

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 17:18:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618570.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_SRR618570 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618570_1.fastq.gz SRR618570_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 17:18:41 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618570.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	216,922,566
Mapped reads	210,412,403 / 97%
Unmapped reads	6,510,163 / 3%
Mapped paired reads	210,412,403 / 97%
Mapped reads, first in pair	105,602,901 / 48.68%
Mapped reads, second in pair	104,809,502 / 48.32%
Mapped reads, both in pair	208,080,656 / 95.92%
Mapped reads, singletons	2,331,747 / 1.07%
Secondary alignments	0
Supplementary alignments	2,212,451 / 1.02%
Read min/max/mean length	30 / 100 / 100.42
Duplicated reads (estimated)	81,121,881 / 37.4%
Duplication rate	31.54%
Clipped reads	49,854,218 / 22.98%

2.2. ACGT Content

Number/percentage of A's	5,263,947,989 / 26.5%
Number/percentage of C's	4,480,365,979 / 22.55%
Number/percentage of T's	5,312,462,377 / 26.74%
Number/percentage of G's	4,808,665,717 / 24.2%
Number/percentage of N's	1,956,111 / 0.01%

GC Percentage	46.76%
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2.3. Coverage

Mean	6.4221
Standard Deviation	24.5232

2.4. Mapping Quality

Mean Mapping Quality	52.39
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2.5. Insert size

Mean	122,946.38
Standard Deviation	3,488,036.54
P25/Median/P75	166 / 185 / 206

2.6. Mismatches and indels

General error rate	1.31%
Mismatches	255,281,034
Insertions	3,336,007
Mapped reads with at least one insertion	1.56%
Deletions	9,795,690
Mapped reads with at least one deletion	4.54%
Homopolymer indels	52.03%

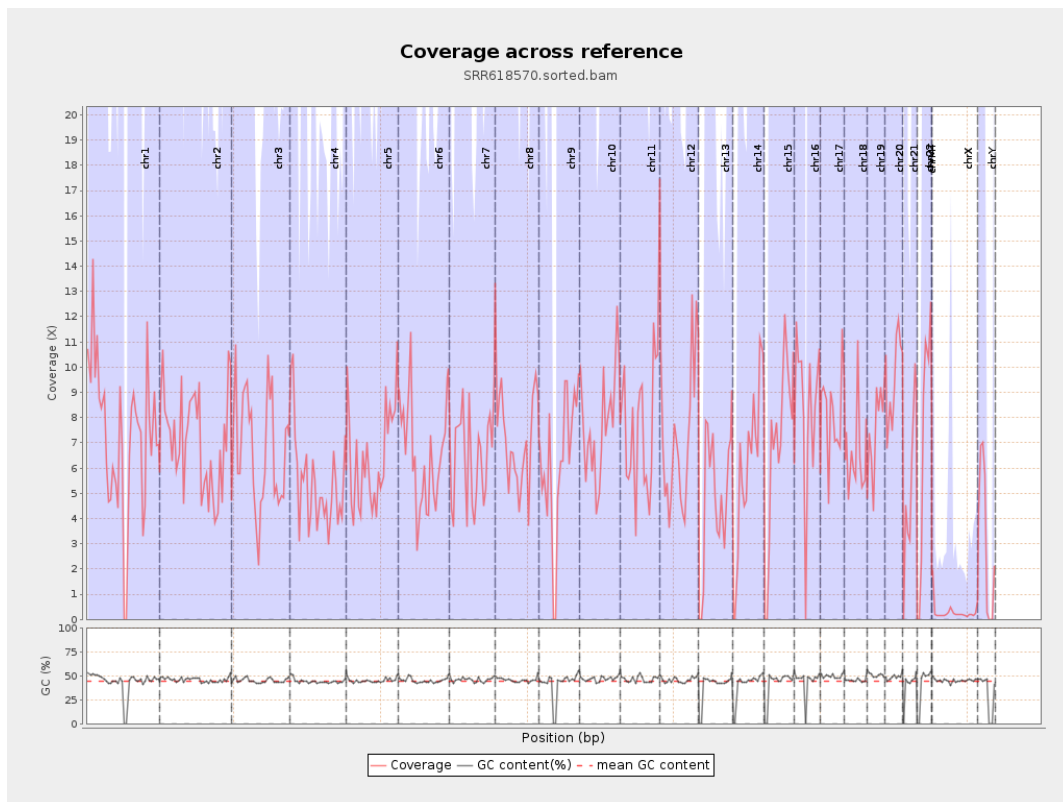
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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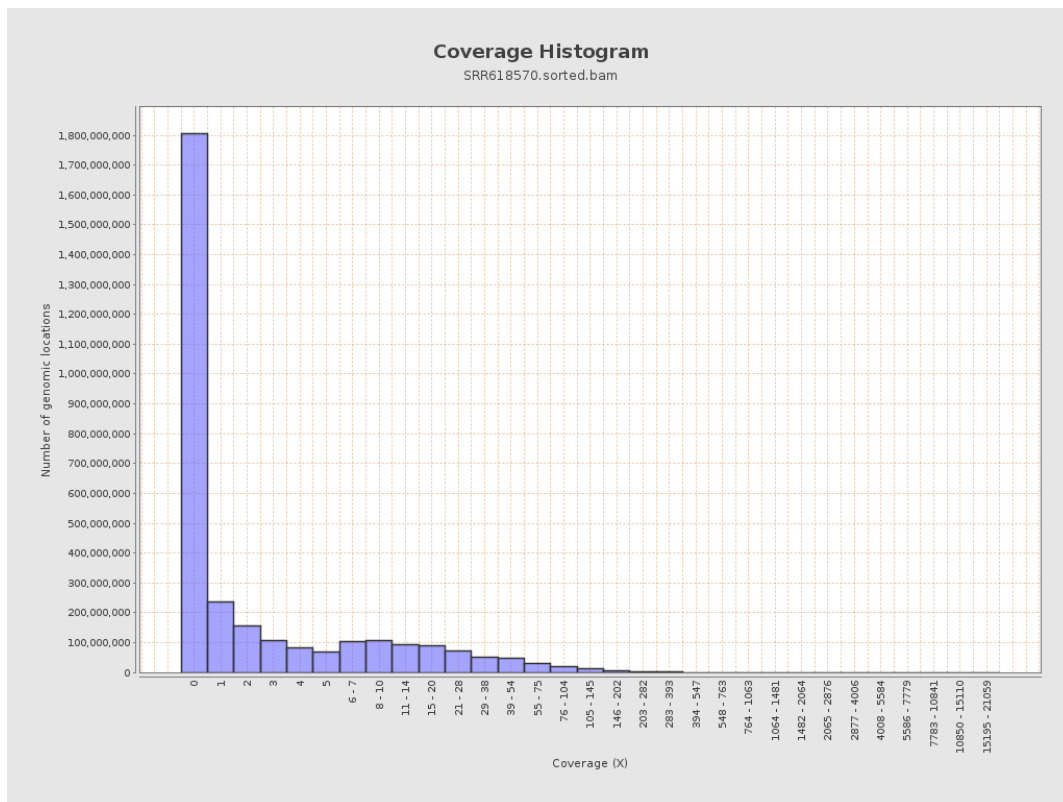
		bases	coverage	deviation
chr1	249250621	1813283054	7.2749	29.2523
chr2	243199373	1724282991	7.09	28.2501
chr3	198022430	1333751466	6.7354	20.6199
chr4	191154276	1027294843	5.3742	20.7454
chr5	180915260	1172389666	6.4803	20.2651
chr6	171115067	1115691729	6.5201	21.0906
chr7	159138663	1029068589	6.4665	20.7028
chr8	146364022	1024622394	7.0005	21.3471
chr9	141213431	884329682	6.2624	26.73
chr10	135534747	1050988181	7.7544	23.6884
chr11	135006516	1019880997	7.5543	27.3793
chr12	133851895	955563483	7.139	22.5057
chr13	115169878	546290148	4.7433	16.8478
chr14	107349540	646251234	6.0201	21.4809
chr15	102531392	701506912	6.8419	23.6817
chr16	90354753	747380380	8.2716	41.1356
chr17	81195210	666765491	8.2119	26.92
chr18	78077248	514033269	6.5836	27.8316
chr19	59128983	442521876	7.484	27.8677
chr20	63025520	603734395	9.5792	28.6513
chr21	48129895	261285573	5.4288	37.1685
chr22	51304566	365063647	7.1156	27.763
chrMT	16571	29647	1.7891	4.9518
chrX	155270560	41836973	0.2694	5.1912

chrY	59373566	193133445	3.2529	21.5491
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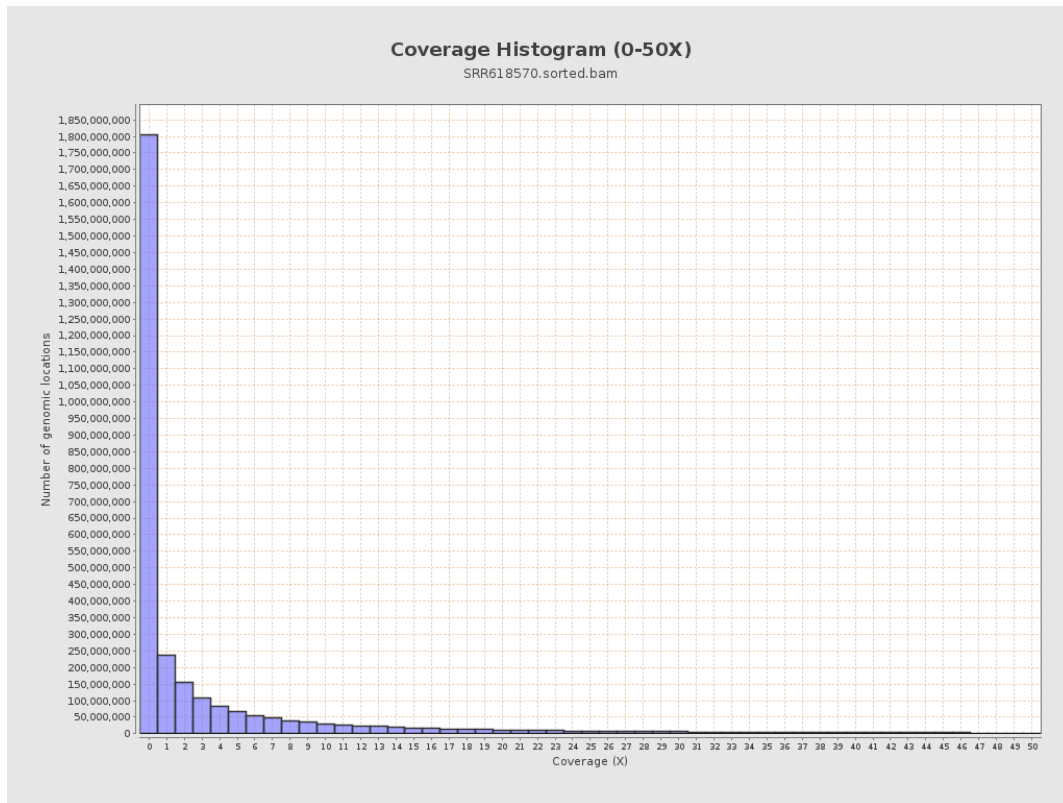
3. Results : Coverage across reference



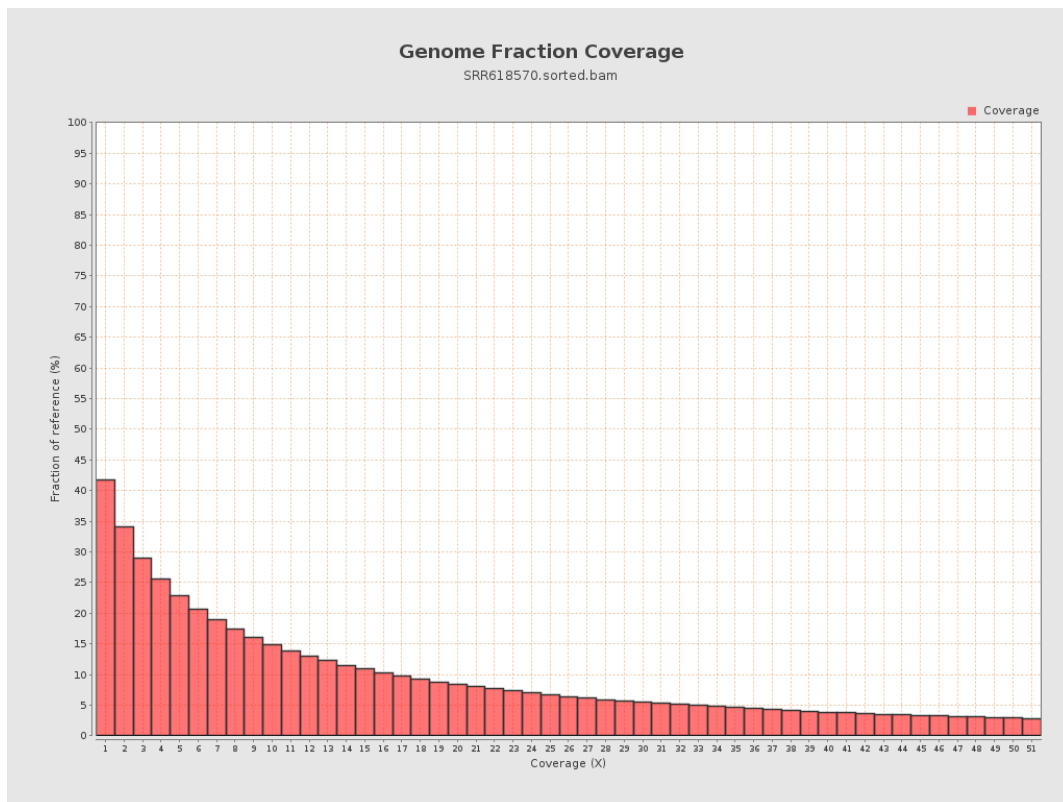
4. Results : Coverage Histogram



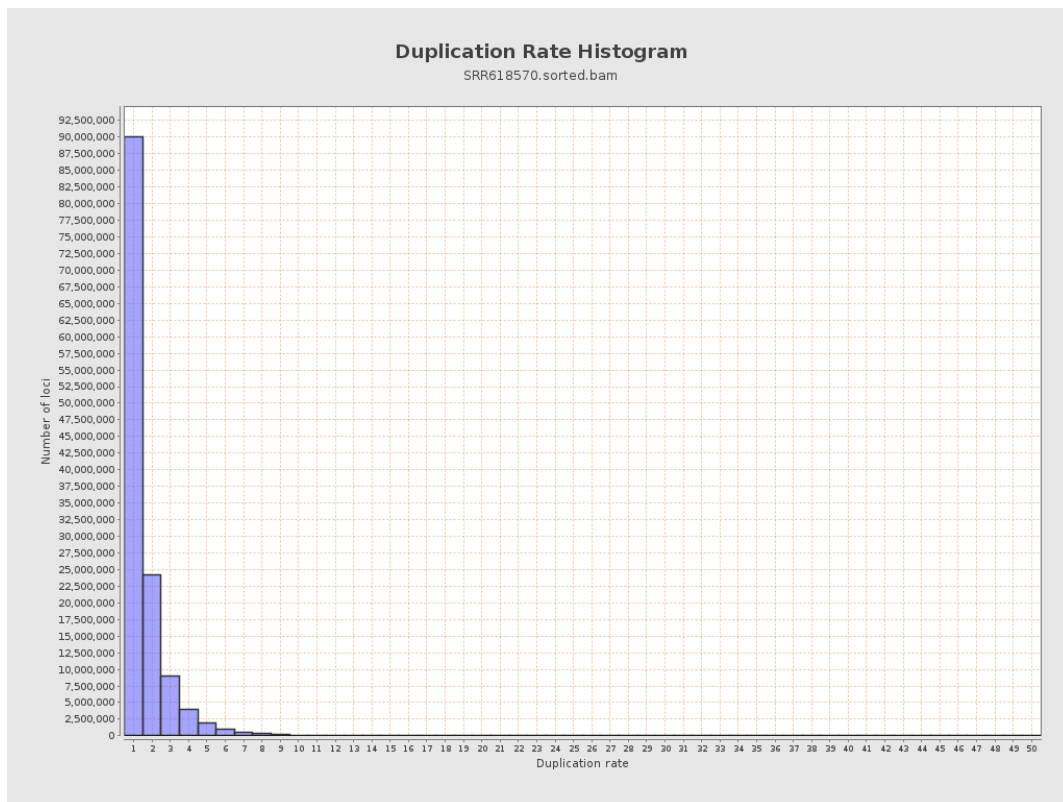
5. Results : Coverage Histogram (0-50X)



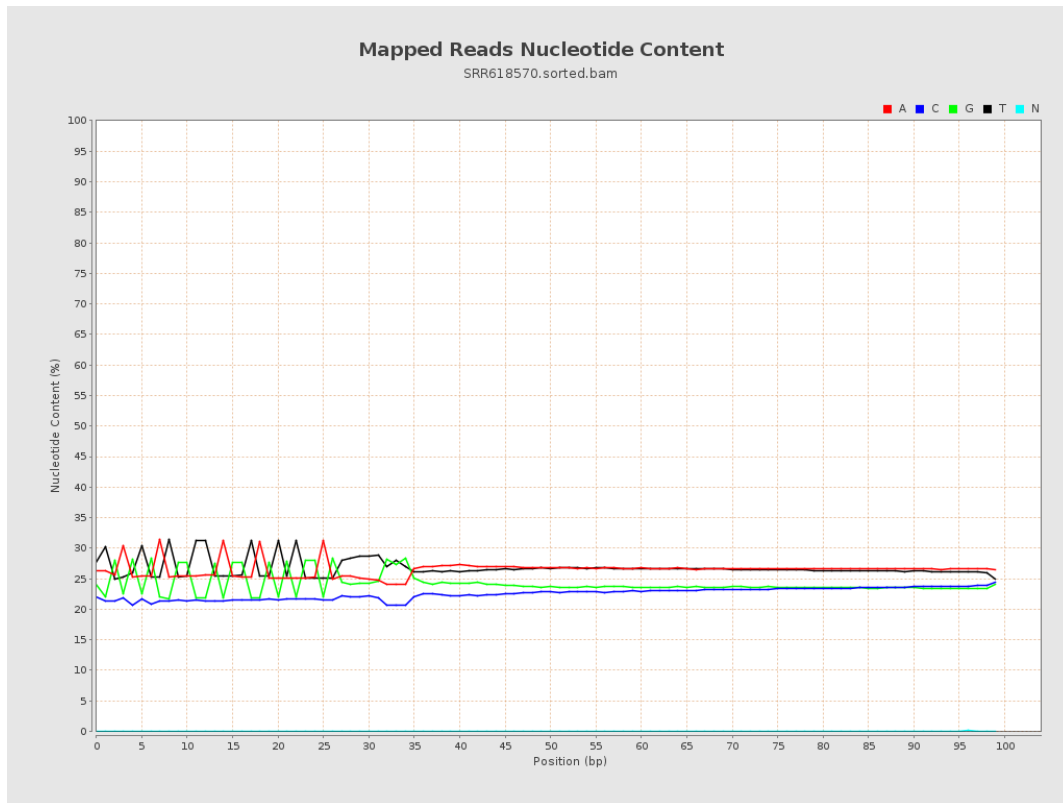
6. Results : Genome Fraction Coverage



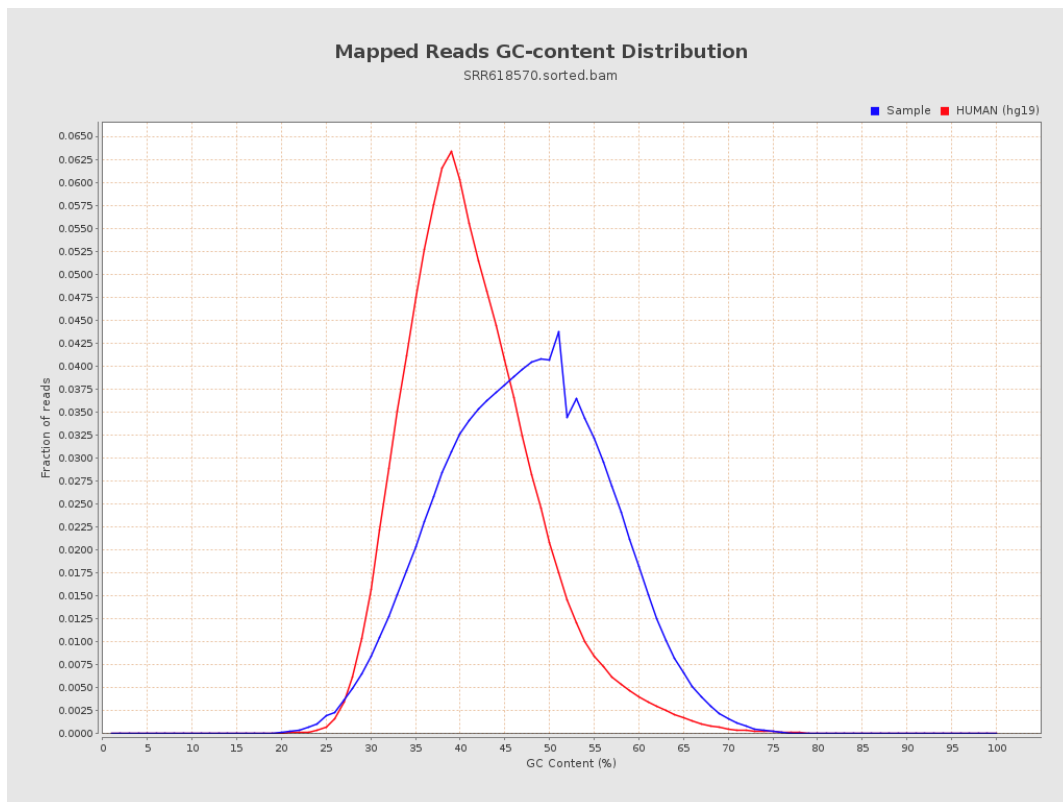
7. Results : Duplication Rate Histogram



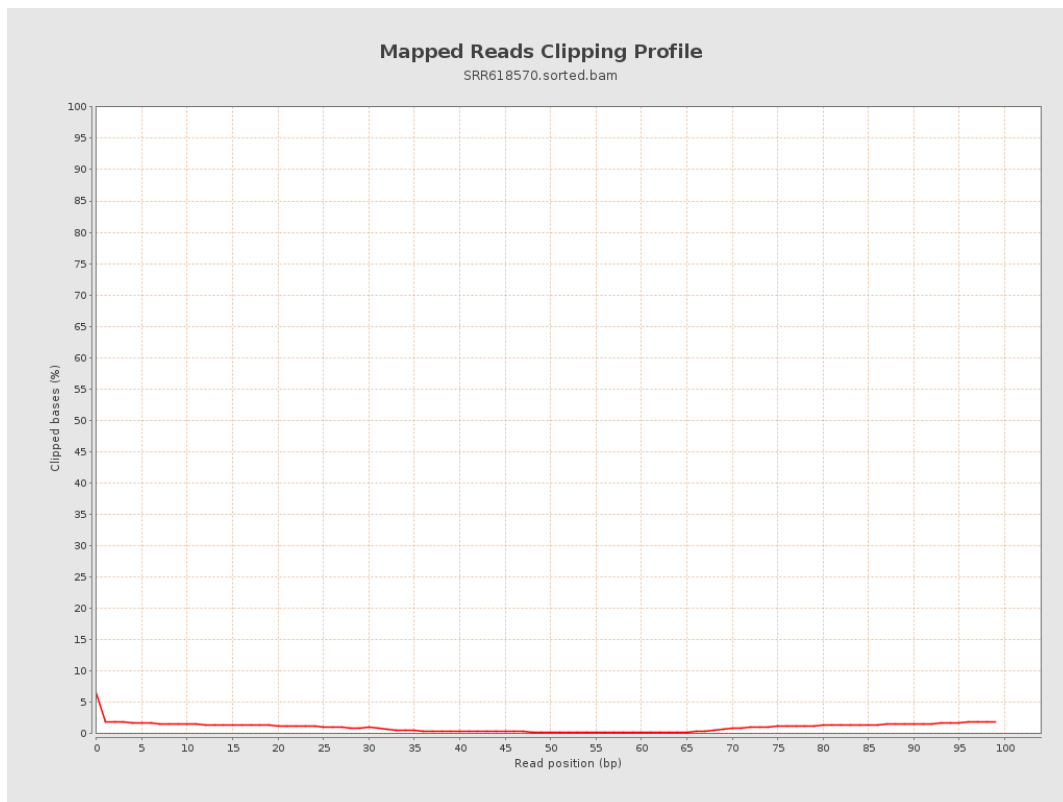
8. Results : Mapped Reads Nucleotide Content



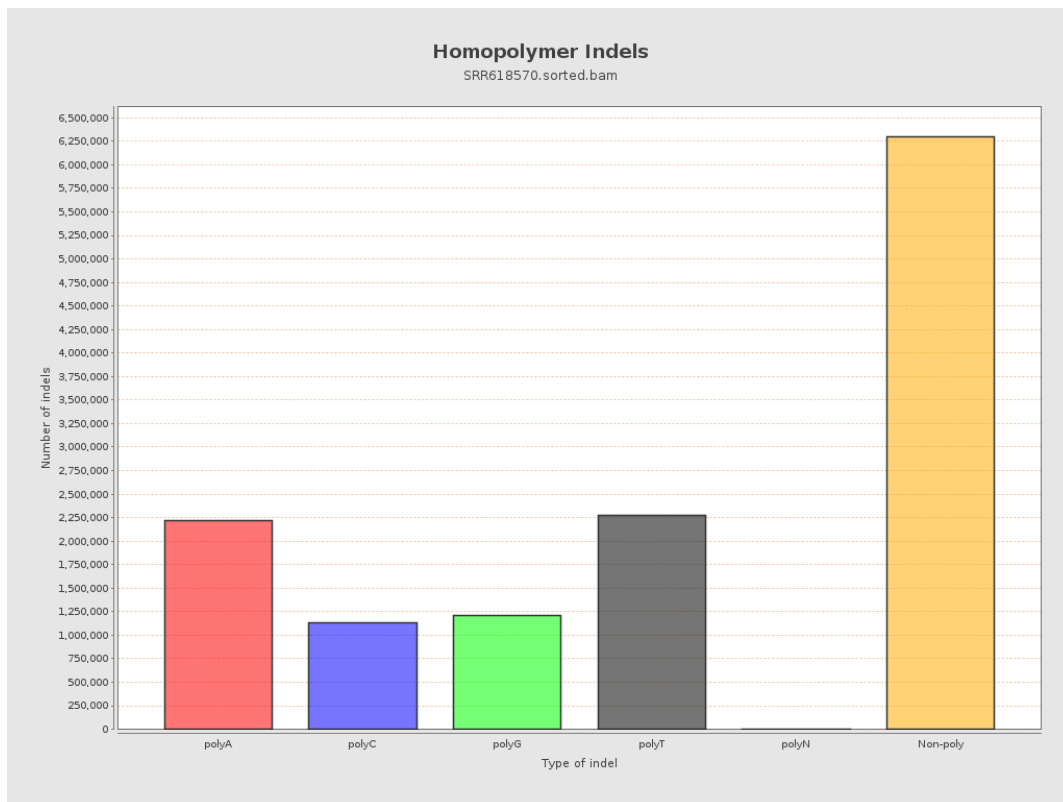
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



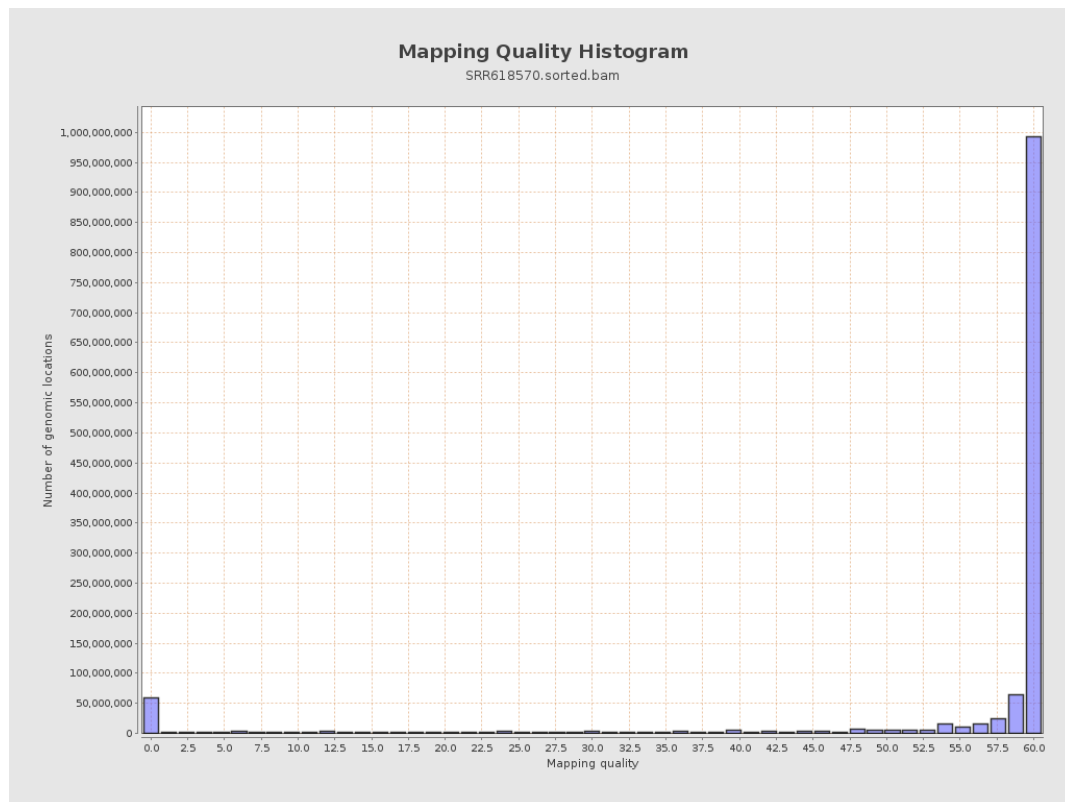
11. Results : Homopolymer Indels



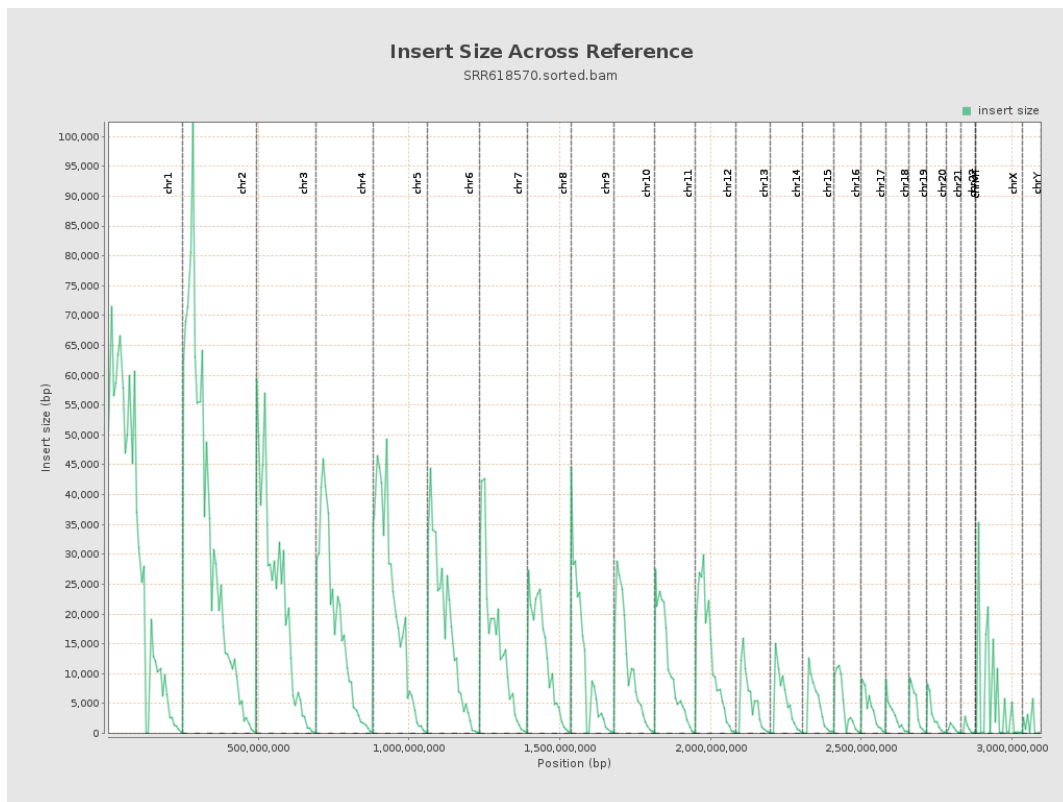
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

