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Commissaire aux brevets
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Titre de l'invention / Title of invention

BIOCAPTEUR BIOLUMINESCENT DE PARCOURS HIPPO

HIPPO PATHWAY BIOLUMINESCENT BIOSENSOR

Breveté(s) / Patentee(s)

QUEEN'S UNIVERSITY AT KINGSTON

Inventeur(s) / Inventor(s)

XIAOLONG YANG; TAHA AZAD; KAZEM NOURI

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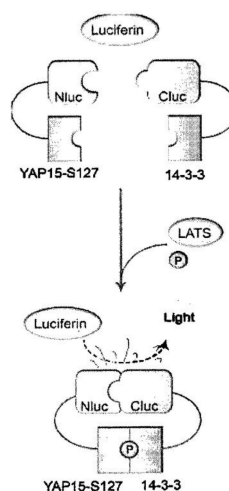
(72) **Inventeur/Inventor:** YANG, XIAOLONG, CA
AZAD, TAHA, CA
NOURI, KAZEM, CA

(73) **Propriétaire/Owner:** QUEEN'S UNIVERSITY AT
KINGSTON, CA

(74) **Agent:** SCRIBNER, STEPHEN J.

(54) **Titre:** BIOCAPTEUR BIOLUMINESCENT DE PARCOURS HIPPO

(54) **Title:** HIPPO PATHWAY BIOLUMINESCENT BIOSENSOR



(57) **Abrégé:**

Il est décrit des biocapteurs bioluminescents utiles pour la quantification et/ou la quantification in vitro ou in vivo d'une activité du parcours de signalisation Hippo. Les biocapteurs surveillent l'activité de kinase suppresseur de grande tumeur ou l'interaction de la protéine associée à Yes et du domaine associé à l'activateur transcriptionnel. Les biocapteurs peuvent être utilisés dans des procédés de surveillance et/ou de quantification en temps réel, in vitro ou in vivo d'une activité du parcours de signalisation Hippo, l'activité pouvant être de kinase suppresseur de grande tumeur et/ou l'interaction de la protéine associée à Yes et du domaine associé à l'activateur transcriptionnel. Les biocapteurs peuvent être fournis dans des trousse de surveillance et/ou de quantification en temps réel, in vitro ou in vivo d'une activité du parcours de signalisation Hippo, l'activité pouvant être de kinase suppresseur de grande tumeur et/ou l'interaction de la protéine associée à Yes et du domaine associé à l'activateur transcriptionnel.

(57) **Abstract:**

Bioluminescent biosensors useful for monitoring and/or quantifying, in vitro or in vivo, activity of the Hippo signaling pathway. The biosensors monitor LATS kinase activity or YAPTEAD interaction. The biosensors may be used in methods for monitoring and/or quantifying in real-time, in vitro or in vivo, activity of the Hippo signaling pathway, wherein the activity may be LATS kinase activity and/or YAP-TEAD interaction. The biosensors may be provided in kits for monitoring and/or quantifying in real-time, in vitro or in vivo, activity of the Hippo signaling pathway, wherein the activity may be LATS kinase activity and/or YAP-TEAD interaction

Hippo Pathway Bioluminescent Biosensor

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Field

This invention relates to bioluminescent biosensors for non-invasively monitoring and/or quantifying in real-time, *in vitro* or *in vivo*, activity of the Hippo signaling pathway.

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Background

Detailed understanding of biochemical pathways will elucidate signaling mechanisms in physiological and pathological processes, yielding insight into approaches for controlling, treating, and preventing many diseases. The ability to gain such insight is severely limited by the complexity of such pathways and the difficulty in monitoring the activity of key components once identified.

The Hippo pathway is a signaling cascade that plays important roles in development (e.g., organ size control, 3D body shape, and early embryo development), cancer (tumorigenesis, metastasis, drug resistance, and immune evasion), regeneration medicine (stem cell renewal and differentiation and tissue homeostasis/regeneration), heart development and disease (cardiomyocyte proliferation and heart infarction/cardiac injury) and in the neuronal system (neural fate and dendrite tiling)¹⁻⁹. Dysregulation of the Hippo pathway is frequently observed in human cancers. When Hippo signaling is activated by upstream regulators, MST1/2 serine/threonine (S/T) kinases (mammalian homologs of *Drosophila* Hippo) phosphorylate/activate LATS1/2 kinases which subsequently phosphorylate/inactivate their downstream effectors, transcriptional co-activator Yes-associated protein (YAP) and its paralog transcriptional co-activator with PDZ-binding motif (TAZ). S127-phosphorylated YAP (YAP-pS127) or S89-phosphorylated TAZ (TAZ-pS89) bind to cytoplasmic protein 14-3-3 and are

prevented from binding to transcription factor TEAD to trans-activate downstream gene targets in the nucleus (e.g., CTGF, CYR61, FGF1, etc.)¹⁰⁻¹⁴. Although a few regulatory factors of the Hippo pathway have been uncovered (actin dynamics, cell matrix stiffness, cell-cell contact, and lysophosphatidic acid (LPA)^{3,6}, comprehensive regulator screens have been technically limited.

- 5 An absence of available tools precludes measuring the dynamics and activity of the Hippo pathway core components in a quantitative, high-throughput and non-invasive manner.

Summary

- 10 One aspect of the invention relates to a luminescent biosensor, comprising: one or more fragments of firefly or NanoBiT luciferase or a functional equivalent thereof; at least one fragment of human YAP or a functional equivalent thereof; and at least one vector.

- 15 In one embodiment, the biosensor comprises: a first construct comprising an N-terminal luciferase fragment (Nluc) or a functional equivalent thereof fused to the at least one YAP fragment; a second construct comprising a C-terminal luciferase fragment (Cluc) or a functional equivalent thereof fused to human cytoplasmic 14-3-3 protein or a functional equivalent thereof; wherein the first construct and the second construct are on separate vectors; wherein LATS-dependent phosphorylation of the at least one YAP fragment leads to binding with the human cytoplasmic 14-3-3 protein, which results in binding of Nluc and Cluc to produce luminescence.

- 20 In one embodiment, the biosensor comprises Nluc luciferase amino acids 1-416 (SEQ ID NO:6) or a functional equivalent thereof; Cluc luciferase amino acids 394-550 (SEQ ID NO:6) or a functional equivalent thereof; and YAP fragment including 15 amino acids (residues 120-134; (SEQ ID NO:7) or a functional equivalent thereof.

- 25 In one embodiment, the biosensor comprises a single construct including: an N-terminal luciferase fragment (Nluc) or a functional equivalent thereof fused to the at least one YAP fragment; and a C-terminal luciferase fragment (Cluc) or a functional equivalent thereof fused to human cytoplasmic 14-3-3 protein; wherein LATS-dependent phosphorylation of the at least one YAP fragment leads to a conformational change and binding of Nluc and Cluc to produce luminescence.

In one embodiment, the biosensor comprises Nluc luciferase amino acids 1-416 (SEQ ID NO:6) or a functional equivalent thereof; Cluc luciferase amino acids 394-550 (SEQ ID NO:6) or a functional equivalent thereof; and YAP fragment including 15 amino acids (residues 120-134; (SEQ ID NO:7) or a functional equivalent thereof.

5 In one embodiment, the biosensor comprises a single construct including a luciferase engineered at the C-terminal fused to the one or more YAP fragment; wherein LATS-dependent phosphorylation of the one or more YAP fragment modulates luciferase activity to increase luminescence. In one embodiment, the luciferase is engineered at the C-terminal consisting of amino acids 1-544 (SEQ ID NO:6) or a functional equivalent thereof.

10 In one embodiment, the biosensor comprises a first construct comprising a LgBiT luciferase fragment or a functional equivalent thereof fused to the at least one YAP fragment or a functional equivalent thereof; a second construct comprising a SmBiT luciferase fragment or a functional equivalent thereof fused to human cytoplasmic 14-3-3 protein or a functional equivalent thereof; wherein the first construct and the second construct are on separate vectors;
15 wherein binding of the at least one YAP fragment with the human cytoplasmic 14-3-3 protein and leads to binding of LgBiT and SmBiT to produce luminescence. In one embodiment, the biosensor comprises YAP fragment including 15 amino acids (residues 120-134) (SEQ ID NO:7) or a functional equivalent thereof.

In one embodiment, the biosensor comprises: a first construct comprising a LgBiT
20 luciferase fragment or a functional equivalent thereof fused to the at least one YAP fragment or a functional equivalent thereof; a second construct comprising a SmBiT luciferase fragment or a functional equivalent thereof fused to a TEAD fragment or a functional equivalent thereof; or a first construct comprising a LgBiT luciferase fragment or a functional equivalent thereof fused to a TEAD fragment or a functional equivalent thereof; a second construct comprising a SmBiT
25 luciferase fragment or a functional equivalent thereof fused to the at least one YAP fragment or a functional equivalent thereof; wherein the first construct and the second construct are on separate vectors; wherein interaction of the at least one YAP fragment with the TEAD fragment leads to binding of LgBiT and SmBiT to produce luminescence.

In one embodiment, the biosensor comprises: YAP fragment comprising amino acids 50-171 of SEQ ID NO:2 or a functional equivalent thereof; and TAED fragment comprising amino acids 194-411 of SEQ ID NO:11 or a functional equivalent thereof.

5 Another aspect of the invention relates to a method, comprising: non-invasively monitoring and/or quantifying in real-time, *in vitro* or *in vivo*, activity of the Hippo signaling pathway, comprising transfecting a cell with a luminescent biosensor as described herein, and detecting luminescence; wherein an intensity of the luminescence is indicative of amount of activity of the Hippo signaling pathway.

10 Another aspect of the invention relates to a method for monitoring and/or quantifying activity of the Hippo signaling pathway, comprising: treating a cell with a luminescent biosensor as described herein; and detecting luminescence of the treated cell; wherein an intensity of the luminescence is indicative of amount of activity of the Hippo signaling pathway. In one embodiment, an intensity of the luminescence is indicative of amount of LATS kinase activity in the Hippo signaling pathway. In one embodiment, an intensity of the luminescence is indicative
15 of amount of YAP-TEAD interaction in the Hippo signaling pathway. In one embodiment, treating a cell comprises transfecting a cell with the luminescent biosensor. In one embodiment, treating a cell comprises lysing the cell and combining a cell lysate with the luminescent biosensor.

20 In one embodiment, the method comprises: non-invasively monitoring and/or quantifying in real-time, *in vitro* or *in vivo*, activity of LATS kinase, comprising transfecting the cell with a luminescent biosensor as described herein, and detecting luminescence; wherein an intensity of the luminescence is indicative of amount of LATS kinase activity in the Hippo signaling pathway.

25 In one embodiment, the method comprises: non-invasively monitoring and/or quantifying in real-time, *in vitro* or *in vivo*, YAP-TEAD interaction, comprising transfecting the cell with a luminescent biosensor as described herein, and detecting luminescence; wherein an intensity of the luminescence is indicative of amount of YAP-TEAD interaction in the Hippo signaling pathway.

Another aspect of the invention relates to a method, comprising: monitoring and/or quantifying activity of one or more proteins of the Hippo signaling pathway, comprising combining the one or more proteins with a luminescent biosensor as described herein and at least one substance, and detecting luminescence of the luminescent biosensor; wherein an intensity of the luminescence is indicative of effect of the at least one substance on activity of the one or more proteins of the Hippo signaling pathway.

In various embodiments of the above method, the at least one substance is selected from a chemical compound such as a small molecule inhibitor (e.g., molecular weight below about 500 Daltons), a large molecule inhibitor (e.g., molecular weight above about 500 Daltons), a biological agent (e.g., antibody), protein, polypeptide, peptide, DNA aptamer, microRNA, interfering RNA (shRNA, siRNA), a sugar, lipid, glycoprotein, and glycolipid.

Another aspect of the invention relates to a method for monitoring and/or quantifying activity of the Hippo signaling pathway in a biological sample obtained from a subject, comprising: treating cells of the biological sample with at least one reagent comprising the a luminescent biosensor as described herein; and detecting luminescence of the treated biological sample; wherein an intensity of the luminescence is indicative of amount of activity of the Hippo signaling pathway. In one embodiment, an intensity of the luminescence is indicative of amount of LATS kinase activity in the Hippo signaling pathway. In one embodiment, an intensity of the luminescence is indicative of amount of YAP-TEAD interaction in the Hippo signaling pathway. In various embodiments, the biological sample comprises at least one of tissue and blood. In one embodiment, the biological sample comprises blood. In one embodiment, an intensity of the luminescence is indicative of the cells being cancer cells.

Another aspect of the invention relates to a kit, comprising: a luminescent biosensor as described herein; at least one reagent; and, optionally, instructions for using the kit.

Brief Description of the Drawings

For a greater understanding of the invention, and to show more clearly how it may be carried into effect, embodiments will be described, by way of example, with reference to the accompanying drawings, wherein:

Fig. 1A is a schematic diagram of YAP1 protein structure (SEQ ID NO:2) showing LATS phosphorylation site (S127) and the surrounding 15 amino acid sequence (YAP15; SEQ ID NO:7).

Fig. 1B is a western blot for GST pulldown assays showing results confirming that
5 YAP15 is sufficient for interaction with cytoplasmic protein 14-3-3 *in vitro*.

Fig. 2A shows schematic diagrams of domain structures of a LATS intermolecular biosensor, referred to as Nluc-YAP15 (upper; SEQ ID NOs:6, 7) and 14-3-3-Cluc (lower; SEQ ID NOs:4, 6), according to an embodiment of the invention.

Fig. 2B is a schematic diagram showing the mechanism by which a LATS intermolecular
10 biosensor determines LATS kinase activity.

Fig. 2C shows experimental results validating LATS intermolecular biosensor activity, where biosensor activity or Nluc-YAP15-S127 phosphorylation status were determined in HEK293 cells 48 hours after transfection by luciferase assay or western blot, respectively. Data are presented as mean $\pm$ SD, n = 3.

Fig. 2D shows experimental results confirming that a LATS intermolecular biosensor
15 responds specifically to LATS kinase activity, by mutation of the LATS kinase consensus motif (HXRXXS/T; H, histidine; R, arginine; X, any amino acid; S, serine; T, threonine; SEQ ID NOs:71, 72) in Nluc-YAP15 (SEQ ID NOs:7, 8). Data are presented as mean $\pm$ SD, n = 3.

Fig. 2E shows experimental results confirming that LATS intermolecular biosensor
20 activity is reduced by MST or LATS knockout. Data are presented as mean $\pm$ SD, n = 3.

Fig. 2F shows experimental results confirming that LATS intermolecular biosensor can
be stably expressed to detect LATS kinase activity, wherein biosensor activity and
phosphorylation status were monitored in a HEK293A cell line with doxycycline (Dox)-
inducible LATS2 overexpression and stable LATS biosensor (LATS-BS) expression, and
25 biosensor activity and phosphorylation status of endogenous YAP (YAP-pS127) and Nluc-
YA15P-S127 (Nluc-YAP15-pS127) were determined at the indicated times by luciferase assay
and western blot, respectively. Data are presented as mean $\pm$ SD, n = 3.

Fig. 3A is a schematic diagram showing the domain structure of a LATS intramolecular biosensor based on SEQ ID NOs:6, 7, 73, according to one embodiment.

Fig. 3B is a schematic diagram showing the mechanism by which a LATS intramolecular biosensor determines LATS kinase activity.

Fig. 3C is a bar chart showing results of a validation study of an intramolecular LATS biosensor according to the embodiment of Fig. 3A.

5 Fig. 4A is a schematic diagram showing the domain structure of an engineered LATS biosensor based on SEQ ID NOs:6, 7, according to one embodiment.

Fig. 4B is a schematic diagram showing the mechanism by which an engineered LATS biosensor determines LATS kinase activity.

10 Fig. 4C is a bar chart showing results of a validation study of an engineered LATS biosensor according to the embodiment of Fig. 4A.

Figs. 5A-5D show diagrams of multiple cloning sites of vectors (pBiT1.1-N [TK/LgBiT; 5A]; pBiT2.1-C [TK/SmBiT; 5B]; pET16b (5C)) and domain structures of constructs (5D) used to make NanoBiT (NanoLuc) biosensors based on Nluc and CLuc (SEQ ID NO:6), YAP15 (SEQ ID NO:7), LgBiT (SEQ ID NO:52), SmBiT (SEQ ID NO:54), and 14-3-3 (SEQ ID NO:4),
15 according to embodiments of the invention.

Fig. 6 is a schematic diagram showing an overview of a NanoBiT interaction system of a LATS NanoBiT biosensor according to an embodiment of the invention.

Fig. 7 shows a coomassie brilliant blue (CBB) stained SDS-PAGE of purified proteins for a LATS NanoBiT biosensor.

20 Fig. 8A shows results of a NanoBiT biosensor assay of overexpressed LgBiT-YAP15 WT and mutant (MUT) and 14-3-3-SmBiT in HEK293T cells as relative luminescence to YAP15MUT-14-3-3.

Fig. 8B shows results of a NanoBiT LATS biosensor assay for cancer cells.

Fig. 8C shows results of a NanoBiT LATS biosensor assay for blood.

25 Fig. 9 shows results of an *in vitro* NanoBiT biosensor assay using purified LgBiT-YAP15 (WT and mutant), 14-3-3-SmBiT, and LATS2 kinase; upper panel shows the result of the NanoBiT assay for YAP15WT or mutant at two different concentrations of biosensor (5 and 100 ng) as a ratio of luminescence signal at different time points; lower panel shows immunoblotting analysis and ponceau staining of the respective samples with 100 ng of biosensor.

Fig. 10 shows the results of a kinase assay with purified proteins; upper panel shows the NanoBiT LATS biosensor assay for YAP15 WT and mutant (100 ng) with and without lambda phosphatase after 30 min; the lower panels show the relative immunoblotting and Ponceau staining for the respective samples.

5 Fig. 11 shows diagrams of domain structures of eight constructs used to make a YAP-TEAD biosensor based on LgBiT (SEQ ID NO:52), SmBiT (SEQ ID NO:54), YAP50-171 (SEQ ID NO:2), and TEAD1-194-411 (SEQ ID NO:50), according to one embodiment.

Fig. 12 shows a schematic overview of a NanoBiT interaction system of a YAP-TEAD NanoBiT biosensor according to an embodiment of the invention.

10 Fig. 13 shows the results of an assay of overexpressed YAP50-171 of SEQ ID NO:2 and TEAD1-194-411 of SEQ ID NO:50 in HEK293T cells lysed with passive lysis buffer, for a biosensor with a combination of SmBiT-YAP50-171 (SEQ ID NO:2) and LgBiT-TEAD1-194-411 of SEQ ID NO:50 constructs.

15 Fig. 14 shows the results of an assay for analyzing LATS kinase activity under various stimuli regulating Hippo signaling by live cell luciferase imaging, using an intermolecular LATS-BS as described herein.

Fig. 15 is a photomicrograph showing the results of an experiment to determine subcellular LATS kinase activity using an intermolecular LATS-BS as described herein, obtained by bioluminescent microscopy.

20 Fig. 16 is a photograph showing LATS kinase activity in mice by *in vivo* luciferase imaging, using an intermolecular LATS-BS as described herein.

Fig. 17A is a schematic diagram showing a method for a screening assay, and Fig. 17B shows the results of a screening assay for identifying novel regulators of LATS using an intermolecular LATS-BS as described herein and a kinase inhibitor screen.

25 Detailed Description of Embodiments

In practicing the embodiments described herein, many conventional techniques in cell biology, molecular biology, protein biochemistry, immunology, and bacteriology are used. These techniques are well-known in the art and are provided in any number of available

publications, such as *Current Protocols in Molecular Biology*, Vols. I-III, Ausubel, Ed. (1997); Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Ed. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989). Unless specifically defined herein, all technical and scientific terms used herein generally have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

One aspect of the invention relates to bioluminescence-based biosensor constructs that non-invasively monitor real-time *in vitro* and *in vivo* activity of LATS kinase, the central player of the Hippo signaling pathway. A LATS biosensor (LATS-BS) as described herein quantifies LATS kinase activity by split luciferase assay, a bioluminescence-based technique that non-invasively monitors protein-protein interactions *in vitro* and *in vivo* in real-time with accurate quantification, high sensitivity, and excellent reproducibility. Embodiments of the biosensor constructs include fragments of firefly (*Photinus sp.*, e.g., *Photinus pyralis*) or NanoBiT (also referred to as NanoLuc) luciferase and human *YAP1*. Some embodiments include human cytoplasmic protein 14-3-3 or a fragment thereof.

Another aspect of the invention relates to a method for non-invasively monitoring real-time *in vitro* and *in vivo* activity of LATS kinase. In various embodiments, the method includes using a LATS biosensor as described herein to quantify LATS kinase activity. The embodiments provide a bioluminescence-based technique for monitoring LATS kinase activity with accurate quantification, high sensitivity, and excellent reproducibility (see Examples for details).

A third aspect of the invention relates to bioluminescent biosensor constructs and methods for non-invasively monitoring YAP-TEAD interaction, a critical step in regulation of downstream target by the Hippo pathway. Embodiments of the biosensor constructs include fragments of NanoBiT luciferase and fragments of human *YAP1* and *TEAD1*, or functional equivalents thereof, and provide a bioluminescent-based technique for monitoring YAP and TEAD interactions both *in vitro* and *in vivo* with high sensitivity, stability, and reproducibility.

At least eight isoforms of *YAP1* are known. SEQ ID NO:1 shows the full human *YAP2L* isoform mRNA (accession number: AB567720) and SEQ ID NO:2 shows the amino acid sequence. The fragments used in the embodiments described herein were obtained from the *YAP2L* isoform of *YAP1* (SEQ ID NO:2). However, the fragments used in the embodiments described herein may be obtained from any of the isoforms, or may be functional equivalents

thereof. In this disclosure, the terms “YAP1” and “YAP” are used interchangeably to refer to an isoform of YAP1. SEQ ID NO:3 shows the full human 14-3-3 protein theta mRNA (accession number: P27348) and SEQ ID NO:4 shows the amino acid sequence. SEQ ID NO:5 shows the full length firefly luciferase mRNA and SEQ ID NO:6 shows the luciferase protein.

5 Since LATS phosphorylates S127 on YAP1 and cytoplasmic protein 14-3-3 binds specifically to phosphorylated but not un-phosphorylated S127-YAP, embodiments were constructed for monitoring LATS kinase activity by measuring the pS127-YAP/14-3-3 interaction.

In various embodiments, a LATS-BS includes a minimal *YAP1* fragment that interacts
10 with 14-3-3 in a phosphorylation-dependent manner. The full length YAP1 protein was not used to avoid confounding signals by post-translational modifications of YAP1 by other upstream regulators. In one embodiment, the minimal YAP1 fragment includes 15 amino acids (YAP15) surrounding the S127 LATS phosphorylation site (amino acids 120-134; SEQ ID NO:7; Fig. 1A). Functional equivalents may be used, such as other sizes of YAP1 fragments, such as, for
15 example, longer (e.g., 16-20 amino acids) or shorter (e.g., 12-14 amino acids) surrounding the S127 (SEQ ID NO:2). Embodiments may include a YAP fragment with a HxRxxS motif (SEQ ID NO:71). Since H, R, and S residues but not other amino acids in the HxRxxS motif (SEQ ID NO:71) on the YAP fragment are essential for LATS biosensor function (see, e.g., Fig. 2D), variants of YAP fragments with changes of amino acids other than H/R/S may also be used.
20 Larger fragments (e.g., 20-100 amino acids) may result in confounding signals.

Minimal YAP1 fragments were tested for interaction with 14-3-3 after phosphorylation by LATS2 kinase. Using *in vitro* GST-pulldown assays, it was found that like full-length YAP-GST, YAP15-GST could directly bind to 14-3-3 after LATS phosphorylation while a phosphorylation-mutant YAP15-S127A-GST (A, alanine) could not. Fig. 1B shows that YAP15
25 is sufficient for interaction with 14-3-3 *in vitro*. To collect the data, GST-tagged full length YAP (YAP-GST), YAP15 with wild type sequence (YAP15-S127-GST), or mutant YAP15 that cannot be phosphorylated by LATS (YAP15-S127A-GST) was purified from bacterial cells and 1 µg of GST fusion protein was incubated for 20 minutes at 30°C with recombinant LATS kinase. 100 µg of cell lysate from human embryonic kidney cells (HEK293) transiently
30 expressing 14-3-3-Flag was added and YAP or YAP15-S127 or YAP15-S127A/14-3-3 binding

was assessed by GST pull-down with protein S-agarose beads, followed by western blot with anti-Flag (14-3-3-Flag) and anti-YAP-pS127 antibodies. The membrane was stained with Ponceau S to visualize the fusion proteins.

Since the TEAD family consists of four members, other TEADs (TEAD2-4) may also be used to replace TEAD1 to make biosensors similar to the YAP-TEAD1 biosensor. Throughout this disclosure, "TEAD1" and "TEAD" are used interchangeably to refer to any one of the TEAD family members.

In the following descriptions of various embodiments of the biosensor, references to sequences and sequence listings are made. Those of ordinary skill in the art will readily appreciate that the invention is not limited to the specific sequences described, as many variants are possible without departing from the invention. For example, substitutions, mutations, deletions, and/or additions of one or more nucleotides or amino acids may be made, or may occur, without substantial effect on functional properties of a biosensor. Such a functional equivalent may have, for example, 60%, or 70%, or 80%, or 90%, or more sequence identity with a sequence described herein. Such functional equivalents are intended to be included in the embodiments of the invention.

1. LATS Biosensor

1.1 Intermolecular Biosensor

The biosensor was made by overlapping PCR using firefly luciferase as a template. YAP15 and 14-3-3 were fused with N-terminal and C-terminal luciferase fragments (Nluc and Cluc), respectively, to create a LATS-BS. As shown in Fig. 2A, for Nluc-YAP15, firefly luciferase amino acids 1-416 (N-luciferase, Nluc) (SEQ ID NO:6) were fused to the N-terminal of YAP15 (120-134; (SEQ ID NO:7) separated by a glycine/alanine linker (GGAGG; SEQ ID NO:73); and for 14-3-3-Cluc, luciferase amino acids 394-550 (C-luciferase, Cluc; SEQ ID NO:6) were fused to the C-terminal of 14-3-3 (SEQ ID NO:4) separated by a glycine/serine linker (GGSGGGGSGG; SEQ ID NO:74). Biosensors were cloned into the BamHI/NotI sites of the pcDNA3.1/hygro (+) vector (SEQ ID NO:9, purchased from Invitrogen, Dublin, Ireland). Primers are shown in SEQ ID NOs:10-16. The full length sequences for Nluc-YAP15 and 14-3-

3-Cluc in pcDNA3.1/hygro (+) vector are given in SEQ ID NOs:57 and 58, respectively, wherein the underlined portions are the main constructs and the rest is the vector.

The mechanism of action for how the LATS-BS determines LATS kinase activity is shown in Fig. 2B. At baseline, there is no interaction between YAP15 and 14-3-3 so the LATS-BS shows minimal bioluminescence activity. However, LATS-dependent phosphorylation of YAP15-S127 leads to 14-3-3 binding, luciferase complementation, and high bioluminescence signal.

In a validation study, LATS-BS was transfected alone or together with LATS2 or/and MST2 into HEK293 cells and biosensor activity or Nluc-YAP15-S127 phosphorylation status were determined 48 hours after transfection by luciferase assay or western blot, respectively. As depicted in Fig. 2C, HEK293 cells transfected with LATS-BS alone had low luciferase activity and this was correlated with a low degree of Nluc-YAP15-S127 phosphorylation. Co-transfection of LATS-BS with MST2 was associated with increases in both Nluc-YAP-S127 phosphorylation and luciferase activity, and this effect was suppressed with lysophosphatidic acid (LPA), an inhibitor of the Hippo pathway. For lysophosphatidic acid (LPA) treatment, cells were stimulated with 10 μ M LPA for 1 hour before collection (n = 3). LATS-BS co-expression with both MST2 and LATS2 was correlated with further increases in Nluc-YAP15-S127 phosphorylation and luciferase activity. Collectively, these observations are consistent with a model where MST2 activates LATS2, which phosphorylates Nluc-YAP15-S127, leading to binding with Cluc-14-3-3 and reconstitution of active luciferase.

To further validate the biosensor construct model, conserved residues (H, histidine; R, arginine; S) within the LATS consensus phosphorylation motif (HxRxxS/T; x, any amino acid; SEQ ID NOs:71, 72) on Nluc-YAP15-S127 were mutated to A (H122A, R124A, and S127A). Each individual mutation completely abolished Nluc-YAP15-S127 phosphorylation and LATS-BS luciferase activity, as shown in Fig. 2D. In addition, the basal LATS-BS signal was reduced by knockout of endogenous MST1/2 in HEK293A (50% reduction) or more dramatically by LATS1/2 knockout (~90% reduction), as shown in Fig. 2E. LATS-BS was transfected into CRISPR-Cas9-generated LATS1/2 or MST1/2 knockout HEK293A and basal biosensor activity was determined 48 hours after transfection (n = 3). Furthermore, inducible expression of LATS2 in HEK293A cells stably expressing LATS-BS showed that the levels of LATS2 are correlated

with the level of endogenous YAP-pS127, Nluc-YAP15-pS127 as well as with LATS-BS activity, as shown in Fig. 2F. Biosensor activity and phosphorylation status were monitored in a HEK293A cell line with doxycycline (Dox)-inducible LATS2 overexpression and stable LATS-BS expression. Cells were treated with 1 μ g/mL Dox for the indicated times and biosensor activity and phosphorylation status of endogenous YAP (YAP-pS127) and Nluc-YA15P-S127 (Nluc-YAP15-pS127) were determined by luciferase assay and western blot, respectively (n = 3).

This LATS biosensor was also used to examine LATS kinase activity in living cells and mice and to perform a screening assay for regulators of LATS (see details in Examples).

1.2 Intramolecular Biosensor

An intramolecular biosensor was made by overlapping PCR using firefly luciferase as a template. In one embodiment, firefly luciferase amino acids 1-416 (N-luciferase, Nluc; SEQ ID NO:6) were fused to the N-terminal of YAP15 (120-134) (SEQ ID NO:7) separated by a glycine/alanine linker (GGAGG; SEQ ID NO:73). Within the same open reading frame, luciferase amino acids 394-550 (C-luciferase, Cluc; SEQ ID NO:6) were fused to the C-terminal of 14-3-3 separated by a glycine/alanine linker. For this biosensor, LATS phosphorylates YAP15-S127 to cause a conformational change in the intramolecular LATS-BS, leading to luciferase complementation and detectable biosensor activity. Primers are shown in SEQ ID NOs:10, 16, 17, and 18.

The domain structure is shown in Fig. 3A and the mechanism of action for how the LATS-BS determines LATS kinase activity is shown in Fig. 3B. At baseline, there is no interaction between YAP15 and 14-3-3 so the LATS-BS shows minimal bioluminescence activity. However, LATS-dependent phosphorylation of YAP15-S127 leads to 14-3-3 binding, luciferase complementation, and high bioluminescence signal.

To validate the intramolecular biosensor, the biosensor was transfected alone or together with LATS2 or/and MST2 into HEK293 cells and biosensor activity was determined 48 hours after transfection by luciferase assay. For LPA treatment, cells were stimulated with 10 μ M LPA, an inhibitor of the Hippo pathway, for 1 hour before collection (n = 3). Results are shown in Fig. 3C.

1.3 Engineered Biosensor

The biosensor was made by overlapping PCR using firefly luciferase as a template. In one embodiment, the C-terminal seven amino acids from firefly luciferase were removed to create Eng-luc (544 amino acids). This construct was fused to the N-terminal of YAP15 (amino acids 120-134; SEQ ID NO:7). This brings the luciferase site in close proximity to YAP15-S127 such that LATS-dependent phosphorylation of YAP-S127 modulates luciferase activity directly. Primers are shown in SEQ ID NOs:10 and 19.

The domain structure of the Eng-luc LATS biosensor according to one embodiment is shown in Fig. 4A and the mechanism of action for how the biosensor determines LATS kinase activity is shown in Fig. 4B.

For validation of the Eng-luc LATS-BS, the biosensor was transfected alone or together with LATS2 or/and MST2 into HEK293 cells and biosensor activity was determined 48 hours after transfection by luciferase assay. For LPA treatment, cells were stimulated with 10 μ M LPA for 1 hour before collection (n = 3). Results are shown in Fig. 4C.

1.4. NanoBiT biosensor

For this biosensor YAP15 (aa 120-134; SEQ ID NO:7) and 14-3-3 full length (aa 1-245; SEQ ID NO:4) were used. As shown in Fig. 7-10, a YAP15 mutant was used as a negative control in these experiments.

To clone YAP15 and 14-3-3 in NanoBiT (also referred to as NanoLuc) vectors (purchased from Promega Corporation, Madison, Wisconsin, U.S.A.), primers with EcoR1 and BglII restriction sites were used. For the LgBiT-YAP15 construct, primers shown in SEQ ID NOs:20-23 were used. For the 14-3-3-SmBiT construct, primers shown in SEQ ID NOs:24-25 were used.

In the case of YAP15WT (S127; SEQ ID NO:7) and mutant (A127; SEQ ID NO:8), primers with EcoR1 and BglII flanking ends were annealed first and then they were ligated into digested pBiT 1.1 N (TK-LgBiT) vector (SEQ ID NO:26; purchased from Promega Corporation) with N-terminal LgBiT domain. Fig. 5A shows the multiple cloning site. For making the 14-3-3-SmBiT construct, in order to amplify 14-3-3 gene, standard PCR using the above mentioned primers was done by using 14-3-3 as a template. PCR product was digested using EcoR1 and BglII restriction enzymes and was ligated into pBiT 2.1 C (TK-SmBiT; purchased from Promega

Corporation) (SEQ ID NO:27) with SmBiT (11 amino acid) sequence at the C-terminus. Fig. 5B shows the multiple cloning site.

To make LgBiT-YAP15 (WT and mutant) and 14-3-3-SmBiT constructs for protein expression and purification in *E.coli*, the primers shown in SEQ ID NOs:28-30 were used for the LgBiT-YAP15 construct, and the primers shown in SEQ ID NOs:31-32 were used for the 14-3-3-SmBiT construct. For PCR, LgBiT-YAP15 and 14-3-3-SmBiT in NanoBiT vectors were used as template. pET16b vector (SEQ ID NO:33; purchased from Novagen (Millipore (Canada) Ltd., Etobicoke, Canada) was used for overexpression of LgBiT-YAP15 (WT and mutant) and 14-3-3-SmBiT as His-tagged proteins. Fig. 5C shows the multiple cloning site.

Fig. 5D shows a schematic representation of the LgBiT-YAP15 and 14-3-3-SmBiT constructs. SEQ ID NOs:59, 60, 61, and 62 give the full length sequences for LgBiT-YAP15 in pBiT 1.1 N vector, 14-3-3-LgBiT in pBiT2.1-C vector, LgBiT-YAP15 in pET16b vector, and SmBiT in pET16b vector, respectively, wherein the underlined portions are the main constructs and the rest is the vector.

Fig. 6 is a schematic diagram showing an overview of the NanoBiT interaction system. YAP15 and 14-3-3 are fused to LgBiT and SmBiT, respectively. Interaction of purified fusion proteins or overexpressed proteins in the cells leads to structural complementation of LgBiT with SmBiT that consequently generates a functional enzyme with bright luminescence.

For protein expression, the *E. coli* strain CodonPlus (DE3)-RIPL was transformed and used to purify the respective proteins. *E.coli* with the respective construct were grown until an OD600 value of 0.6-0.8 and then induced with 0.3 mM isopropyl- β -D-thiogalactopyranoside (IPTG) overnight at 20 °C. Protein purification was carried out by incubating cells at 4°C with DNase I (10 μ g/ml) followed by cell lysis by sonication. Bacterial lysates were centrifuged to collect soluble fractions and His-tagged proteins were purified from the supernatant via Ni-affinity purification. After eluting and concentrating, proteins were subjected to dialysis against standard buffer containing 30 mM Tris-HCl, pH 7.5, 150 mM NaCl, 5 mM MgCl₂, and 2 mM DTT. All purified proteins were analyzed by SDS-PAGE and stored at -80°C. Fig. 7 shows coomassie brilliant blue (CBB) stained SDS-PAGE of purified proteins for the biosensor.

NanoBiT assay for YAP15-14-3-3 in cells. A NanoBiT assay was prepared for YAP15-14-3-3 in cells. HEK293T cells (3×10^5) were transfected using Polyjet transfection reagent according to the manufacturer's instructions in 12-well plates by using 250 ng of each plasmid DNA per transfection. After 48 h the cells were lysed with passive lysis buffer and the NanoBiT assay of overexpressed LgBiT-YAP15 WT and mutant and 14-3-3-SmBiT was performed. Relative luminescence to YAP15MUT-14-3-3 was determined as shown in Fig. 8A.

NanoBiT assay for YAP15-14-3-3 using cancer cells. Cancer cells (A549, H1299, and HEK293) were treated with okadaic acid for 1 h to activate LATS before lysing with passive lysis buffer. Then, 350 μ g cell lysate was untreated or treated with calf intestine phosphatase (CIP) to inactivate the biosensor, followed by LATS pulldown and measurement of LATS kinase activity *in vitro* using purified LATS BS. As shown in Fig. 8B, the NanoBiT LATS-BS produced a strong signal for all three types of cancer cells.

NanoBiT assay for YAP15-14-3-3 using blood. Mononuclear cells were separated from fresh human blood and then lysed with passive lysis buffer. Then, 350 μ g cell lysate was used to pull-down LATS kinase and measure its activity *in vitro* using purified NanoBiT LATS-BS. As shown in Fig. 8C, the NanoBiT LATS-BS produced a strong signal.

NanoBiT assay using purified proteins. In order to test the LATS NanoBiT biosensor *in vitro*, a kinase assay was done using purified LgBiT-YAP15 (WT and mutant), 14-3-3-SmBiT and LATS2 as the kinase. The assay was done with two different concentrations of biosensor (100 ng and 5 ng). After 1, 10, 20, 30 min and 1, 2, 4 and 20 h luminescence was measured and also phosphorylation level was checked using WB. Results are shown in Fig. 9. The upper panel shows the result of NanoBiT assay for YAP15WT and mutant at the two different concentrations of biosensor (5 and 100 ng) as a ratio of luminescence signal in the presence to absence of LATS as a kinase in different time points. The lower panel shows immunoblotting analysis and Ponceau staining of the respective samples from the experiment with 100 ng of biosensor.

Kinase assay with and without phosphatase. To confirm that the biosensor is phosphorylation dependent and works through LATS, lambda phosphatase was used and luminescence as well as phosphorylation was determined. The results show that treating with lambda phosphatase abolishes luminescence. In Fig. 10 the upper panel shows the result of an assay for the biosensor with YAP15 WT or mutant (100 ng) with and without lambda

phosphatase after 30 min. The Y axis shows the ratio of luminescence in the presence of LATS and in the absence of LATS. The lower panels show the relative immunoblotting and Ponceau staining for the respective samples.

2. YAP-TEAD Biosensor

YAP transcriptionally activates downstream genes by interacting with the TEAD family of transcription factors (i.e., TEAD1-4). To monitor interaction between YAP and TEAD, a NanoBiT split luciferase biosensor was developed that quantifies YAP1 and TEAD1 interaction. This biosensor is based on a YAP fragment (residues 50–171; SEQ ID NO:2)–TEAD1 fragment (residues 194–411; SEQ ID NO:50) complex, in which YAP wraps around the globular structure of TEAD1. Fig. 12 shows a schematic overview of the NanoBiT interaction system of a YAP-TEAD NanoBiT biosensor as described herein. The YAP1 mRNA and amino acid sequences are given in SEQ ID NOs:1 and 2, respectively. The TEAD1 mRNA and protein sequences are given in SEQ ID NOs:49 and 50, respectively. The Large BiT (LgBiT) mRNA and protein sequences are given in SEQ ID NOs:51 and 52, respectively. The Small BiT (SmBiT) mRNA and protein sequences are given in SEQ ID NOs:53 and 54, respectively. The vectors were pcDNA3.1/hygro(+) (SEQ ID NO:9), pcDNA3.1/hygro(+)-Flag (SEQ ID NO:55), and pcDNA3.1/hygro(+)-Myc (SEQ ID NO:56).

Eight NanoBit split luciferase constructs were made using the primers as listed below. The domain structures of the eight constructs are shown in Fig. 11.

Construct 1: LgBiT-YAP50-171-Flag (overlapping PCR):

SEQ ID NO:34. B1-Kozak-LgBiT-F primer (41 nucleotides):

SEQ ID NO:35. LgBiT-(GS)-R primer (54 nucleotides):

SEQ ID NO:36. (GS)-YAP50-F primer (69 nucleotides):

SEQ ID NO:37. N1-YAP171-Flag-R primer (63 nucleotides)

Construct 2: Flag-YAP50-171-LgBiT (overlapping PCR):

SEQ ID NO:38. B1-YAP50-F primer (32 nucleotides):

SEQ ID NO:39. (GS)-YAP171-R primer (68 nucleotides):

SEQ ID NO:40. (GS)-LgBiT-F primer (66 nucleotides):

SEQ ID NO:41. N1-LgBiT-R primer (43 nucleotides):

Construct 3: SmBiT- YAP50-171-Flag (tandem PCR):

SEQ ID NO:42. B1-Kozak -SmBiT-(GS)-F primer (98 nucleotides):

SEQ ID NO:36. (GS)-YAP50-F primer (69 nucleotides):

5 SEQ ID NO:37. N1-YAP171-Flag-R primer (63 nucleotides)

Construct 4: Flag-YAP50-171-SmBiT (tandem PCR):

SEQ ID NO:38. B1-YAP50-F primer (32 nucleotides)

SEQ ID NO:39. (GS)-YAP171-R primer (68 nucleotides)

SEQ ID NO:43. N1-SmBiT-(GS)-R primer (97 nucleotides):

10 Construct 5: LgBiT- TEAD1-194-411-Myc (overlapping PCR):

SEQ ID NO:34. B1-Kozak-LgBiT-F primer (41 nucleotides)

SEQ ID NO:35. LgBiT-(GS)-R primer (54 nucleotides)

SEQ ID NO:44. (GS)-TEAD-194-F primer (73 nucleotides):

SEQ ID NO:45. N1-TEAD411-Myc-R primer (73 nucleotides):

15 Construct 6: Myc-TEAD1-194-411-LgBiT (overlapping PCR)

SEQ ID NO:46. B1-TEAD194-F primer (36 nucleotides):

SEQ ID NO:47. GS-TEAD-411-R primer (69 nucleotides):

SEQ ID NO:40. (GS)-LgBiT-F primer (66 nucleotides)

SEQ ID NO:41. N1-LgBiT-R primer (43 nucleotides)

20 Construct 7: SmBiT- TEAD1-194-411-Myc (tandem PCR)

SEQ ID NO:42. B1-Kozak-SmBiT-(GS)-F primer (98 nucleotides)

SEQ ID NO:48. (GS)-TEAD194-F primer (73 nucleotides):

SEQ ID NO:45. N1-TEAD411-Myc-R primer (73 nucleotides)

Construct 8: Myc-TEAD1-194-411-SmBiT (tandem PCR)

SEQ ID NO:46. B1-TEAD194-F primer (36 nucleotides)

SEQ ID NO:47. GS-TEAD-411-R primer (69 nucleotides)

SEQ ID NO:43. N1-SmBiT-(GS)-R primer (97 nucleotides)

Cloning. To make constructs 1 and 5, overlapping PCR was performed using the above
5 primers, and they were inserted into BamH1/Not1 cloning site of pcDNA3.1/hygro. For
construct 1, pBiT1.1-N(TK/LgBiT) and full length YAP were used as templates to perform PCR.
For construct 5, pBiT1.1-N(TK/LgBiT) and full length TEAD1 were used to perform PCR.

To make constructs 2 and 6, overlapping PCR was performed using the above primers,
and they were inserted into BamH1/Not1 cloning site of pcDNA3.1/hygro-Flag/Myc. For
10 construct 2, pBiT1.1-C(TK/LgBiT) and full length YAP were used to perform PCR. For
construct 6, pBiT1.1-C(TK/LgBiT) and full length TEAD1 were used to perform PCR.

To make constructs 3 and 7, tandem PCR was performed using the above primers, and
they were inserted into BamH1/Not1 cloning site of pcDNA3.1/hygro. For both constructs full
length YAP and TEAD1 were used respectively to perform PCR.

15 To make construct 4 and 8, overlapping PCR was performed using the above primers,
and they were inserted into BamH1/Not1 cloning site of pcDNA3.1/hygro-Flag/Myc. For both
constructs full length YAP and TEAD1 were used respectively to perform PCR.

SEQ ID NOS:63-70 give the full length sequences for constructs 1-8, respectively,
wherein, in each sequence, the underlined portion is the main construct and the rest is the vector.

20 Validation. Different combinations of the eight constructs were used in assays in order to
find the best orientation for the biosensor. The assays used overexpressed YAP50-171 and
TEAD1-194-411 in HEK293T cells lysed with passive lysis buffer. All combinations of SmBiT
and LgBiT biosensors worked, but the combination of SmBiT-YAP50-171 and LgBiT-TEAD1-
194-411 showed the highest signal and sensitivity (Fig. 13).

25 Discussion

The embodiments and experiments described herein establish the LATS biosensor
embodiments as the first LATS biosensor that can accurately monitor LATS kinase activity and
intensity of Hippo signaling *in vitro* and *in vivo*, and its use in a new bioluminescence (BLI)

method. In addition, the embodiments and experiments described herein establish the YAP-TEAD biosensor embodiments as the first biosensor that can accurately monitor YAP and TEAD interaction, which is essential for elucidating the function of YAP in the Hippo pathway.

Although BLI is widely used for reporting promoter activity and imaging tumors in mice, few studies have used it to measure protein function at the cellular level and even fewer studies have examined subcellular protein function using bioluminescence microscopy. The ability to detect LATS kinase activity in individual cells and in blood as provided by the embodiments described herein has applications for evaluating heterogeneous dynamics of LATS kinase activity in cell culture as well as for the real-time monitoring of Hippo signaling responses to various drug treatments, and in applications such as detecting Hippo pathway signaling in biological samples such as tissue and blood obtained from subjects. In particular, the results show that a biosensor as described herein may be useful for detecting cancerous cells in biological samples such as tissue. The results of *in vivo* experiments in mice further illustrate how LATS-BS embodiments may be used to preclinically examine the effects of a variety of drugs on LATS kinase activity *in vivo*.

A biosensor as described herein may be provided in a kit to measure the Hippo signaling pathway, for use *in vitro* and *in vivo*. For example, a kit may include one or more LATS biosensor such as an intermolecular biosensor, intramolecular biosensor, engineered biosensor, or NanoBiT biosensor, and/or a YAP-TEAD biosensor as described herein, optionally with one or more reagents suitable for using the kit in an assay for a specified biological sample or cell type, and instructions for proper use of the kit. The reagent may be, for example, a reagent appropriate for *in vitro* use or for *in vivo* use, a buffer, cell lysis buffer, etc.

Example

The following example provides details of the methods used to make and use an intermolecular LATS biosensor as described herein.

1. Determine activity of purified LATS protein and LATS in cells by *in vitro* luciferase assay (described above and shown in Figs. 2C, 2D, 3C, 8, and 13).

2. Determine interaction of YAP and TEAD in cells by *in vitro* luciferase assay (described above and shown in Fig. 13).

3. Determine LATS kinase activity under various stimuli regulating Hippo signaling by live cell luciferase imaging.

For live cell imaging, LATS-BS or a pGL3-control vector were transfected into HEK293, MDA-MB-231 or A549 cells. After 48 hours, cells were trypsinized and collected in a black, clear bottomed, 96-well plate. 150 µg/mL D-luciferin (D-Luciferin, Potassium Salt, GoldBio # LUCK-250) in media was added to each well 5–10 min before imaging. Exposure time for images was approximately 3 min/plate. Imaging was performed using a LightTools Research system (Synopsys, Ltd., Mountain View, California, USA) dark box and a Hamamatsu ORCA-Flash4.0 V2 digital CMOS camera over the course of 20 minutes to establish optimal peak luciferase activity. The bioluminescence of the regions of interest was analyzed for total emission flux using Image-Pro® Plus software (Media Cybernetics, Inc., Rockville, Maryland, USA).

Experiments were conducted to further validate the LATS intermolecular biosensor and explore potential applications for its use. The LATS-BS responded to numerous signals reported to modulate Hippo pathway activity, including cell confluency, drugs activating Hippo signaling (Forskolin, PI3K inhibitor, PDK inhibitor, F-IBMX, and 2-deoxy-glucose) and Hippo signaling inhibitors (LPA, EGF, Insulin, S1P, and TPA). The LATS-BS is activated by LATS in various cell lines (e.g., A549, MDA-MB231). Notably, in these experiments biosensor activity was measured in both cell lysates and in live cells using luciferase assay and BLI respectively. Collectively, these data illustrate the broad range of potential applications for the LATS-BS in monitoring Hippo pathway activity.

The following compound treatments were used for *in vitro* luciferase assay and live cells imaging: RAF inhibitor (GW5054, Cayman Chemical, Ann Arbor, Michigan, USA), ATR inhibitor (CGK733, Cayman Chemical), PI3K inhibitor 1 (GDC0941, Cayman Chemical), PI3K inhibitor 2 (LY294002, Cayman Chemical), PDK inhibitor (GSK2334470, Cayman Chemical)-10 µM for 4 hours; EGF-100 ng/mL for 1 hour; insulin (Sigma #91077C)-10 µg/ml for 1 hour; F/IBMX (Forskolin, Cayman Chemical /IBMX, Cayman Chemical)-0.1-10 µM for Forskolin and 100 µM for IBMX for 1 hour; L-α -lysophosphatidic acid (LPA) (Sigma#L7260)-0.1-10 µM for 1 hour; sphingosine 1-phosphophate (S1P)-1 µM for 1 hour; 12-O-tetradecanoylphorbol-13-acetate (TPA) (#41745; Cell Signaling Technology, Inc., Danvers, Massachusetts, USA)-5 nM

for 1 hour; 2-deoxy glucose (#D8375, Sigma-Aldrich Canada Co., Oakville, Ontario, Canada)-25 mM for 1 hour. The results are shown in Fig. 14.

4. Determine subcellular LATS kinase activity by bioluminescent microscopy.

Using the intermolecular LATS-BS, a new method was developed for the Olympus
5 LV200 Bioluminescence Imager, and LATS kinase activity was visualized and quantified at the individual cell level in cancer cell lines. 3.5 mM D-luciferin was added to the media culturing HEK293A, A549 or MDA-MB231 cells stably expressing LATS-BS at 5-10 min before imaging. Images were captured using Olympus LV200 Bioluminescence Imager with exposure times ranging from 30 seconds (HEK293A) to 10 min (MDA-MB-231, A549). The results are
10 shown in Fig. 15. The difference in biosensor signal intensity among individual cells represents altered endogenous LATS kinase activity rather than differential LATS-BS expression levels since only the LATS-phosphorylated fraction of LATS-BS should emit bioluminescence. In addition, data showed that both the levels and subcellular localization of LATS-BS bioluminescence (cytoplasm where LATS is expressed) and GFP (control, nucleus/cytoplasm)
15 were different in the same cell. This technology also allowed comparison of the heterogeneity of LATS kinase activity among cancer cell lines by assessing the distribution of luciferase activity. Further, and of particular significance, using biophotonics BLI, LATS kinase activity was detected *in vivo* in mice. The subcellular activity of LATS kinase can be also visualized by bioluminescent imaging.

5. Measuring LATS kinase activity in mice by *in vivo* luciferase imaging.

Further, and of particular significance, using biophotonics BLI, LATS kinase activity was detected *in vivo* in mice. All mouse procedures were approved by the Queen's University Animal Care Committee (UACC) and performed in accordance with institutional policies. To visualize LATS kinase activity *in vivo*, 12-week-old female BALB/c mice were anesthetized by exposure
25 to 1-3% isoflurane. 3 x 10⁶ HEK293 cells transfected with an intermolecular LATS-BS alone (LATS-) or together with LATS (LATS+) were suspended in 100 µL of sterile PBS and injected into the mammary fat pad. Two days after the injection, post-surgery mice received 150mg/kg of D-luciferin (Cedarlane) dissolved in PBS by intraperitoneal injection. Imaging of ventral view was performed using a LightTools Research system (Encinitas, CA) dark box and a Hamamatsu
30 ORCA-Flash4.0 V2 digital CMOS camera over a course of 30 minutes to establish optimal peak

luciferase activity. Pseudo-colored parametric overlays of BLI with anatomical reference images were dynamically constructed for each individual animal at comparative time points. The bioluminescence (BLI) of the regions of interest (ROI) was then analyzed for total emission flux using Image Pro Plus software. The results are shown in Fig. 16, where the arrow (right panel) points to the area where high intensity luminescence (red in heatmap) was detected.

6. Identifying novel regulators of LATS by a kinase inhibitor screen.

The intermolecular LATS-BS was used to search for novel kinases regulating Hippo signaling with a small-scale kinase inhibitor screen. The LATS-BS was transfected into HEK293A. Cells were passed into a 384-well plate the following day. 48 hours after transfection, cells were treated with the Tocriscreen Kinase Inhibitor Toolbox (Tocris Bioscience #3514) with each drug administered at 10 μ M in DMSO for 4 hours in duplicate. Biosensor activity was then measured by luciferase assay. Fold change ratios were generated by comparing biosensor activity for each drug with that of DMSO-treated controls. The screening schematic and results are shown in Figs. 17A and 17B, respectively. Of 80 kinase inhibitors screened, six kinase inhibitors activated the biosensor (i.e., inhibitors of VEGFR, MEK, GSK-3, PKB/Akt, EGFR, and CDK) while six inhibitors reduced the biosensor signal (i.e., inhibitors of TrkA, Broad, SYK, ATR/ATM, CHK1, and SGK). From these candidate LATS regulators, VEGFR1/2, GSK-3a/b, CDK4, TrkA, SYK, Broad, and SGK are novel. The screen results were confirmed by luciferase assays using the LATS-BS and an STBS-luciferase reporter that measures the transactivating function of YAP/TAZ32. The kinase inhibitors had the opposite effects on LATS-BS and STBS reporter, suggesting that the screen had identified true regulators of Hippo signaling. It is expected that future large-scale screens using the LATS-BS will identify additional new activators or inhibitors of the Hippo signaling pathway.

Sequences

SEQ ID NO:1. Human YAP1 (yes-associated protein beta) isoform 2L mRNA (1,401 nucleotides) (accession number: AB567720)

ATGGATCCCGGGCAGCAGCCGCCCTCAACCGGCCCCCCAGGGCCAAGGGCAGCCGCCTTCGC
AGCCCCCGCAGGGGCAGGGCCCGCGTCCGGACCCGGGCAACCGGCACCCGCGGCGACCCAGGC
GGCGCCGCAGGCACCCCCCGCGGGCATCAGATCGTGCACGTCCGCGGGGACTCGGAGACCGAC

CTGGAGGCGCTCTTCAACGCCGTCATGAACCCCAAGACGGCCAACGTGCCCCAGACCGTGCCCA
 TGAGGCTCCGGAAGCTGCCCCACTCCTTCTTCAAGCCGCCGGAGCCCAAATCCCCTCCCGACA
 GGCCAGTACTGATGCAGGCACTGCAGGAGCCCTGACTCCACAGCATGTTGAGCTCATTCTCTCT
 CCAGCTTCTCTGCAGTTGGGAGCTGTTTCTCCTGGGACACTGACCCCCACTGGAGTAGTCTCTG
 5 GCCCAGCAGCTACACCCACAGCTCAGCATCTTCGACAGTCTTCTTTTGAGATACCTGATGATGT
 ACCTCTGCCAGCAGGTTGGGAGATGGCAAAGACATCTTCTGGTCAGAGATACTTCTTAAATCAC
 ATCGATCAGACAACAACATGGCAGGACCCCAGGAAGGCCATGCTGTCCCAGATGAACGTCACAG
 CCCCCACCAGTCCACCAGTGCAGCAGAATATGATGAACTCGGCTTCAGCCATGAACCAGAGAAT
 CAGTCAGAGTGCTCCAGTGAAACAGCCACCACCCCTGGCTCCCCAGAGCCCACAGGGAGGCGTC
 10 ATGGGTGGCAGCAACTCCAACCAGCAGCAACAGATGCGACTGCAGCAACTGCAGATGGAGAAGG
 AGAGGCTGCGGCTGAAACAGCAAGAACTGCTTCGGCAGGCAATGCGGAATATCAATCCCAGCAC
 AGCAAATCTCCAAAATGTCAGGAGTTAGCCCTGCGTAGCCAGTTACCAACACTGGAGCAGGAT
 GGTGGGACTCAAAATCCAGTGTCTTCTCCCGGGATGTCTCAGGAATTGAGAACAAATGACGACCA
 ATAGCTCAGATCCTTTCCTTAACAGTGGCACCTATCACTCTCGAGATGAGAGTACAGACAGTGG
 15 ACTAAGCATGAGCAGCTACAGTGTCCCTCGAACCCCAGATGACTTCCTGAACAGTGTGGATGAG
 ATGGATACAGGTGATACTATCAACCAAAGCACCCCTGCCCTCACAGCAGAACCGTTTCCCAGACT
 ACCTTGAAGCCATTCCTGGGACAAATGTGGACCTTGGAACTGGAAGGAGATGGAATGAACAT
 AGAAGGAGAGGAGCTGATGCCAAGTCTGCAGGAAGCTTTGAGTTCTGACATCCTTAATGACATG
 GAGTCTGTTTTGGCTGCCACCAAGCTAGATAAAGAAAGCTTTCTTACATGGTTATAG

20 SEQ ID NO:2. Human YAP1 isoform 2L protein (504 amino acids)

MDPGQQPPPQPAPQGQGQPPSQPPQGQPPSPGPGQPAPAAATQAAPQAPPAGHQIVHVRGDSETD
 LEALFNAVMPNPKTANVPQTVPMLRLKLPDSFFKPPPEPKSHSRQASTDAGTAGALTPQHVRHSS
 PASLQLGAVSPGTLTPTGVVSGPAATPTAQHLRQSSFEPDDVPLPAGWEMAKTSSGQRYFLNH
 IDQTTTWQDPRKAMLSQMNVTAPTSPPVQONMMNSASGPLPDGWEQAMTQDGEIYYINHKNKTT
 25 SWLDPRLDPRFAMNQRISSAPVKQPPPLAPQSPQGGVMGGSNSNQQQQMRLQQLQMEKERLRL
 KQQELLRQAMRNINPSTANSPKCQELALRSQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDP
 FLNSGTYHSRDESTDSGLSMSSYSVPRTPDDEFNSVDEMDTGDTINQSTLPSQQNRFPDYLEAI
 PGTNVDLGTLEGDMNIEGEELMPSLQEALSSDILNDMESVLAATKLDKESFLTWL

30 SEQ ID NO:3. Human 14-3-3 protein theta mRNA (738 nucleotides) (accession number: P27348)

ATGGAGAAGACTGAGCTGATCCAGAAGGCCAAGCTGGCCGAGCAGGCCGAGCGCTACGACGACA
 TGGCCACCTGCATGAAGGCAGTGACCGAGCAGGGCGCCGAGCTGTCCAACGAGGAGCGCAACCT
 GCTCTCCGTGGCCTACAAGAACGTGGTGGGGGGCCGAGGTCCGCCTGGAGGGTCATCTCTAGC
 ATCGAGCAGAAGACCGACACCTCCGACAAGAAGTTGCAGCTGATTAAGGACTATCGGGAGAAAAG
 5 TGGAGTCCGAGCTGAGATCCATCTGCACCACGGTGCTGGAATTGTTGGATAAATATTTAATAGC
 CAATGCAACTAATCCAGAGAGTAAGGTCTTCTATCTGAAAATGAAGGGTGATTACTTCCGGTAC
 CTTGCTGAAGTTGCGTGTGGTGATGATCGAAAACAAACGATAGATAATTCCCAAGGAGCTTACC
 AAGAGGCATTTGATATAAGCAAGAAAGAGATGCAACCCACACACCCAATCCGCCTGGGGCTTGC
 TCTTAACTTTTCTGTATTTTACTATGAGATTCTTAATAACCCAGAGCTTGCCTGCACGCTGGCT
 10 AAAACGGCTTTTGATGAGGCCATTGCTGAACTTGATACACTGAATGAAGACTCATACAAAGACA
 GCACCCTCATCATGCAGTTGCTTAGAGACAACCTAACACTTTGGACATCAGACAGTGCAGGAGA
 AGAATGTGATGCGGCAGAAGGGGCTGAAAACATA

SEQ ID NO:4. Human 14-3-3 protein theta (245 amino acids)

MEKTELIQKAKLAEQAERYDDMATCMKAVTEQGAELSNEERNLLSVAYKNVVGRRSAWRVISS
 15 IEQKTDTSDDKKLQLIKDYREKVESELRSICTTVLELLDKYLIANATNPESKVFYLMKMGDYFRY
 LAEVACGDDRKQTIDNSQGAYQEAFDISKEMQPTHPIRLGLALNFSVFYYEILNNPELACTLA
 KTAFFDEAIAELDTLNEDSYKDSTLIMQLLRDNLTLWTSDSAGEECDAAEGAEN

SEQ ID NO:5. Firefly (*Photinus pyralis*) luciferase mRNA (1,653 nucleotides)

ATGGAAGACGCCAAAAACATAAAGAAAGGCCCGCGCCATTCTATCCGCTGGAAGATGGAACCG
 20 CTGGAGAGCAACTGCATAAGGCTATGAAGAGATACGCCCTGGTTCCTGGAACAATTGCTTTTAC
 AGATGCACATATCGAGGTGGACATCACTTACGCTGAGTACTTCGAAATGTCCGTTTCGGTTGGCA
 GAAGCTATGAAACGATATGGGCTGAATACAAATCACAGAATCGTCGTATGCAGTGAAAACCTCTC
 TTCAATTCTTTATGCCGGTGTGGGCGCGTTATTTATCGGAGTTGCAGTTGCGCCCCGGAACGA
 CATTTATAATGAACGTGAATTGCTCAACAGTATGGGCATTTTCGCAGCCTACCGTGGTGTTCGTT
 25 TCCAAAAAGGGGTTGCAAAAAATTTTGAACGTGCAAAAAAGCTCCCAATCATCCAAAAAATTA
 TTATCATGGATTCTAAACGGATTACCAGGGATTTTCAGTCGATGTACACGTTTCGTCACATCTCA
 TCTACCTCCCGGTTTTTAATGAATACGATTTTGTGCCAGAGTCCTTCGATAGGGACAAGACAATT
 GCACTGATCATGAACTCCTCTGGATCTACTGGTCTGCCTAAAGGTGTCGCTCTGCCTCATAGAA
 CTGCCTGCGTGAGATTCTCGCATGCCAGAGATCCTATTTTTGGCAATCAAATCATTCGGGATAC
 30 TGCGATTTTAAGTGTGTTCCATTCCATCACGGTTTTGGAATGTTTACTACACTCGGATATTTG

ATATGTGGATTTTCGAGTCGTCTTAATGTATAGATTTGAAGAAGAGCTGTTTCTGAGGAGCCTTC
 AGGATTACAAGATTCAAAGTGCCTGCTGGTGCCAACCTATTCTCCTTCTTCGCCAAAAGCAC
 TCTGATTGACAAATACGATTTATCTAATTTACACGAAATTGCTTCTGGTGGCGCTCCCCCTCTCT
 AAGGAAGTCGGGGAAGCGGTTGCCAAGAGGTTCCATCTGCCAGGTATCAGGCAAGGATATGGGC
 5 TCACTGAGACTACATCAGCTATTCTGATTACACCCGAGGGGGATGATAAACCGGGCGCGGTCGG
 TAAAGTTGT'TCCATTTTTTTGAAGCGAAGGTTGTGGATCTGGATAACCGGAAAACGCTGGGCGTT
 AATCAAAGAGGCGAACTGTGTGTGAGAGGTCTATGATTATGTCCGGTTATGTAAACAATCCGG
 AAGCGACCAACGCCTTGATTGACAAGGATGGATGGCTACATTCTGGAGACATAGCTTACTGGGA
 CGAAGACGAACACTTCTTCATCGTTGACCGCCTGAAGTCTCTGATTAAGTACAAAGGCTATCAG
 10 GTGGCTCCCGCTGAATTGGAATCCATCTTGCTCCAACACCCCAACATCTTCGACGCAGGTGTCTG
 CAGGTCTTCCCGACGATGACGCCGGTGAAGTCTCCCGCCGCCGTTGTTGTTTTGGAGCACGGAAA
 GACGATGACGGAAAAAGAGATCGTGGATTACGTCGCCAGTCAAGTAACAACCGCGAAAAAGTTG
 CGCGGAGGAGTTGTGTTTGTGGACGAAGTACCGAAAGGTCTTACCGGAAAACCTCGACGCAAGAA
 AAATCAGAGAGATCCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAA

15 **SEQ ID NO:6. Firefly (*Photinus pyralis*) luciferase protein (555 amino acids)**

MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTDAHIEVDITYAEYFEMSVRLA
 EAMKRYGLNTNHRIVVCSNSLQFFMPVLGALFIGVAVAPANDIYNERELLNSMGISQPTVVFV
 SKKGLQKILNVQKKLPPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGFNEYDFVPESFDRDKTI
 ALIMNSSGSTGLPKGVALPHRTACVRFSHARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYL
 20 ICGFRVVLMYRFEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIASGGAPLS
 KEVGEAVAKRFHLPGIRQGYGLTETTSAILITPEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGV
 NQRGELCVRGPMIMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGQ
 VAPAELESILLQHPNIFDAGVAGLPDDDAGELPAVVVLEHGKTMTEKEIVDYVASQVTTAKKL
 RGGVVFVDEVKGLTGKLDARKIREILIKAKKGGKIAV

25 **SEQ ID NO:7. YAP15 S127 wildtype (WT) protein fragment (15 amino acids)**

PQHVRHASSPASLQL

SEQ ID NO:8. YAP15 A127 mutant protein fragment (15 amino acids)

PQHVRHAASPASLQL

**SEQ ID NO:9. pcDNA3.1/hygro(+)
vector (5,597 nucleotides)**

GACGGATCGGGAGATCTCCCGATCCCCTATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGC
ATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAA
ATTTAAGCTACAACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGC
5 GTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGACATTGATTATTGACTAGTTA
TTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA
CTTACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGA
CGTATGTTCCCATAGTAACGCCAATAGGGACTTTCATTGACGTCAATGGGTGGAGTATTTACG
GTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTC
10 AATGACGGTAAATGGCCCGCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTT
GGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAA
TGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCTAAGTCTCCACCCCATGACGTCAATGGG
AGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCTAAGTGTGTAACAACCTCCGCCCCATTGA
CGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAG
15 AGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACCCAAGCTGGC
TAGCGTTTTAACTTAAGCTTGGTACCGAGCTCGGATCCACTAGTCCAGTGTGGTGGAATTCTGC
AGATATCCAGCACAGTGGCGGCCGCTCGAGTCTAGAGGGCCCGTTTTAAACCCGCTGATCAGCCT
CGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTGACCCT
GGAAGGTGCCACTCCCCTGTCCTTTTCTAATAAAATGAGGAAATTGCATCGCATTTGTCTGAGT
20 AGGTGTCATTCTATTCTGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACA
ATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGG
CTCTAGGGGGTATCCCCACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACG
CGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCT
TTCTCGCCACGTTTCGCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCG
25 ATTTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG
CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGAC
TCTTGTTCCAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGAT
TTTGCCGATTTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTAA
TTCTGTGGAATGTGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTAT
30 GCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGC
AGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCA

TCCCGCCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTAT
TTATGCAGAGGCCGAGGCCGCCTCTGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTT
GGAGGCCTAGGCTTTTGCAAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCAGC
ACGTGATGAAAAAGCCTGAACTCACCGCGACGTCTGTGCGAGAAGTTTCTGATCGAAAAGTTCGA
5 CAGCGTCTCCGACCTGATGCAGCTCTCGGAGGGCGAAGAATCTCGTGCTTTCAGCTTCGATGTA
GGAGGGCGTGGATATGTCCTGCGGGTAAATAGCTGCGCCGATGGTTTCTACAAAGATCGTTATG
TTTATCGGCACTTTGCATCGGCCGCGCTCCCGATTCCGGAAGTGCTTGACATTGGGGAATTCAG
CGAGAGCCTGACCTATTGCATCTCCCGCCGTGCACAGGGTGTACGTTGCAAGACCTGCCTGAA
ACCGAACTGCCCCGCTGTTCTGCAGCCGGTGC GCGAGGCCATGGATGCGATCGCTGCGGCCGATC
10 TTAGCCAGACGAGCGGGTTTCGGCCCATTTCGGACCGCAAGGAATCGGTCAATACACTACATGGCG
TGATTTTCATATGCGCGATTGCTGATCCCCATGTGTATCACTGGCAAACGTGATGGACGACACC
GTCAGTGCGTCCGTGCGCGAGGCTCTCGATGAGCTGATGCTTTGGGCCGAGGACTGCCCCGAAG
TCCGGCACCTCGTGACGCGGATTTTCGGCTCCAACAATGTCCTGACGGACAATGGCCGCATAAC
AGCGGTCAATTGACTGGAGCGAGGCGATGTTCTGGGGATTCCCAATACGAGGTGCGCAACATCTTC
15 TTCTGGAGGCCGTGGTTGGCTTGTATGGAGCAGCAGACGCGCTACTTCGAGCGGAGGCATCCGG
AGCTTGCAGGATCGCCGCGGCTCCGGGCGTATATGCTCCGCATTGGTCTTGACCAACTCTATCA
GAGCTTGGTTGACGGCAATTCGATGATGCAGCTTGGGCGCAGGGTCGATGCGACGCAATCGTC
CGATCCGGAGCCGGGACTGTGCGGCGTACACAAATCGCCCGCAGAAGCGCGGCCGTCTGGACCG
ATGGCTGTGTAGAAGTACTCGCCGATAGTGGAACCGACGCCCCAGCACTCGTCCGAGGGCAAA
20 GGAATAGCACGTGCTACGAGATTTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGA
ATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCG
CCCACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTT
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCT
TATCATGTCTGTATACCGTCGACCTCTAGCTAGAGCTTGGCGTAATCATGGTCATAGCTGTTTC
25 CTGTGTGAAATTGTTATCCGCTCACAATTCACACACATACGAGCCGGAAGCATAAAGTGTA
AGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCCGCTTTC
CAGTCGGGAAACCTGTGCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
TGCATATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTTCGCTGCG
GCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCA
30 GGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGG
CGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTG
GCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCT

CCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGC
 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTG
 TGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC
 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGA
 5 GGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAC
 AGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGA
 TCCGGCAAACAAACCACCGCTGGTAGCGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAA
 AAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAA
 CTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAAT
 10 TAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAAT
 GCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACT
 CCCCCTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATA
 CCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCG
 AGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGC
 15 TAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTG
 GTGTCACGCTCGTCGTTTTGGTATGGCTTCATTACGCTCCGGTTCCCAACGATCAAGGCGAGTTA
 CATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAG
 TAAGTTGGCCGAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATG
 CCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA
 20 TGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAAC
 TTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTG
 TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACCTGATCTTCAGCATCTTTTACTTTCA
 CCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGAC
 ACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTATCAGGGTTAT
 25 TGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCA
 CATTTCCCCGAAAAGTGCCACCTGACGTC

SEQ ID NO:10. B1-Kozak-Nluc-F primer (41 nucleotides)

CTGGATCCGCCGCCACCATGGAAGACGCCAAAAACATAAAG

SEQ ID NO:11. Nluc-416-Yap-15-S127-(GGAGG)-R primer (84 nucleotides)

TTACAACTGCAGAGAAGCTGGAGAGGAATGAGCTCGAACATGCTGTGGGCCTCCAGCTCCTCCT
CCATCCTTGTCAATCAAGGC

SEQ ID NO:12. N1-Yap-5-Overlapping PCR-R primer (36 nucleotides)

ATGAAACTGCGGCCGCTTACAACTGCAGAGAAGCTG

5 **SEQ ID NO:13. B1-Kozak-14-3-3-F primer (38 nucleotides)**

CTGGATCCGCCGCCACCATGGAGAAGACTGAGCTGATC

SEQ ID NO:14. (GGGGS)2-14-3-3-R primer (51 nucleotides)

ACTACCTCCTCCTCCACTACCTCCTCCTCCGTTTTTCAGCCCCCTTCTGCCGC

SEQ ID NO:15. (GGGGS)2-Cluc394-F primer (39 nucleotides)

10 GGTAGTGGAGGAGGAGGTAGTGGTCCTATGATTATGTCC

SEQ ID NO:16. N1-Cluc-R primer (34 nucleotides)

ATGAAACTGCGGCCGCTTACACGGCGATCTTTCC

SEQ ID NO:17. Nluc398-15-S127-(GGAGG)-R primer (81 nucleotides)

CAACTGCAGAGAAGCTGGAGAGGAATGAGCTCGAACATGCTGTGGGCCTCCAGCTCCTCCCATA

15 ATCATAGGACCTCTCAC

SEQ ID NO:18. Yap15-S127-Cluc394-F primer (42 nucleotides)

TCTCCAGCTTCTCTGCAGTTGGGTCCTATGATTATGTCCGGT

SEQ ID NO:19. N1-Yap15-S127-Cluc443 (engineered C-terminus of luciferase)-R primer (86 nucleotides)

20 ATGAAACTGCGGCCGCTTACAACTGCAGAGAAGCTGGAGAGGAATGAGCTCGAACATGCTGTGG
CTTCTTGGCCTTTATGAGGATC

SEQ ID NO:20. EcoR1-YAP-S127-BglII-S primer (55 nucleotides)

AATTCACCACAGCATGTTTCGAGCTCATTCCTCTCCAGCTTCTCTGCAGTTGTGAA

SEQ ID NO:21. ECoR1-YAP-S127-BglII-AS primer (55 nucleotides)

GATCTTCACAACCTGCAGAGAAGCTGGAGAGGAATGAGCTCGAACATGCTGTGGTG

SEQ ID NO:22. EcoR1-YAP-A127-BglII-S primer (55 nucleotides)

5 AATTCACCACAGCATGTTTCGAGCTCATGCGTCTCCAGCTTCTCTGCAGTTGTGAA

SEQ ID NO:23. ECoR1-YAP-A127-BglII-AS primer (55 nucleotides)

GATCTTCACAACCTGCAGAGAAGCTGGAGACGCATGAGCTCGAACATGCTGTGGTG

SEQ ID NO:24. BglII-14-3-3-F primer (31 nucleotides)

GGAAGATCTAATGGAGAAGACTGAGCTGATC

10 **SEQ ID NO:25. ECoR1-14-3-3-R primer (34 nucleotides)**

CGCCGGAATTCCTCGTTTTCAGCCCCCTCTGCCGC

SEQ ID NO:26. pBiT 1.1 N (TK-Larg BiT) whole vector (3,858 nucleotides)

GGCCTAACTGGCCGGTACCTGAGTCTAAATGAGTCTTCGGACCTCGCGGGGGCCGCTTAAGCGG
TGGTTAGGGTTTGTCTGACGCGGGGGGAGGGGGAAGGAACGAAACACTCTCATTCGGAGGCGGC
15 TCGGGGTTTGGTCTTGGTGGCCACGGGCACGCAGAAGAGCGCCGCGATCCTCTTAAGCACCCCC
CCGCCCTCCGTGGAGGCGGGGGTTTGGTCGGCGGGTGGTAACTGGCGGGCCGCTGACTCGGGCG
GGTCGCGCGCCCCAGAGTGTGACCTTTTCGGTCTGCTCGCAGACCCCCGGGCGGCGCCCGCG
GCGGCGACGGGCTCGCTGGGTCTTAGGCTCCATGGGGACCGTATACGTGGACAGGCTCTGGAGC
ATCCGCACGACTGCGGTGATATTACCGGAGACCTTCTGCGGGACGAGCCGGGTCACGCGGCTGA
20 CGCGGAGCGTCCGTGGGCGACAAACACCAGGACGGGGCACAGGTACACTATCTTGTCAACCGG
AGGCGCGAGGGACTGCAGGAGCTTCAGGGAGTGGCGCAGCTGCTTCATCCCCGTGGCCCGTTGC
TCGCGTTTGTCTGGCGGTGTCCCCGGAAGAAATATATTTGCATGTCTTTAGTTCTATGATGACAC
AAACCCCGCCCAGCGTCTTGTCAATTGGCGAAGTCGAACACGCAGATGCAGTCGGGGCGGCGCGG
TCCCAGGTCCACTTCGCATATTAAGGTGACGCGTGTGGCCTCGAACACCGAGCGACCCCTGCAGC
25 GACCCGCTTAAAAGCTTGGCAATCCGGTACTGTTGGTAAAGCCACCATGGTCTTCACACTCGAA
GATTTTCGTTGGGGACTGGGAACAGACAGCCGCCTACAACCTGGACCAAGTCCTTGAACAGGGAG

GTGTGTCCAGTTTGCTGCAGAATCTCGCCGTGTCCGTAACCTCCGATCCAAAGGATTGTCCGGAG
 CGGTGAAAATGCCCTGAAGATCGACATCCATGTCATCATCCCGTATGAAGGTCTGAGCGCCGAC
 CAAATGGCCCAGATCGAAGAGGTGTTTAAGGTGGTGTACCCTGTGGATGATCATCACTTTAAGG
 TGATCCTGCCCCTATGGCACACTGGTAATCGACGGGGTTACGCCGAACATGCTGAACTATTTTCGG
 5 ACGGCCGTATGAAGGCATCGCCGTGTTTCGACGGGCAAAAAGATCACTGTAACAGGGACCCTGTGG
 AACGGCAACAAAATTATCGACGAGCGCCTGATCACCCCGACGGCTCCATGCTGTTCCGAGTAA
 CCATCAACAGTGGGAGTTCCGGTGGTGGCGGGAGCGGAGGTGGAGGCTCGAGCGGTGGAGCTCA
 GGGGAATTCAGTCTAAGCTAGCAGATCTTCTAGAGTCGGGGCGGCCGGCCGCTTCGAGCAGACA
 TGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTAT
 10 TTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAC
 AACAACAATTGCATTCAATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTTAAAGCA
 AGTAAAACCTCTACAAATGTGGTAAAATCGATAAGGATCCGTCGACCGATGCCCTTGAGAGCCT
 TCAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACTATCGTCGCCGCACTTATGACTGT
 CTTCTTTATCATGCAACTCGTAGGACAGGTGCCGGCAGCGCTCTTCCGCTTCCTCGCTCACTGA
 15 CTCGCTGCGCTCGGTGCTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG
 TTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA
 GGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTCATAGGCTCCGCCCCCCTGACGAGCATCA
 CAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTT
 CCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCG
 20 CCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGT
 GTAGGTCGTTGCTCCAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCC
 TTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAG
 CCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTG
 GCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC
 25 TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTT
 TTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC
 TACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATCA
 AAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTAAATCAATCTAAAGTATAT
 ATGAGTAAACTTGGTCTGACAGCGGCCGCAAATGCTAAACCACTGCAGTGGTTACCAGTGCTTG
 30 ATCAGTGAGGCACCGATCTCAGCGATCTGCCTATTTTCGTTTCGTCCATAGTGGCCTGACTCCCCG
 TCGTGTAGATCACTACGATTCGTGAGGGCTTACCATCAGGCCCCAGCGCAGCAATGATGCCGCG
 AGAGCCGCGTTACCCGGCCCCCGATTGTGTCAGCAATGAACCAGCCAGCAGGGAGGGCCGAGCGA

AGAAGTGGTCCTGCTACTTTGTCCGCCTCCATCCAGTCTATGAGCTGCTGTCGTGATGCTAGAG
 TAAGAAGTTCGCCAGTGAGTAGTTTCCGAAGAGTTGTGGCCATTGCTACTGGCATCGTGGTATC
 ACGCTCGTCGTTTCGGTATGGCTTCGTTCAACTCTGGTTCACGCGGTCAAGCCGGGTACATGA
 TCACCCATATTATGAAGAAATGCAGTCAGCTCCTTAGGGCCTCCGATCGTTGTCAGAAGTAAGT
 5 TGGCCGCGGTGTTGTCGCTCATGGTAATGGCAGCACTACACAATTCTCTTACCGTCATGCCATC
 CGTAAGATGCTTTTCCGTGACCGGCGAGTACTCAACCAAGTCGTTTTGTGAGTAGTGTATACGG
 CGACCAAGCTGCTCTTGCCCGGCGTCTATACGGGACAACACCGCGCCACATAGCAGTACTTTGA
 AAGTGCTCATCATCGGGAATCGTTCTTCGGGGCGGAAAGACTCAAGGATCTTGCCGCTATTGAG
 ATCCAGTTCGATATAGCCCACTCTTGACCCAGTTGATCTTCAGCATCTTTTACTTTTACCAGC
 10 GTTTCGGGGTGTGCAAAAACAGGCAAGCAAAATGCCGCAAGAAGGGAATGAGTGCACACGAA
 AATGTTGGATGCTCATACTCGTCCTTTTTTCAATATTATTGAAGCATTTATCAGGGTTACTAGTA
 CGTCTCTCAAGGATAAGTAAGTAATATTAAGGTACGGGAGGTATTGGACAGGCCGCAATAAAAT
 ATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGATAGTACTAACATACGCT
 CTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAG
 15 GTGCCAGAACATTTCTCT

SEQ ID NO:27. pBiT 2.1 C (TK-SmBiT) whole vector (3,423 nucleotides)

GGCCTAACTGGCCGGTACCTGAGTCTAAATGAGTCTTCGGACCTCGCGGGGGCCGCTTAAGCGG
 TGGTTAGGGTTTGTCTGACGCGGGGGGAGGGGGAAGGAACGAAACACTCTCATTCGGAGGCGGC
 TCGGGGTTTGGTCTTGGTGGCCACGGGCACGCAGAAGAGCGCCGCGATCCTCTTAAGCACCCCC
 20 CCGCCCTCCGTGGAGGCGGGGTTTGGTCGGCGGGTGGTAACTGGCGGGCCGCTGACTCGGGCG
 GGTGCGCGCCCCAGAGTGTGACCTTTTCGGTCTGCTCGCAGACCCCCGGGCGGCGCCGCGCG
 GCGGCGACGGGCTCGCTGGGTCTTAGGCTCCATGGGGACCGTATACGTGGACAGGCTCTGGAGC
 ATCCGCACGACTGCGGTGATATTACCGGAGACCTTCTGCGGGACGAGCCGGGTACGCGGCTGA
 CGCGGAGCGTCCGTGCGGCGACAAACACCAGGACGGGGCACAGGTACACTATCTTGTACCCGG
 25 AGGCGCGAGGGACTGCAGGAGCTTCAGGGAGTGGCGCAGCTGCTTCATCCCCGTGGCCCGTTGC
 TCGCGTTTGCTGGCGGTGTCCCCGGAAGAAATATATTTGCATGTCTTTAGTTCTATGATGACAC
 AAACCCCGCCCAGCGTCTTGTCAATTGGCGAAGTCGAACACGCAGATGCAGTCGGGGCGGCGCGG
 TCCAGGTCCACTTCGCATATTAAGGTGACGCGTGTGGCCTCGAACACCGAGCGACCCTGCAGC
 GACCCGCTTAAAGCTTGGCAATCCGGTACTGTGGTAAAGCCACCAGATCTGCTAGCGATCGCC
 30 TAAGTGGGAGCTCAGGGGAATTCTGGCTCGAGCGGTGGTGGCGGGAGCGGAGGTGGAGGGTCGT
 CAGGTGTGACCGGCTACCGGCTGTTTCGAGGAGATTCTGTAATCTAGAGTCGGGGCGGCGGCCG

CTCGAGCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAA
 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAA
 TAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAG
 GTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTAAAATCGATAAGGATCCGTCGACCGATG
 5 CCCTTGAGAGCCTTCAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACTATCGTCGCCC
 CACTTATGACTGTCTTCTTTATCATGCAACTCGTAGGACAGGTGCCGGCAGCGCTCTTCCGCTT
 CCTCGCTCACTGACTCGCTGCGCTCGGTCTGCTCGGCTGCGGCGAGCGGTATCAGCTCACTCAA
 GGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGC
 CAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTGTGCTGGCGTTTTTCCATAGGCTCCGCCCC
 10 CTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAG
 ATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACC
 GGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGT
 ATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCC
 CGACCGCTGCGCCTTATCCGGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCG
 15 CCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGT
 TCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCT
 GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGT
 AGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATC
 CTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGT
 20 CATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTAAATCA
 ATCTAAAGTATATATGAGTAACTTGGTCTGACAGCGGCCGCAAATGCTAAACCACTGCAGTGG
 TTACCAGTGCTTGATCAGTGAGGCACCGATCTCAGCGATCTGCCTATTTTCGTTTCGTCCATAGTG
 GCCTGACTCCCCGTCGTGTAGATCACTACGATTCGTGAGGGCTTACCATCAGGCCCCAGCGCAG
 CAATGATGCCGCGAGAGCCGCGTTACCGGGCCCCCGATTGTGTCAGCAATGAACCAGCCAGCAGG
 25 GAGGGCCGAGCGAAGAAGTGGTCCTGCTACTTTGTCCGCCTCCATCCAGTCTATGAGCTGCTGT
 CGTGATGCTAGAGTAAGAAGTTCGCCAGTGAGTAGTTTCCGAAGAGTTGTGGCCATTGCTACTG
 GCATCGTGGTATCACGCTCGTCGTTTCGGTATGGCTTCGTTCAACTCTGGTTCCAGCGGTCAAG
 CCGGGTCACATGATCACCCATATTATGAAGAAATGCAGTCAGCTCCTTAGGGCCTCCGATCGTT
 GTCAGAAGTAAGTTGGCCGCGGTGTTGTGCTCATGGTAATGGCAGCACTACACAATTCTCTTA
 30 CCGTCATGCCATCCGTAAGATGCTTTTCCGTGACCGGCGAGTACTCAACCAAGTCGTTTTGTGA
 GTAGTGTATACGGCGACCAAGCTGCTCTTGCCCGGCGTCTATACGGGACAACACCGCGCCACAT
 AGCAGTACTTTGAAAGTGCTCATCATCGGAATCGTTCTTCGGGGCGGAAAGACTCAAGGATCT

TGCCGCTATTGAGATCCAGTTCGATATAGCCCACTCTTGCACCCAGTTGATCTTCAGCATCTTT
TACTTTTACCAGCGTTTCGGGGTGTGCAAAACAGGCAAGCAAAATGCCGCAAAGAAGGGAATG
AGTGCGACACGAAAATGTTGGATGCTCATACTCGTCCTTTTCAATATTATTGAAGCATTTATC
AGGGTTACTAGTACGTCTCTCAAGGATAAGTAAGTAATATTAAGGTACGGGAGGTATTGGACAG
5 GCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGATAGT
ACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCC
AGTGCAAGTGCAGGTGCCAGAACATTTCTCT

SEQ ID NO:28. NdeI- LgBiT-YAP15-F primer (38 nucleotides)

GGAATTCATATGATGGTCTTCACACTCGAAGATTTCGT

10 **SEQ ID NO:29. B1-LgBiT-YAP15-R primer (40 nucleotides)**

CGCGGGATCCTTACAACCTGCAGAGAAGCTGGAGAGGAATG

SEQ ID NO:30. B1-LgBiT-YAP15A127-R primer (43 nucleotides)

CGCGGGATCCTTACAACCTGCAGAGAAGCTGGAGACGCATGAGC

SEQ ID NO:31. NdeI-14-3-3-SmBiT-F primer (38 nucleotides)

15 GGAATTCATATGATGGAGAAGACTGAGCTGATCCAGAA

SEQ ID NO:32. B1-14-3-3-SmBiT-R primer (40 nucleotides)

CGCGGGATCCTTACAGAATCTCCTCGAACAGCCGGTAGCC

SEQ ID NO:33. pET 16b (6 his N-terminal) whole vector (5,711 nucleotides)

TTCTCATGTTTGACAGCTTATCATCGATAAGCTTTAATGCGGTAGTTTATCACAGTTAAATTGC
20 TAACGCAGTCAGGCACCGTGTATGAAATCTAACAATGCGCTCATCGTCATCCTCGGCACCGTCA
CCCTGGATGCTGTAGGCATAGGCTTGGTTATGCCGGTACTGCCGGGCCTCTTGCGGGATATCCG
GATATAGTTCCTCCTTTCAGCAAAAAACCCCTCAAGACCCGTTTAGAGGCCCAAGGGGTATG
CTAGTTATTGCTCAGCGGTGGCAGCAGCCAACTCAGCTTCCTTTCGGGCTTTGTTAGCAGCCGG
ATCCTCGAGCATATGACGACCTTCGATATGGCCGCTGCTGTGATGATGATGATGATGATGATGA
25 TGATGGCCCATGGTATATCTCCTTCTTAAAGTTAAACAAAATTATTTCTAGAGGGGAATTGTTA

TCCGCTCACAATTCCCCTATAGTGAGTCGTATTAATTTTCGCGGGATCGAGATCTCGATCCTCTA
 CGCCGGACGCATCGTGGCCGGCATCACCGGCGCCACAGGTGCGGTTGCTGGCGCCTATATCGCC
 GACATCACCGATGGGGAAGATCGGGCTCGCCACTTCGGGCTCATGAGCGCTTGTTTTCGGCGTGG
 GTATGGTGGCAGGCCCGTGGCCGGGGGACTGTTGGGCGCCATCTCCTTGCCATGCACCATTCCCT
 5 TCGGCGGCGGTTGCTCAACGGCCTCAACCTACTACTGGGCTGCTTCCTAATGCAGGAGTCGCAT
 AAGGGAGAGCGTCGAGATCCCGGACACCATCGAATGGCGCAAAACCTTTTCGCGGTATGGCATGA
 TAGCGCCCGGAAGAGAGTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCCG
 CAGAGTATGCCGGTGTCTCTTATCAGACCGTTTCCCGCGTGGTGAACCAGGCCAGCCACGTTTC
 TGCGAAAACGCGGGAAAAAGTGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTG
 10 GCACAACAACCTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC
 ACGCGCCGTCGCAAATTGTGCGGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCGTGGT
 GGTGTGATGGTAGAACGAAGCGGCGTGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCG
 CAACGCGTCAGTGGGCTGATCATTAACCTATCCGCTGGATGACCAGGATGCCATTGCTGTGGAAG
 CTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTAT
 15 TATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTGCATTGGGTACCCAG
 CAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCTCTGCGTCTGGCTGGCTGGC
 ATAAATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTGCCAT
 GTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGATGCTGGTT
 GCCAACGATCAGATGGCGCTGGGCGCAATGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTG
 20 CGGATATCTCGGTAGTGGGATACGACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAAC
 CACCATCAAACAGGATTTTCGCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCT
 CAGGGCCAGGCGGTGAAGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCAACC
 TGGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACG
 ACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTAAGTTAGCTCACTCA
 25 TTAGGCACCGGGATCTCGACCGATGCCCTTGAGAGCCTTCAACCCAGTCAGCTCCTTCCGGTGG
 GCGCGGGGCATGACTATCGTCGCCGCACTTATGACTGTCTTCTTTATCATGCAACTCGTAGGAC
 AGGTGCCGGCAGCGCTCTGGGTCAATTTTCGGCGAGGACCGCTTTCGCTGGAGCGCGACGATGAT
 CGGCCTGTGCTTGCGGTATTCGGAATCTTGACGCGCCCTCGCTCAAGCCTTCGTCACTGGTCCC
 GCCACCAAACGTTTCGGCGAGAAGCAGGCCATTATCGCCGGCATGGCGGGCCGACGCGCTGGGCT
 30 ACGTCTTGCTGGCGTTTCGCGACGCGAGGCTGGATGGCCTTCCCCATTATGATTCTTCTCGCTTC
 CGGCGGCATCGGGATGCCCCGCTTGCAAGGCCATGCTGTCCAGGCAGGTAGATGACGACCATCAG
 GGACAGCTTCAAGGATCGCTCGCGGCTCTTACCAGCCTAACTTCGATCACTGGACCGCTGATCG

TCACGGCGATTTATGCCGCCTCGGCGAGCACATGGAACGGGTGGCATGGATTGTAGGCGCCGC
 CCTATACCTTGTCTGCCTCCCCGCGTTGCGTCGCGGTGCATGGAGCCGGGCCACCTCGACCTGA
 ATGGAAGCCGGCGGCACCTCGCTAACGGATTCAACACTCCAAGAATTGGAGCCAATCAATTCTT
 GCGGAGAACTGTGAATGCGCAAACCAACCCTTGGCAGAACATATCCATCGCGTCCGCCATCTCC
 5 AGCAGCCGCACGCGGCGCATCTCGGGCAGCGTTGGGTCTGGCCACGGGTGCGCATGATCGTGC
 TCCTGTCTGTTGAGGACCCGGCTAGGCTGGCGGGGTTCCTTACTGGTTAGCAGAATGAATCACC
 GATACGCGAGCGAACGTGAAGCGACTGCTGCTGCAAAACGTCTGCGACCTGAGCAACAACATGA
 ATGGTCTTCGGTTTCCGTGTTTCGTAAAGTCTGGAAACGCGGAAGTCAGCGCCCTGCACCATTA
 TGTTCGGATCTGCATCGCAGGATGCTGCTGGCTACCCTGTGGAACACCTACATCTGTATTAAC
 10 GAAGCGCTGGCATTGACCCTGAGTGATTTTTCTCTGGTCCCGCCGCATCCATACCGCCAGTTGT
 TTACCCTCACAACGTTCCAGTAACCGGGCATGTTTCATCATCAGTAACCCGTATCGTGAGCATCC
 TCTCTCGTTTCATCGGTATCATTACCCCCATGAACAGAAATCCCCCTTACACGGAGGCATCAGT
 GACCAAACAGGAAAAAACCGCCCTTAACATGGCCCGCTTTATCAGAAGCCAGACATTAACGCTT
 CTGGAGAACTCAACGAGCTGGACGCGGATGAACAGGCAGACATCTGTGAATCGCTTCACGACC
 15 ACGCTGATGAGCTTTACCGCAGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACA
 CATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGT
 CAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCGCAGCCATGACCCAGTCACGTAGCGATA
 GCGGAGTGATACTGGCTTAACATGCGGCATCAGAGCAGATTGTACTGAGAGTGACCATATA
 TGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTC
 20 CTCGCTCACTGACTCGCTGCGCTCGGTGCTTCGGCTGCGGGCAGCGGTATCAGCTCACTCAAAG
 GCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCC
 AGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC
 TGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA
 TACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCG
 25 GATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTA
 TCTCAGTTCGGTGAGTTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCC
 GACCGCTGCGCCTTATCCGGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGC
 CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTT
 CTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTG
 30 AAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTA
 GCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCC
 TTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAACTCACGTAAAGGGATTTTGGTC

ATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAA
 TCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTAT
 CTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACG
 ATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC GG
 5 CTCCAGATTTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAAC
 TTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTTCGCCAGTT
 AATAGTTTGC GCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTTCGTTTGGTA
 TGGCTTCATT CAGCTCCGGTTC CCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAA
 AAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCA
 10 CTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTG
 TGA CTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTG
 CCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGA
 AAACGTTCTTCGGGGCGAAA ACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTTCGATGTAAC
 CCACTCGTGCACCCA ACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAA
 15 AACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATA
 CTCTTCCTTTTTC AATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATAT
 TTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACC
 TGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
 TTTCGTCTTCAAGAA

20 SEQ ID NO:34. B1-Kozak-LgBiT-F primer (41 nucleotides)

CTGGATCCGCCGCCACCATGGTCTTCACACTCGAAGATTTC

SEQ ID NO:35. LgBiT-(GS)-R primer (54 nucleotides)

ACCGCTCGAGCCTCCACCTCCGCTCCCGCCACCACCGGAACTCCCACTGTTGAT

SEQ ID NO:36. (GS)-YAP50-F primer (69 nucleotides)

25 GGGAGTTCCGGTGGTGGCGGGAGCGGAGGTGGAGGCTCGAGCGGTGCCGGGCATCAGATCGTGC
 ACGTC

SEQ ID NO:37. N1-YAP171-Flag-R primer (63 nucleotides)

ATGAAACTGCGGCCGCCTTGTCGTCATCGTCTTTGTAGTCTACATCATCAGGTATCTCAAAAG

SEQ ID NO:38. B1-YAP50-F primer (32 nucleotides)

CTGGATCCGCCGGGCATCAGATCGTGCACGTC

SEQ ID NO:39. (GS)-YAP171-R primer (68 nucleotides)

5 ACCTGACGACCCTCCACCTCCGCTCCCGCCACCACCGCTCGAGCCTACATCATCAGGTATCTCA
AAAG

SEQ ID NO:40. (GS)-LgBiT-F primer (66 nucleotides)

GGCTCGAGCGGTGGTGGCGGGAGCGGAGGTGGAGGGTCGTCAGGTGTCTTCACACTCGAAGATT
TC

10 **SEQ ID NO:41. N1-LgBiT-R primer (43 nucleotides)**

ATGAAACTGCGGCCGCTTAACTGTTGATGGTTACTCGGAACAG

SEQ ID NO:42. B1-Kozak -SmiBiT-(GS)-F primer (98 nucleotides)

CTGGATCCGCCGCCACCATGGTGACCGGCTACCGGCTGTTCGAGGAGATTCTCGGGAGTTCCGG
TGGTGGCGGGAGCGGAGGTGGAGGCTCGAGCGGT

15 **SEQ ID NO:43. N1-SmBiT-(GS)-R primer (97 nucleotides)**

ATGAAACTGCGGCCGCTTAGAGAATCTCCTCGAACAGCCGGTAGCCGGTCACACCTGACGACCC
TCCACCTCCGCTCCCGCCACCACCGCTCGAGCC

SEQ ID NO:44. (GS)-TEAD-194-F primer (73 nucleotides)

GGGAGTTCCGGTGGTGGCGGGAGCGGAGGTGGAGGCTCGAGCGGTGAGCCTGCATCGGCCCCAG
20 CTCCCTCAG

SEQ ID NO:45. N1-TEAD411-Myc-R primer (73 nucleotides)

ATGAAACTGCGGCCGCTTACAGATCCTCTTCTGAGATGAGTTTTTGTTCATTTGAAACTTCAA
CACACAGGC

SEQ ID NO:46. B1-TEAD194-F primer (36 nucleotides)

CTGGATCCGAGCCTGCATCGGCCCCAGCTCCCTCAG

SEQ ID NO:47. GS-TEAD-411-R primer (69 nucleotides)

ACCTGACGACCCTCCACCTCCGCTCCCGCCACCACCGCTCGAGCCATTTGAAACTTCAAACACA
5 CAGGC

SEQ ID NO:48. (GS)-TEAD194-F primer (73 nucleotides)

GGGAGTTCCGGTGGTGGCGGGAGCGGAGGTGGAGGCTCGAGCGGTGAGCCTGCATCGGCCCCAG
CTCCCTCAG

**SEQ ID NO:49. TEAD1_HUMAN transcriptional enhancer factor TEF-1 (accession number
10 P28347) mRNA (1,281 nucleotides)**

ATTGAGCCCAGCAGCTGGAGCGGCAGTGAGAGCCCTGCCGAAAACATGGAAAGGATGAGTGACT
CTGCAGATAAGCCAATTGACAATGATGCAGAAGGGGTCTGGAGCCCCGACATCGAGCAAAGCTT
TCAGGAGGGCCCTGGCTATCTATCCACCATGTGGGAGGAGGAAAATCATCTTATCAGACGAAGGC
AAAATGTATGGTAGGAATGAATTGATAGCCAGATACATCAAACCTCAGGACAGGCAAGACGAGGA
15 CCAGAAAACAGGTGTCTAGTCACATTCAGGTTCTTGCCAGAAGGAAATCTCGTGATTTTCATTC
CAAGCTAAAGGATCAGACTGCAAAGGATAAGGCCCTGCAGCACATGGCGGCCATGTCTTCAGCC
CAGATCGTCTCGGCCACTGCCATTTCATAACAAGCTGGGGCTGCCTGGGATTCCACGCCCGACCT
TCCCAGGGGCGCCGGGGTTCTGGCCGGGAATGATTCAAACAGGGCAGCCAGGATCCTCACAAGA
CGTCAAGCCTTTTGTGCAGCAGGCCTACCCCATCCAGCCAGCGGTCACAGCCCCCATTCAGGG
20 TTTGAGCCTGCATCGGCCCCAGCTCCCTCAGTCCCTGCCTGGCAAGGTCGCTCCATTGGCACAA
CCAAGCTTCGCCTGGTGGAAATTTTCAGCTTTTCTCGAGCAGCAGCGAGACCCAGACTCGTACAA
CAAACACCTCTTCGTGCACATTGGGCATGCCAACCATTCTTACAGTGACCCATTGCTTGAATCA
GTGGACATTCGTTCAGATTTATGACAAATTTCTGAAAAGAAAGGTGGCTTAAAGGAACTGTTTG
GAAAGGGCCCTCAAAATGCCTTCTTCCTCGTAAAATTCTGGGCTGATTTAAACTGCAATATTCA
25 AGATGATGCTGGGGCTTTTTATGGTGTAAACCAGTCAGTACGAGAGTTCTGAAAATATGACAGTC
ACCTGTTCCACCAAAGTTTGCTCCTTTGGGAAGCAAGTAGTAGAAAAAGTAGAGACGGAGTATG
CAAGGTTTGAGAATGGCCGATTTGTATACCGAATAAACCGCTCCCCAATGTGTGAATATATGAT
CAACTTCATCCACAAGCTCAAACACTTACCAGAGAAATATATGATGAACAGTGTTTTGGAAAAC

TTCACAATTTTATTGGTGGTAACAAACAGGGATACACAAGAACTCTACTCTGCATGGCCTGTG
TGTTTGAAGTTTCAAATAGTGAACACGGAGCACAAATCATATTTACAGGCTTGTAAGGACTG
A

SEQ ID NO:50. TEAD1_HUMAN protein (426 amino acids)

5 MEPSSWSGSESPAENMERMSDSADKPIDNDAEGVWSPDIEQSFQEALAIYPPCGRRKIILSDEG
KMYGRNELIARYIKLRTGKTRTRKQVSSHIQVLARRKSRDFHSLKDQTAKDKALQHMAAMSSA
QIVSATAIHNLKGLPGIPRPTFPGAPGFWPGMIQTGQPGSSQDVKPFVQQAYPIQPAVTAPIPG
FEPASAPAPSVPAWQGRSIGTTKLRLVEFSAFLEQQRDPDSYNKHLFVHIGHANHSYSDPLLES
VDIRQIYDKFPEKKGGLKELFGKGPQNAFFLVKFWADLNCNIQDDAGAFYGVTSQYESSNMTV
10 TCSTKVCSFGKQVVEKVETEARFENGFRVYRINRSPMCEYMINFIHKLKHLPEKYMMNSVLEN
FTILLVVTNRDTQETLLCMACVFEVSNSEHGAQHIIYRLVKD

SEQ ID NO:51. Large BiT (LgBiT) mRNA (477 nucleotides)

ATGGTCTTCACACTCGAAGATTTTCGTTGGGGACTGGGAACAGACAGCCGCCTACAACCTGGACC
AAGTCCTTGAACAGGGAGGTGTGTCCAGTTTGCTGCAGAATCTCGCCGTGTCCGTAACCTCCGAT
15 CCAAAGGATTGTCCGGAGCGGTGAAAATGCCCTGAAGATCGACATCCATGTCATCATCCCGTAT
GAAGGTCTGAGCGCCGACCAAATGGCCCAGATCGAAGAGGTGTTAAGGTGGTGTACCCTGTGG
ATGATCATCACTTTAAGGTGATCCTGCCCTATGGCACACTGGTAATCGACGGGGTTACGCCGAA
CATGCTGAACTATTTTCGGACGGCCGTATGAAGGCATCGCCGTGTTTCGACGGCAAAAAGATCACT
GTAACAGGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCACCCCCGACGGCT
20 CCATGCTGTTCCGAGTAACCATCAACAGT

SEQ ID NO:52. Large BiT (LgBiT) protein (159 amino acids)

MVFTLEDFVGDWEQTAAYNLDQVLEQGGVSSLLQNLAHSVTPIQRIVRSGENALKIDIHVIIPY
EGLSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPYEGIAVFDGKKIT
VTGTLWNGNKIIDERLITPDGSMLFRVTINS

25 **SEQ ID NO:53. Small BiT (SmBiT) mRNA (36 nucleotides)**

ATGGTGACCGGCTACCGGCTGTTCGAGGAGATTCTC

SEQ ID NO:54. Small BiT (SmBiT) protein (11 amino acids)

MVTGYRLFEIL

SEQ ID NO:55. pcDNA3.1/hygro(+)-Flag vector (5,490 nucleotides)

GACGGATCGGGAGATCTCCCGATCCCCTATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGC
ATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGC GCGAGCAAA
5 ATTTAAGCTACACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCG
TTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGACATTGATTATTGACTAGTTAT
TAATAGTAATCAATTACGGGGTTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAAC
TTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGAC
GTATGTTCCCATAGTAACGCCAATAGGGACTTTCATTGACGTCAATGGGTGGAGTATTTACGG
10 TAAACTGCCCCTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA
ATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTG
GCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAAT
GGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGA
GTTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAATGTCTAACAACCTCCGCCCCATTGAC
15 GCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAGA
GAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACCCAAGCTGGCT
AGCGTTTAACTTAAGCTTGGTACCATGGACTACAAAGACGATGACGGTGATTATAAAGATCAT
GACATCTACCTGATGTTTTCTGGTACTGCCAGGATCCACTAGTCCAGTGTGGTGGAATTCTGCAG
ATATCCAGCACAGTGGCGGCCGCTCGAGTCTAGAGGGCCGTTTAAACCCGCTGATCAGCCTCG
20 ACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTGACCCTGG
AAGGTGCCACTCCCCTGTCTTTTCCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAAT
AGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCT
CTAGGGGGTATCCCCACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCG
25 CAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCTTT
CTCGCCACGTTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT
TTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTACGTAGTGGGCC
ATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTC
TTGTTCCAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTATAAGGGATTT
30 TGCCGATTTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTAATT
CTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGC

AAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAG
AAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATC
CCGCCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTT
ATGCAGAGGCCGAGGCCGCTCTGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGG
5 AGGCCTAGGCTTTTGCAAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCAAGAG
ACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTT
GGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGT
GTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTG
AATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAG
10 CTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCA
GGATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGG
CGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGCATCGAGC
GAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGG
GCTCGCGCCAGCCGAACCTGTTGCCAGGCTCAAGGCGCGCATGCCCCGACGGCGAGGATCTCGTC
15 GTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAATGGCCGCTTTTCTGGATTCA
TCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATAT
TGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCC
GATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTT
CGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCCTTC
20 TATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGG
ATCTCATGCTGGAGTTCTTCGCCACCCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATA
AAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTG
TCCAAACTCATCAATGTATCTTATCATGTCTGTATACCGTCGACCTCTAGCTAGAGCTTGGCGT
AATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACG
25 AGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCG
TTGCGCTCACTGCCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCC
AACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCGCTTCCTCGCTCACTGACTCGCT
GCGCTCGGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCC
ACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACC
30 GTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAA
TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCT
GGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTC

TCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGT
 CGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTAGCCCGACCGCTGCGCCTTATCC
 GGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG
 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA
 5 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA
 AAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTTTTTTTGTGTTGCA
 AGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC
 TGACGCTCAGTGGAACGAAAACCTCACGTAAAGGGATTTTGGTCATGAGATTATCAAAAAGGATC
 TTCACCTAGATCCTTTTAAATTAATAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAA
 10 CTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCG
 TTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCT
 GGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC GGCTCCAGATTTATCAGCAATAA
 ACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTC
 TATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC GCAACGTTGTT
 15 GCCATTGCTACAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTT
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SEQ ID NO:56. pcDNA3.1/hygro(+)-Myc vector (5,455 nucleotides)

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SEQ ID NO:57. Intermolecular biosensor Nluc-YAP15 in pcDNA3.1/hygro(+) vector (6,693 nucleotides)

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SEQ ID NO:58. Intermolecular biosensor 14-3-3-Cluc in pcDNA3.1/hygro(+) vector (6,621 nucleotides)

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30 GCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAG
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 5 GCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGA
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 5 TCGGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAAC
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 TTGAGATCCAGTTTCGATGTAACCCACTCGTGCACCCAAGTATCTTCAGCATCTTTTACTTTCA
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 10 TGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCA
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SEQ ID NO:59. NanoBiT Biosensor: LgBiT-YAP15 in pBiT 1.1 N vector (3,890 nucleotides)

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 25 ACCCGCTTAAAAGCTTGGCAATCCGGTACTGTTGGTAAAGCCACCATGGTCTTCACACTCGAAG
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 5 GTTGATCTTCAGCATCTTTTACTTTACCCAGCGTTTTCGGGGTGTGCAAAAACAGGCAAGCAAAA
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 10 AGCAAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGGTGCCAGAACATTTCTCT

SEQ ID NO:60. NanoBIT Biosensor: 14-3-3-LgBiT in pBiT2.1-C vector (4,131 nucleotides)

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 15 CCGCCCTCCGTGGAGGCGGGGTTTGGTCGGCGGGTGGTAACTGGCGGGCCGCTGACTCGGGCG
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 20 AGGCGCGAGGGACTGCAGGAGCTTCAGGGAGTGGCGCAGCTGCTTCATCCCCGTGGCCCGTTGC
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5 **GGCAGAAGGGGCTGAAAACCCGAATTCTGGCTCGAGCGGTGGTGGCGGGAGCGGAGGTGGAGGG**
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25 GATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTT
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 5 GTGAGTAGTGTATACGGCGACCAAGCTGCTCTTGCCCGGCGTCTATACGGGACAACACCGCGCC
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 10 TATCAGGGTTACTAGTACGTCTCTCAAGGATAAGTAAGTAATATTAAGGTACGGGAGGTATTGG
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SEQ ID NO:61. NanoBiT Biosensor: LgBiT-YAP15 in pET16b vector (6,291 nucleotides)

15 TTCTTGAAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATG
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 20 TGGGTGCACGAGTGGGTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCG
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 30 AGCACCGCCGCCGCAAGGAATGGTGCATGCAAGGAGATGGCGCCCAACAGTCCCCCGGCCACGG
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 5 TGGACCAAGTCCTTGAACAGGGAGGTGTGTCCAGTTTGCTGCAGAAATCTCGCCGTGTCCGTAAC
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 10 ATCACTGTAACAGGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCACCCCG
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SEQ ID NO:62. NanoBiT Biosensor: SmBiT in pET16b vector (6,531 nucleotides)

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 25 GGGTGACGGTGCCGAGGATGACGATGAGCGCATTGTTAGATTTTCATACACGGTGCCTGACTGCG
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 GAA

**SEQ ID NO:63. YAP-TEAD NanoBiT biosensor construct 1: LgBiT-YAP50-171-Flag in pcDNA3.1-
 hygro vector (6,297 nucleotides)**

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TCCCCGAAAAGTGCCACCTGACGTC

**SEQ ID NO:64. YAP-TEAD NanoBiT biosensor construct 2: Flag-YAP50-171-LgBiT in pcDNA3.1-
5 hygro vector (6,270 nucleotides)**

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10 **SEQ ID NO:65. YAP-TEAD NanoBiT biosensor construct 3: SmBiT-YAP50-171-Flag in pcDNA3.1-
 hygro vector (5,856 nucleotides)**

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10 **SEQ ID NO:66. YAP-TEAD NanoBiT biosensor construct 4: Flag-YAP50-171-SmBiT in pcDNA3.1-
 hygro vector (5,829 nucleotides)**

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10 **SEQ ID NO:67. YAP-TEAD NanoBiT biosensor construct 5: LgBiT-TEAD1-194-411-Myc in
 pcDNA3.1-hygro vector (6,592 nucleotides)**

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**SEQ ID NO:68. YAP-TEAD NanoBiT biosensor construct 6: Myc-TEAD1-194-411-LgBiT in
 pcDNA3.1-hygro vector (6,559 nucleotides)**

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SEQ ID NO:69. YAP-TEAD NanoBiT biosensor construct 7: SmBiT-TEAD1-194-411-Myc in pcDNA3.1-hygro vector (6,151 nucleotides)

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10 **Equivalents**

While the invention has been described with respect to illustrative embodiments thereof, it will be understood that various changes may be made to the embodiments without departing from the scope of the invention. Accordingly, the described embodiments are to be considered merely exemplary and the invention is not to be limited thereby.

15

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30

Claims

1. A DNA construct comprising a nucleic acid sequence encoding a fusion protein comprising a fragment of firefly luciferase fused to at least one fragment of Yes-associated protein (YAP);
5 wherein the fragment of firefly luciferase is capable of binding to a different fragment of firefly luciferase to produce luminescence;
 wherein the at least one YAP fragment is capable of phosphorylation by large tumour suppressor (LATS) kinase.
- 10 2. The DNA construct of claim 1, wherein the fragment of firefly luciferase comprises amino acids 1-416 of SEQ ID NO:6 and is N-terminal to the at least one fragment of YAP comprising amino acids 120-134 of SEQ ID NO:2.
- 15 3. The DNA construct of claim 1, wherein the fragment of firefly luciferase comprises amino acids 1-544 of SEQ ID NO:6 and is N-terminal to the at least one fragment of YAP comprising amino acids 120-134 of SEQ ID NO:2.
- 20 4. A DNA construct comprising a nucleic acid sequence encoding a fusion protein comprising a fragment of firefly luciferase fused to at least one fragment of 14-3-3 protein;
 wherein the fragment of firefly luciferase is capable of binding to a different fragment of firefly luciferase to produce luminescence;
 wherein the at least one fragment of 14-3-3 protein is capable of binding to Yes-associated protein (YAP).
- 25 5. The DNA construct of claim 4, wherein the at least one fragment of 14-3-3 protein comprises SEQ ID NO:4 and is N-terminal to the fragment of firefly luciferase comprising amino acids 394-550 of SEQ ID NO:6.
- 30 6. A DNA construct comprising a nucleic acid sequence encoding a fusion protein comprising a fragment of NanoBiT luciferase fused to at least one fragment of Yes-associated protein (YAP);

wherein the fragment of NanoBiT luciferase is capable of binding to a different fragment of NanoBiT luciferase to produce luminescence;

wherein the at least one YAP fragment is capable of phosphorylation by large tumour suppressor (LATS) kinase.

5

7. The DNA construct of claim 6, wherein the fragment of NanoBit luciferase is LgBiT comprising amino acid sequence SEQ ID NO:52 and is N-terminal to the at least one fragment of YAP comprising amino acids 120-134 of SEQ ID NO:2.

10

8. A DNA construct comprising a nucleic acid sequence encoding a fusion protein comprising a fragment of NanoBiT luciferase fused to at least one fragment of 14-3-3 protein; wherein the fragment of NanoBiT luciferase is capable of binding to a different fragment of NanoBiT luciferase to produce luminescence;

15

wherein the at least one fragment of 14-3-3 protein is capable of binding to Yes-associated protein (YAP).

20

9. The DNA construct of claim 8, wherein the at least one fragment of 14-3-3 protein comprises SEQ ID NO:4 and is N-terminal to the fragment of NanoBit luciferase that is SmBiT comprising amino acid sequence SEQ ID NO:54.

25

10. A DNA construct comprising a nucleic acid sequence encoding a fusion protein comprising a fragment of NanoBit luciferase that is LgBiT comprising amino acid sequence SEQ ID NO:52 and a fragment of Yes-associated protein (YAP) comprising amino acids 50-171 of SEQ ID NO:2.

30

11. A DNA construct comprising a nucleic acid sequence encoding a fusion protein comprising a fragment of NanoBit luciferase that is SmBiT comprising amino acid sequence SEQ ID NO:54 and a fragment of Yes-associated protein (YAP) comprising amino acids 50-171 of SEQ ID NO:2.

12. A DNA construct comprising a nucleic acid sequence encoding a fusion protein comprising a fragment of NanoBiT luciferase fused to at least one fragment of TEAD protein; wherein the fragment of NanoBiT luciferase is capable of binding to a different fragment of NanoBiT luciferase to produce luminescence;

5 wherein the at least one fragment of TEAD protein is capable of binding to Yes-associated protein (YAP).

13. The DNA construct of claim 12, wherein the fragment of NanoBit luciferase is LgBiT comprising amino acid sequence SEQ ID NO:52 and the at least one fragment of TEAD protein
10 comprises amino acids 194-411 of SEQ ID NO:50.

14. The DNA construct of claim 12, wherein the fragment of NanoBit luciferase is SmBiT comprising amino acid sequence SEQ ID NO:54 and the at least one fragment of TEAD protein
15 comprises amino acids 194-411 of SEQ ID NO:50.

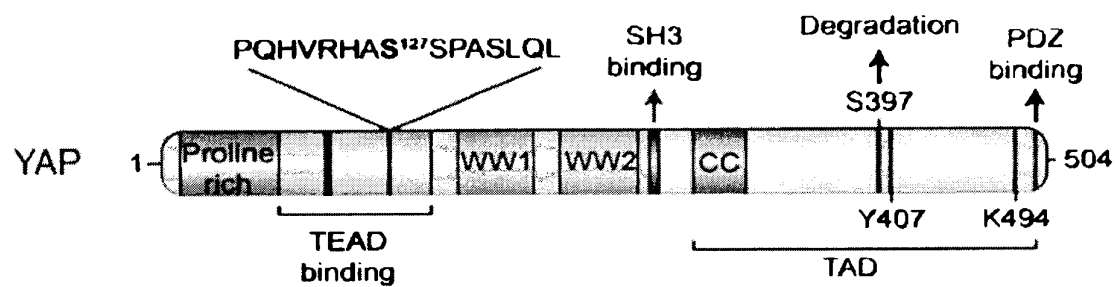


Fig. 1A

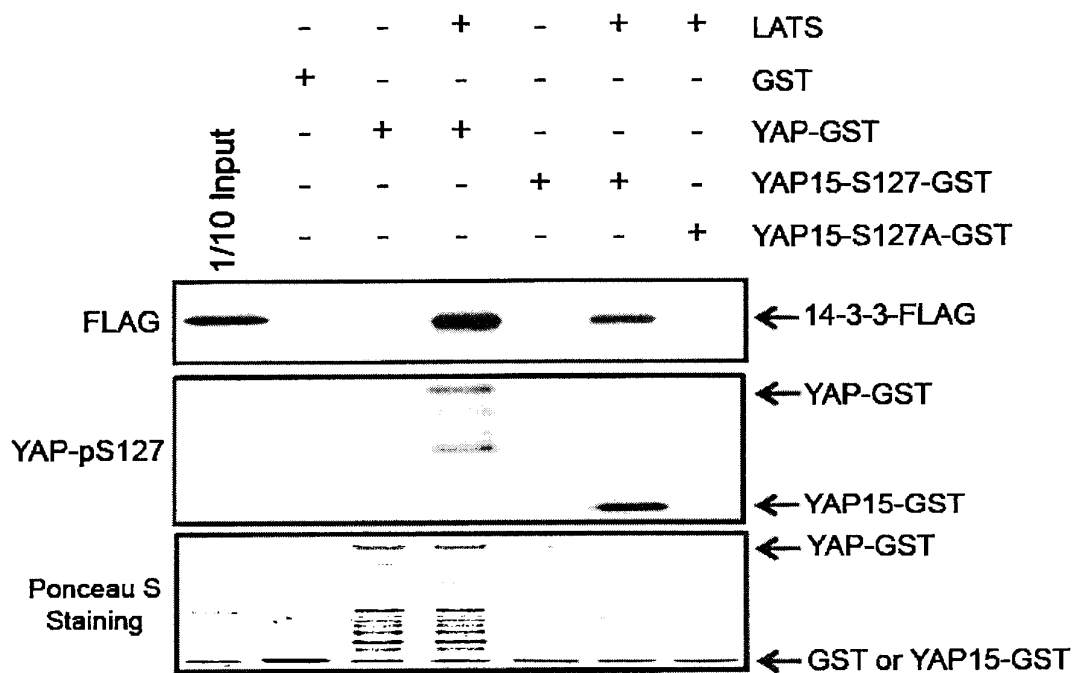


Fig. 1B

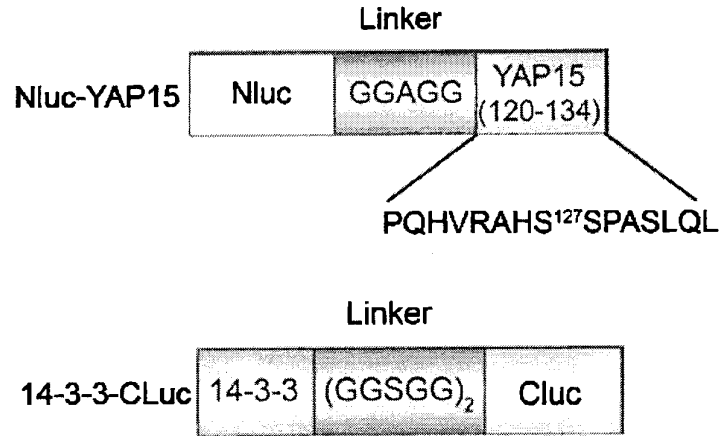


Fig. 2A

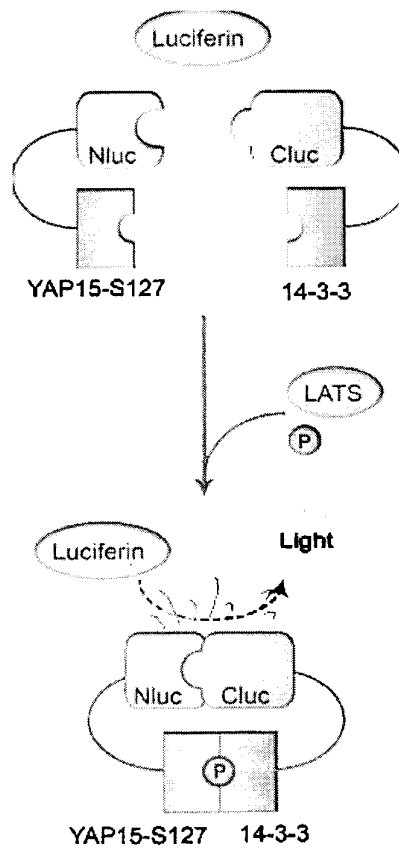


Fig. 2B

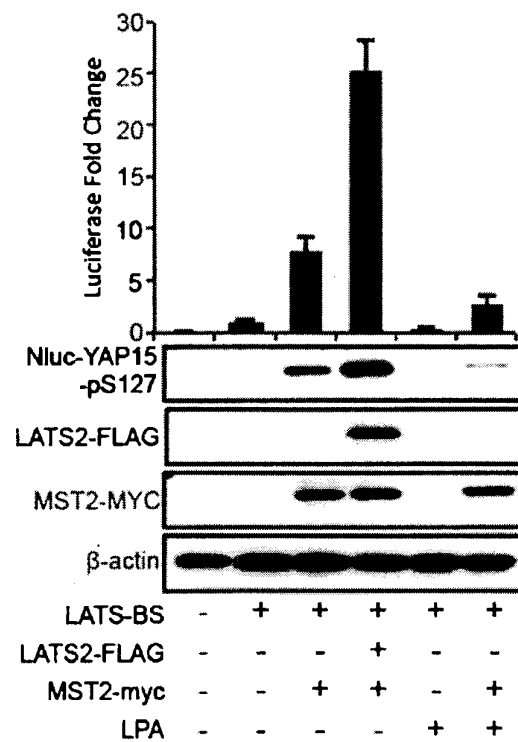


Fig. 2C

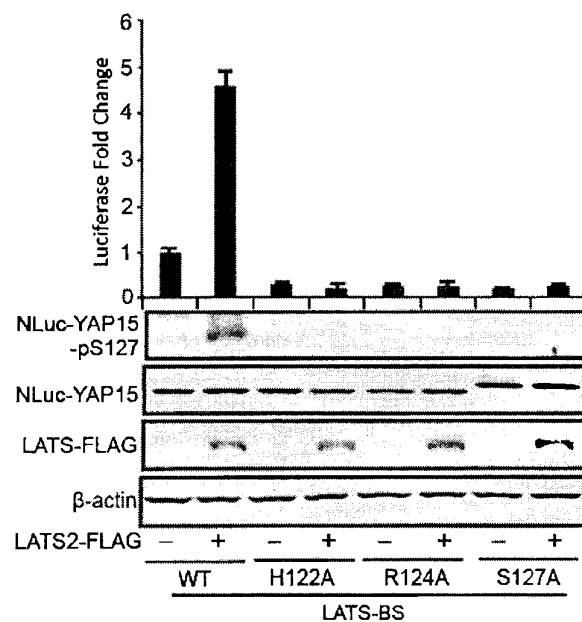


Fig. 2D

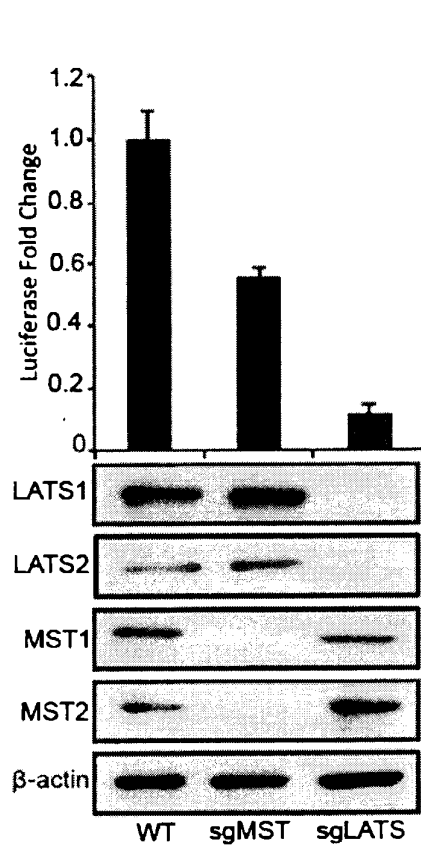


Fig. 2E

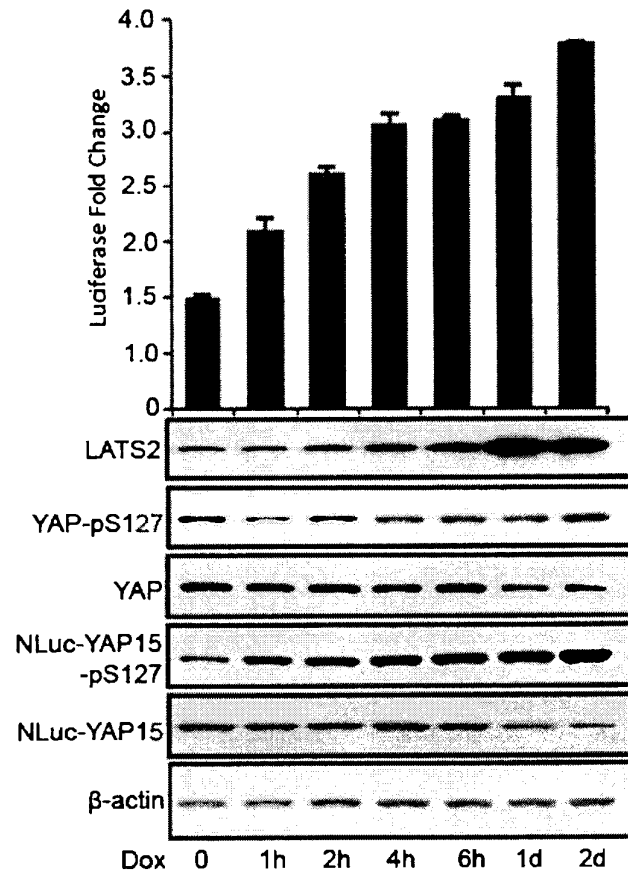


Fig. 2F

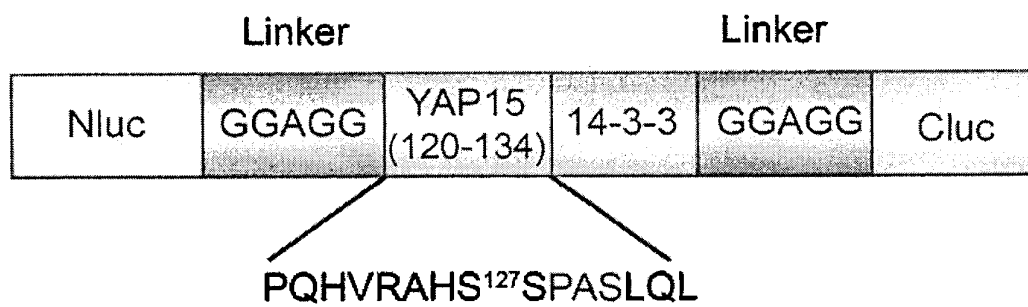


Fig. 3A

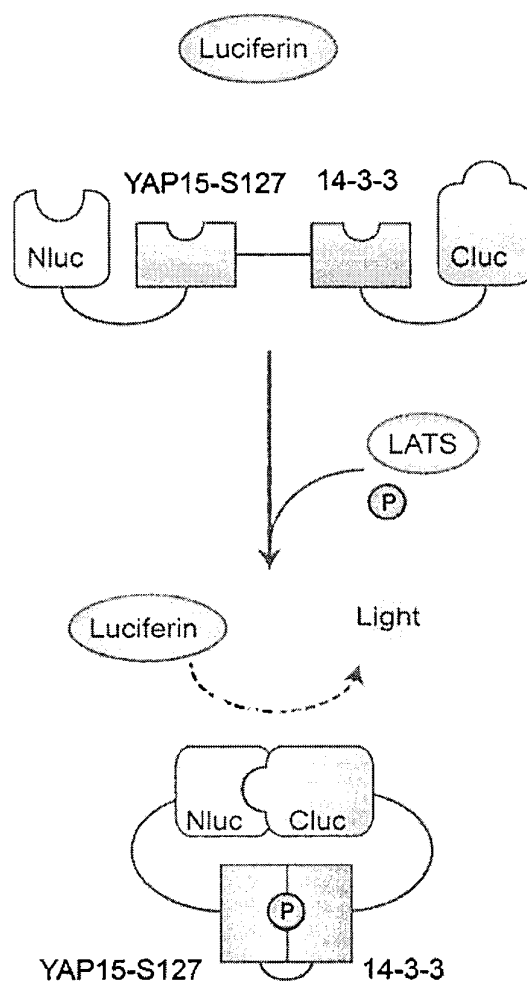


Fig. 3B

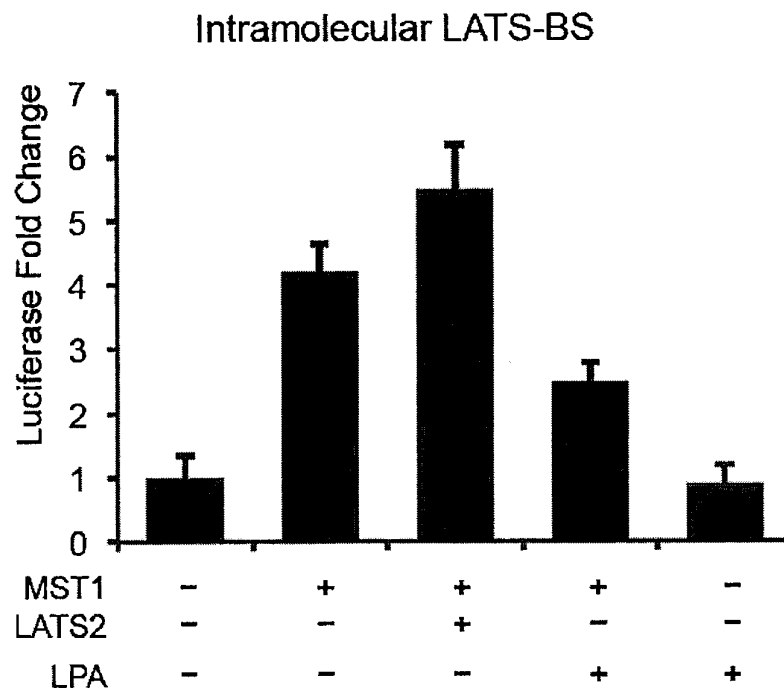


Fig. 3C

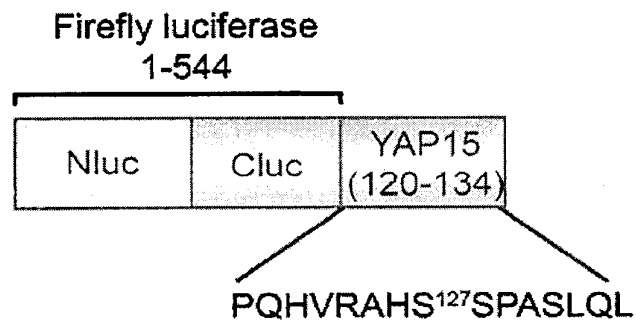


Fig. 4A

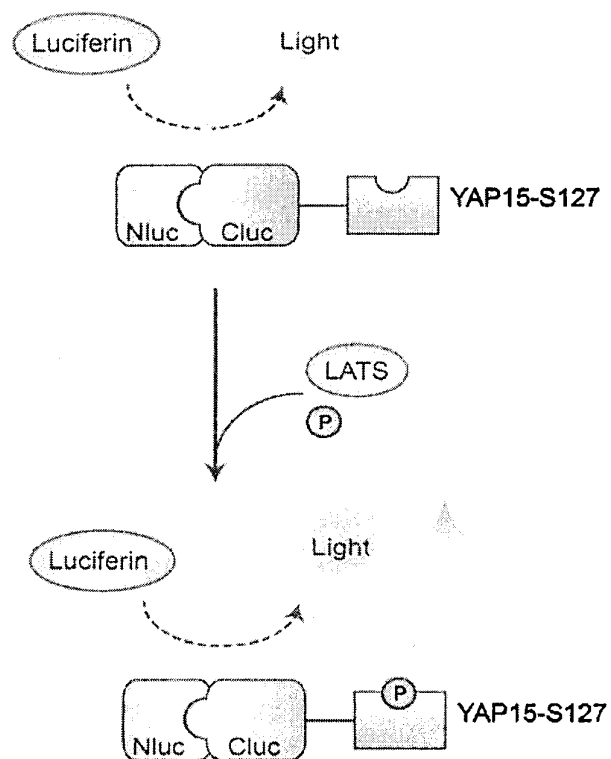


Fig. 4B

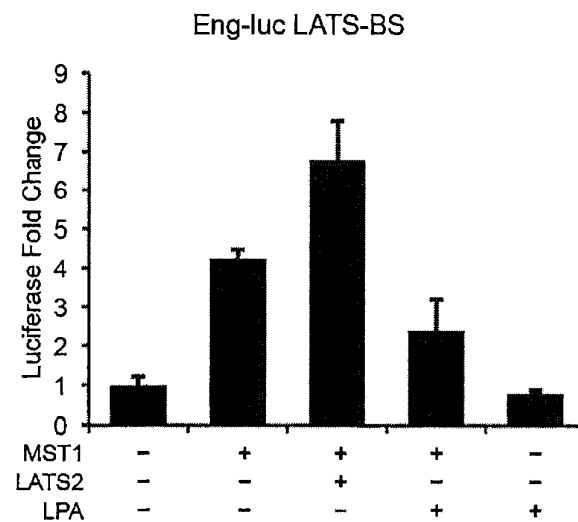


Fig. 4C

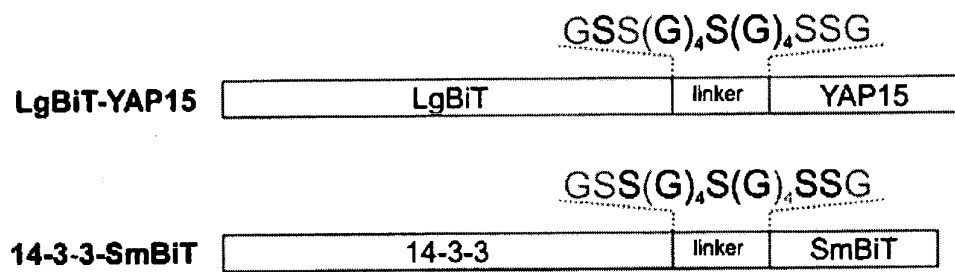


Fig. 5D

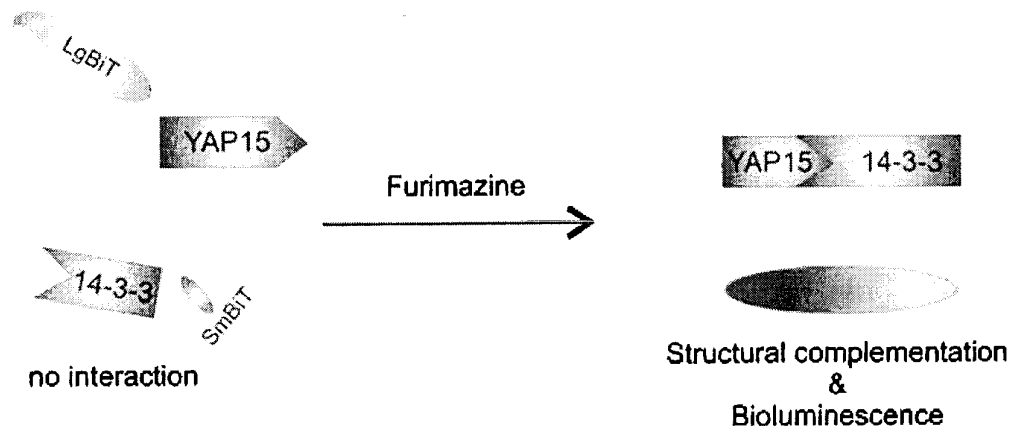


Fig. 6

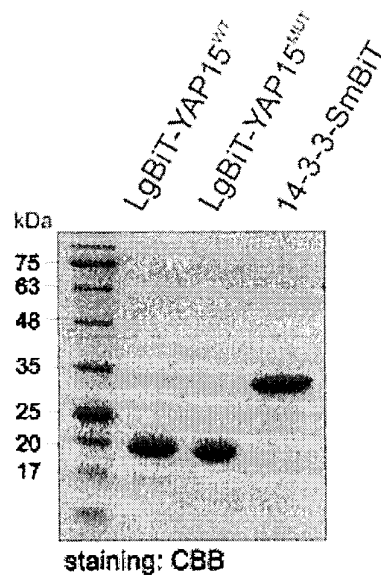


Fig. 7

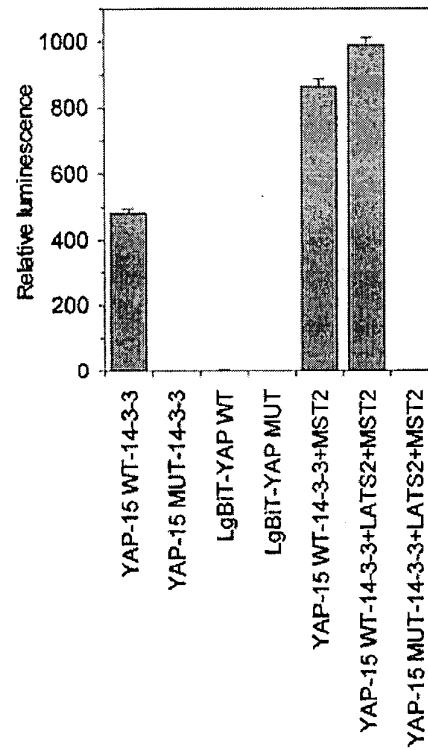


Fig. 8A

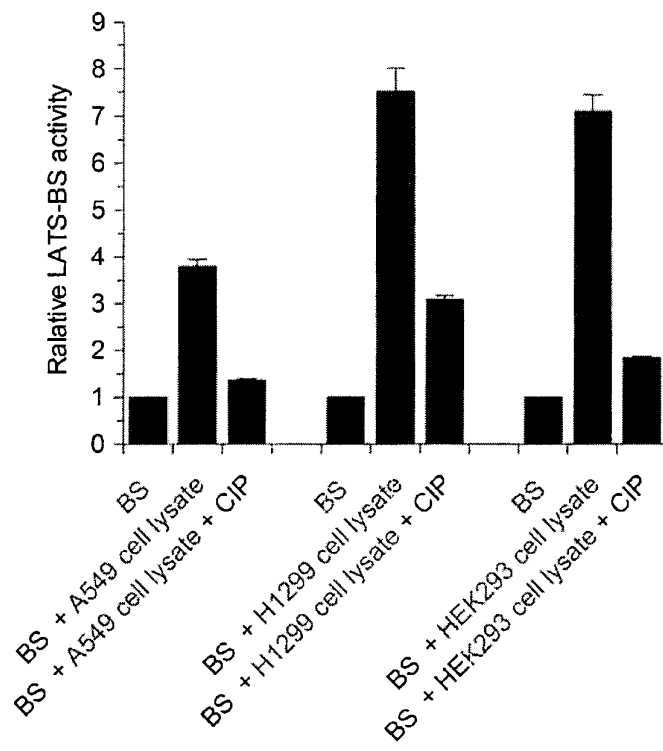


Fig. 8B

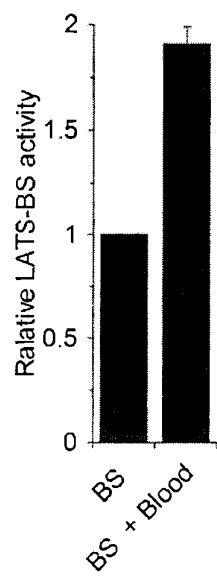


Fig. 8C

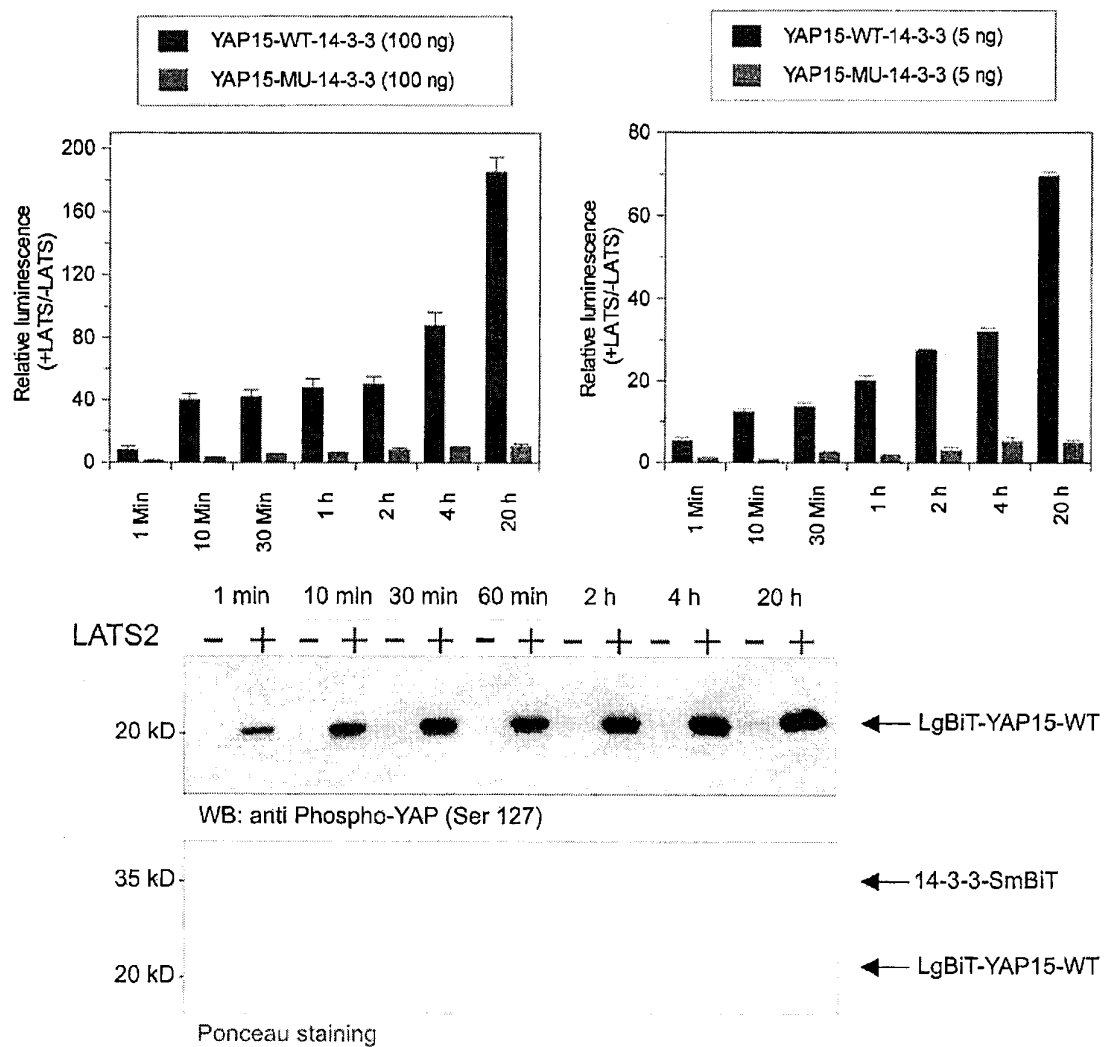


Fig. 9

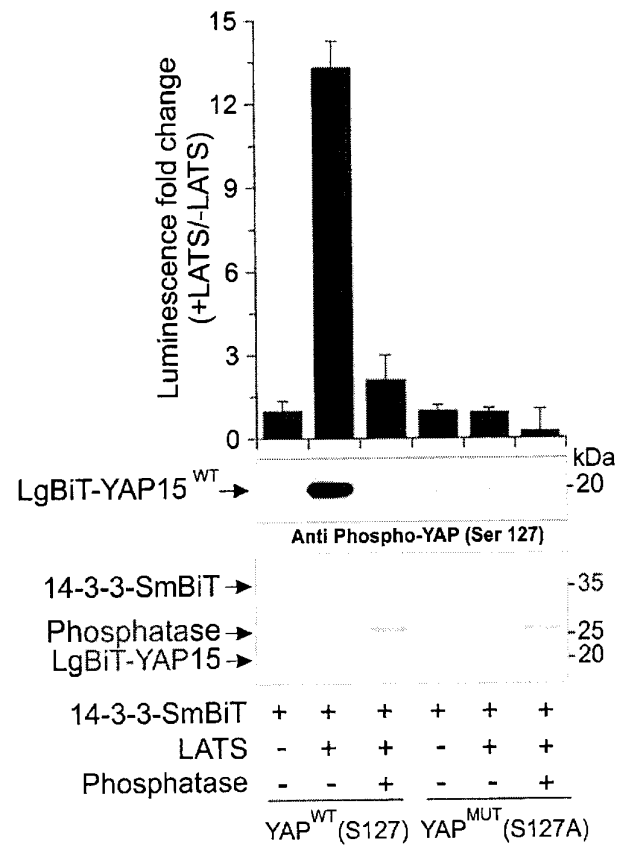


Fig. 10

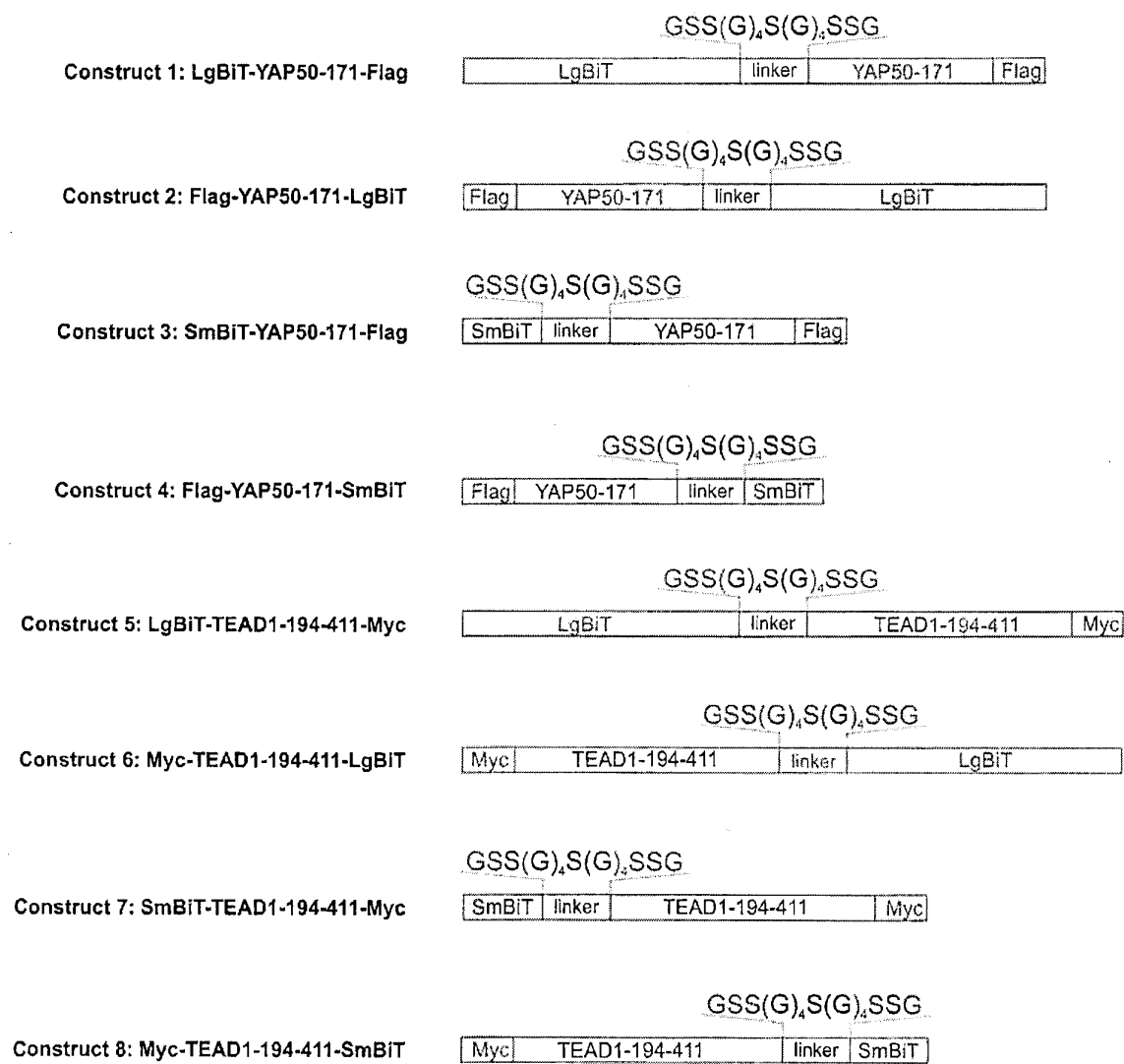


Fig. 11

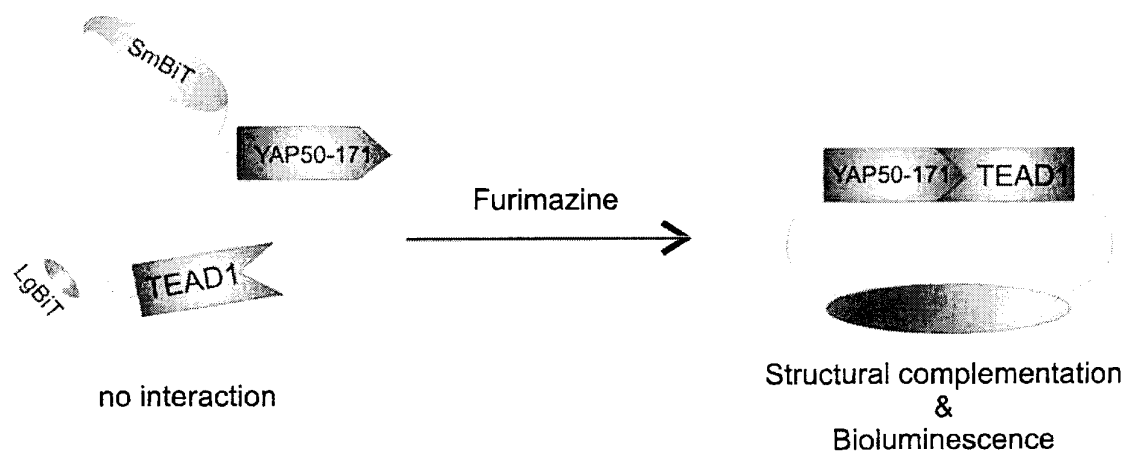


Fig. 12

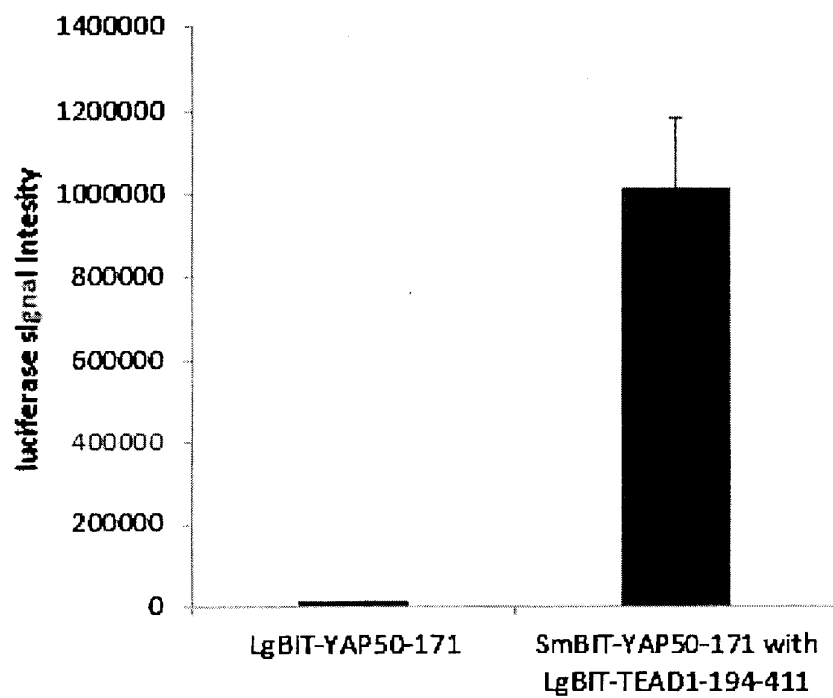


Fig. 13

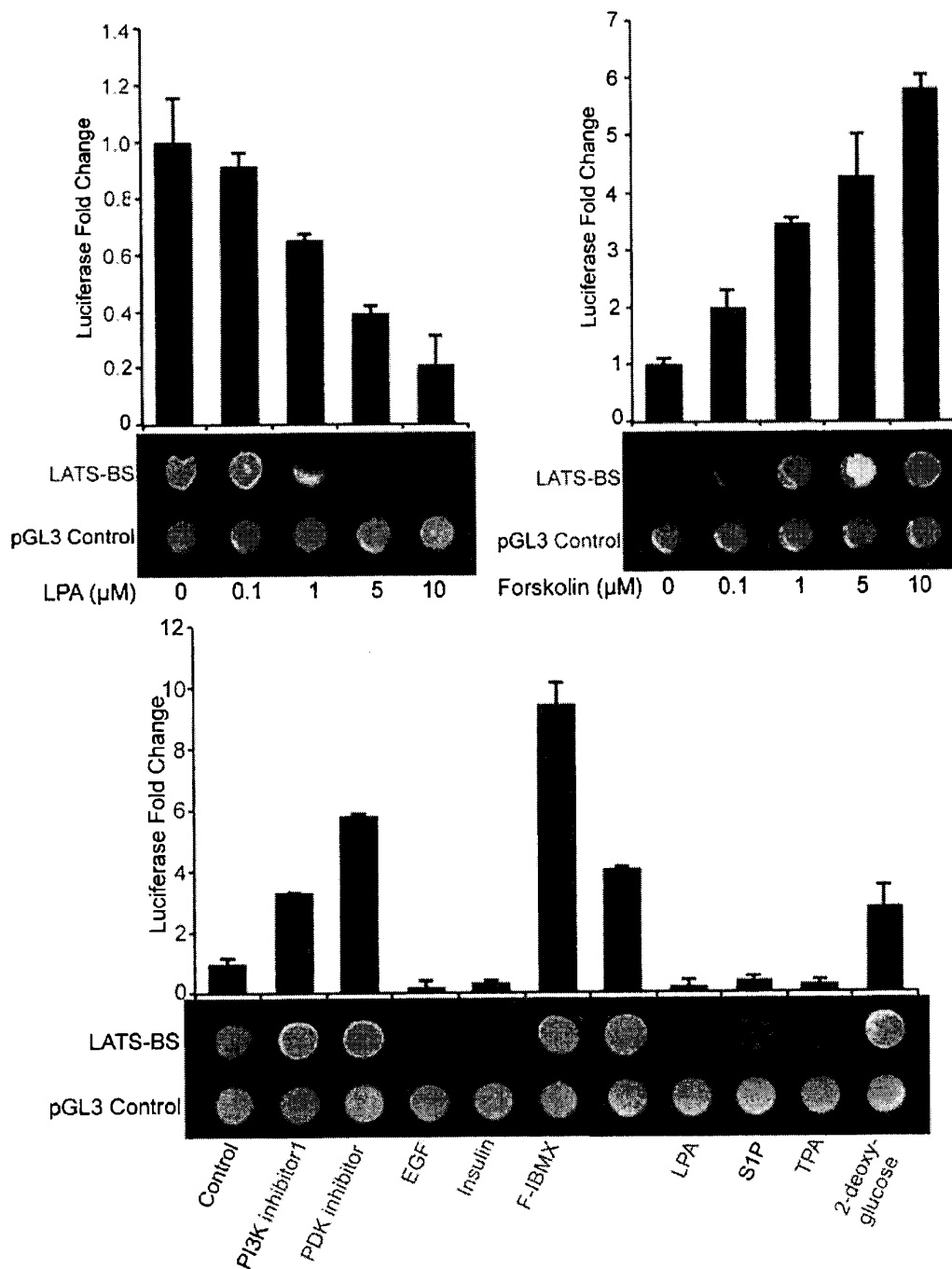


Fig. 14

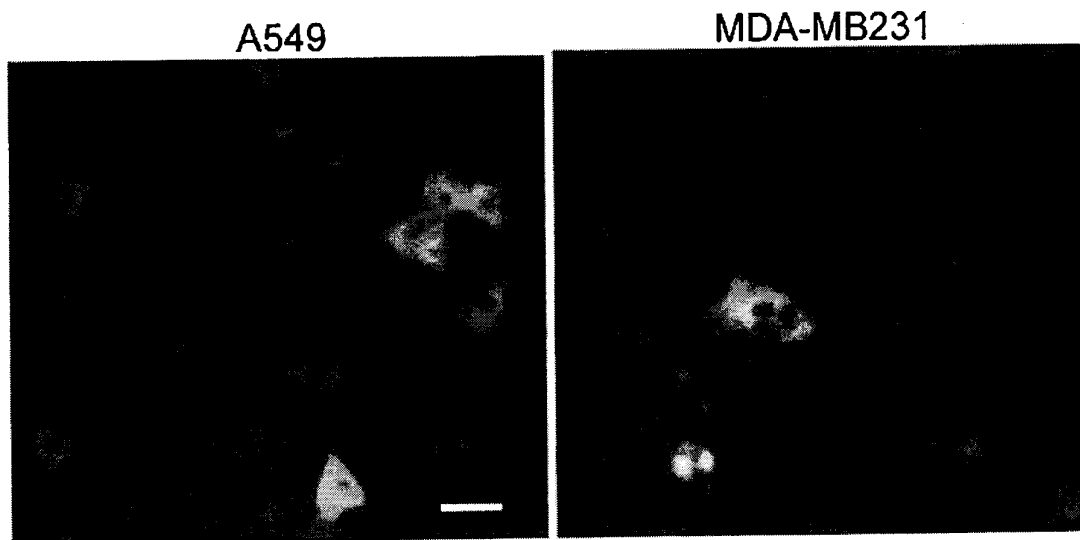


Fig. 15

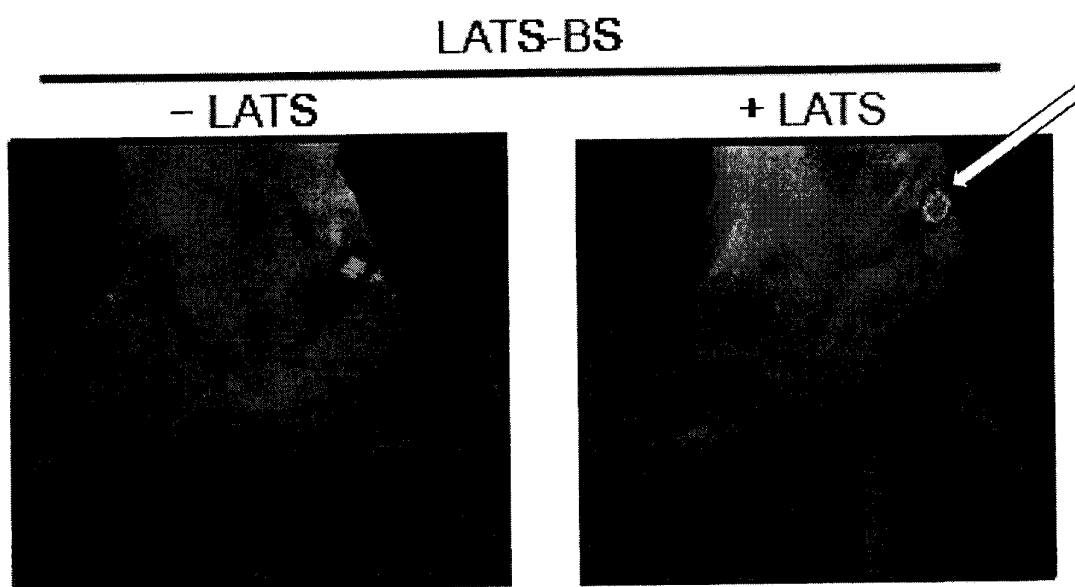


Fig. 16

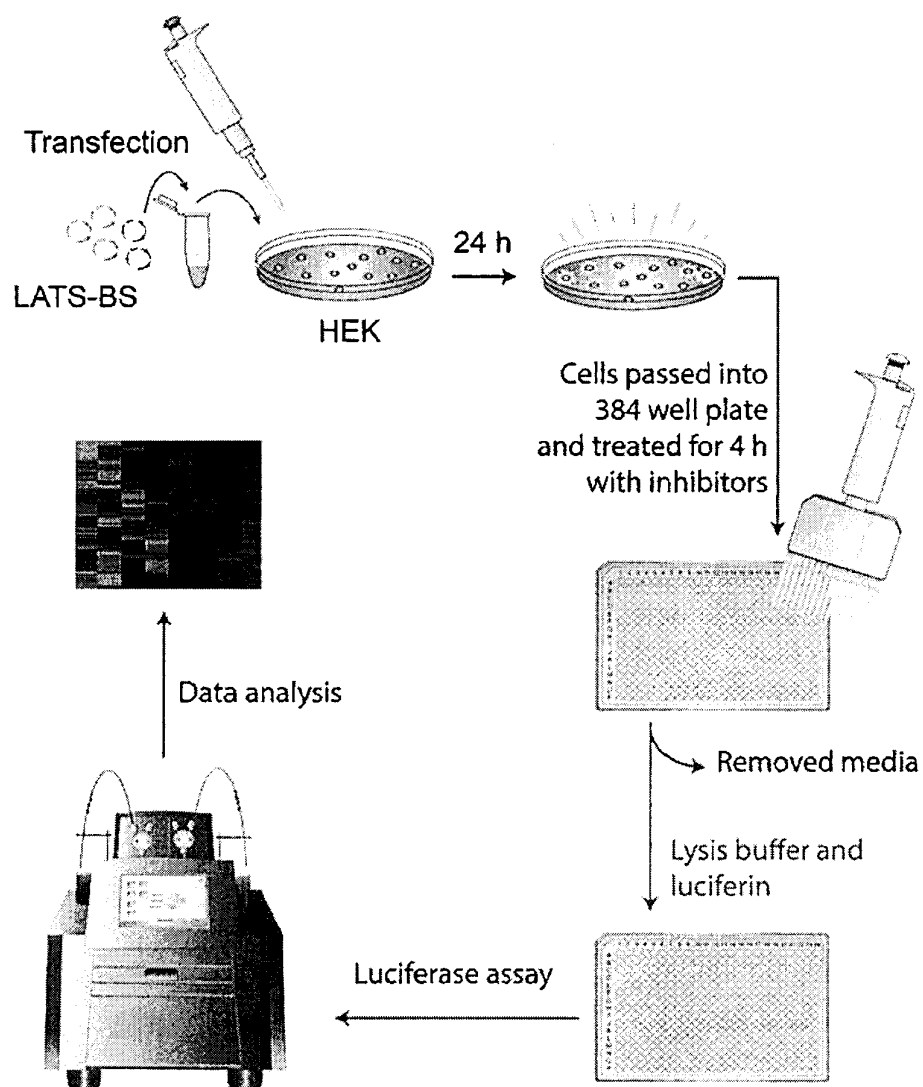


Fig. 17A

