Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/16 23:13:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365363.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_SRR5365363 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365363_1.fastq.gz SRR5365363_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 16 23:13:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365363.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	859,328,356
Mapped reads	778,937,010 / 90.64%
Unmapped reads	80,391,346 / 9.36%
Mapped paired reads	778,937,010 / 90.64%
Mapped reads, first in pair	389,035,804 / 45.27%
Mapped reads, second in pair	389,901,206 / 45.37%
Mapped reads, both in pair	771,035,106 / 89.73%
Mapped reads, singletons	7,901,904 / 0.92%
Secondary alignments	0
Supplementary alignments	75,887,493 / 8.83%
Read min/max/mean length	30 / 150 / 154.52
Duplicated reads (estimated)	494,344,827 / 57.53%
Duplication rate	39.35%
Clipped reads	499,355,194 / 58.11%

2.2. ACGT Content

Number/percentage of A's	28,462,727,289 / 27.78%
Number/percentage of C's	22,842,499,518 / 22.29%
Number/percentage of T's	27,701,709,558 / 27.03%
Number/percentage of G's	23,450,329,417 / 22.89%
Number/percentage of N's	10,547,479 / 0.01%

GC Percentage	45.18%

2.3. Coverage

Mean	33.1393
Standard Deviation	940.3496

2.4. Mapping Quality

Mean Mapping Quality	53.08

2.5. Insert size

Mean	139,588.95
Standard Deviation	3,127,472.93
P25/Median/P75	123 / 159 / 212

2.6. Mismatches and indels

General error rate	1.57%
Mismatches	1,464,462,260
Insertions	33,497,038
Mapped reads with at least one insertion	3.88%
Deletions	29,961,731
Mapped reads with at least one deletion	3.5%
Homopolymer indels	36.04%

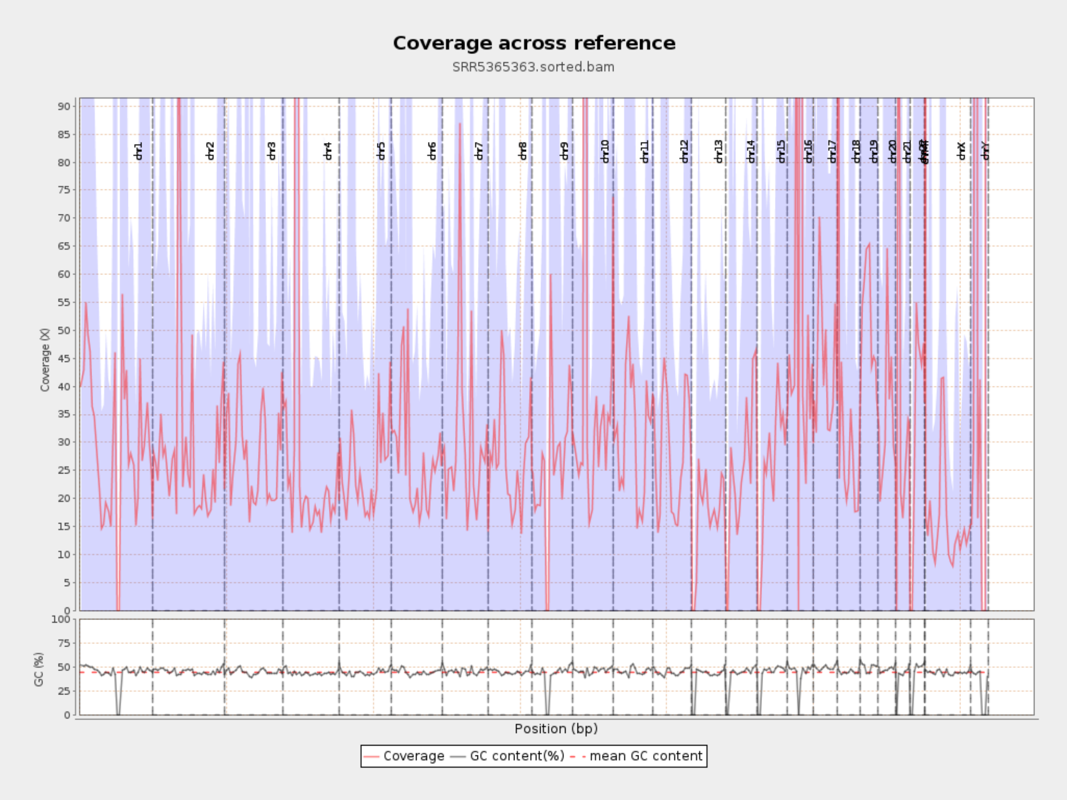
2.7. Chromosome stats

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

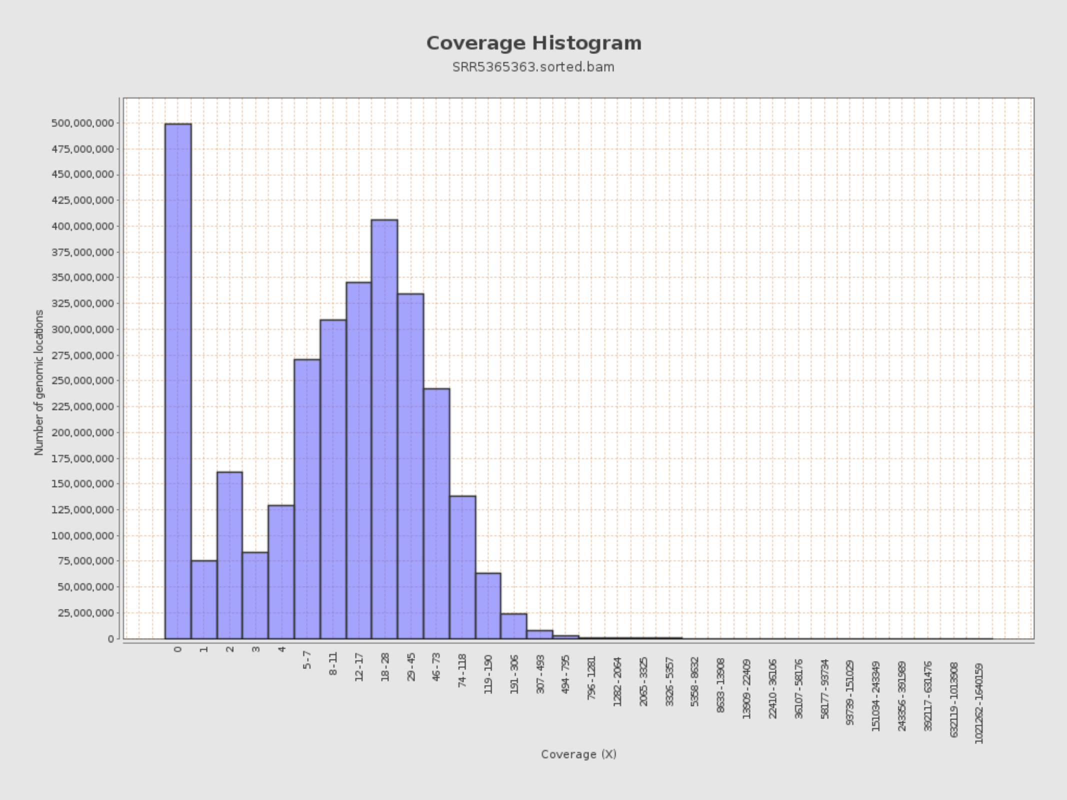
		bases	coverage	deviation
chr1	249250621	7425290141	29.7905	441.6744
chr2	243199373	7257492946	29.8417	535.6289
chr3	198022430	5516583275	27.8584	212.0083
chr4	191154276	6321522451	33.0703	1,607.5717
chr5	180915260	4603455016	25.4454	83.1743
chr6	171115067	4689681463	27.4066	328.0142
chr7	159138663	4824048161	30.3135	187.9015
chr8	146364022	4003524963	27.3532	143.6128
chr9	141213431	3686393671	26.1051	401.5997
chr10	135534747	7241609159	53.4299	2,303.4175
chr11	135006516	4295956645	31.8204	153.7048
chr12	133851895	3776984527	28.2176	102.7627
chr13	115169878	1945948693	16.8963	33.6076
chr14	107349540	2631597635	24.5143	81.1344
chr15	102531392	2508493654	24.4656	53.4008
chr16	90354753	5653921777	62.5747	1,379.8264
chr17	81195210	3564612064	43.9018	734.5228
chr18	78077248	2762408341	35.3805	1,936.6952
chr19	59128983	3096541008	52.3693	330.7411
chr20	63025520	2216640644	35.1705	624.131
chr21	48129895	1988981367	41.3253	1,005.9274
chr22	51304566	1761669411	34.3375	110.9935
chrMT	16571	61713213	3,724.1695	2,002.7997
chrX	155270560	2433964092	15.6756	159.3311

chrY	59373566	8320034469	140.1303	3,544.4655

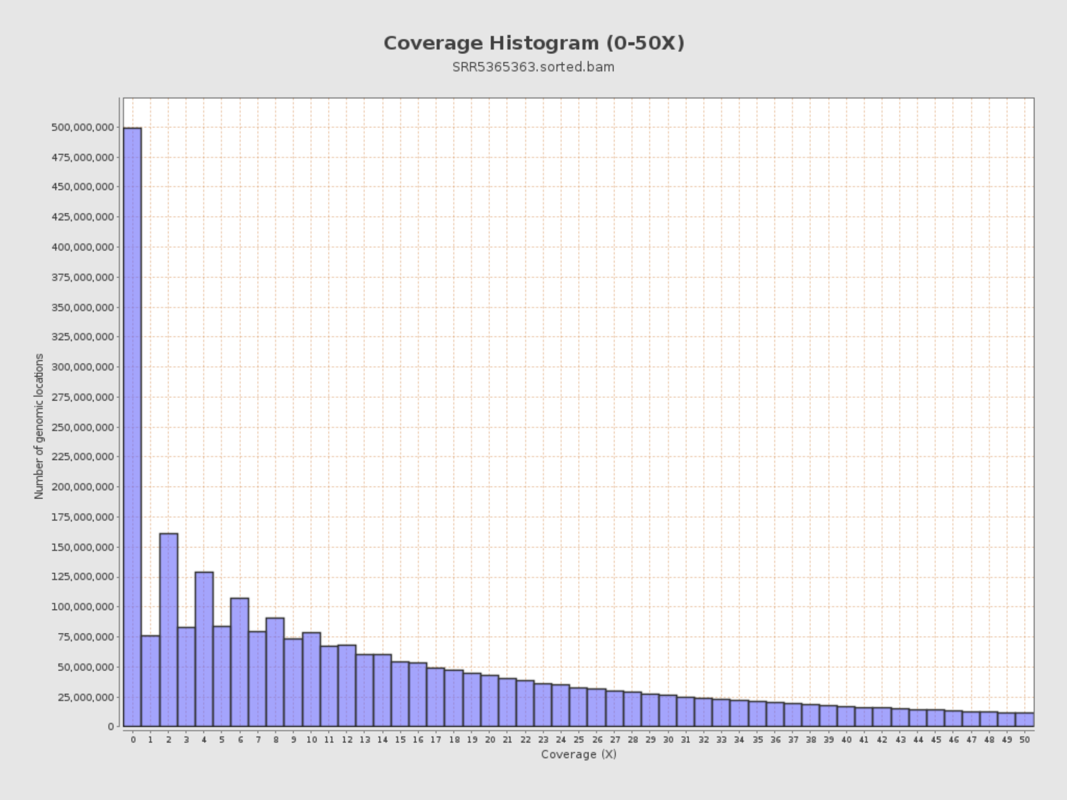
3. Results : Coverage across reference



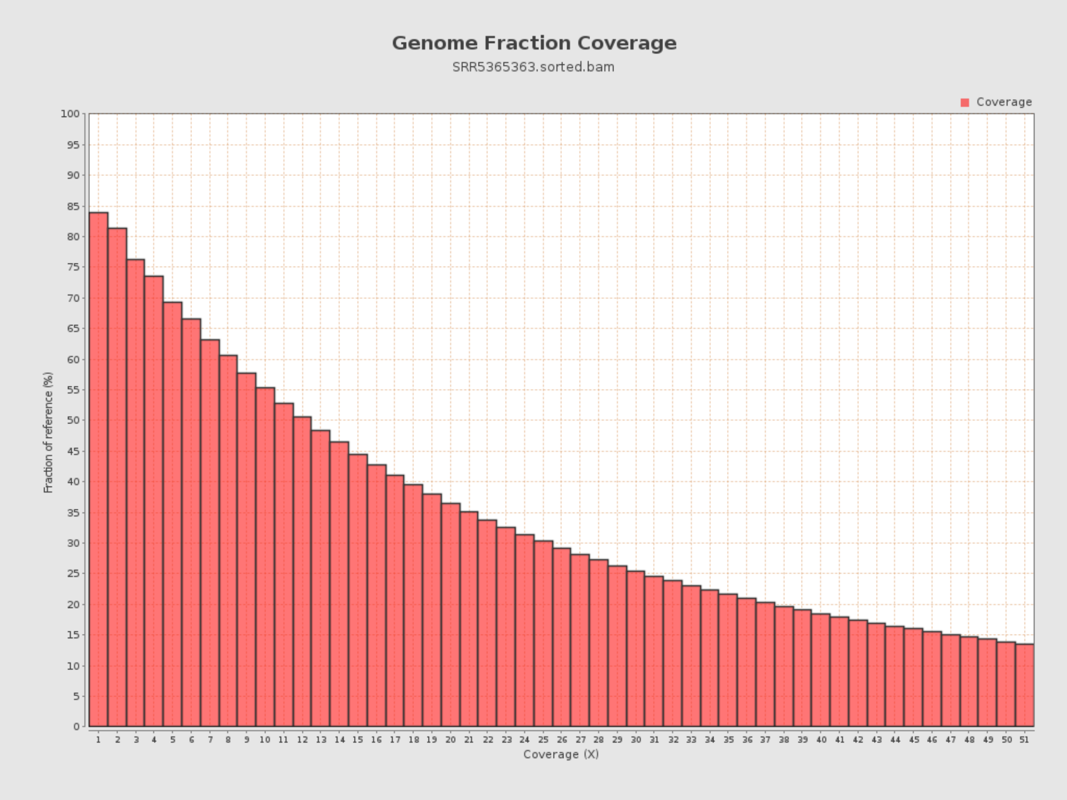
4. Results : Coverage Histogram



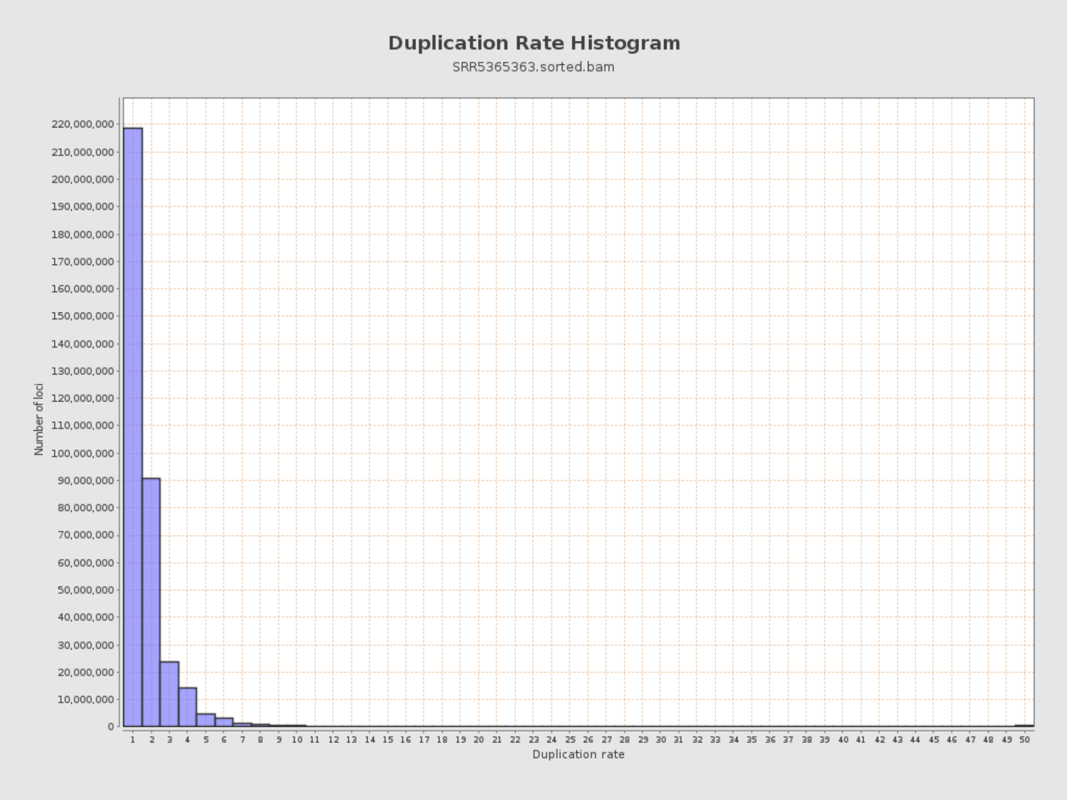
5. Results : Coverage Histogram (0-50X)



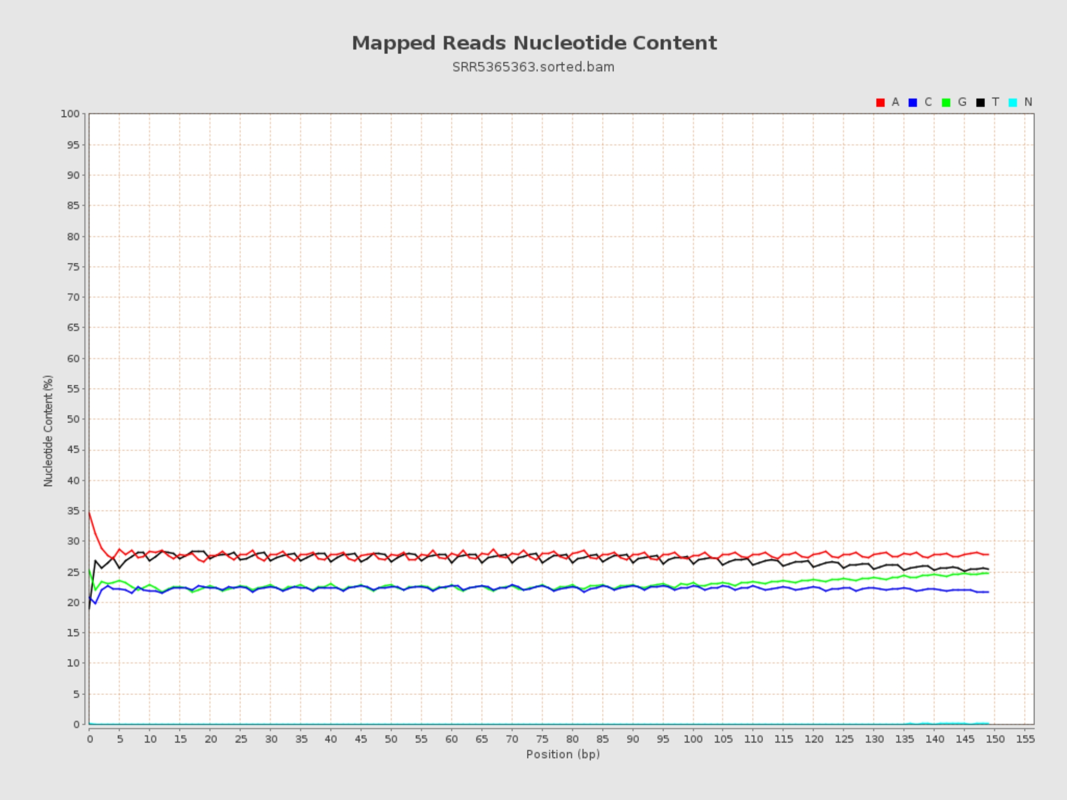
6. Results : Genome Fraction Coverage



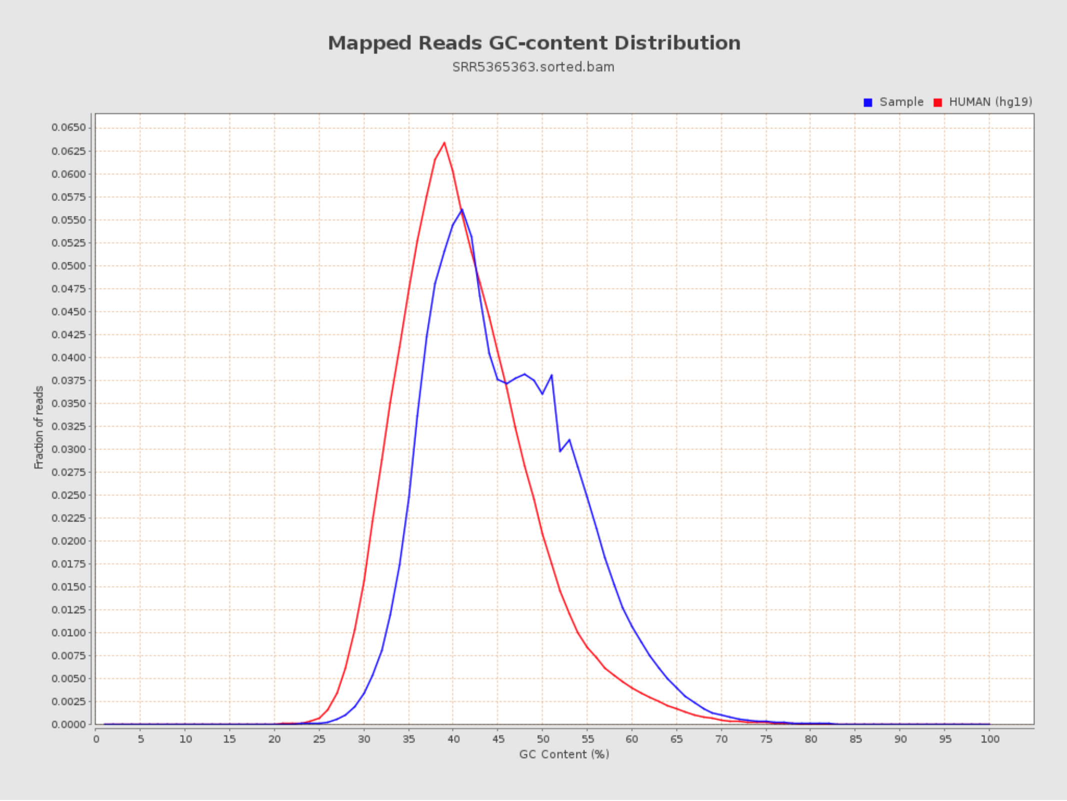
7. Results : Duplication Rate Histogram



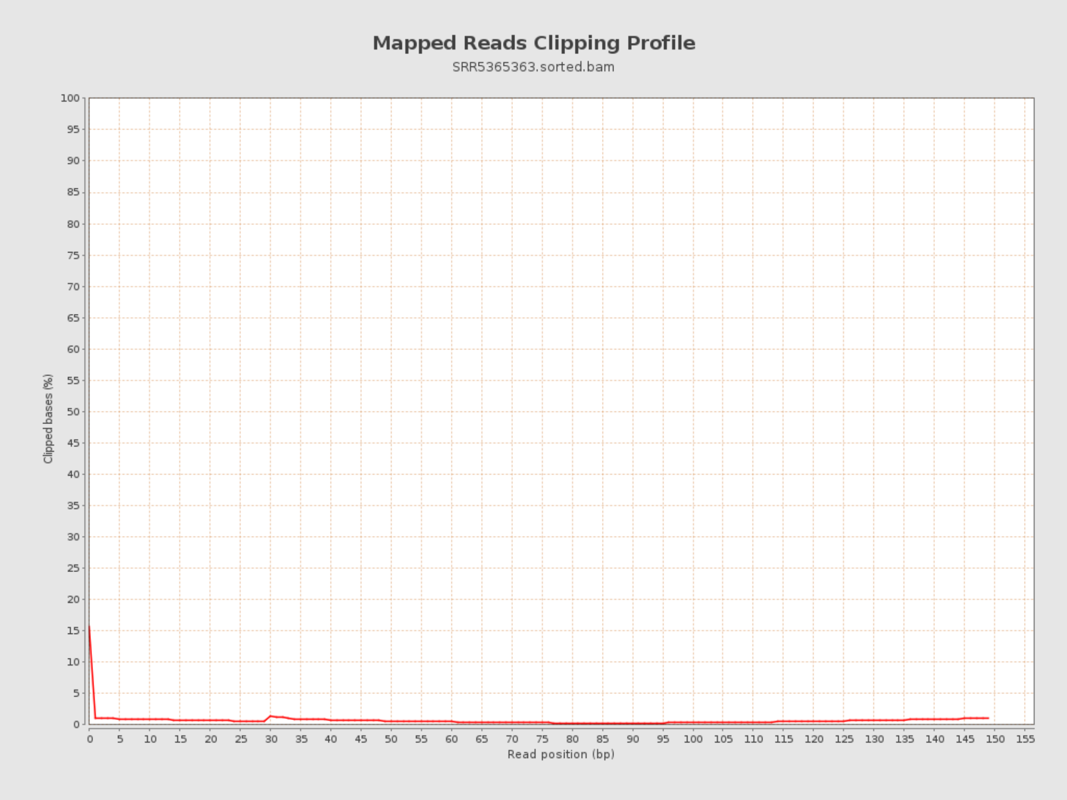
8. Results : Mapped Reads Nucleotide Content



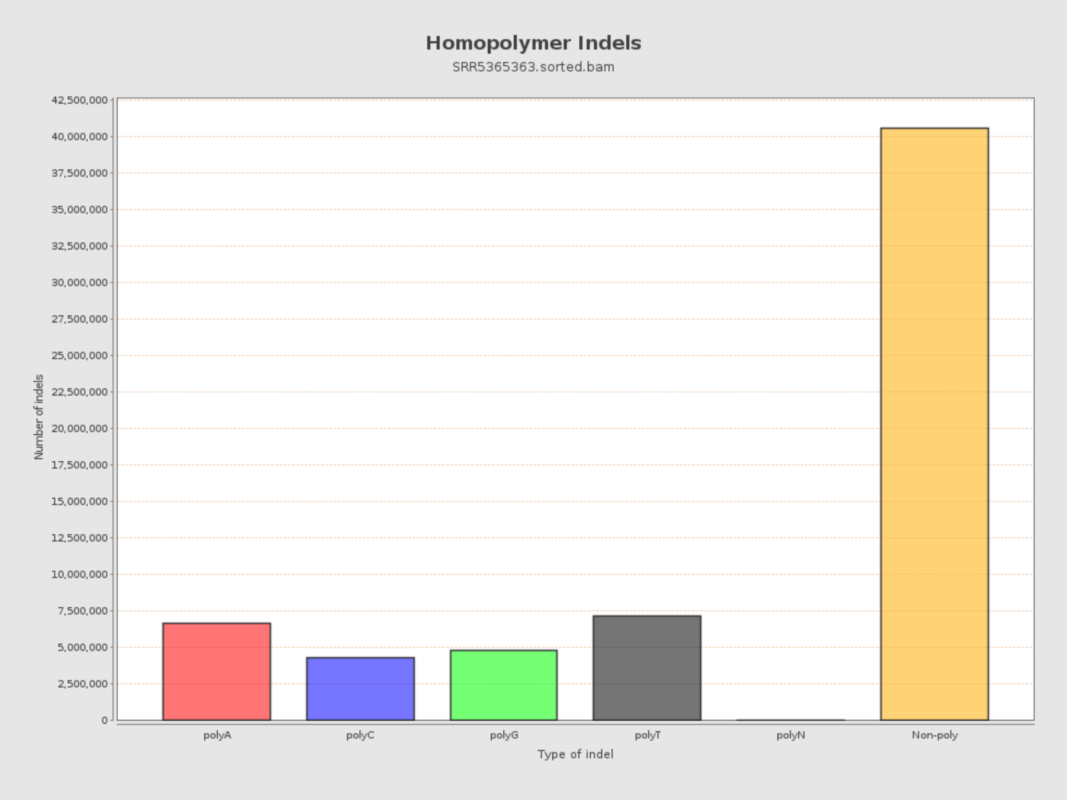
9. Results : Mapped Reads GC-content Distribution



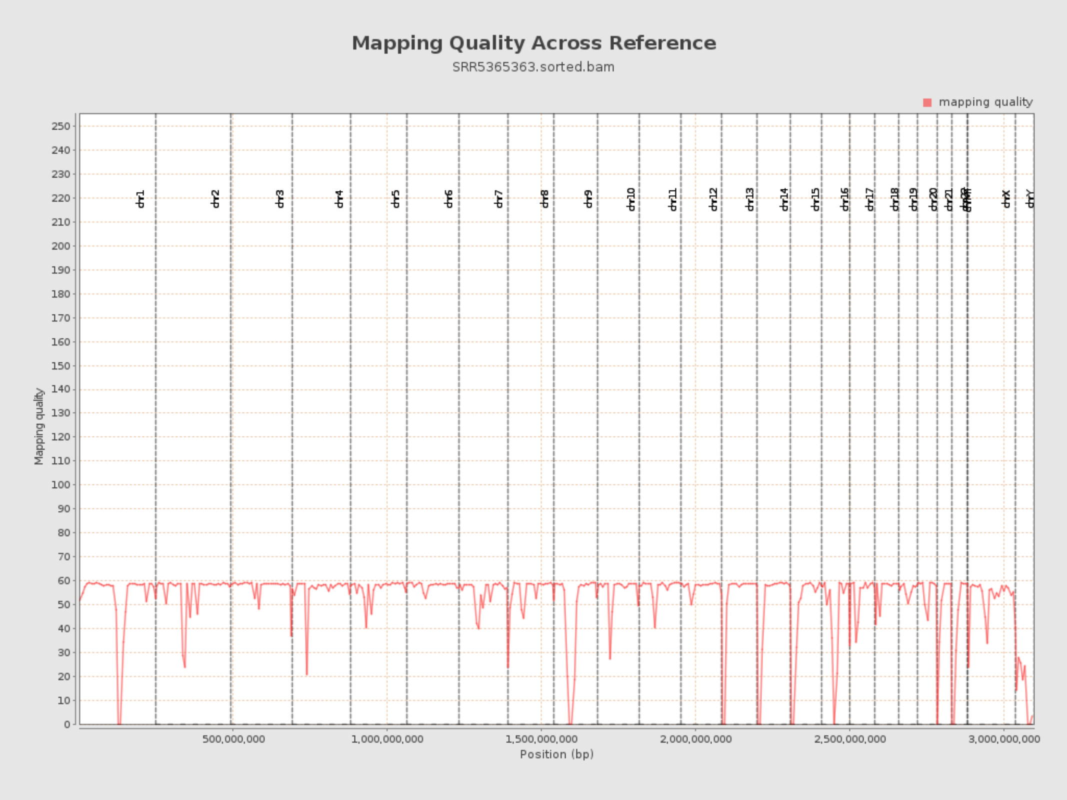
10. Results : Mapped Reads Clipping Profile



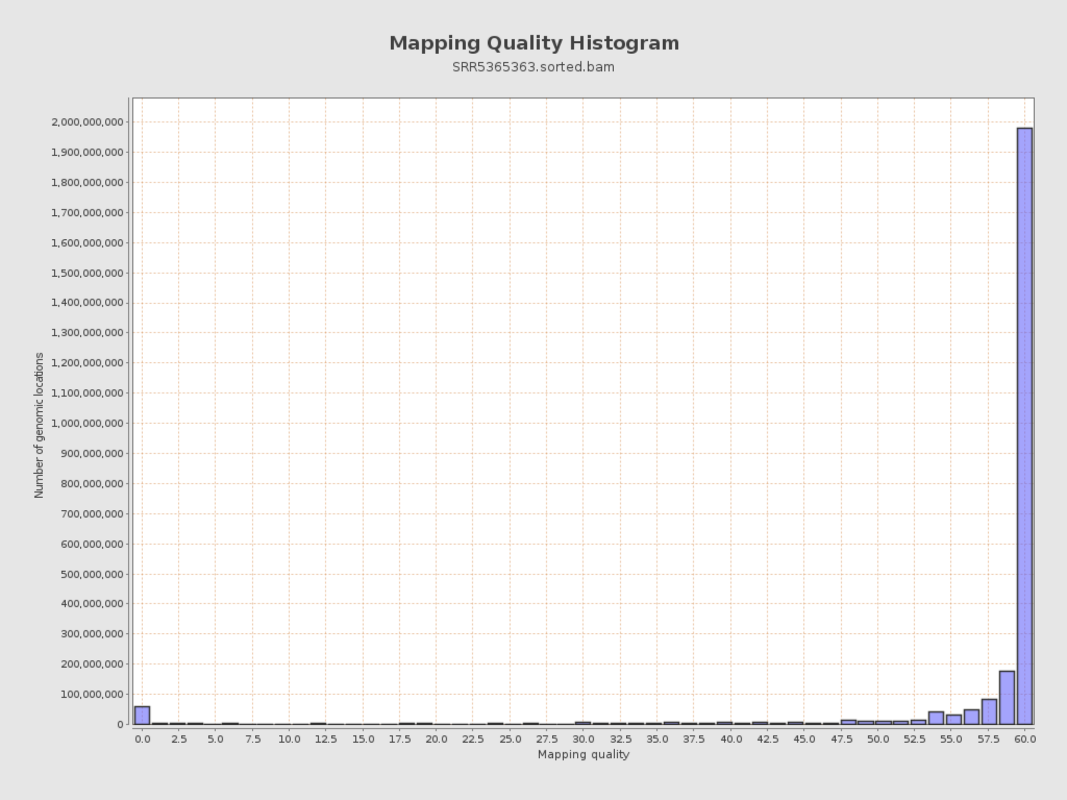
11. Results : Homopolymer Indels



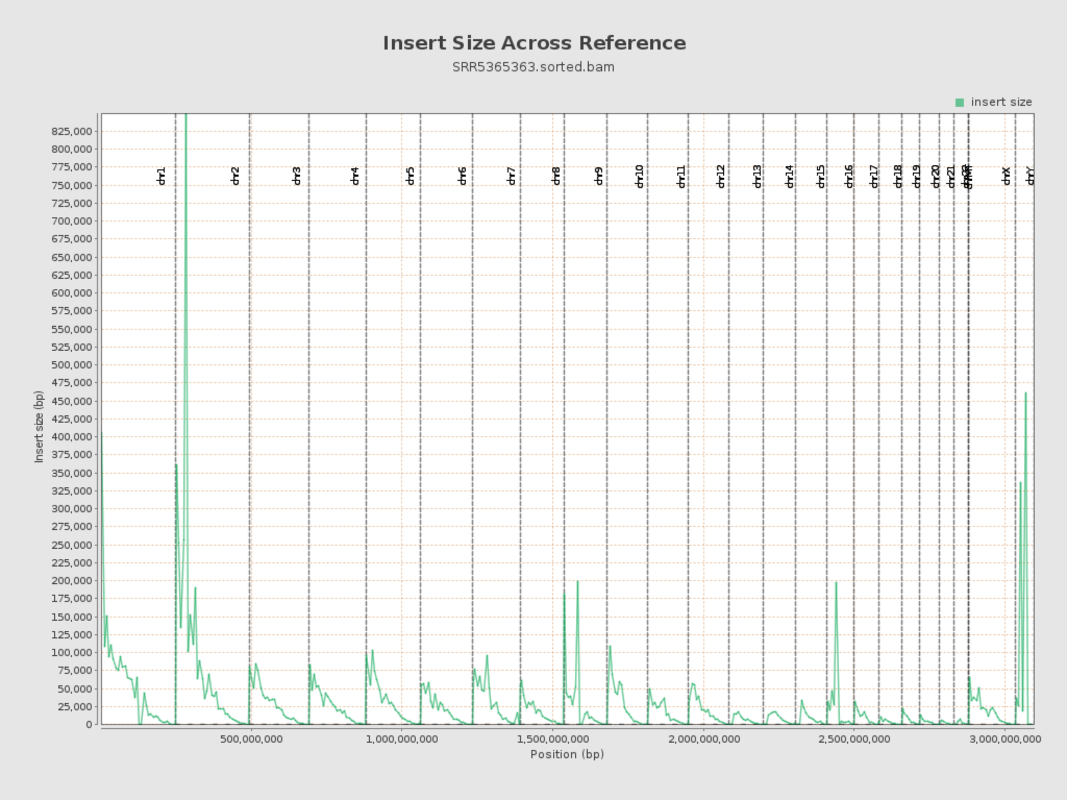
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram