Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/01 23:09:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365378.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_SRR5365378 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365378_1.fastq.gz SRR5365378_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 01 23:09:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365378.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	927,732,918
Mapped reads	893,588,339 / 96.32%
Unmapped reads	34,144,579 / 3.68%
Mapped paired reads	893,588,339 / 96.32%
Mapped reads, first in pair	445,393,449 / 48.01%
Mapped reads, second in pair	448,194,890 / 48.31%
Mapped reads, both in pair	889,349,910 / 95.86%
Mapped reads, singletons	4,238,429 / 0.46%
Secondary alignments	0
Supplementary alignments	7,864,252 / 0.85%
Read min/max/mean length	30 / 125 / 125.38
Duplicated reads (estimated)	213,721,048 / 23.04%
Duplication rate	19.44%
Clipped reads	156,721,198 / 16.89%

2.2. ACGT Content

Number/percentage of A's	31,967,444,205 / 29.61%
Number/percentage of C's	22,048,744,904 / 20.42%
Number/percentage of T's	31,602,431,331 / 29.27%
Number/percentage of G's	22,325,450,646 / 20.68%
Number/percentage of N's	19,751,474 / 0.02%

GC Percentage	41.1%

2.3. Coverage

Mean	34.8871
Standard Deviation	453.6793

2.4. Mapping Quality

Mean Mapping Quality	54.02

2.5. Insert size

Mean	96,235.64
Standard Deviation	3,022,623.69
P25/Median/P75	148 / 204 / 287

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	567,126,893
Insertions	11,062,521
Mapped reads with at least one insertion	1.17%
Deletions	13,550,487
Mapped reads with at least one deletion	1.45%
Homopolymer indels	40.75%

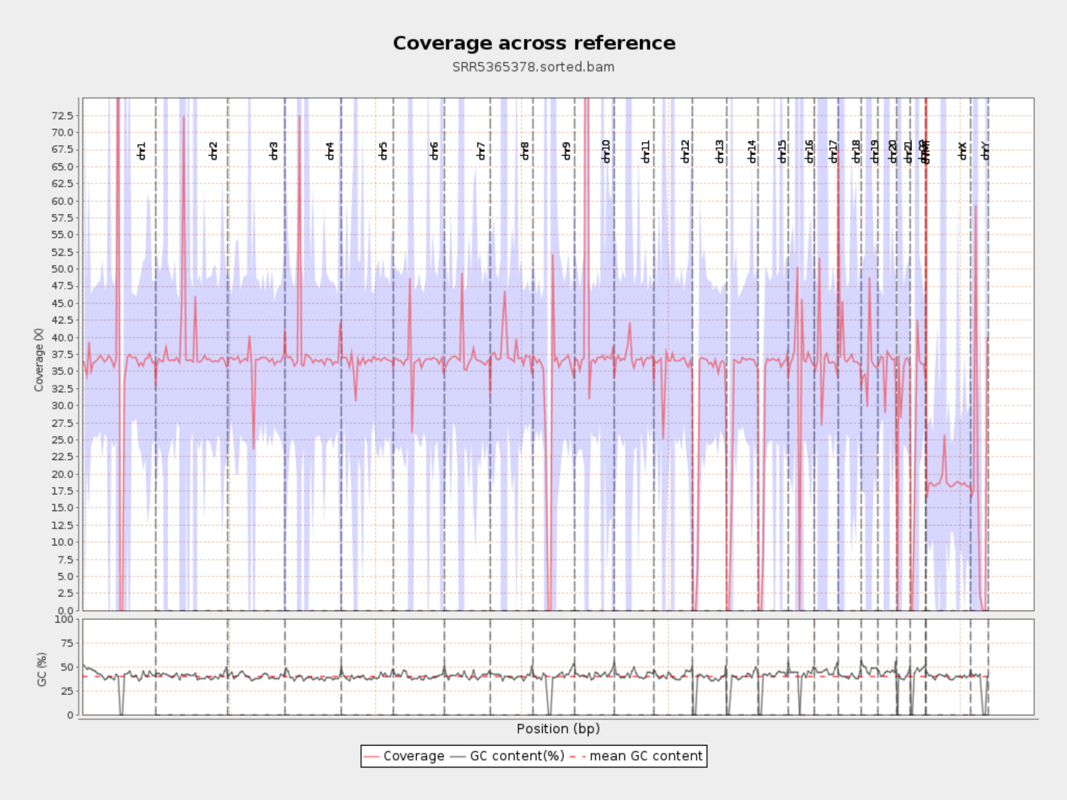
2.7. Chromosome stats

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

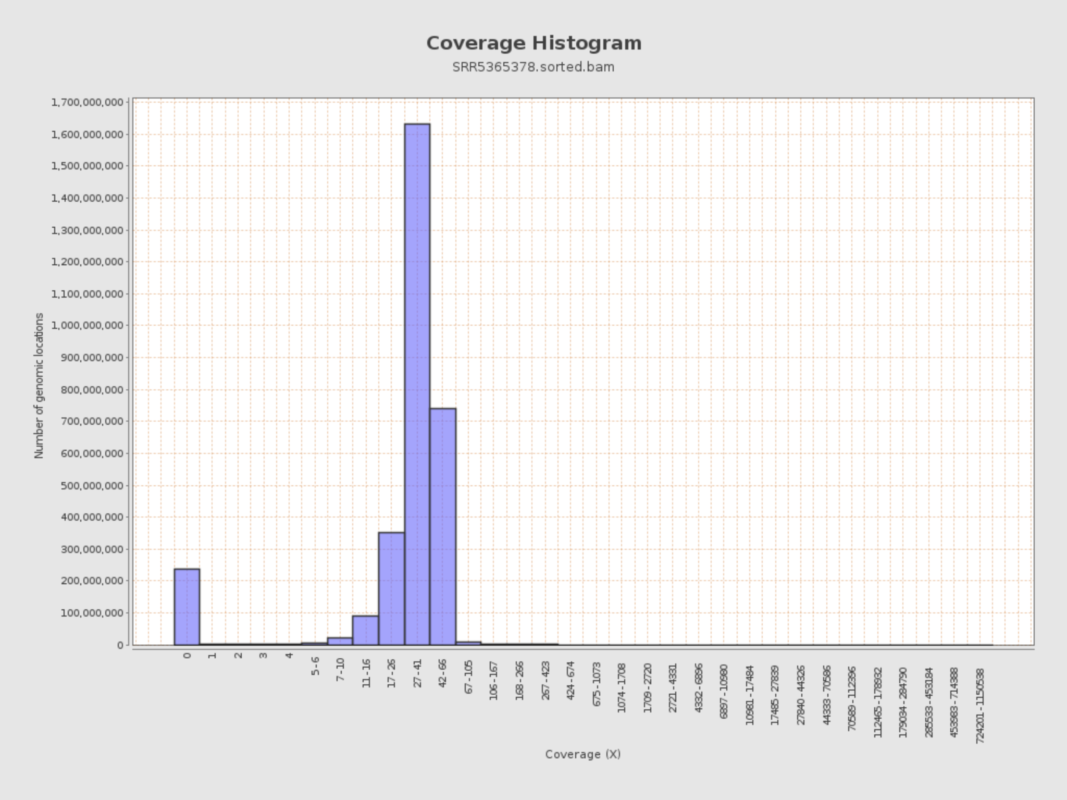
		bases	coverage	deviation
chr1	249250621	8979037055	36.0241	1,187.097
chr2	243199373	9335845550	38.3876	247.7287
chr3	198022430	7206551485	36.3926	50.398
chr4	191154276	7312052348	38.2521	314.4594
chr5	180915260	6583531135	36.3901	30.228
chr6	171115067	6271973476	36.6535	141.843
chr7	159138663	5916416634	37.1777	293.1137
chr8	146364022	5528953546	37.7754	373.9116
chr9	141213431	4612636167	32.6643	416.1334
chr10	135534747	5858333517	43.2238	949.222
chr11	135006516	5007652867	37.0919	246.3114
chr12	133851895	4816464494	35.9835	54.1942
chr13	115169878	3483782548	30.2491	17.5728
chr14	107349540	3283288312	30.585	28.4745
chr15	102531392	3003705074	29.2955	27.9635
chr16	90354753	3202944424	35.4485	136.0574
chr17	81195210	2999715465	36.9445	203.3343
chr18	78077248	3039070523	38.9239	454.3384
chr19	59128983	2149269656	36.3488	524.4499
chr20	63025520	2260677447	35.8692	90.5117
chr21	48129895	1531591001	31.822	155.2364
chr22	51304566	1341044491	26.1389	106.6281
chrMT	16571	197461501	11,916.0884	876.3674
chrX	155270560	2925376307	18.8405	95.1107

chrY	59373566	1152559736	19.412	502.2972

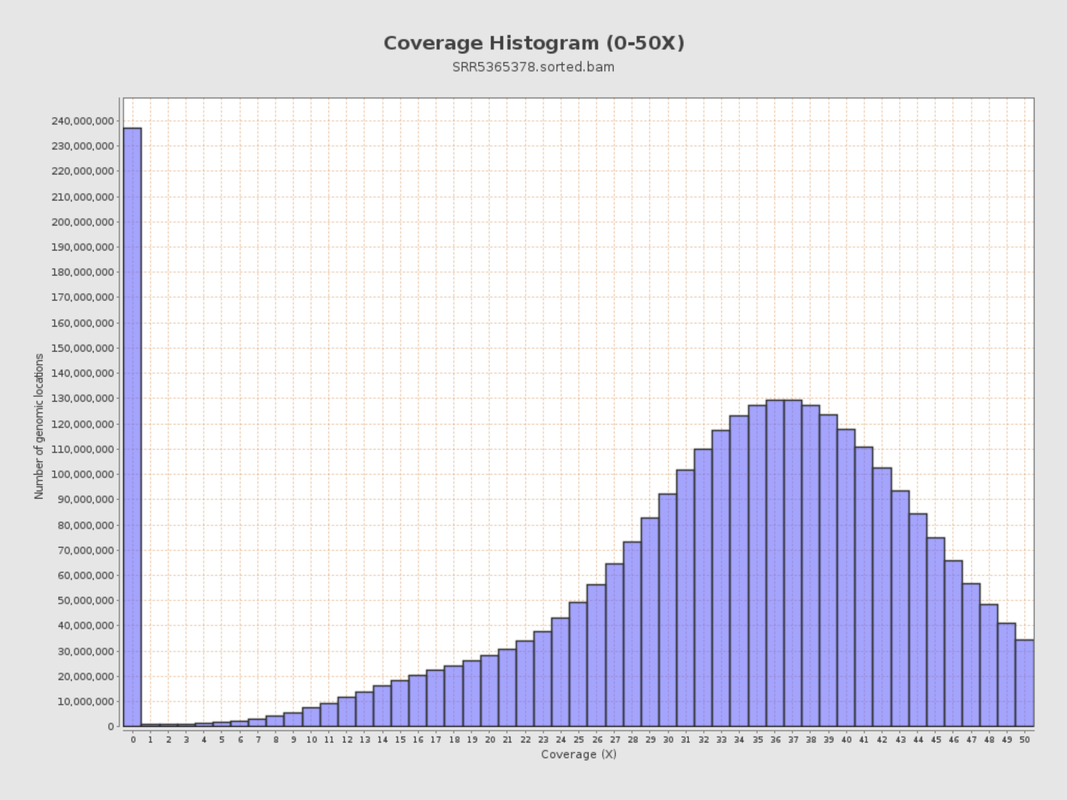
3. Results : Coverage across reference



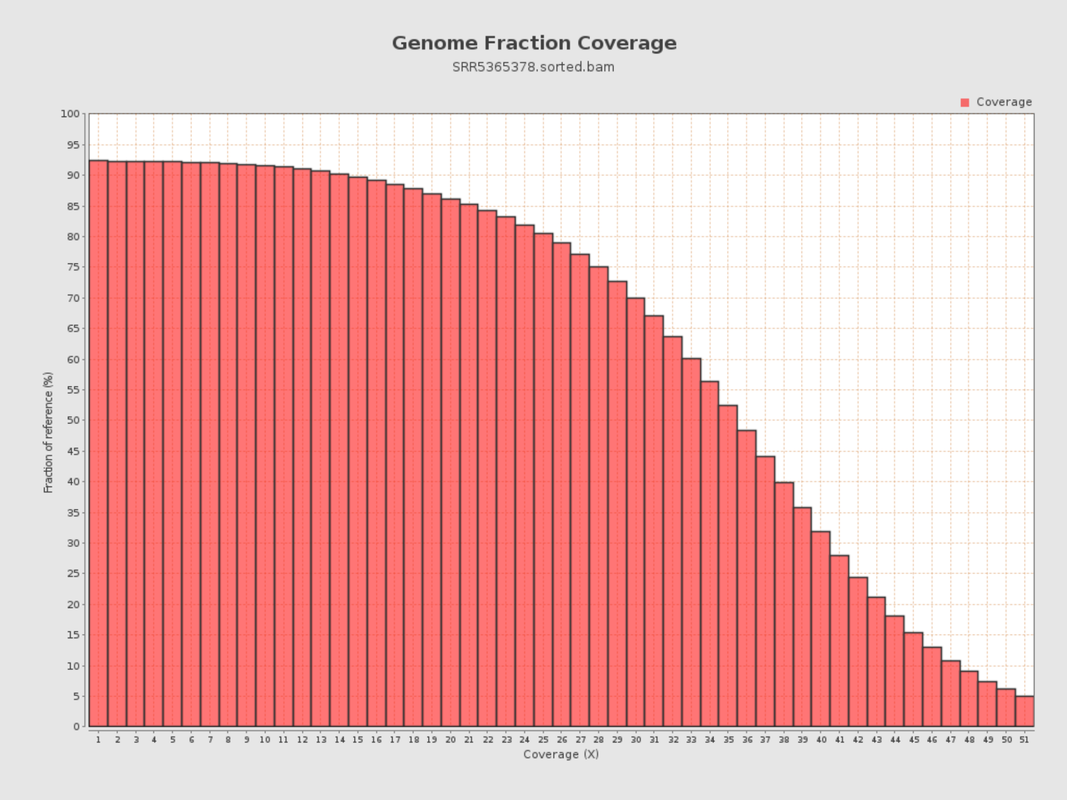
4. Results : Coverage Histogram



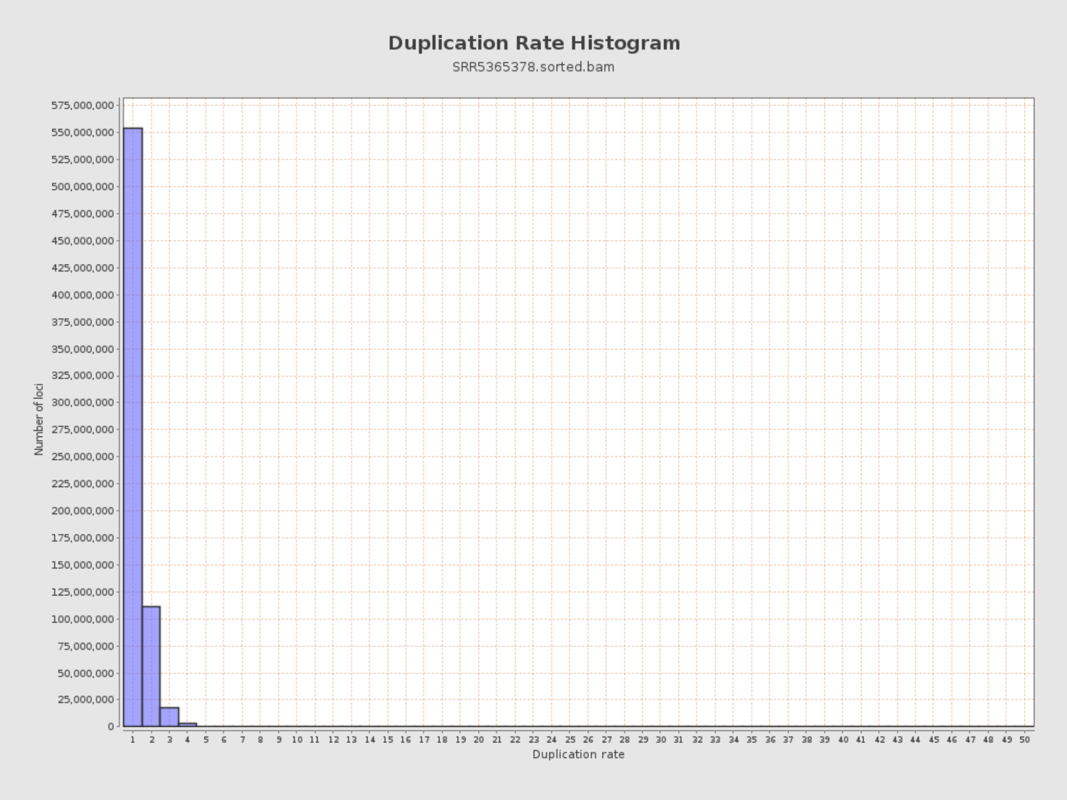
5. Results : Coverage Histogram (0-50X)



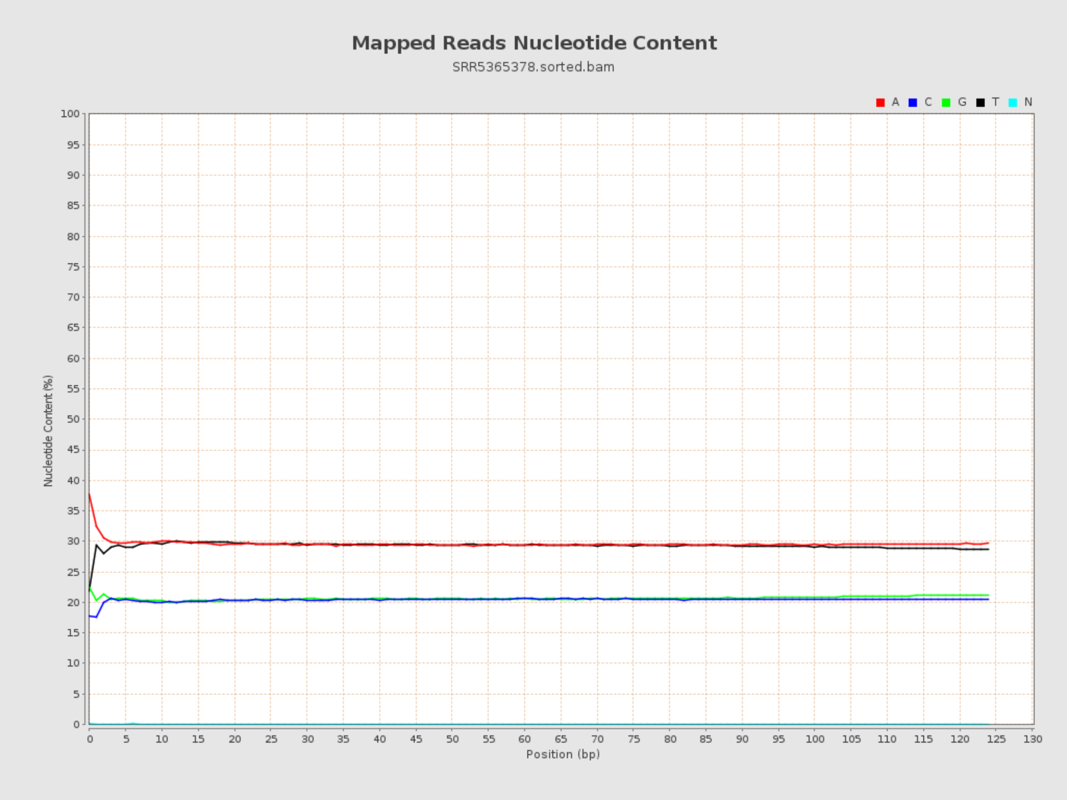
6. Results : Genome Fraction Coverage



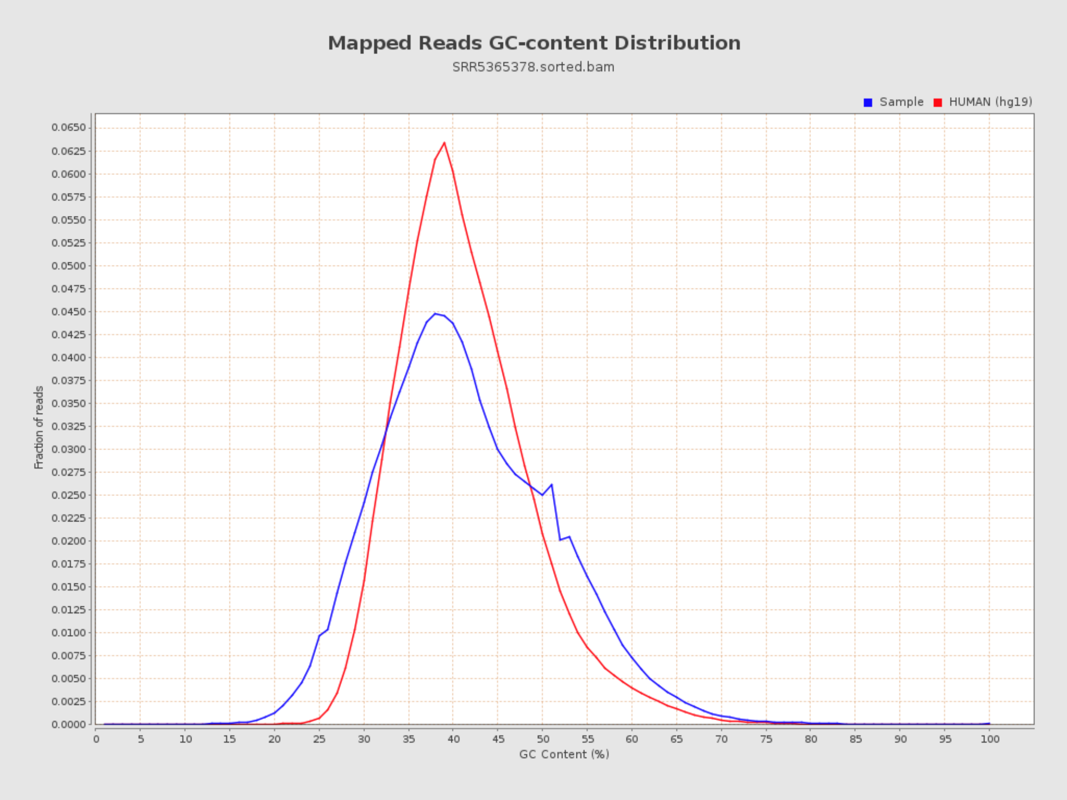
7. Results : Duplication Rate Histogram



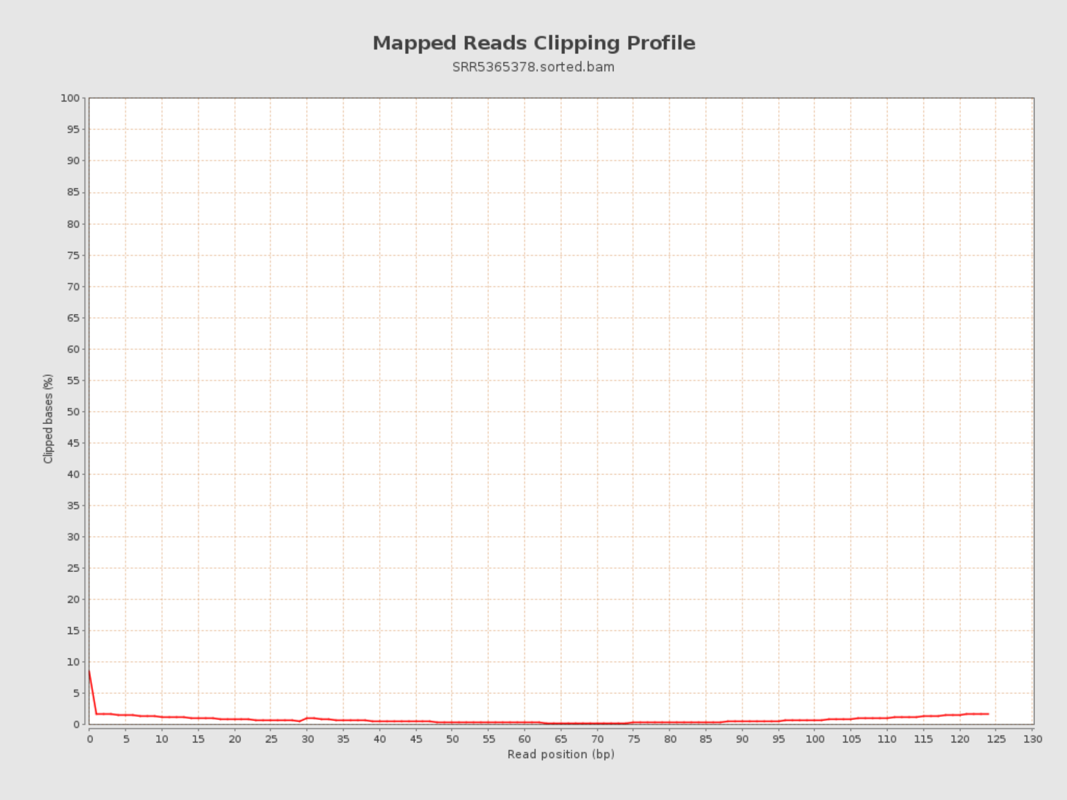
8. Results : Mapped Reads Nucleotide Content



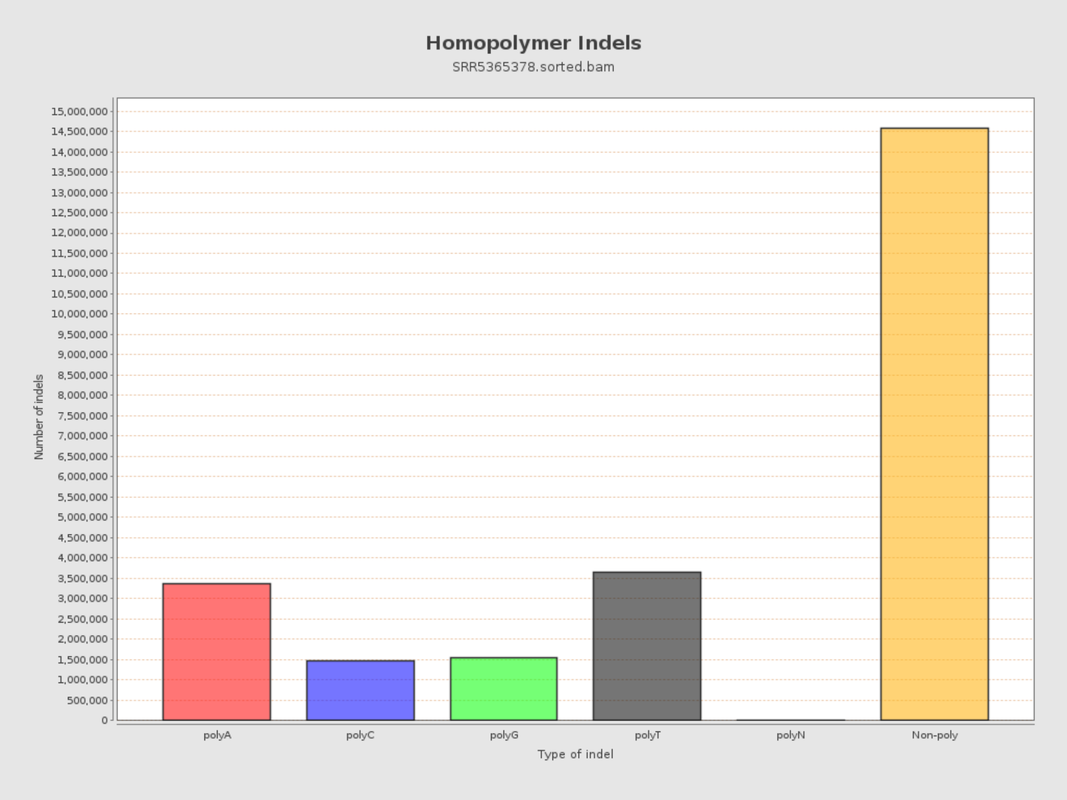
9. Results : Mapped Reads GC-content Distribution



