

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 09:27:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618568.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_SRR618568 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618568_1.fastq.gz SRR618568_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 09:27:11 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618568.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	239,567,132
Mapped reads	231,060,690 / 96.45%
Unmapped reads	8,506,442 / 3.55%
Mapped paired reads	231,060,690 / 96.45%
Mapped reads, first in pair	116,120,505 / 48.47%
Mapped reads, second in pair	114,940,185 / 47.98%
Mapped reads, both in pair	228,036,496 / 95.19%
Mapped reads, singletons	3,024,194 / 1.26%
Secondary alignments	0
Supplementary alignments	2,464,696 / 1.03%
Read min/max/mean length	30 / 100 / 100.43
Duplicated reads (estimated)	95,472,687 / 39.85%
Duplication rate	33.48%
Clipped reads	56,612,144 / 23.63%

2.2. ACGT Content

Number/percentage of A's	5,830,241,817 / 26.79%
Number/percentage of C's	4,831,680,507 / 22.2%
Number/percentage of T's	5,886,474,147 / 27.05%
Number/percentage of G's	5,209,485,882 / 23.94%
Number/percentage of N's	2,296,544 / 0.01%

GC Percentage	46.14%
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2.3. Coverage

Mean	7.034
Standard Deviation	24.4325

2.4. Mapping Quality

Mean Mapping Quality	53.56
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2.5. Insert size

Mean	130,736.49
Standard Deviation	3,581,372.96
P25/Median/P75	169 / 189 / 213

2.6. Mismatches and indels

General error rate	1.34%
Mismatches	285,084,974
Insertions	3,637,363
Mapped reads with at least one insertion	1.55%
Deletions	10,775,057
Mapped reads with at least one deletion	4.55%
Homopolymer indels	52.35%

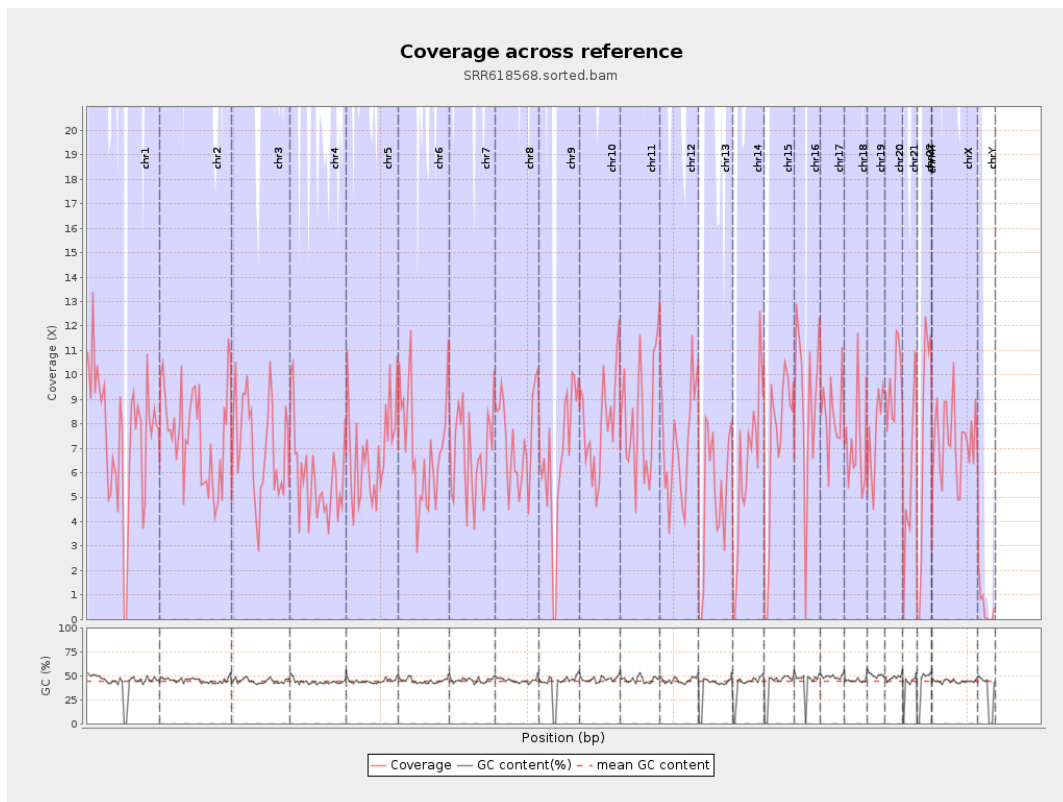
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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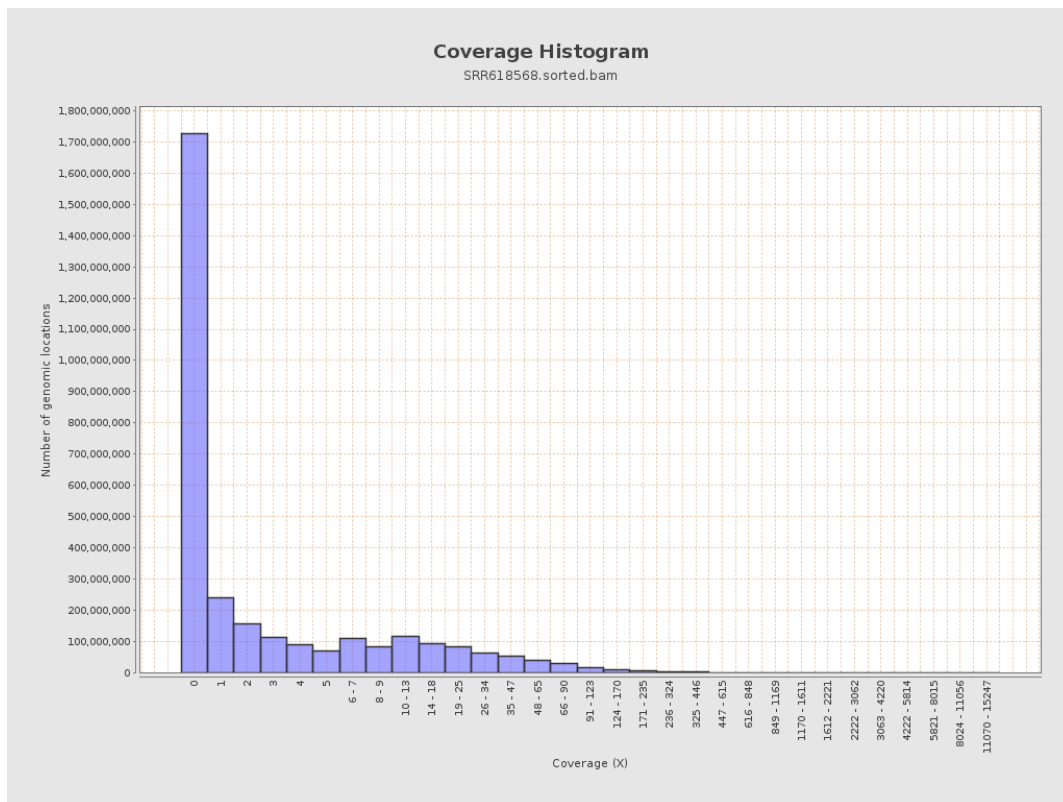
		bases	coverage	deviation
chr1	249250621	1870661589	7.5051	29.6397
chr2	243199373	1839417646	7.5634	26.5437
chr3	198022430	1406700316	7.1037	21.0836
chr4	191154276	1095691189	5.732	19.6535
chr5	180915260	1241379016	6.8617	20.5036
chr6	171115067	1197071530	6.9957	21.7118
chr7	159138663	1072725423	6.7408	21.2604
chr8	146364022	1068964092	7.3035	21.9074
chr9	141213431	926473759	6.5608	26.0049
chr10	135534747	1085139786	8.0064	24.368
chr11	135006516	1110257351	8.2237	30.9329
chr12	133851895	959879263	7.1712	21.6178
chr13	115169878	585051078	5.0799	16.7478
chr14	107349540	665742432	6.2016	20.7197
chr15	102531392	724600214	7.0671	23.0949
chr16	90354753	799568030	8.8492	35.7026
chr17	81195210	675299097	8.317	26.5913
chr18	78077248	563145982	7.2127	26.4472
chr19	59128983	452861768	7.6589	28.06
chr20	63025520	606484618	9.6228	28.225
chr21	48129895	286975384	5.9625	33.1037
chr22	51304566	378862175	7.3846	27.1302
chrMT	16571	45229	2.7294	7.3238
chrX	155270560	1132309183	7.2925	21.0413

chrY	59373566	29675130	0.4998	11.6531
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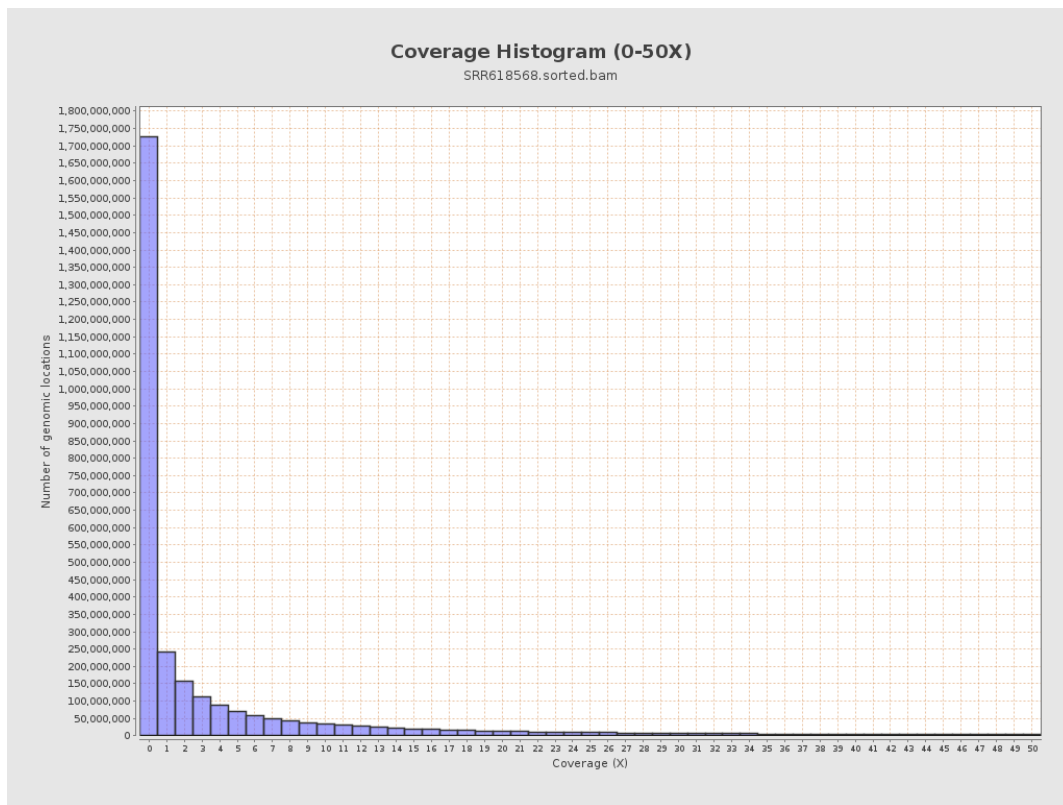
3. Results : Coverage across reference



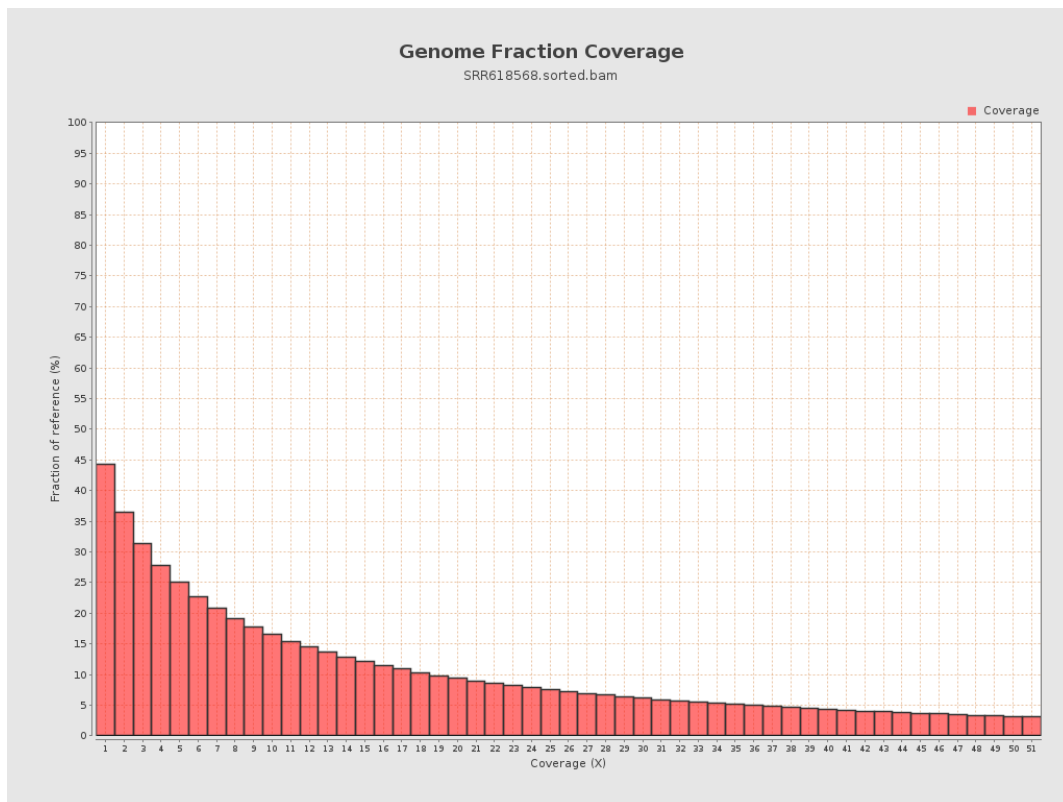
4. Results : Coverage Histogram



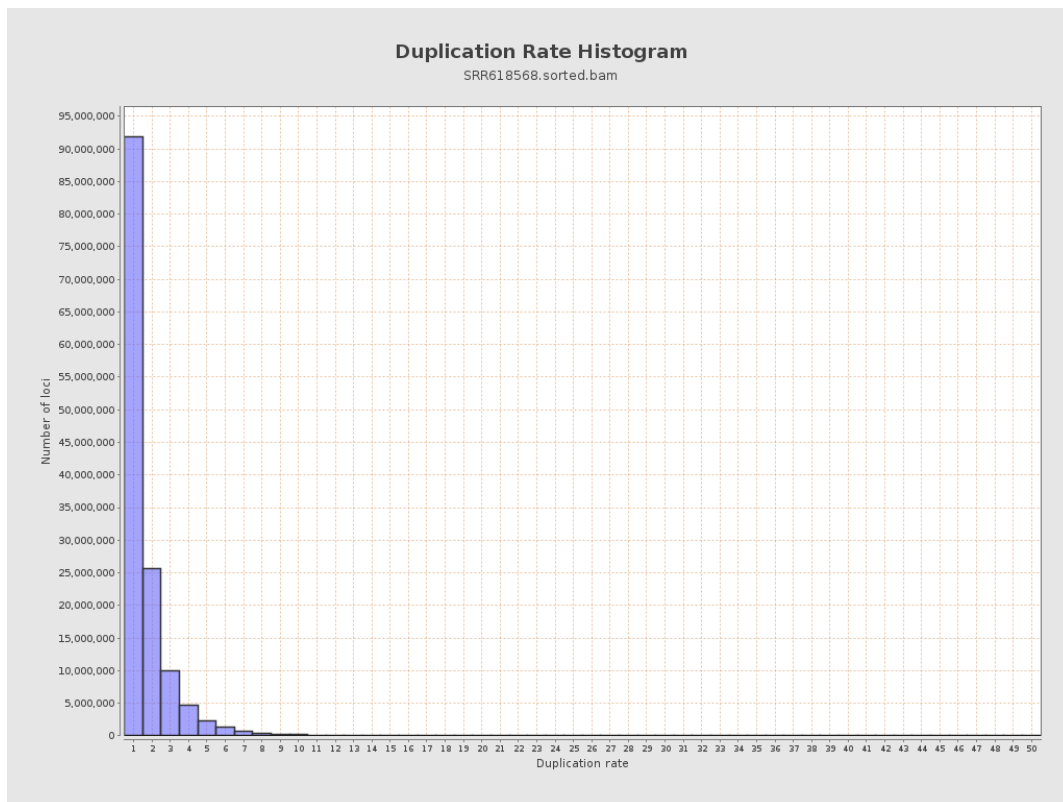
5. Results : Coverage Histogram (0-50X)



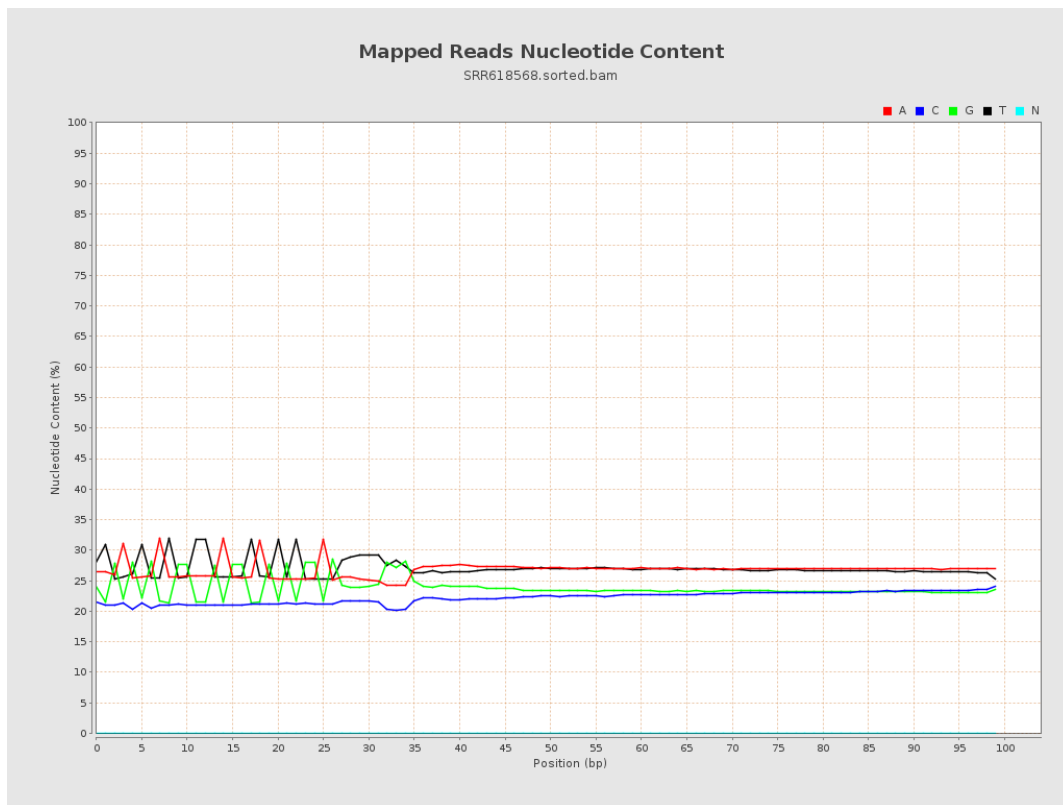
6. Results : Genome Fraction Coverage



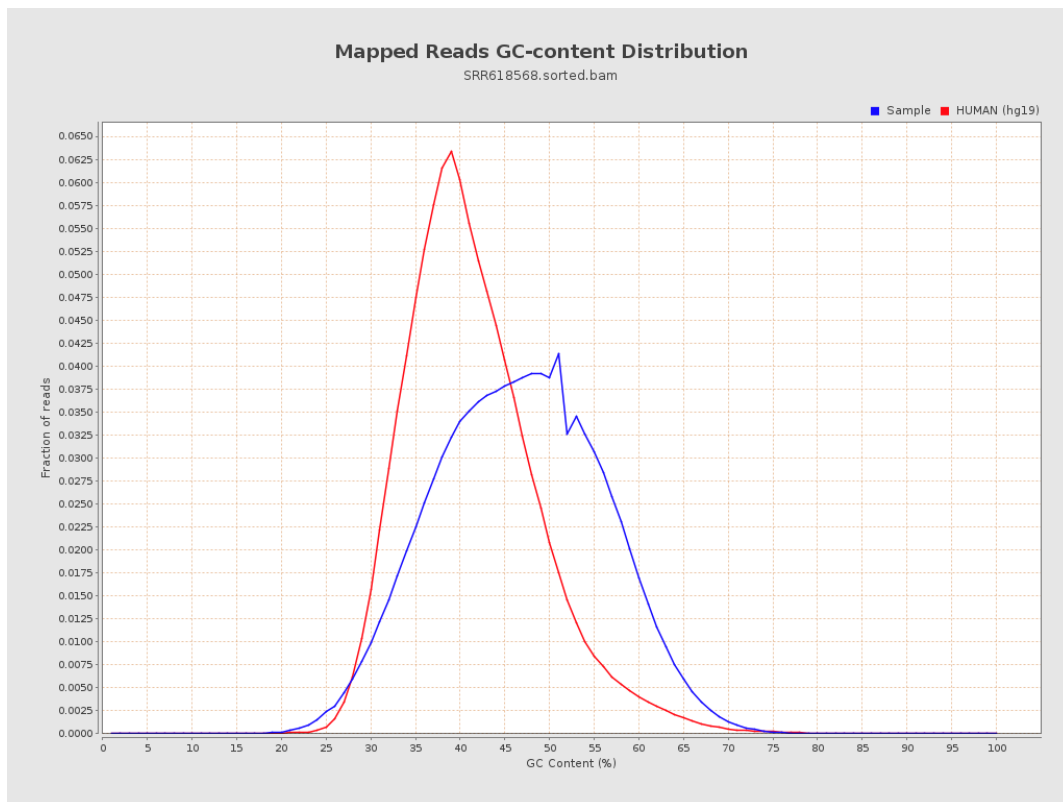
7. Results : Duplication Rate Histogram



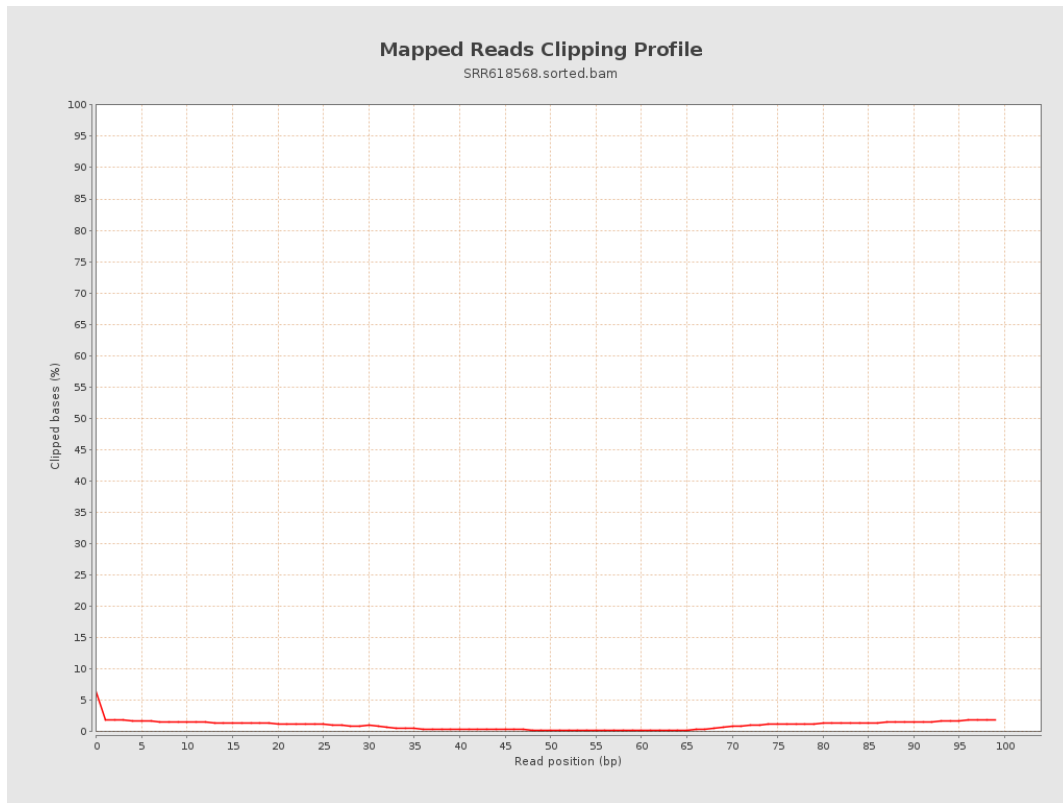
8. Results : Mapped Reads Nucleotide Content



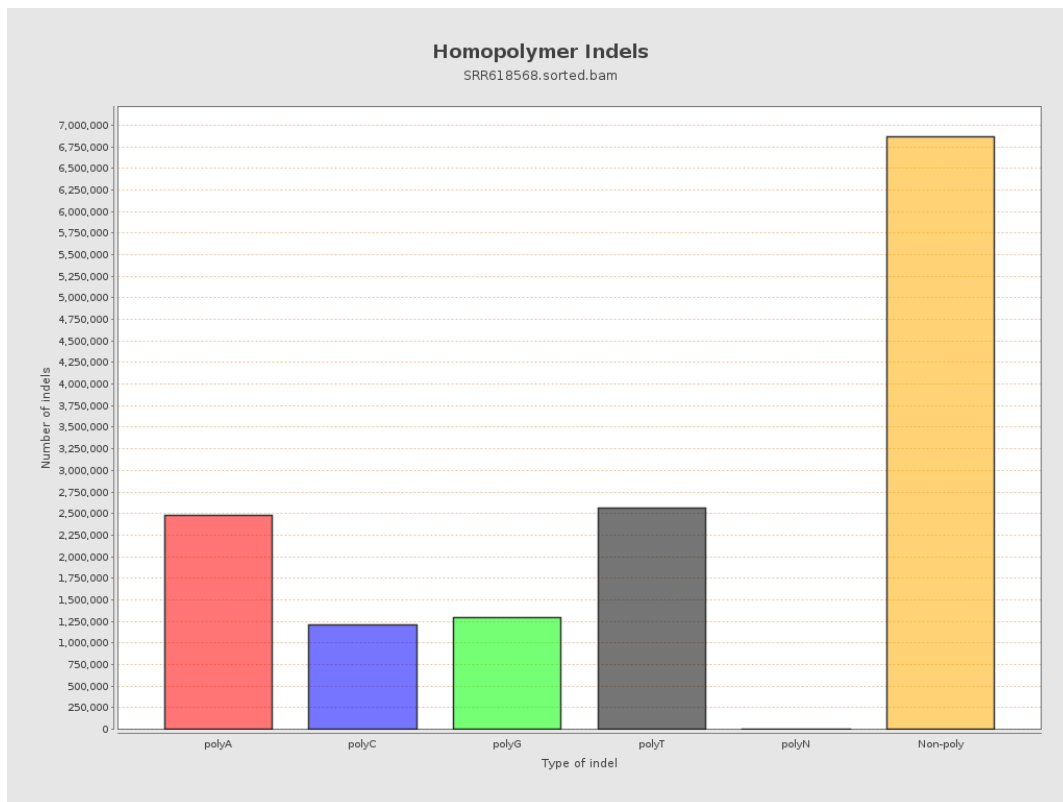
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



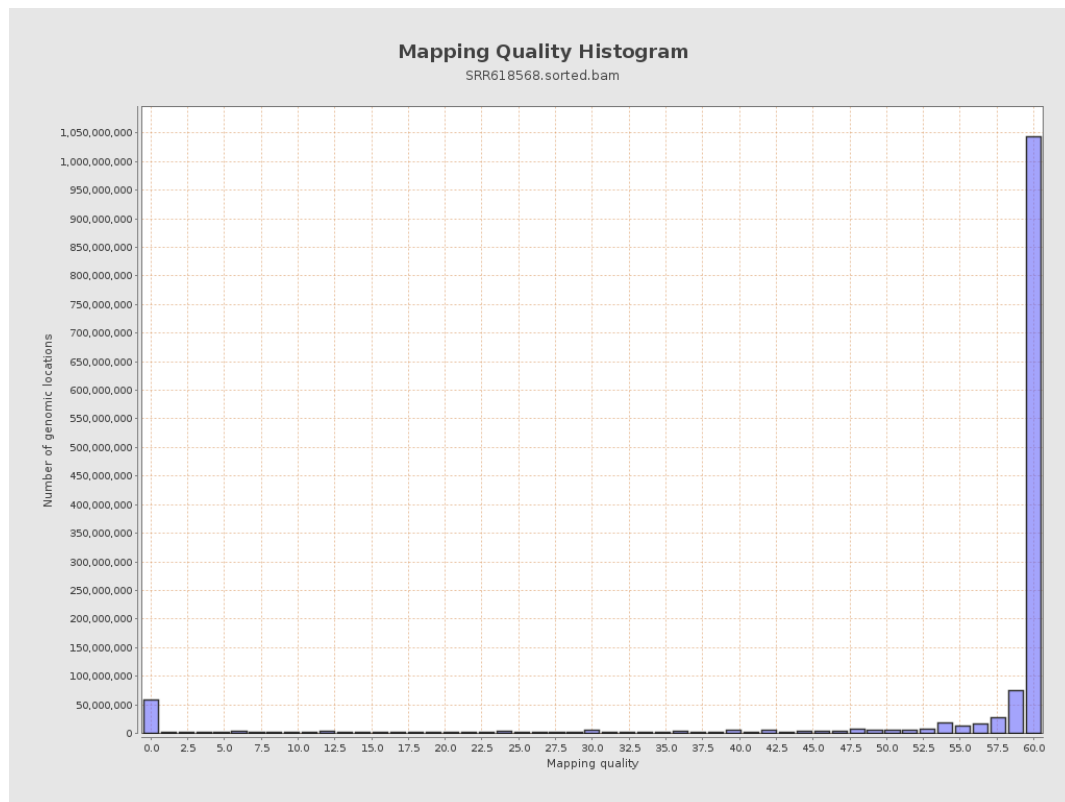
11. Results : Homopolymer Indels



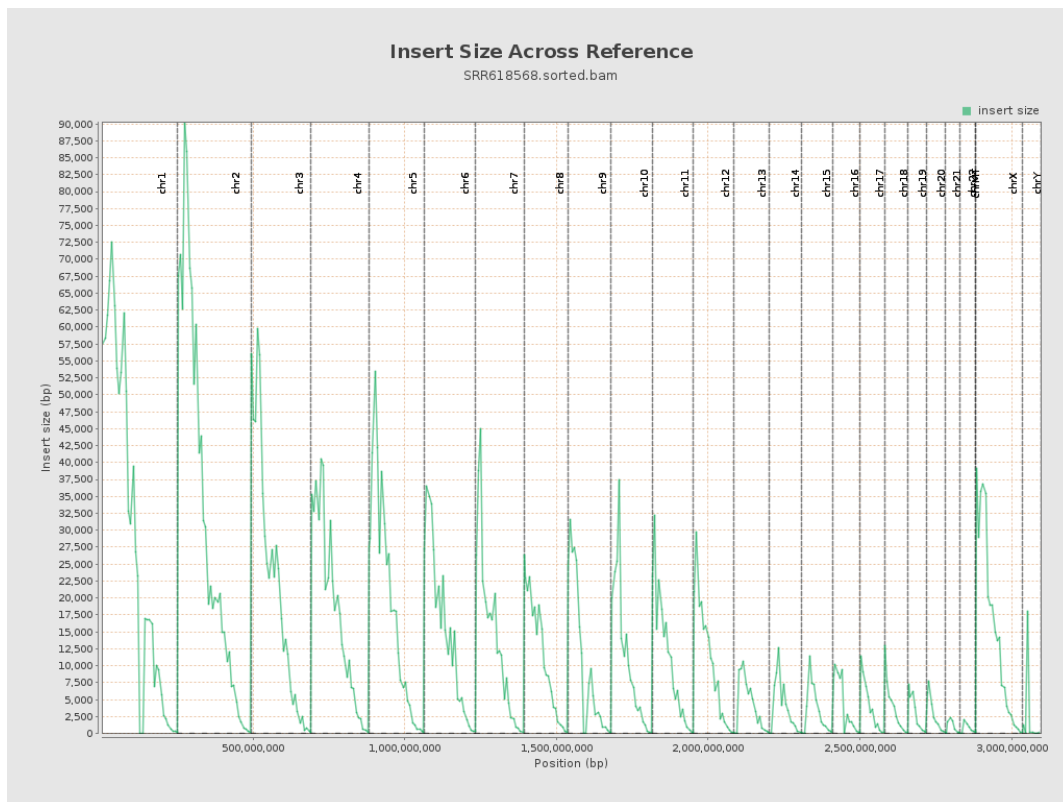
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

