

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 13:02:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618588.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_SRR618588 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618588_1.fastq.gz SRR618588_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 13:02:28 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618588.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	57,255,644
Mapped reads	55,006,413 / 96.07%
Unmapped reads	2,249,231 / 3.93%
Mapped paired reads	55,006,413 / 96.07%
Mapped reads, first in pair	27,804,139 / 48.56%
Mapped reads, second in pair	27,202,274 / 47.51%
Mapped reads, both in pair	54,117,380 / 94.52%
Mapped reads, singletons	889,033 / 1.55%
Secondary alignments	0
Supplementary alignments	234,622 / 0.41%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	19,527,078 / 34.11%
Duplication rate	29.27%
Clipped reads	10,161,373 / 17.75%

2.2. ACGT Content

Number/percentage of A's	1,411,132,830 / 26.86%
Number/percentage of C's	1,182,505,201 / 22.51%
Number/percentage of T's	1,412,566,113 / 26.89%
Number/percentage of G's	1,247,240,402 / 23.74%
Number/percentage of N's	254,354 / 0%

GC Percentage	46.25%
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2.3. Coverage

Mean	1.6984
Standard Deviation	7.8352

2.4. Mapping Quality

Mean Mapping Quality	52.84
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2.5. Insert size

Mean	81,221.91
Standard Deviation	2,820,596.96
P25/Median/P75	193 / 220 / 258

2.6. Mismatches and indels

General error rate	1.34%
Mismatches	68,586,982
Insertions	1,007,754
Mapped reads with at least one insertion	1.79%
Deletions	2,733,182
Mapped reads with at least one deletion	4.84%
Homopolymer indels	51.17%

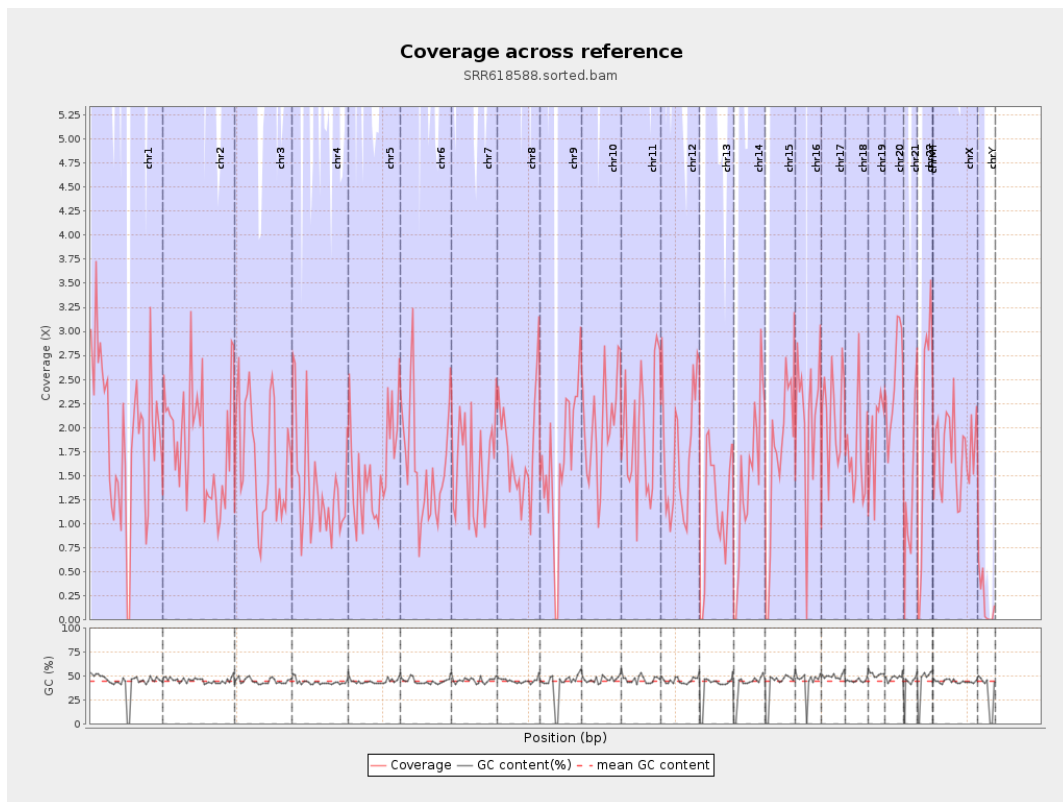
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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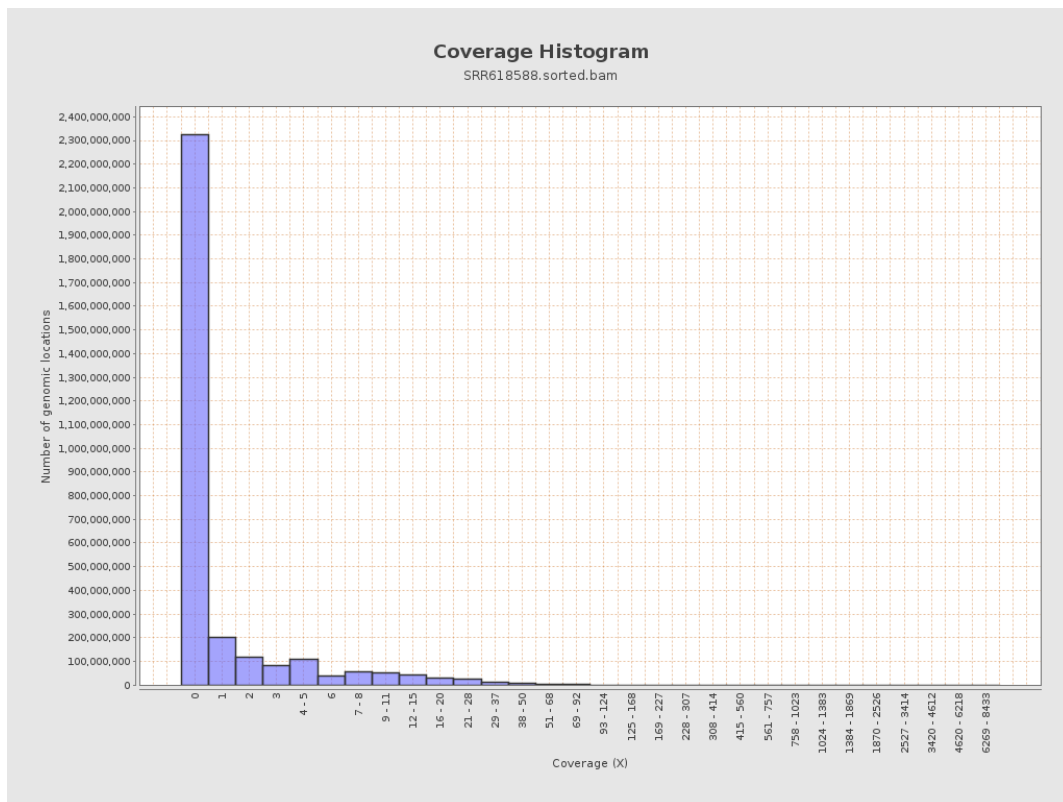
		bases	coverage	deviation
chr1	249250621	472657567	1.8963	7.6017
chr2	243199373	445380468	1.8313	10.7592
chr3	198022430	327112717	1.6519	5.6087
chr4	191154276	261843675	1.3698	9.4074
chr5	180915260	287022985	1.5865	5.5955
chr6	171115067	271679549	1.5877	5.9358
chr7	159138663	255407232	1.6049	5.9475
chr8	146364022	258551492	1.7665	6.4387
chr9	141213431	232756073	1.6483	9.702
chr10	135534747	270612921	1.9966	10.6921
chr11	135006516	261170629	1.9345	6.8086
chr12	133851895	232999287	1.7407	6.5844
chr13	115169878	131614357	1.1428	4.5048
chr14	107349540	157105745	1.4635	5.6502
chr15	102531392	172893972	1.6863	6.1341
chr16	90354753	190186320	2.1049	10.7498
chr17	81195210	174164954	2.145	8.3311
chr18	78077248	132561713	1.6978	11.0997
chr19	59128983	114795384	1.9414	7.2696
chr20	63025520	156820895	2.4882	8.1774
chr21	48129895	66478287	1.3812	11.1706
chr22	51304566	102579818	1.9994	7.6138
chrMT	16571	34367	2.0739	8.1661
chrX	155270560	270043482	1.7392	5.7126

chrY	59373566	11154747	0.1879	7.1962
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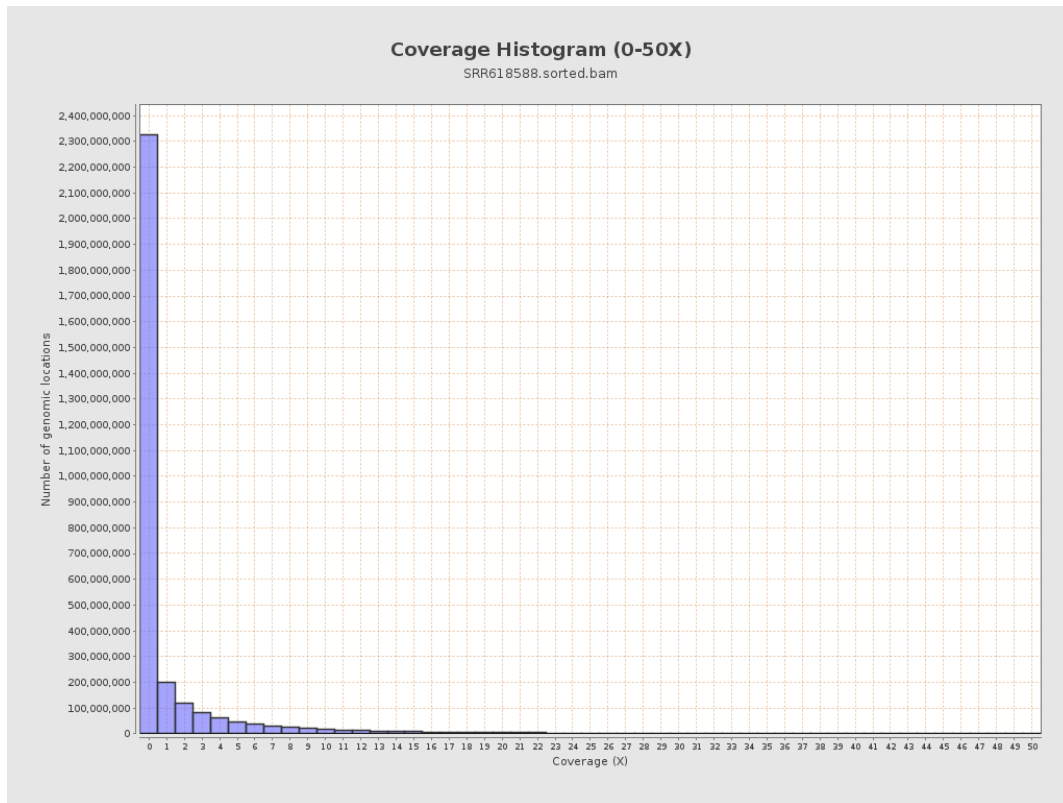
3. Results : Coverage across reference



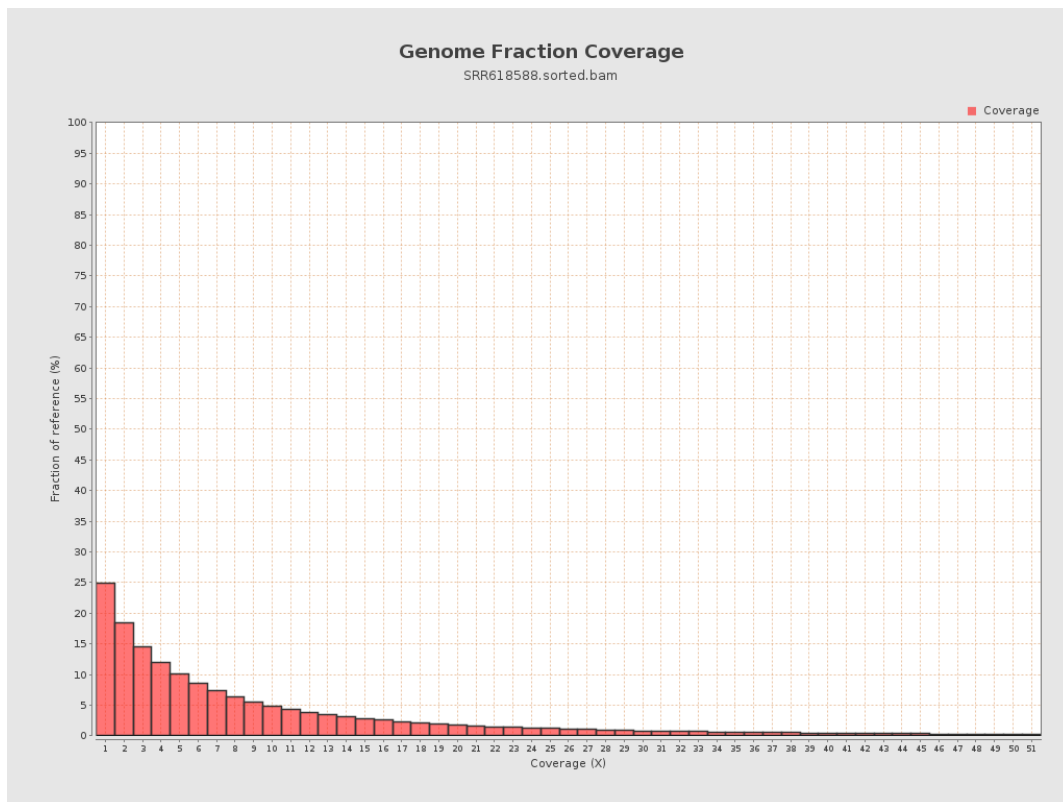
4. Results : Coverage Histogram



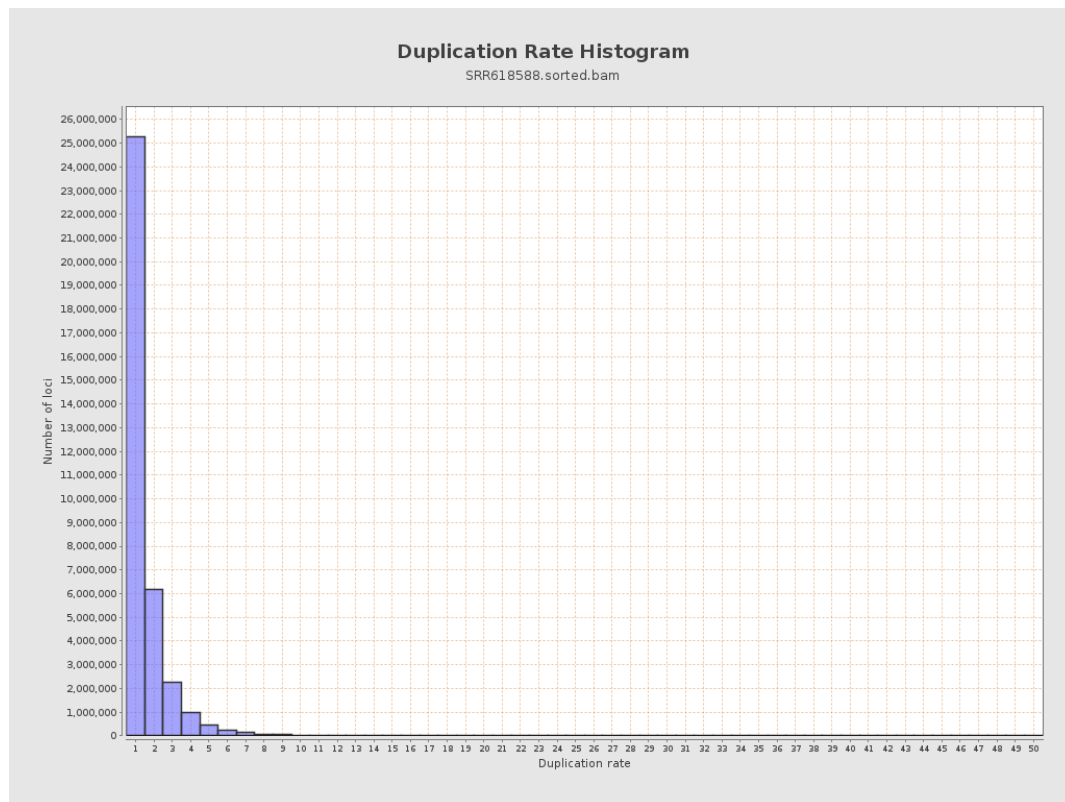
5. Results : Coverage Histogram (0-50X)



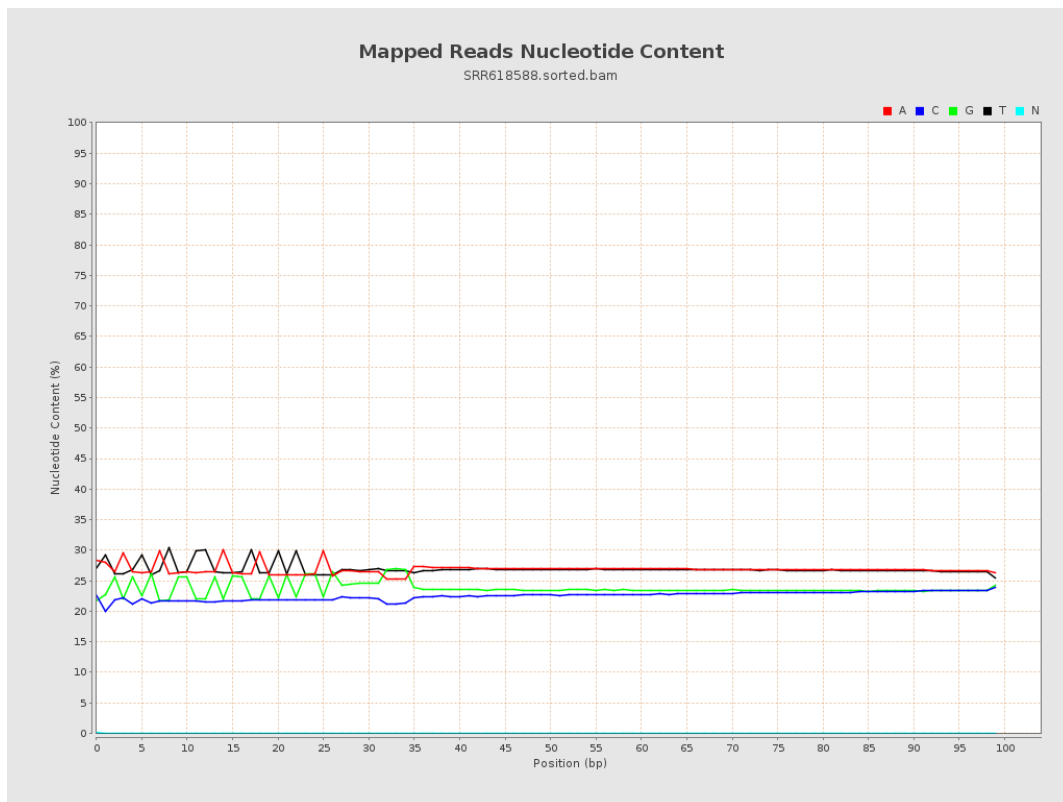
6. Results : Genome Fraction Coverage



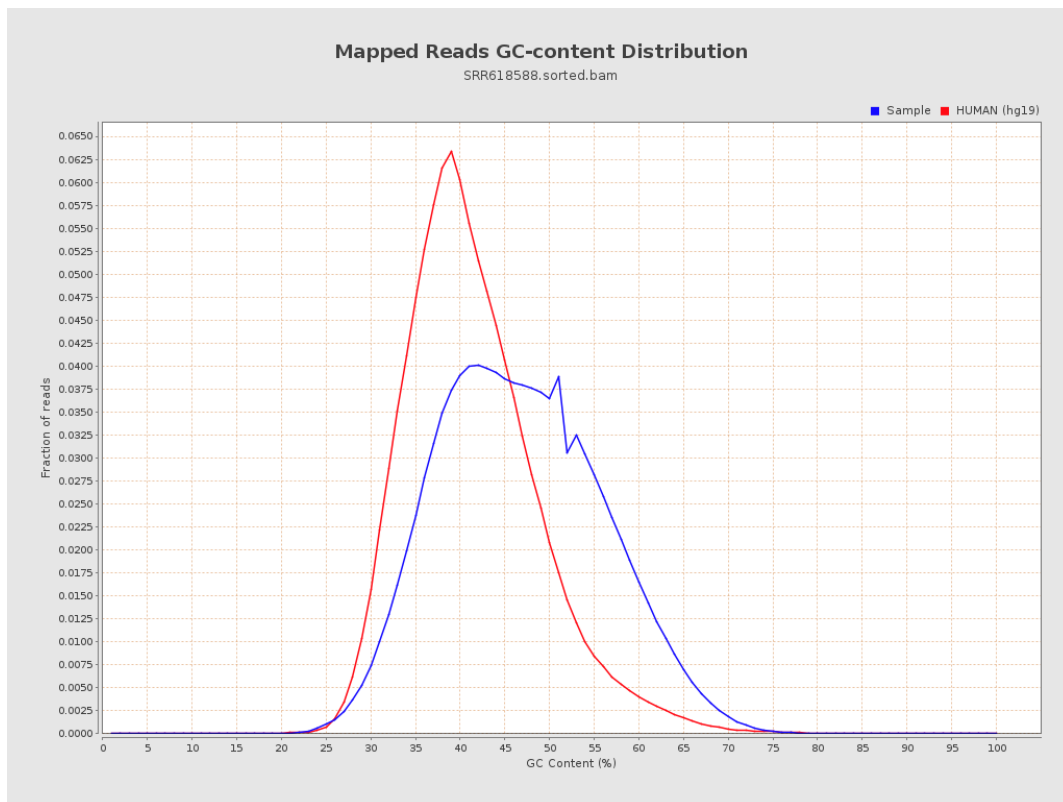
7. Results : Duplication Rate Histogram



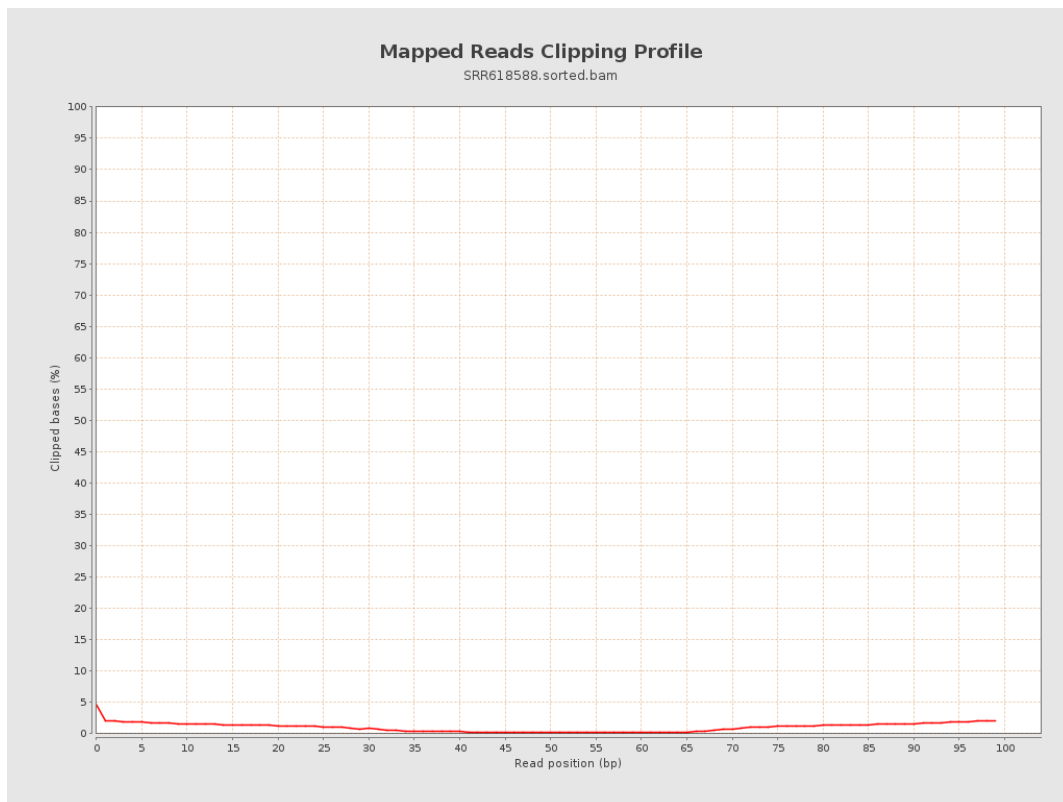
8. Results : Mapped Reads Nucleotide Content



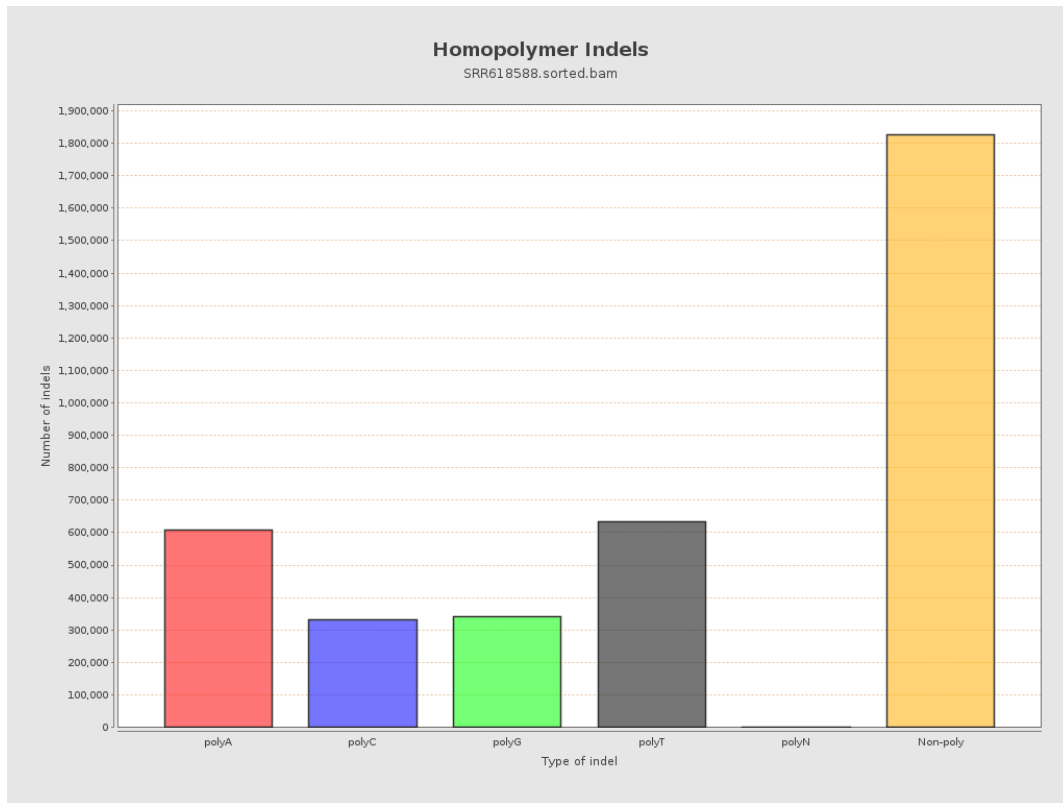
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



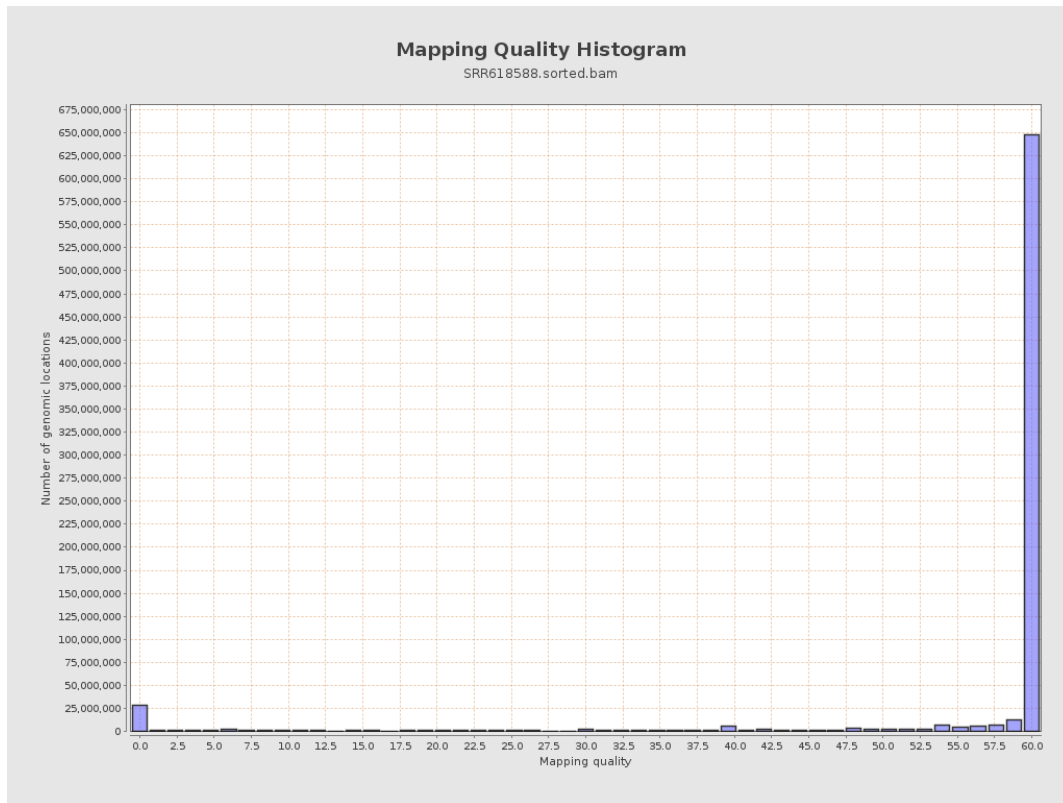
11. Results : Homopolymer Indels



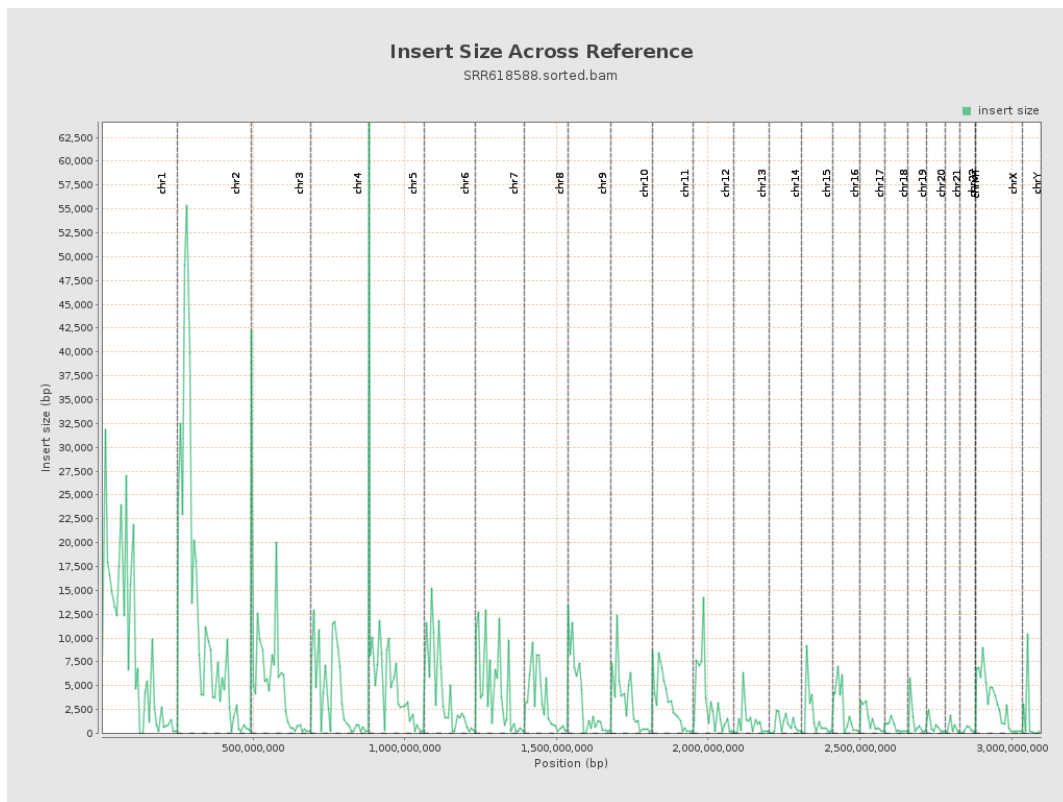
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

