Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/02 19:44:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365339.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_SRR5365339 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365339_1.fastq.gz SRR5365339_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 02 19:44:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365339.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	114,630,740
Mapped reads	111,368,544 / 97.15%
Unmapped reads	3,262,196 / 2.85%
Mapped paired reads	111,368,544 / 97.15%
Mapped reads, first in pair	55,970,528 / 48.83%
Mapped reads, second in pair	55,398,016 / 48.33%
Mapped reads, both in pair	110,622,546 / 96.5%
Mapped reads, singletons	745,998 / 0.65%
Secondary alignments	0
Supplementary alignments	913,788 / 0.8%
Read min/max/mean length	30 / 151 / 151.36
Duplicated reads (estimated)	47,729,748 / 41.64%
Duplication rate	30.11%
Clipped reads	66,007,031 / 57.58%

2.2. ACGT Content

Number/percentage of A's	4,380,875,607 / 29.87%
Number/percentage of C's	2,906,227,013 / 19.82%
Number/percentage of T's	4,325,434,774 / 29.5%
Number/percentage of G's	3,051,404,524 / 20.81%
Number/percentage of N's	866,299 / 0.01%

GC Percentage	40.63%

2.3. Coverage

Mean	4.739
Standard Deviation	53.0095

2.4. Mapping Quality

Mean Mapping Quality	54.23

2.5. Insert size

Mean	73,268.3
Standard Deviation	2,655,252.56
P25/Median/P75	149 / 203 / 277

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	112,852,929
Insertions	4,451,521
Mapped reads with at least one insertion	3.87%
Deletions	2,300,908
Mapped reads with at least one deletion	2%
Homopolymer indels	49.96%

