

Supplementary Fig. S4 Wheat *TaSINA* gene sequences from Kukri, RAC875, Drsydale and Gladius generated by Sanger sequencing using primers designed for TraesCS3B02G572900 of Chinese Spring RefSeq v2 and described in Supplementary Table 3. The fasta sequences include exons and introns.

>Kukri TaSINA (4,812-4,814..Start codon) (4,812-4,985..exon 1) (5,093-5,934...exon 2) (4,696-4,811..5' UTR)

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>RAC875 TaSINA (4,816-4,818..Start codon) (4,816-4,989..exon 1) (5,097-5,936..exon 2) (4,700-4,815..5' UTR)

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>Drysdale TaSINA (4,814-4,816..Start codon) (4,814-4,987..exon 1) (5,095-5,935..exon 2) (4,698-4,813..5'
UTR)

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TGCGCCCGGCGCTGACTTCCCCGTCGCCGCCACCCCTCCTCCCTGCCCGGCCACCATCCCGCCTTCTCGTCCG
TCCTCCGCCGGCTCCTCCGACA

>Gladius TaSINA (4,809-4,811..Start codon) (4,809-4,982..exon 1) (5,090-5,920..exon 2) (4,693-4,808..5'
UTR)

ATAATGAGTTATCACTCCCTATTTGGGTGAATCACAAAAGTTTAAATTAAGAACAATCCATTCCATCAAACCTTGGAT
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AGGCGTCGTCATCTCAACGACAACGACGACGACGACGCGCCGCCACCGCCACCGGTCCGCCATGGCGACGCCGG

Supplementary Fig. S5 Wheat *TaSINA* gene sequences retrieved from 10+Genome dataset (<https://wheat.pw.usda.gov/blastn>) using Chinese Spring TraesCS3B01G572900 gene as query. The fasta sequences include exons and introns.

>**Mace** TraesMAC3B01G633400.1 chr3B:822719144..822720339 (- strand) class=mRNA length=1196

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CAAGCTCGCCGTGGAGAGCGACGGCTGCAGGCTGACCCTGGAGTCGCCGCTGGTGTGCAGCAGCTCCCTGTCCG
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TCCACATCGAGAAGCTCCCGTTGCCCCGCTCCTCCTTAGGACCAGGAGTGCGCCGGCCTGTACCTCCCCGGT
CGCCGCCACGCTCCTCCTTGCCCGGCGGCCACCATCCCGCTTCCCGTCCGTCCTCCGCGGCTCCTCCGACAACG
TCGCAGTCAAGACGGTGATCACCGATCAGAGCTACAAGAAACGGAAGTCTGCCAACCCAAGGAAGCTGTAG
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ESPLVSSSLSGGLPGEVKCLPVPKDFLSGDSVPLSIHIEKLPVAPAPPLGPGVAPACTSPVAATPPPCPAATIPPSRPSSA
GSSDNVAVKTVITDQSYKKRKSANPRKL
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Blastn score: 2695.52 (2988), E value: 0, Identity: 1494/1494 (100%), Gaps: 0/1494 (0%), Strand: + / -

> **Longreach Lancer** TraesLAC3B01G635900.1 chr3B:812952783..812953978 (- strand) class=mRNA length=1196

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GCGGCTGCCCGGCGAGGTCAAGTGCTGCCGGTGCCCAAAGACTTTCTCTCCGGCGACAGTGTGCCCCCTCAGCA
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TCGCAGTCAAGACGGTGATCACCGATCAGAGCTACAAGAAACGGAAGTCTGCCAACCAAGGAAGCTGTAG

ESPLVCSSSLGGLPGEVKCLPVPKDFLSGDSVPLSIHIEKLPVAPAPPLGPGVAPACTSPVAATPPPCPAATIPPSRPSSA
GSSDNVAVKTVITDQSYKKRKSANPRKL

Blastn score: 2674.78 (2965), E value: 0, Identity: 1492/1498 (99.6%), Gaps: 4/1498 (0.3%), Strand: + / -

> **CDC Stanley** chr3B TraesSTA3B01G630200.1 chr3B:829890824..829892019 (- strand) class=mRNA
length=1196

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TCTGCTCCTCCTGCCGCGGCGCCACGCCGAGGCCTGCGGCGGCCGCGCCGCCGCTCCACTCCGCGCTCGCCGACAT
CTTCGCGGCCGCCGCCACCGTGCCCTGCGGCTACGAGCGCTACGGCTGCGACGCGGGCGGCGTGGTGTACCACG
AGGCGGCCGACCACGGCGCGCGTGCCAGCACGCGCCCTGCTGCTGCCCGGACCGCGCGGGCGCGGCCGGC
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ESPLVCSSSLGGLPGEVKCLPVPKDFLSGDSVPLSIHIEKLPVAPAPPLGPGVAPACTSPVAATPPPCPAATIPPSRPSSA
GSSDNVAVKTVITDQSYKKRKSANPRKLX

> **CDC Landmark** chr3B chr3B:821846270..821847465 (+ strand) class=mRNA length=1196

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GCGGCTGCCCGGCGAGGTCAAGTGCTGCCGTTGCCAAAGACTTTCTCTCCGGCGACAGTGTGCCCTCAGCA
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ESPLVCSSSLGGLPGEVKCLPVPKDFLSGDSVPLSIHIEKLPVAPAPPLGPGVAPACTSPVAATPPPCPAATIPPSRPSSA
GSSDNVAVKTVITDQSYKKRKSANPRKLX

Blastn score: 2695.52 (2988), E value: 0, Identity: 1494/1494 (100%), Gaps: 0/1494 (0%), Strand: + / +

> **PI190962 *Triticum aestivum ssp. spelta*** chr3B chr3B:807307688..807308883 (- strand) class=mRNA
length=1196

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ESPLVCSSSLGGLPGEVKCLPVPKDFLSGDSVPLSIHIEKLPAPPAPPLGPGVAPACTSPVAATPPPCPAATIPPSRPSSA
GSSDNVAVKTVITDQSYKKRKSANPRKLX

Blastn score: 2538.63 (2814), E value: 0, Identity: 1460/1493 (97.8%), Gaps: 3/1493 (0.2%), Strand: + / -

> **Norin 61** chr3B chr3B:823641574..823642769 (+ strand) class=mRNA length=1196

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ESPLVCSSSLGGLPGEVKCLPVPKDFLSGDSVPLSIHIEKLPAPPAPPLGPGVAPACTSPVAATPPPCPAATIPPSRPSSA
GSSDNVAVKTVITDQSYKKRKSANPRKLX

Blastn score: 2538.63 (2814), E value: 0, Identity: 1460/1493 (97.8%), Gaps: 3/1493 (0.2%), Strand: + / +

>**SY Mattis** TraesSYM3B01G629300.1 chr3B:808881627..808882822 (- strand) class=mRNA length=1196
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ESPLVCSSSLGGLPGEVKCLPVPKDFLSGDSVPLSIHIEKLPAPPAPPLGPGVAPACTSPVAATPPPCPAATIPPSRPSSA
GSSDNVAVKTVITDQSYKKRKSANPRKLX

Blastn score: 2538.63 (2814), E value: 0, Identity: 1460/1493 (97.8%), Gaps: 3/1493 (0.2%), Strand: + / -

>**Julius** TraesJUL3B01G636200.1 chr3B chr3B:830706300..830707495 (- strand) class=mRNA
length=1196

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GGCTGCCGGGCGAGGTCAAGTGCTGCCGGTGCCCAAAGACTTCTGTCCGGCGACAGTGTGCCCCTCAGCATC
CACATCGAGAAGCTCCCGGCTCCCCAGCTCCTCTAGGACCAGGAGTGGCGCCGGCCTGTACTTCCCCGGTGC
CCGCCACCCCTCCTCCCTGCCGGCGCCACCATCCCGCCTTCTCGTCCGTCTCCGCCGGCTCCTCCGACAACGTC
GCCGTTAAGACGGTGATCACCGATCAGAGCTACAAGAAACGGAAGTCCGCCAACCAAGGAAGCTGTAG

ESPLVCSSSLGGLPGEVKCLPVPKDFLSGDSVPLSIHIEKLPAPPAPPLGPGVAPACTSPVAATPPPCPAATIPPSRPSSA
GSSDNVAVKTVITDQSYKKRKSANPRKLX

Blastn score: 2538.63 (2814), E value: 0, Identity: 1460/1493 (97.8%), Gaps: 3/1493 (0.2%), Strand: + / -

>**Jagger** TraesJAG3B01G629200.1 chr3B chr3B:827852942..827854137 (+ strand) class=mRNA
length=1196

ATGGGCCTCGGCGGCGGCGGCGGAGAGGGGATCCTGGCCGTGGCCGTGGTGGCCATGGAGGCCATCCCCATGG
CGGAGCCGCAGATCCTCGCCGGCGGCAAGACCgTCGGCTGCGGGCGGACCTGCTCGACTGCCACAACCTGCCGC
TCCCCCTCAAGCCCCCATATTCAAGGTGAGATCCGCCGGCCGCCCTTCTCCAAGATTCATTTTTCCGTTTTCTT
GAATCTGGCACGGCGTGACCGAGCGTATCTGGTGTGCATGAATCTTGCCGGCAGTGCACGCCGAGCACCTGGT
CTGCTCCTCCTGCCGCGGCGCCACGCCGAGGCCTGCGGCGGCCGCGCCGCGCCGTCCACTCCGCGCTCGCCGACAT
CTTCGCGGCCGCCACCGTGCCCTGCGGCTACGAGCGCTACGGCTGCGACGCCGGCGGCGTGGTGTACCACGA
GGCCGCCGACCACCGGCGCGCGTGCAGCACGCGCCCTGCTGCTGCCGGACCGCGCGGGCGCGGCCGGCATCG
GGGGCTGCGGCTTCGTGGCTCCCGCCAGGACCTGCTCGACCACATCTCCGGCCCCGACCACTCGCGCCCCATCAT
CGTCGTCCGCTACGGCCAGCCGTGGAACCTCAGCCTGCCGCTCTCGCGCCGCTGGCACATCCTCGTCGGCGAGGA
GGACAAGGCGGTGGCCGCCGCCGGCGGGCGCCGACCGGCACCGCAACCTCTTCCTCGTCTCCCTCGGCGAGCGCG
GCGCCACCACGGCCGTGTCGCTGGTGTGCGTCCGGGCGGACGGCACGGCGCCGGGCGCGCCGAGTTCGCGTGC
AAGCTCGCCGTGGAGAGCGACGGCTGCAGGCTGACCCTGGAGTCGCCTCTGGTGTGCAGCAGCTCCCTGTCCGGC
GGCCTGCCGGGCGAGGTCAAGTGCTGCCGGTGCCCAAAGACTTCTGTCCGGCGACAGTGTGCCCCTCAGCATC
CACATCGAGAAGCTCCCGGCTCCCCAGCTCCTCTAGGACCAGGAGTGGCGCCGGCCTGTACTTCCCCGGTGC
CCGCCACCCCTCCTCCCTGCCGGCGCCACCATCCCGCCTTCTCGTCCGTCTCCGCCGGCTCCTCCGACAACGTC
GCCGTTAAGACGGTGATCACCGATCAGAGCTACAAGAAACGGAAGTCCGCCAACCAAGGAAGCTGTAG

LESPLVCSSSLGGLPGEVKCLPVPKDFLSGDSVPLSIHIEKLPAPPAPPLGPGVAPACTSPVAATPPPCPAATIPPSRPSSA
GSSDNVAVKTVITDQSYKKRKSANPRKL

Blastn score: 2538.63 (2814), E value: 0, Identity: 1460/1493 (97.8%), Gaps: 3/1493 (0.2%), Strand: + / +

>**Arina** TraesARI3B01G636300.1 chr3B chr3B:861871096..861872291 (- strand) class=mRNA
length=1196

ATGGGCCTCGGCGGCGGCGGCGGAGAGGGGATCCTGGCCGTGGCCGTGGTGGCCATGGAGGCCATCCCCATGG
CGGAGCCGCAGATCCTCGCCGGCGGCAAGACCgTCGGCTGCGGGCGGACCTGCTCGACTGCCACAACCTGCCGC
TCCCCCTCAAGCCCCCATATTCAAGGTGAGATCCGCCGGCCGCCCTTCTCCAAGATTCATTTTTCCGTTTTCT
TGAATCTGGCACGGCGTGACCGAGCGTATCTGGTGTGCATGAATCTTGCCGGCAGTGCACGCCGAGCACCTGG
TCTGCTCCTCCTGCCGCGGCGCCACGCCGAGGCCTGCGGCGGCCGCGCCGCGCCGTCCACTCCGCGCTCGCCGACAT

CTTCGCGGCCGCGCCACCGTGCCCTGCGGCTACGAGCGCTACGGCTGCGACGCCGGCGGGCGTGGTGTACCACGA
GGCCGCCGACCACCGGCGCGCTGCCAGCACGCGCCCTGCTGCTGCCCGGACCGCGCGGGCGCGGCCGGCATCG
GGGGCTGCGGCTTCGTTCGGCTCCCGCCAGGACCTGCTCGACCACATCTCCGGCCCCGACCACTCGCGCCCCATCAT
CGTCGTCCGCTACGGCCAGCCGTGGAACCTCAGCCTGCCGCTCTCGCGCCGCTGGCACATCCTCGTCGGCGAGGA
GGACAAGGCGGTGGCCGCCCGCGGGCGCCGACCGGCACCGCAACCTTCTCCTCGTCTCCCTCGGCGAGCGCG
GCGCCACCACGGCCGTGTCGCTGGTGTGCGTCCGGGCGGACGGCACGGCGCCGGGCGCGCCGAGTTCGCGTGC
AAGCTCGCCGTGGAGAGCGACGGCTGCAGGCTGACCCTGGAGTCGCCTCTGGTGTGCAGCAGCTCCCTGTCCGGC
GGCCTGCCGGGCGAGGTCAAGTGCCTGCCGGTGCCCAAAGACTTCTGTCCGGCGACAGTGTGCCCTCAGCATC
CACATCGAGAAGCTCCCGGCTCCCCAGCTCCTCCTTAGGACCAGGAGTGGCGCCGGCCTGTACTTCCCCGGTGC
CCGCCACCCCTCCTCCCTGCCCGGCCGCCACCATCCCGCCTTCTCGTCCGTCTCCGCCGGCTCCTCCGACAACGTC
GCCGTTAAGACGGTGATCACCGATCAGAGCTACAAGAAACGGAAGTCCGCCAACCCAAGGAAGCTGTAG

ESPLVCSSSLGGLPGEVKCLPVPKDFLSGDSVPLSIHIEKLPAPPAPPLGPGVAPACTSPVAATPPPCPAATIPPSRPSSA
GSSDNVAVKTVITDQSYKKRKSANPRKL

Blastn score: 2538.63 (2814), E value: 0, Identity: 1460/1493 (97.8%), Gaps: 3/1493 (0.2%), Strand: + / -