Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/29 03:03:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264626.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_SRR1264626 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264626_1.fastq.gz SRR1264626_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 29 03:03:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264626.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,231,064,828
Mapped reads	1,225,179,454 / 99.52%
Unmapped reads	5,885,374 / 0.48%
Mapped paired reads	1,225,179,454 / 99.52%
Mapped reads, first in pair	614,119,858 / 49.89%
Mapped reads, second in pair	611,059,596 / 49.64%
Mapped reads, both in pair	1,221,109,644 / 99.19%
Mapped reads, singletons	4,069,810 / 0.33%
Secondary alignments	0
Supplementary alignments	9,211,003 / 0.75%
Read min/max/mean length	30 / 101 / 101.31
Duplicated reads (estimated)	391,075,229 / 31.77%
Duplication rate	31.59%
Clipped reads	54,522,439 / 4.43%

2.2. ACGT Content

Number/percentage of A's	38,011,180,942 / 30.9%
Number/percentage of C's	23,446,176,046 / 19.06%
Number/percentage of T's	37,901,214,374 / 30.81%
Number/percentage of G's	23,639,175,923 / 19.22%
Number/percentage of N's	18,772,779 / 0.02%

GC Percentage	38.28%

2.3. Coverage

Mean	39.7471
Standard Deviation	38.8196

2.4. Mapping Quality

Mean Mapping Quality	54.51

2.5. Insert size

Mean	108,345.42
Standard Deviation	3,159,743.62
P25/Median/P75	313 / 342 / 376

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	421,035,941
Insertions	13,486,344
Mapped reads with at least one insertion	1.09%
Deletions	12,715,975
Mapped reads with at least one deletion	1.02%
Homopolymer indels	48.55%