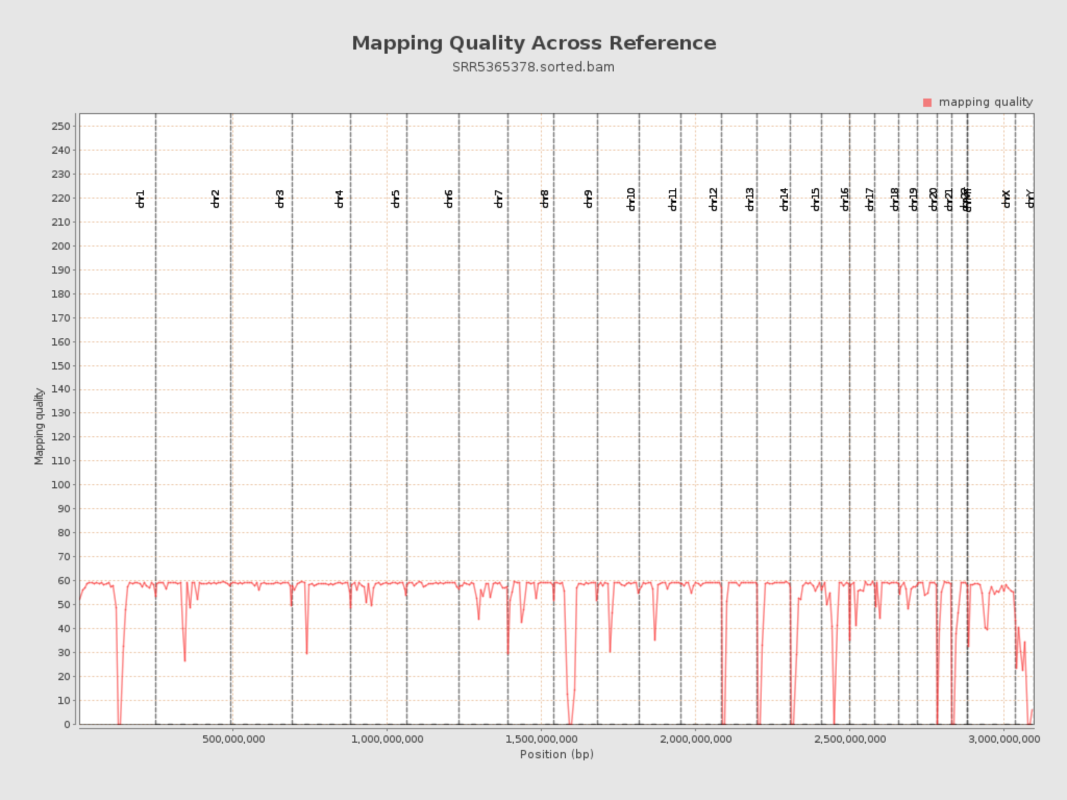
10. Results : Mapped Reads Clipping Profile



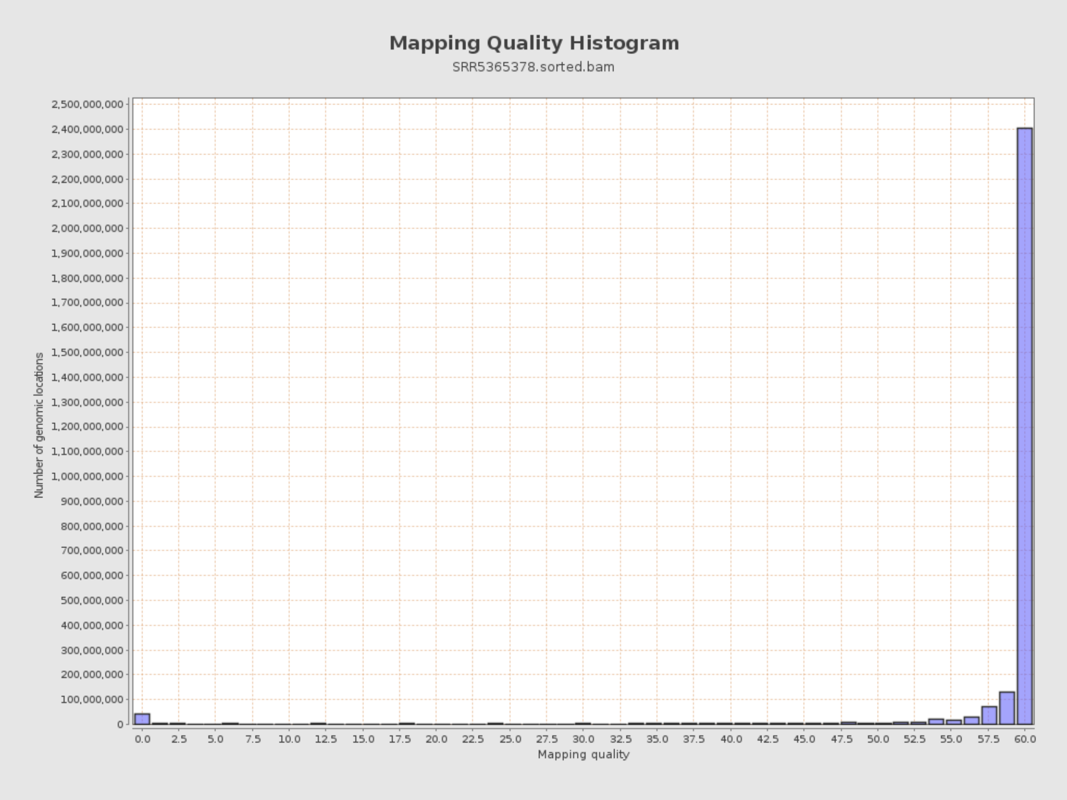
11. Results : Homopolymer Indels



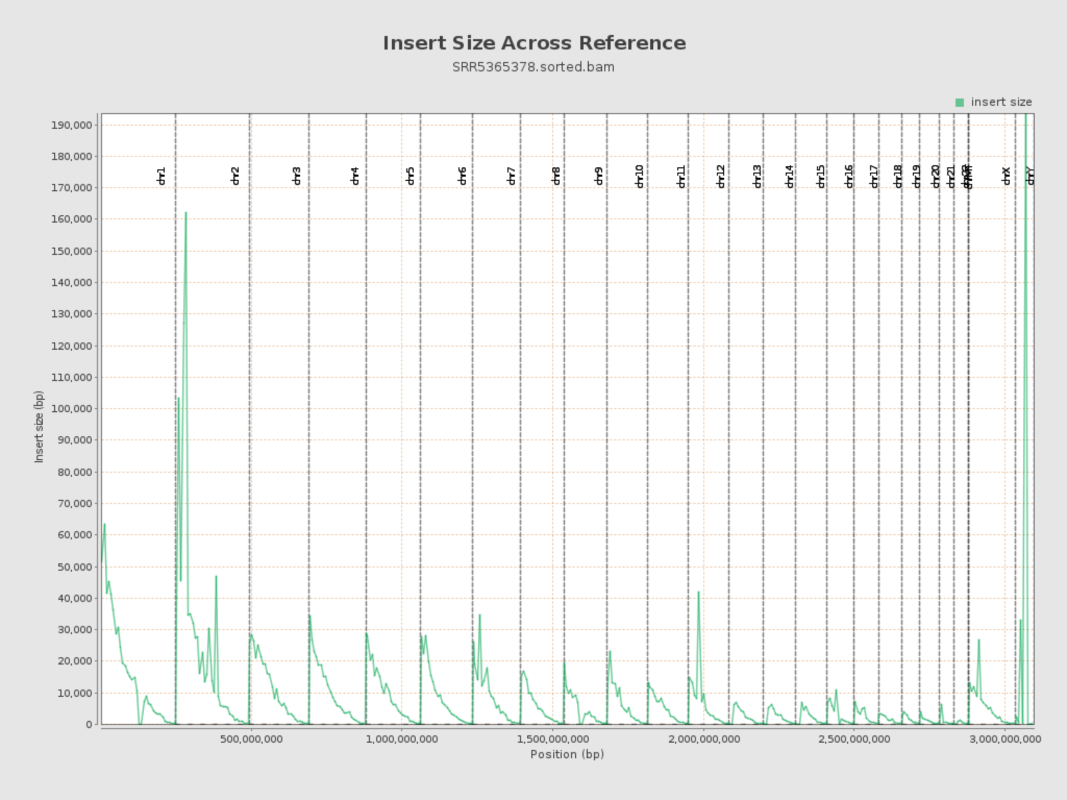
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram