

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/19 14:24:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16328242.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_SRR16328242 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16328242_1.fastq.gz SRR16328242_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Feb 19 14:24:09 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16328242.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	342,502,082
Mapped reads	309,530,403 / 90.37%
Unmapped reads	32,971,679 / 9.63%
Mapped paired reads	309,530,403 / 90.37%
Mapped reads, first in pair	156,918,575 / 45.82%
Mapped reads, second in pair	152,611,828 / 44.56%
Mapped reads, both in pair	304,244,078 / 88.83%
Mapped reads, singletons	5,286,325 / 1.54%
Secondary alignments	0
Supplementary alignments	15,056,168 / 4.4%
Read min/max/mean length	30 / 150 / 152.18
Duplicated reads (estimated)	112,386,699 / 32.81%
Duplication rate	29.94%
Clipped reads	206,964,088 / 60.43%

2.2. ACGT Content

Number/percentage of A's	12,470,329,978 / 29.2%
Number/percentage of C's	8,867,230,831 / 20.76%
Number/percentage of T's	12,416,933,113 / 29.07%
Number/percentage of G's	8,953,402,333 / 20.96%
Number/percentage of N's	3,045,979 / 0.01%

GC Percentage	41.72%
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2.3. Coverage

Mean	13.809
Standard Deviation	155.8986

2.4. Mapping Quality

Mean Mapping Quality	53.45
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2.5. Insert size

Mean	172,646.54
Standard Deviation	3,977,982.18
P25/Median/P75	229 / 323 / 463

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	451,397,963
Insertions	7,631,456
Mapped reads with at least one insertion	2.33%
Deletions	20,305,538
Mapped reads with at least one deletion	6.27%
Homopolymer indels	44.16%

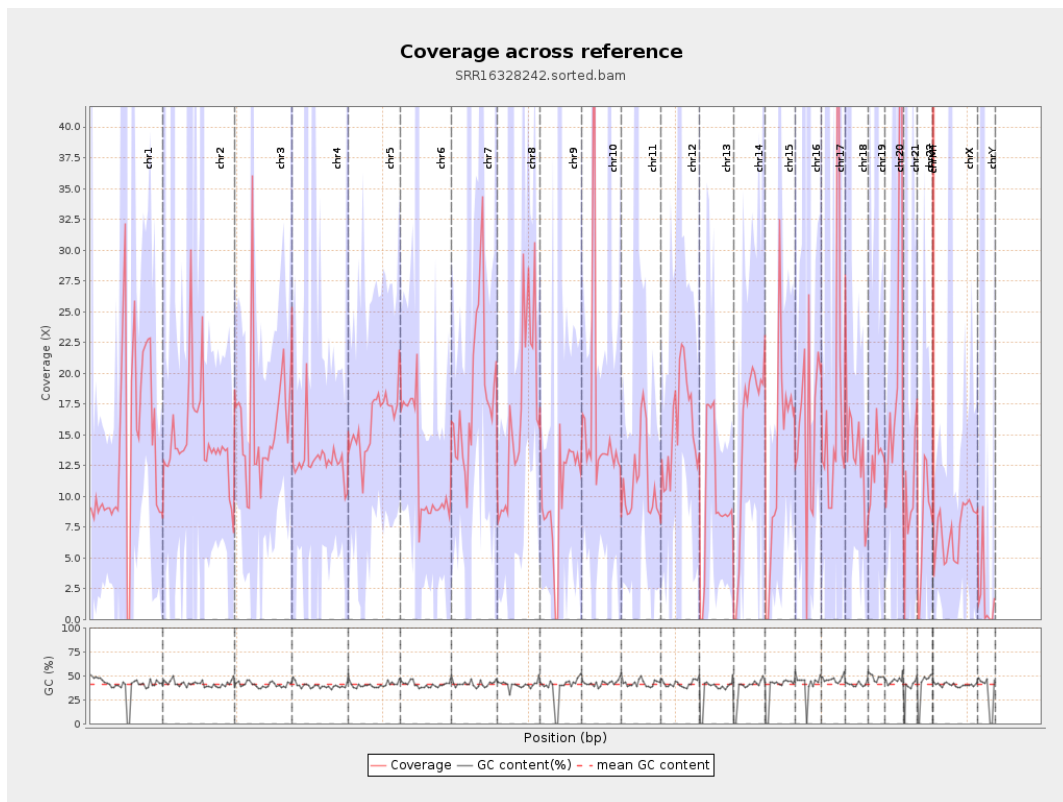
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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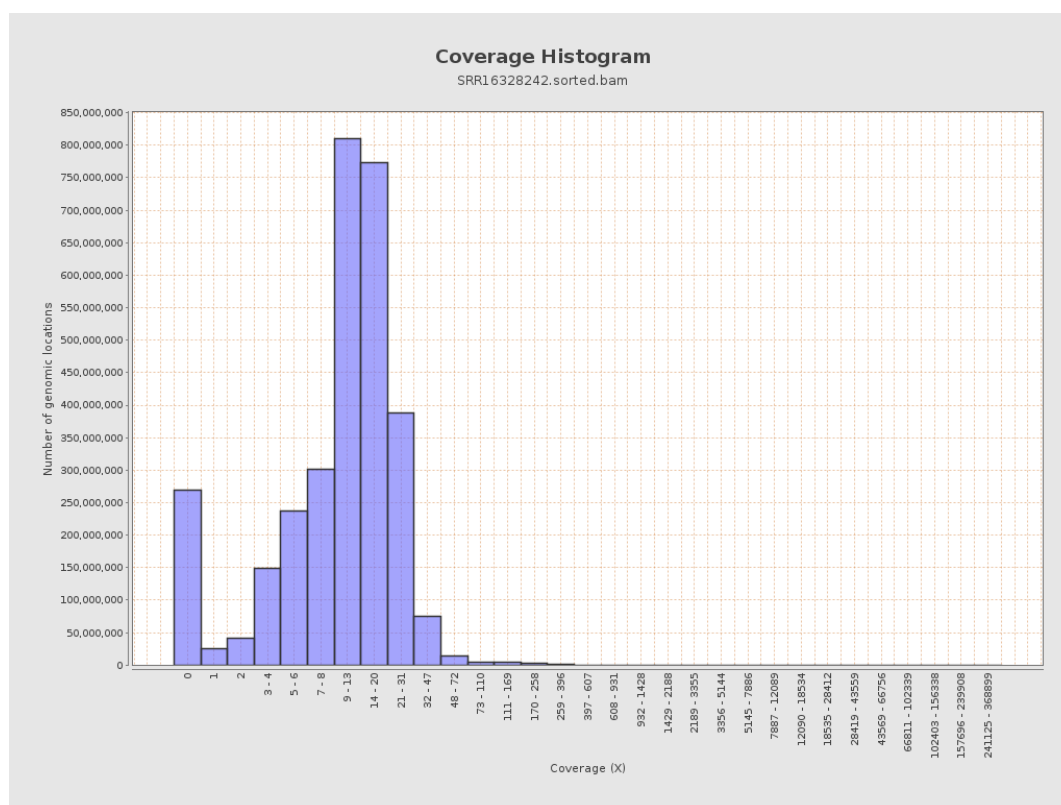
		bases	coverage	deviation
chr1	249250621	3383812139	13.5759	330.2043
chr2	243199373	3585158678	14.7416	144.3762
chr3	198022430	3132100044	15.8169	19.3565
chr4	191154276	2474843332	12.9468	81.4833
chr5	180915260	2925777941	16.1721	10.8187
chr6	171115067	2060426488	12.0412	52.6487
chr7	159138663	2935101023	18.4437	87.5965
chr8	146364022	2464198398	16.8361	290.1406
chr9	141213431	1415862574	10.0264	133.8436
chr10	135534747	2132069448	15.7308	309.2112
chr11	135006516	1498024552	11.0959	49.6892
chr12	133851895	2117058049	15.8164	27.7567
chr13	115169878	1105402802	9.598	10.2407
chr14	107349540	1594055834	14.8492	15.6668
chr15	102531392	1344417010	13.1122	14.6937
chr16	90354753	1405309649	15.5532	117.1261
chr17	81195210	1478803781	18.2129	65.7544
chr18	78077248	1063542347	13.6217	134.4681
chr19	59128983	758737347	12.8319	188.0822
chr20	63025520	1460155585	23.1677	46.3111
chr21	48129895	493279642	10.2489	42.2241
chr22	51304566	393355061	7.6671	12.7474
chrMT	16571	298227712	17,996.9653	4,184.6469
chrX	155270560	1119460128	7.2097	20.0701

chrY	59373566	109319276	1.8412	96.9166
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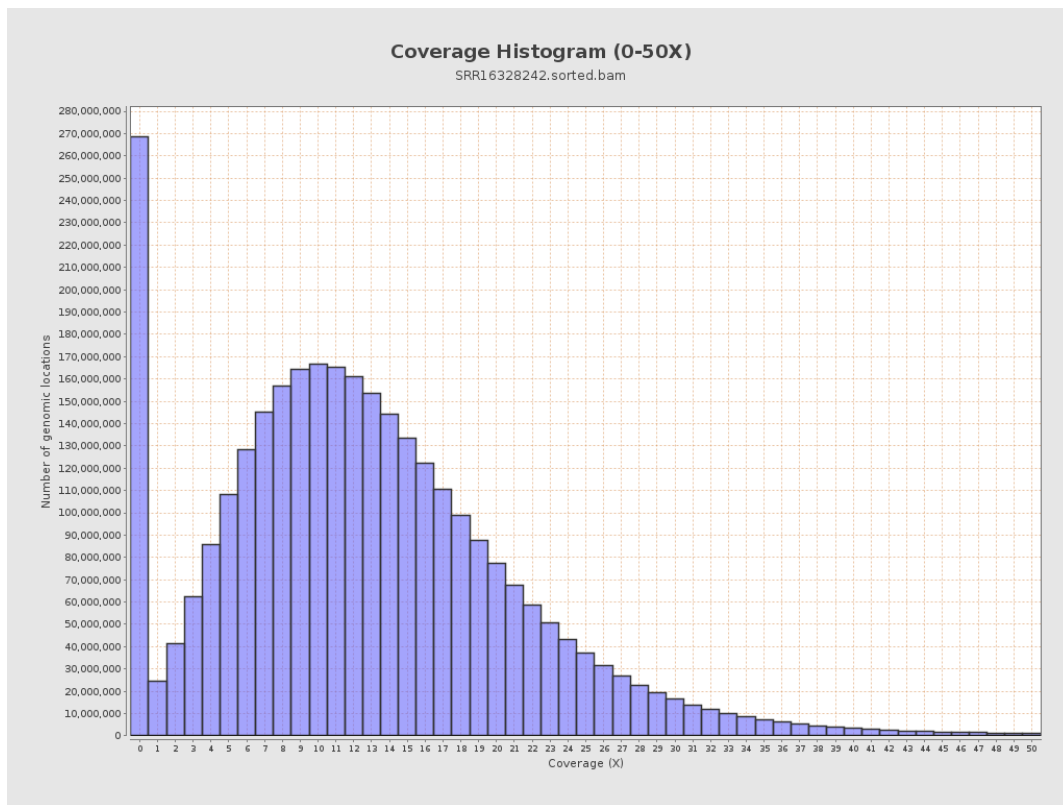
3. Results : Coverage across reference



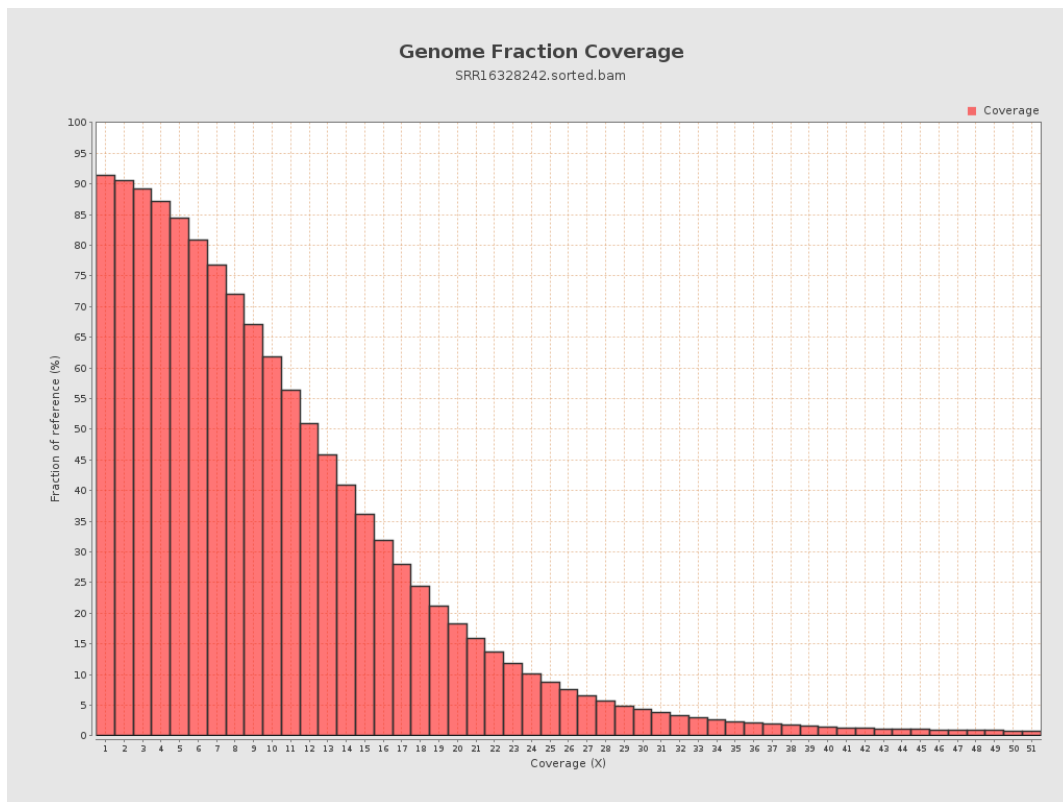
4. Results : Coverage Histogram



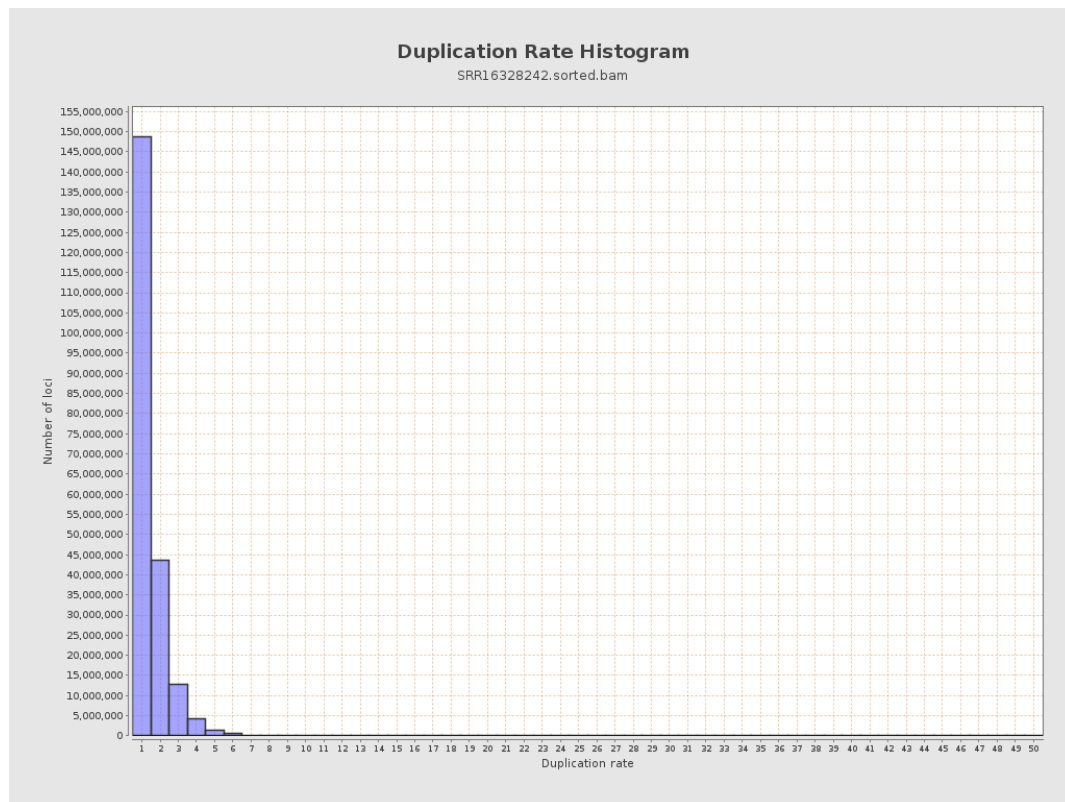
5. Results : Coverage Histogram (0-50X)



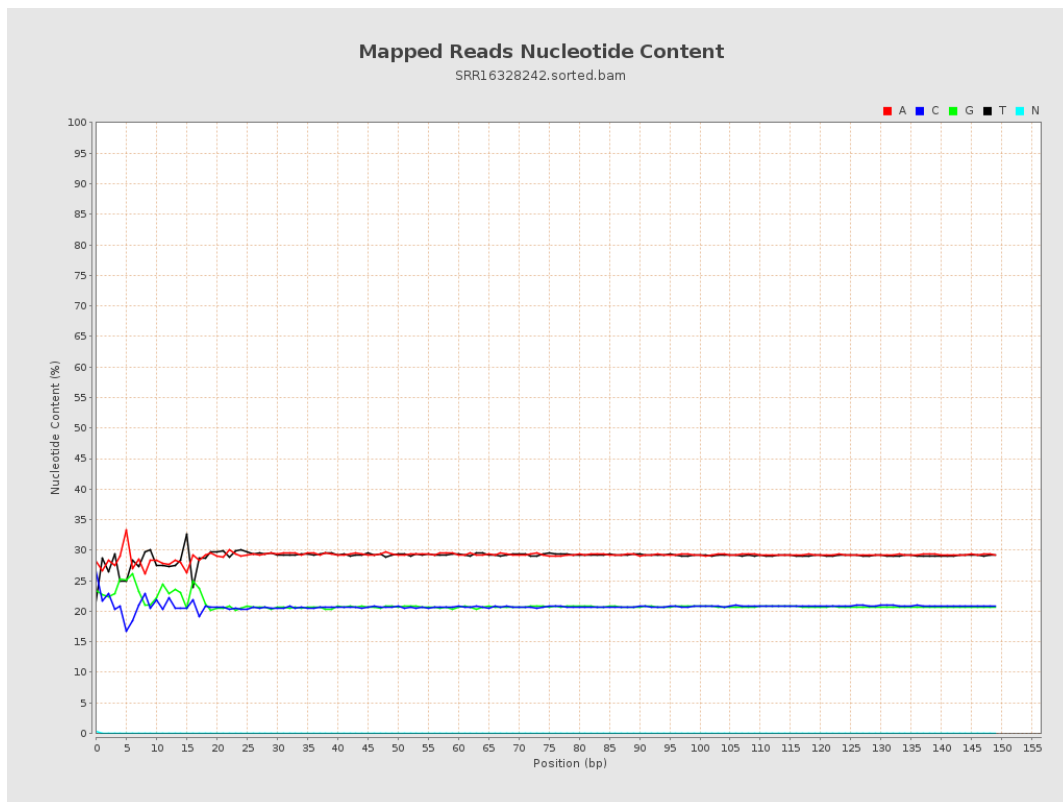
6. Results : Genome Fraction Coverage



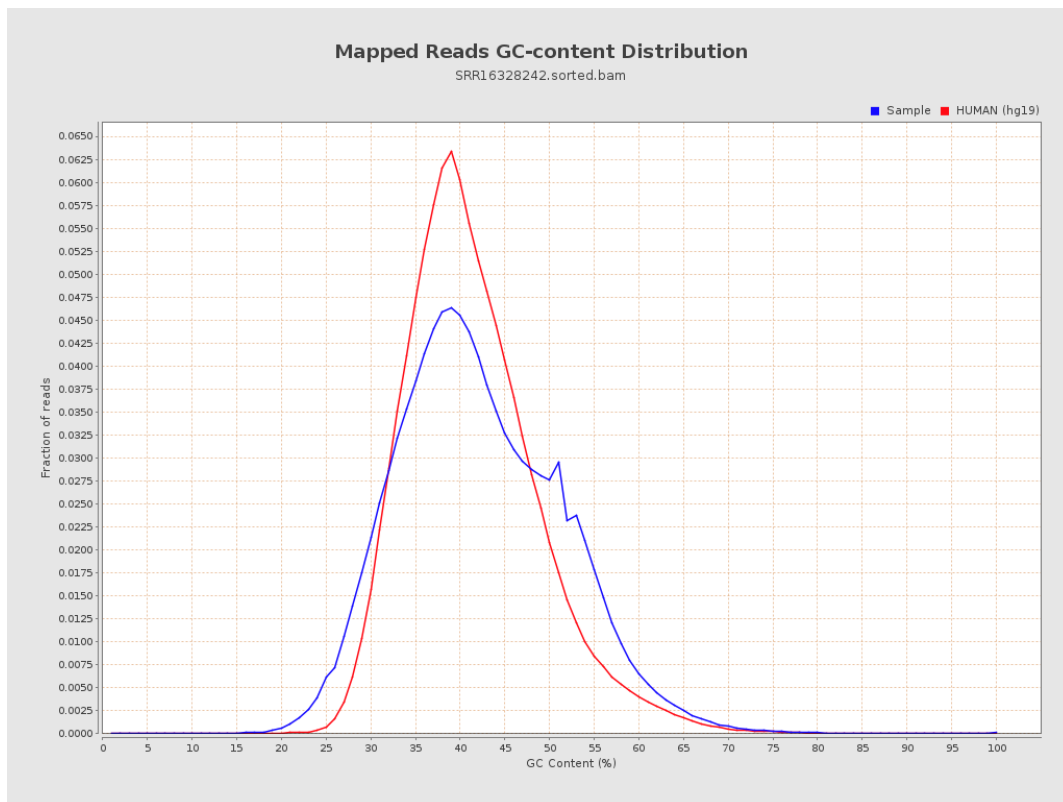
7. Results : Duplication Rate Histogram



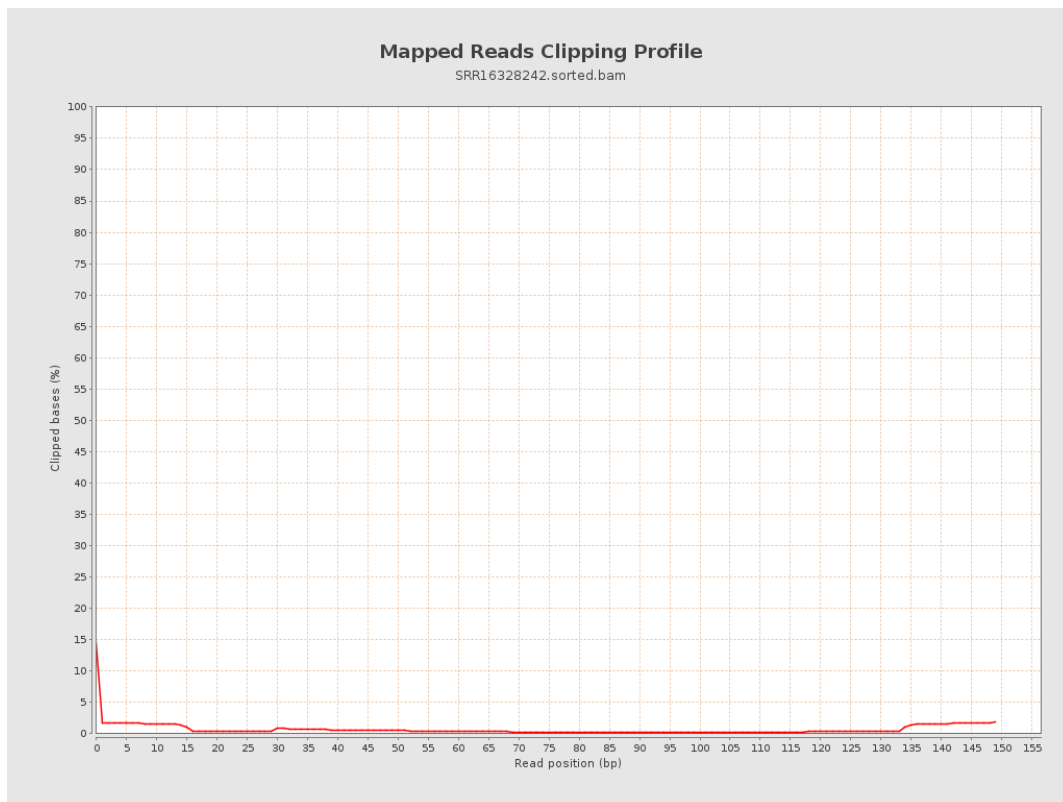
8. Results : Mapped Reads Nucleotide Content



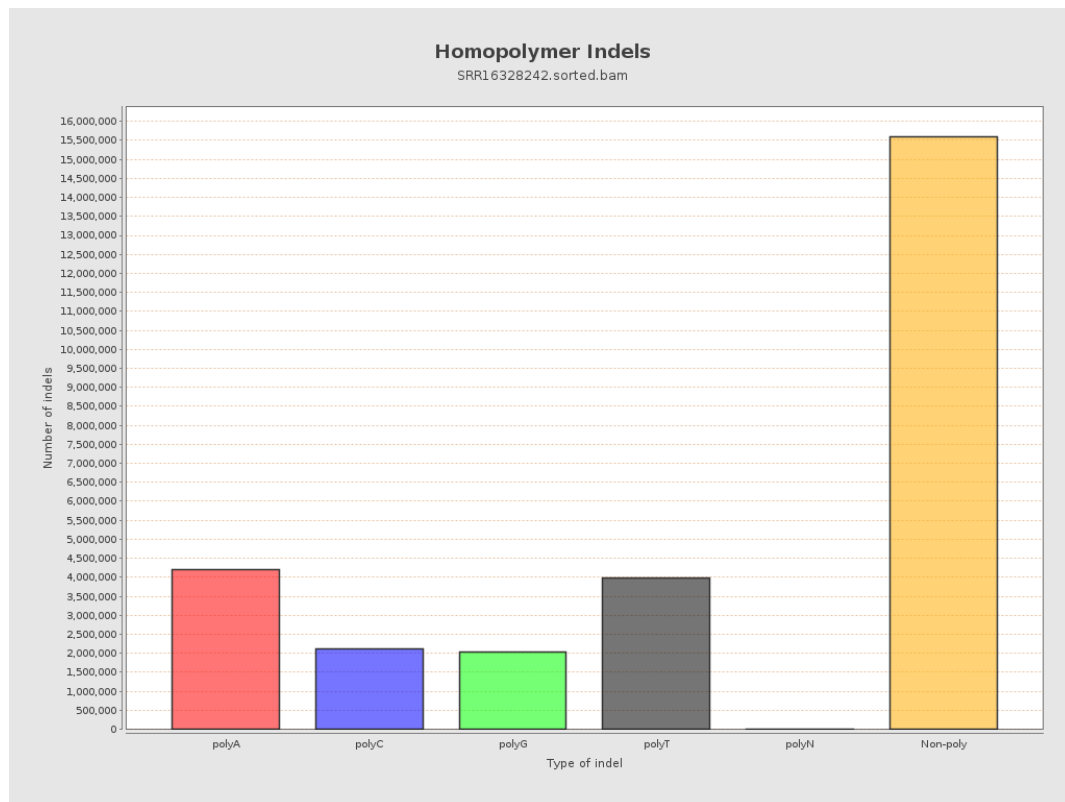
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



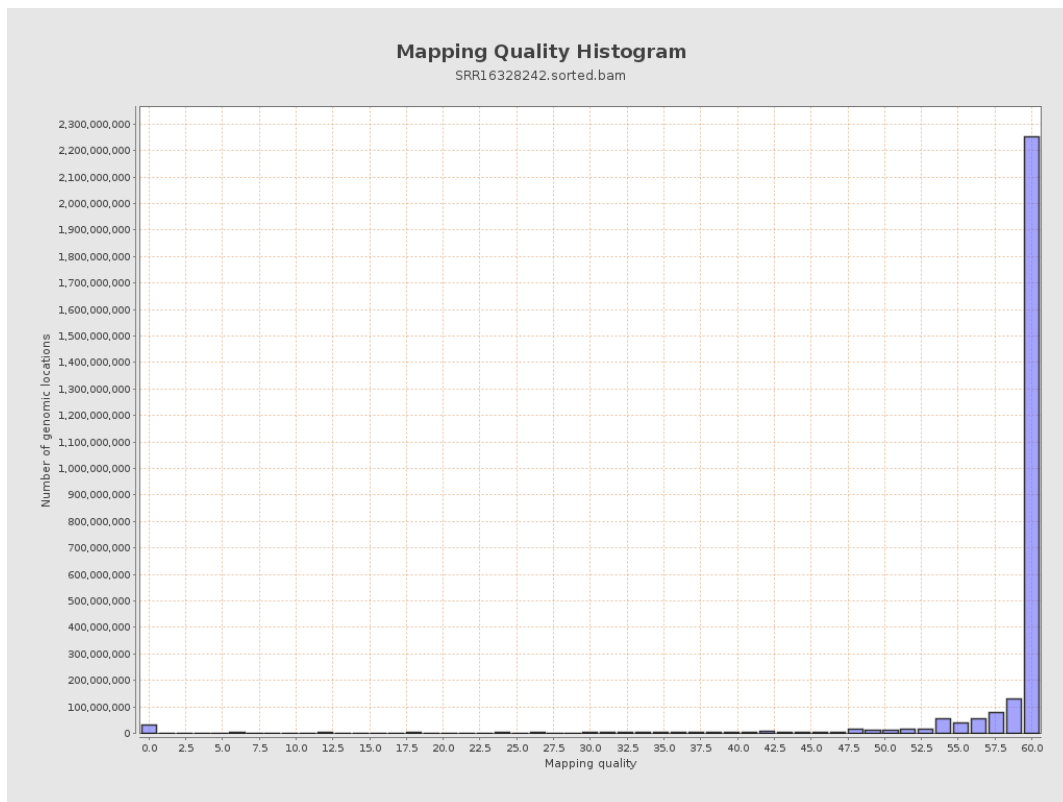
11. Results : Homopolymer Indels



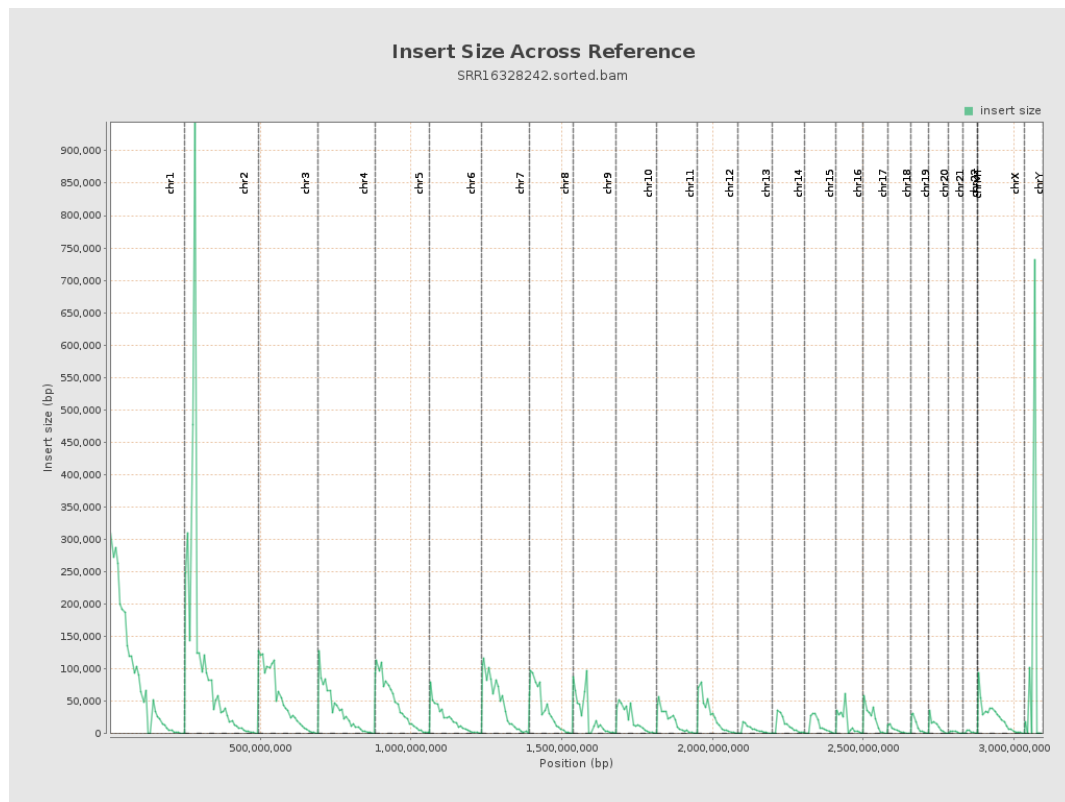
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

