

# *A Novel High-Throughput Acceleration Engine for Read Alignment*

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# Read Alignment: An Approximate Matching Problem

An individual's Genome Samples

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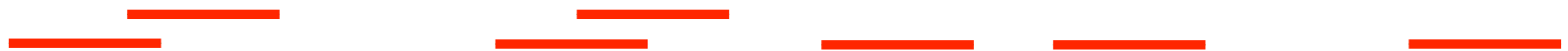
Fragmented into Pieces



Sequenced by Chemical Sequencer



Mapped by Software Aligner INDEPENDENTLY



# However...it is not as easy as we thought

## ◆ In theory

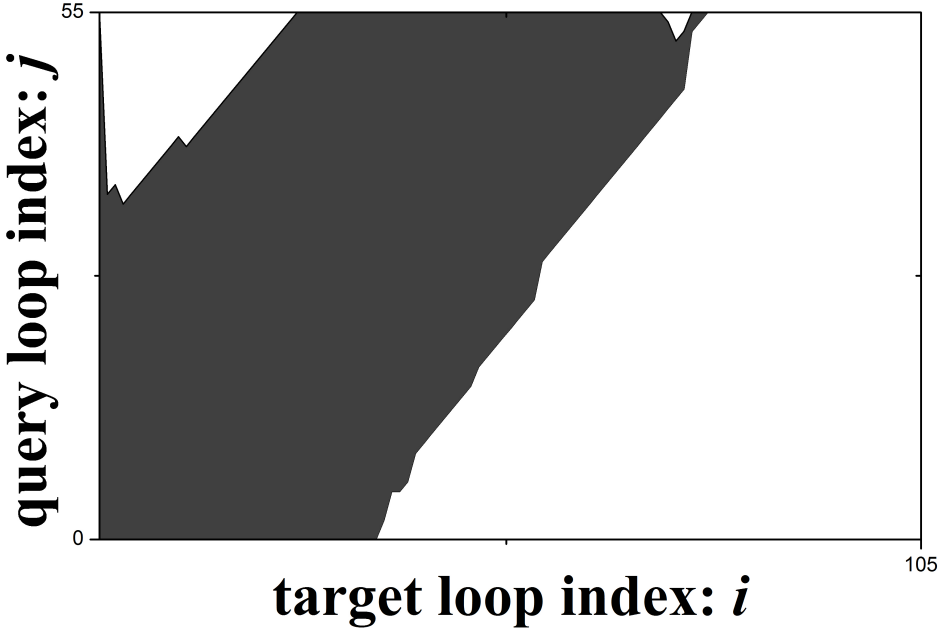
$$H(i, j) = \max \left\{ \begin{array}{l} 0 \\ H(i-1, j-1) + w(a_i, b_j) \quad \text{Match/Mismatch} \\ H(i-1, j) + w(a_i, -) \quad \text{Deletion} \\ H(i, j-1) + w(-, b_j) \quad \text{Insertion} \end{array} \right\}, 1 \leq i \leq m, 1 \leq j \leq n$$

~ 30 Lines of C Code, Simple, Well-shaped, Anti-diagonal Parallelism, Well Studied

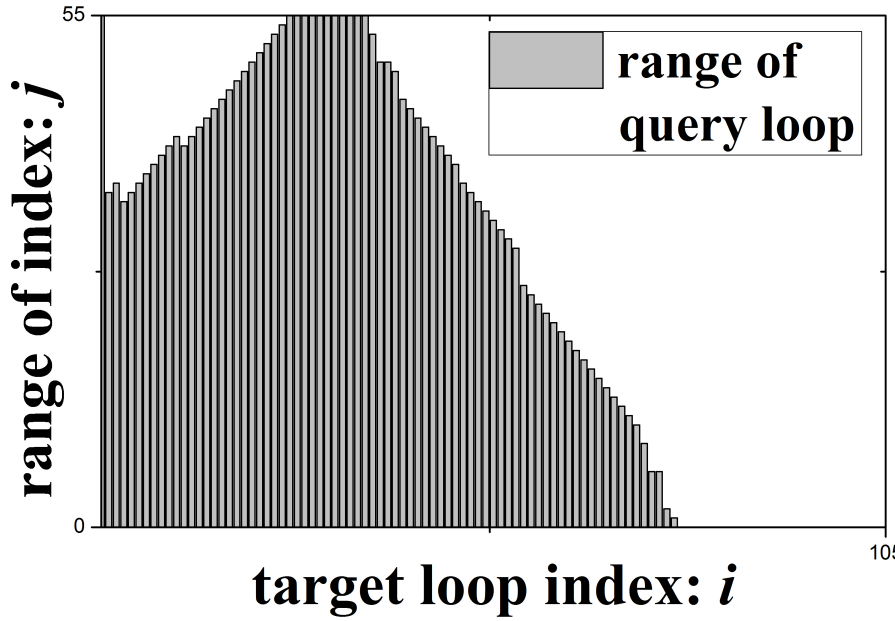
## ◆ In practice...

~ 150 Lines of C Code, Complicated, Full of Dependencies, No Parallelism,  
Existing work can not even achieve the same results

# Challenge 1: Bioinformaticians have done something we dislike



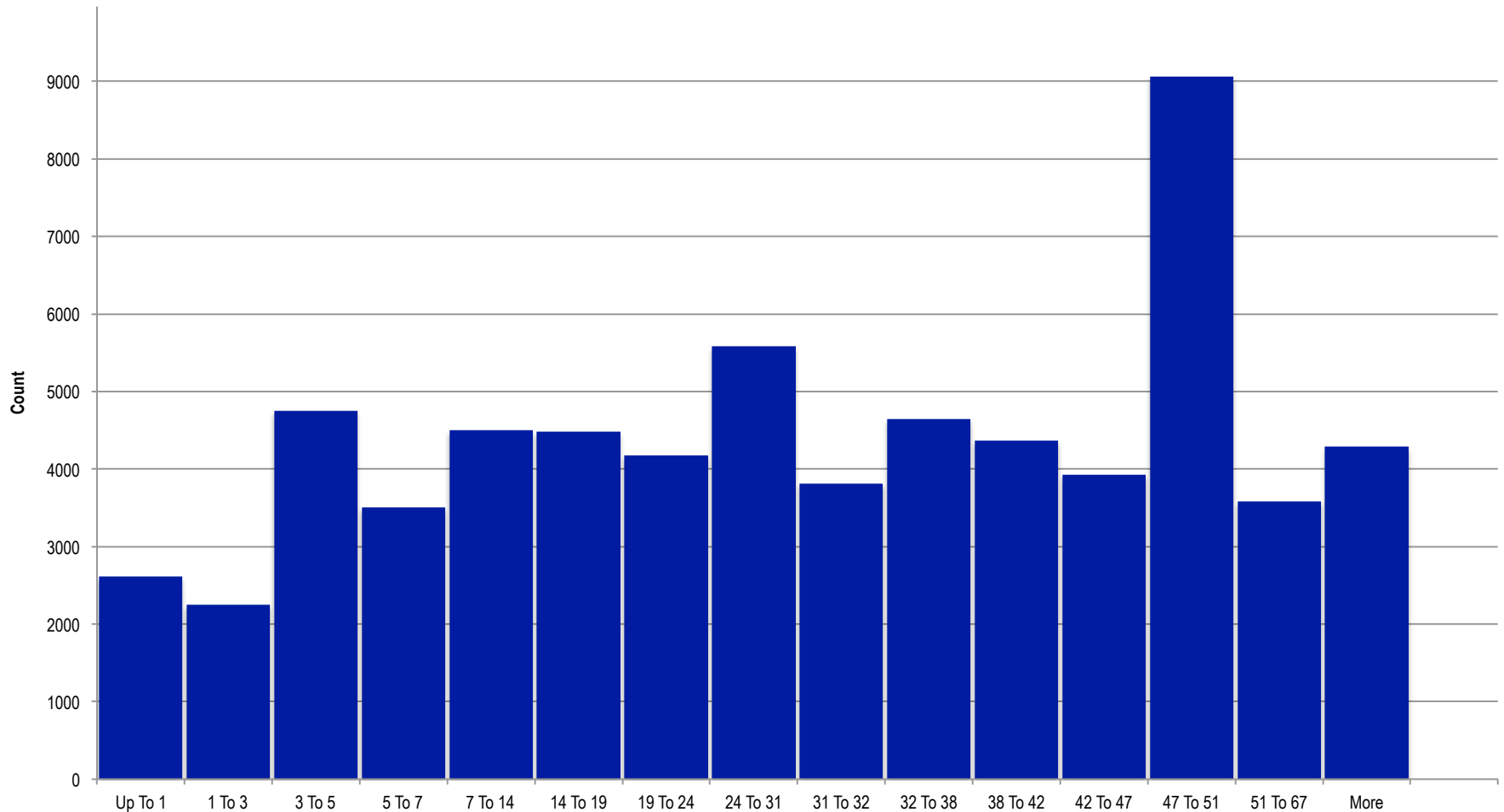
|   |   |   |   |   |    |    |    |    |
|---|---|---|---|---|----|----|----|----|
| - | A | C | A | C | A  | C  | T  | A  |
| 0 | 0 | 0 | 0 | 0 | 0  | 0  | 0  | 0  |
| 0 | 2 | 1 | 2 | 1 | 2  | 1  | 0  | 2  |
| 0 | 1 | 1 | 1 | 1 | 1  | 1  | 0  | 1  |
| 0 | 0 | 3 | 2 | 3 | 2  | 3  | 2  | 1  |
| 0 | 2 | 2 | 5 | 4 | 5  | 4  | 3  | 4  |
| 0 | 1 | 4 | 4 | 7 | 6  | 7  | 6  | 5  |
| 0 | 2 | 3 | 6 | 6 | 9  | 8  | 7  | 8  |
| 0 | 1 | 4 | 5 | 8 | 8  | 11 | 10 | 9  |
| 0 | 2 | 3 | 6 | 7 | 10 | 10 | 10 | 12 |



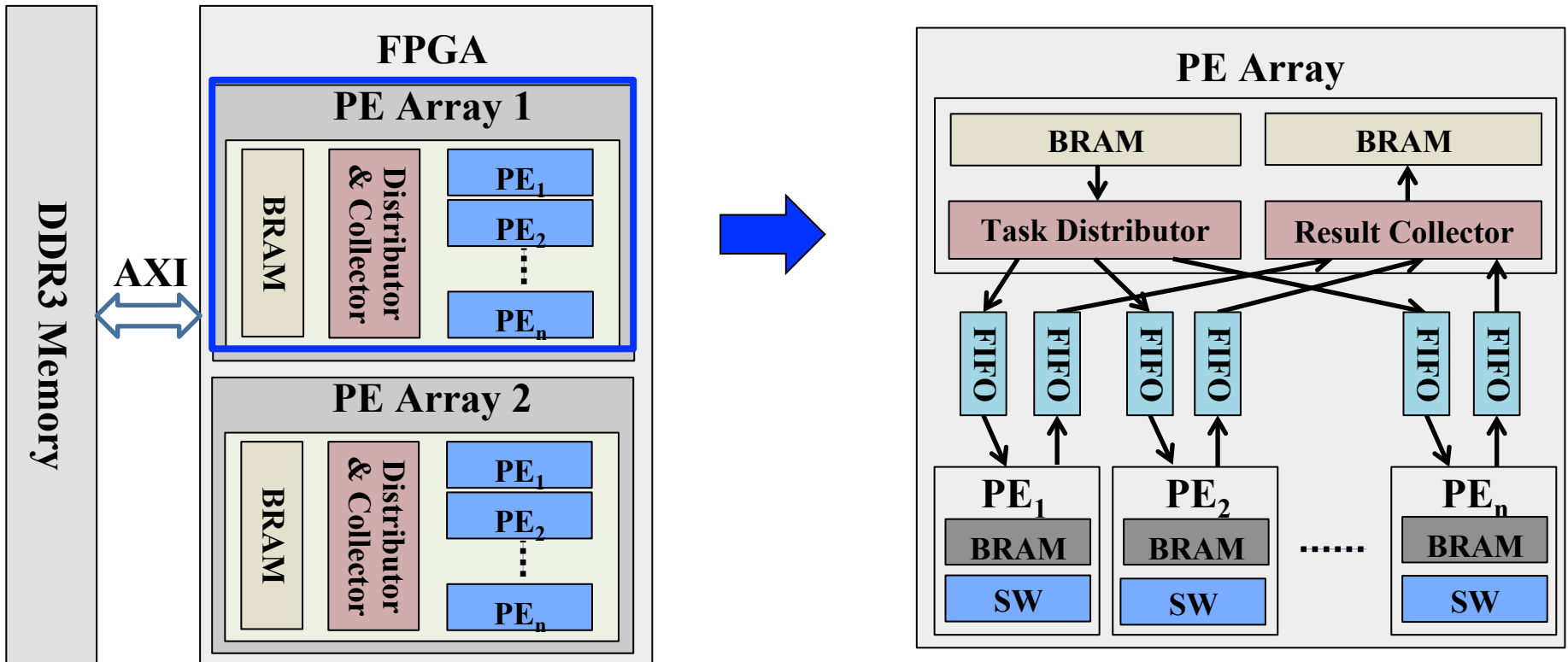
- Calculate ~50% of Matrix[i][j]-s
- Anti-diagonal parallelism disappears.
- It changes the results, raising a correctness issue.

## Challenge 2: Input Size Varies Dramatically

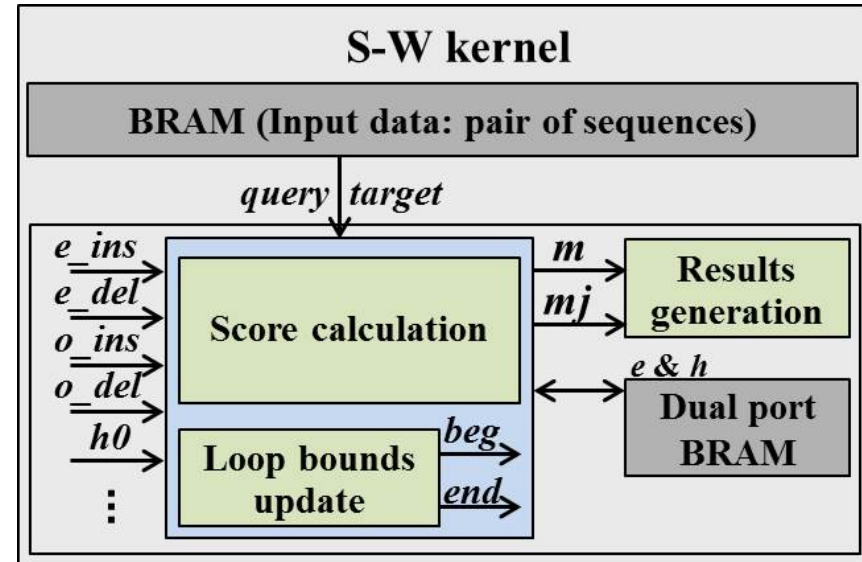
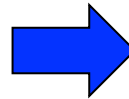
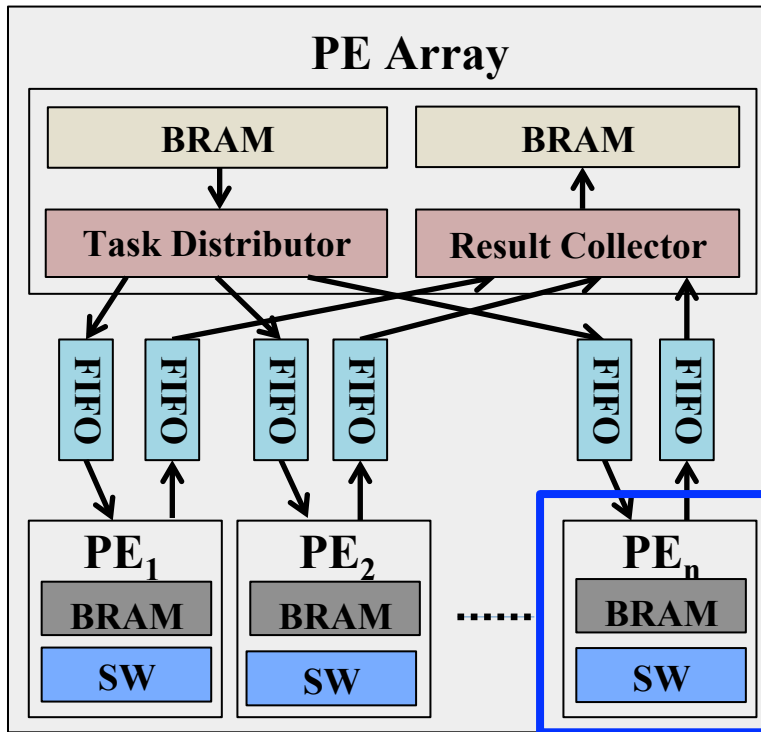
Query Length Histogram



# Accelerator Architecture

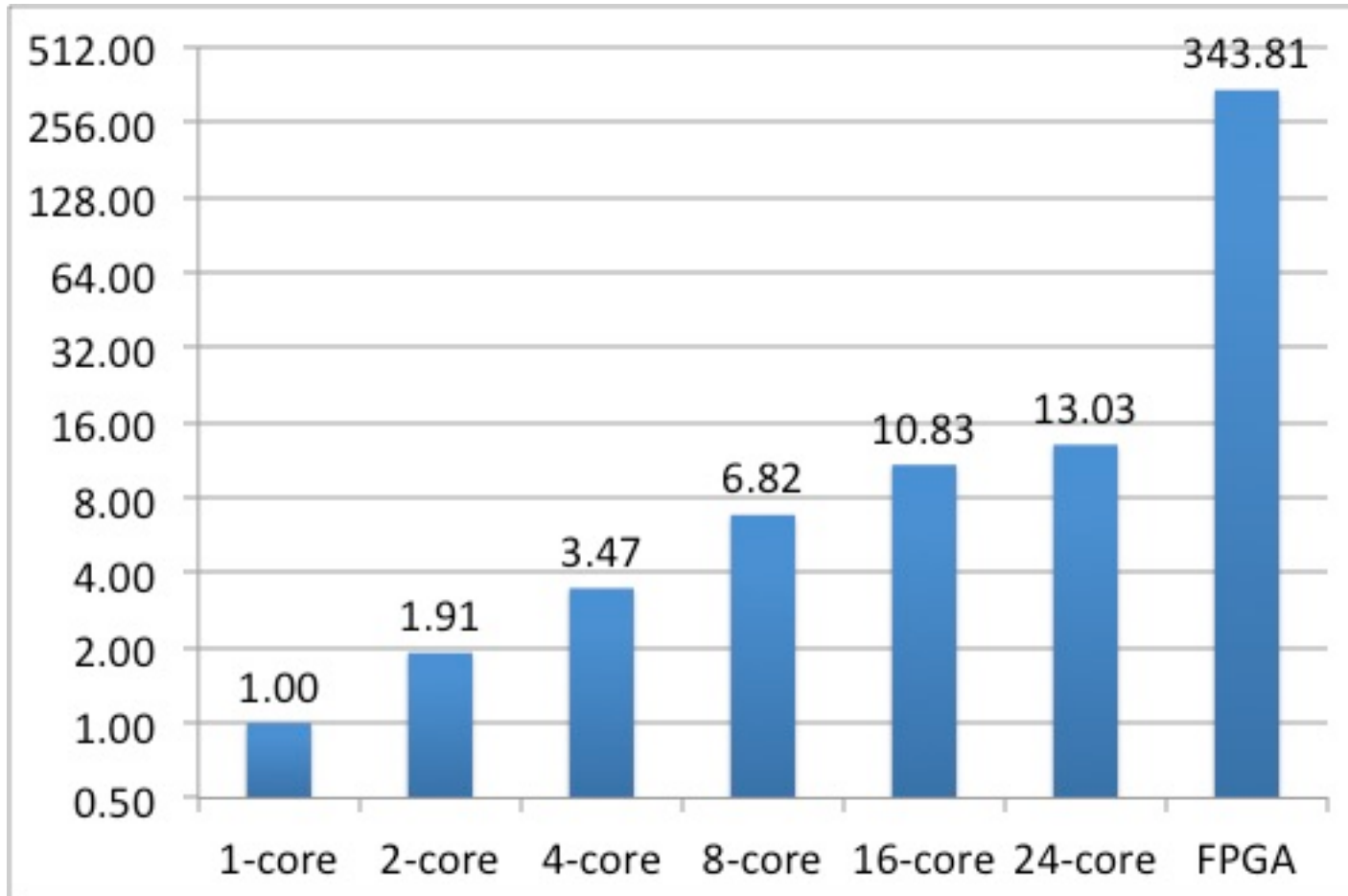


# Accelerator Architecture



# Experimental Results

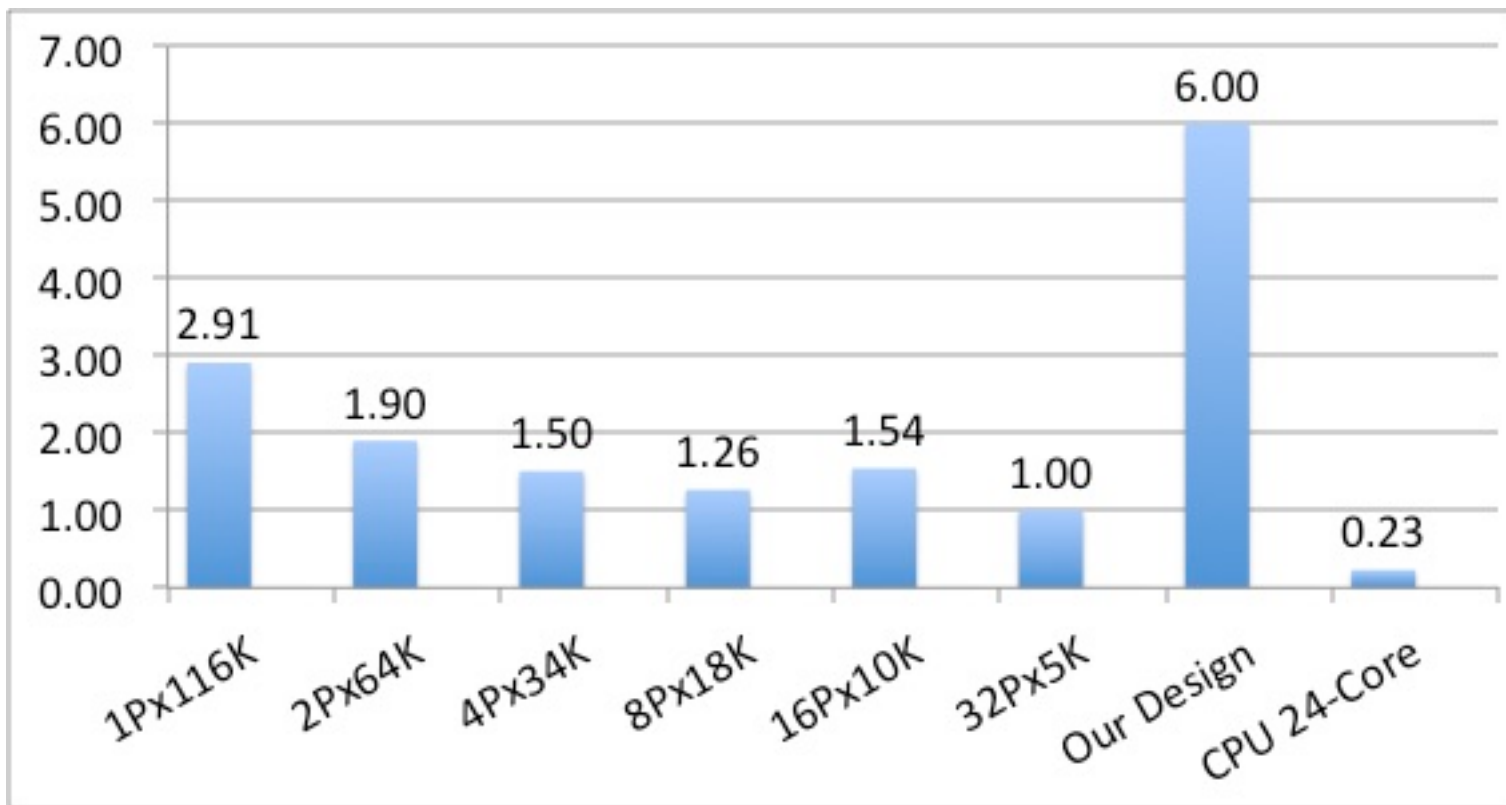
## ◆ Performance Improvement over CPU





# Experimental Results

## ◆ Performance Improvement Over Wavefront-based Designs





***THANKS!***