

Supplementary File 7: Sequence of Vgll4l, Vgll4b, Yap, Taz, and Tead3a mutants.

Vgll14l E2 (Δ7)

WT open reading frame is underlined. Aminoacids coded by another coding frame after the mutation site are in *red* italics.

WT TGTGCGTTGAAGATTCAGGAATGGCGGTCCTAATTTCCACTACATAACCAGGATGAGCA 120
|||||
Vgll14l E2Δ7 TGTGCGTTGAAGATTCAGGAATGGCGGTCCTAATTTCCACTACATAACCAGGATGAGCA 120
C A L K I Q E W R S L I S T T * P G * A
V R * R F R N G G H * F P L H N Q D E Q
C V E D S G M A V T N F H Y I T R M S S

WT GTGGTTTCAAAGTATACATCTTAGAGGGACAGCCCAATCTGAGGAGCGAAGACAGATTCC 180
|||||
Vgll14l E2Δ7 GTGGTTTCAAAGTATACATCTTAGAGGGACAGCCCAATCTGAGGAGCGAAGACAGATTCC 180
V V S K Y T S * R D S P I * G A K T D S
W F Q S I H L R G T A Q S E E R R Q I P
G F K V Y I L E G Q P N L R S E D R F R

WT GGCACATGACCAGCGACAGAGTGCGCATGCGCCCGCACACCCCATGAAGCGCAAGCACA 240
|||||
Vgll14l E2Δ7 GGCACAT-----GACAGAGTGCGCATGCGCCCGCACACCCCATGAAGCGCAAGCACA 233
G T * A H A P R T P H E A Q A Q A Q
A H R V R M R P A H P M K R K H S
H M *T E C A C A P H T P* * S A S T

peptide

WT MAVTNFHYITRMSSGFKVYILEGQPNLRSEDRFRHMTSDRVRMRPAHPMKRKHSSDRGRT 60
|||||
Vgll14l E2Δ7 MAVTNFHYITRMSSGFKVYILEGQPNLRSEDRFRHM*TECACAPHTP*
WT LEERRERALS KCVANSARRSSGF S I P E S P T S T W S P T A S P T H L I P S P V F S S P V M D E P L A L I 120
WT KKPRPEPEKTESQN KAT T Q I Q M R P S V I T C V S S A S R S T K Q D C C N H S T A V S K H S Y D H V E E H F 180
WT Q R S L G I N Y H R A T S I S V S V D D H F A K A L G D K W L Q L K A S S S S C H S S S S S S S S S P P S S P T F I H S 240
WT P G Y S P K R A R K D S S S P T T T T P N F W S D K 266

Vg114b E3(Δ4+6)

WT open reading frame is underlined. Aminoacids coded by another coding frame after the mutation site are in *red* italics.

WT	CTTTCGCGATTAAAAGTCCATAA ATG CTTTTTTACCAAAATGGACCTGTTGAACTACCAG	180
Vg114b E3Δ4+6	CTTTCGCGATTAAAAGTCCATAAATGCTTTTTTACCAAAATGGACCTGTTGAACTACCAG L S A I K S P * <u>M L F T K M D L L N Y Q</u> F L R L K V H K C F L P K W T C * T T S F C D * K S I N A F Y Q N G P V E L P V	180
WT	TACTTGGACAAAATGAACAACAACATCGGCATCCTGTGCTACGAAGGAGATGCGGCTCTG	240
Vg114b E3Δ4+6	TACTTGGACAAAATGAACAACAACATCGGCATCCTGTGCTACGAAGGAGATGCGGCTCTG Y <u>L D K M N N N I G I L C Y E G D A A L</u> T W T K * T T T S A S C A T K E M R L * L G Q N E Q Q H R H P V L R R R C G S E	240
WT	AGAGGCGAGTCCAGAATGCAGTCTCTGTCGTCTGCAGTCAGCAACCACCGGACCGGCCCT	300
Vg114b E3Δ4+6	AGAGGCGAGTCCAGAATGCAGTCTCTGTCGTCTGCAGTCAGCAACCACCGGACCGGCCCT <u>R G E S R M Q S L S S A V S N H R T G P</u> E A S P E C S L C R L Q S A T T G P A L R R V Q N A V S V V C S Q Q P P D R P S	300
WT	CCTCCCATCAGCCCCAGCAAGAGGAAACACAGCGCGGAGCAAGCAGACGACGACATCGAC	360
Vg114b E3Δ4+6	CCTCCCATCAGCCCCAGCAAGAGGAAACACAGCGCGGAGCAAGCAGACGACGACATCGAC <u>P P I S P S K R K H S A E Q A D D D I D</u> L P S A P A R G N T A R S K Q T T T S T S H Q P Q Q E E T Q R G A S R R R H R L	360
WT	TGCAACAGTGAGCATGTGGCCAAGATGAGCCGCCTGTTCGCCGCACAGCTAGGAAAGCCT	420
Vg114b E3Δ4+6	TGCAACAGTGAGCATGTGGCCAAGATGAGCCGCCTGTTCGCCGCACAGCTAGGAAAGCCT <u>C N S E H V A K M S R L F A A Q L G K P</u> A T V S M W P R * A A C S P H S * E S L Q Q * A C G Q D E P P V R R T A R K A C	420
WT	GCCAACGGGGACTACCGCAAGGACCCCCGGGAGCGCAGCCGACGCCCATC GAGC --GCA	478
Vg114b E3Δ4+6	GCCAACGGGGACTACCGCAAGGACCTCCGGGAGCGCAGCCGACGCCCATC ATCCCA GCA <u>A N G D Y R K D L R E R S R S P I</u> <i>I P A</i> P T G T T A R T S G S A A A A P S S Q H Q R G L P Q G P P G A Q P Q P H H P S <u>M</u>	480
WT	TGGCGGCCCCAGCATGAGTCTGGTTGGTGGGCATCATCTCTACATGCCCAGCCTGGCCC	538
Vg114b E3Δ4+6	TGGCGGCCCCAGCATGAGTCTGGTTGGTGGGCATCATCTCTACATGCCCAGCCTGGCCC <i>W R P P A</i> * V W L V G I I S T C P A W P G G P Q H E S G W W A S S L H A Q P G P <u>A A P S M S L V G G H H L Y M P S L A L</u>	540

Peptide

WT	MLFTKMDLLNYQYLDKMNNNIGILCYEGDAALRGESRMQSLSSAVSNHRTGPPPIPSKR	60
Vg114b E3Δ4+6	MLFTKMDLLNYQYLDKMNNNIGILCYEGDAALRGESRMQSLSSAVSNHRTGPPPIPSKR	60
WT	KHSAEQADDDIDCNSEHVAKMSRLFAAQLGKPANGDYRKDPRERSRSPIERMAAPMSLV	120
Vg114b E3Δ4+6	KHSAEQADDDIDCNSEHVAKMSRLFAAQLGKPANGDYRKDLRERSRSP <i>IPAWRPPA</i>	
WT	GGHLYMPSLALDQPLALTKNMDSSRSMGISPTASPVERQQNRPSVITCAPANNRNCNLS	180
WT	HCTGSHNGCSPGLNASYRRASNSNTACDPVIEEHFRRLGKNYKEPEFVTNSVSITGSVD	240
WT	DHFAKALGETWLQIKAKGSSSPDASPNTHMVNHNHSPSLVS	282

Yap E3 (Δ8)

WT open reading frame is underlined. Aminoacids coded by another coding frame after the mutation site are in *red* italics.

WT	TTCAGTTGGATAGAAAGAAGAGTTTACTTTTATCTGGAGTCA TGG GATCCGAACCAGCACAAACCTCCAGCCGGCCACCA	440
Yap E3Δ8	TTCAGTTGGATAGAAAGAAGAGTTTACTTTTATCTGGAGTCA TGG GATCCGAACCAGCACAAACCTCCAGCCGGCCACCA F S W I E R R V L L L S G V M D P N Q H N P P A G H Q S V G * K E E F Y F Y L E S W I R T S T T L Q P A T R Q L D R K K S F T F I W S H G S E P A Q P S S R P P	440
WT	GATCGTCCATGTTTCGGGGAGACTCCGAGACCGATCTGGAGGCTCTTTTAAACGCTGTGATGAACCCGAAAAACACCATCG	520
Yap E3Δ8	GATCGTCCATGTTTCGGGGAGACTCCGAGACCGATCTGGAGGCTCTTTTAAACGCTGTGATGAACCCGAAAAACACCATCG I V H V R G D S E T D L E A L F N A V M N P K N T I V S S M F G E T P R P I W R L F L T L * * T R K T P S D R P C S G R L R D R S G G S F * R C D E P E K H R	520
WT	TCCCCCTTCCGTGCCGATGAGGTTGAGAAAGCTGCCAGACTCATTTCTCACGCCGCCAGAGCCAAAGTCCCACTCCAGA	600
Yap E3Δ8	TCCCCCTTCCGTGCCGATGAGGTTGAGAAAGCTGCCAGACTCATTTCTCACGCCGCCAGAGCCAAAGTCCCACTCCAGA P P S V P M R L R K L P D S F F T P P E P K S H S R S P L P C R * G * E S C Q T H S S R R Q S Q S P T P D P P F R A D E V E K A A R L I L H A A R A K V P L Q T	600
WT	CAAGCCAGTACAGATGCAGGTACTGCTGGTACCGTCACGCCCCATCACGTCCGGGCACACTCCTCACCTGCCTCCCTGCA	680
Yap E3Δ8	CAAGCCAGTACAGATGCAGGTACTGCTGGTACCGTCACGCCCCATCACGTCCGGGCACACTCCTCACCTGCCTCCCTGCA Q A S T D A G T A G T V T P H H V R A H S S P A S L Q K P V Q M Q V L L V P S R P I T S G H T P H L P P C S S Q Y R C R Y C W Y R H A P S R P G T L L T C L P A	680
WT	GCTGGGCGCAGTTTCTCCTGGTGCCTGACTGACCAGCATGGGTCCAGCAAACGCCCCACCTCAGCACCTCCGCCAGTCTCTT	760
Yap E3Δ8	GCTGGGCGCAGTTTCTCCTGGTGCCTGACTGACCAGCATGGGTCCAGCAAACGCCCCACCTCAGCACCTCCGCCAGTCTCTT L G A V S P G A L T S M G P A N A P P Q H L R Q S S Y W A Q F L L V H * P A W V Q Q T P H L S T S A S P L A G R S F S W C T D Q H G S S K R P T S A P P P V L L	760
WT	ACGAGATACCTGA TGACATGC CGCTGCCCCAGGCTGGGAGATGGCCAAGACCCCTTCGGGACAGAGATACTTCCTAAACCATAA	847
Yap E3Δ8	ACGAGATACCTGA-----CGCTGCCCCAGGCTGGGAGATGGCCAAGACCCCTTCGGGACAGAGATACTTCCTAAACCATAA E I P D <i>A A P R L G D G Q D P F G T E I L P K P *</i> T R Y L T L P P G W E M A K T P S G Q R Y F L N H N R D T * R C P Q A G R W P R P L R D R D T S * T I M	847

Peptide

WT	MDPNQHNPAGHQIVHVRGDSETDLEALFNAVMPKNTIVPPSVPMRLRKLPDSFFTPPE	60
Yap E3Δ8	MDPNQHNPAGHQIVHVRGDSETDLEALFNAVMPKNTIVPPSVPMRLRKLPDSFFTPPE	60
WT	PKSHSRQASTDAGTAGTVTPHHVRAHSSPASLQLGAVSPGALTSMGPANAPPQHRLRQSSY	120
Yap E3Δ8	PKSHSRQASTDAGTAGTVTPHHVRAHSSPASLQLGAVSPGALTSMGPANAPPQHRLRQSSY	120
WT	EIPDDMPLPPGWEMAKTPSGQRYFLNHNDQTTWQDPRKALLQMNQAAPASPVVQQQNI	180
Yap E3Δ8	EIPD <i>AAPRLGDGQDPFGTEILPKP</i>	
WT	MNPASGPLPDGWEQAITSEGEIYYINHKNKTTSWLDPRLDPRFAMNQQRISQSAPVKQGS	240
WT	QLPSSPQSGVMSGNNPIRLQQIHIEKERLRIKQELLRQRPQELALRNQLPTSMEQDGGTQ	300
WT	NPVSSPGMGQDARNMTTNSSDPFLNSGTYHSRDESTDGLSMSSYSVPRTPDDFLNSVDE	360
WT	METGDTLGP GSMATQPSRFPDYDLAIPGTDVDLGTLEGESMAVEGEELMPSLQEALSSDI	420
WT	LNDMESVLAATKIDKENFLTWL	442

TAZ E1 (Δ4)

WT open reading frame is underlined. Aminoacids coded by another coding frame after the mutation site are in *red* italics.

WT	CAAACACTTTTCAACTCGGCTGAAACTACTTAAGGACGAAAAACAGGAAAAGTTCCTACA	60
Taz E1Δ4	CAAACACTTTTCAACTCGGCTGAAACTACTTAAGGACGAAAAACAGGAAAAGTTCCTACA Q T L F N S A E T T * G R K T G K V P T K H F S T R L K L L K D E K Q E K F L Q N T F Q L G * N Y L R T K N R K S S Y R	60
WT	GGAAttttttttCCATCGGCCATTTTAATCGAAGTTTGTTTTGACCATGAGCGGTAATC	120
Taz E1Δ4	GGAATTTTTCATCGGCCATTTTAATCGAAGTTTGTTTTGACCATGAGCGGTAATC G I F F S I G H F N R S L F * P * A V I E F F F P S A I L I E V C F D H E R * S N F F F H R P F * S K F V L T <u>M S G N P</u>	120
WT	CTCTCCAGCCGATACCGGGCCACCAGGTGATCCATGTCGCCAAAGACCTGGACACGGATC	180
Taz E1Δ4	CTCTCCAGCCGATACCGGGCCACCAGGTGATCCATGTCGCCAAAGACCTGGACACGGATC L S S R Y R A T R * S M S P K T W T R I S P A D T G P P G D P C R Q R P G H G S <u>L Q P I P G H Q V I H V A K D L D T D L</u>	180
WT	TGGAGGCTCTTTTAACTCGGTTCATGAACCCGAAACCGAGCTCCTGGAGGAACAAGGATA	240
Taz E1Δ4	TGGAGGCTCTTTTAACTCGGTTCATGAACCCGAAACCGAGCTCCTGGAGGAACAAGGATA W R L F L T R S * T R N R A P G G T R I G G S F * L G H E P E T E L L E E Q G Y <u>E A L F N S V M N P K P S S W R N K D M</u>	240
WT	TGCCGAGTCTTTCTTCCAGGAGCCGACTCGGGCTCCCACTCCCGGCAGTCCAGCGCGG	300
Taz E1Δ4	TGCCGAGTCTTTCTTCCAGGAGCCGACTCGGGCTCCCACTCCCGGCAGTCCAGCGCGG C R S L S S R S R T R A P T P G S P A R A A V F L P G A G L G L P L P A V Q R G <u>P Q S F F Q E P D S G S H S R Q S S A D</u>	300
WT	ATTCGGTTCTCTCCCGCCGAGGGTCCACTTTCGCTCGCGCTCATCTCCGGCGTCCCTAC	360
Taz E1Δ4	ATTCGGTTCTCTCCCGCCGAGGGTCCACTTTCGCTCGCGCTCATCTCCGGCGTCCCTAC I P V L S R R G S T F A R A H L R R P Y F R F S P A E G P L S L A L I S G V P T <u>S G S L P P R V H F R S R S S P A S L Q</u>	360
WT	AGCTGCGCGGGCTCCGTGAGCGGCCCCGAGCCCCGGGAGACTCCACTCCCACACCCGGC	420
Taz E1Δ4	AG----CGGCGGGCTCCGTGAGCGGCCCCGAGCCCCGGGAGACTCCACTCCCACACCCGGC S G L R E R P E P R E T P L P H P A A <u>A G S V S G P S P G R L H S H T R H</u> <i>R R A P *</i> A A R A P G D S T P T P G	416

Peptide

WT	MSGNPLQPIPGHQVIHVAKDLDTDLEALFNSVMNPKPSSWRNKDMPQSFFQEPDSGSHSR	60
TAZ E1Δ4	MSGNPLQPIPGHQVIHVAKDLDTDLEALFNSVMNPKPSSWRNKDMPQSFFQEPDSGSHSR	60
WT	QSSADSGSLPPRVHFRSRSSPASLQLPAGSVSGPSPGRLHSHTRHQSCDVAEELPLPPGW	120
TAZ E1Δ4	QSSADSGSLPPRVHFRSRSSPASLQRRAP	120
WT	EMAFTPNGQKYFLNHIEKITTTWHDPKSMTPSVAQLSLHNQVSNTASIQQRSMALSQPNL	180
WT	VLNQQAHQQQQHLQQQQQVPVQVPVQAPQQQSSQPMNLSAQQHQQKMRLQRIQMERE	240
WT	RIQRQEELMRQEVALRQLFMDSDNLPVAPAGSPAMSGNMPNNSADPFLNSGPYHSR	300
WT	EQSTDGSLGLGCYSIPTTPEDFLNNMEDMDTGENMVPVSMNVPPQSRFPDFLDSMPGTNV	360
WT	DLGTLEGTDLMPIINDVESVLNKSEPFLLTWL	391

Tead3a^{SA14593}

WT open reading frame is underlined. Aminoacids coded by another coding frame after the mutation site are in *red* italics.

WT	CCAGCGAGAGCCCGGAGGAGGGCCAGGAGGATGAGGTGGACGGGATGGACAAAACCGGAA	360
Tead3a SA14593	CCAGCGAGAGCCCGGAGGAGGGCCAGGAGGATGAGGTGGACGGGATGGACAAAACCGGAA P A R A R R R A R R M R W T G W T K P E Q R E P G G G P G G * G G R D G Q N R N S E S P E E G Q E D E V D G M D K T G <u>M</u>	360
WT	TGACCGGGGATGCGGAGGGCGTCTGGAGTCCTGACATTGAACAAAGCTTCCAGGAGGCTC	420
Tead3a SA14593	TGACCGGGGATGCGGAGGGCGTCTGGAGTCCTGACATTGAACAAAGCTTCCAGGAGGCTC W T G M R R A S G V L T L N K A S R R L G R G C G G R L E S * H * T K L P G G S <u>D G D A E G V W S P D I E Q S F Q E A L</u>	420
WT	TGGCCATTTATCCACCCTGTGGCCGAGAAAGATCATCCTCTCAGATGAAGGAAAGATGT	480
Tead3a SA14593	TGGCCATTTATCCACCCTGTGGCCGAGAAAGATCATCCTCTCAGATGAAGGAAAGATGT W P F I H P V A A E R S S S Q M K E R C G H L S T L W P Q K D H P L R * R K D V <u>A I Y P P C G R R K I I L S D E G K M Y</u>	480
WT	ATGGTCGTAATGAATTGATAGCAAGATATATAAAGCTGCGAACTGGAAAAACACGCACAC	540
Tead3a SA14593	ATGGTCGTAATGAATTGATAGCAAGATATATAAAGCTGCGAACTGGAAAAACACGCACAC M V V M N * * Q D I * S C E L E K H A H W S * * I D S K I Y K A A N W K N T H T <u>G R N E L I A R Y I K L R T G K T R T R</u>	540
WT	GGAAACAGGTATCTAGTCACATACAGGTGTTAGCAAGGAAGAAAATGCGGGAATATCAAG	600
Tead3a SA14593	GGAAACAGGTATCTAGTCACATACAGGTGTTAGCAAGGAAGAAAATGCGGGAATATCAAG G N R Y L V T Y R C * Q G R K C G N I K E T G I * S H T G V S K E E N A G I S S <u>K Q V S S H I Q V L A R K K M R E Y Q A</u>	600
WT	CAGGCATAAAGGCCATGAATTTGGATCAGGCTTCAAAAGACAAAGCTCTTCAGAACATGG	660
Tead3a SA14593	CAGGCATAAAGGCCATGAATTTGGATCAGGCTTCAAAAGACAAAGCTCTTCAGAACATGG Q A * R P * I W I R L Q K T K L F R T W R H K G H E F G S G F K R Q S S S E H G <u>G I K A M N L D Q A S K D K A L Q N M A</u>	660
WT	CGGCTCTGTCCTCAGCTCAGATCGTGTCTGCCAGTGTGATGAAGAGTCAGCTTCCTCCTC	720
Tead3a SA14593	CGGCTCTGTCCTCAGCTCAGATCGTGTCTGCCAGTGTGATGAAGAGTCAGCTTCCTCCTC R L C P Q L R S C L P V * * R V S F L L G S V L S S D R V C Q C D E E S A S S S <u>A L S S A Q I V S A S V M K S Q L P P L</u>	720
WT	TTCCTCAGCACCCATACCTCCTCCAGCCCGGTTTGGCCCGGCCCATCCCAGGACAGC	780
Tead3a SA14593	TTCCTCAGCACCCATACCTCCTCCAGCCCGGTTTGGCCCGGCCCATCCCAGGACAGC F L S T H T L L Q P G F G P A P S Q D S S S A P I P S S S P V L A R P H P R T A <u>P Q H P Y P P P A R F W P G P I P G Q P</u>	780
WT	CTGGACCTTCTCAGGACATCAAGCCCTTTGCACCGAGCCCGTACCCTACCCTTCAGCCTC	840
Tead3a SA14593	CTGGACCTTCTCAGGA ■ gagtatttcagaccacatttgatctaagaacagtactcctgc L D L L R R E Y F R P T F D L R T V L L W T F S G G S I S D P H L I * E Q Y S C	840

G P S Q E G V F Q T H I * S K N S T P A

Tead3a^{SA14593} Peptide

WT	MDKTGMDGDAEGVWSPDIEQSFQEALAIYPPCGRRKIILSDEGKMYGRNELIARYIKLRT	60
Tead3a SA14593	MDKTGMDGDAEGVWSPDIEQSFQEALAIYPPCGRRKIILSDEGKMYGRNELIARYIKLRT	60
WT	GKTRTRKQVSSHIQVLARKKMREYQAGIKAMNLDQASKDKALQNMAALSSAQIVSASVMK	120
Tead3a SA14593	GKTRTRKQVSSHIQVLARKKMREYQAGIKAMNLDQASKDKALQNMAALSSAQIVSASVMK	120
WT	SQLPPLPQHYPYPPPARFWPGPIPGQPGPSQDIKPFAPSPYPTLQPPPISSYQLPAPLPP	180
Tead3a SA14593	SQLPPLPQHYPYPPPARFWPGPIPGQPGPSQEGVFQTHI	
WT	SATAVPVWQDRTIASSKLRMLEYSAFMEVQRDPDTYSKHLFVHIAQTNPSYTDPLLEAVD	240
WT	IRQIYDKFPEKKGGLKELYEKGPQNAFFLVKFWADLNSSNVQDGAGSFYGVSSQYSSAEN	300
WT	MTITVSTKVCSEFGKQVVEKVEYARVEGGRYVYRIHRSPMCEYMINFIHKLKHLPEKYM	360
WT	MNSVLENFTILQVVTNRDTQETLLCIAFVFEVSTSDHGAQYHVYRLVKD	409