

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 14:01:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618589.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_SRR618589 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618589_1.fastq.gz SRR618589_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 14:01:51 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618589.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	57,387,688
Mapped reads	55,207,699 / 96.2%
Unmapped reads	2,179,989 / 3.8%
Mapped paired reads	55,207,699 / 96.2%
Mapped reads, first in pair	27,924,806 / 48.66%
Mapped reads, second in pair	27,282,893 / 47.54%
Mapped reads, both in pair	54,039,940 / 94.17%
Mapped reads, singletons	1,167,759 / 2.03%
Secondary alignments	0
Supplementary alignments	185,727 / 0.32%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	10,738,353 / 18.71%
Duplication rate	16.73%
Clipped reads	13,131,550 / 22.88%

2.2. ACGT Content

Number/percentage of A's	1,402,829,360 / 27.13%
Number/percentage of C's	1,130,985,799 / 21.87%
Number/percentage of T's	1,424,538,552 / 27.55%
Number/percentage of G's	1,211,798,381 / 23.44%
Number/percentage of N's	464,483 / 0.01%

GC Percentage	45.31%
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2.3. Coverage

Mean	1.6714
Standard Deviation	6.3534

2.4. Mapping Quality

Mean Mapping Quality	53.56
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2.5. Insert size

Mean	67,395.48
Standard Deviation	2,606,494.7
P25/Median/P75	169 / 198 / 235

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	66,776,533
Insertions	934,971
Mapped reads with at least one insertion	1.67%
Deletions	2,576,464
Mapped reads with at least one deletion	4.55%
Homopolymer indels	52.68%

