

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 02:08:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438268.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_SRR8438268 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438268_1.fastq.gz SRR8438268_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 02:08:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438268.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	646,716,700
Mapped reads	644,728,361 / 99.69%
Unmapped reads	1,988,339 / 0.31%
Mapped paired reads	644,728,361 / 99.69%
Mapped reads, first in pair	322,558,010 / 49.88%
Mapped reads, second in pair	322,170,351 / 49.82%
Mapped reads, both in pair	643,342,874 / 99.48%
Mapped reads, singletons	1,385,487 / 0.21%
Secondary alignments	0
Supplementary alignments	10,637,362 / 1.64%
Read min/max/mean length	28 / 151 / 144.95
Duplicated reads (estimated)	246,900,318 / 38.18%
Duplication rate	35.56%
Clipped reads	114,301,669 / 17.67%

2.2. ACGT Content

Number/percentage of A's	28,042,769,798 / 30.28%
Number/percentage of C's	18,499,241,462 / 19.97%
Number/percentage of T's	26,738,459,560 / 28.87%
Number/percentage of G's	19,345,478,594 / 20.89%
Number/percentage of N's	701,362 / 0%

GC Percentage	40.86%
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2.3. Coverage

Mean	29.9292
Standard Deviation	101.0006

2.4. Mapping Quality

Mean Mapping Quality	55.03
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2.5. Insert size

Mean	37,251.95
Standard Deviation	1,861,359.64
P25/Median/P75	188 / 253 / 374

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	476,017,848
Insertions	11,346,463
Mapped reads with at least one insertion	1.73%
Deletions	10,095,788
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.32%

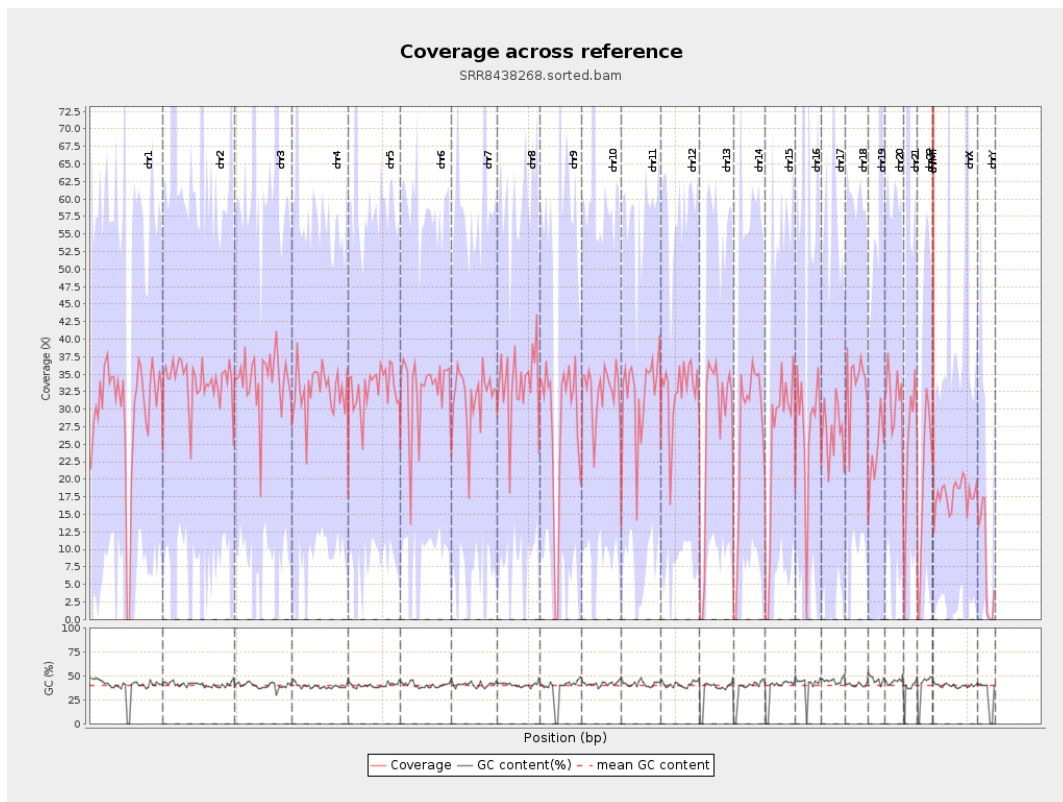
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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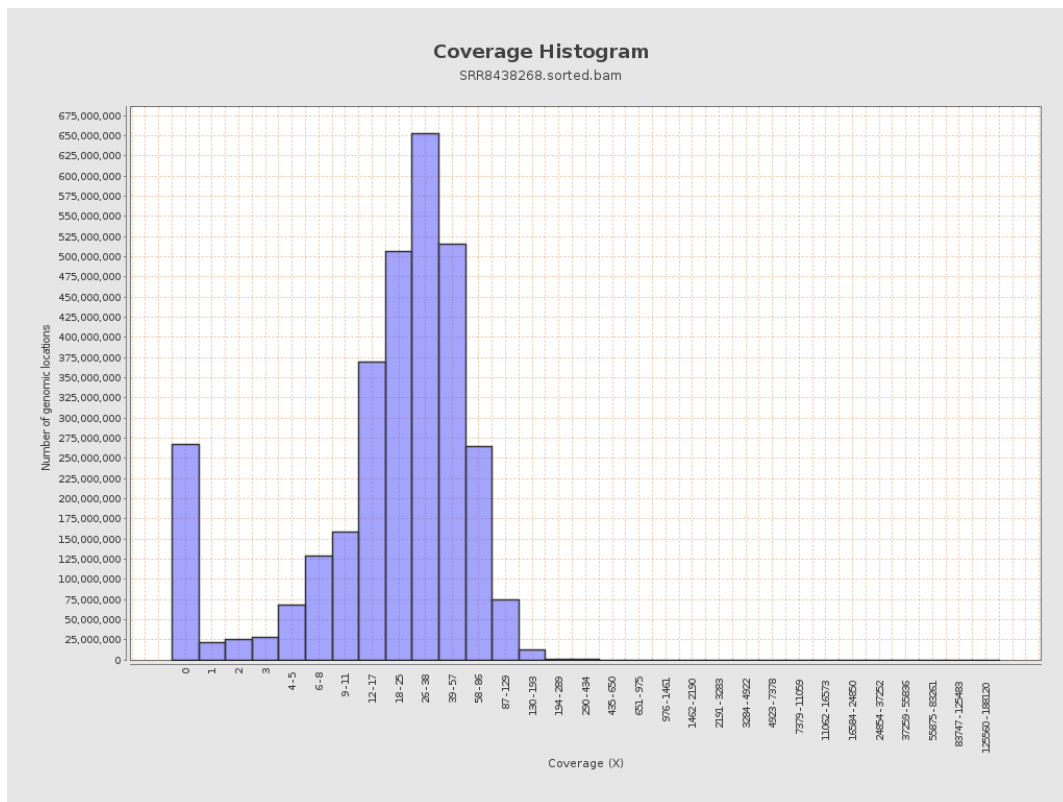
		bases	coverage	deviation
chr1	249250621	7425253009	29.7903	29.1066
chr2	243199373	8256244492	33.9485	96.2755
chr3	198022430	6759200746	34.1335	210.1
chr4	191154276	6277452092	32.8397	25.6834
chr5	180915260	5943330060	32.8515	29.1508
chr6	171115067	5646976150	33.001	25.9426
chr7	159138663	5038885623	31.6635	29.0425
chr8	146364022	4905031436	33.5125	26.3193
chr9	141213431	3936530556	27.8765	31.1926
chr10	135534747	4432160793	32.7013	36.8916
chr11	135006516	4349255641	32.2152	25.0695
chr12	133851895	4388855984	32.7889	25.0202
chr13	115169878	3187497027	27.6765	24.514
chr14	107349540	2930595229	27.2996	27.8134
chr15	102531392	2629798408	25.6487	26.6771
chr16	90354753	2431651981	26.9123	42.9274
chr17	81195210	2197881759	27.0691	31.6273
chr18	78077248	2622924626	33.594	26.2797
chr19	59128983	1413920599	23.9125	262.1509
chr20	63025520	1994474092	31.6455	27.5997
chr21	48129895	1168276291	24.2734	121.981
chr22	51304566	1028159508	20.0403	25.9232
chrMT	16571	442457900	26,700.7362	10,187.0702
chrX	155270560	2756559267	17.7533	39.403

