

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 10:48:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618586.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_SRR618586 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618586_1.fastq.gz SRR618586_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 10:48:29 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618586.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	66,580,650
Mapped reads	61,360,840 / 92.16%
Unmapped reads	5,219,810 / 7.84%
Mapped paired reads	61,360,840 / 92.16%
Mapped reads, first in pair	31,007,564 / 46.57%
Mapped reads, second in pair	30,353,276 / 45.59%
Mapped reads, both in pair	60,037,472 / 90.17%
Mapped reads, singletons	1,323,368 / 1.99%
Secondary alignments	0
Supplementary alignments	244,903 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	14,524,529 / 21.81%
Duplication rate	20.13%
Clipped reads	15,744,801 / 23.65%

2.2. ACGT Content

Number/percentage of A's	1,562,650,884 / 27.36%
Number/percentage of C's	1,225,734,439 / 21.46%
Number/percentage of T's	1,587,882,090 / 27.8%
Number/percentage of G's	1,334,344,203 / 23.37%
Number/percentage of N's	217,649 / 0%

GC Percentage	44.83%
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2.3. Coverage

Mean	1.8461
Standard Deviation	6.7795

2.4. Mapping Quality

Mean Mapping Quality	51.96
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2.5. Insert size

Mean	71,113.24
Standard Deviation	2,655,411.39
P25/Median/P75	176 / 203 / 238

2.6. Mismatches and indels

General error rate	1.35%
Mismatches	75,627,192
Insertions	1,043,532
Mapped reads with at least one insertion	1.68%
Deletions	2,938,630
Mapped reads with at least one deletion	4.67%
Homopolymer indels	52.69%

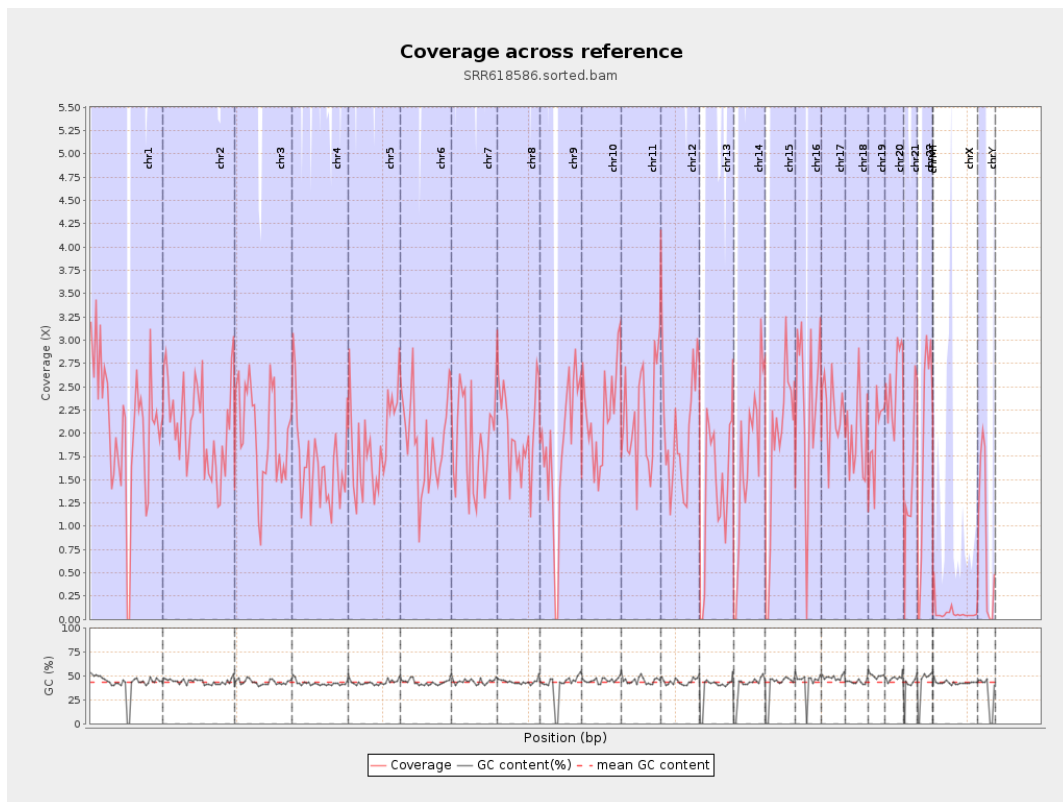
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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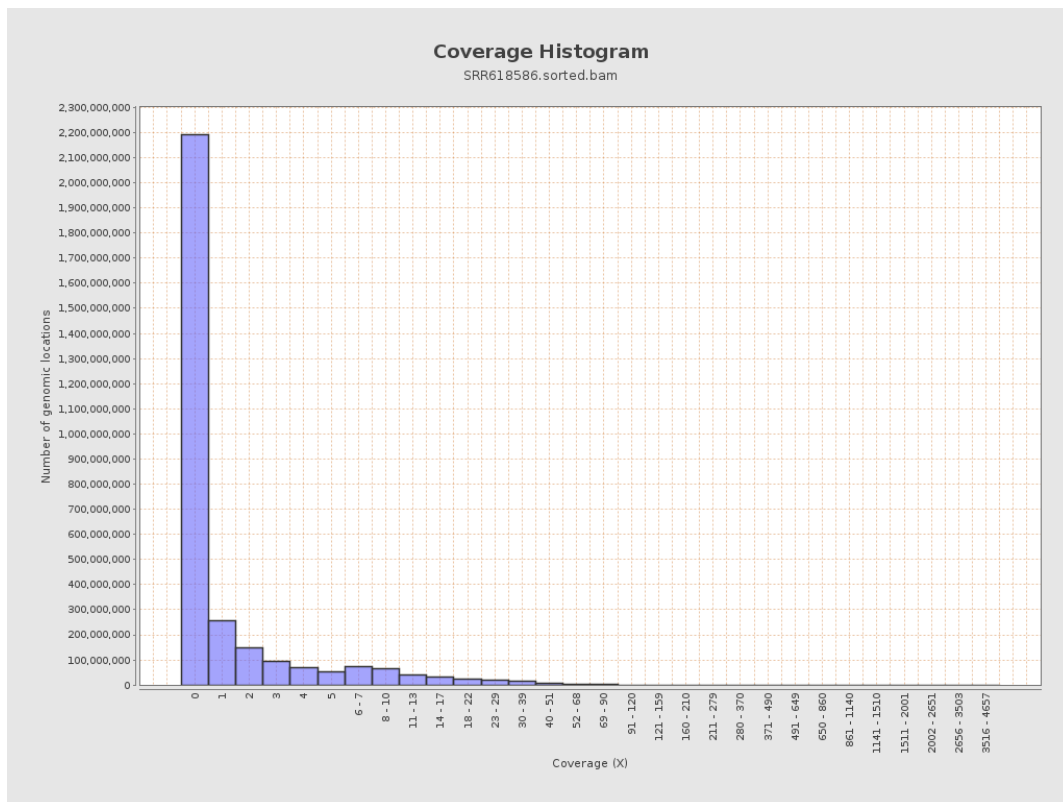
		bases	coverage	deviation
chr1	249250621	516139050	2.0708	8.5513
chr2	243199373	505948618	2.0804	7.3778
chr3	198022430	392412906	1.9817	5.8602
chr4	191154276	319341456	1.6706	5.8748
chr5	180915260	344862825	1.9062	5.7347
chr6	171115067	324593634	1.8969	6.082
chr7	159138663	303540031	1.9074	6.0712
chr8	146364022	292751328	2.0002	6.2828
chr9	141213431	257021969	1.8201	8.2551
chr10	135534747	298026364	2.1989	6.7715
chr11	135006516	294563932	2.1818	7.7012
chr12	133851895	271518265	2.0285	6.304
chr13	115169878	161477496	1.4021	4.7558
chr14	107349540	185467170	1.7277	5.8839
chr15	102531392	189719830	1.8504	6.1256
chr16	90354753	209106097	2.3143	9.2357
chr17	81195210	182779806	2.2511	7.4248
chr18	78077248	151572182	1.9413	8.4417
chr19	59128983	115915078	1.9604	7.3926
chr20	63025520	161022433	2.5549	7.6251
chr21	48129895	73611709	1.5294	9.317
chr22	51304566	97853465	1.9073	7.2601
chrMT	16571	748	0.0451	0.3557
chrX	155270560	11338681	0.073	1.8049