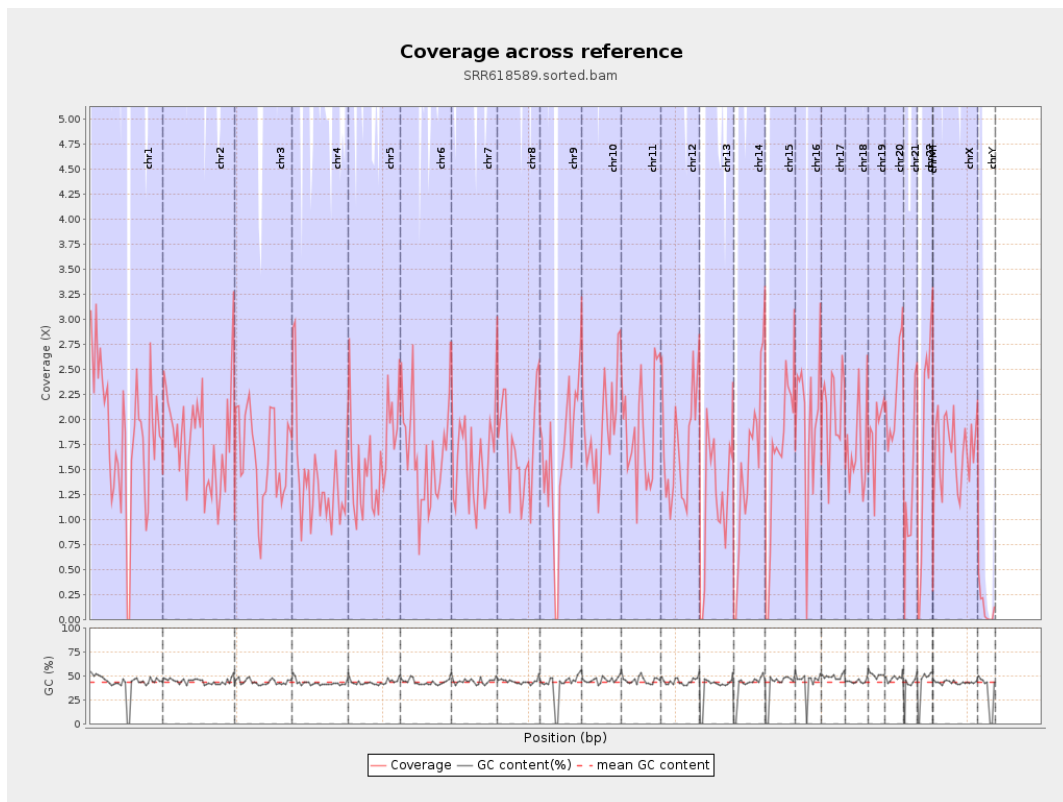
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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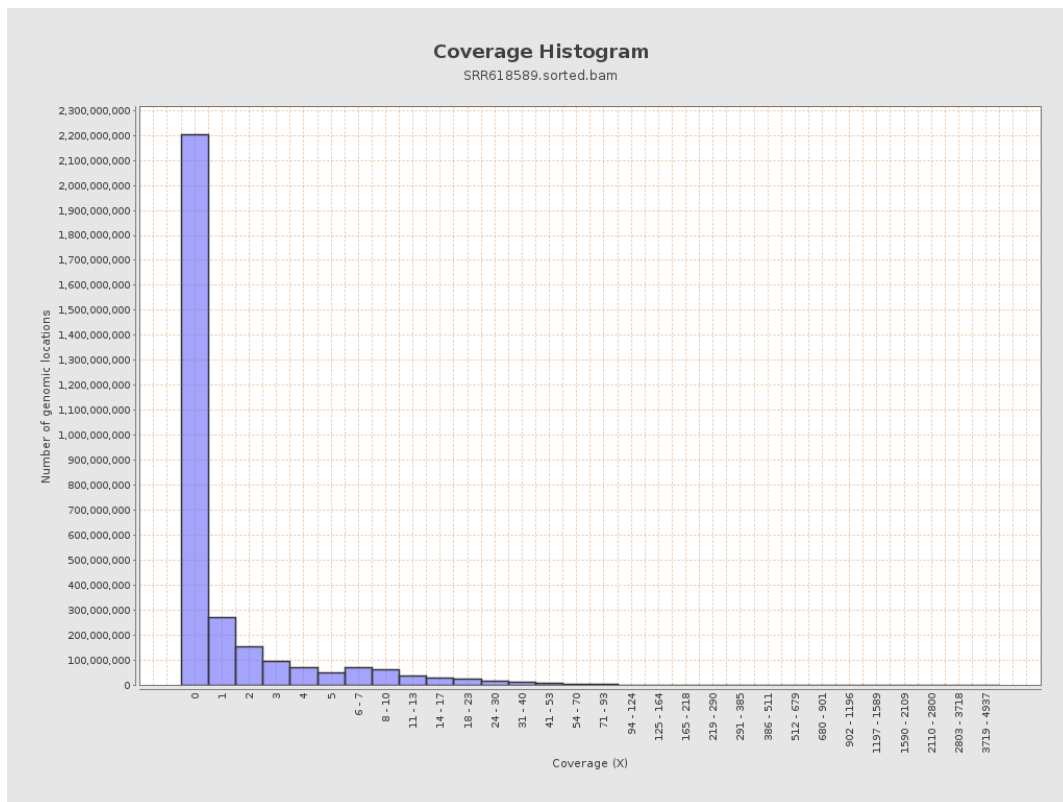
		bases	coverage	deviation
chr1	249250621	459611767	1.844	7.8089
chr2	243199373	438165239	1.8017	6.9091
chr3	198022430	321861510	1.6254	5.0479
chr4	191154276	266088045	1.392	5.34
chr5	180915260	292989289	1.6195	5.2408
chr6	171115067	279983035	1.6362	5.4824
chr7	159138663	257101325	1.6156	5.358
chr8	146364022	252672980	1.7263	5.4557
chr9	141213431	227123668	1.6084	7.4893
chr10	135534747	259396514	1.9139	6.2971
chr11	135006516	255814200	1.8948	6.8219
chr12	133851895	233614578	1.7453	6.969
chr13	115169878	139804350	1.2139	4.3368
chr14	107349540	162698910	1.5156	5.3692
chr15	102531392	165247685	1.6117	5.6319
chr16	90354753	179220991	1.9835	10.0883
chr17	81195210	171095545	2.1072	7.0195
chr18	78077248	130680155	1.6737	7.2131
chr19	59128983	110826391	1.8743	7.0642
chr20	63025520	141992727	2.2529	6.7664
chr21	48129895	65474746	1.3604	8.6869
chr22	51304566	92139690	1.7959	6.6546
chrMT	16571	4651	0.2807	0.8543
chrX	155270560	263689302	1.6983	5.2056

chrY	59373566	6824103	0.1149	3.0417
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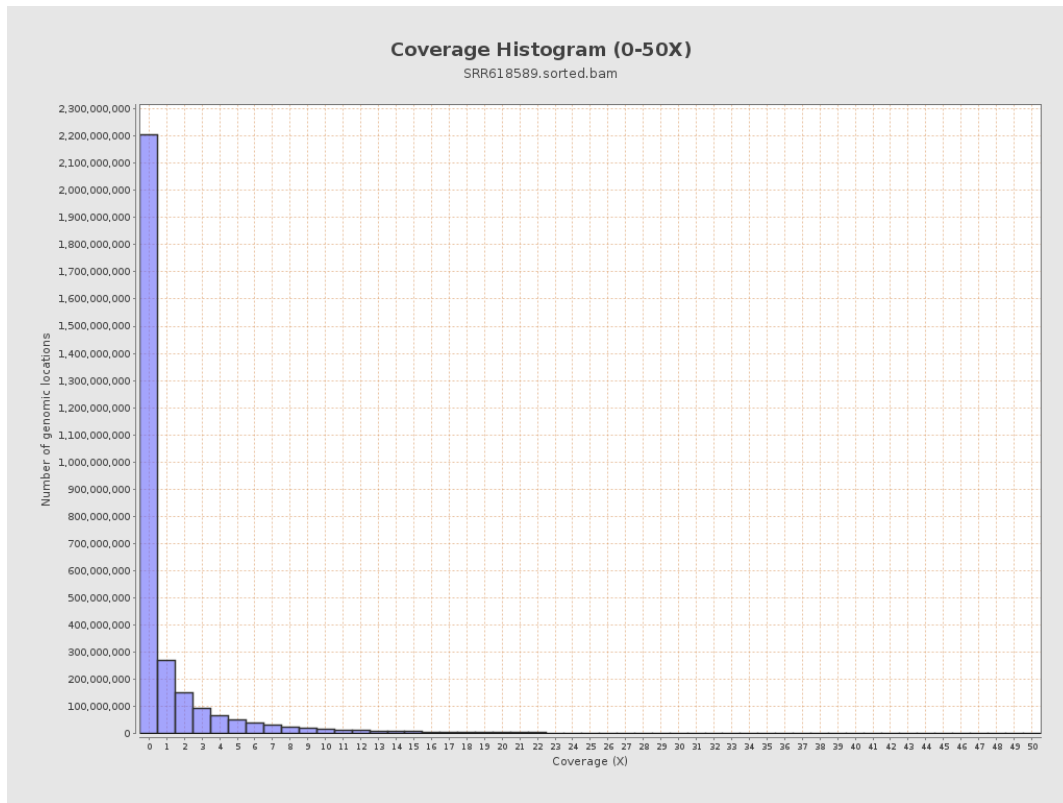
3. Results : Coverage across reference



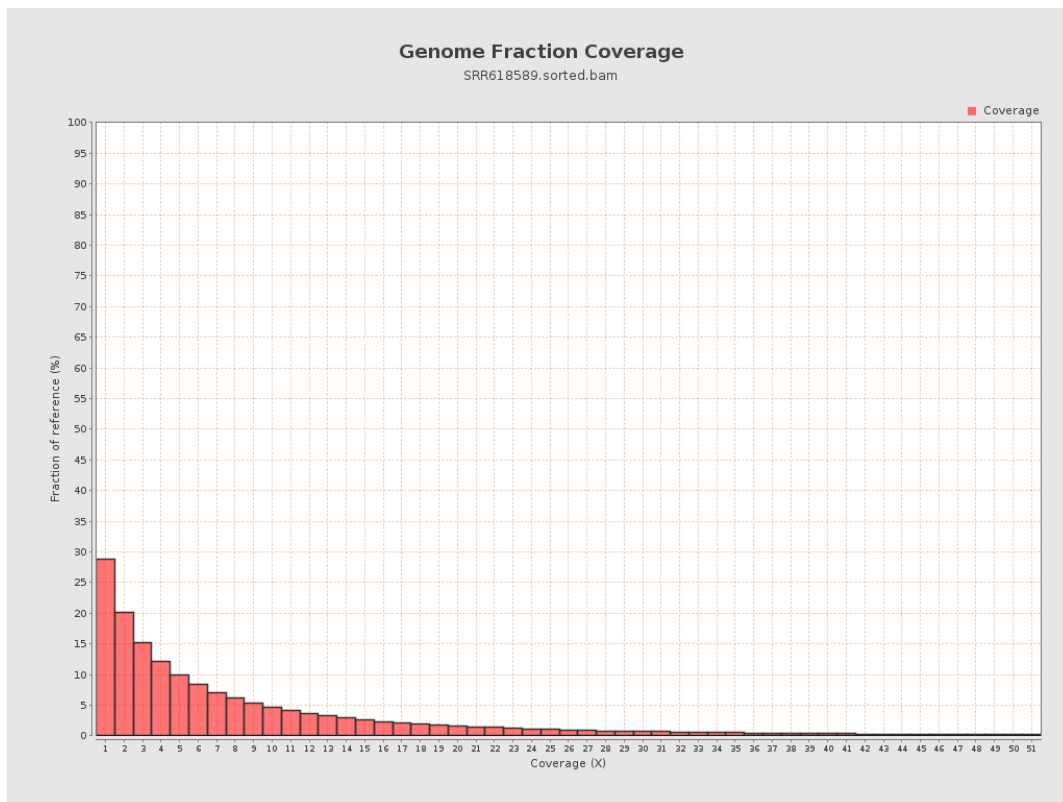
4. Results : Coverage Histogram



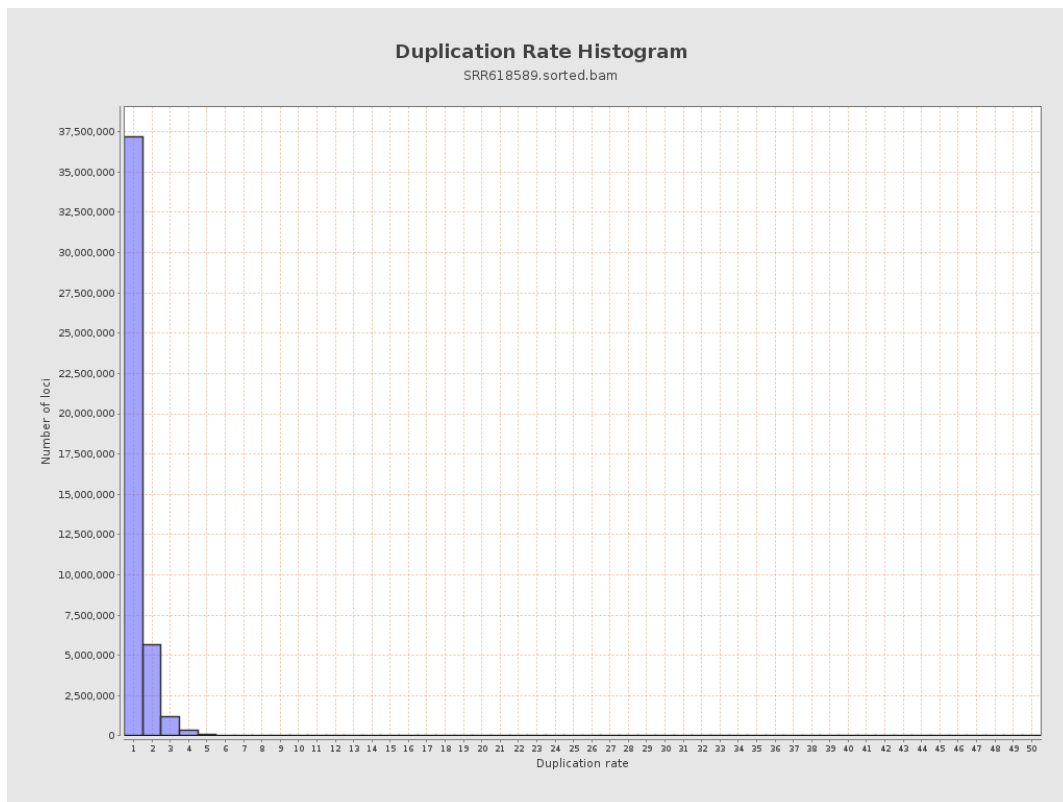
5. Results : Coverage Histogram (0-50X)



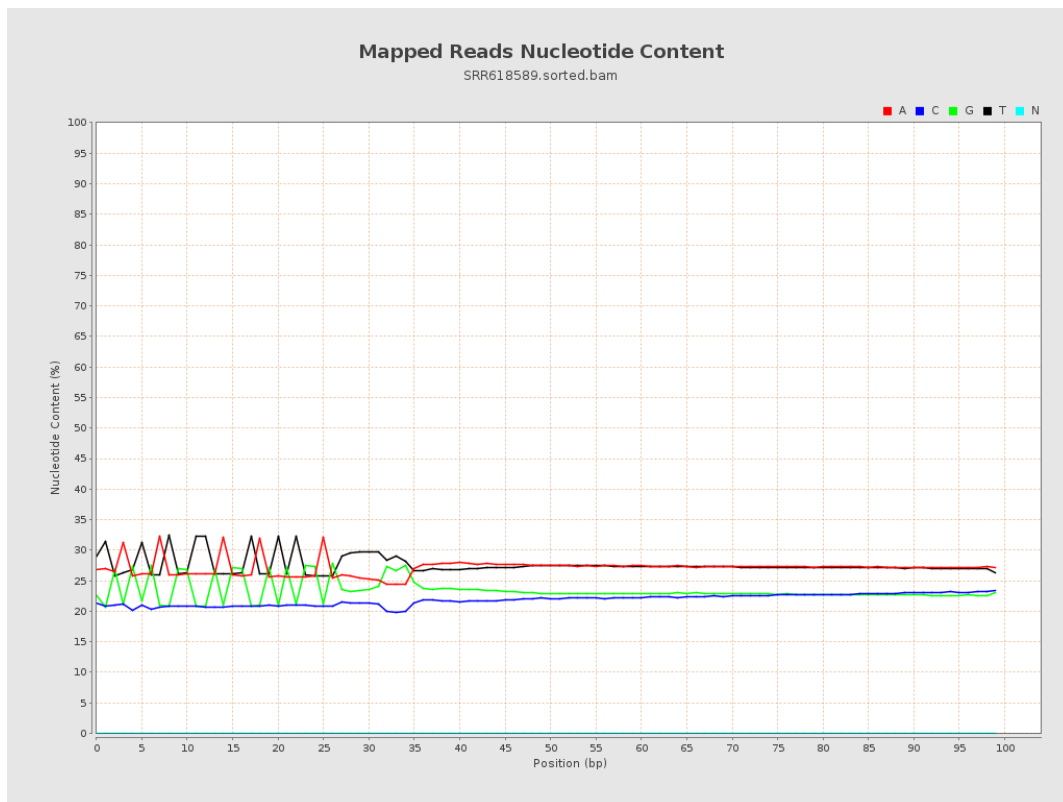
6. Results : Genome Fraction Coverage



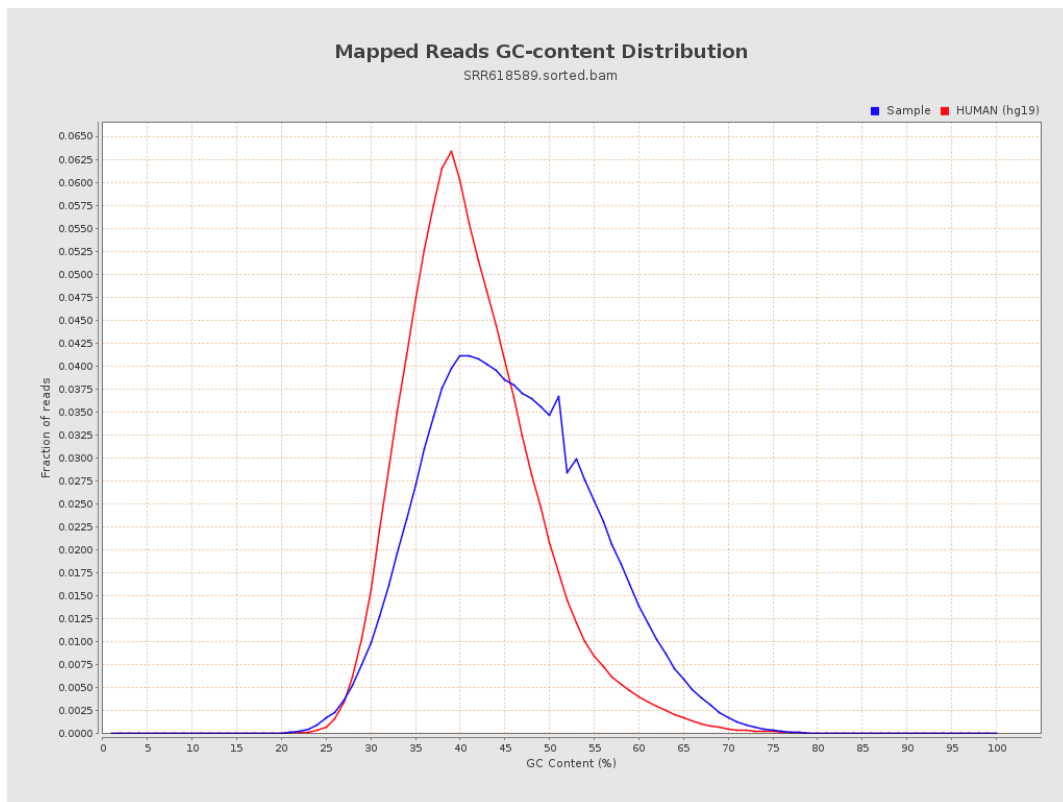
7. Results : Duplication Rate Histogram



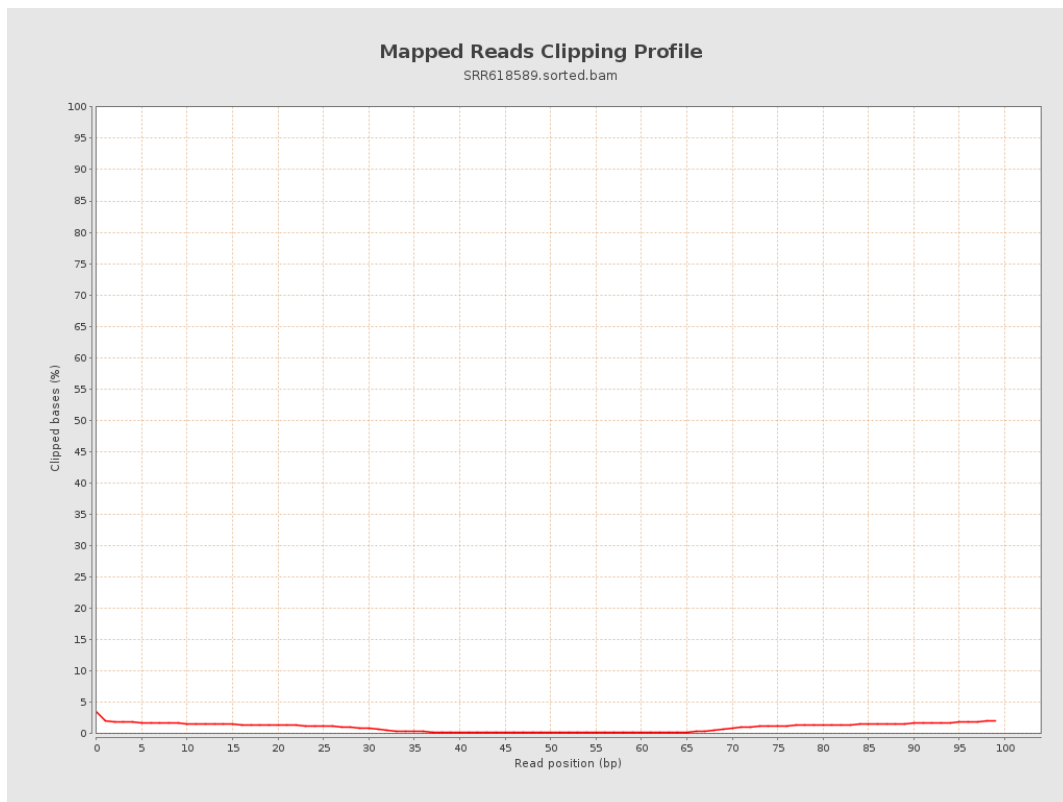
8. Results : Mapped Reads Nucleotide Content



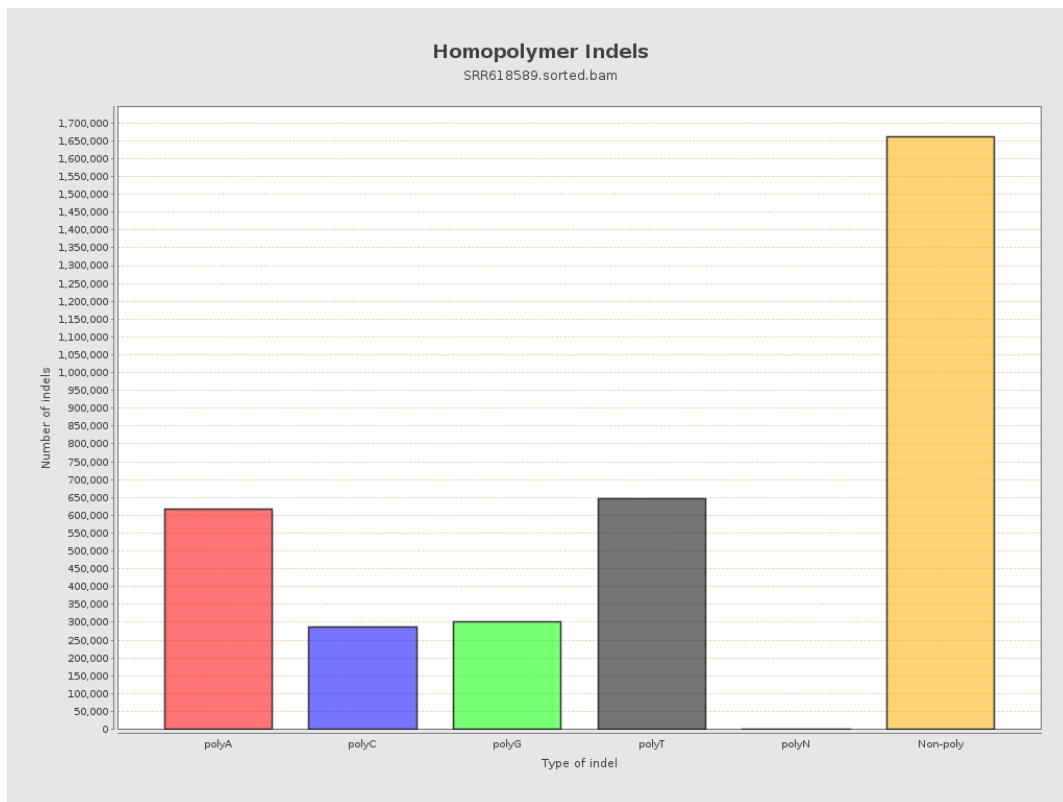
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



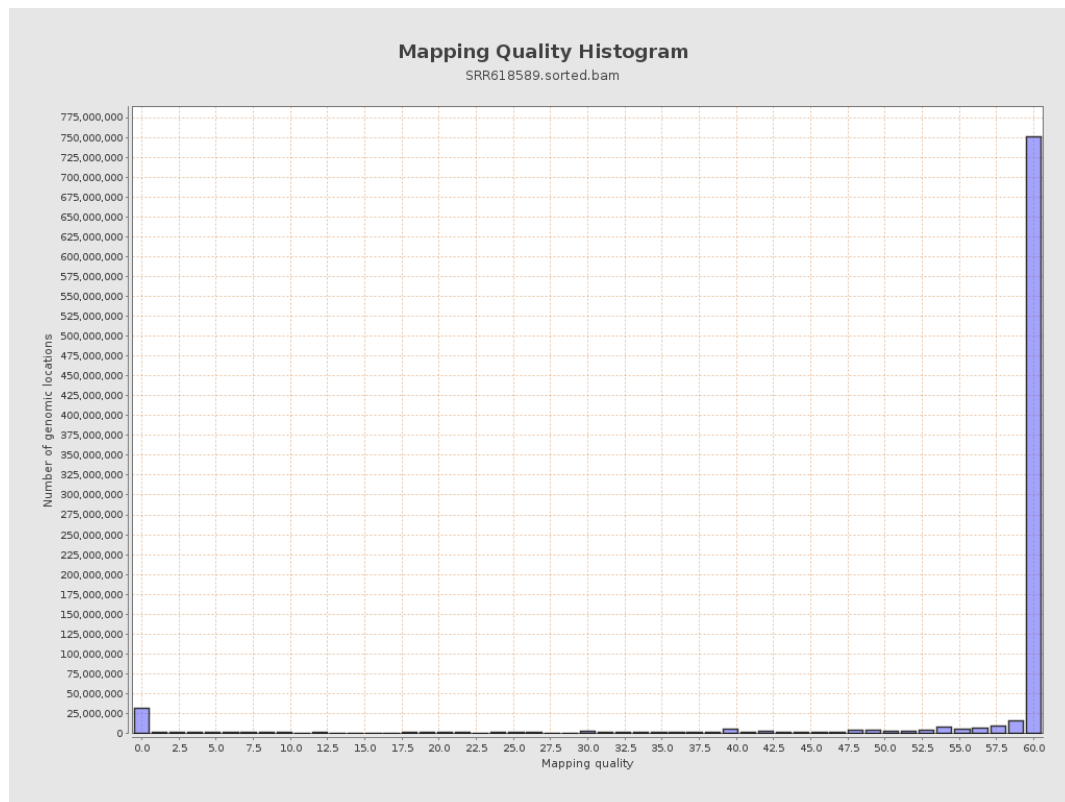
11. Results : Homopolymer Indels



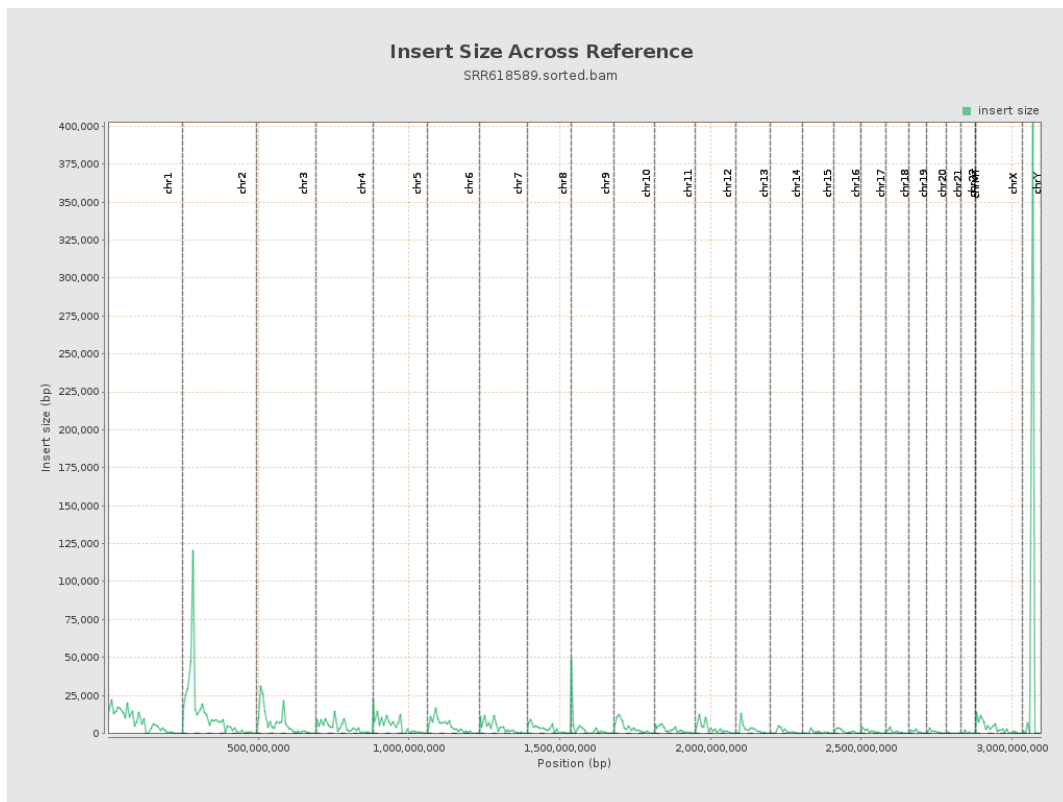
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

