The mechanism of transactivation regulation due to polymorphic short tandem repeats (STRs) using *IGF1* promoter as a model

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Supplementary Information

Supplementary Table 1. Haplotypes of IGF1[a] promoter in the Chinese population of 169 normal subjects[b]

(A) Common haplotypes [c]

Haplotypes	Polymorphisms in the haplotypes			
	rs35767	Microsatellite	rs5742612	rs2288377
C17TT	C	17	T	T
C18TT	C	18	T	T
C19TT	C	19	T	T
T21CA	T	21	C	A

(B) Uncommon haplotypes[d] (most of them were constructed by in-vitro mutagenesis)

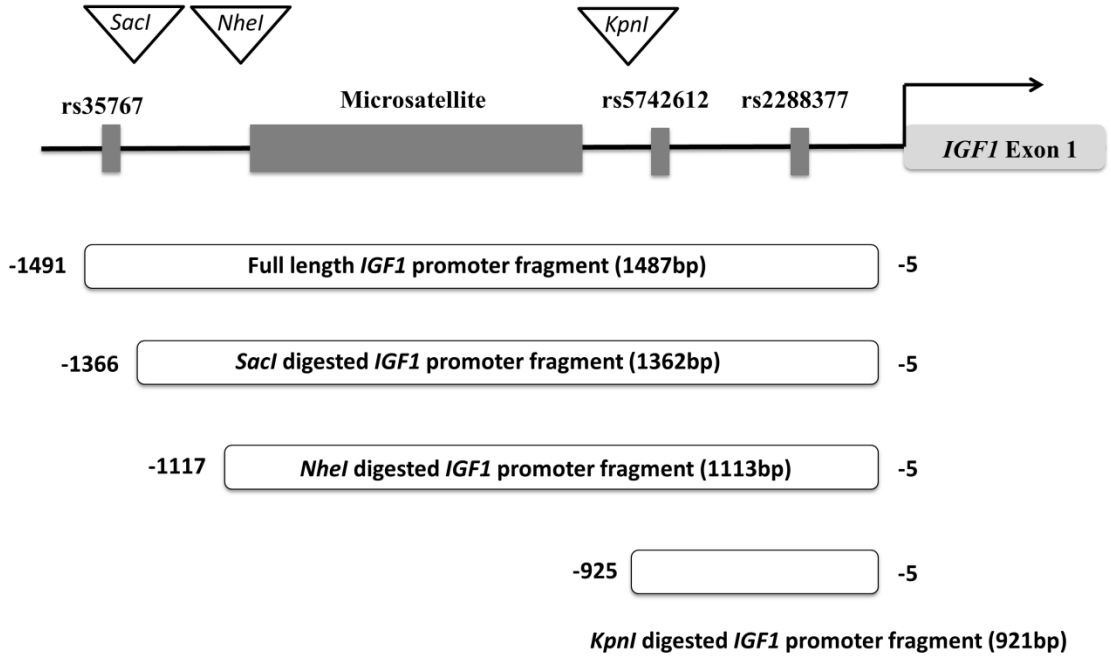
Haplotypes	Polymorphisms in the haplotypes			
	rs35767	Microsatellite	rs5742612	rs2288377
T17CA	T	17	C	A
T18CA	T	18	C	A
T19CA	T	19	C	A
C21TT	C	21	T	T
T17TT	T	17	T	T
T18TT	T	18	T	T
T19TT	T	19	T	T
T21TT	T	21	T	T

[a]IGF1 is short for insulin-like growth factor 1.

[b]The study subjects were described previously [23].

[c]Common haplotype is defined as a haplotype with frequency greater than 5%.

[d]Uncommon haplotype is defined as a haplotype with frequency less than 5%.



Supplementary Fig. 1 Serial 5' deletion of IGF1 promoter fragment. The horizontal line at the top of the figure depicts the IGF1 promoter region, and the arrow indicates the translation start site (TSS) of IGF1. The tagging genetic variants in this study are highlighted by rectangles, according to their relative positions in the promoter region. The triangles indicate the relative position of the restriction enzymes, *SacI*, *NheI* and *KpnI*. Bars at the lower part of the figure depict full length and digested promoter fragments. The number on the left of bars indicates the position of 5' end of fragments relative to TSS of IGF1, while the number on the right indicates the position of 3' end of fragments relative to TSS of IGF1.