

**Figure S1.** Sequences of the  $\gamma$ -gliadin,  $\delta$ -gliadin and avenin-like genes reported in Table 1 and their deduced translation products. The stop codons are highlighted in red.

***Gli-γ1a***

[illegible]

*Gli-γ2a\**

[illegible]

*Gli-γ3a*

[illegible]

*Gli-γ4a*

[illegible]

## Gli- $\gamma 1b$

1 M K T L L I L T I L A M A T T I A T A N M Q V D P S G Q V Q W P Q Q  
ATGAAGACCT TACTCATCCT AACAAATCCTT GCGATGGCAA CAACCATCGC CACCGCCAAT ATGCAAGTCG ACCCCAGCGG CCAAGTACAA TGGCCACAAC  
· Q P F P Q P Q Q P F C E Q P Q R T I P Q P H Q T F H H Q P Q Q T F  
101 AACAAACCATT CCCCCAGCCC CAACAACCAT TCTGCGAGCA ACCACAACGA ACTATTCCCC AACCCCATCA AACATTCCAC CATCAACCAC AACAAACATT  
· P Q P E Q T Y P H Q P Q Q Q F P Q T Q Q P Q Q P F P Q P Q Q T F P  
201 TCCCCAACCC GAACAAACAT ACCCCCATCA ACCACAACAA CAATTTCCCC AGACCCAACA ACCACAACAA CCATTTCCCC AGCCCCAACA AACATTCCCC  
Q Q P Q L P F P Q Q P Q Q P F P Q P Q Q P F P Q S Q Q P Q Q P  
301 CAACAACCCC AACTACCATT TCCCAACAA CCCCACAAC CATTCCCCCA GCCTCAGCAA CCCCACAAC CATTCCCCCA GTCACAACAA CCACAACAAC  
· F P Q P Q Q Q F P Q P Q Q P Q Q S F P Q Q Q Q P A I Q S F L Q Q Q  
401 CTTTTCCTT GCCCCAACAA CAATTTCCGC AGCCCCAACA ACCACAACAA TCATTCCCC AACACAACA ACCGGCGATT CAGTCATTTC TACAACAACA  
· M N P C K N F L L Q Q C N H V S L V S S L V S I I L P R S D C Q V  
501 GATGAACCCC TGCAAGAATT TCCTCTTGCA GCAATGCAAC CATGTGTCAT TGGTGTATC TCTCGTGTCA ATAATTTTGC CACGAAGTGA TTGCCAGGTG  
M Q Q Q C C Q Q L A Q I P Q Q L Q C A A I H S V A H S I I M Q Q E Q  
601 ATGCAGCAAC AATGTTGCCA ACAACTAGCA CAAATTCCTC AACAGCTCCA GTGCGCAGCC ATCCACAGCG TCGCGCATTC CATCATCATG CAACAAGAAC  
· Q Q G V P I L R P L F Q L A Q G L G I I Q P Q Q P A Q L E G I R S  
701 AACACAAGG CGTGCCGATC CTGCGGCCAC TATTTAGCT CGCCAGGGT CTGGGTATCA TCCAACCTCA ACAACCAGCT CAATTGGAGG GGATCAGGTC  
· L V L K T L P T M C N V Y V P P D C S T I N V P Y A N I D A G I G  
801 ATTGGTATTG AAAACTCTTC CAACCATGTG CAACGTGTAT GTGCCACCTG ACTGCTCCAC CATCAACGTA CCATATGCCA ACATAGACGC TGGCATTGGT  
G Q  
901 GGCCAAATGA

## Gli- $\gamma 2b$

1 M K T L L I L T I L A M A T I I A T A N M Q V D P S S R V Q W P Q E  
ATGAAGACCT TACTCATCCT AACAAATCCTT GCGATGGCAA CAATAATCGC CACTGCCAAT ATGCAGGTCG ACCCTAGCAG CCGAGTACAA TGGCCACAAG  
· Q P S P Q S Q Q P F S Q Q P Q Q I F P Q P Q Q T L P H Q P Q Q A F  
101 AACAAACCAT CCCCCAGTCC CAACAACCAT TCTCCCAGCA ACCACAACAA ATATTTCCCC AACCCCAACA AACATTGCCC CATCAACCAC AACAAACATT  
· P Q P Q Q T F P H R P Q Q Q F P Q P Q Q P Q Q P F P Q P Q Q P Q L  
201 TCCCCAACCT CAACAAACAT TCCCCCATCG ACCACAACAA CAATTTCCCC AGCCCCAGCA ACCACAACAA CCATTTCCCTC AGCCCCAACA ACCCCAACTA  
P F P Q Q T Q Q P F P Q P Q Q P Q Q P F P Q S Q Q P Q Q P F P Q P Q  
301 CCATTTCCCC AACAAACACA ACAACCATTC CCCAGCCTC AACAAACCCA ACAACCATTT CCCAGTCAC AGCAACCACA ACAACCTTTT CCCAGCCCC  
· Q Q F P Q P Q Q P Q Q S F P Q Q Q Q W M I Q S F L Q Q Q M N P C K  
401 AACAAACATT TCCGCAGCCC CAACAACCAC AACAAATCATT CCCCACAACA CAACAATGGA TGATTAGTC ATTTCTACAA CAACAGATGA ACCCTGCAA  
· N F L L Q Q C N P V S L V S S L V S I I L P R S D C Q L M Q Q C  
501 GAATTTCCCTC TTGCAGCAAT GCAACCCTGT GTCATTGGTG TCATCTCTCG TGTCAATAAT CTTGCCACGA AGTGATTGCC AGCTGATGCA GCAACAATGT  
C Q Q L A Q I P Q Q L Q C A A I H S V A H S I V M Q Q E Q Q R G V Q  
601 TGCCAACAAC TAGCACAAT TCCTCAACAG CTCCAGTGCG CAGCCATCCA CAGCGTCGCG CATTCCATCG TCATGCAGCA AGAACAACAA CGAGGCGTGC  
· I L R P L F Q L A Q G L G I I Q P Q Q P A Q L E G I R S L V L K T  
701 AGATCCTGCG GCCACTATTT CAGCTCGCCC AGGGTCTGGG TATCATCCAA CCTCAACAAC CAGCTCAATT GGAGGGGATC AGGTCATTGG TATTGAAAAC  
· L P T M C N V Y V P P D C S T I N V P Y A S I D A V I G G Q  
801 TCTTCCAACC ATGTGCAATG TGTATGTCCC ACCTGACTGC TCCACCATCA ACGTGCCATA TGCCAGCATA GACGCTGTCA TTGGTGGCCA ATGA

## Gli- $\beta$ b

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      M K T L L I L T I L A M A I T I S T A N M Q V D P S G Q V Q W P Q Q
1  ATGAAGACCT TACTCATCCT GACGATCCTT GCGATGGCAA TAACCATCAG CACCGCCAAT ATGCAGGTCG ACCCTAGTGG CCAAGTACAA TGGCCACAAC
   · Q L V P Q P Q Q P L S Q Q P Q Q A F P Q P Q Q T F P H Q P Q Q Q V
101 AACAACTAGT CCCCCAACCC CAACAGCCAT TATCCCAGCA ACCGCAACAA GCATTTCCCC AACCCCAACA AACATTTCCC CATCAACCAC AACAACAAGT
   · P Q P Q Q P Q Q P F L Q P Q Q A F P Q Q P Q Q P F P Q T Q Q P Q Q
201 TCCCCAGCCT CAGCAACCAC AACCAACCATT TCTCCAGCCC CAACAAGCAT TCCCCAACA ACCACAACAA CCATTCCCTC AGACTCAACA ACCACAACA

      P F P Q Q P Q Q P F P Q T Q Q P Q Q P F P Q T Q Q P
301 CCATTTCCCC AGCAACCACA ACAACCATT CCCCAGACTC AACCAACCACA ACAACCATTT CCCCAGCAAC CACAACAACC ATTCCCCCAG ACTCAACAAC
   · Q Q P F P Q F Q Q P H Q P F P Q P Q Q Q F P Q P Q Q P Q Q S F L Q
401 CACAACAACC ATTTCCCCAG TTCCAGCAAC CACACCAACC TTTTCCCCAG CCCCAACAAC AATTCCCGCA GCCCAACAA CCGCAACAAT CATTCCCTCA
   · Q Q R P F I Q P S L Q Q R L N P C K N I L L Q Q C K P A S L V S S
501 GCAACAACGA CCATTCAATC AGCCATCTCT ACAACAACGT TTGAACCCAT GCAAGAATAT CCTCTTGCAA CAATGCAAAC CTGCGTCATT GGTGTCATCC
   L W S I I W P Q S D C Q V M Q Q Q C C Q E L A Q I P Q Q L Q C A A I
601 CTCTGGTCTGA TAATCTGGCC ACAAGCGAT TGCCAAGTGA TGCAGCAACA ATGCTGCCAA GAACTAGCAC AGATTCTCTCA GCAGCTCCAG TGCGCAGCCA
   · H S V V H S I I M Q Q Q Q Q Q Q Q Q Q G M H I L L T L S Q
701 TCATAGCGT CGTGATTC ATCATCATGC AGCAGCAACA ACAACAACA CAACAACAAC AACACAACA AGGCATGCAT ATCCTGCTGA CACTATCTCA
   · Q Q Q L G Q G T L V Q G Q G I I Q P Q Q L A Q L E A I R S L V L Q
801 ACAACAACGA TTGGGTCAAG GTACTCTCGT CCAAGGCCAG GGCATCATCC ACTAGCTCAA TTGGAGGCGA TCAGGTCATT GGTGTTGCAA
   T L P T M C N V Y V P P E C S I I R A P F A S I V A G I G G Q
901 ACTCTTCCAA CCATGTGCAA CGTGTATGTC CCACCTGAGT GCTCCATCAT CAGGGCACCA TTTGCCAGCA TAGTCGCGGG GATTGGTGGC CAATGA
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## Gli- $\gamma$ b\*

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      M K T L L I L T I L A M A V T I G T A N M Q V G P S G Q V Q W P Q Q
1  ATGAAGACCT TACTCATCCT AACAAATCCTT GCGATGGCAG TAACCATCGG CACCGCCAAT ATGCAGGTCG GCCCTAGCGG CCAAGTACAA TGGCCACAAC
   · Q P V L L P Q Q P F S Q Q P Q Q T F P Q P Q Q T F P H Q P Q Q
101 AACCAACCAGT CCTGCTGCCT CAGCAACCAT TCTCCCAGCA ACCACAACAA ACATTTCCCC AACCCCAACA AACATTCCCC CATCAACCAC AACAAATA
201 TCCCCAGCCT CAACAACCAC AACAAACAATT TCTCCAGCCA CAACAACCAT TCCCCAACA ACCACAACA CCATATCCCC AACCAACCACA ACAACCATT
301 CCCCAGACTC AACCAACCCA ACAACTATTT CCCCAGTCCC AGCAACCACA ACAACCATAT CCCCAGCAAC CACAACAACC ATTCCCCCAG ACTCAACAAC
401 CCAACAACA ATTTCCCCAA TCCCAGCAAC CACAACAACC ATTTCCCCAA CCCCAACAAC TGCAACAATC ATTCCCCCAG CAACAACCAT CGTTCATTCA
501 GGCATCTCTA CAACAACCTG TGAACCCATG CAAGAATTTA CTCTTGAGC AATGTAGACC TGTGTCATTG GTCTCATCCC TCTGGTCAAT GATCTGGCCA
601 CAAAGCGCTT GCCAAGTGAT GAGGAAACAA TGCTGCCAAC AACTAGCACA GATTCCTCAG CAGCTCCAGT GTGCAGCCAT CCATAGCGTC GTGCATTCCA
701 TCAGCATGTA GCAAGAACA CAACAACAAC AACACAACA ACAACAACA CAACAACAAC AACACAACA ACAAGGCATG CGTATCCTGC TGCCACTATA
801 TCAGCAACAA CAGGTGGGTC AAGGTACTCT CGTCCAGGGC CAGGGCATCA TCCAACCCA ACAACCAGCT CAATTGGAGG CGATCAGGTC ATTGGTGTG
901 CAAACTCTTC CAACCATGTG CAACGTGTAT GTCCCACCTG AGTGCTCTAT CATCAAGGCA CCATTTGCCA GCATAGTCAC CGGAATTGGT GGCCAATGA
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*Gli-γ5b*

[illegible]

*Gli- $\delta 1a^*$*

[illegible]

*Gli- $\delta 2a^*$*

[illegible]

*Gli- $\delta 1b^*$*

	M	K	I	F	L	V	F	A	L	L	V	V	S	T	T	I	T	T	A	I	V	Q	L	D	P	S	V	H	V	Q	E	R	P	Q																																																	
1	ATGAAGATCT	TCTTGGTCTT	TGCCCTCCTC	GTTGTATCAA	CGACCATCAC	CACCGCGATC	GTGCAGCTCG	ACCCTAGTGT	CCATGTCCAA	GAAAGGCCAC	.	Q	S	F	P	Q	Q	Q	P	L	T	Q	Q	Q	P	F	F	P	L	Q	E	P	Q	Q	P																																																
101	ACAACATTATT	TCCGCGAGCAG	CAACCACTTA	CCCAGCAACA	ACCATTCCCG	CTGCAAGAAC	CACAACAACC	ACTATTCCCG	CAAAAAGAGC	CACAACAACC	.	F	L	L	Q	Q	P	Q	P	Q	E	Q	Q	P	Y	P	Q	Q	P	L	L	Q	Q	Q	L	P																																															
201	ATTTTTGCTG	CAGCAACCAC	AACCCAGGA	ACAACAACCA	TATCCACAAC	AGCCACTTCT	CCAACAACAA	CTTCCCTAGC	AACATCTATT	CCCGCAGCAG	301	CCACCACAAC	AACAATTTCC	GCAGCAGATG	CCACTTCCAT	ATGACAACA	AACATTCCCG	CTACAACAGC	AACGCGAACC	ACAATTTCCG	CAACCACAAC	401	CATTTCCCCA	ATATCAATAC	CCATTAAAC	AACAACCATA	CCCGCAAGAG	CAACCATTGC	CACAACAACA	ACCTTCTATG	GAGGAAAAAC	AACAATTGAA	501	CGTGTCGAAG	GAGTTCCTCC	TGCAACAGTG	CAACCCGGAG	GAGAACTGT	CATTACTCCA	GTCAAGTATC	CCGTTCTCTC	GACCAAGAAC	CTCGCAACAG	601	AATAGCTGCC	AGTTGAAGCG	TCTACAATGT	TGTACAACAAC	TTGCACATAT	CAATGAACCG	TCCCGATGCC	CGGCCATCCA	CAACATTGTG	CACGCCATCG	701	TCGTTCAACA	ACAACATGTG	GATAGAGGTT	TCGCCCAGCC	TCAACCACAA	CAGTTGGGCC	AGGGAATGCC	CATGCAGCCT	CAATATCAAT	TGGGCCAGGG	801	CTTTATCTTA	CCTCAACAAC	TAGCCAGTT	CAAGTTGGTT	AGGTTACTTG	TGATTACAG	CCTGCCTATG	TTATGCAACG	TGCATGTCCC	ATCTGATTGC	901	TATACCCTA	GTGCACCATC	TGGTAGCATG	ACTGCCTTGA	AGGTTGGACA	GTGA

$$Av-la^*$$
[illegible]

*Av-2a*

[illegible]
$$Av-1b^*$$
[illegible]

*Av-2b*

[illegible]