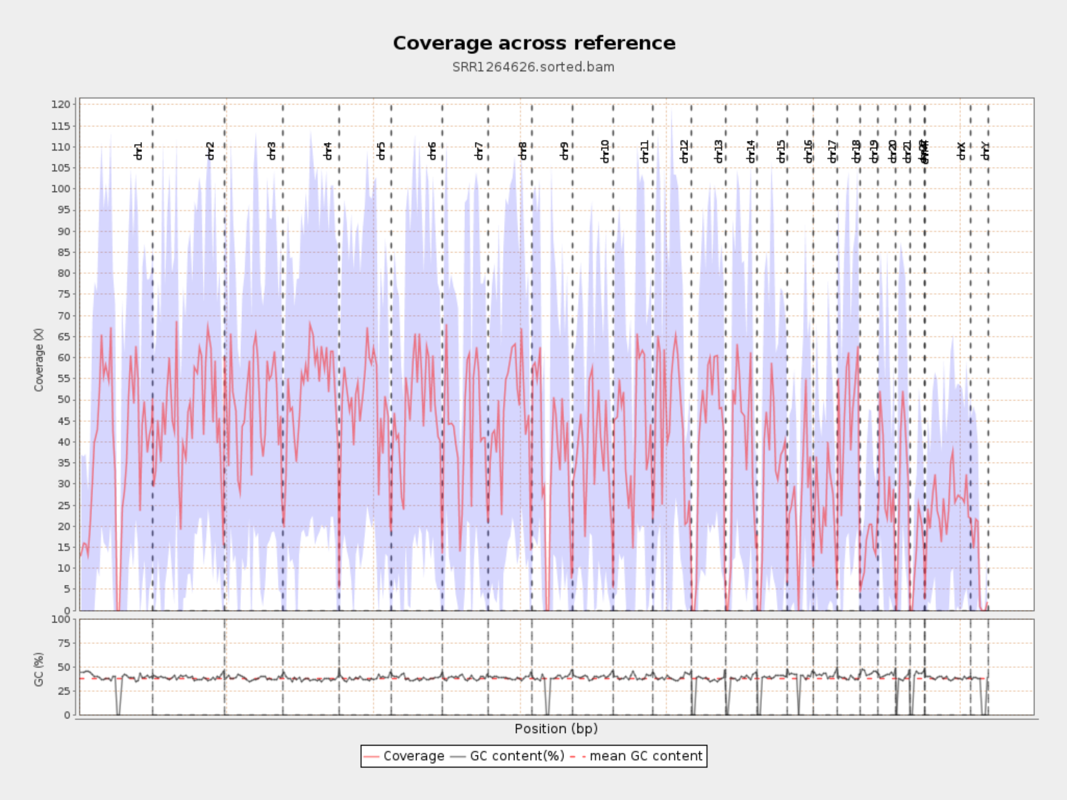
2.7. Chromosome stats

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

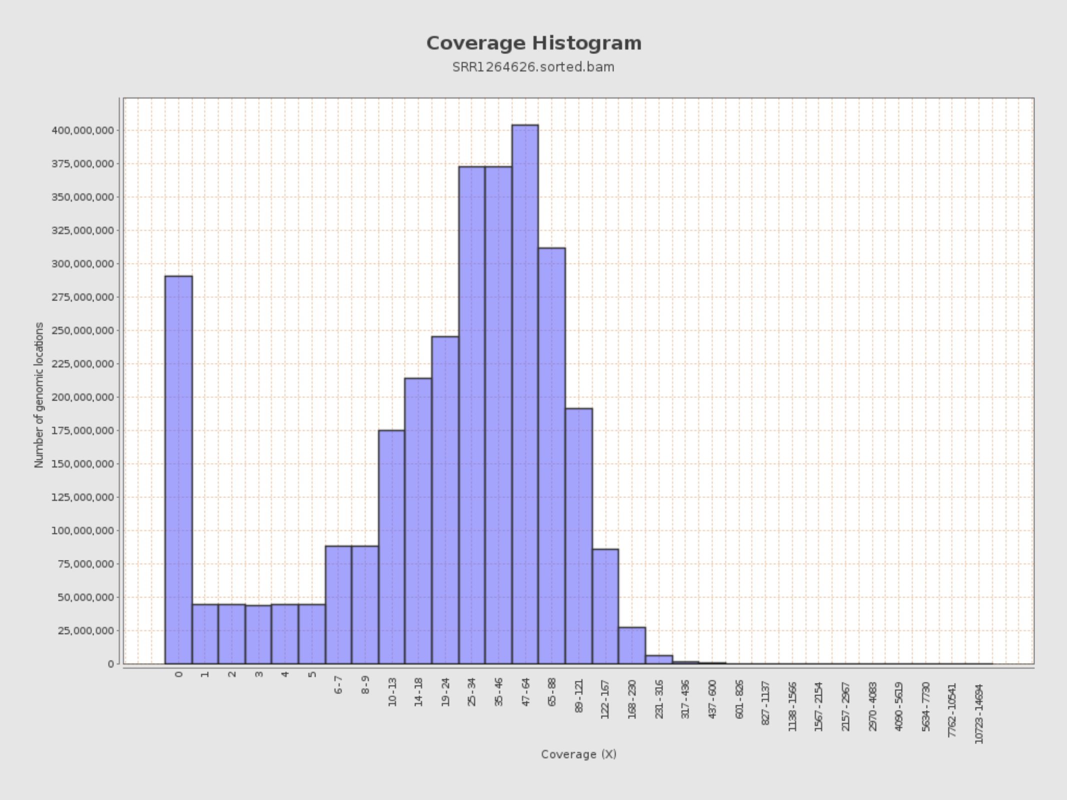
		bases	coverage	deviation
chr1	249250621	9571661818	38.4018	39.932
chr2	243199373	11282247124	46.3909	39.8544
chr3	198022430	9632722984	48.6446	39.1778
chr4	191154276	10029711330	52.4692	40.0082
chr5	180915260	8732480871	48.2683	38.3845
chr6	171115067	8307701955	48.5504	40.4012
chr7	159138663	6860080649	43.1076	39.2695
chr8	146364022	6945930498	47.4565	39.5015
chr9	141213431	5084566997	36.0063	39.9847
chr10	135534747	5233195115	38.6115	34.6964
chr11	135006516	5837434344	43.2382	39.6932
chr12	133851895	6012894727	44.922	42.0384
chr13	115169878	4800278287	41.68	38.7515
chr14	107349540	3978141549	37.0578	39.1956
chr15	102531392	3395044825	33.1122	38.3617
chr16	90354753	2269071254	25.1129	29.9621
chr17	81195210	1943785097	23.9397	28.4492
chr18	78077248	3706033627	47.4662	39.2426
chr19	59128983	840137142	14.2086	20.4616
chr20	63025520	1880034760	29.8297	36.3791
chr21	48129895	1539112366	31.9783	40.2224
chr22	51304566	656707785	12.8002	21.1844
chrMT	16571	45234	2.7297	7.7306
chrX	155270560	3935051612	25.3432	25.3656

chrY	59373566	570866988	9.6148	20.8501

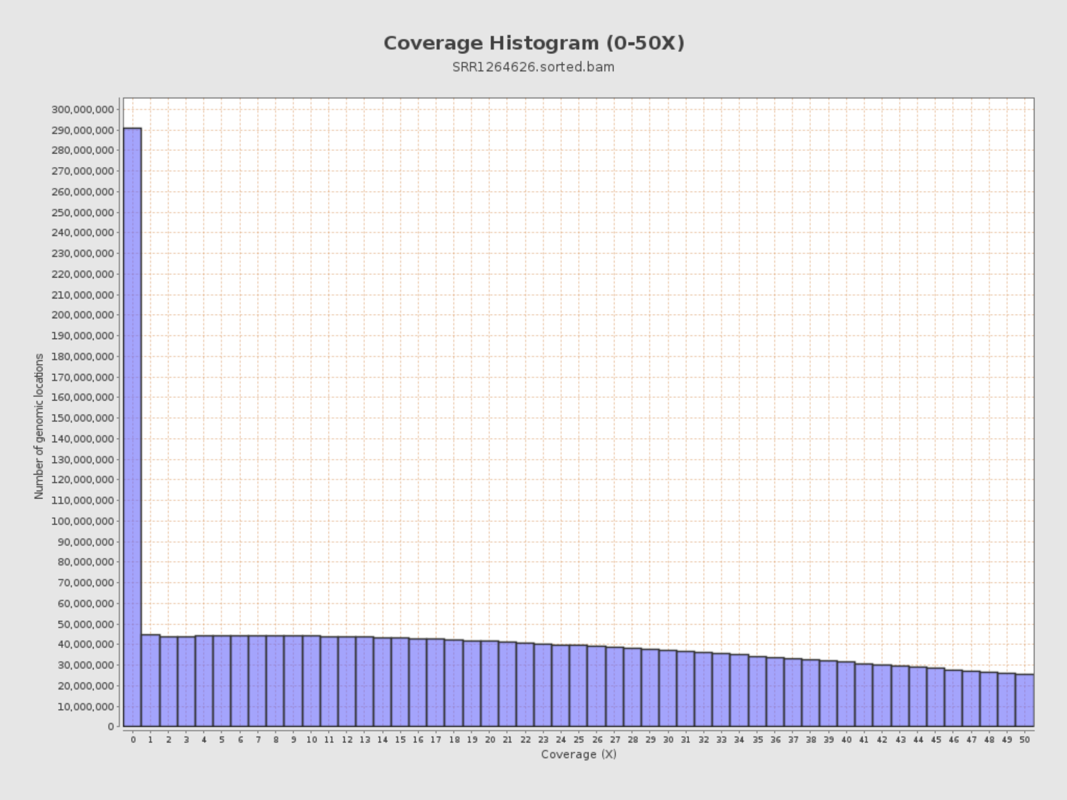
3. Results : Coverage across reference



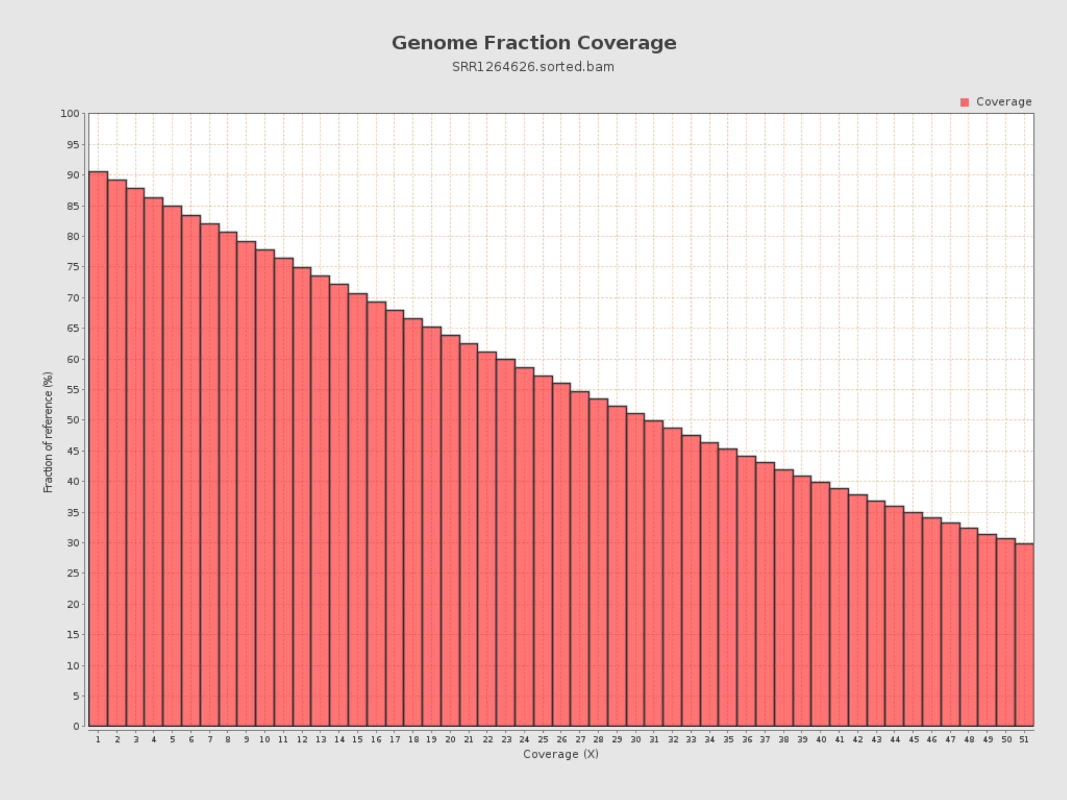
4. Results : Coverage Histogram



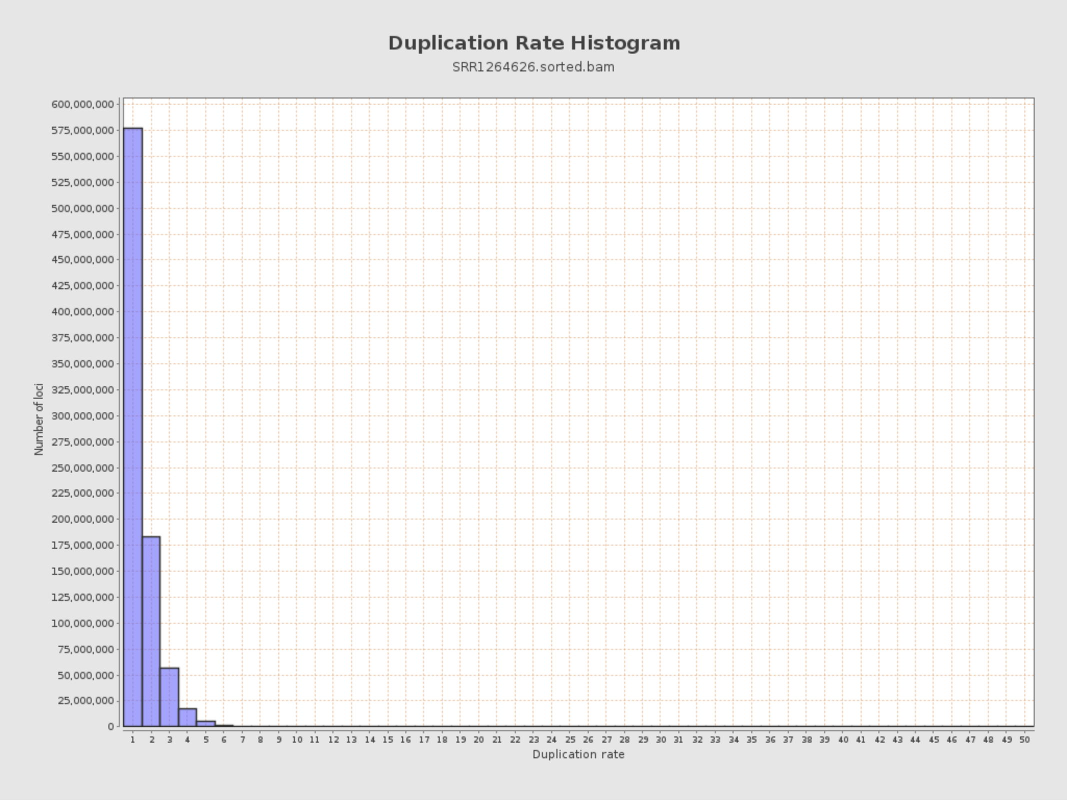
5. Results : Coverage Histogram (0-50X)



