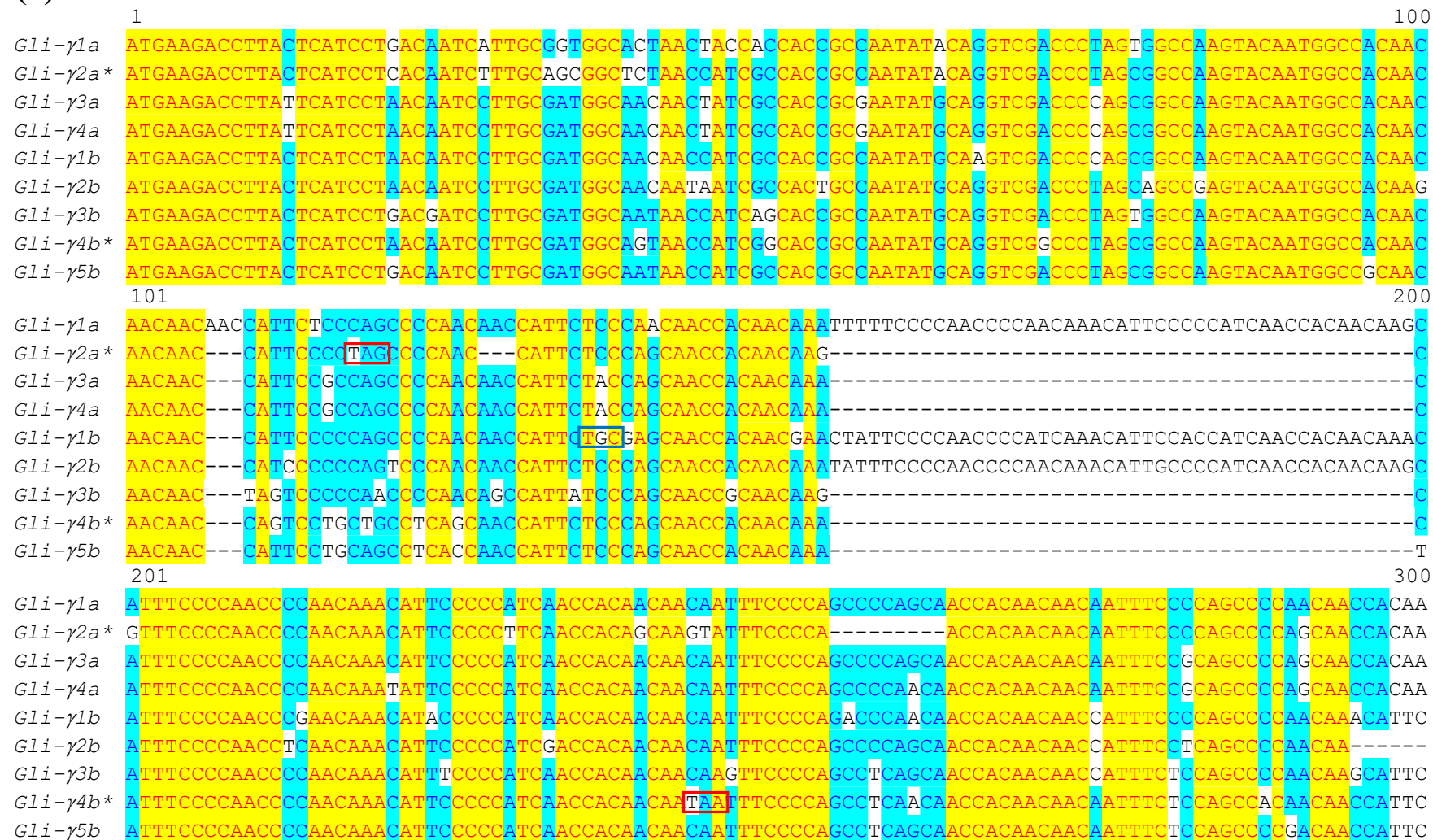


Figure S2. Alignment of the γ -gliadin **(a)** and δ -gliadin **(b)** gene sequences from the durum wheat cv. Svevo. The premature stop codons are boxed in red, the TGC codon that encodes the extra cysteine in the *Gli- γ 1b* is boxed in blue, the region of Domain IV rich in glutamine codons is boxed in green.

(a)



301 400

Gli-γ1a CAACCATTTCCCCAGCAACCAACAACAATTTCCCCGGC-----CCCAACAACCACAACAACCAATTCCCCCAGC-----CCCAACAACCCCAAC

*Gli-γ2a** CAACCATTTCCCCAGC-----CCCAACAACCCCAAC

Gli-γ3a CAACCATTTCCCAAC-----CCCAACAAGCCCAAC

Gli-γ4a CAACCATTTCCCCAGC-----CCCAACAAGCCCAAC

Gli-γ1b CCCAACAAACCCCAACTACCATTTC-----CCCAACAACCCCAAC

Gli-γ2b -----CCCAACTACCATTTC-----CCCAACAACCAACAAC

Gli-γ3b CCCAACAAACCAACCAACCATTCTCAGACTCAACAACCACAACAACCATTCCCCCAGCAACCACAACAACCAATCCCCCAGACTCAACAACCCCAACAACCTATTTCCCCCAGTCTCAACAACCAACAAC

*Gli-γ4b** CCCAACAAACCAACCAACCATTCCCCCAGACTCAACAACCCCAACAACCTATTTCCCCCAGTCCCAGCAACCAACAAC

Gli-γ5b CCCAACAAACCAACCAACCATTCCCA-----

401 500

Gli-γ1a TACCATTTC-----GCAACAACCAACAACCAATTCCCCCAGCCTCAACAACCCCAACAACCAATTTCCCAGTTACAGCAACCAACAACCTTTTACC

*Gli-γ2a** AACCATTCCCCCAGCCCTCAACAACCCCAACAACCAATTCCCCCAGTCAAGCAACCAACAACCTTTCCCCAG-----CCCAACAACAAATTTCC

Gli-γ3a TACCATTTC-----TCAACAACCAACAACCAATTCCCCCAGCCTCAACAACCCCAACAACCAATTTCCCCAGTCAAGCAACCAACAACCTTTTCC

Gli-γ4a TACCATTTC-----TCAACAACCAACAACCAATTCCCCCAGCCTCAACAACCCCAACAACCAATTTCCCCAGTCAAGCAACCAACAACCTTTTCC

Gli-γ1b AACCATTCCCCCAGCCCTCAGCAACCCCAACAACCAATTCCCCCAGTCAACAACCAACAACCTTTCCCCAG-----CCCAACAACAAATTTCC

Gli-γ2b AACCATTCCCCCAGCCCTCAACAACCCCAACAACCAATTCCCCCAGTCAAGCAACCAACAACCTTTCCCCAG-----CCCAACAACAAATTTCC

Gli-γ3b AACCATTTCCT-----CAGCAACCAACAACCAATTCCCCCAGACTCAACAACCAACAACCAATTTCCCCAGTTCAGCAACCAACAACCTTTTCC

*Gli-γ4b** AACCATTTCCT-----CAGCAACCAACAACCAATTCCCCCAGACTCAACAACCCCAACAACCAATTTCCCCAATCCAGCAACCAACAACCAATTTCC

Gli-γ5b -----GCAACCAACAACCGTTCCCCCAGACTCAACAACCCCAACAACCAATTTCCCCAGTCCAAGCAACCAACAACCTTTTCC

501 600

Gli-γ1a CCAGCCCCAACAAAT-----CGCAACAACCATTCCTCCAGCAACAACAATCATTGATTAGCCATACCTACAACAACAGATGAAC

*Gli-γ2a** GCAGCCCCAACAAAC-----CGCAACAATCATTCCCCAGCAGCAACAACCTGTTGATTAGCCATATCTACAACAACAGATGAAC

Gli-γ3a CCAGCCCCAACAAAC-----CGCAACAATCATTCCCCAGCAACAACCCGTTGATTAGCCATATCTACAACAACAGATGAAC

Gli-γ4a CCAGCCCCAACAAAC-----CGCAACAATCATTCCCCAGCAACAACCCGTTGATTAGCCATATCTACAACAACAGATGAAC

Gli-γ1b GCAGCCCCAACAAAC-----CACAACAATCATTCCCCCAACAACAACCCGGCGATTAGCTCATTCTACAACAACAGATGAAC

Gli-γ2b GCAGCCCCAACAAAC-----CACAACAATCATTCCCCCAACAACAACATGGATGATTAGCTCATTCTACAACAACAGATGAAC

Gli-γ3b CCAGCCCCAACAAACAATTCGCGAGCCCCAACAAACCGCAACAATCATTCCTCCAGCAACAACGACCATTATTAGCCATCTCTACAACAACGTTTGAAC

*Gli-γ4b** CCAACCCCCAACAAAC-----TGCAACAATCATTCCCCAGCAACAACCATCGTTATTAGCCATCTCTACAACAACGCTGAAC

Gli-γ5b CCAGCCCCAACAAAC-----CGCAACAATCATTCCCCCAACAACAACCATATTGATTCAACAATCTCTACAACAACAGTGAAC

601 700

Gli-γ1a CCTGCAAGAATTACCTCTTGCAAGCAATGCAACCCTGTGTCATTGGTGTGTCATCCCTCGTGTCAATGATCTTGCCACGAAGTGATTGCCAGGTGATGCGGC

*Gli-γ2a** CCTGCAAGAATTACCTCTTGCAAGCAATGCAACCCTGTGTCATTAGTGTGTCGTCCTCGTGTCAATGATCTTGCCACGAAGTGATTGCCAGGTGATGCAGC

Gli-γ3a CCTGCAAGAATTACCTCTTGCAAGCAATGCAACCCTGTGTCATTGGTGTGTCATCCCTCGTGTCAATGATCTTGCCACGAAGTGATTGCCAGGTGATGCAGC

Gli-γ4a CCTGCAAGAATTACCTCTTGCAAGCAATGCAACCCTGTGTCATTGGTGTGTCATCCCTCGTGTCAATGATCTTGCCACGAAGTGATTGCCAGGTGATGCAGC

Gli-γ1b CCTGCAAGAATTTCTCTTGCAAGCAATGCAACCCTGTGTCATTGGTGTGTCATCTCTCGTGTCAATAATTTTGCCACGAAGTGATTGCCAGGTGATGCAGC

Gli-γ2b CCTGCAAGAATTTCTCTTGCAAGCAATGCAACCCTGTGTCATTGGTGTGTCATCTCTCGTGTCAATAATCTTGCCACGAAGTGATTGCCAGCTGATGCAGC

Gli-γ3b CCAATGCAAGAATATCTCTTGCAACAATGCAACCCTGCGTCATTGGTGTGTCATCCCTCTGGTGCATAATCTGGCCACAAGCGATTGCCAAGTGATGCAGC

*Gli-γ4b** CCAATGCAAGAATTTACTCTTGCAAGCAATGTAGACCTGTGTCATTGGTCTCATCCCTCTGGTGCATAATGATCTGGCCACAAGCGCTTGCCAAGTGATGAGGA

Gli-γ5b CCAATGCAAGAATTTCTCTTGCAAGCAATGCAACCCTGTGTCCTGGTGTGTCATCCCTCTGGTGCATAATCATCTTGCCACCAAGCGATTGCCAGGTGATGCGG

	701		800
<i>Gli-γ1a</i>	AACAATGTTGCCAACAACCTAGCACAGATTTCCTCAGCAGCTCCAGTGCAGCCATCCATGGTGTGCTGCATTCCATCATCATGCAGCAAGAACAACAACA		
<i>Gli-γ2a*</i>	AACAATGTTGCCAACAACCTAGCACAGATTTCCTCAGTGTGCTGCATTCCATCATCATGCAGCAAGAACAAC---A		
<i>Gli-γ3a</i>	AACAATGTTGCCAACAACCTAGCACAGATTTCCTCGCCAGCTCCAGTGTGCAGCCATCCATAGCGTGTGCTGCATTCCATCGTCATGCAGCAAGAACAACAACA		
<i>Gli-γ4a</i>	AACAATGTTGCCAACAACCTAGCACAGATTTCCTCGCCAGCTCCAGTGTGCAGCCATCCATAGCGTGTGCTGCATTCCATCATCATGCAGCAAGAACAACAACA		
<i>Gli-γ1b</i>	AACAATGTTGCCAACAACCTAGCACAAATTTCCTCAACAGCTCCAGTGCAGCCATCCACAGCGTGTGCTGCATTCCATCATCATGCAACAAGAACAACAACA		
<i>Gli-γ2b</i>	AACAATGTTGCCAACAACCTAGCACAAATTTCCTCAACAGCTCCAGTGCAGCCATCCACAGCGTGTGCTGCATTCCATCGTCATGCAGCAAGAACAACAACG		
<i>Gli-γ3b</i>	AACAATGCTGCCAAGAACCTAGCACAGATTTCCTCAGCAGCTCCAGTGCAGCCATCCATAGCGTGTGCTGCATTCCATCATCATGCAGCAGCAACAACAACA		
<i>Gli-γ4b*</i>	AACAATGCTGCCAACAACCTAGCACAGATTTCCTCAGCAGCTCCAGTGTGCAGCCATCCATAGCGTGTGCTGCATTCCATCAGCATGTAGCAAGAACAACAACA		
<i>Gli-γ5b</i>	AACAATGTTGTCACAACAACCTAGCACAAATTTCCTCAGCAACTCCAGTGTGCAGCCATCCATAGCGTGTGCTGCATTCCATCATCATGCAGCAAGAACAACAAGA		
	801		900
<i>Gli-γ1a</i>	ACAACAA-----GGCATACAGATCATGCGGCCACTTTTCAGC-----		
<i>Gli-γ2a*</i>	A-----GGCATACAGATCCTGCGACCACTGTTTCAGC-----		
<i>Gli-γ3a</i>	A-----GGCATACAGATCCTCGGCCACTGTTTCAGC-----		
<i>Gli-γ4a</i>	A-----GGCATACAGATCCTCGGCCACTGTTTCAGC-----		
<i>Gli-γ1b</i>	A-----GGCGTGCCGATCCTGCGGCCACTATTTTCAGC-----		
<i>Gli-γ2b</i>	A-----GGCGTGCGATCCTGCGGCCACTATTTTCAGC-----		
<i>Gli-γ3b</i>	ACAACAACAACAACAACAACAACA-----GGCATGCATATCCTGTGTGACACTATCTCAACAACAACAGTTGGGTCAAGGT		
<i>Gli-γ4b*</i>	ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA-----GGCATGCGTATCCTGTGTGCACTATATCAGCAACAACAGGTGGGTCAAGGT		
<i>Gli-γ5b</i>	ACAACCTACAG-----SGTGTGCAAAATCCTGGTGCCACTGTCTCAACAGCAACAGGTGGGTCAAGGT		
	901		1000
<i>Gli-γ1a</i>	----TCATCCAGGGTCAGGGCATCATCCAACCTCAACAACCAGCTCAATTGGAGGTGATCAGGTCATTGGTATTGGGAACCTCTTCCAACCATGTGCAATG		
<i>Gli-γ2a*</i>	----TTGTCCAAGGACAGGGCATCATCCAACCTCAACAACCAGCTCAATATGAGGTGATCAGGTCATTGGTATTGAGAACCCTTCCAACCATGTGCAACG		
<i>Gli-γ3a</i>	----TCATCCAAGGTCAGGGCATCATCCAACCTCAACAACCAGCTCAATATGAGGTGATCAGGTCATTGGTATTGAGAACCCTTCCAACCATGTGCAACG		
<i>Gli-γ4a</i>	----TCGTCCAAGGTCAGGGCATCATCCAACCTCAACAACCAGCTCAATATGAGGTGATCAGGTCATTGGTATTGAGAACCCTTCCAACCATGTGCAACG		
<i>Gli-γ1b</i>	----TCGCCCAGGGTCTGGGTATCATCCAACCTCAACAACCAGCTCAATTGGAGGGGATCAGGTCATTGGTATTGAAAACCTCTTCCAACCATGTGCAACG		
<i>Gli-γ2b</i>	----TCGCCCAGGGTCTGGGTATCATCCAACCTCAACAACCAGCTCAATTGGAGGGGATCAGGTCATTGGTATTGAAAACCTCTTCCAACCATGTGCAATG		
<i>Gli-γ3b</i>	ACTCTCGTCCAAGGCCAGGGCATCATCCAACCTCAACAACCTAGCTCAATTGGAGGCGATCAGGTCATTGGTGTGCAAACTCTTCCAACCATGTGCAACG		
<i>Gli-γ4b*</i>	ACTCTCGTCCAAGGCCAGGGCATCATCCAACCTCAACAACCAGCTCAATTGGAGGCGATCAGGTCATTGGTGTGCAAACTCTTCCAACCATGTGCAACG		
<i>Gli-γ5b</i>	ATTCTCGTCCAAGGGTCAAGGCATCATCCAACCTCAACAACCAGCTCAATTGGAGGTGATCAGGTCATTGGTGTGCAAACTCTTCCAACCATGTGCAACG		
	1001		1074
<i>Gli-γ1a</i>	TATTTGTTCACCTGAGTGCTCCACCACCAAGGCACCATTTGCCAGCATAGTTGCCGACATTGGTGGCCAATGA		
<i>Gli-γ2a*</i>	TGTATGTCCGACCTGACTGCTCCACCATCAACGCACCATTTGCCAGCATAGTTGCCGGCATTTGGTGGCCAATGA		
<i>Gli-γ3a</i>	TGTATGTCCGACCTGACTGCTCCACCATCAACGCACCATTTGCCAGCATAGTCGCCGGCATCAGTGGACAATGA		
<i>Gli-γ4a</i>	TGTATGTCCGACCTGACTGCTCCACCATCAACGCACCATTTGCTAGCATAGTCGCCGGCATCAGTGGACAATGA		
<i>Gli-γ1b</i>	TGTATGTGCCACCTGACTGCTCCACCATCAACGTACCATATGCCAACATAGACGCTGGCATTTGGTGGCCAATGA		
<i>Gli-γ2b</i>	TGTATGTGCCACCTGACTGCTCCACCATCAACGTGCCATATGCCAGCATAGACGCTGTTCATTGGTGGCCAATGA		
<i>Gli-γ3b</i>	TGTATGTGCCACCTGAGTGCTCCATCATCAGGGCACCATTTTGCCAGCATAGTCGCCGGGATTGGTGGCCAATGA		
<i>Gli-γ4b*</i>	TGTATGTGCCACCTGAGTGCTCTATCATCAAGGCACCATTTGCCAGCATAGTCACCGGAATTGGTGGCCAATGA		
<i>Gli-γ5b</i>	TGTATGTGCCACCTTACTGCTCCACCATCAGGGCACCATTTTGCTAGCATAGTCGCCAGCATTTGGTGGCCAATGA		

(b)

1 100

Gli- δ 1a* ATGAAGATCTTCTTGGTCTTTGCCCTCCTCGTTGTATCAACGATCATCACCACCGCGACCGTGCAGCTCGACCCTAGCATCCATGTACAAGAAAGGCCAC

Gli- δ 1b* ATGAAGATCTTCTTGGTCTTTGCCCTCCTCGTTGTATCAACGACCATCACCACCGCGATCGTGCAGCTCGACCCTAGTGTCCATGTCCAAGAAAGGCCAC

Gli- δ 2a* ATGAAGATCTTCTTGGTCTTTGCCCTCCTGGTTGCCACAACGATCAGCACCACCGGCACCTGCAGCTCGACCCTAGCGTCCATGACTTAGAAAGGCCAC

101 200

Gli- δ 1a* AACAAATCATTTCACAGCAGCAACCACTTAATCAACAACAACCATTCCCCTGCAAGAGCCACAACAACCACTATTCCAGCAA-----

Gli- δ 1b* AACAAATCATTTCGAGCAGCAACCACTTACCAGCAACAACCATTCCCCTGCAAGAACCAACAACCACTATTCCCGCAA--AAAGAGCCACAACAACC

Gli- δ 2a* ACCAAATCATTTCACAAAGCAGCAGCACTTCCCCTGCTACAACCATTCCCCTGCAAGAGCCATTAACCA---TTTCCGTTG-----

201 300

Gli- δ 1a* -----CAACAACCGTATCCACAACAGTCACTTCCCACAACAACACTTCCCAGCAACATTATTTCCTAGCAA

Gli- δ 1b* ATTTTTGCTGCAGCAACCACAACCCAGGAACAACAACCATATCCACAACAGCCACTTCTCCAACAACAACACTTCCCAGCAACATCTATTCCCAGCAG

Gli- δ 2a* -----CAGCAACCACAACAAC---CTGCAACAACAACCACTTCCCACAACAACATCTATTTCCTAGCAAC

301 400

Gli- δ 1a* CCGCGCAACAACAATTTCCACAGCAGATGCCACTTCCGTATCAACAACAAATATTCCCCTCAACAACAACAC---CCCACAACAACAAC

Gli- δ 1b* CCACCAACAACAACAATTTCCGAGCAGATGCCACTTCCATATGAACAACAAATATTCCCCTTACAACAGCAACGGCAACCACAATTCCCAGCAACACAAC

Gli- δ 2a* CCGCCAACAACAACAATTTCCACAGCA-----ACAACAACATTTCCCCTCAACCTCATCAACA---ACCACAATTCCCGAACAACAAC

401 500

Gli- δ 1a* CATTTTACCAATATCAACAACCATTAAACAACAACCATAACCGCAAGAGCAACCATTGCCACAACAACAACCTTCTGTGGAGGAAAACAACAATTGAA

Gli- δ 1b* CATTTCCCAATATCAACAACCATTAAACAACAACCATAACCGCAAGAGCAACCATTGCCACAACAACAACCTTCTATGGAGGAAAACAACAATTGAA

Gli- δ 2a* CATTTTACCAATATCAACAACCATTAAACAACAACCATAACCGCAAGAGCAACCATTGGCAGCAACAACCTTGTGTAGAGGAAAACAACAAGACTGAA

501 600

Gli- δ 1a* CTGTGTGAAGGAGTTTCCTGCTGCAGCAGTGCAACCCGGAGGAGAACTGTGCTATTACTGCAGTCAGTGATCCCGTTCCTCCGACCAAGACCTCGCAACAG

Gli- δ 1b* CGTGTGTGAAGGAGTTTCCTCCTGCAACAGTGCAACCCGGAGGAGAACTGTGCTATTACTCCAGTCAGTGATCCCGTTCCTCCGACCAAGACCTCGCAACAG

Gli- δ 2a* CTGTGTGAAGGAATTTCCTCTGCAGCAGTGCAACCCGGAGGAGAAAGGTGTGCTACTCCATTCTGGTGATCCCGTTCCTCTGACCAAGACCTCGCAACAG

601 700

Gli- δ 1a* AACAACTGCCAGTTGAAGCGGCAACAATGTTGTGCAAACTTGACATATCAGCGAGCCGTCCGATGCCCGAACATCCACAACATTGTGCACGCCATCA

Gli- δ 1b* AATAGCTGCCAGTTGAAGCGTCTACAATGTTGTGCAAACTTGACATATCAATGAACCGTCCGATGCCCGGCCATCCACAACATTGTGCACGCCATCG

Gli- δ 2a* AATAGCTGCCAGTTGAAGCGACAAGAATGTTGTGCGCAAACTTGACATATCCGTGAGCAGTCTTGATGCCCGGCCATCCAAAGCCCTGTGTGATGCCATCA

701 800

Gli- δ 1a* TTATGCAACAACAACAACAACAACAACAACAACAACAACATGTGGATAGAGGTTTGTCCAGCCTCAACC-ACAACAGTTGGGCCAGGGAATGCCCATGC

Gli- δ 1b* TCGTTCAACAACAACA-----TGTGGATAGAGGTTTCCGCCAGCCTCAACC-ACAACAGTTGGGCCAGGGAATGCCCATGC

Gli- δ 2a* TTGTGCAACAACAACAACAACAACAACAACAACAACA-----GTTGGATAGAGGTTTCCGCCAGCCTCAACCACACAGTTGGGCCAGGGAATGCCCATGC

801 900

Gli- δ 1a* AGCCTCAACATCAATTGGGCCAGGGCTTAAGCCTACCTCAACAACCTAGCCCAGTTCAAGTTGGTTAGGTTACTTGTGATTTCAGACCTTGCCTATGTTATG

Gli- δ 1b* AGCCTCAATATCAATTGGGCCAGGGCTTTATCCTACCTCAACAACCTAGCCCAGTTCAAGTTGGTTAGGTTACTTGTGATTTCAGACCTTGCCTATGTTATG

Gli- δ 2a* AACCTCAATAGCCACTGGGCCAGGGCTTTATCCTACCTCAGCAACCTAGCCCAGTTTAAGTTGGTTAGGTTACTTGTGATTTCAGACCTTGCCTATGTTATG

901 979

Gli- δ 1a* CAATGTGCATGTCCCCTCTGATTGCTACACCATTAGTGCACCATTTGGTGGCATCACTGCCTACAACAGTGGACAATGA

Gli- δ 1b* CAACGTGCATGTCCCCTCTGATTGCTACACCATTAGTGCACCATTTGGTAGCATGACTGCCTTGAACGGTGGACAGTGA

Gli- δ 2a* CAACGTGCATGTCCCCTCTGATTGCTACACCATTAGTGCATATTTGGTAGCATGACTGCCTGCAGCTGTGGACAATGA