

Supplementary Tables and Figures

Physical Peculiarity of Two Sites in Human Promoters: Universality and Diverse Usage in Gene Function

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Supplementary Table S1. Known human CPEs for transcription by Pol II.

CPE ¹	Consensus sequence ²	Position ³	Reference
TATA box	TATAWAWR	−31 - −24	Goldberg, M. L., Thesis, Stanford University, Stanford, CA, USA, 1979 Bucher, P., <i>J. Mol. Biol.</i> 1990 , <i>212</i> , 563–578
Inr	BBCABW	−3 - +3	Javahery, R.; et al., <i>Mol. Cell Biol.</i> 1994 , <i>14</i> , 116–127 Smale, S. T.; et al., <i>Cold Spring Harb. Symp. Quant. Biol.</i> 1998 , <i>63</i> , 21–31
TCT	YYCTTTY	−2 - +6	Parry, T. J.; et al., <i>Genes Dev.</i> 2010 , <i>24</i> , 2013–2018
DPE (RGWCGTG)	RGWCGTG	+28 - +34	Burke, T. W.; Kadonaga, J. T., <i>Genes Dev.</i> 1997 , <i>11</i> , 3020–3031
DPE (RGWYVT)	RGWYVT	+28 - +33	Burke, T. W.; Kadonaga, J. T., <i>Genes Dev.</i> 1997 , <i>11</i> , 3020–3031
BREu	SSRCGCC	−38 - −32	Lagrange, T.; et al., <i>Genes Dev.</i> 1998 , <i>12</i> , 34–44
BREd	RTDKKKK	−23 - −17	Deng, W.; Roberts, S.G.E.; <i>Genes Dev.</i> 2005 , <i>19</i> , 2418–2423
DRE	WATCGATW	−100 - −1	Hirose, F.; et al., <i>J. Biol. Chem.</i> 1993 , <i>268</i> , 2092–2099
XCPE1	DSGYGGRASM	−8 - +2	Tokusumi, Y.; et al., <i>Mol. Cell. Biol.</i> 2007 , <i>27</i> , 1844–1858
XCPE2	VCYCRTTRCMY	−9 - +2	Anish, R.; et al., <i>PLoS ONE</i> 2009 , <i>4</i> , e5103
Pause button	KCGRWCG	+25 - +35	Hendrix, D.A.; et al., <i>Proc. Natl Acad. Sci. USA</i> 2008 , <i>105</i> , 7762–7767
DCEI	CTTC	+6 - +11	Lewis, B. A., et al., <i>Proc. Natl Acad. Sci. USA</i> 2000 , <i>97</i> , 7172–7177
DCEII	CTGT	+16 - +21	Lewis, B. A., et al., <i>Proc. Natl Acad. Sci. USA</i> 2000 , <i>97</i> , 7172–7177
DCEIII	AGC	+30 - +34	Lewis, B. A., et al., <i>Proc. Natl Acad. Sci. USA</i> 2000 , <i>97</i> , 7172–7177

¹Core promoter element, ²B = C or G or T; D = A or G or T; K = G or T; M = A or C; R = A or G; S = C or G; V = A or C or G; W = A or T; Y = C or T.

³Relative to the TSS.

Supplementary Table S2. Ratios of CPE(s)-containing human Pol II gene promoters.

CPE(s) ¹	Count	Ratio (%)
Core-less	12,031	57.1
Inr	5,575	26.5
DPE	598	2.8
BREd	511	2.4
BREu	468	2.2
TATA	295	1.4
Inr + DPE	290	1.4
BREd + Inr	212	1.0
TCT	186	0.9
Inr + TATA	171	0.8
BREu + Inr	158	0.8
Pause button	151	0.7
XCPE1	58	0.3
Inr + Pause button	41	0.2
TATA + DPE	31	0.1
Inr + TCT	29	0.1
BREd + DPE	28	0.1
DCE	19	0.1
Inr + DCE	17	0.1
TCT + DPE	14	0.1
BREd + TATA	13	0.1
BREd + Inr + DPE	12	0.1
BREu + Pause button	11	0.1
BREd + BREu	9	0.0
BREd + TCT	9	0.0
BREu + DPE	9	0.0
Pause button + DPE	8	0.0
Inr + TATA + DPE	7	0.0
Inr + XCPE1	7	0.0
DRE	6	0.0
BREd + XCPE1	5	0.0
BREu + XCPE1	5	0.0
Inr + Pause button + DPE	5	0.0
Inr + XCPE2	5	0.0
BREd + Inr + TATA	4	0.0
BREu + Inr + DPE	4	0.0
BREu + Inr + Pause button + DPE	4	0.0
BREu + TCT	4	0.0
BREd + BREu + Inr	3	0.0
BREd + Inr + TCT	3	0.0

BREd + Pause button	3	0.0
Inr + TCT + DPE	3	0.0
TATA + TCT	3	0.0
TATA + TCT + DPE	3	0.0
BREd + DCE	2	0.0
BREu + Inr + Pause button	2	0.0
BREu + TCT + DPE	2	0.0
Pause button + XCPE1	2	0.0
XCPE2	2	0.0
BREd + BREu + DPE	1	0.0
BREd + Inr + Pause button	1	0.0
BREd + TATA + XCPE1	1	0.0
BREd + XCPE1 + DPE	1	0.0
BREu + Inr + XCPE1	1	0.0
BREu + Pause button + DPE	1	0.0
BREu + Pause button + XCPE1	1	0.0
BREu + TATA	1	0.0
BREu + XCPE2	1	0.0
DCE + DPE	1	0.0
DRE + Inr + TCT	1	0.0
DRE + TATA	1	0.0
Inr + DCE + DPE	1	0.0
Inr + Pause button + TATA + DPE	1	0.0
Inr + TATA + DCE	1	0.0
Inr + XCPE1 + DPE	1	0.0
Pause button + TATA	1	0.0
XCPE1 + DPE	1	0.0
<hr/>		
TATA-containing promoters	533	2.5
Inr-containing promoters	6,559	31.2
Other CPE-containing promoters	1,933	9.2

¹Core promoter element(s).

Supplementary Table S3. Numerical values for DPPs at each position of the aligned all human Pol II gene promoters.

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Supplementary Table S4. Numerical values for DPPs at each position of the aligned core-less promoters.

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Supplementary Table S5. Numerical values for DPPs at each position of the aligned Inr-containing promoters.

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Supplementary Table S6. Numerical values for DPPs at each position of the aligned TATA-containing promoters.

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Supplementary Table S7. Canonical position(s) for the occurrence of distinctive DPPs.

DPPs	Group	Maximum value	Minimum value	Maximum rate of change	Minimum rate of change
DNA denaturability	<i>e</i>	+1 or -27	—	+2 or -26	-2 or -31
Duplex disrupt energy	<i>e</i>	—	0 or -27	-1 or -31	+2 or -26
Duplex DNA free energy	<i>e</i>	0 or -27	—	+2 or -26	-1 or -31
Base stacking energy	<i>e</i>	-1 or -27	-2	-1 or -25	-2 or -32
DNA bending stiffness	<i>m</i>	—	+1 or -27	-2 or -32	+2 or -26
Protein-induced deformability	<i>m</i>	-1	0 or -26	-1 or -29	-2 or -26
Flexibility	<i>m</i>	-1 or -30	0, -4 or -26	-1 or -28	0 or -25
Rigidity	<i>m</i>	-4, 0 or -27	-2	-4 or -26	-1 or -29
Stabilizing energy of Z DNA (AS)	<i>z</i>	0, -2 or -28	-1	-2 or -26	-1 or -31
Stabilizing energy of Z DNA (SA)	<i>z</i>	-1 or -27	-2 or 0	-1 or -25	-2 or -32

Supplementary Table S8. Numerical values for DPPs at each position of the aligned promoters of the cluster 1 genes in Fig. 5a.

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Supplementary Table S9. Numerical values for DPPs at each position of the aligned promoters of the cluster 2 genes in Fig. 5a.

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Supplementary Table S10. Numerical values for DPPs at each position of the aligned promoters of the cluster 3 genes in Fig. 5a.

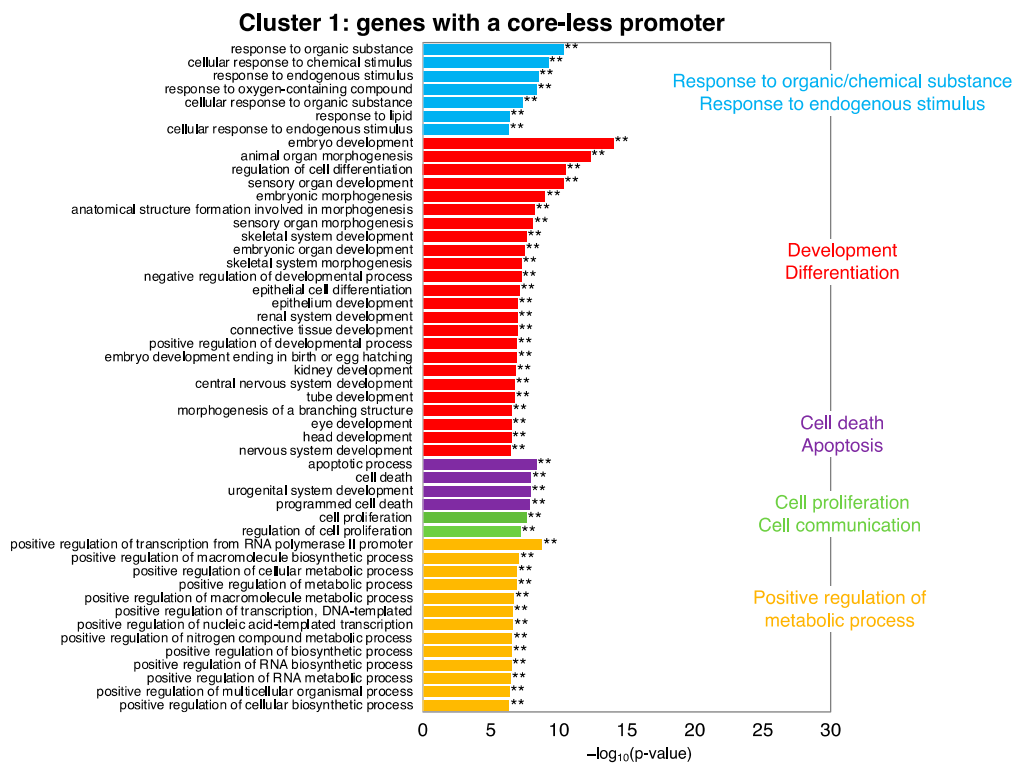
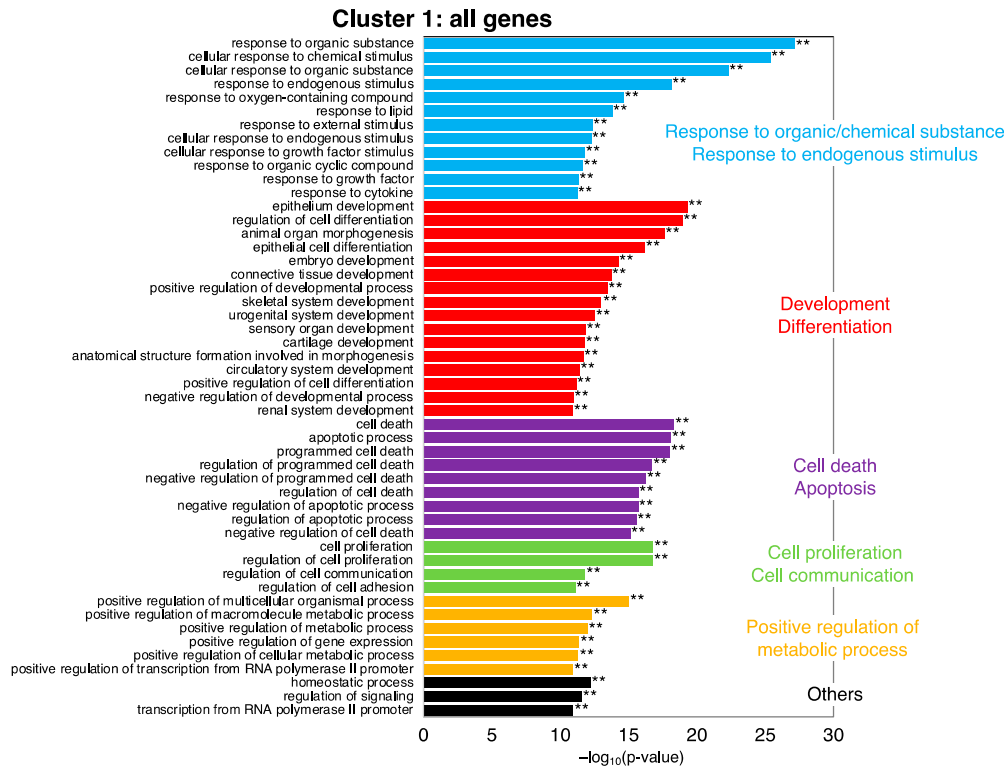
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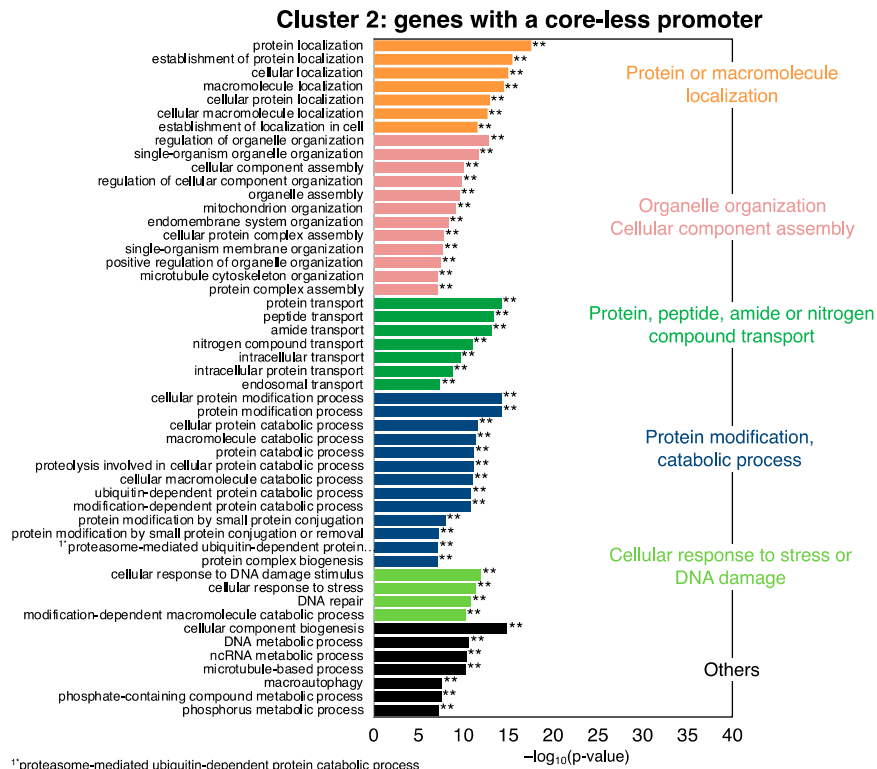
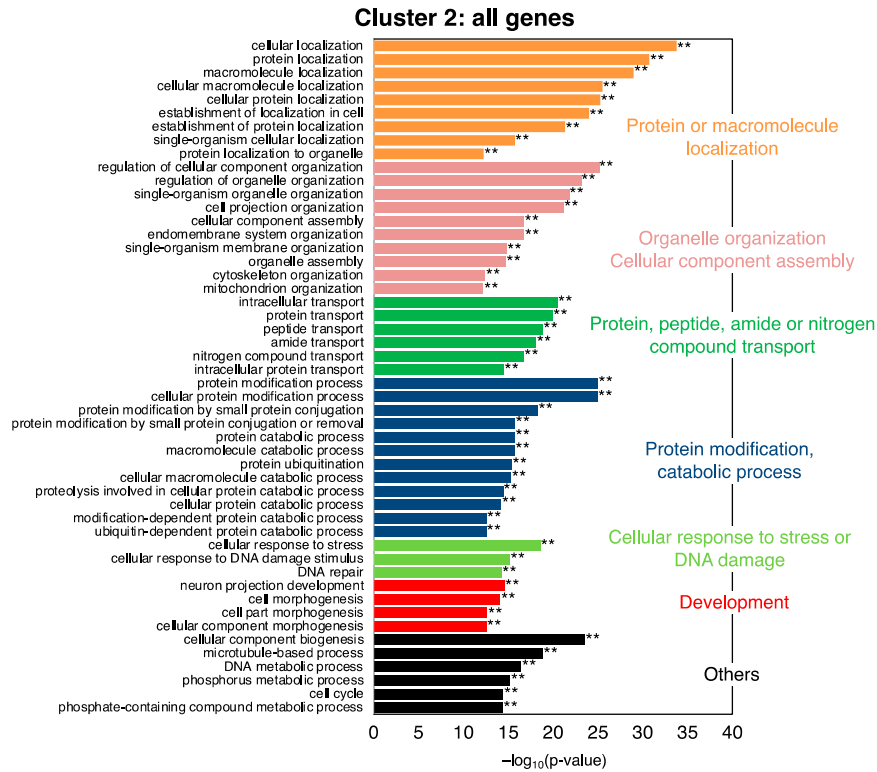
Supplementary Table S11. Numerical values for DPPs at each position of the aligned promoters of the cluster 4 genes in Fig. 5a.

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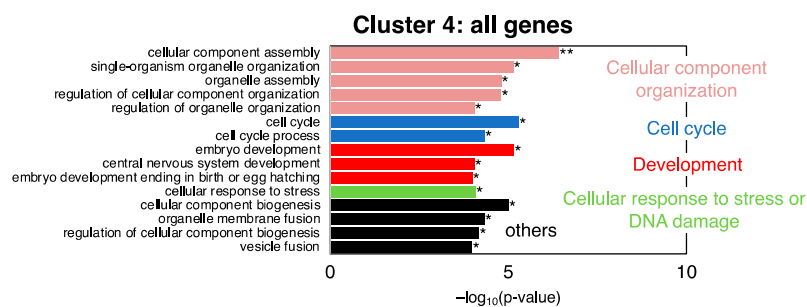
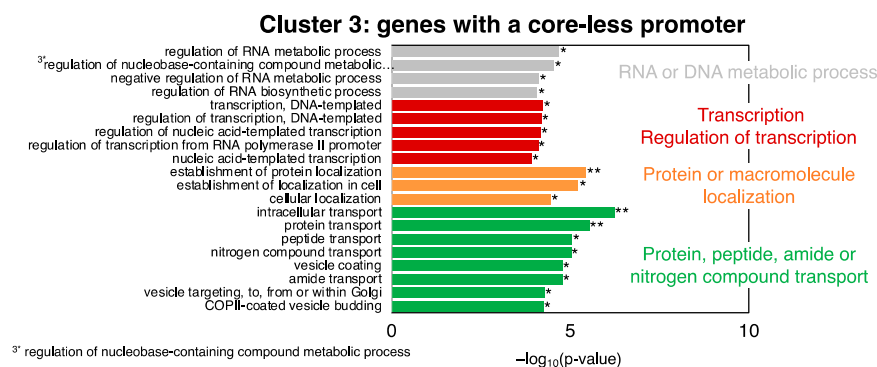
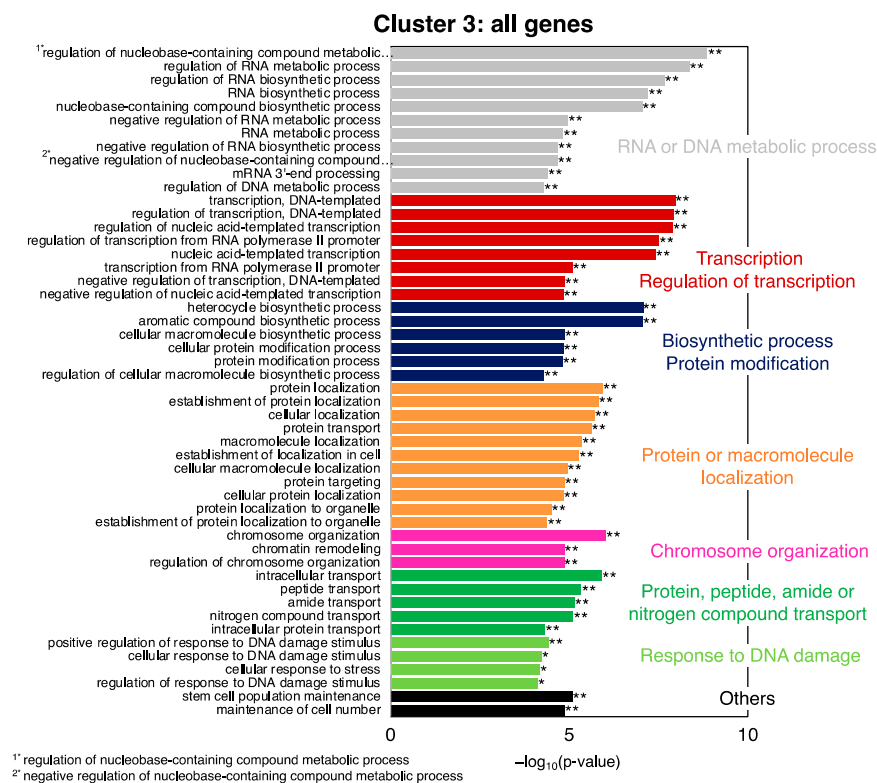
Supplementary Table S12. Proportions of two built-in marks.

The 1st mark	The 2nd mark	All genes		Genes with a core-less promoter	
		Count	Ratio (%)	Count	Ratio (%)
+	+	15,604	74.1	9,032	75.1
+	–	523	2.5	335	2.8
+ or –	+	20,404	96.9	11,619	96.6
–	+	4,800	22.8	2,587	21.5
–	–	129	0.6	77	0.6
+	+ or –	16,127	76.6	9,109	75.7

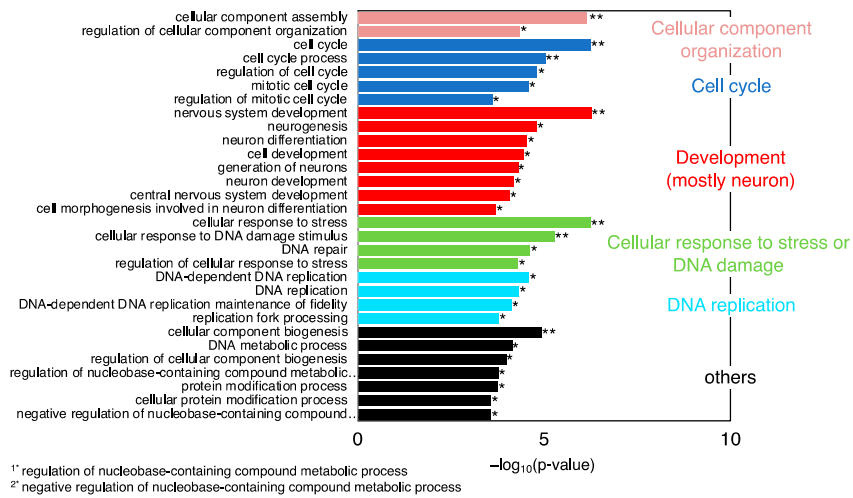


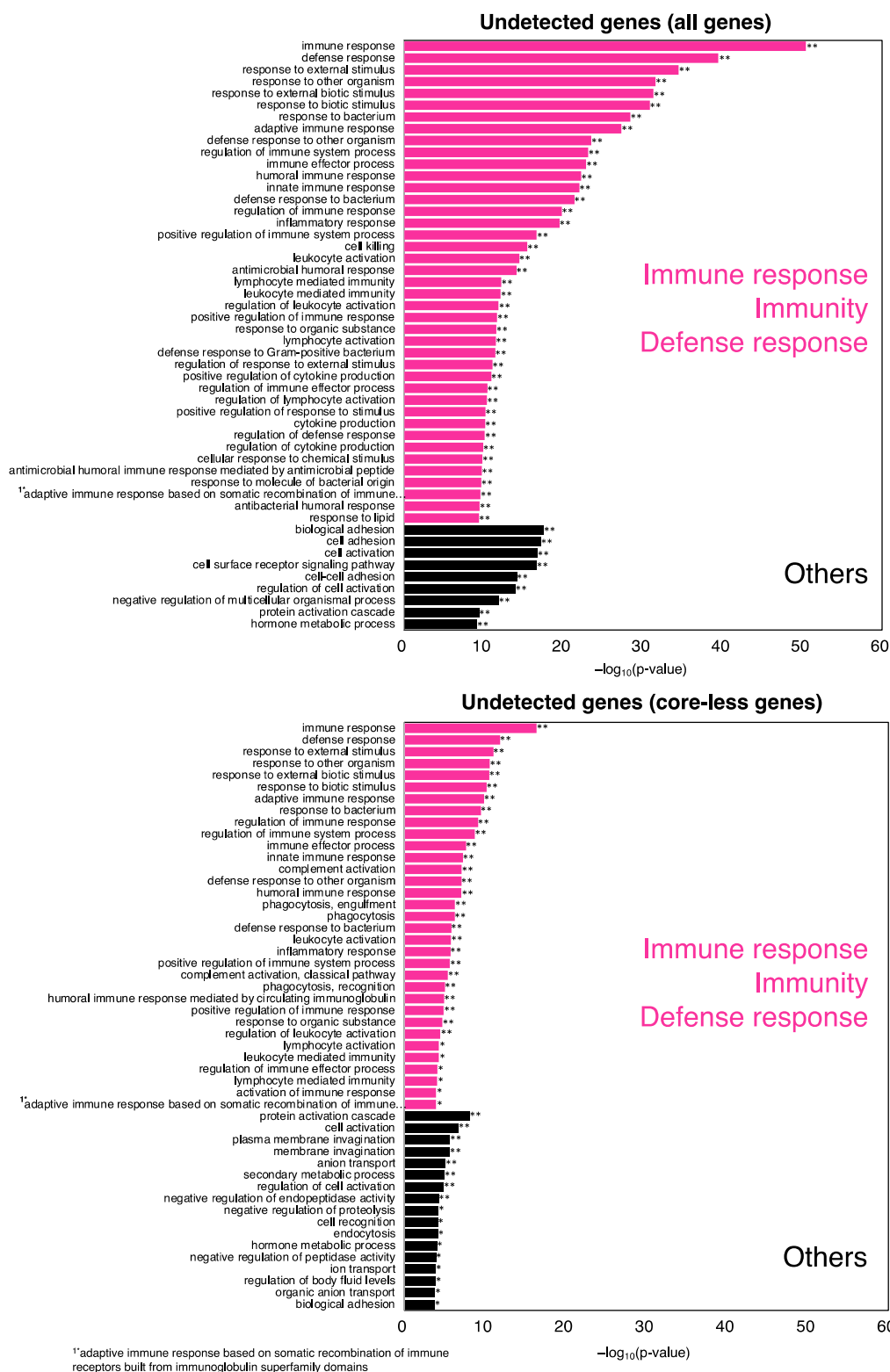


¹proteasome-mediated ubiquitin-dependent protein catabolic process



Cluster 4: genes with a core-less promoter





Supplementary Figure S2. Non-abbreviated version of Fig. 6a.