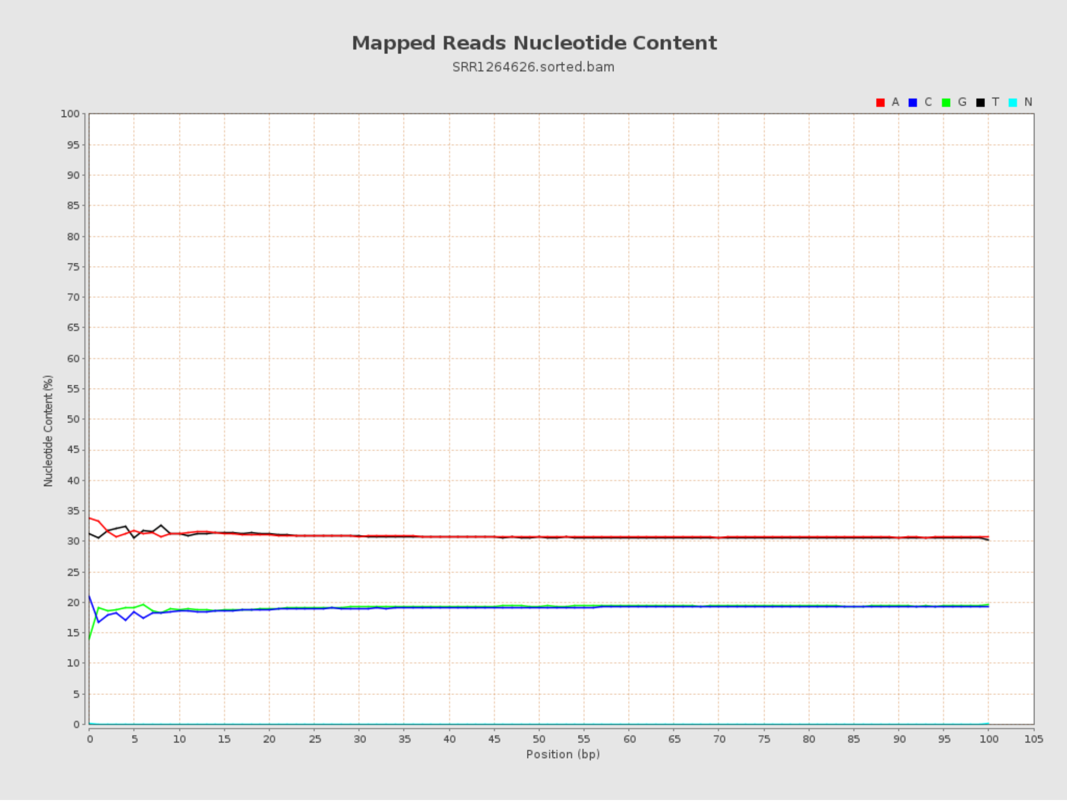
6. Results : Genome Fraction Coverage



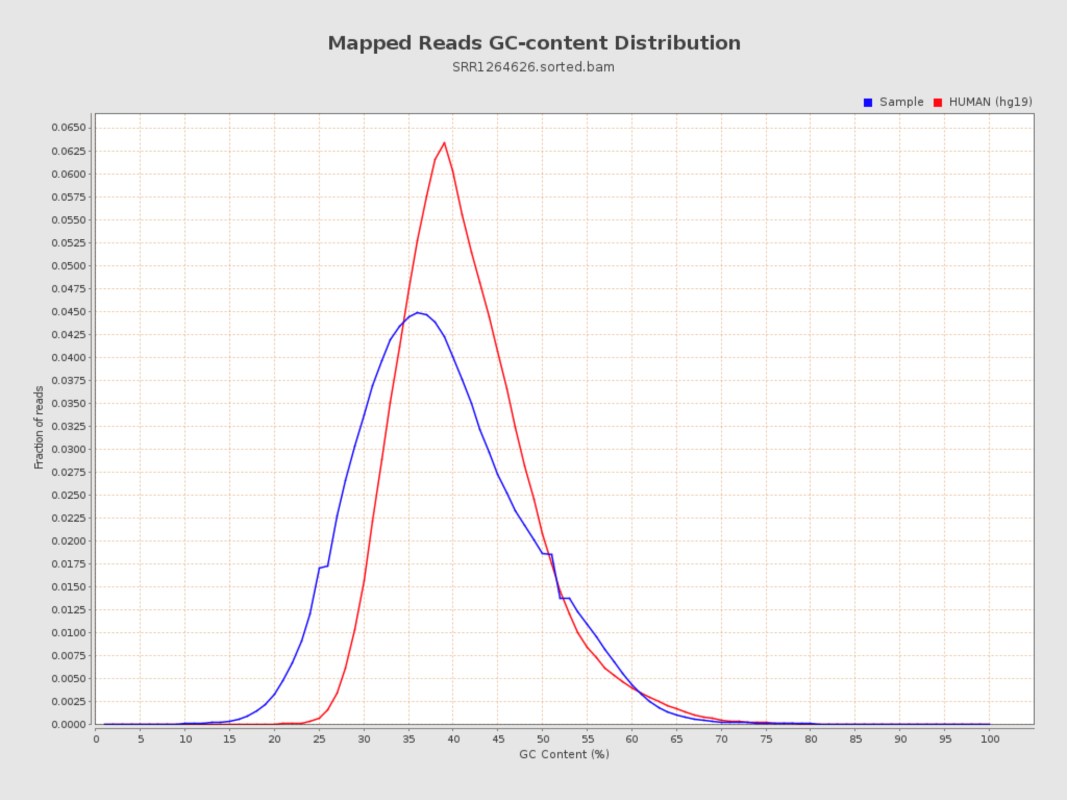
7. Results : Duplication Rate Histogram



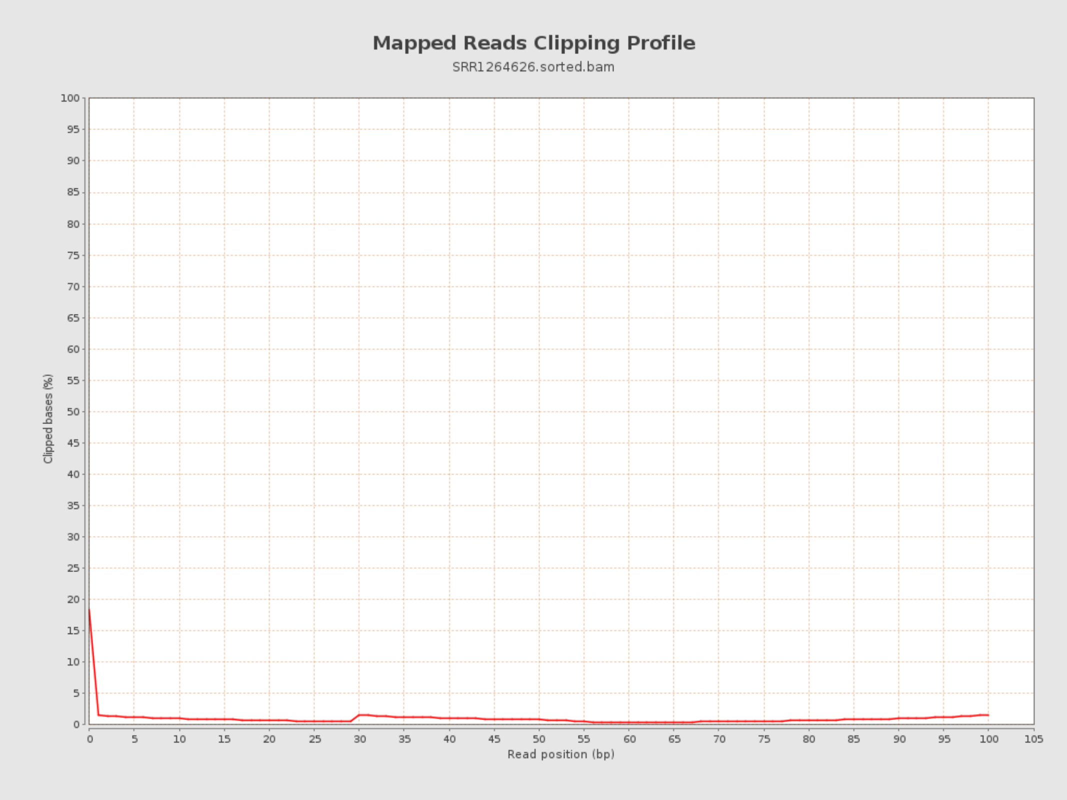
8. Results : Mapped Reads Nucleotide Content



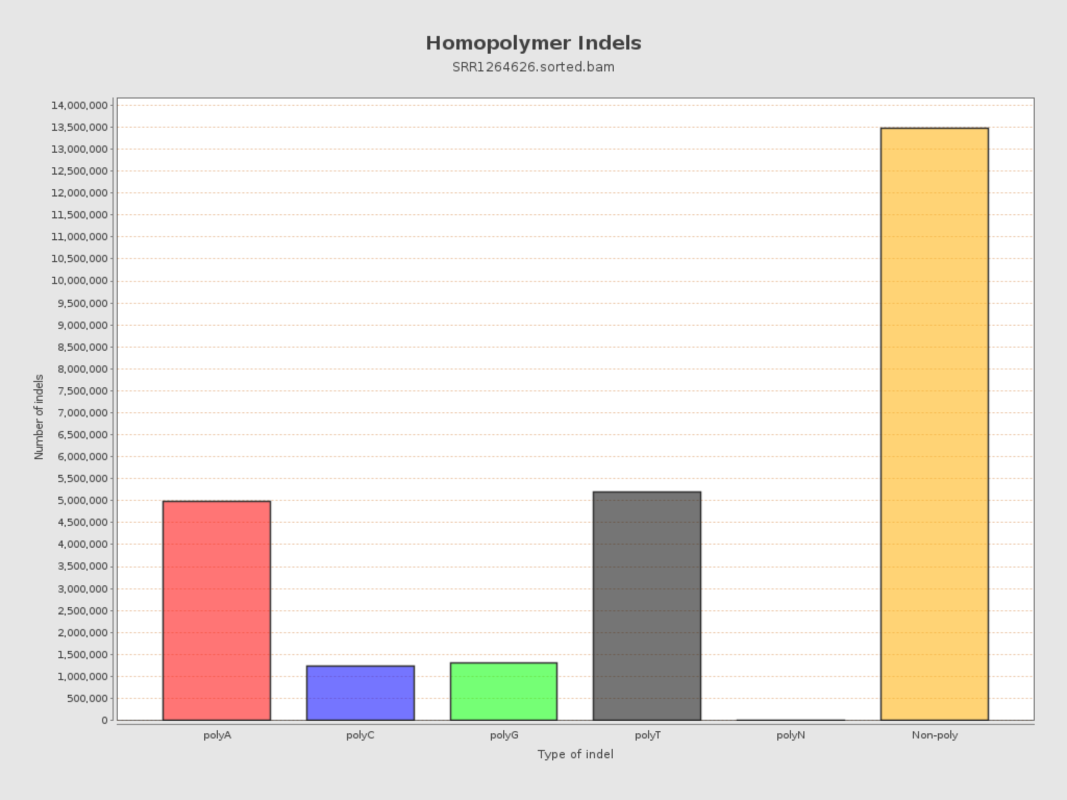
9. Results : Mapped Reads GC-content Distribution



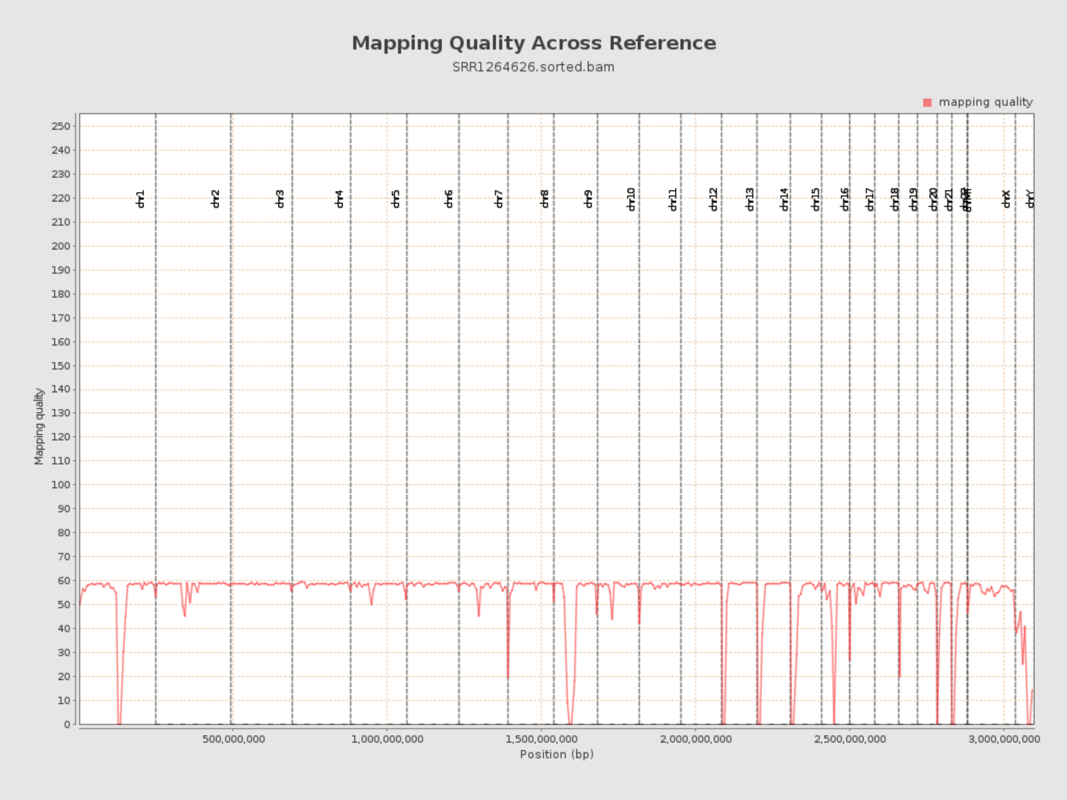
10. Results : Mapped Reads Clipping Profile



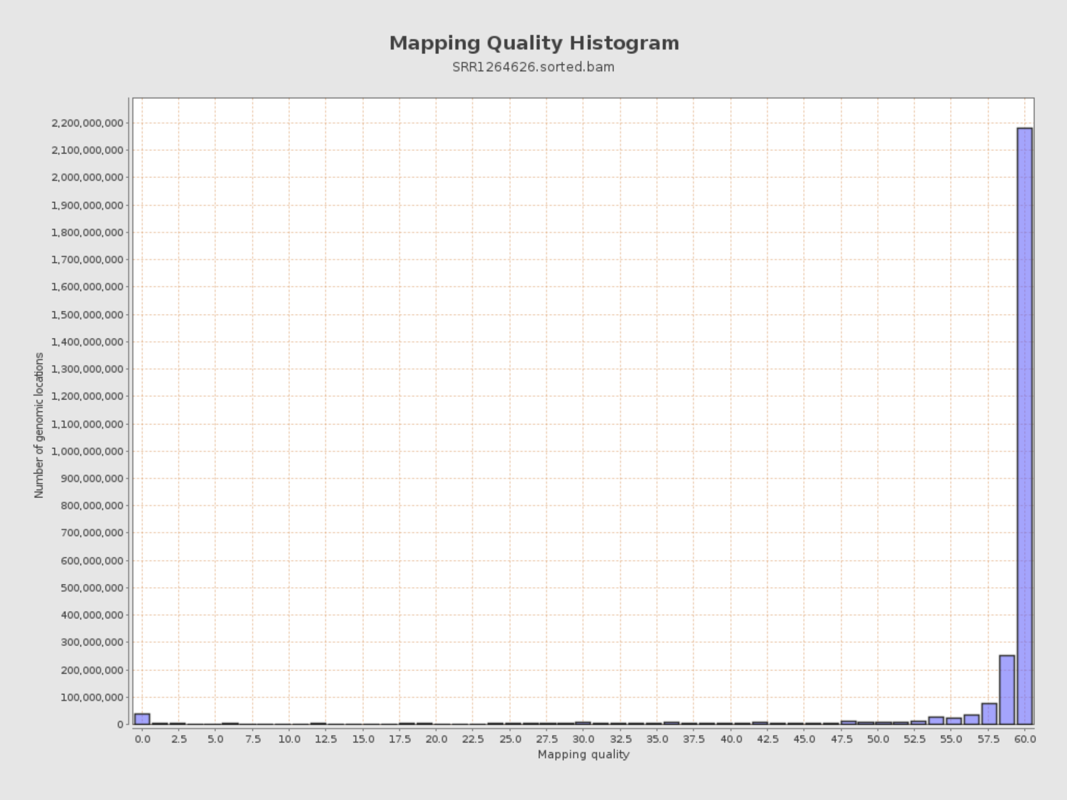
11. Results : Homopolymer Indels



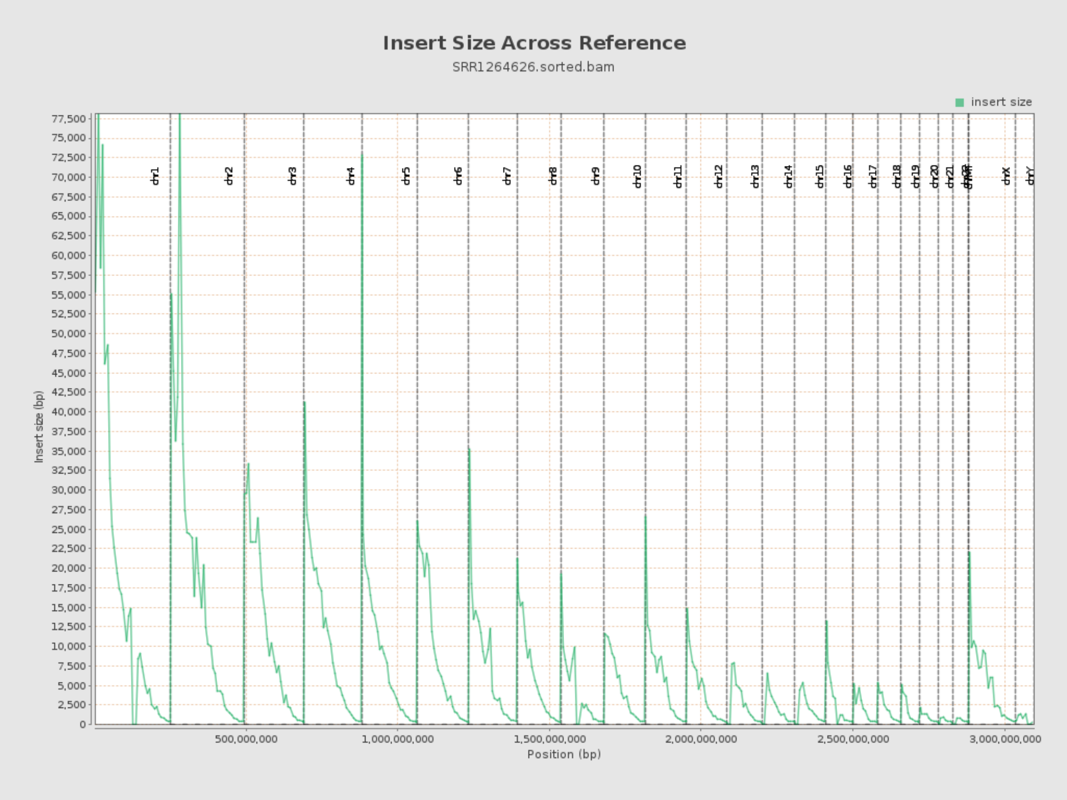
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram