• Clustering Window Size: 700bp
• Individual Site p-value cutoff: .0003
• All binding sequences derived abd-A were removed
even-skipped

- Clustering Window Size: 700bp
- Individual Site p-value cutoff: .0003
- All binding sequences derived from eve were removed
hairy

- Clustering Window Size: 700bp
- Individual Site p-value cutoff: .0003

No clustering constraint (all sites plotted)

Minimum number of sites: 12

Minimum number of sites: 13

Minimum number of sites: 14
- Clustering Window Size: 700bp
- Individual Site p-value cutoff: .0003
- All binding sequences derived from *hb* were removed

**hunchback**

- No clustering constraint (all sites plotted)
- Minimum number of sites: 12
- Minimum number of sites: 13
- Minimum number of sites: 14
Minimum number of sites: 15

Minimum number of sites: 16

Minimum number of sites: 17

Minimum number of sites: 18
knirps

- Clustering Window Size: 700bp
- Individual Site p-value cutoff: .0003
- All binding sequences derived from *knirps* were removed
Krüppel

- Clustering Window Size: 700bp
- Individual Site p-value cutoff: .0003
- All binding sequences derived from Kr were removed

No clustering constraint (all sites plotted)

Minimum number of sites: 12

Minimum number of sites: 13

Minimum number of sites: 14
- Clustering Window Size: 700bp
- Individual Site p-value cutoff: 0.0003
- No binding sequences were derived from *runt*

No clustering constraint (all sites plotted)

Minimum number of sites: 12

Minimum number of sites: 13

Minimum number of sites: 14
spalt

- Clustering Window Size: 700bp
- Individual Site p-value cutoff: .0003
- All binding sequences derived from spalt were removed

No clustering constraint (all sites plotted)

Minimum number of sites: 12

Minimum number of sites: 13

Minimum number of sites: 14
Minimum number of sites: 15

Minimum number of sites: 16

Minimum number of sites: 17

Minimum number of sites: 18
- Ultrabithorax
- Clustering Window Size: 700bp
- Individual Site p-value cutoff: .0003
- All binding sequences derived from Ubx were removed
- Ubx transcription unit not shown due to size
- “Blank” area in first plot is a gap in the BDGP r.1 sequence
- Second unknown cluster contains several Knirps sites. Could represent a novel enhancer.

No clustering constraint (all sites plotted)

Minimum number of sites: 12

Minimum number of sites: 13

Minimum number of sites: 14