Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/25 14:16:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781824.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_SRR1781824 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781824_1.fastq.gz SRR1781824_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 25 14:16:52 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781824.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	174,558,694
Mapped reads	168,665,524 / 96.62%
Unmapped reads	5,893,170 / 3.38%
Mapped paired reads	168,665,524 / 96.62%
Mapped reads, first in pair	84,990,244 / 48.69%
Mapped reads, second in pair	83,675,280 / 47.94%
Mapped reads, both in pair	166,492,758 / 95.38%
Mapped reads, singletons	2,172,766 / 1.24%
Secondary alignments	0
Supplementary alignments	583,169 / 0.33%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	11,548,710 / 6.62%
Duplication rate	6.58%
Clipped reads	8,057,249 / 4.62%

2.2. ACGT Content

Number/percentage of A's	4,981,463,262 / 29.77%
Number/percentage of C's	3,377,944,047 / 20.19%
Number/percentage of T's	4,964,768,685 / 29.67%
Number/percentage of G's	3,406,367,798 / 20.36%
Number/percentage of N's	1,452,009 / 0.01%

GC Percentage	40.55%

2.3. Coverage

Mean	5.406
Standard Deviation	6.9745

2.4. Mapping Quality

Mean Mapping Quality	53.91

2.5. Insert size

Mean	42,626.21
Standard Deviation	2,010,552.68
P25/Median/P75	160 / 197 / 243

2.6. Mismatches and indels

General error rate	0.49%
Mismatches	78,033,636
Insertions	1,855,086
Mapped reads with at least one insertion	1.08%
Deletions	1,561,684
Mapped reads with at least one deletion	0.91%
Homopolymer indels	46.91%

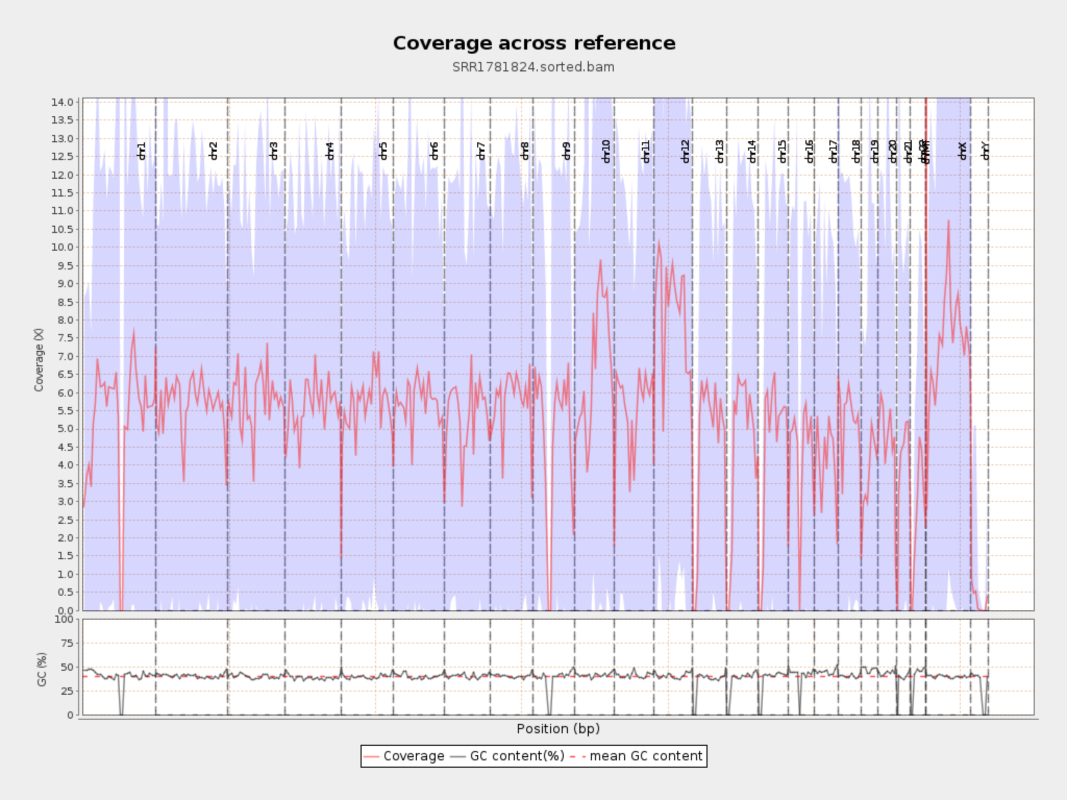
2.7. Chromosome stats

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

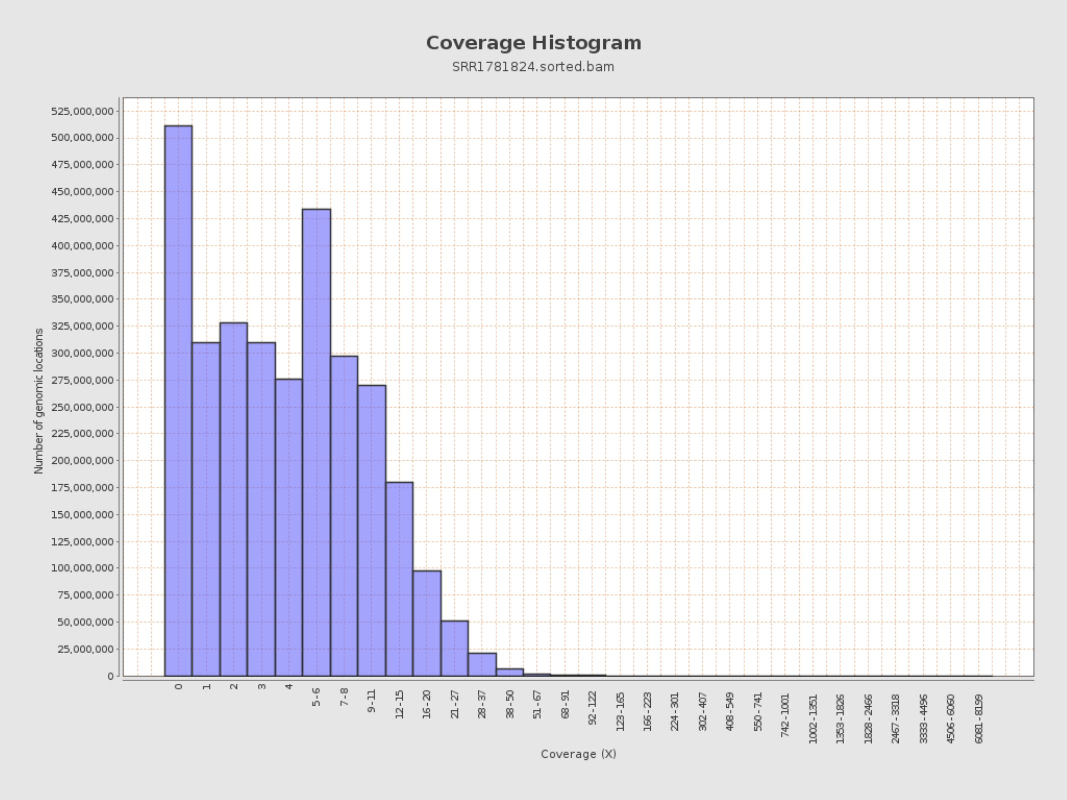
		bases	coverage	deviation
chr1	249250621	1325082550	5.3163	8.6967
chr2	243199373	1380392255	5.676	9.0384
chr3	198022430	1149148969	5.8031	5.7763
chr4	191154276	1083519698	5.6683	5.9131
chr5	180915260	1024086575	5.6606	5.508
chr6	171115067	983701002	5.7488	5.9379
chr7	159138663	853219046	5.3615	6.4808
chr8	146364022	843055625	5.76	5.8331
chr9	141213431	682528655	4.8333	6.9241
chr10	135534747	906742158	6.6901	10.3811
chr11	135006516	757752860	5.6127	5.9543
chr12	133851895	1111069191	8.3007	8.1623
chr13	115169878	530646837	4.6075	5.3286
chr14	107349540	492640831	4.5891	5.5652
chr15	102531392	458621046	4.473	5.5633
chr16	90354753	378559124	4.1897	5.4579
chr17	81195210	341738717	4.2089	5.3295
chr18	78077248	414314682	5.3065	6.1671
chr19	59128983	224548088	3.7976	6.124
chr20	63025520	304855359	4.837	6.4723
chr21	48129895	190628685	3.9607	7.0137
chr22	51304566	136258948	2.6559	4.3275
chrMT	16571	592030	35.7269	10.8072
chrX	155270560	1146016673	7.3808	7.6661

chrY	59373566	15728650	0.2649	2.6372

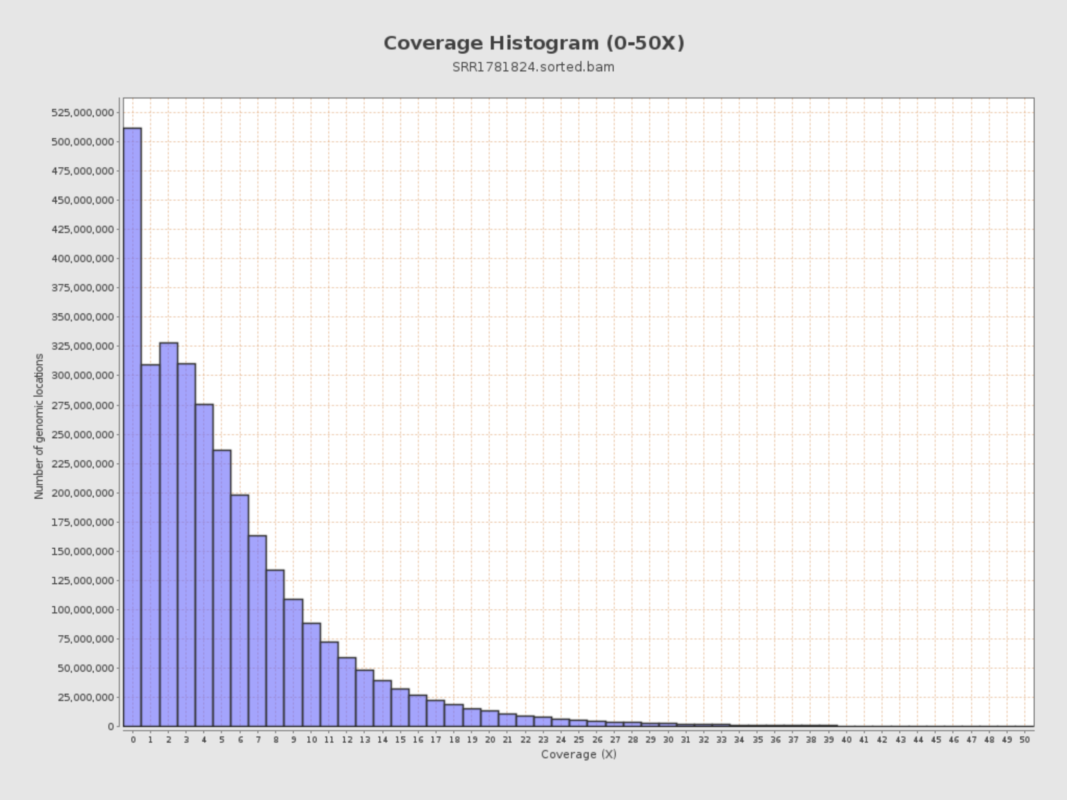
3. Results : Coverage across reference



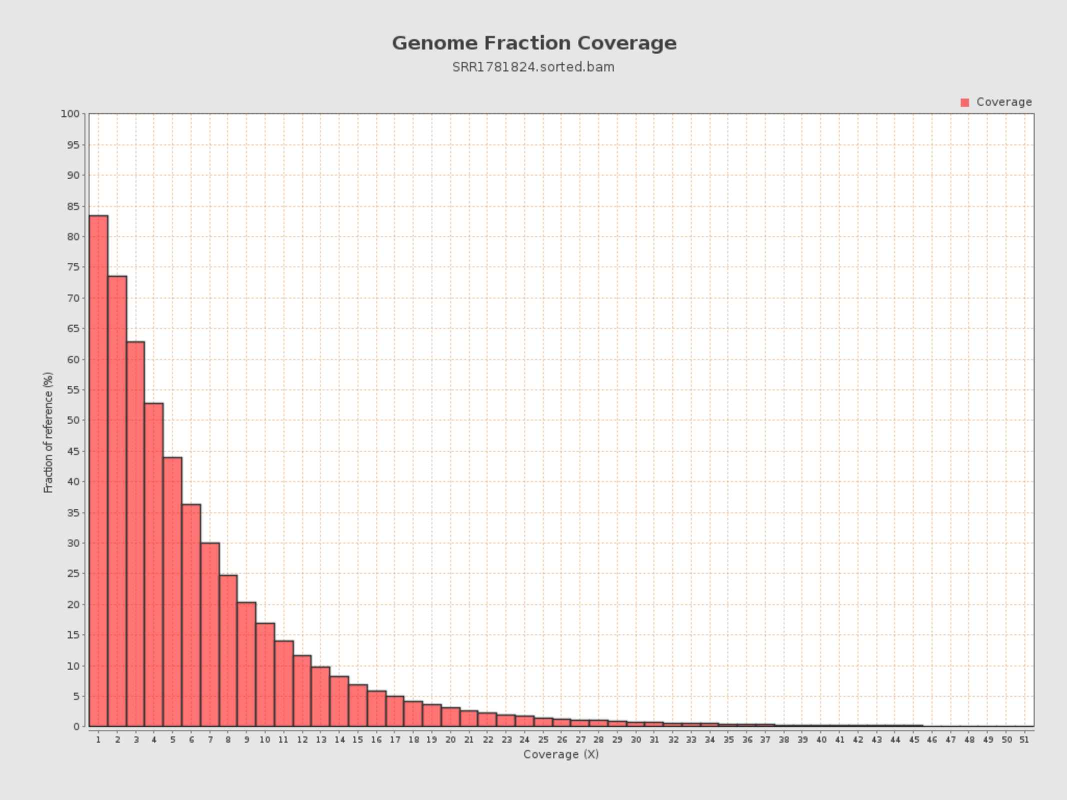
4. Results : Coverage Histogram



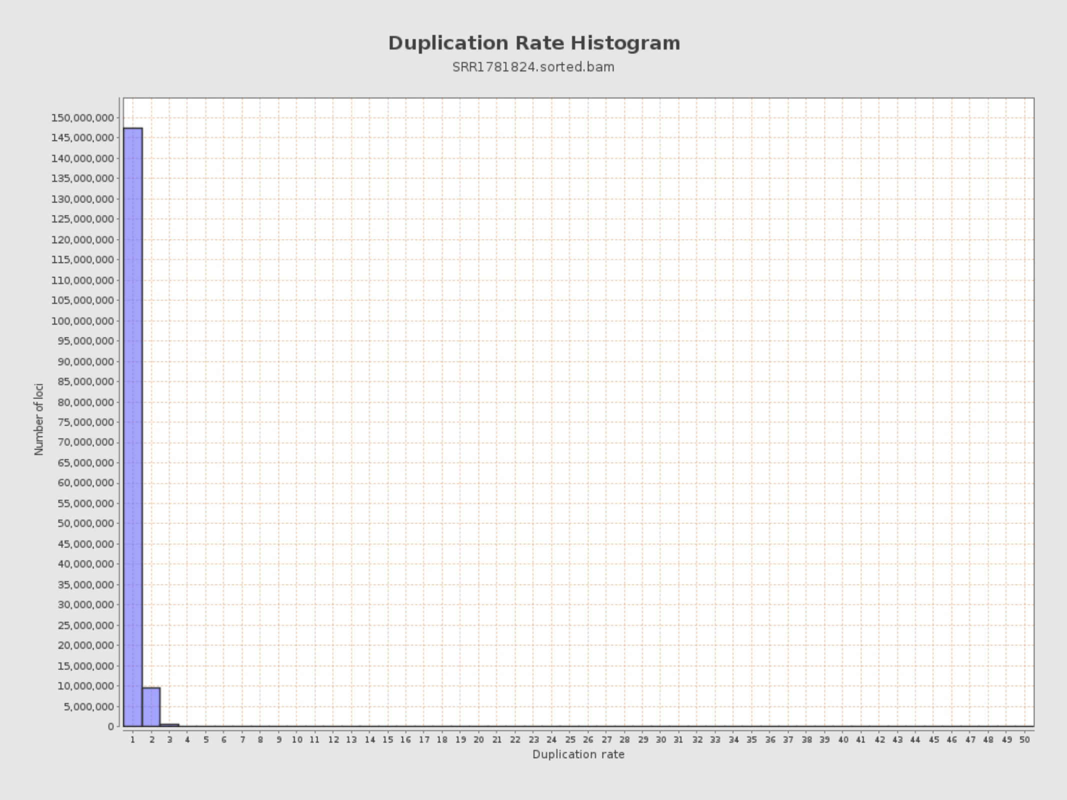
5. Results : Coverage Histogram (0-50X)



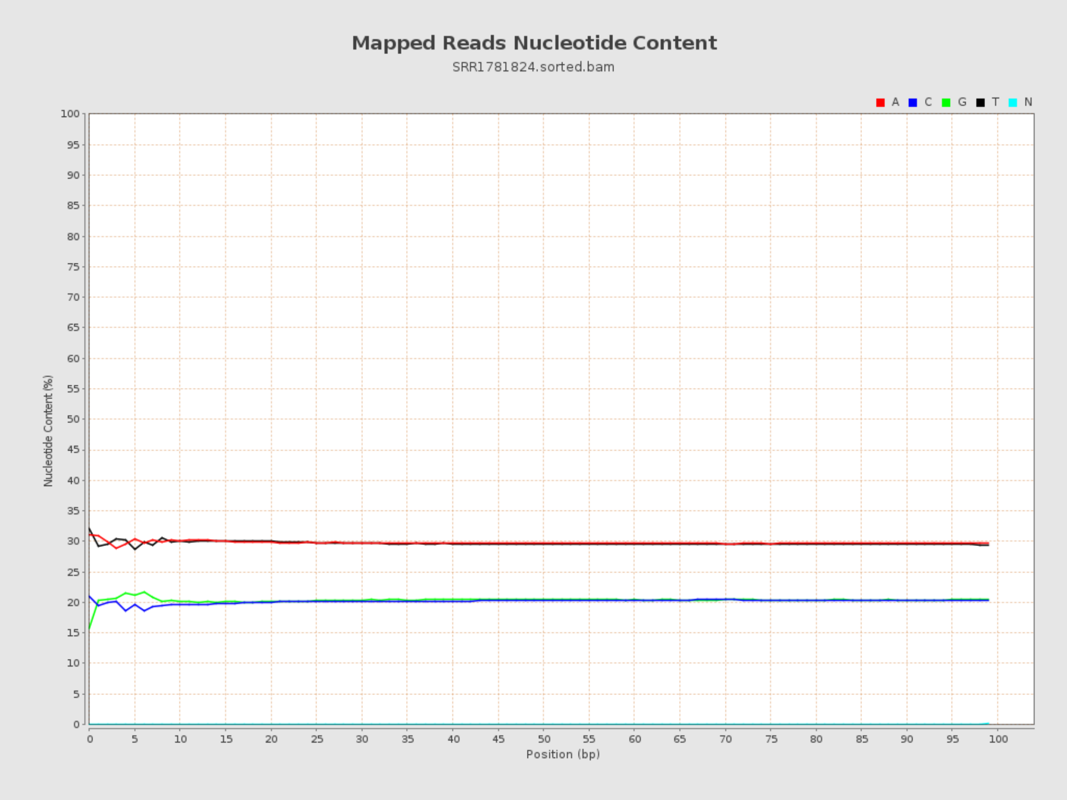
6. Results : Genome Fraction Coverage



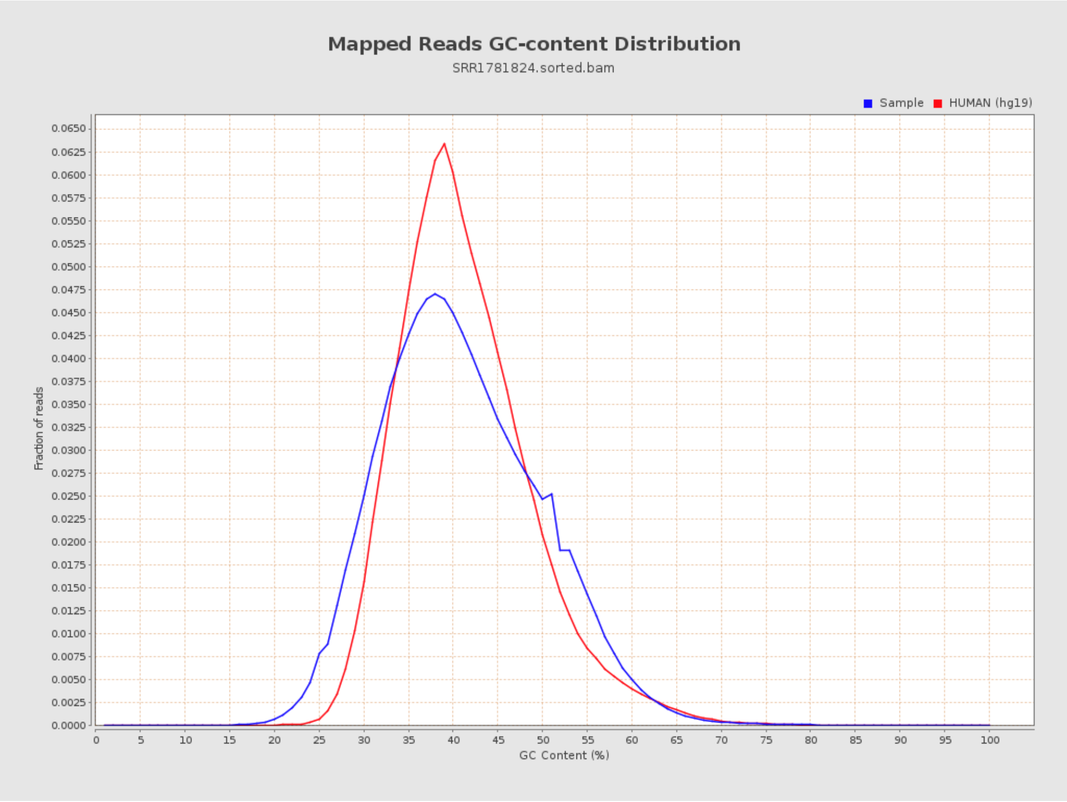
7. Results : Duplication Rate Histogram



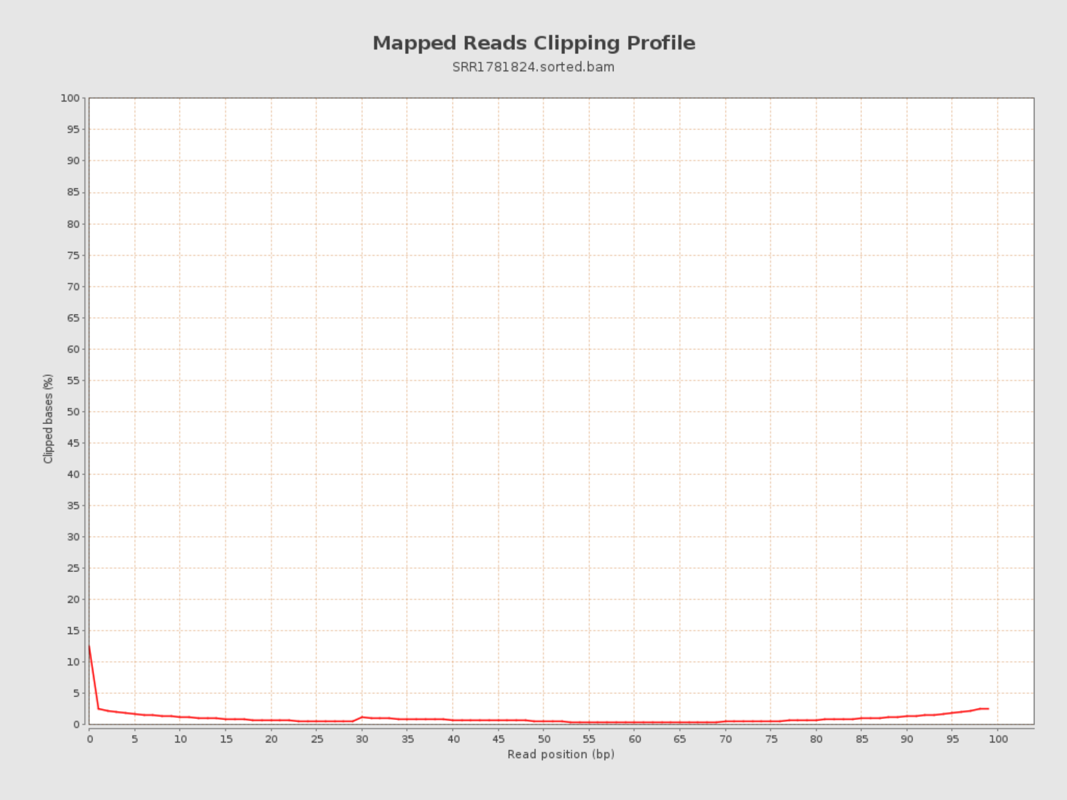
8. Results : Mapped Reads Nucleotide Content



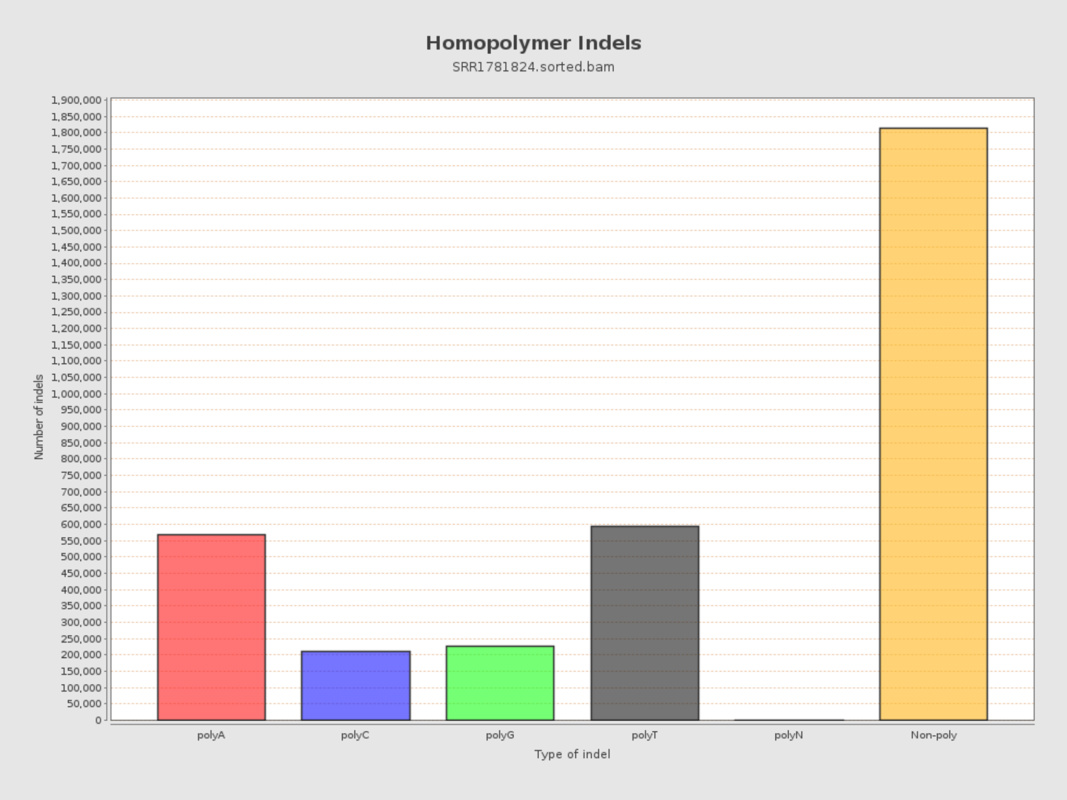
9. Results : Mapped Reads GC-content Distribution



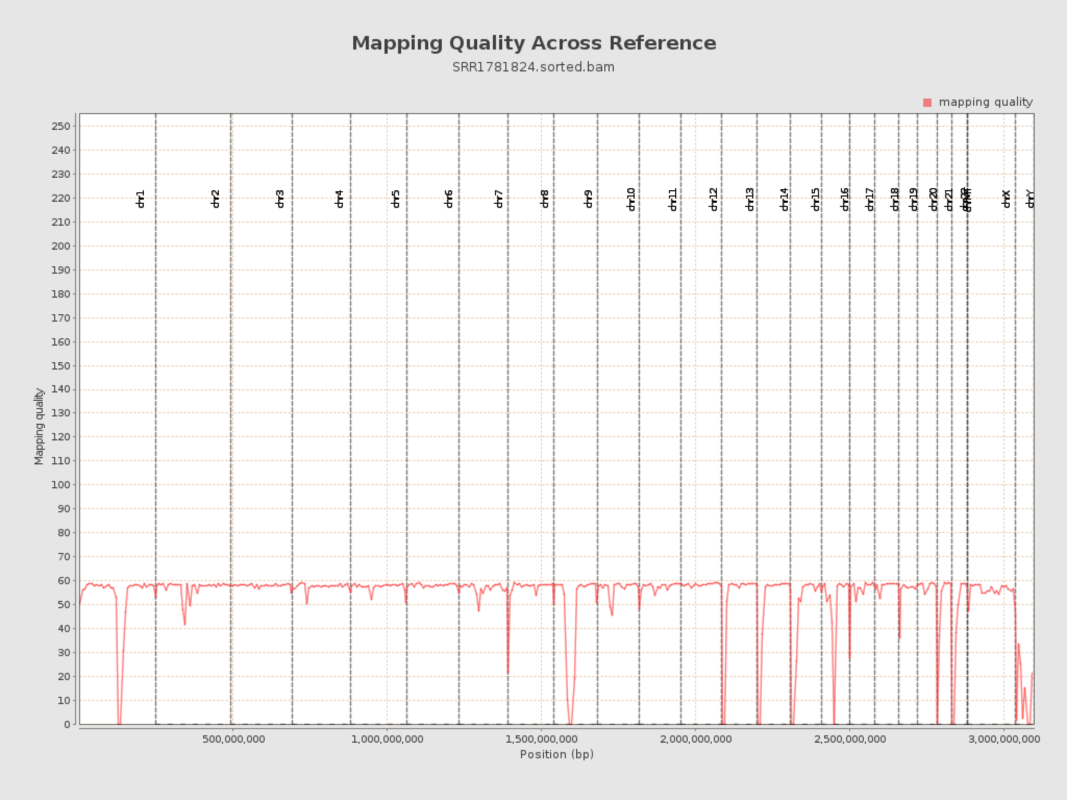
10. Results : Mapped Reads Clipping Profile



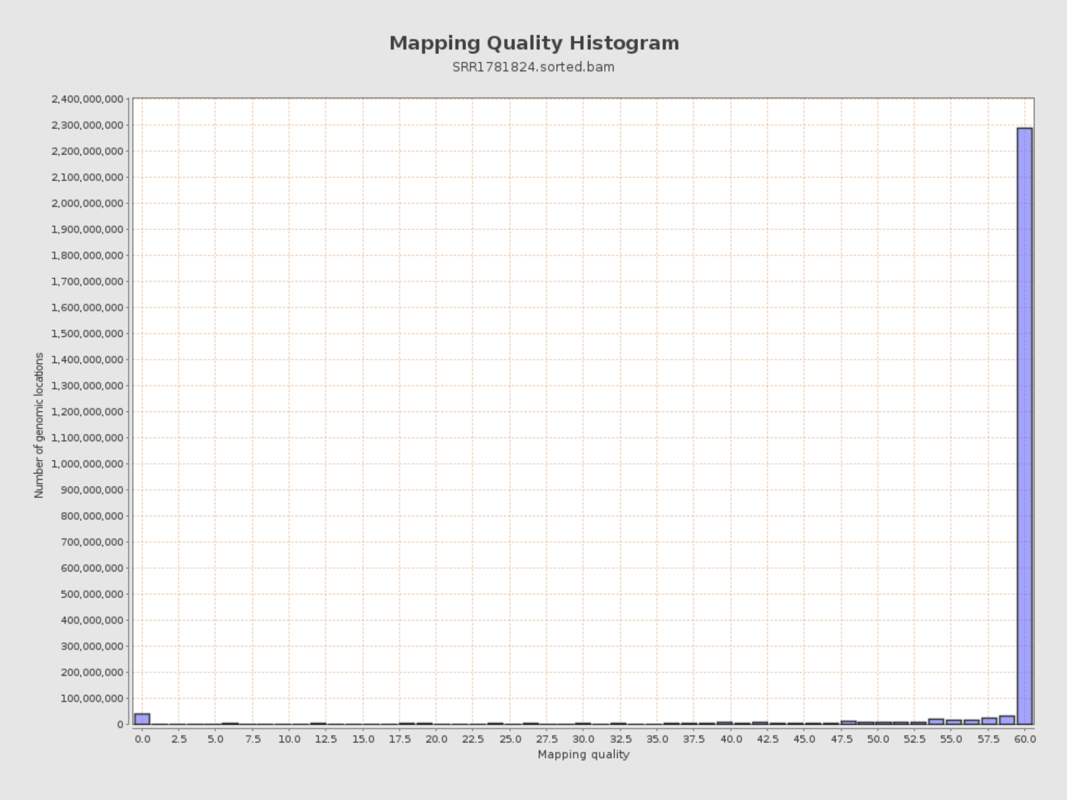
11. Results : Homopolymer Indels



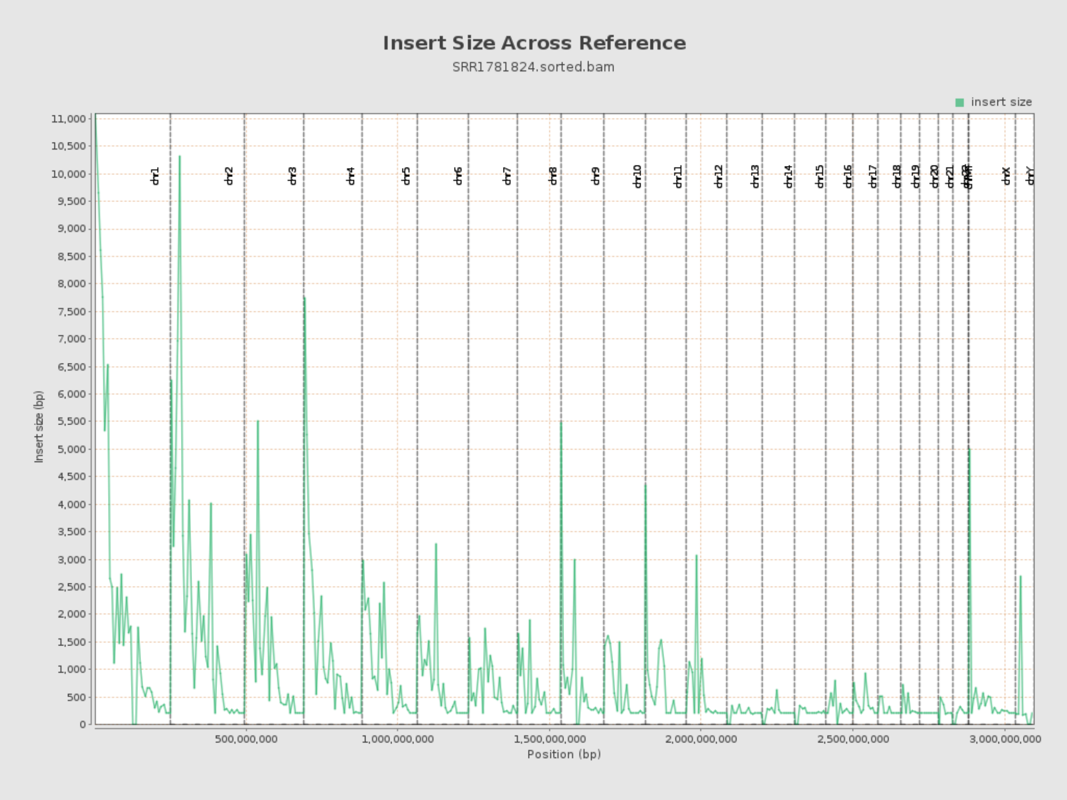
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram