Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/16 03:38:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365362.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_SRR5365362 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365362_1.fastq.gz SRR5365362_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 16 03:38:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365362.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	603,486,254
Mapped reads	577,411,013 / 95.68%
Unmapped reads	26,075,241 / 4.32%
Mapped paired reads	577,411,013 / 95.68%
Mapped reads, first in pair	288,645,628 / 47.83%
Mapped reads, second in pair	288,765,385 / 47.85%
Mapped reads, both in pair	573,028,512 / 94.95%
Mapped reads, singletons	4,382,501 / 0.73%
Secondary alignments	0
Supplementary alignments	68,817,492 / 11.4%
Read min/max/mean length	30 / 150 / 155.86
Duplicated reads (estimated)	405,070,023 / 67.12%
Duplication rate	34.92%
Clipped reads	380,004,398 / 62.97%

2.2. ACGT Content

Number/percentage of A's	20,891,799,800 / 27.52%
Number/percentage of C's	17,113,783,750 / 22.55%
Number/percentage of T's	20,447,603,262 / 26.94%
Number/percentage of G's	17,454,135,274 / 22.99%
Number/percentage of N's	288,526 / 0%

GC Percentage	45.54%

2.3. Coverage

Mean	24.566
Standard Deviation	1,220.6917

2.4. Mapping Quality

Mean Mapping Quality	52.52

2.5. Insert size

Mean	186,228.17
Standard Deviation	3,509,957.14
P25/Median/P75	124 / 165 / 226

2.6. Mismatches and indels

General error rate	2.18%
Mismatches	1,459,331,875
Insertions	40,419,358
Mapped reads with at least one insertion	6.14%
Deletions	33,335,127
Mapped reads with at least one deletion	5.16%
Homopolymer indels	35.1%

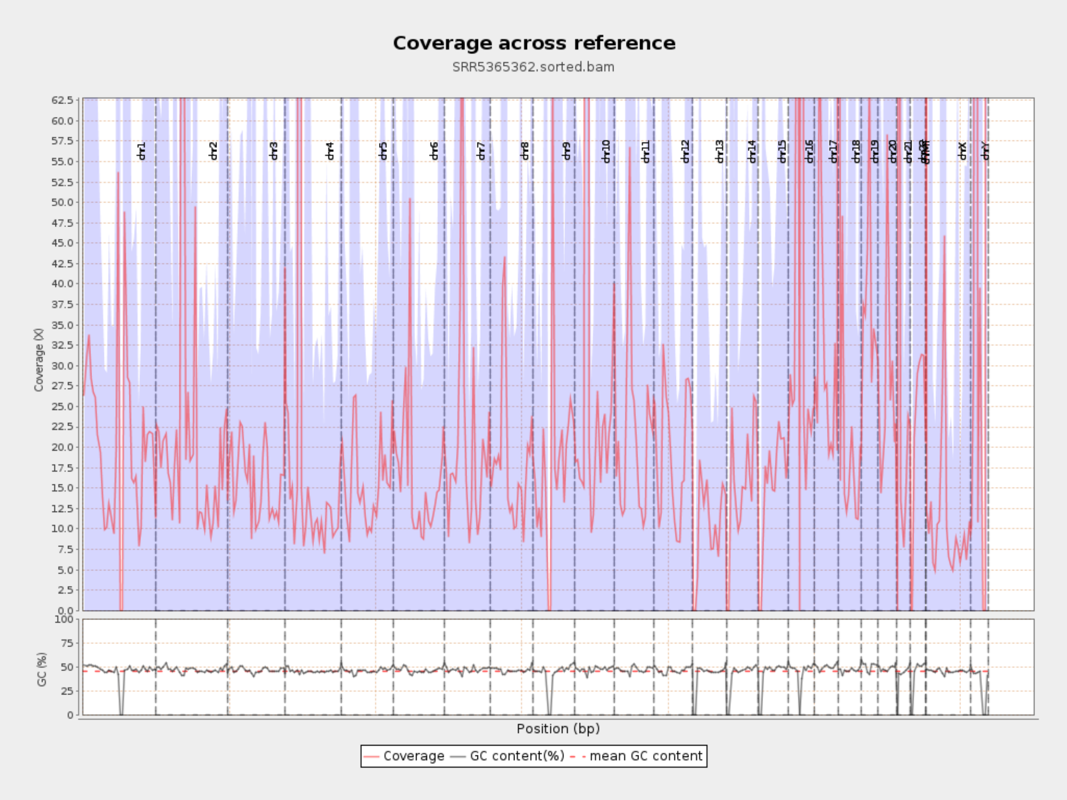
2.7. Chromosome stats

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

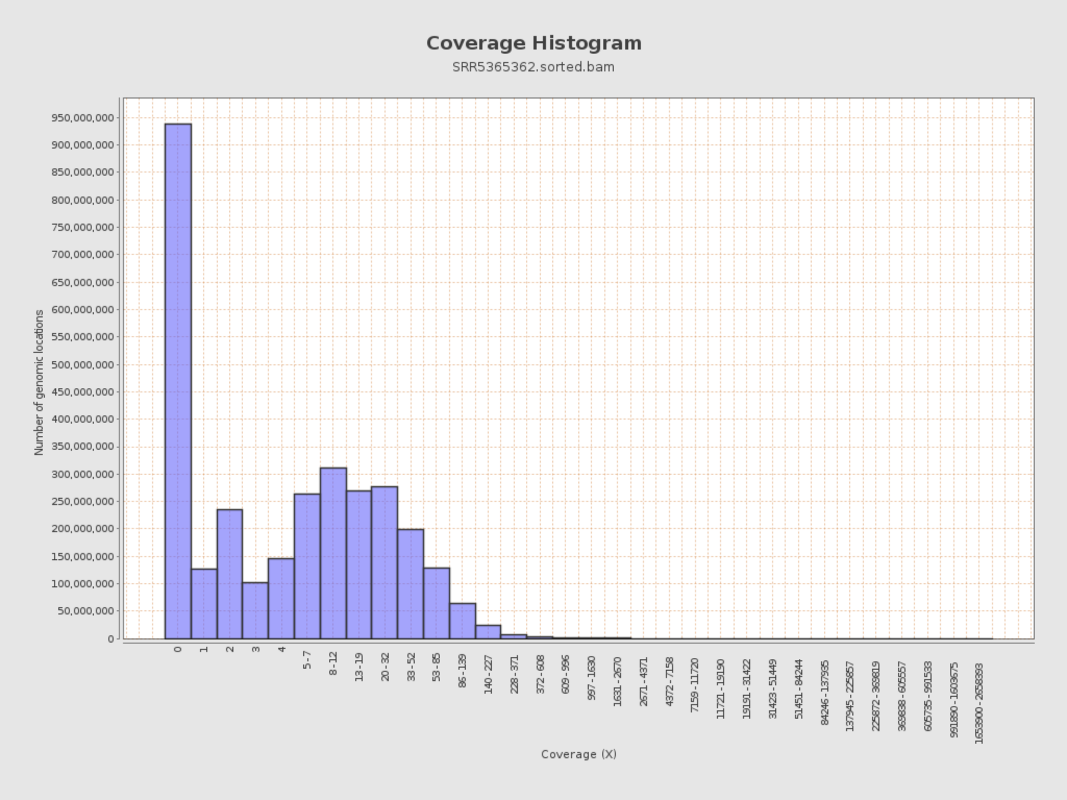
		bases	**coverage**	**deviation**
chr1	249250621	5054070032	20.2771	552.4942
chr2	243199373	5528866435	22.7339	743.7
chr3	198022430	3184220221	16.0801	237.2979
chr4	191154276	5646581740	29.5394	2,495.8191
chr5	180915260	2898074763	16.019	100.3909
chr6	171115067	2839437373	16.5937	411.9158
chr7	159138663	3390291331	21.304	240.2194
chr8	146364022	2672057927	18.2562	189.1716
chr9	141213431	2597555643	18.3945	518.3253
chr10	135534747	6371623159	47.011	2,863.5209
chr11	135006516	2946548642	21.8252	171.9499
chr12	133851895	2570191126	19.2018	96.2537
chr13	115169878	1220240544	10.5951	30.4703
chr14	107349540	1624511308	15.1329	88.2734
chr15	102531392	1541126959	15.0308	44.6843
chr16	90354753	4688063464	51.8851	1,580.3313
chr17	81195210	2576075531	31.7269	928.6969
chr18	78077248	2512765653	32.1831	2,927.7418
chr19	59128983	2271620589	38.4181	448.2277
chr20	63025520	1695990283	26.9096	954.6196
chr21	48129895	1716325921	35.6603	1,393.3116
chr22	51304566	1152812496	22.47	110.4921
chrMT	16571	30134326	1,818.4977	1,197.2213
chrX	155270560	1736409727	11.1831	217.3464

chrY	59373566	7583149437	127.7193	3,812.0358

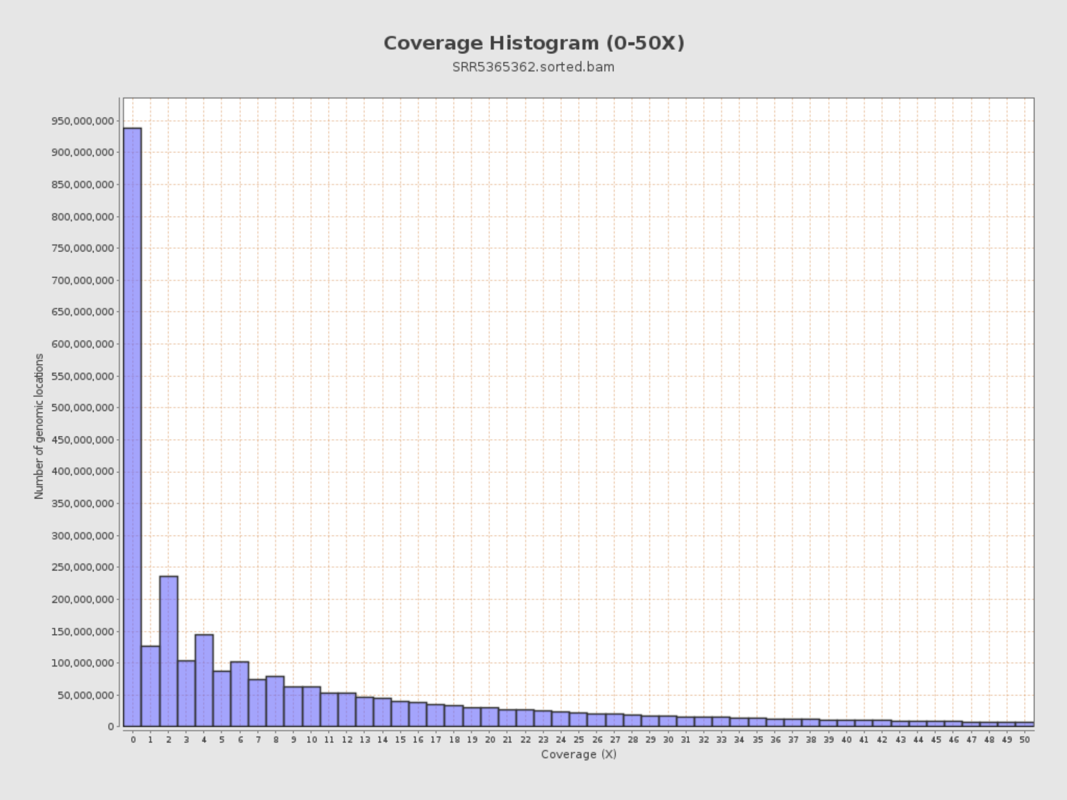
3. Results : Coverage across reference



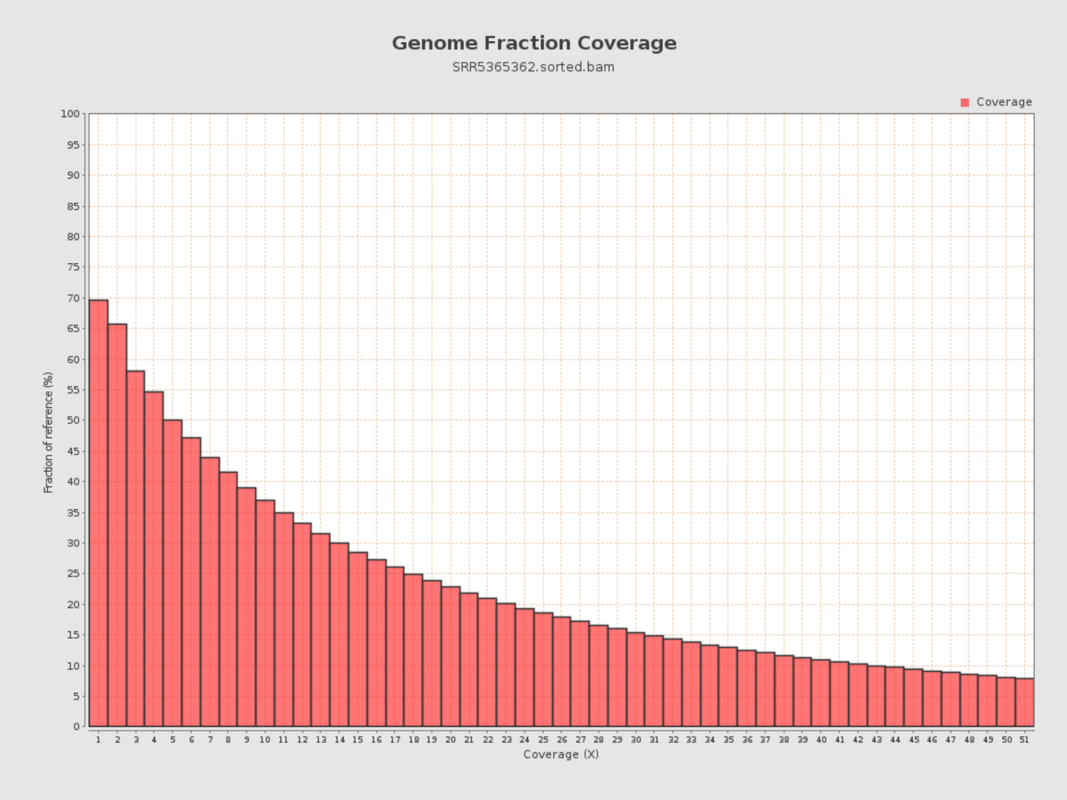
4. Results : Coverage Histogram



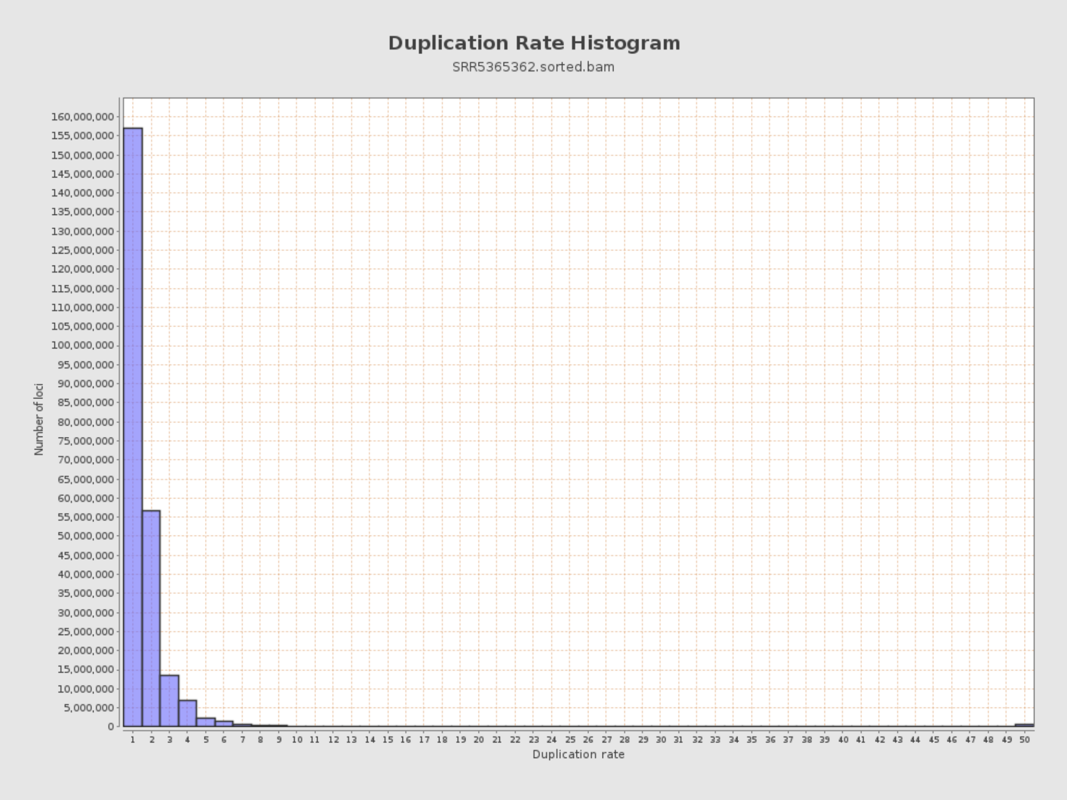
5. Results : Coverage Histogram (0-50X)



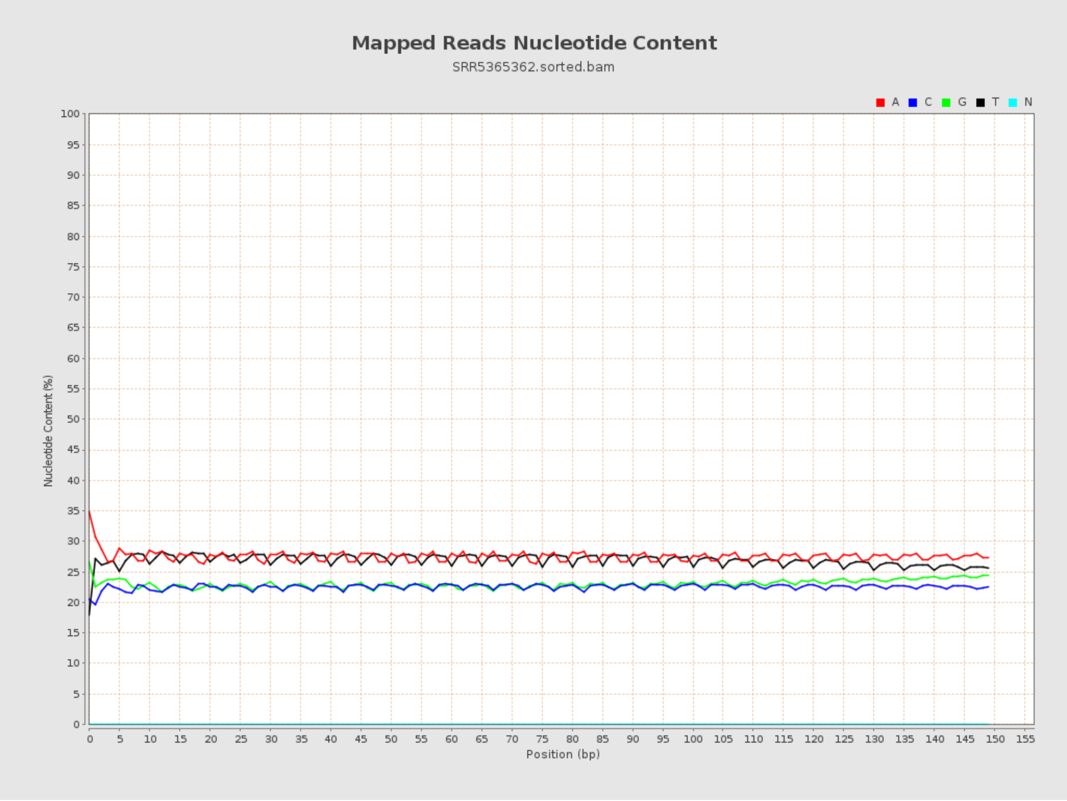
6. Results : Genome Fraction Coverage



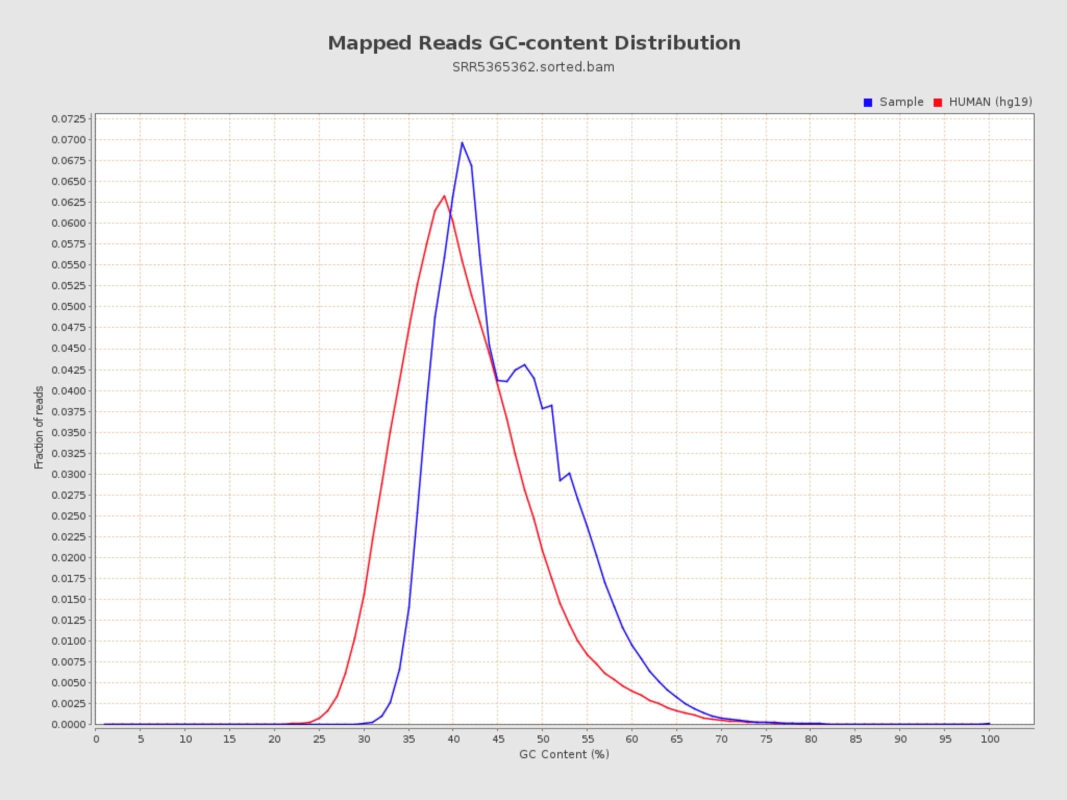
7. Results : Duplication Rate Histogram



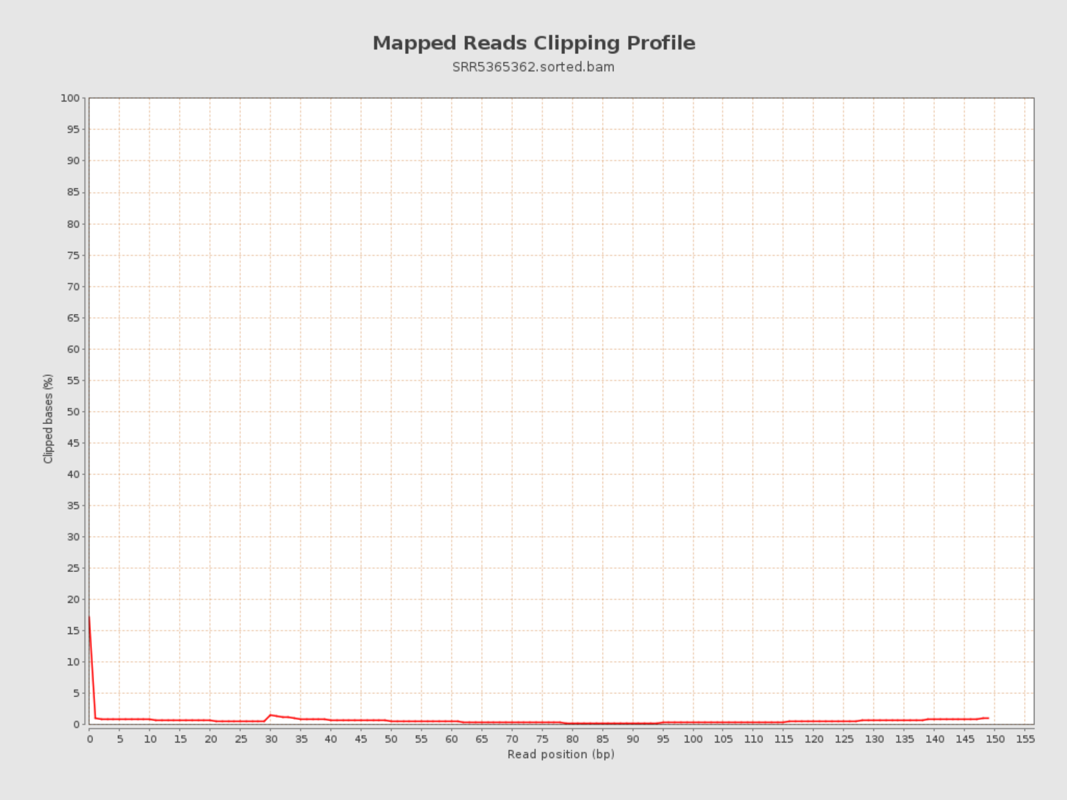
8. Results : Mapped Reads Nucleotide Content



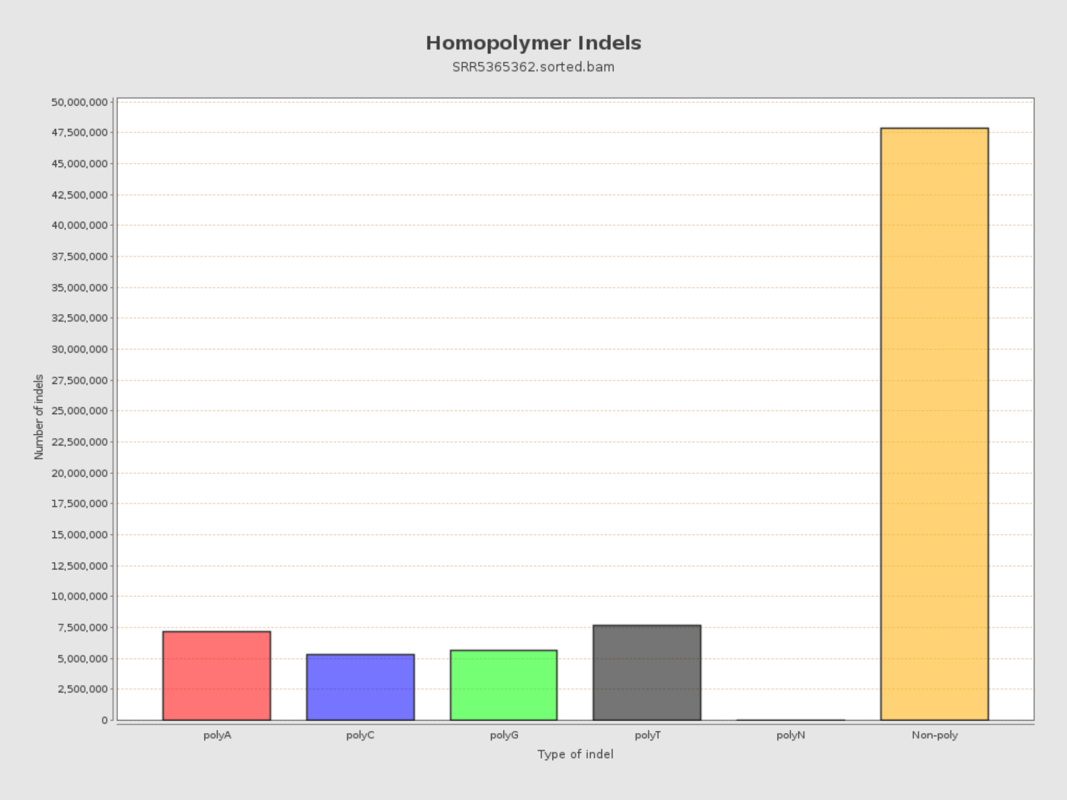
9. Results : Mapped Reads GC-content Distribution



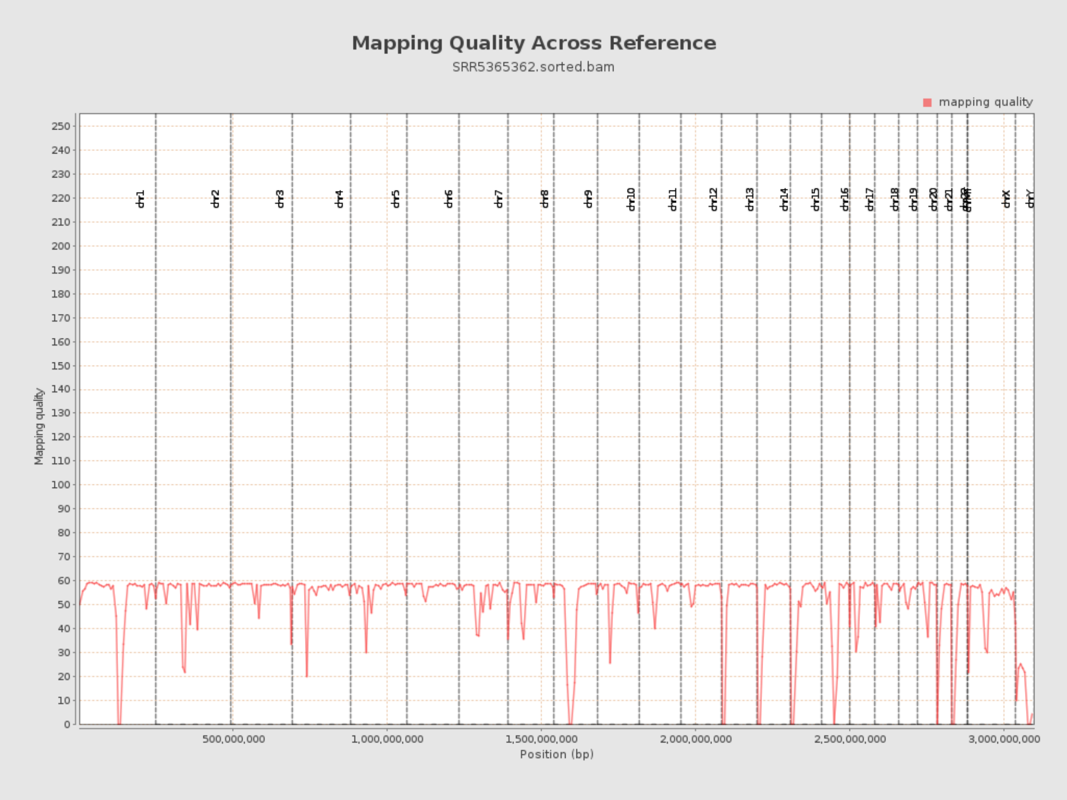
10. Results : Mapped Reads Clipping Profile



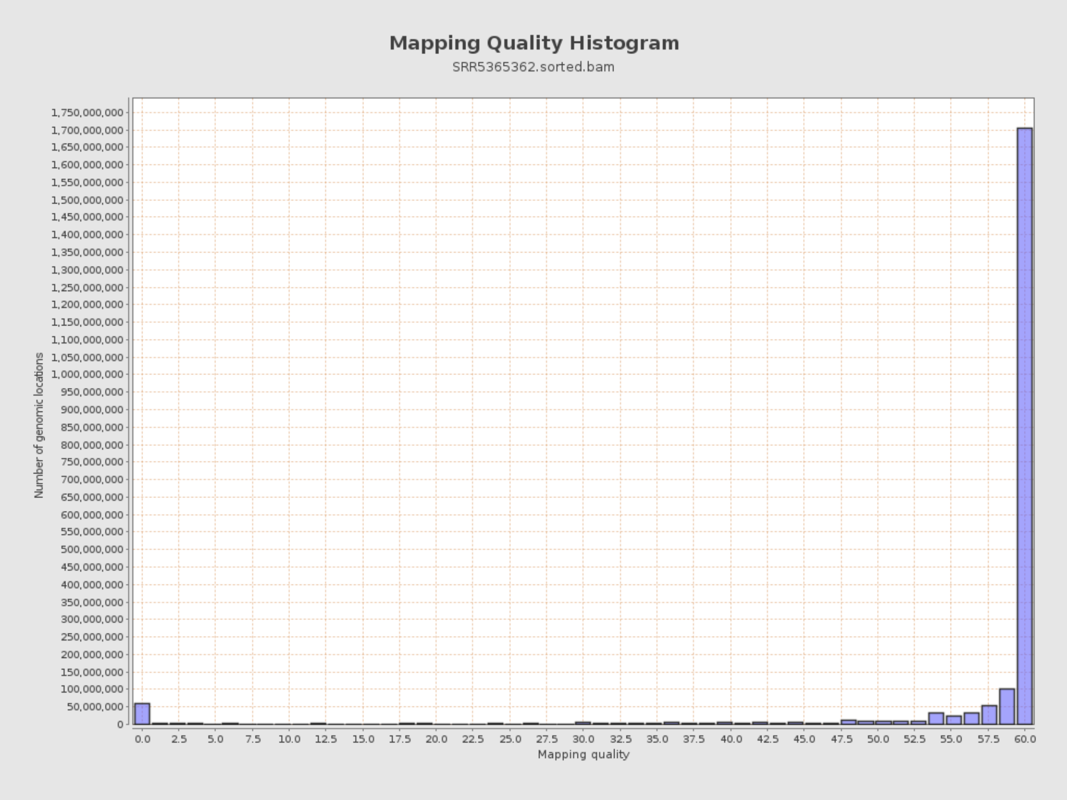
11. Results : Homopolymer Indels



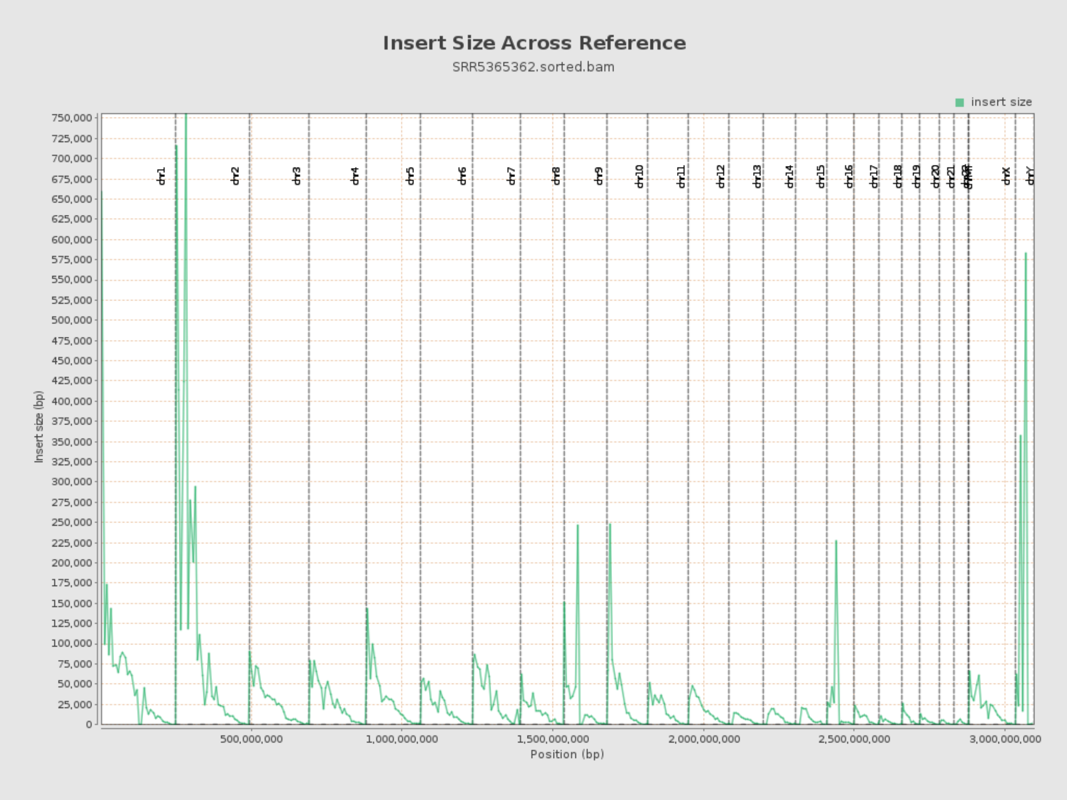
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram