Table S1: Firefly / Renilla activity ratio of the tested vectors determined by GraphPad Prism.

Type of vector	Firefly/Renilla Ration
pGL4.23 [luc2/minP] vector containing full intron 3	0.0513
pGL4.23 [luc2/minP] vector containing partial intron 3	0.0383
Non-cloned pGL4.23 [luc2/minP] vector	0.0283
Renilla control vector (pRL-SV40)	0.00015

Table S2: The standard deviation of the tested vectors determined by GraphPad Prism.

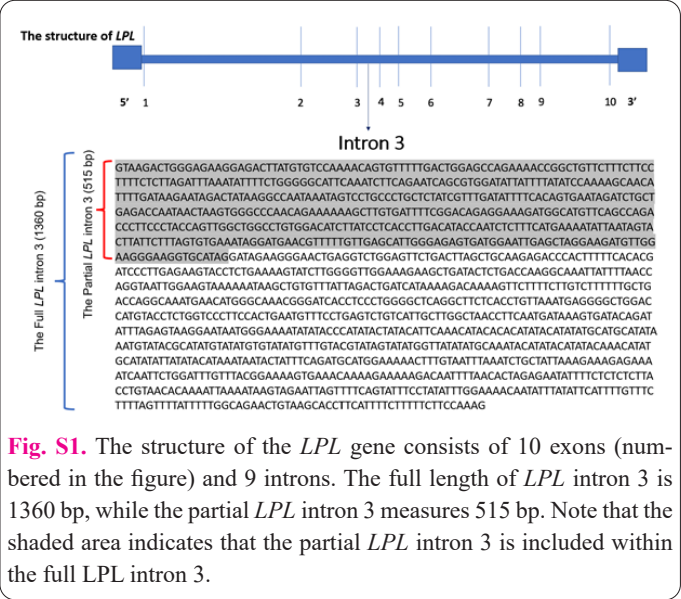| Type of vector	Standard deviation
pGL4.23 [luc2/minP] vector containing full intron 3	0.022
pGL4.23 [luc2/minP] vector containing partial intron 3	0.015
Non-cloned pGL4.23 [luc2/minP] vector	0.007
Renilla control vector (pRL-SV40)	0.0002

Fig. S1. The structure of the *LPL* gene consists of 10 exons (numbered in the figure) and 9 introns. The full length of *LPL* intron 3 is 1360 bp, while the partial *LPL* intron 3 measures 515 bp. Note that the shaded area indicates that the partial *LPL* intron 3 is included within the full LPL intron 3.

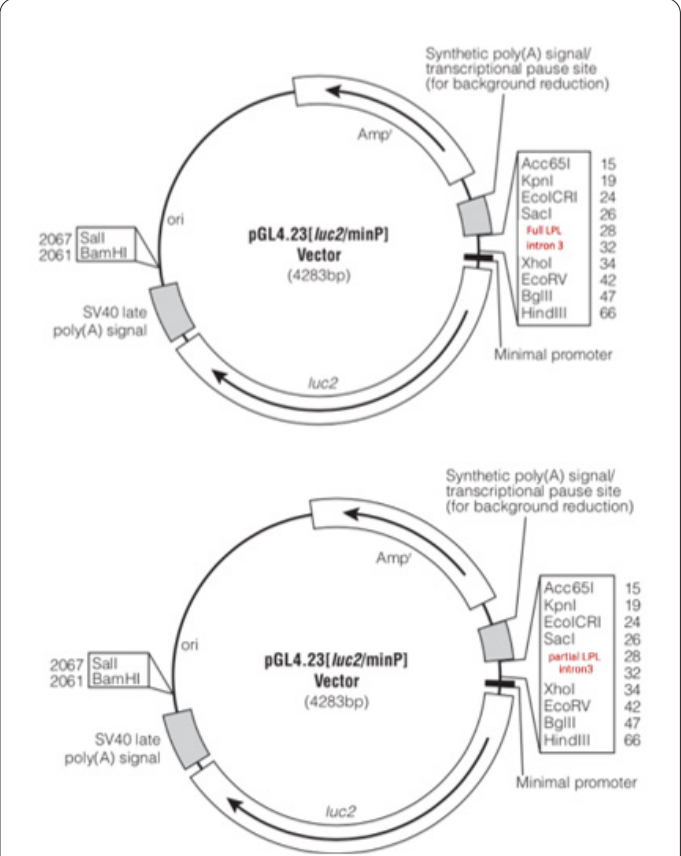**Fig. S2.** Map of **pGL4.23[luc2/minP]** vector including the cloned (A) full and (B) partial *LPL* intron 3 (between SacI & XhoI restriction sites). Image modified from Promega, catalogue no. E841A .
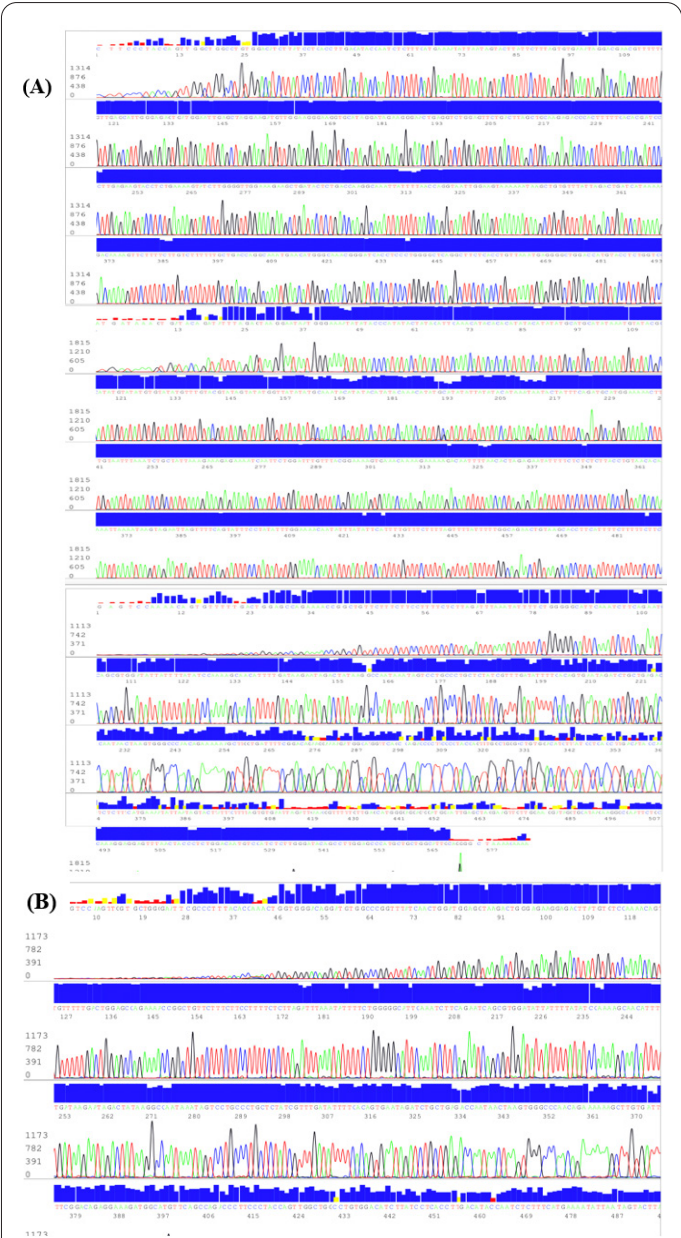

