

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/25 07:41:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16328252.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_SRR16328252 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16328252_1.fastq.gz SRR16328252_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Feb 25 07:41:32 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16328252.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	479,260,756
Mapped reads	449,799,049 / 93.85%
Unmapped reads	29,461,707 / 6.15%
Mapped paired reads	449,799,049 / 93.85%
Mapped reads, first in pair	226,293,414 / 47.22%
Mapped reads, second in pair	223,505,635 / 46.64%
Mapped reads, both in pair	445,793,370 / 93.02%
Mapped reads, singletons	4,005,679 / 0.84%
Secondary alignments	0
Supplementary alignments	20,603,882 / 4.3%
Read min/max/mean length	30 / 150 / 152.15
Duplicated reads (estimated)	174,900,720 / 36.49%
Duplication rate	33.21%
Clipped reads	299,035,930 / 62.4%

2.2. ACGT Content

Number/percentage of A's	17,983,578,407 / 28.89%
Number/percentage of C's	13,118,042,200 / 21.07%
Number/percentage of T's	17,857,552,248 / 28.69%
Number/percentage of G's	13,282,604,106 / 21.34%
Number/percentage of N's	4,737,588 / 0.01%

GC Percentage	42.41%
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2.3. Coverage

Mean	20.1252
Standard Deviation	232.9509

2.4. Mapping Quality

Mean Mapping Quality	53.83
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2.5. Insert size

Mean	157,170.11
Standard Deviation	3,832,998.2
P25/Median/P75	182 / 242 / 335

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	565,258,311
Insertions	10,909,302
Mapped reads with at least one insertion	2.3%
Deletions	30,546,552
Mapped reads with at least one deletion	6.51%
Homopolymer indels	44.46%

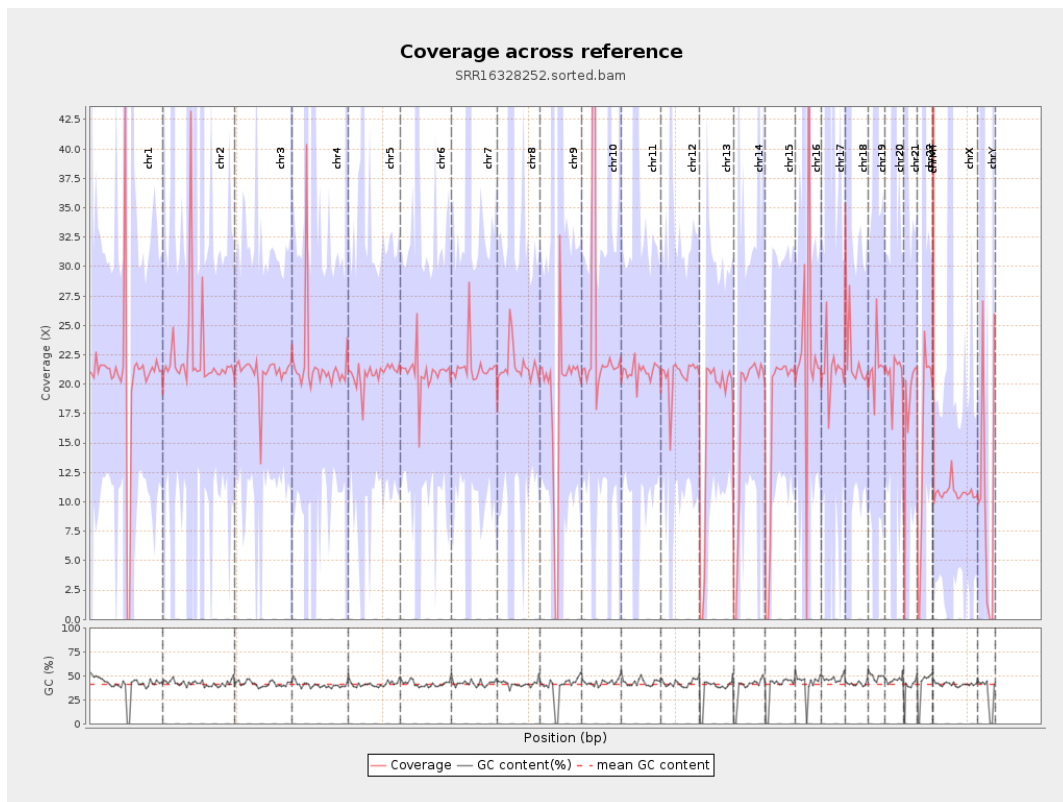
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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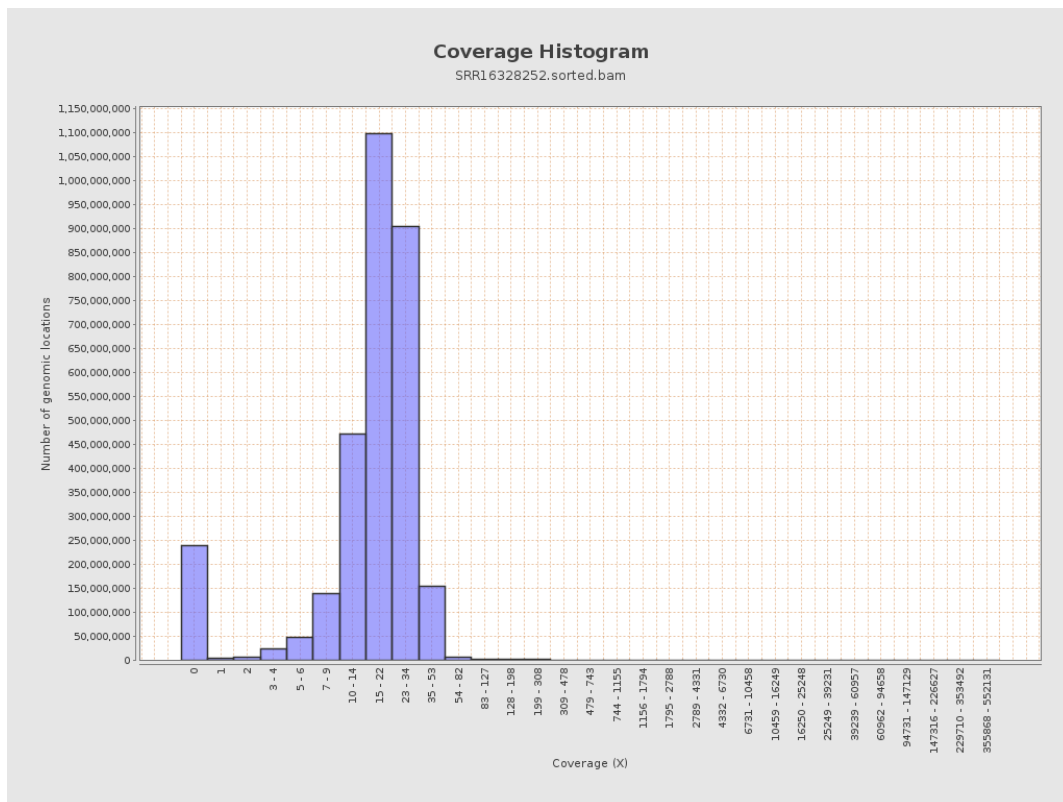
		bases	coverage	deviation
chr1	249250621	5124246475	20.5586	541.2285
chr2	243199373	5437300032	22.3574	180.9639
chr3	198022430	4149771046	20.9561	24.2822
chr4	191154276	4154908998	21.7359	168.2759
chr5	180915260	3772246648	20.8509	15.8965
chr6	171115067	3582801387	20.938	65.363
chr7	159138663	3419772948	21.4893	163.2262
chr8	146364022	3157891712	21.5756	306.4506
chr9	141213431	2684691521	19.0116	276.8294
chr10	135534747	3295877343	24.3176	468.4299
chr11	135006516	2840725459	21.0414	75.7414
chr12	133851895	2782492951	20.7878	14.1566
chr13	115169878	1977311969	17.1687	12.2288
chr14	107349540	1891703272	17.6219	19.417
chr15	102531392	1747129140	17.0399	12.3012
chr16	90354753	2077683918	22.9947	213.1301
chr17	81195210	1733602504	21.351	83.7801
chr18	78077248	1741150043	22.3004	265.1552
chr19	59128983	1271873892	21.5102	297.8894
chr20	63025520	1308712027	20.7648	49.0802
chr21	48129895	867900220	18.0325	104.3382
chr22	51304566	784883851	15.2985	86.4609
chrMT	16571	186395621	11,248.3025	1,712.509
chrX	155270560	1677631014	10.8046	31.8305

chrY	59373566	632840170	10.6586	204.956
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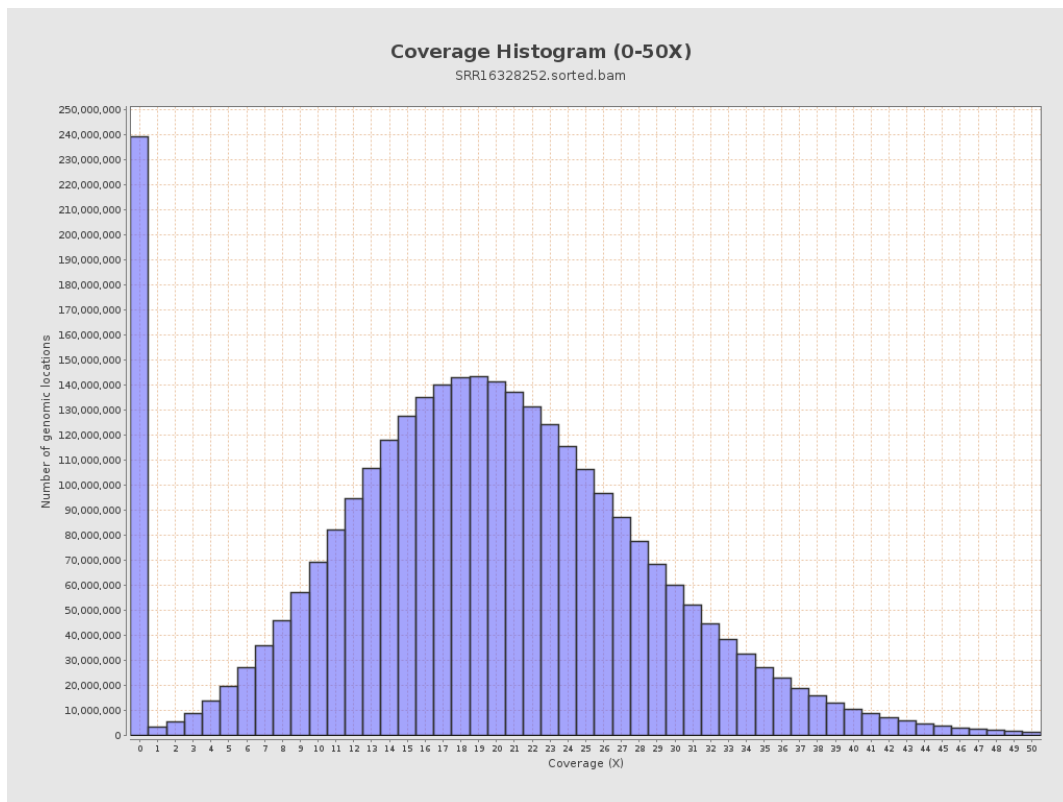
3. Results : Coverage across reference



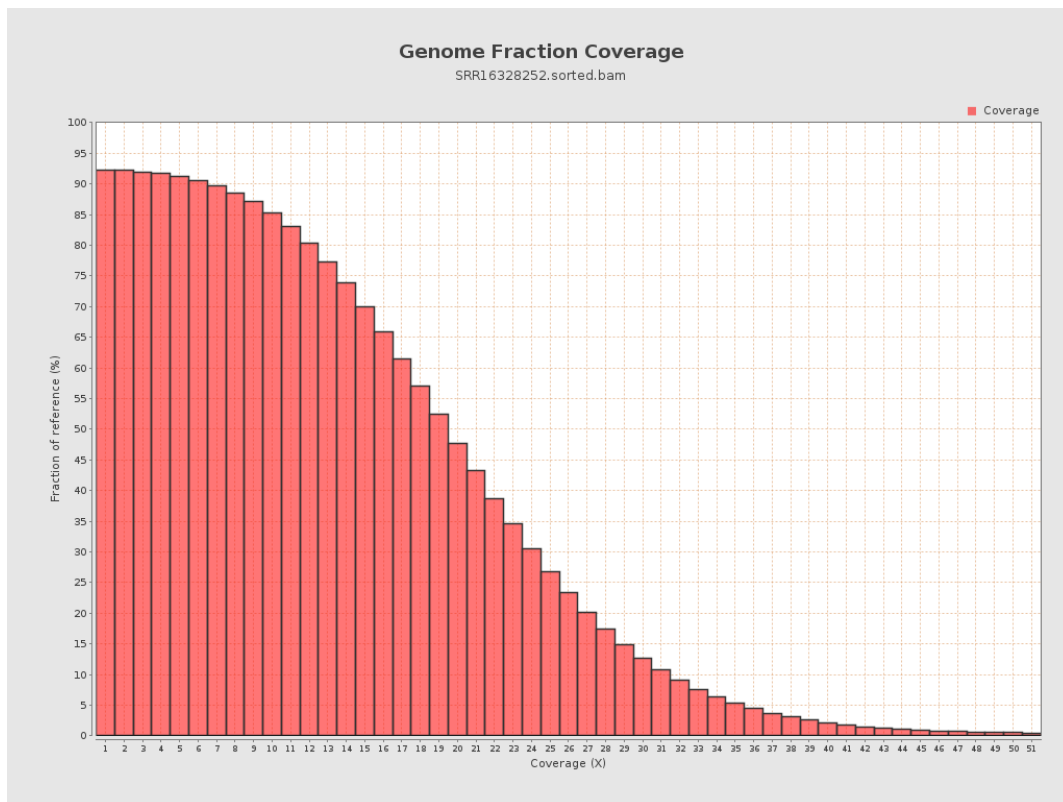
4. Results : Coverage Histogram



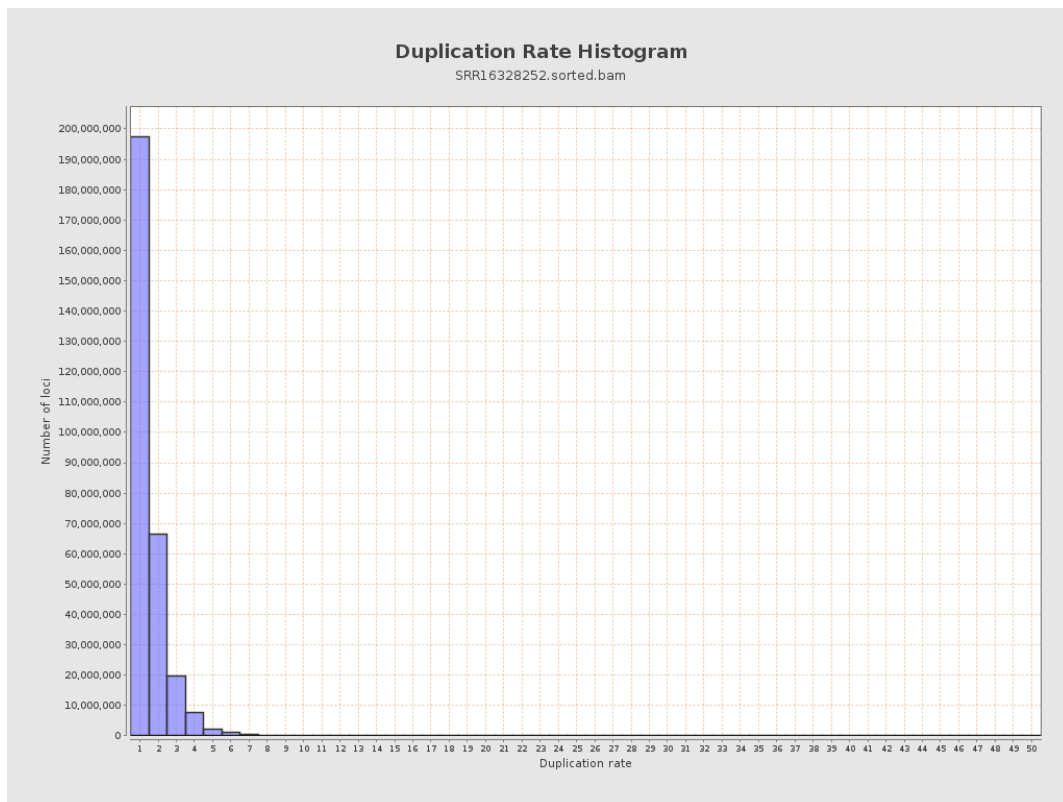
5. Results : Coverage Histogram (0-50X)



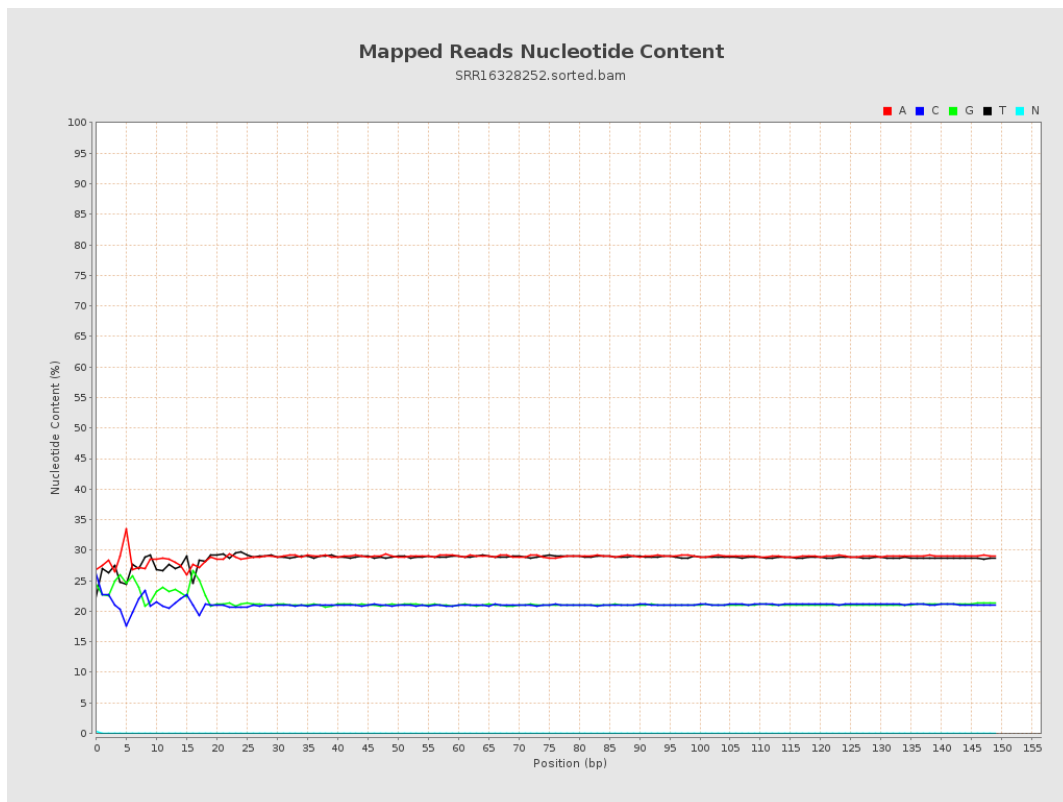
6. Results : Genome Fraction Coverage



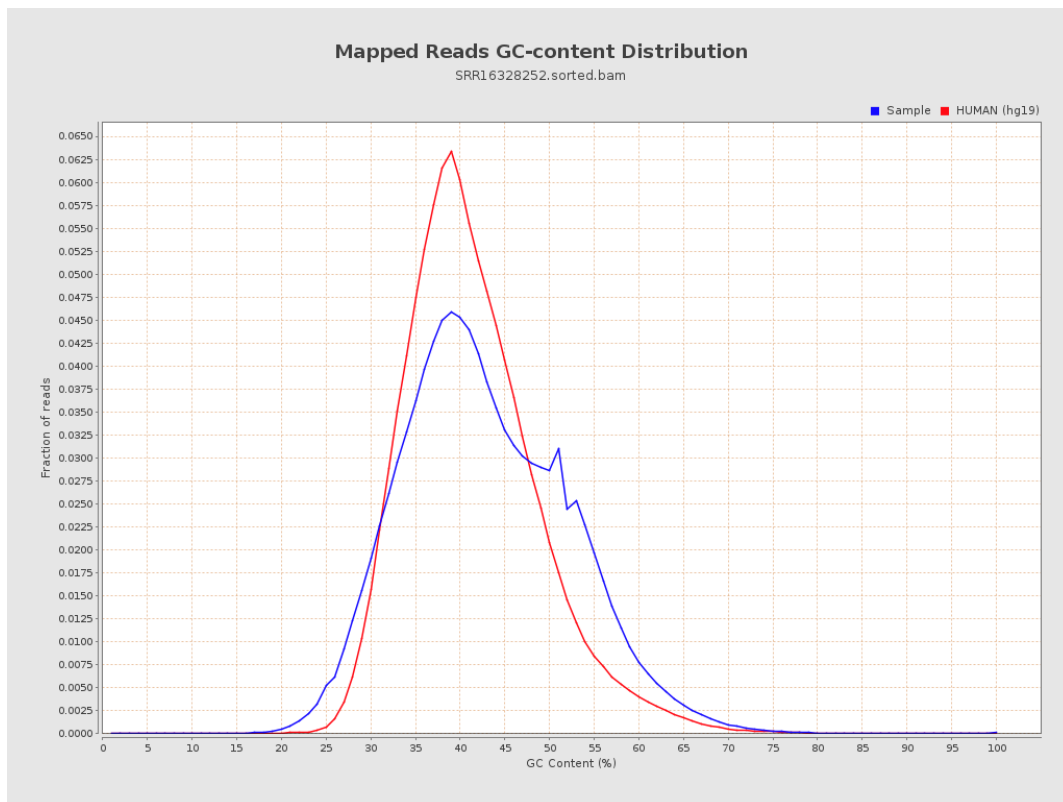
7. Results : Duplication Rate Histogram



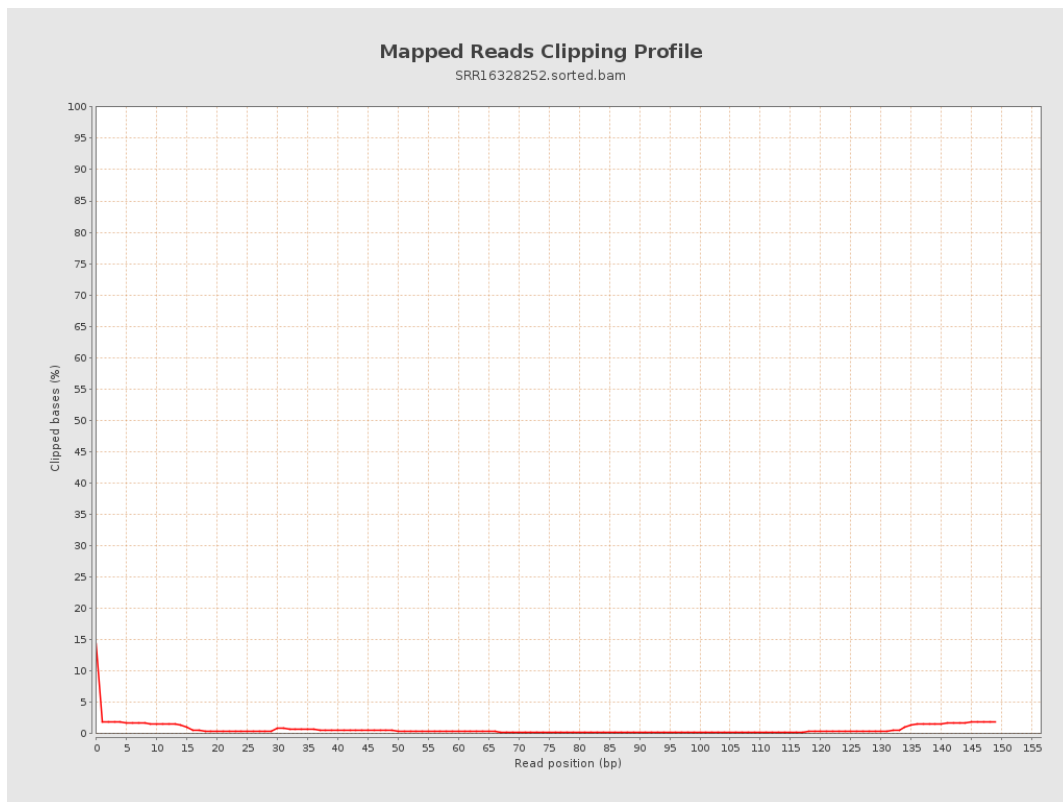
8. Results : Mapped Reads Nucleotide Content



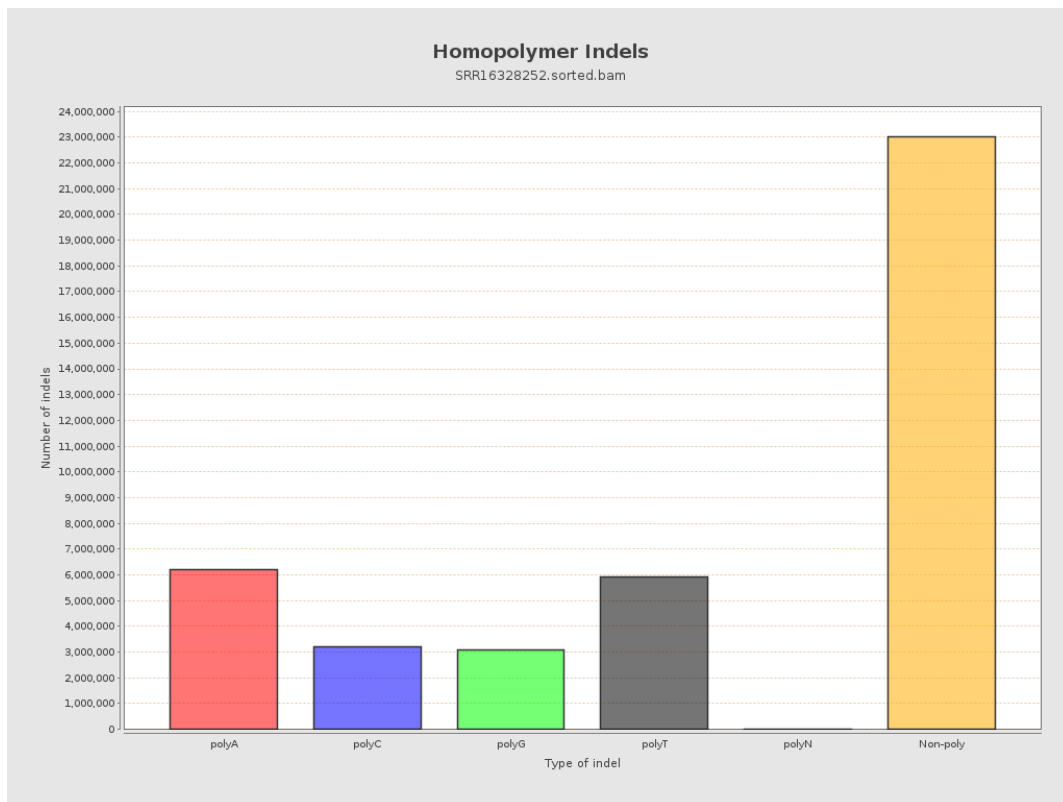
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



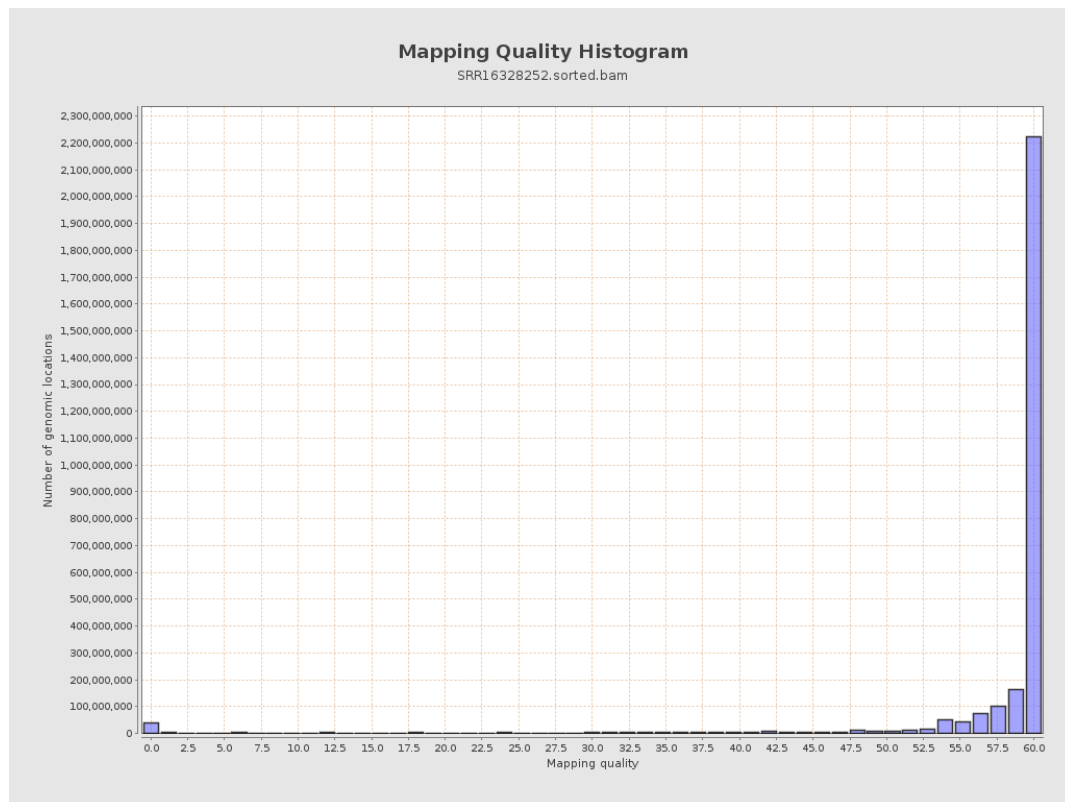
11. Results : Homopolymer Indels



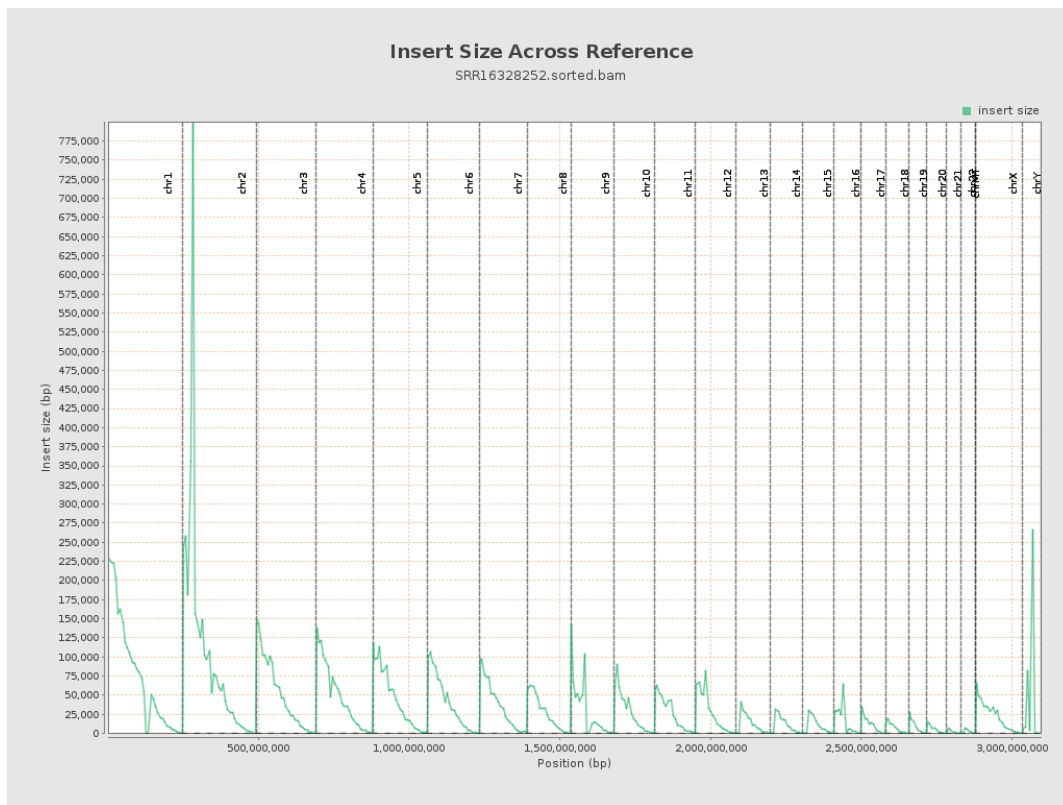
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