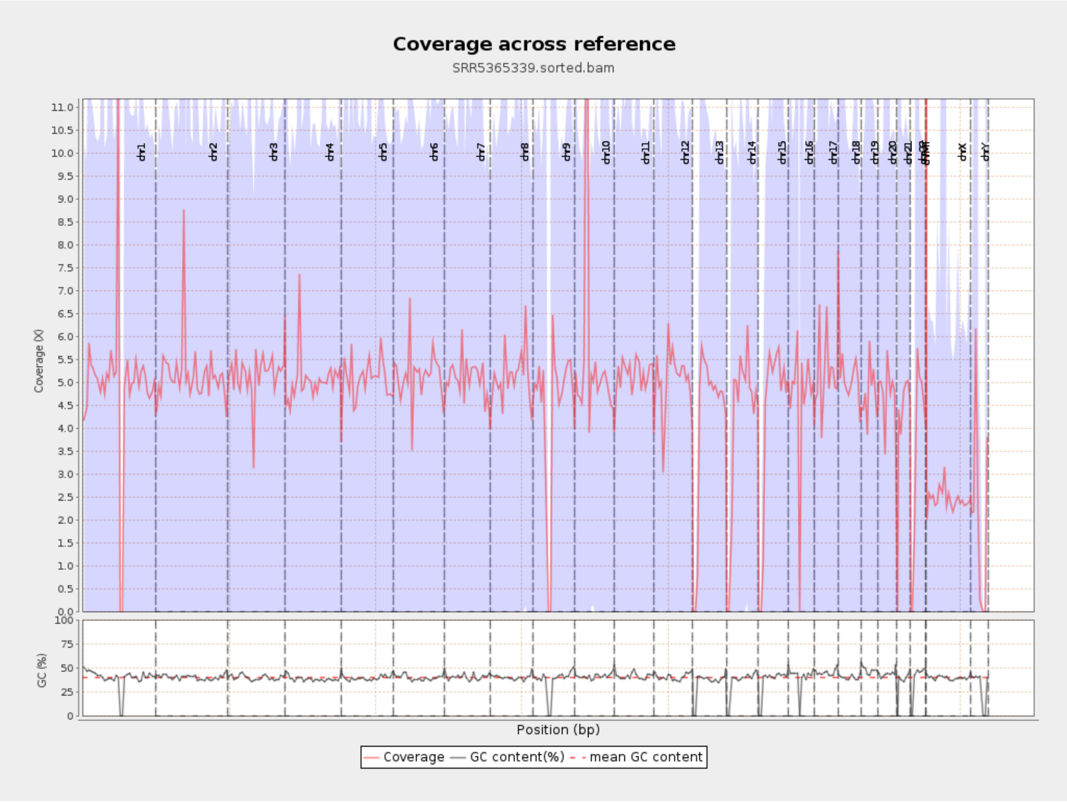
2.7. Chromosome stats

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

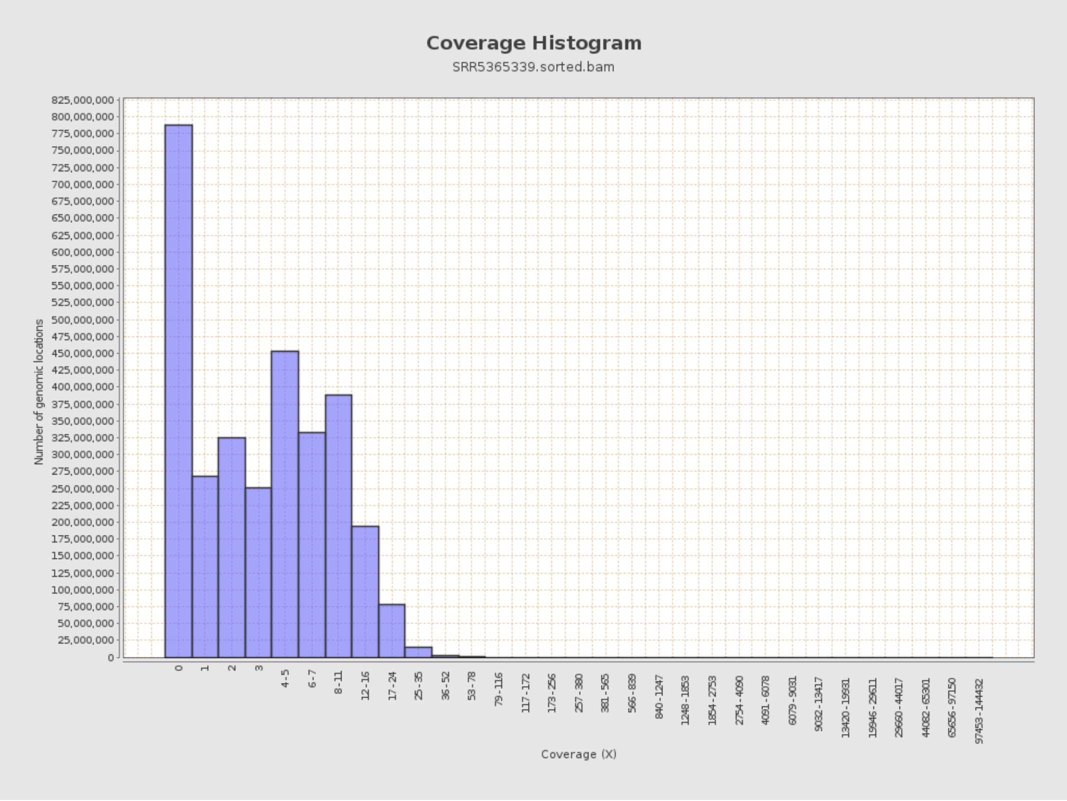
		bases	coverage	deviation
chr1	249250621	1232772955	4.9459	143.4513
chr2	243199373	1261600543	5.1875	31.0447
chr3	198022430	1018413300	5.1429	6.8832
chr4	191154276	965365824	5.0502	25.1216
chr5	180915260	917993248	5.0742	6.3937
chr6	171115067	882967079	5.1601	20.4126
chr7	159138663	806246742	5.0663	33.7799
chr8	146364022	748864835	5.1165	19.5327
chr9	141213431	629285066	4.4563	52.7764
chr10	135534747	755121601	5.5714	104.3356
chr11	135006516	695096597	5.1486	32.0401
chr12	133851895	680363305	5.083	25.577
chr13	115169878	479024294	4.1593	4.9383
chr14	107349540	450112601	4.193	5.5598
chr15	102531392	427175455	4.1663	12.8852
chr16	90354753	417245179	4.6179	16.9771
chr17	81195210	422186195	5.1996	25.7358
chr18	78077248	404993878	5.1871	50.9978
chr19	59128983	280529545	4.7444	72.0231
chr20	63025520	299539246	4.7527	10.3167
chr21	48129895	201195342	4.1803	18.6022
chr22	51304566	178577105	3.4807	15.8741
chrMT	16571	10028462	605.1815	144.4728
chrX	155270560	380357463	2.4496	10.6548