Fig. S3. Electrophoretogram of cloned and desired (A) full and (B) partial fragments of *LPL* intron 3 using the forward primers of intron 3. Blue bars indicate that the quality of the generated nucleotide sequence data was > 95%.

Note: -The sequencing is starting from Position #: 19,951,96 (Nucleotide # 28).
-The sequencing is covered until Position #: 19,952,233 (Nucleotide # 284).
-This ending is the start of the coming sequence

Note: -The sequencing is starting from Position #: 19,952,216 (Nucleotide # 267).
-The sequencing is covered until Position #: 19,952,759 (Nucleotide # 811).
-The ending of the previous sequence is the start of the coming sequence

Note: -The sequencing is starting from Position #: 19,952,743 (Nucleotide # 794).
-The sequencing is covered until Position #: 19,953,309 (Nucleotide # 1360) the end of the intron

Notes:
The yellow highlighted sequence is the Forward primer: Intron part 2
The red highlighted sequence is the Reverse complement: intron part 1
The green highlighted sequence is the Forward primer: Intron part 3

Fig. S4. Sequence analysis of the cloned full intron 3 using 3 primer sets from the recombinant TOPO vector was aligned using the Clustal Omega platform. The alignments between the sequencing result against the nucleotide sequence of intron 3 from the database. The * refers to the identity of the nucleotide in the same column in the alignment.

Note: -The sequencing is starting from position # 19,951,949 (1st nucleotide).
- The sequencing is covered until Position #: 19,952,441(Nucleotide # 492).

Notes:
The red highlighted nucleotide (Nucleotide # 2) is the SNP at Position #: 19,951,950 (splice donor variant)

Fig. S5. Sequence analysis of the purified PCR product of the partial fragment of intron 3 using the first primer set was aligned using the Clustal Omega platform. The alignments between the sequencing result against the nucleotide sequence of intron 3 from the database. The * refers to the identity of the nucleotide in the same column in the alignment.

Fig. S6. Electrophoretogram of the partial fragment of *LPL* intron 3 from the purified recombinant pGL4.23 [luc2/minP] vector using forward primer of intron 3. The blue bars indicate that the quality of the generated nucleotide sequence was above 95%.

Note:
T is The sequence is starting from the 39th nucleotide (position #: 19,951,988).
A is The sequencing is covered until nucleotide # 446 (Position #: 19,952,395).

Fig. S7. Sequence analysis of the partial fragment of intron 3 cloned from the recombinant pGL4.23 [luc2/minP] vector using the first primer set was aligned using the Clustal Omega platform. Alignments between the sequencing results and nucleotide sequences of intron 3 from the database. * Identity of the nucleotide in the same alignment column.