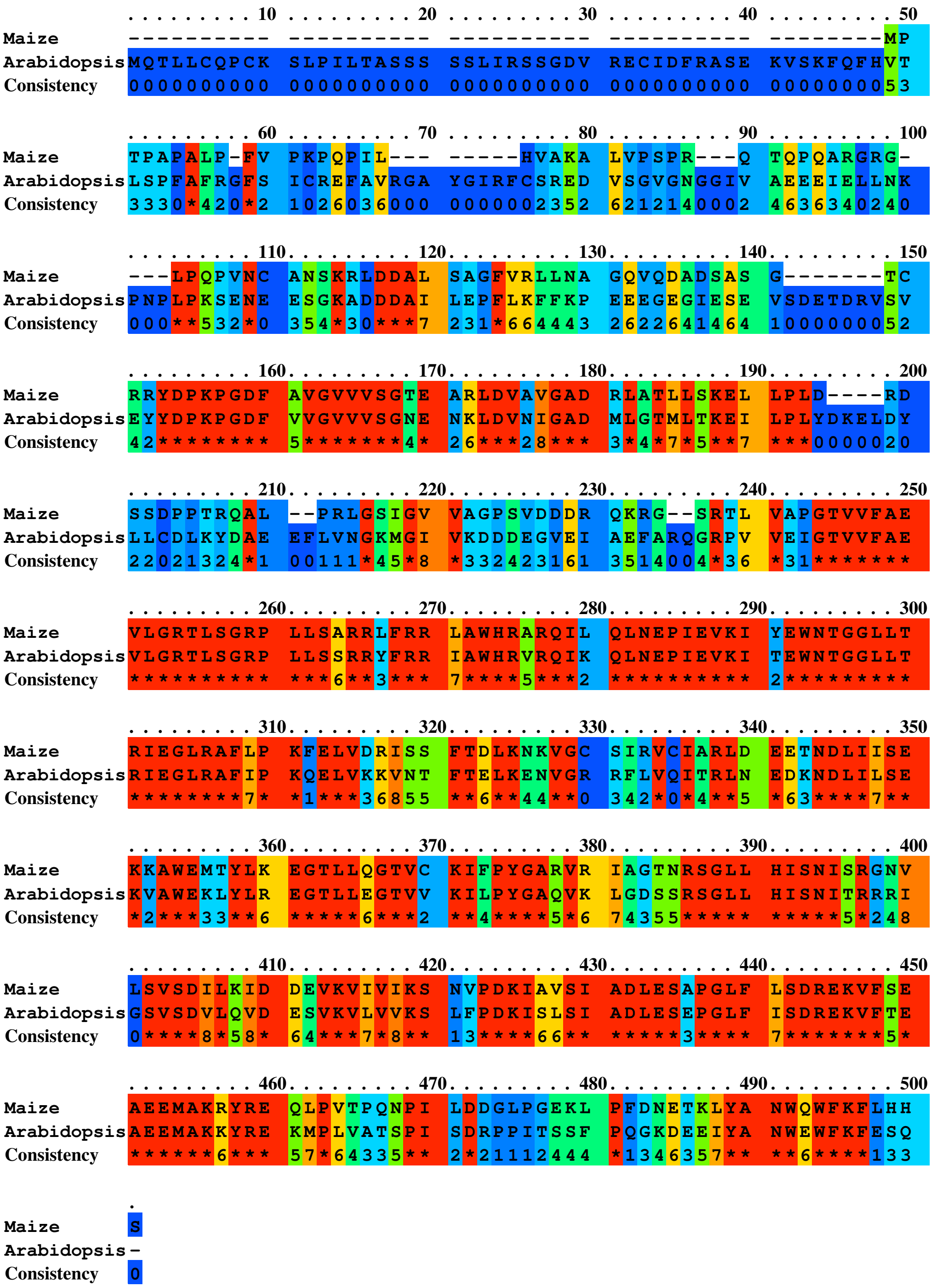
Additional File 2: Figure S2

Results colour-coded for amino acid conservation

The current colourscheme of the alignment is for **amino acid conservation**.

The conservation scoring is performed by PRALINE. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most co
The colour assignments are:

Unconserved 0 1 2 3 4 5 6 7 8 9 10 **Conserved**



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            .........10 .........20 .........30 .........40 .........50
Maize       ---------- ---------- ---------- ---------- ---------MP
Arabidopsis MQTLLCQPCK SLPILTASSS SSLIRSSGDV RECIDFRASE KVSKFQFHVT
Consistency 0000000000 0000000000 0000000000 0000000000 0000000053

            .........60 .........70 .........80 .........90 .........100
Maize       TPAPALP-FV PKPQPIL--- -----HVAKA LVPSPR---Q TQPQARGRG-
Arabidopsis LSPFAFRGFS ICREFAVRGA YGIRFCSRED VSGVGNGGIV AEEEIELLNK
Consistency 3330*420*2 1026036000 0000002352 6212140002 4636340240

            .........110.........120.........130.........140.........150
Maize       ---LPQPVNC ANSKRLDDAL SAGFVRLLNA GQVQDADSAS G-------TC
Arabidopsis PNPLPKSENE ESGKADDDAI LEPFLKFFKP EEEGEGIESE VSDETDRVSV
Consistency 000**532*0 354*30***7 231*664443 2622641464 1000000052

            .........160.........170.........180.........190.........200
Maize       RRYDPKPGDF AVGVVVSGTE ARLDVAVGAD RLATLLSKEL LPLD----RD
Arabidopsis EYYDPKPGDF VVGVVVSGNE NKLDVNIGAD MLGTMLTKEI LPLYDKELDY
Consistency 42******** 5*******4* 26***28*** 3*4*7*5**7 ***0000020

            .........210.........220.........230.........240.........250
Maize       SSDPPTRQAL --PRLGSIGV VAGPSVDDDR QKRG--SRTL VAPGTVVFAE
Arabidopsis LLCDLKYDAE EFLVNGKMGI VKDDDEGVEI AEFARQGRPV VEIGTVVFAE
Consistency 2202132 4*1 00111*45*8 *332423161 3514004*36 *31*******

            .........260.........270.........280.........290.........300
Maize       VLGRTLSGRP LLSARRLFRR LAWHRARQIL QLNEPIEVKI YEWNTGGLLT
Arabidopsis VLGRTLSGRP LLSSRRYFRR IAWHRVRQIK QLNEPIEVKI TEWNTGGLLT
Consistency ********** ***6**3*** 7****5***2 ********** 2*********

            .........310.........320.........330.........340.........350
Maize       RIEGLRAFLP KFELVDRISS FTDLKNKVGC SIRVCIARLD EETNDLIISE
Arabidopsis RIEGLRAFIP KQELVKKVNT FTELKENVGR RFLVQITRLN EDKNDLILSE
Consistency ********7* *1***36855 **6**44**0 342*0*4**5 *63****7**

            .........360.........370.........380.........390.........400
Maize       KKAWEMTYLK EGTLLQGTVC KIFPYGARVR IAGTNRSGLL HISNISRGNV
Arabidopsis KVAWEKLYLR EGTLLEGTVV KILPYGAQVK LGDSSRSGLL HISNITRRRI
Consistency *2***33**6 *****6***2 **4****5*6 74355***** *****5*248

            .........410.........420.........430.........440.........450
Maize       LSVSDILKID DEVKVIVIKS NVPDKIAVSI ADLESAPGLF LSDREKVFSE
Arabidopsis GSVSDVLQVD ESVKVLVVKS LFPDKISLSI ADLESEPGLF ISDREKVFTE
Consistency 0****8*58* 64***7*8** 13****66** *****3**** 7*******5*

            .........460.........470.........480.........490.........500
Maize       AEEMAKRYRE QLPVTPQNPI LDDGLPGEKL PFDNETKLYA NWQWFKFLHH
Arabidopsis AEEMAKKYRE KMPLVATSPI SDRPPITSSF PQGKDEEIYA NWEWFKFESQ
Consistency ******6*** 57*64335** 2*21112444 *1346357** **6****133

            .
Maize       S
Arabidopsis -
Consistency 0
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