chrY	59373566	125385435	2.1118	44.872

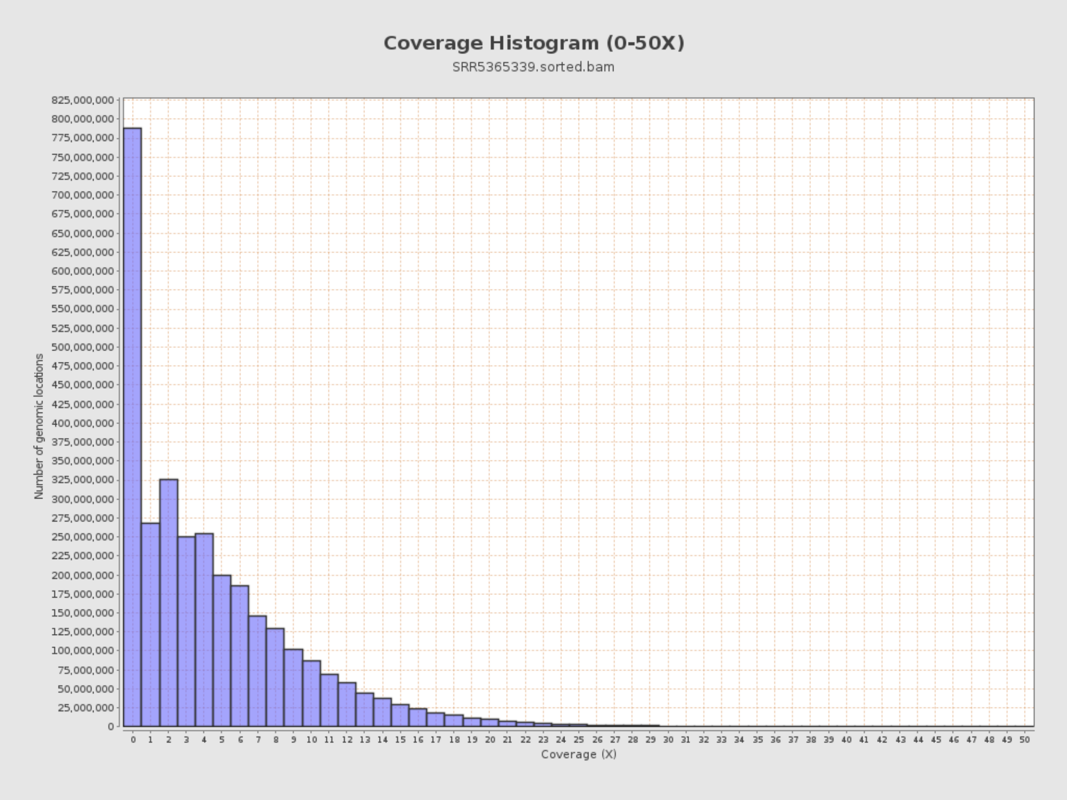
3. Results : Coverage across reference



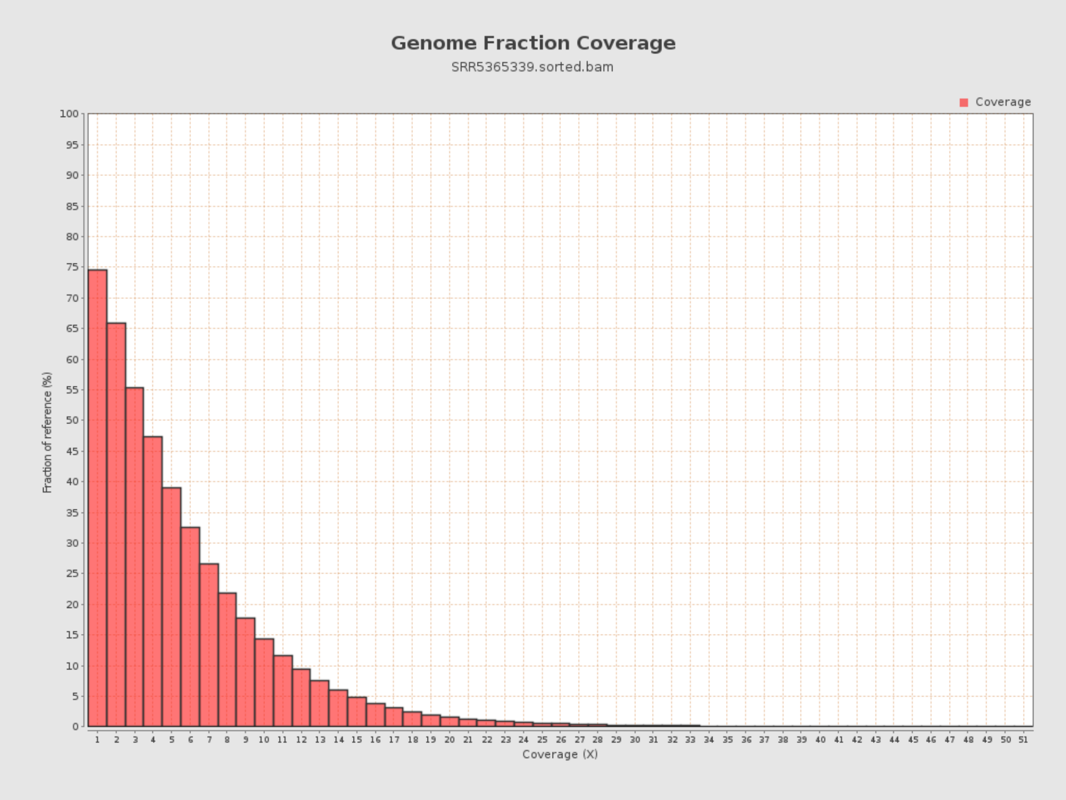
4. Results : Coverage Histogram



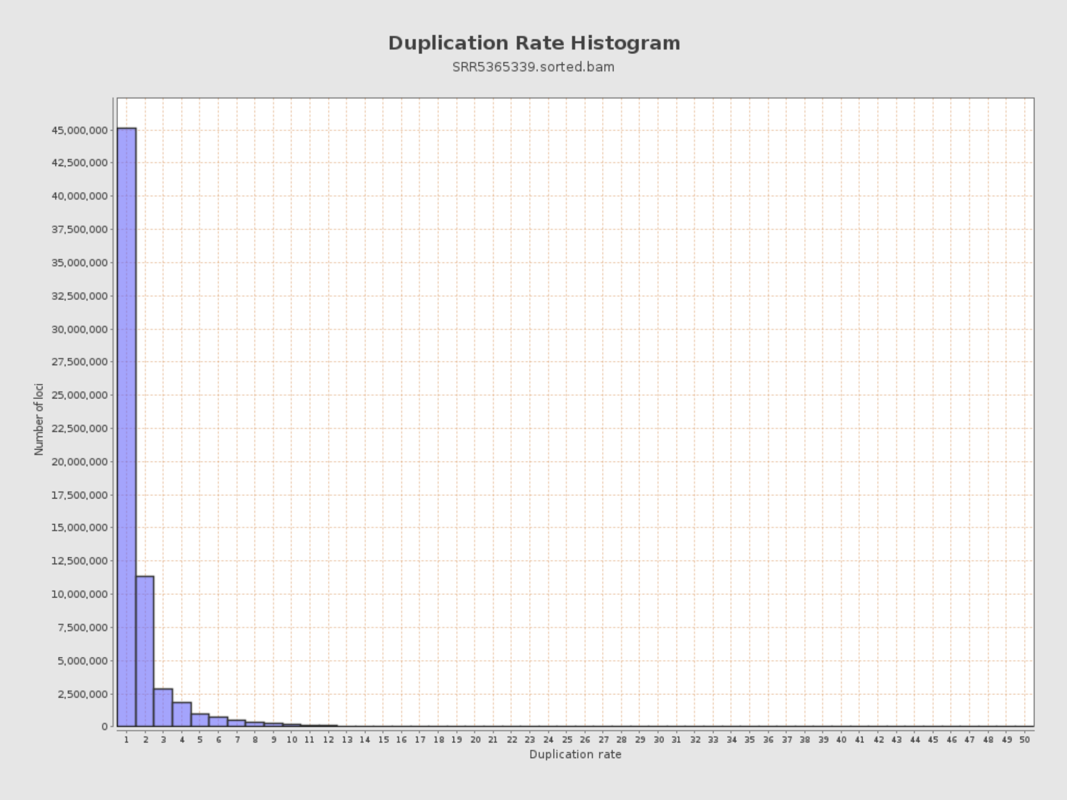
5. Results : Coverage Histogram (0-50X)



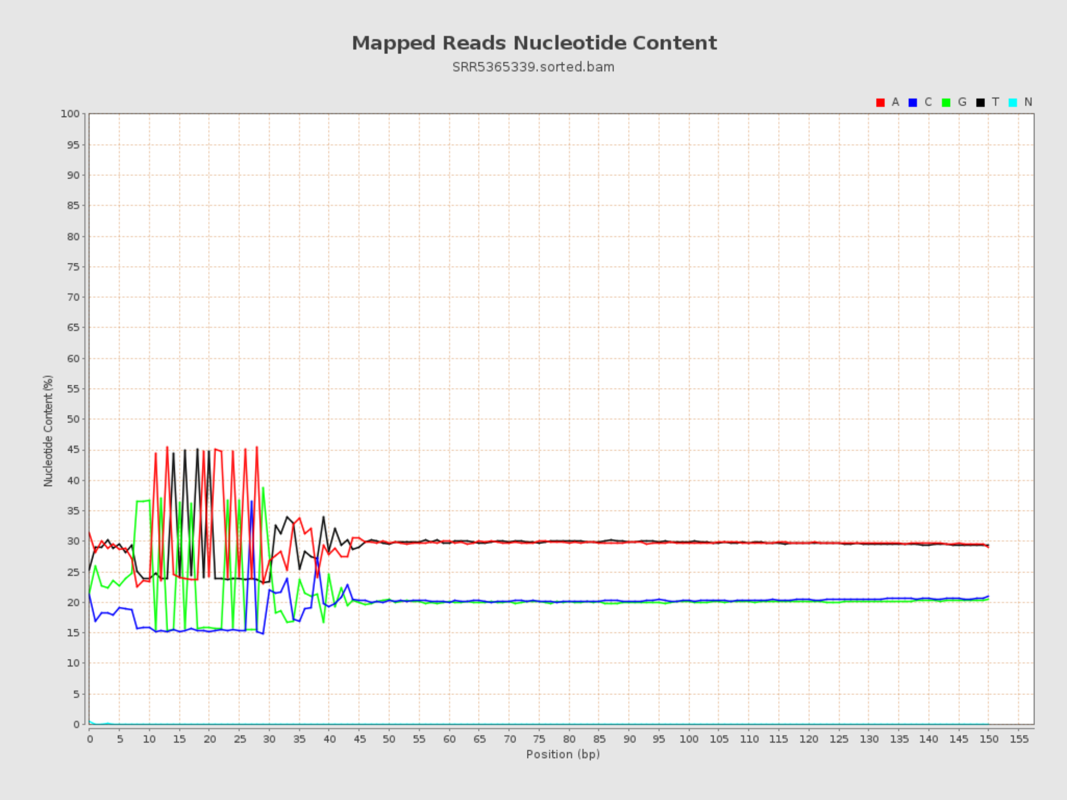
6. Results : Genome Fraction Coverage



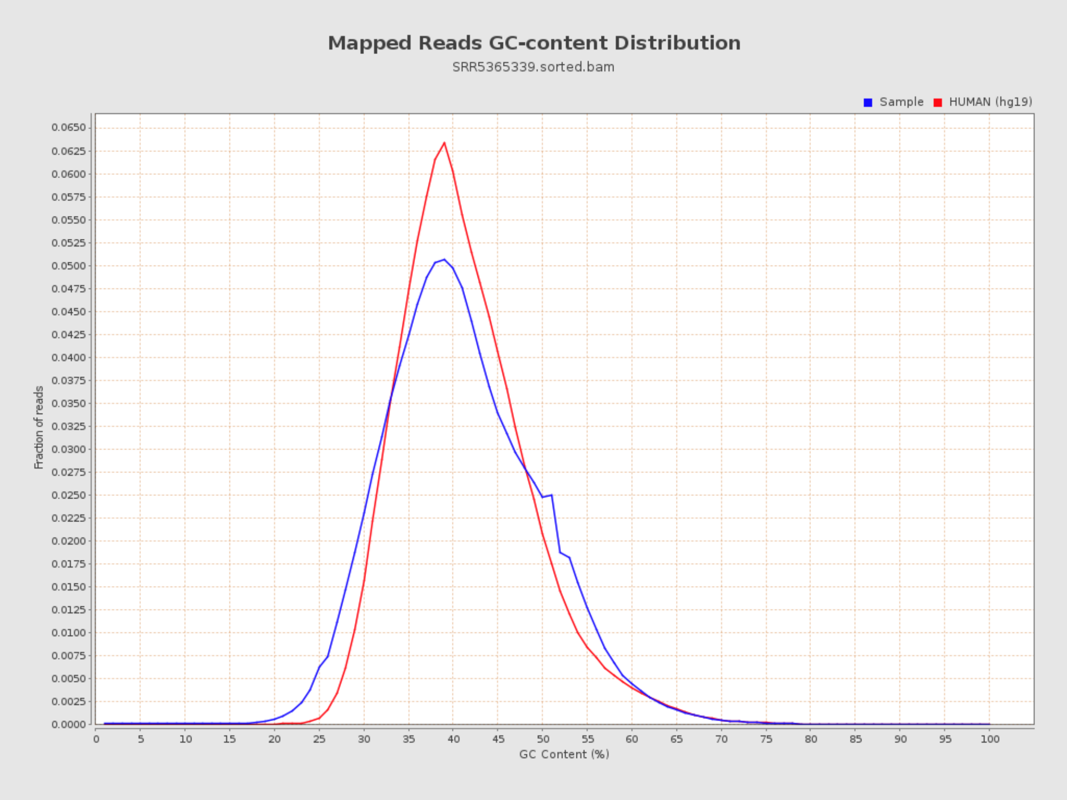
7. Results : Duplication Rate Histogram



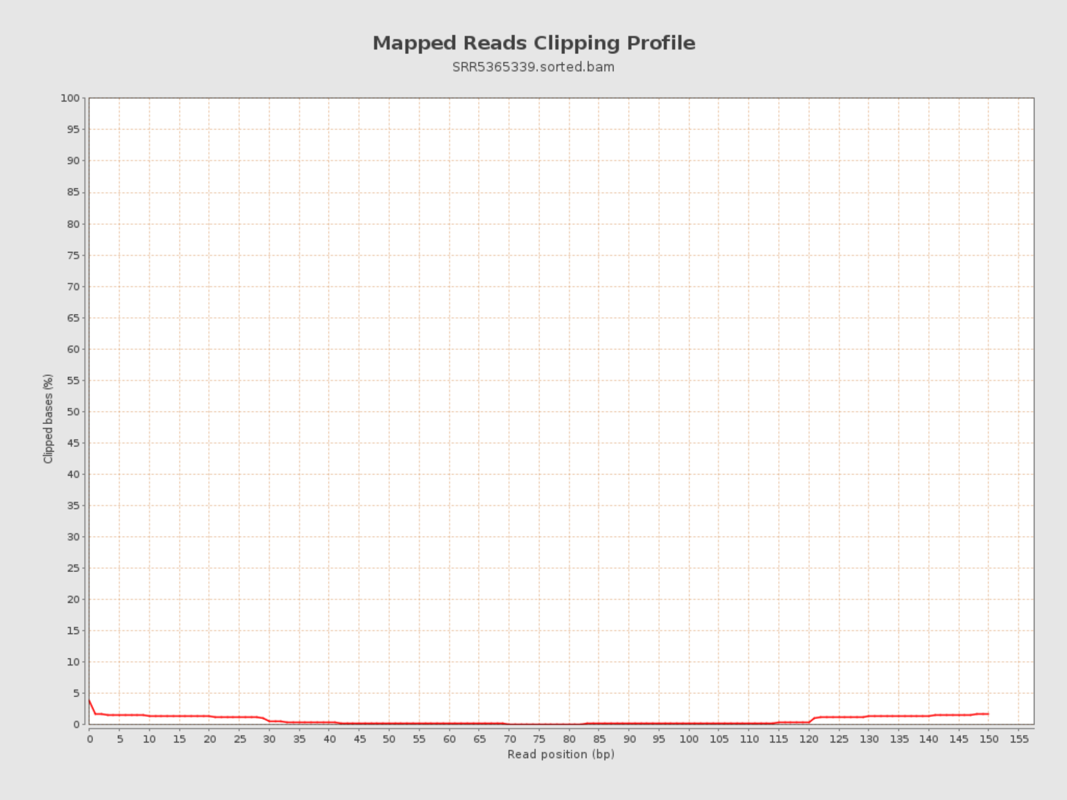
8. Results : Mapped Reads Nucleotide Content



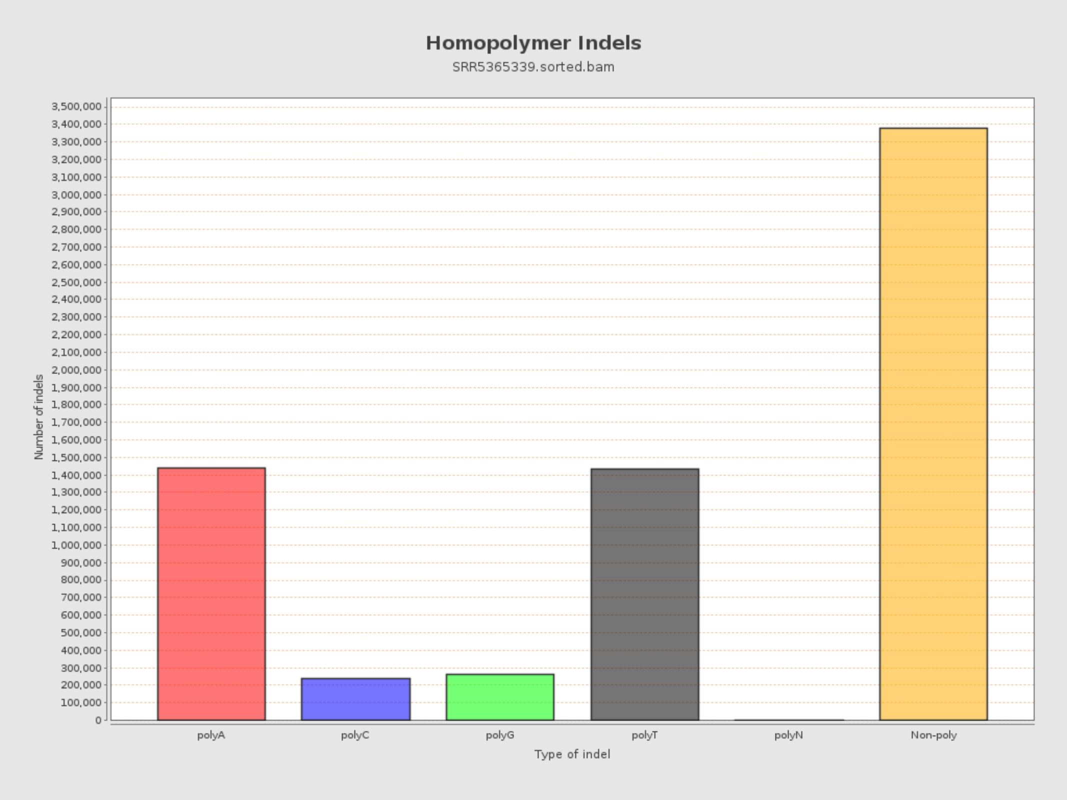
9. Results : Mapped Reads GC-content Distribution



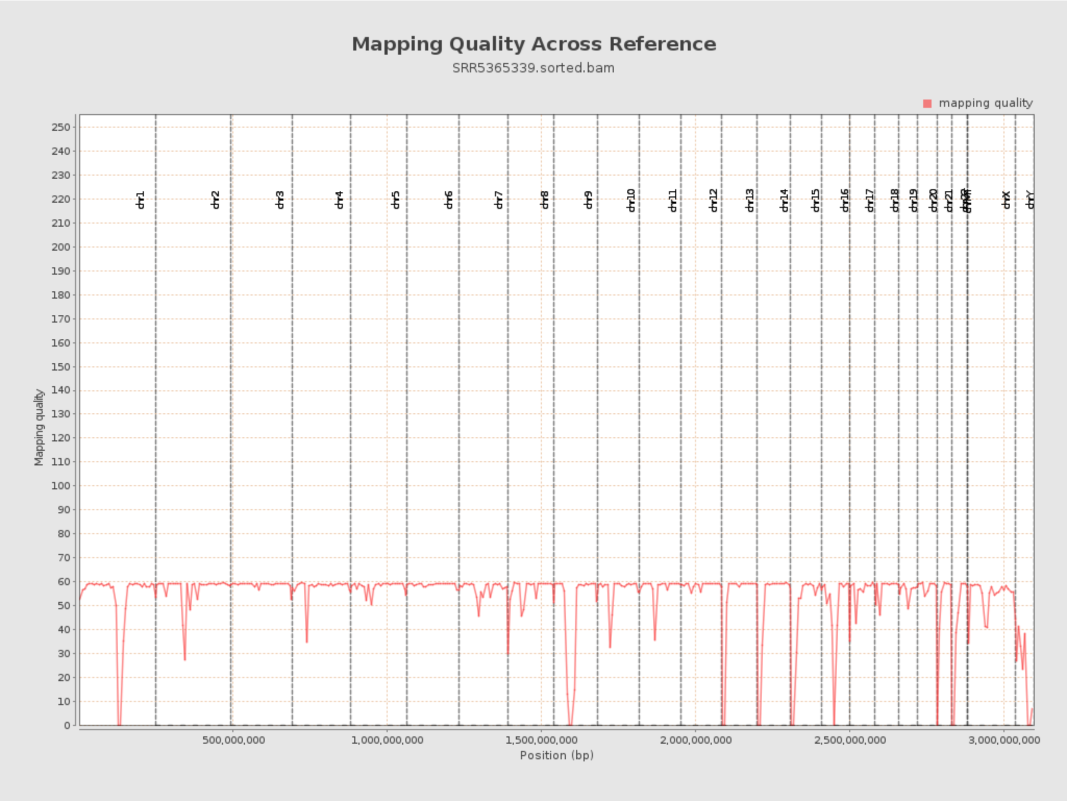
10. Results : Mapped Reads Clipping Profile



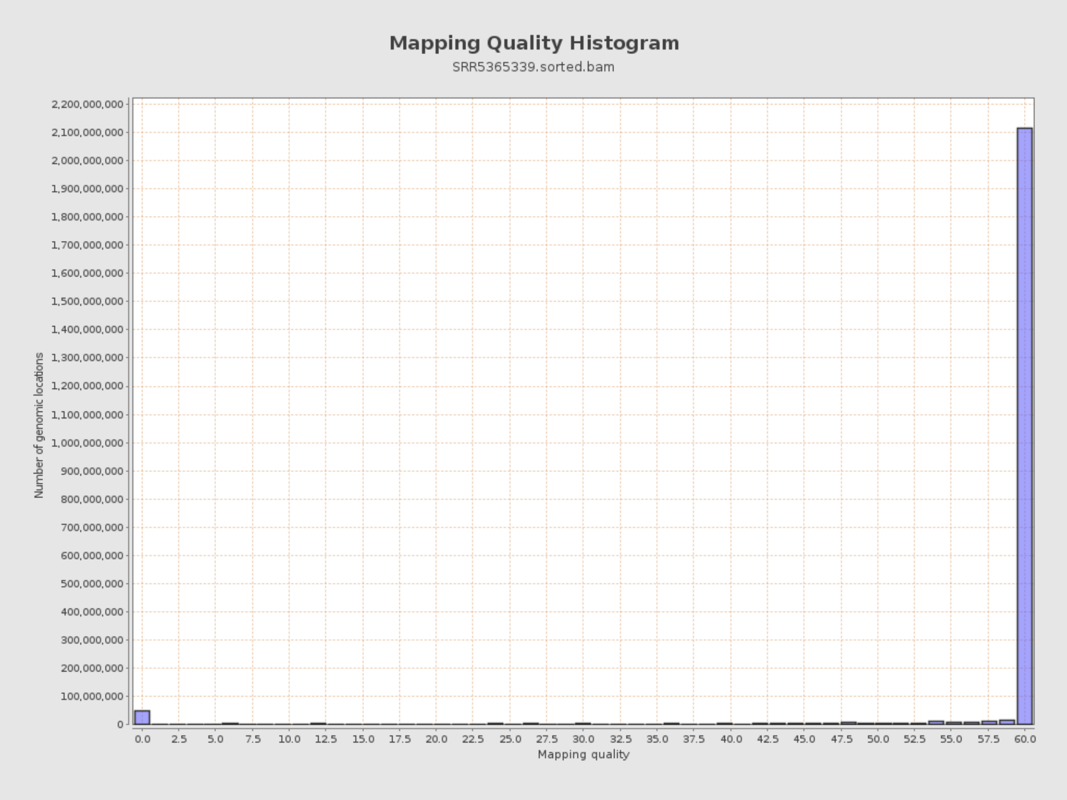
11. Results : Homopolymer Indels



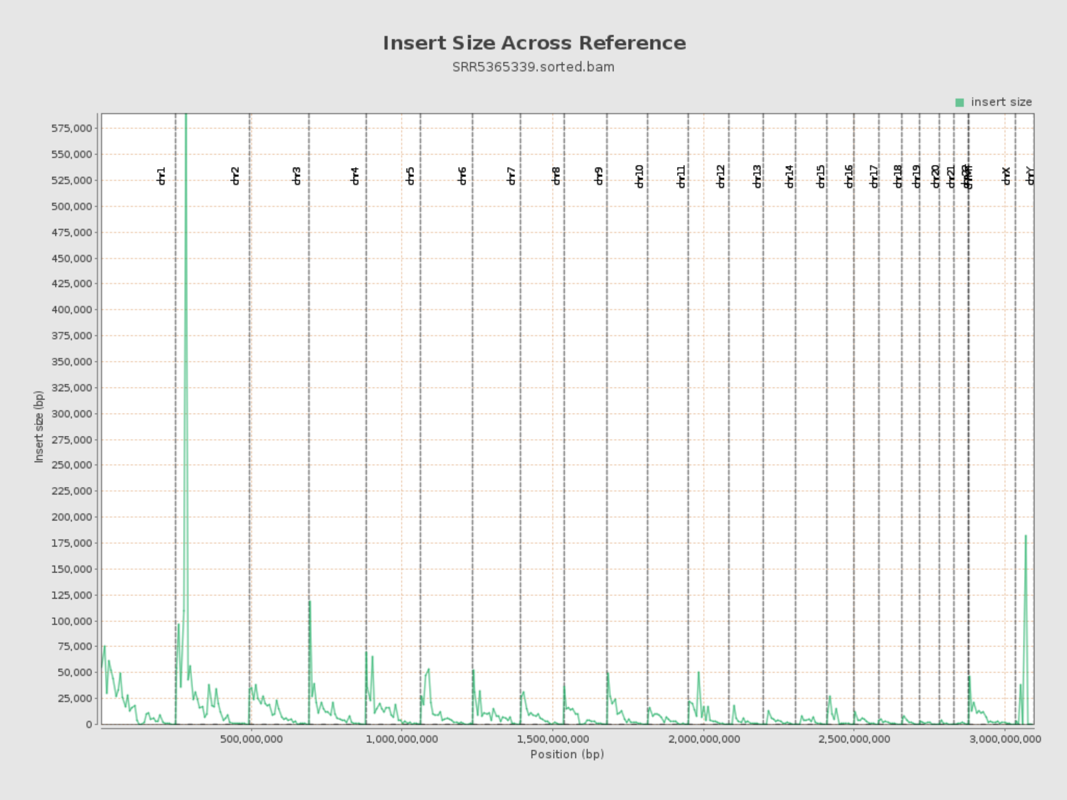
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram