

## **Enriched Domain Detector: a program for detection of wide genomic enrichment domains robust against local variations**

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### **SUPPLEMENTARY DATA**

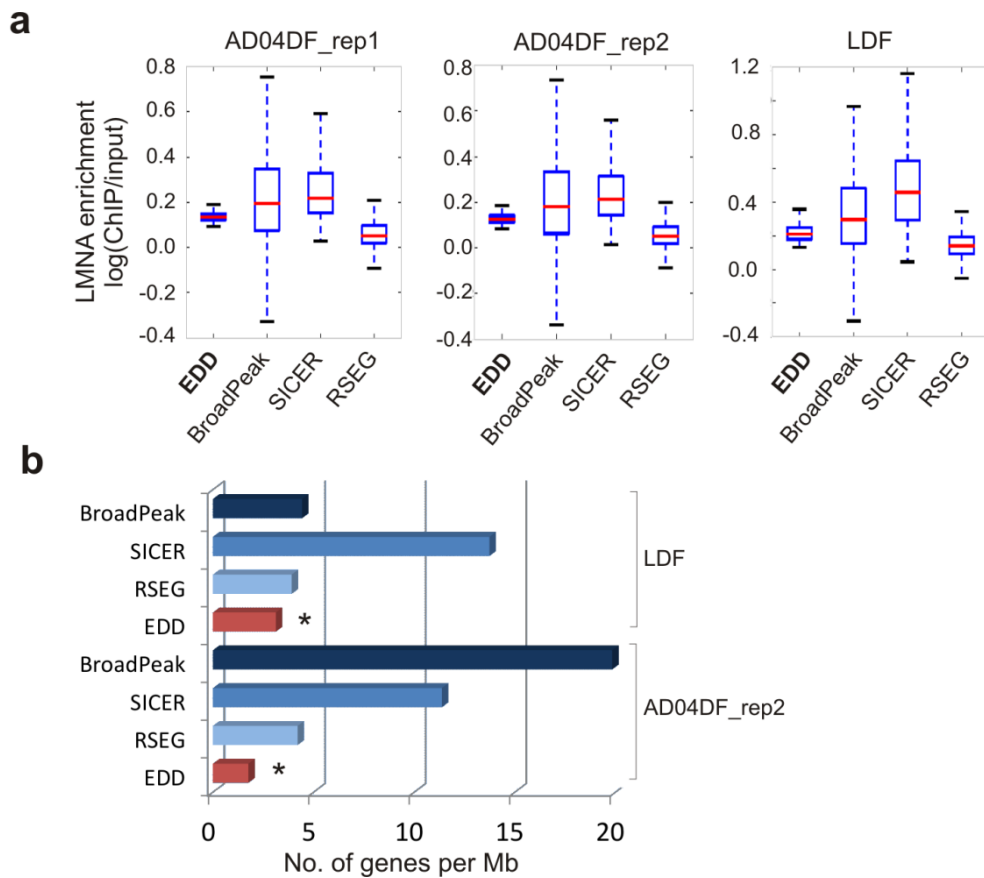
**Figure S1.** LMNA enrichment and gene density within peaks identified by EDD, BroadPeak, SICER and RSEG.

**Figure S2.** LMNA enrichment detected by ChIP-seq negatively correlates with gene expression.

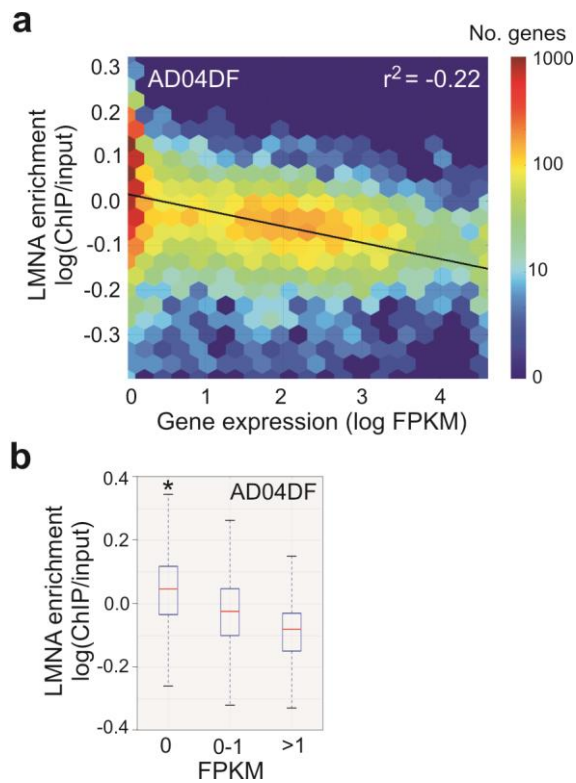
**Table S1.** Effect of including or excluding duplicate LMNA or LMNB1 ChIP-seq reads on genome coverage under LADs identified by EDD

**Table S2.** ChIP-qPCR primers used in this study

**Table S3.** P-values and W values returned by the Wilcoxon rank-sum tests performed in this study



**Figure S1.** LMNA enrichment and gene density within peaks identified by EDD, BroadPeak, SICER and RSEG. **(a)** Median LMNA enrichment within peaks detected by the indicated algorithms. **(b)** Number of protein-coding genes per megabase covered by indicated peak callers in AD04DFs (replicate 2) and LDFs (\* $P < 0.001$ , Wilcoxon rank-sum test;  $W = 0$  for each comparison).



**Figure S2.** LMNA enrichment detected by ChIP-seq negatively correlates with gene expression level. **(a)** Heat map of LMNA enrichment in AD04DFs (y axis) on protein-coding genes of > 1 Kb as a function of gene expression level (log FPKM, x axis). **(b)** Median LMNA enrichment level in protein-coding genes of > 1 Kb that are repressed (FPKM = 0; 3833 genes), weakly expressed (FPKM = 0-1; 3435 genes) and highly expressed (FPKM > 1; 7795 genes). \* $P < 10^{-80}$  relative to FPKM = 0-1 or FPKM > 1; Wilcoxon rank-sum test; see Supplementary Table S3 for W and P values.

## SUPPLEMENTARY DATA

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**Table S1.** Effect of including or excluding duplicate LMNA or LMNB1 ChIP-seq reads on genome coverage under LADs identified by EDD

ChIP sample	Cell type	Genome coverage (Mb)				Jaccard index
		Including duplicate reads	Excluding duplicate reads	Intersect	Union	
LMNA	AD04DF_rep1	676.20	728.18	651.6	752.8	0.865
LMNA	AD04DF_rep2	702.38	721.50	675.7	748.2	0.903
LMNA	LDF	809.15	694.66	654.9	848.9	0.771
LMNB1	IMR90_rep1	1025.74	1041.67	1011.7	1055.7	0.958
LMNB1	IMR90_rep2	1033.64	1078.18	1021.0	1090.8	0.936
LMNB1	IMR90_rep3	1025.74	1041.67	1011.7	1055.7	0.958

**Table S2.** ChIP-qPCR primers used in this study

<b>Gene</b>	<b>Forward primer (F) Reverse primer (R)</b>	<b>Position rel. to TSS (nt)</b>	<b>Product size (bp)</b>
<u>Genic regions</u>			
<i>DNAL4</i>	F: TACGAAGCCACCCACAGTTC R: CTGGCTCTTTCCAAGGAGGG	-2209 / -2077	133
<i>RPA4</i>	F: TAGGGTGGGCTGAAAAACAG R: CCGGATTGCTGGTTAAAGA	-2437 / -2124	139
<i>SCN10A</i>	F: GGAAGAGGGTGAGGGAAAGC R: TGTCACCAGTCCTTCCATGC	-3414 / -3297	149
<i>DEFA3</i>	F: AGCCCTTCACATCCATTGGG R: CCCGGGCATGGTCTAGAATC	-2414 / -2337	78
<i>ACTL7A</i>	F: GGATCAGGTTTCAGGGTGTGG R: GGACCTAGCGTGCAACTCTT	+1723 / +1859	137
<i>BACE2</i>	F: CCCAGCACCATAGGCTTGAA R: GGATGGCAGAGCTGTCTTGT	-1864 / -1732	133
<i>LDHB</i>	F: AAGCCTCTGGAAGGAGACCT R: TTGGAAATCCGAGTACCGCC	-182 / -60	123
<i>STX2</i>	F: CAAAGGACTGTGCACCAAGC R: CCAAGCACCCAGCACTCTAA	+684 / + 757	74
		<b>Genomic position (nt)</b>	
<u>Intergenic regions</u>			
Chr12 r2	F: CTCCCAGGCATGTCTCACTT R: GAATGCTTTGCAGTCACCCC	129887824-129888838	130
Chr8 r1	F: TGCTAGCTGACAGGTGATGC R: GTTGTTTCGTGCTAACGGCTG	6834856-6836060	51
Chr14 r1	F: AGCTAACAGGACAGAGTGCT R: TGTGCATGGGAAGGTCTTGG	104288010-104288880	56
Chr3 r1	F: CCCTCAGCATAGCGGTGTAG R: AGAACTCAGTGAGGGCTTGC	38868181-38873708	138

**Table S3.** P-values and W values returned by the Wilcoxon rank-sum tests performed in this study

<b>Analysis</b>	<b>Component1</b>	<b>Component2</b>	<b>P value</b>	<b>W value</b>
<b>LMNB1_rep1 peak length</b>				
Fig. 2b	EDD	BroadPeak	0	29210230
	EDD	PeakRanger	0	21323779
	EDD	RSEG	0	9385114
	EDD	SICER	0	63677469
<b>LMNA peak length, AD04DF_rep1</b>				
Fig. 4c	EDD	BroadPeak	2.32e-237	4699745
	EDD	PeakRanger	1.77e-205	715728
	EDD	RSEG	7.86e-99	839687
	EDD	SICER	3.42e-175	348564
<b>LMNA peak length, AD04DF_rep2</b>				
Fig. 4c	EDD	BroadPeak	3.42e-228	4510527
	EDD	PeakRanger	6.39e-198	672588
	EDD	RSEG	1.34e-75	617082
	EDD	SICER	7.19e-166	303093
<b>LMNA peak length, LDF</b>				
Fig. 4c	EDD	BroadPeak	3.38e-197	420145
	EDD	PeakRanger	2.72e-292	1369060
	EDD	RSEG	5.16e-93	1031357
	EDD	SICER	1.15e-262	833289
<b>LMNA enrichment as function of FPKM, LDF</b>				
Fig. 5c	FPKM 0	FPKM 0-1	1.47e-54	1135138
	FPKM 0	FPKM > 1	0	3526357
<b>LMNA enrichment as function of FPKM, AD04DF_rep1</b>				
Fig. S2b	FPKM 0	FPKM 0-1	6.71e-82	3145970
	FPKM 0	FPKM > 1	0	9372546