SUPPLEMENTARY INFORMATION

Laminin β3 cDNA constructs and subcloning

Domain VI of the human laminin β3 chain (*HuLAMB3*) spans amino acid residues 1-232 and domain III/V residues 233-561 (1). The first deletion construct (ΔVI) begins at residue 229 thereby containing four amino acids of domain VI, one of which was changed during creation of an *Nhe* I site for cloning purposes (residue 230, a glycine, was exchanged for an alanine). The sequence encoding domain III/V begins with cysteine at aa 233 and the construct ends with the C-terminal stop codon of *HuLAMB3*, (aa 1153), encompassing domains I and II. Three pairs of PCR primers (**supplementary Table 1**): "BM40 forward" and "BM40 reverse", "*Nhe* I VI forward" and "*Acc* I reverse", and "*Acc* I forward" and "LAMB3 Stop reverse" were used to generate three cDNA fragments, which were then ligated together in Zero Blunt® TOPO® via *Hind* III, *Nhe* I, *Acc* I and *Not* I restriction digestions (**Supplementary Fig. 1**). An *Acc* I site, which cuts between aa 581 and aa 582, already existed in the *HuLAMB3* sequence and was exploited during subcloning. The PCR was performed using Pfu Ultra Hot Start polymerase as per the manufacturer's instructions (Stratagene, La Jolla, CA) and a correct clone was verified by sequencing the full length of the assembled insert.

A second deletion mutant, ΔVI-III, begins at residue 560, which for cloning purposes was exchanged from a valine to a leucine to create an *Nhe* I site. The sequence encoding domain II begins at aa 562. The fragments for subcloning were generated by PCR as described above, except that the primer "*Nhe* I VI-III Forward" was used in place of "*Nhe* I VI Forward".

The deletion constructs, fused to a BM40 signal sequence, were sub-cloned into the *Eco*R I sites of pENTR™ 1A (Invitrogen, Carlsbad, CA) and then transferred into the

retroviral vector pLZRS-GATEWAY via a GATEWAY® recombination reaction (Invitrogen).

Supplementary Table 1: PCR primers used to synthesize laminin β3 cDNA constructs

Primer	Sequence
BM40 (*Hind* III)[1] forward	5'-GCCAGCTGATCAAGCTTCT-3'
BM40 reverse	5'-CTTGCAGGGGTCTTTGTAGT-3'
Nhe I VI forward	5'-CATGCTAGCAGGGAGCTGCTTCTGTCAC-3'
Nhe I VI-III forward	5'-CATGCTAGCCTGCCACCCTTGCTTCCAG-3'
Acc I reverse	5'-TGGCATTGCGGAGTCTACCAAAGC-3'
Acc I forward	5'-CGCTTTGGTAGACTCCGCAATGCCAC-3'
LAMB3 stop[2] (*Not* I) reverse	5'-TAGCGGCCGC**TCA**CTTGCAGGTGGCATAG-3'

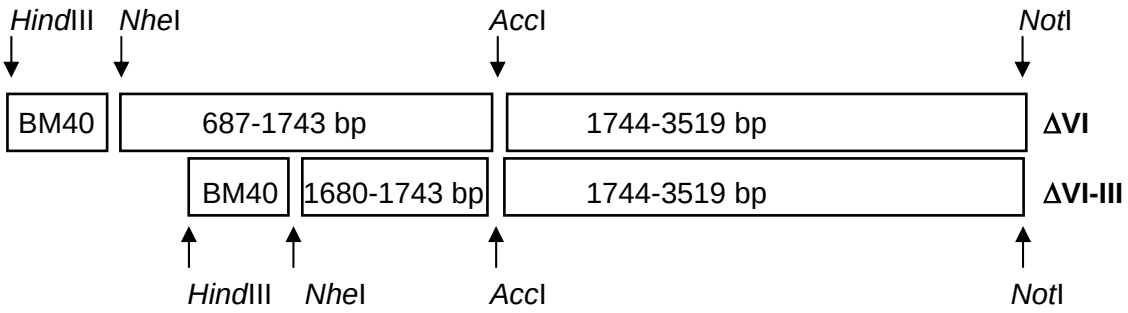
[1]Restriction sites are underlined

[2]Stop codon is shown in bold.

Supplementary Figure Legend

Figure 1. Laminin β3 cDNAs used in generating ΔVI and ΔVI-III constructs. Numbers in boxes indicate position in base pairs (bp) in the *LAMB3* gene. Arrows indicate restriction enzyme sites used during subcloning.

Supplementary Figure 1



Reference

1. Gerecke DR, Wagman DW, Champliaud MF, Burgeson RE. The complete primary structure for a novel laminin chain, the laminin B1k chain. J Biol Chem. 1994;269:11073-80.