(a) Binding models generated using the top affinity binders from EMSA-Seq

from top 1000 binders

- RELARELA
- RELAp50
- RELAp52

Number of distinct 11-mers enriched during EMSA-Seq from a starting pool of 2,097,152 sequences:

<table>
<thead>
<tr>
<th>11-mers</th>
<th>RELARELA</th>
<th>RELAp50</th>
<th>RELAp52</th>
</tr>
</thead>
<tbody>
<tr>
<td>64847</td>
<td>15347</td>
<td>40478</td>
<td></td>
</tr>
<tr>
<td>(3.1%)</td>
<td>(0.7%)</td>
<td>(1.9%)</td>
<td></td>
</tr>
<tr>
<td>117942</td>
<td>19407</td>
<td>115552</td>
<td></td>
</tr>
<tr>
<td>(5.6%)</td>
<td>(0.9%)</td>
<td>(5.5%)</td>
<td></td>
</tr>
<tr>
<td>28411</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(1.4%)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

% non-canonical: 80% (MATCH<0.75)

% non-canonical: 72.3% (MATCH<0.75)

(b) RELAp50

% non-canonical: 72.3% (MATCH<0.75)

% non-canonical: 48% (MATCH<0.75)

% non-canonical: 59.3% (MATCH<0.75)

RELARELA

% non-canonical: 80% (MATCH<0.75)

% non-canonical: 72.3% (MATCH<0.75)

RELAp52

% non-canonical: 96% (MATCH<0.75)

% non-canonical: 90.1% (MATCH<0.75)

Figure 4