chrY	59373566	488258429	8.2235	23.6104
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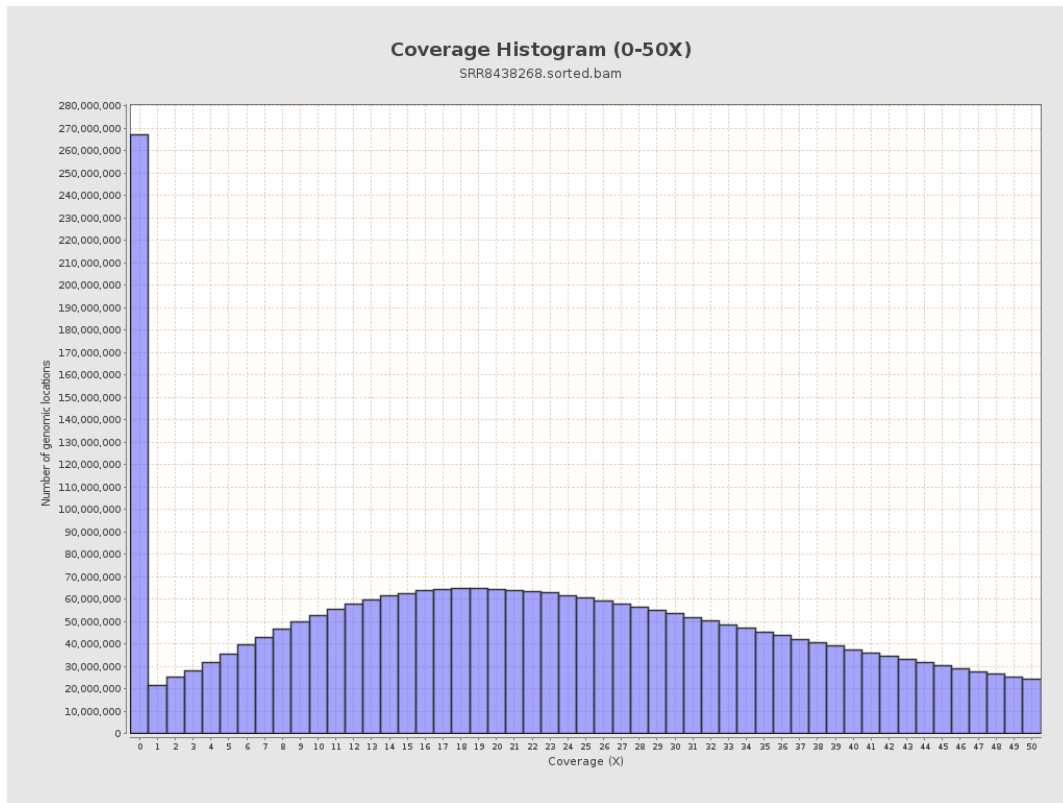
3. Results : Coverage across reference



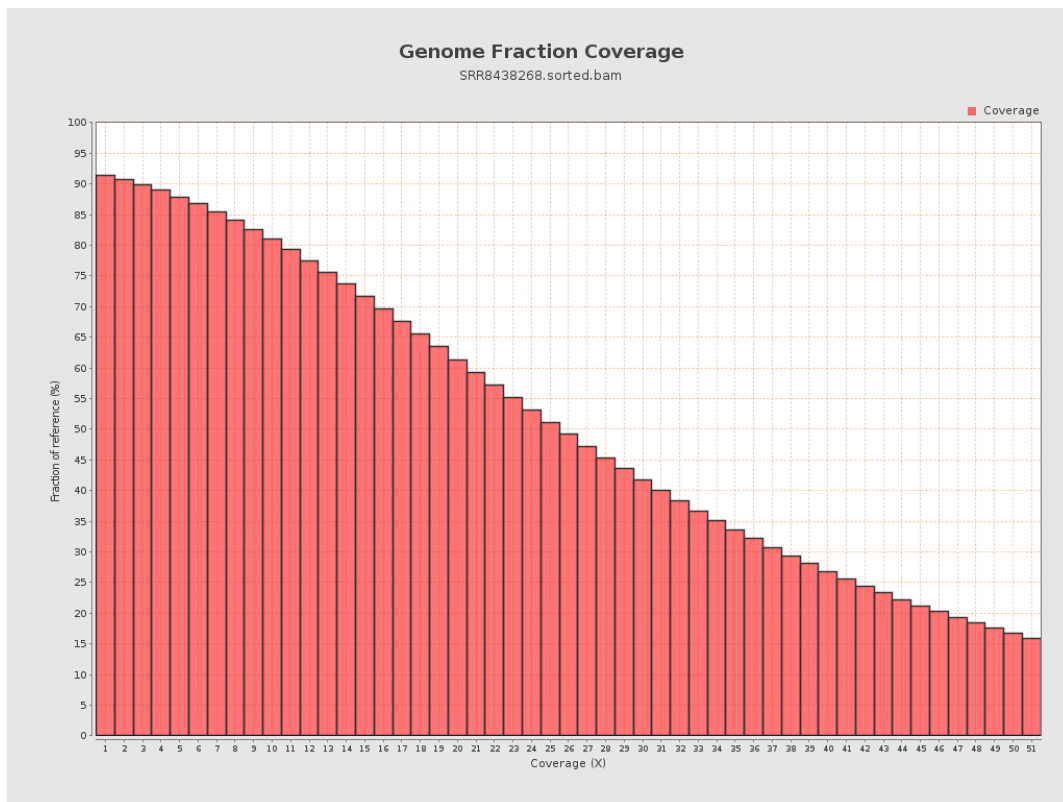
4. Results : Coverage Histogram



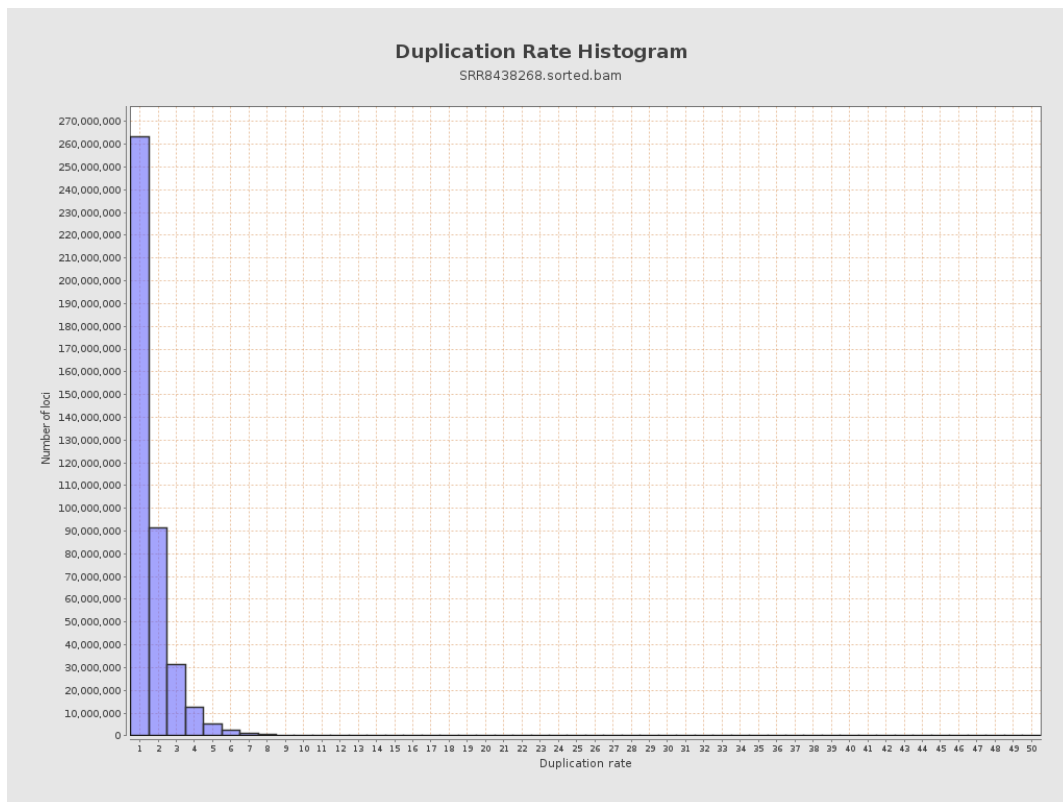
5. Results : Coverage Histogram (0-50X)



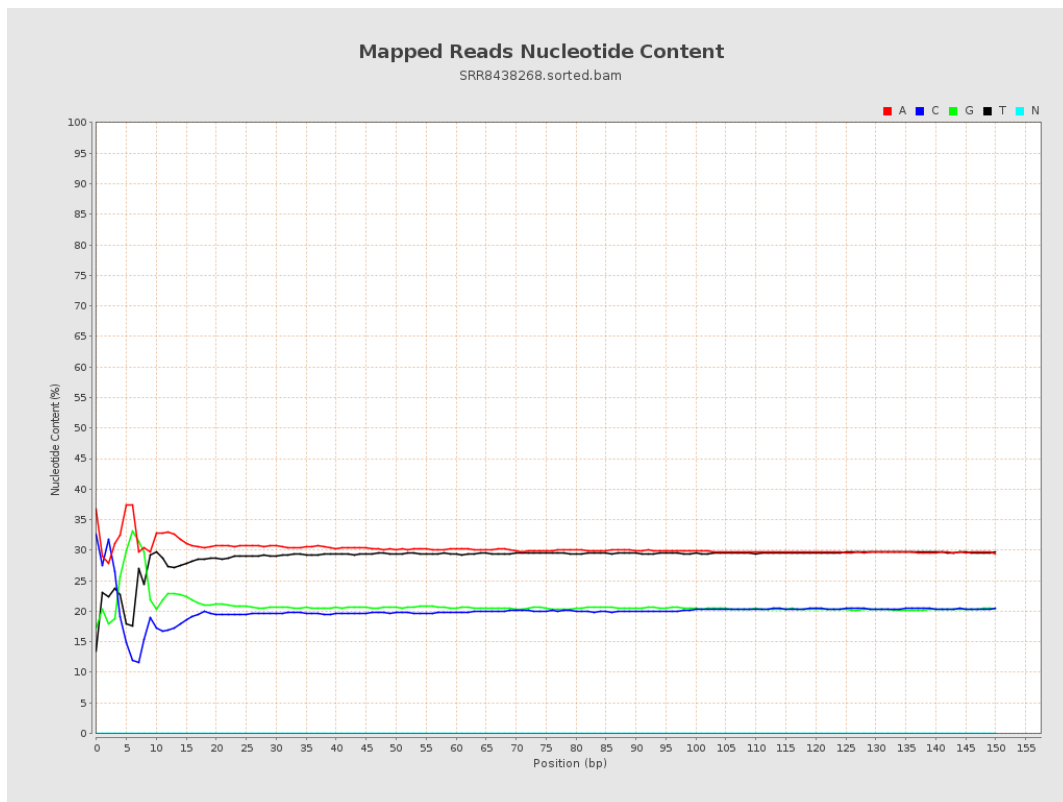
6. Results : Genome Fraction Coverage



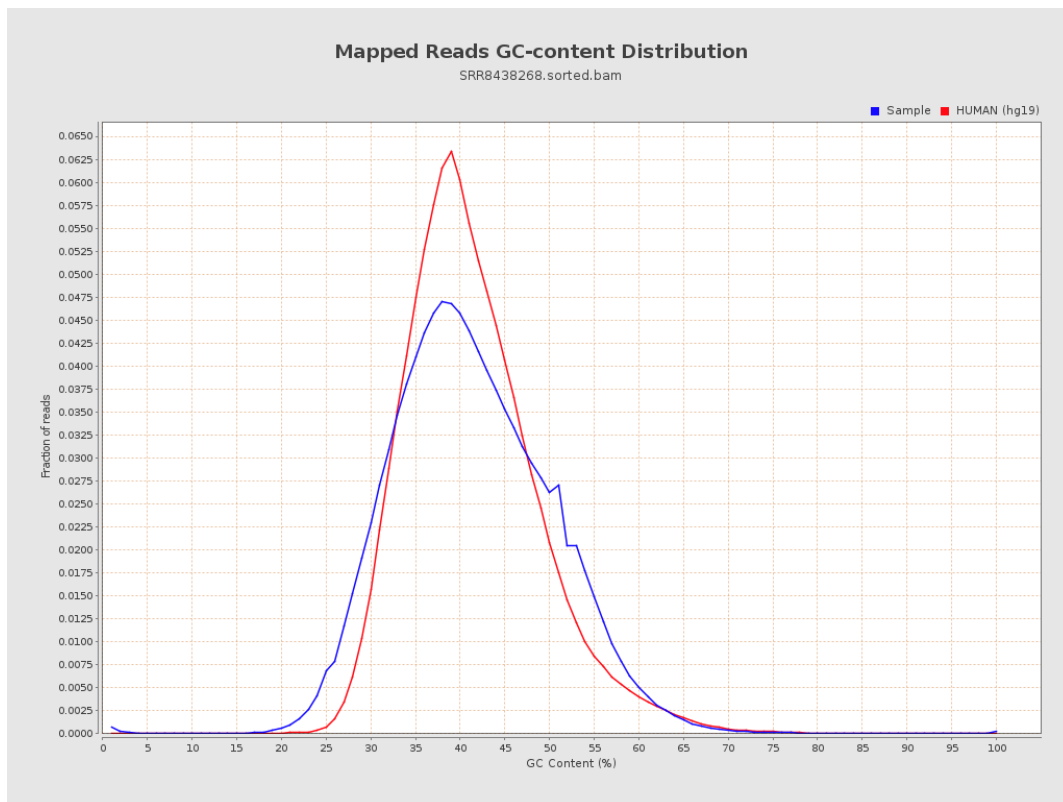
7. Results : Duplication Rate Histogram



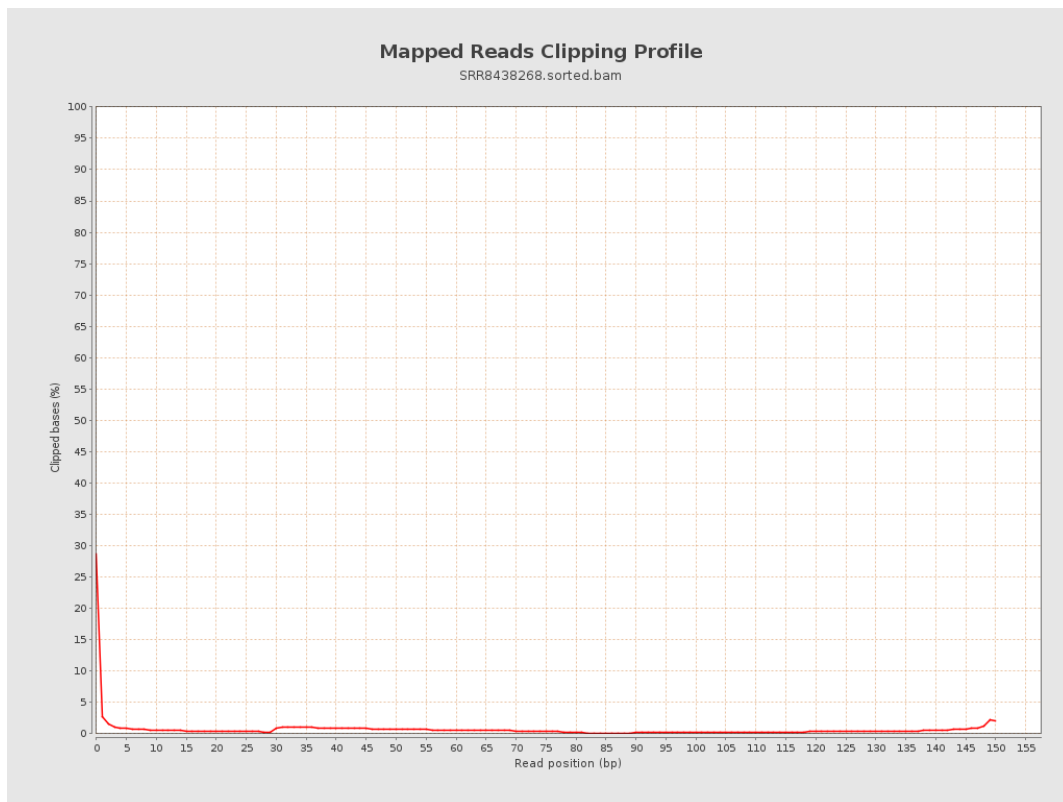
8. Results : Mapped Reads Nucleotide Content



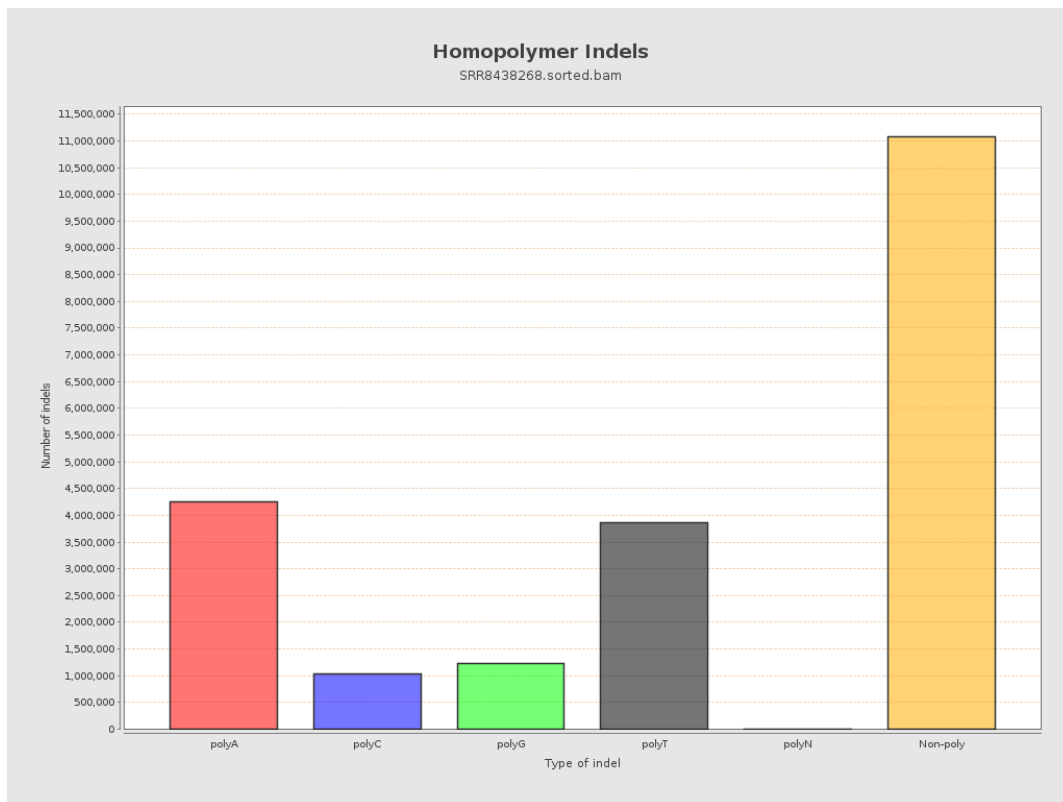
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



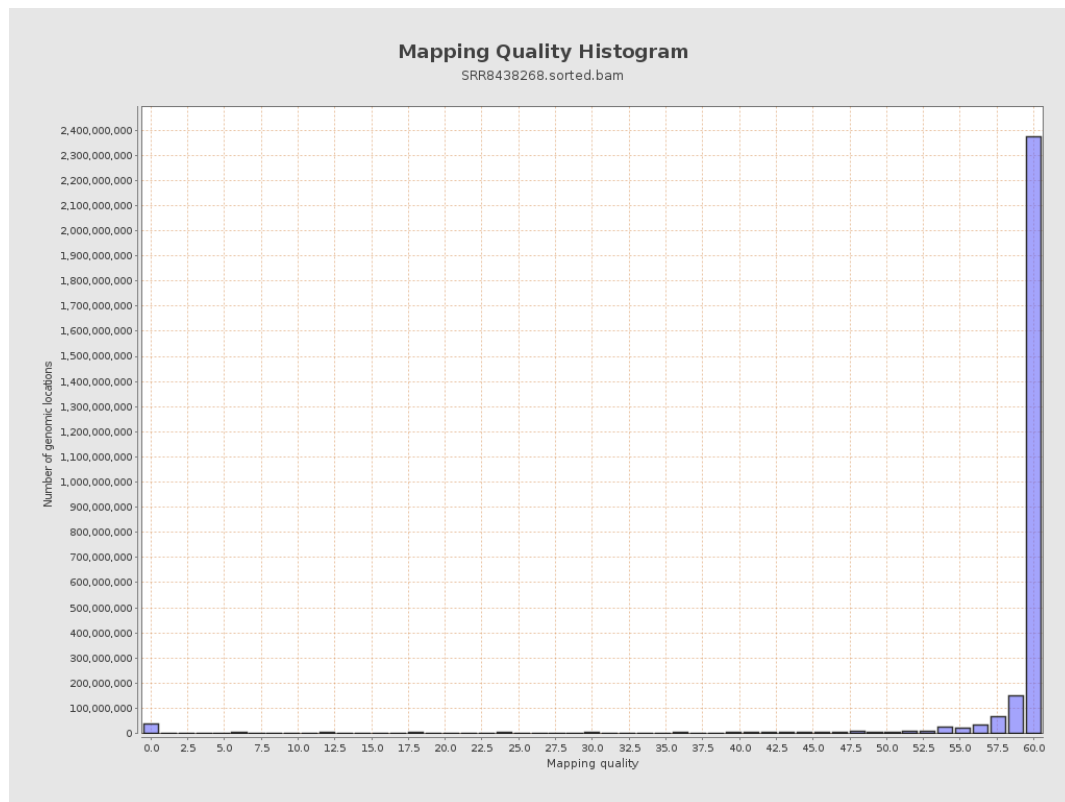
11. Results : Homopolymer Indels



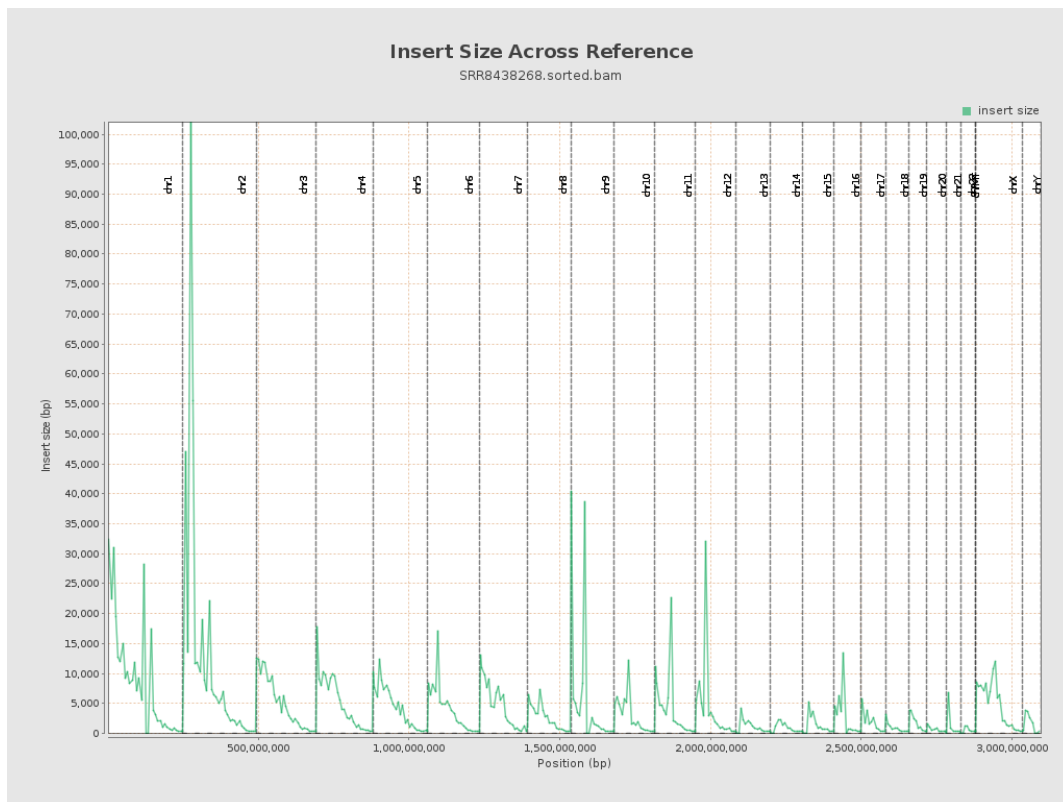
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

