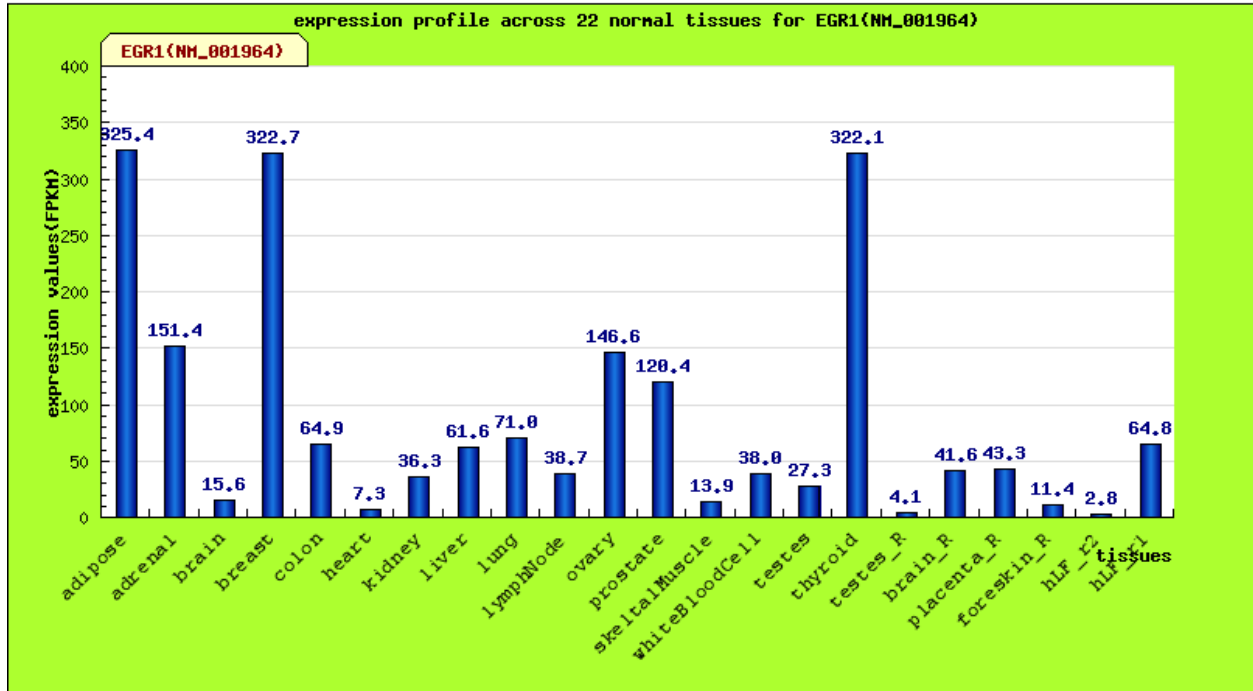


**Supplementary Table 1 – Comparison between mmHG-Finder and other motif discovery tools**

We evaluated the performance of mmHG-Finder in comparison to other state-of-the-art methods: MEME, DREME and XXmotif over 18 datasets. This table is more comprehensive than Table 1 and contains it.

The protein and its consensus binding motif	mmHG-Finder results	MEME results	DREME results	XXmotif results
<b>Synthetic TNWMNG</b>	6.28e-14 * 	2.2e+6 	Nothing found	2.98e+00 
<b>Synthetic CTNNAT</b>	2.37e-28 * 	5.8e+7 	Nothing found	1.84e+01 
<b>Synthetic MMMMMMM</b>	1.69e-39 * 	4.1e+6 * 	Nothing found	1.58e+01 * 
<b>P53 (DNA)</b> 	1.09e-174 * 	4.6e-7 * 	4.9e-133 * 	1e-490 * 
<b>REB1 (DNA)</b> <b>TTACCCG</b>	1.54e-132 * 	4.3e-88 * 	1.1e-80 * 	3.15e-89 * 
<b>CBF1 (DNA)</b> <b>tCACGTG</b>	1.84e-75 * 	2.3e-59 * 	1.1e-39 2.0e-023 (4 <sup>th</sup> best) * 	5.00e-15 2.72e-10 (3 <sup>rd</sup> best) * 
<b>UME6 (DNA)</b> <b>taGCCGCCsa</b>	5.11e-83 * 	3.8e-76 * 	3.1e-45 5.1e-030 (3 <sup>rd</sup> best) * 	3.52e-47 * 
<b>TYE7 (DNA)</b> <b>tCACGTGa</b>	1.39e-38 * 	2.1e-30 * 	7.3e-43 1.7e-018 (4 <sup>th</sup> best) * 	9.26e-21 1.11e-10 (3 <sup>rd</sup> best) * 
<b>GCN4 (DNA)</b> <b>TGAsTCa</b>	1.8e-45 * 	1.7e-16 * 	2.0e-32 2.5e-005 (9 <sup>th</sup> best) * 	4.00e-17 
<b>Puf5 (RNA)</b> 	6.95e-80 * 	8.9e+1 * 	6.8e-42 3.1e-012 * 	9.76e-21 1.61e-20 * 





**Supplementary Figure 1 – EGR1 expression profile**

The expression profile of EGR1 in 22 tissues is shown below. As can be seen, EGR1 is highly expressed in thyroid, adipose and breast. We note that the expression values for the lncRNAs were obtained for the same set of tissues (in our analysis we excluded replicates and focused on 19 distinct tissues).