chrY	59373566	54224658	0.9133	4.8937
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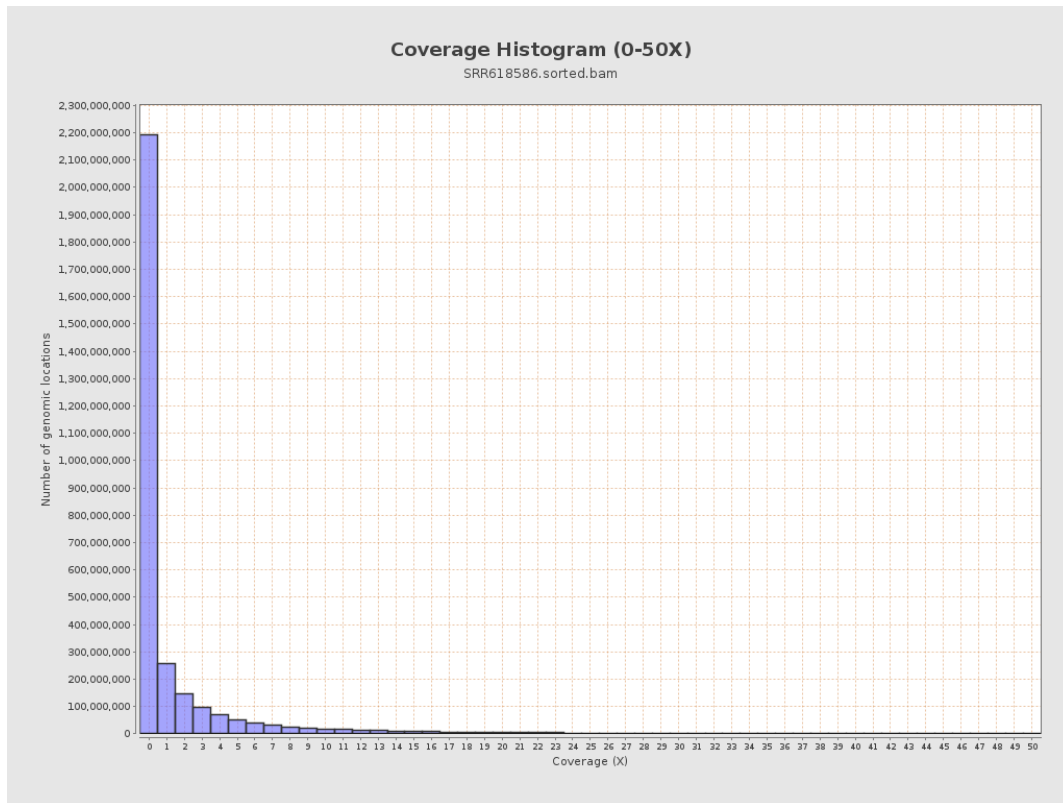
3. Results : Coverage across reference



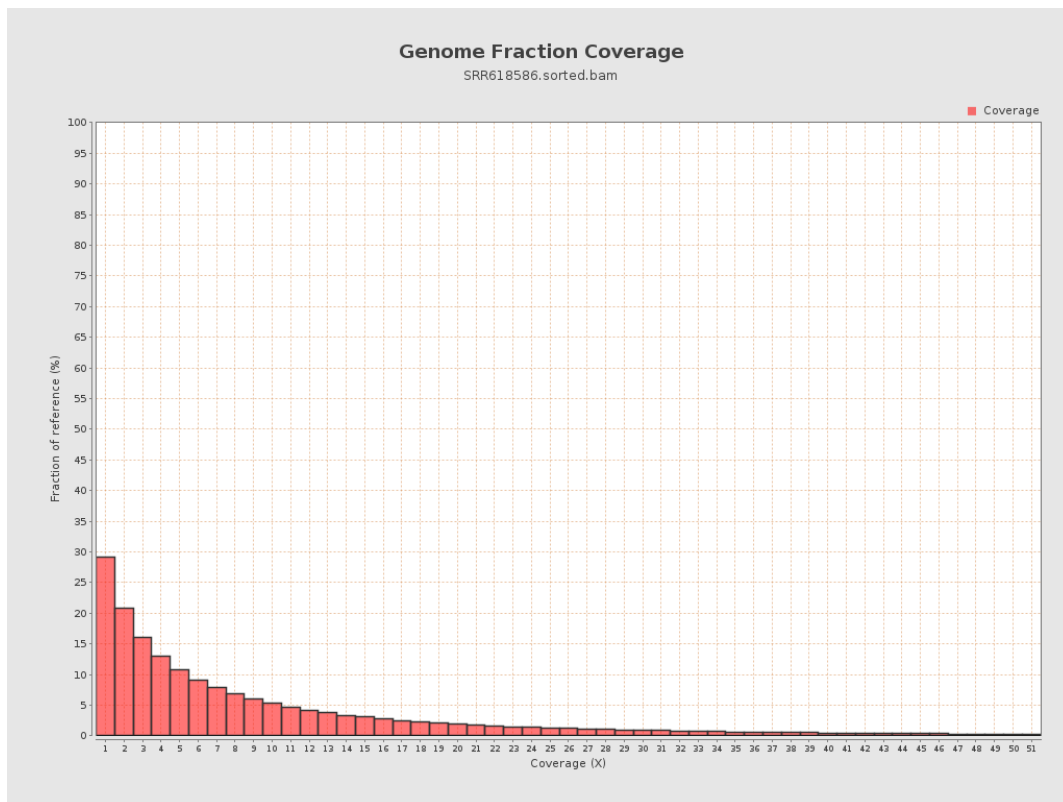
4. Results : Coverage Histogram



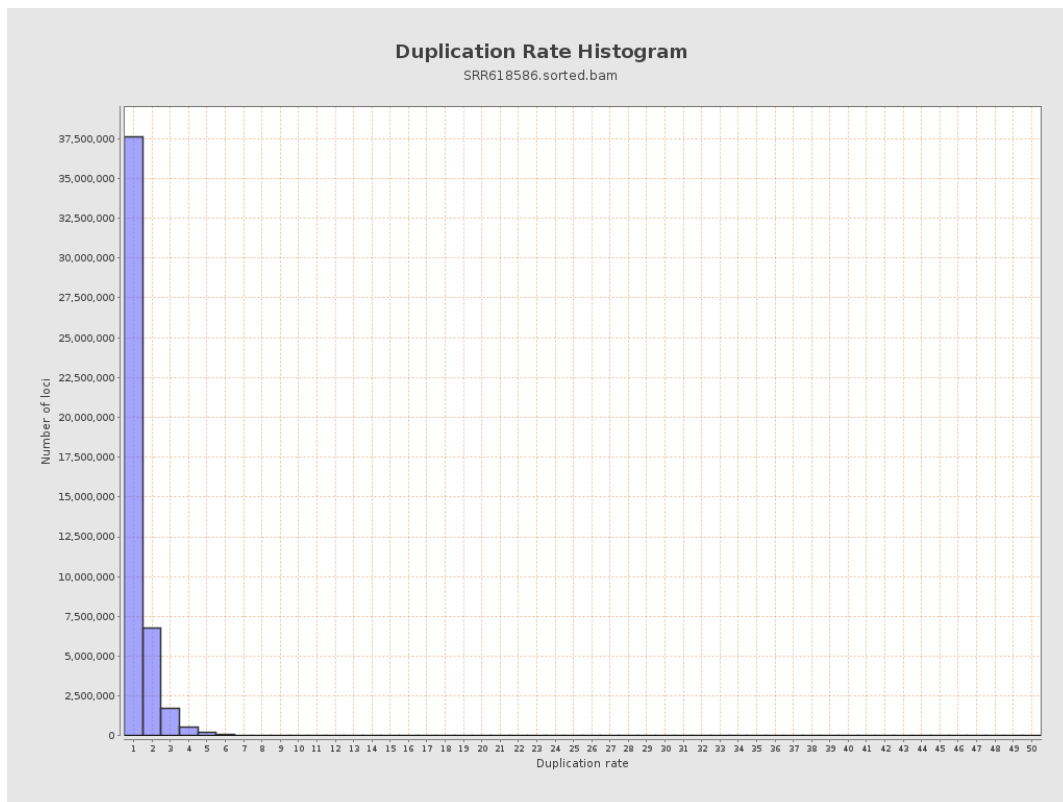
5. Results : Coverage Histogram (0-50X)



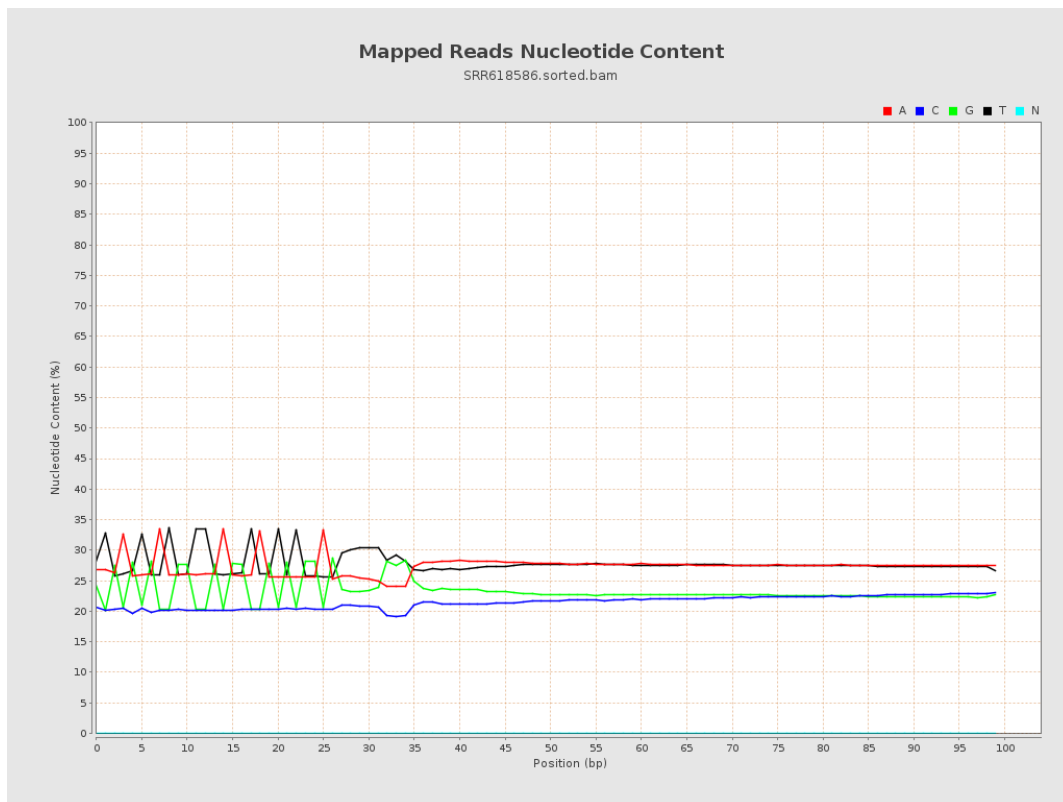
6. Results : Genome Fraction Coverage



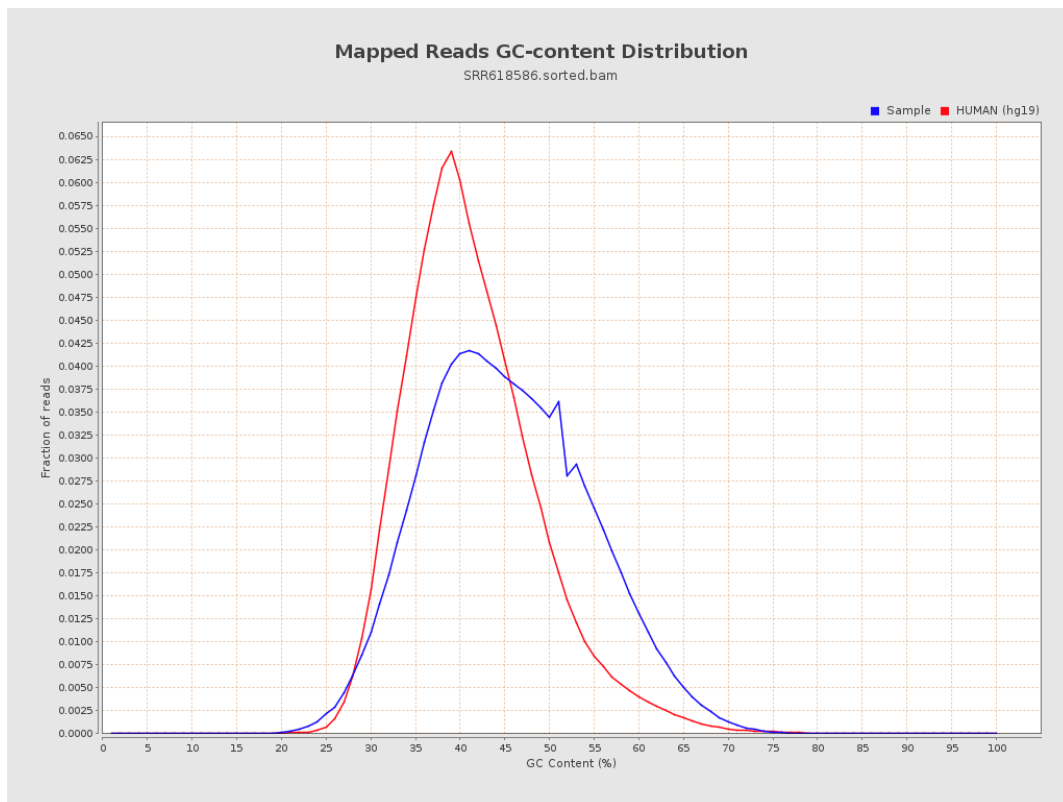
7. Results : Duplication Rate Histogram



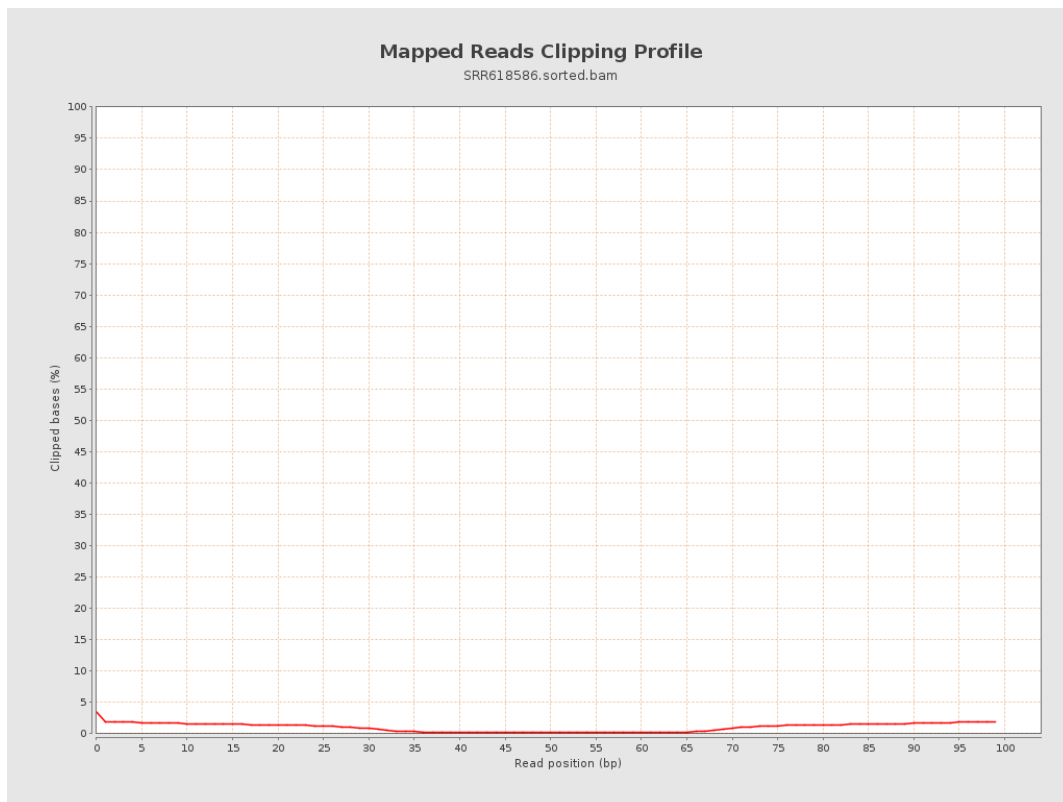
8. Results : Mapped Reads Nucleotide Content



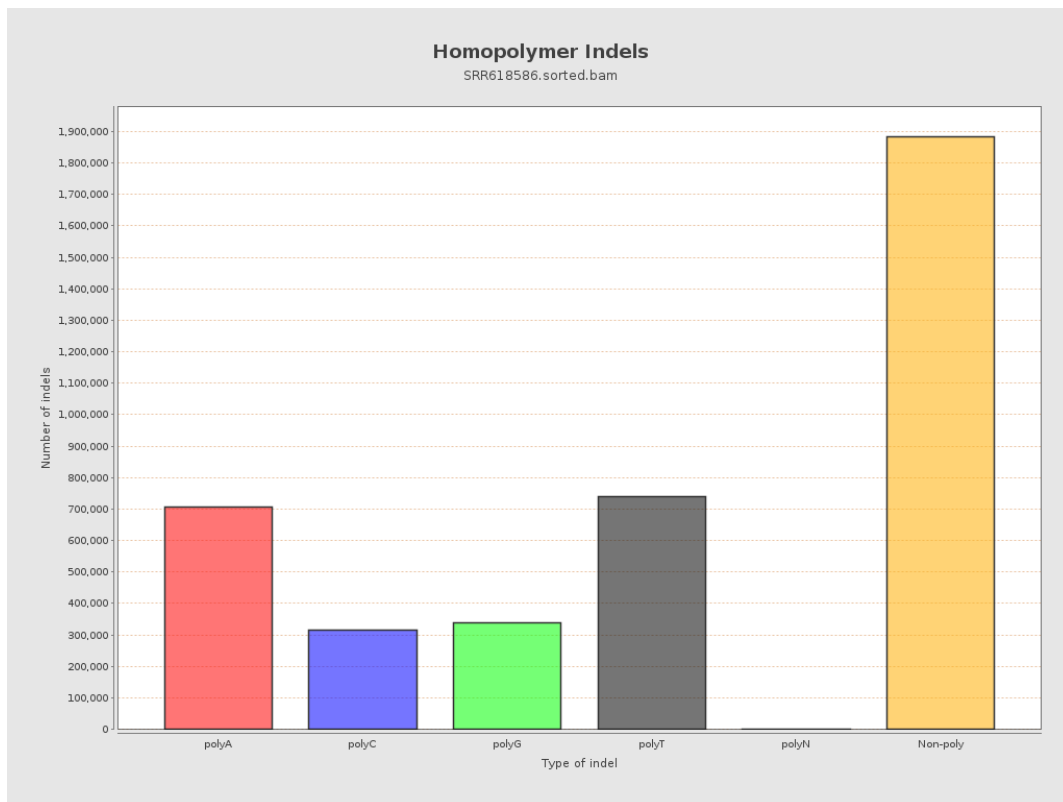
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



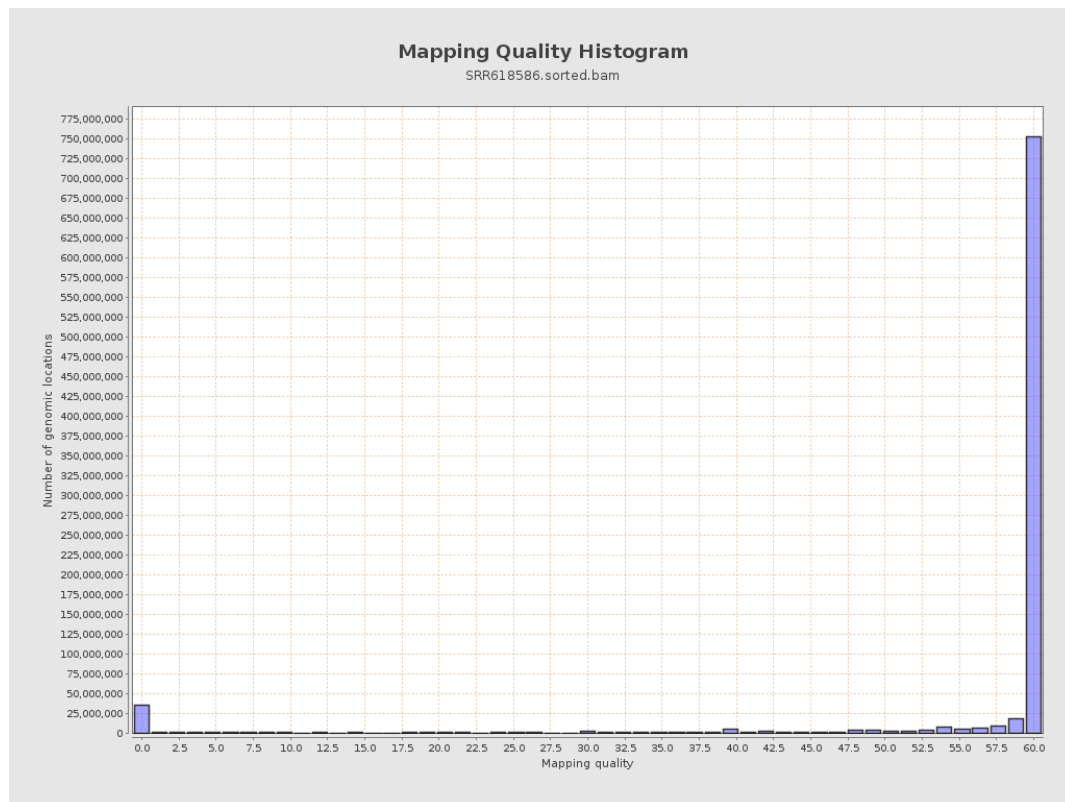
11. Results : Homopolymer Indels



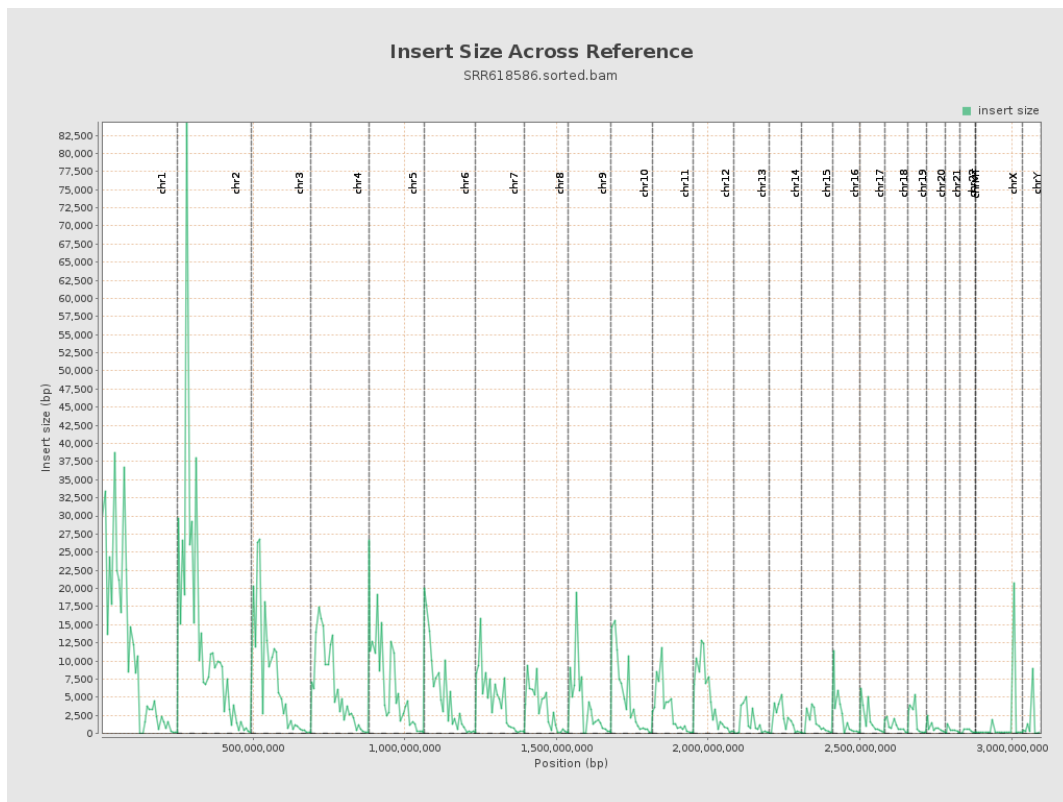
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

