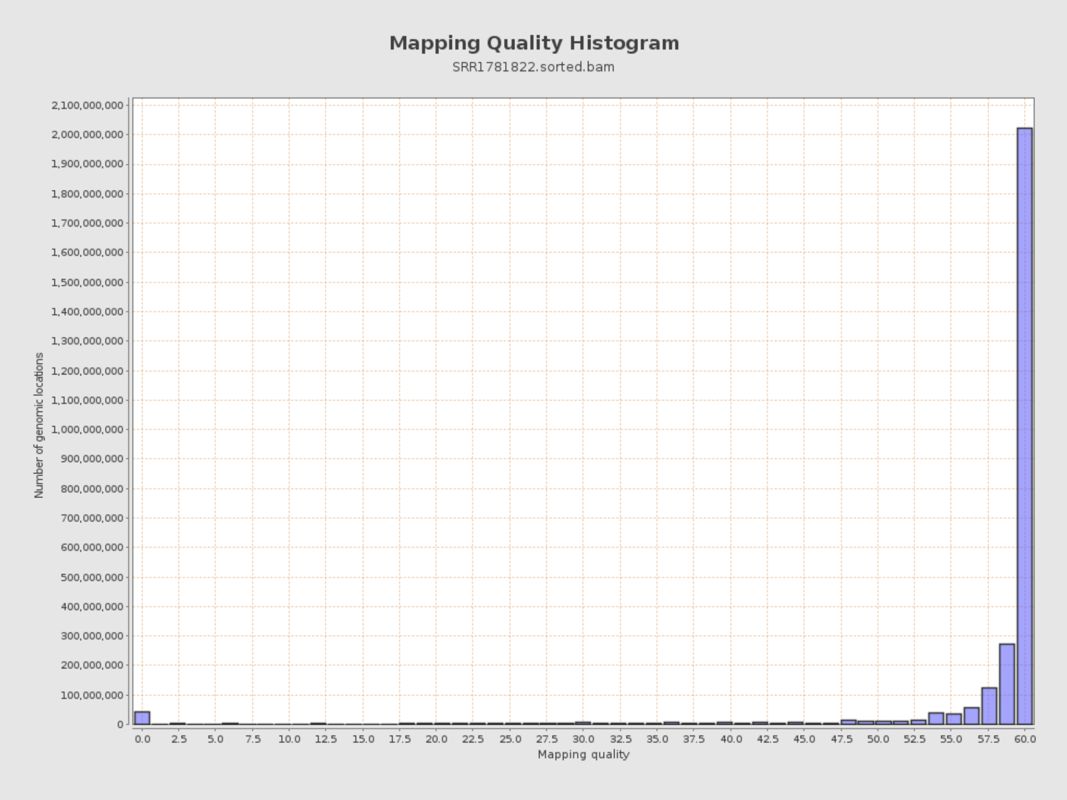
11. Results : Homopolymer Indels



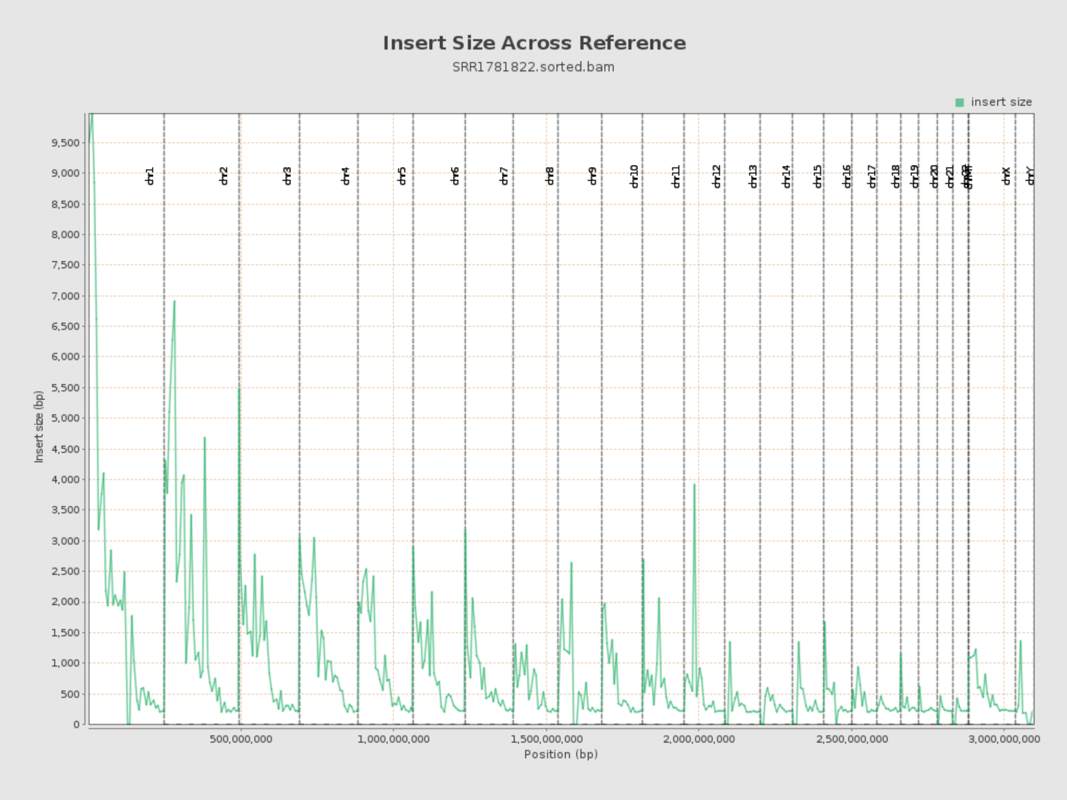
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram