Figure S1 – UPGMA tree for ASB1 orthologs

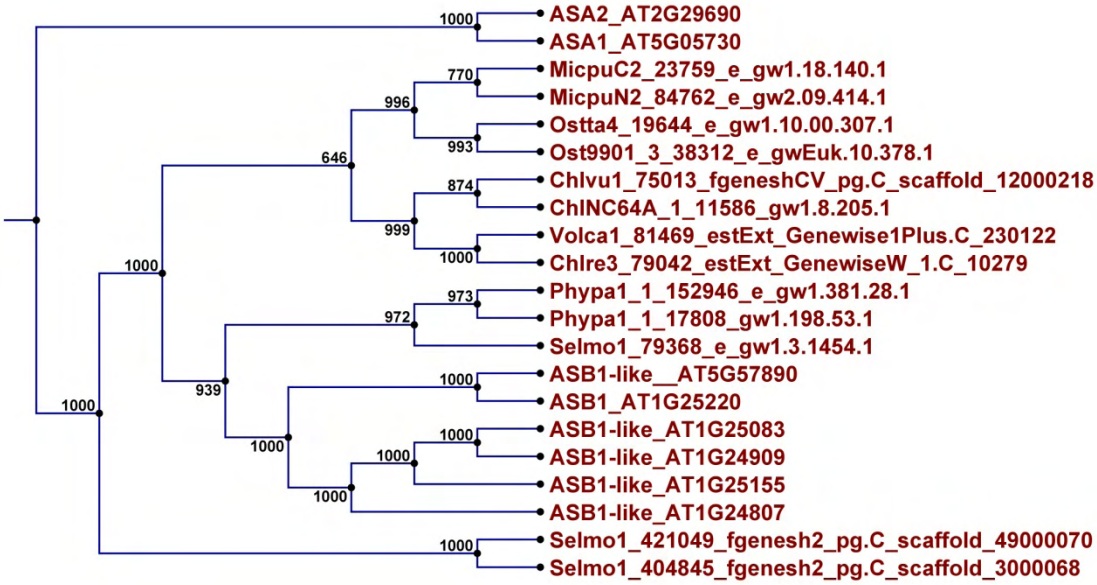


Figure S2 – UPGMA tree for ASA1-ASA2 orthologs

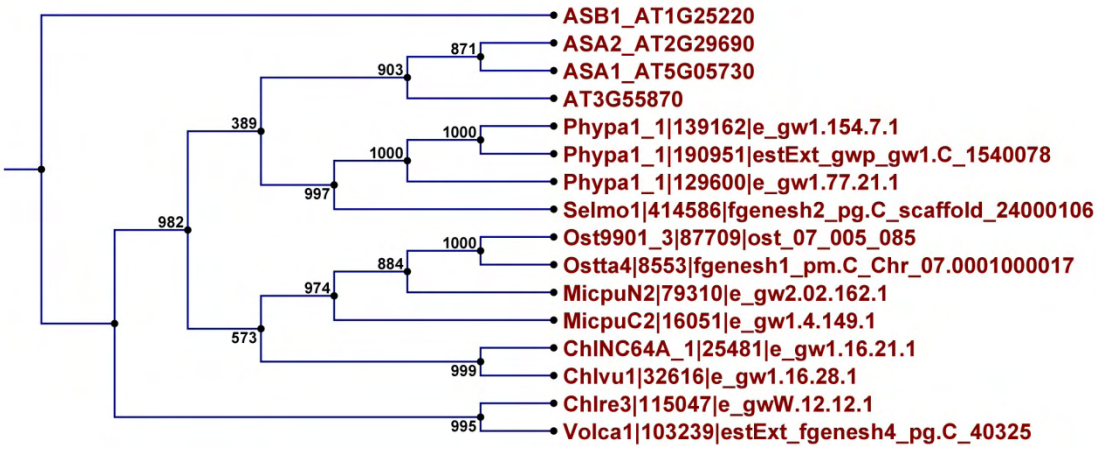


Figure S3 – UPGMA tree for PAT1 orthologs

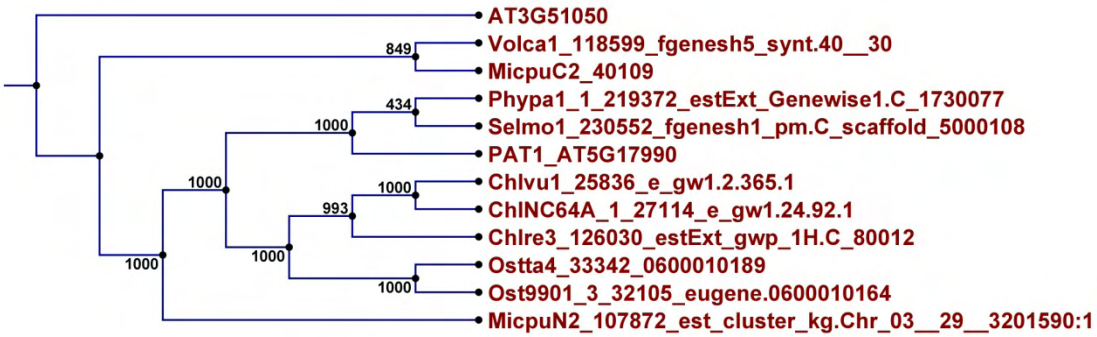


Figure S4 – UPGMA tree for PAI1,2,3 orthologs

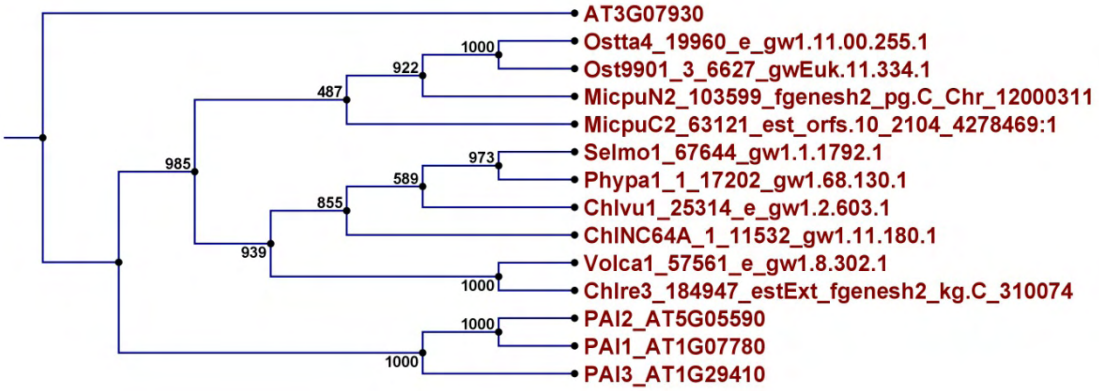


Figure S5 – UPGMA tree for IGPS orthologs

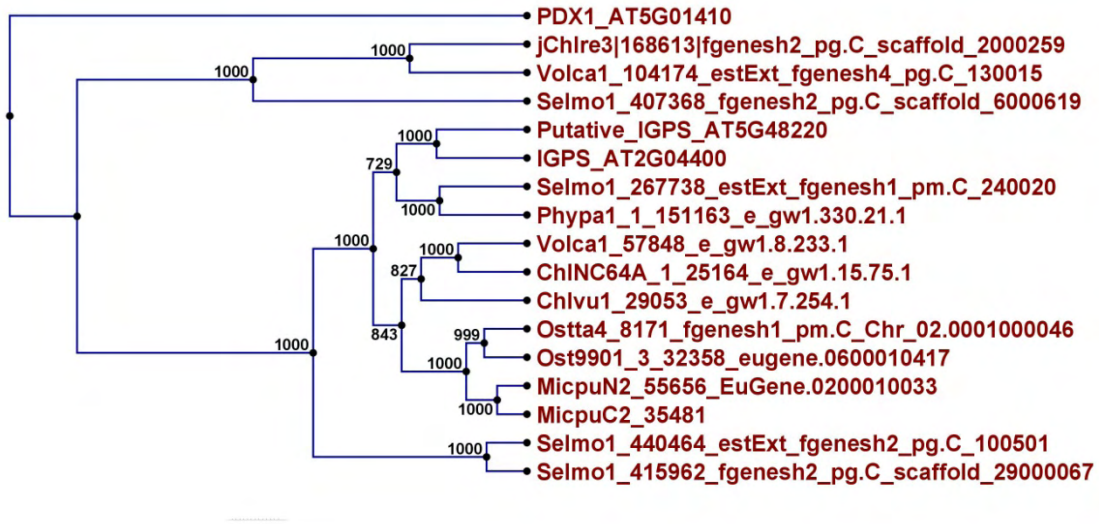


Figure S6 – UPGMA tree for TSA1 orthologs

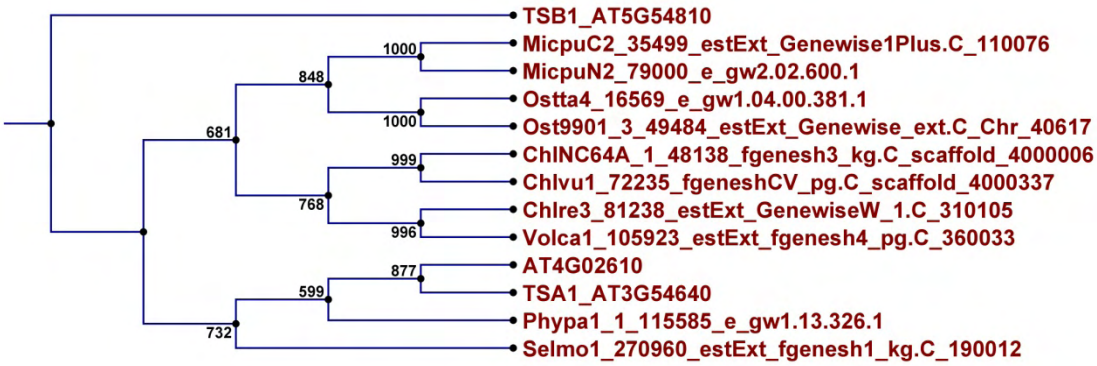


Figure S7 – UPGMA tree for TSB1-TSB2 orthologs

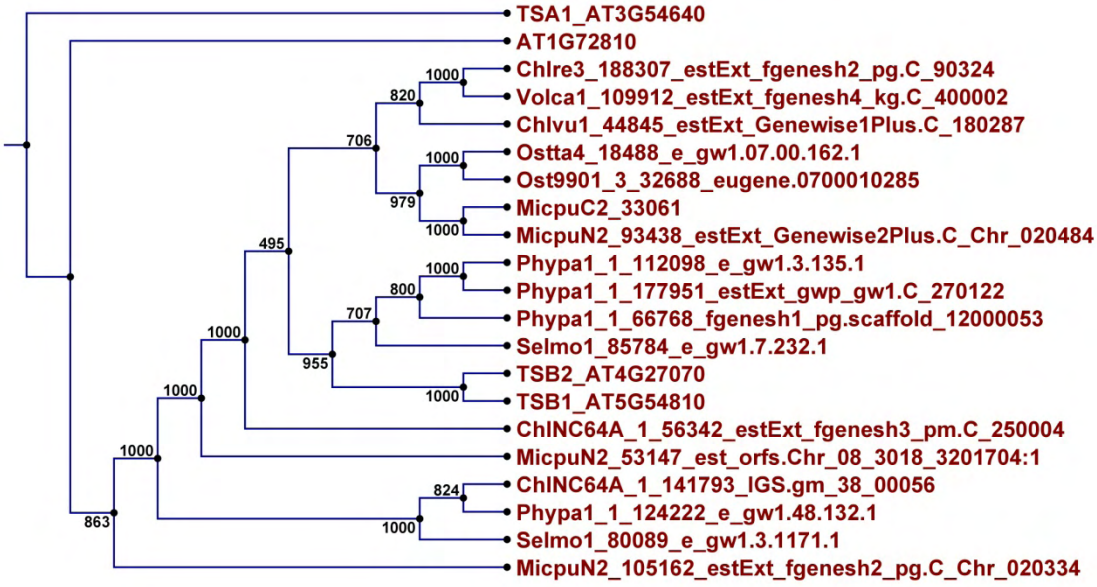


Figure S8 – UPGMA tree for TAA1-TAR1-TAR2-TAR3-TAR4 orthologs

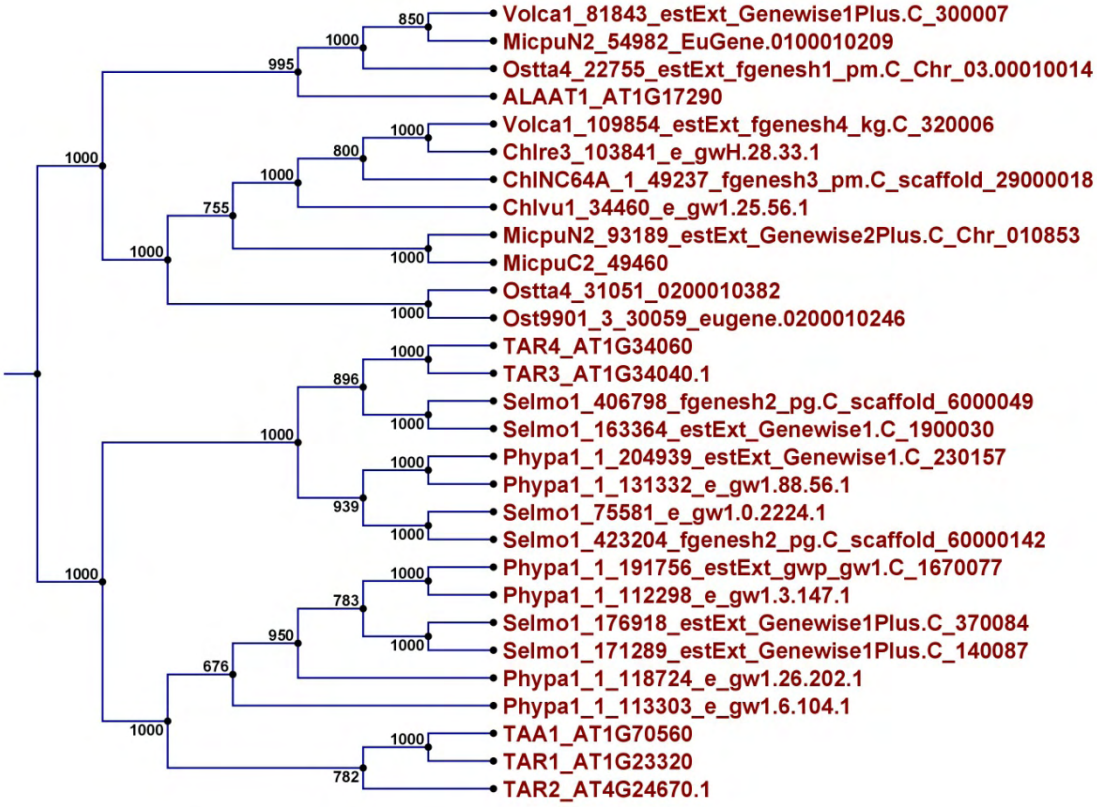


Figure S9 – UPGMA tree for SUR1 orthologs

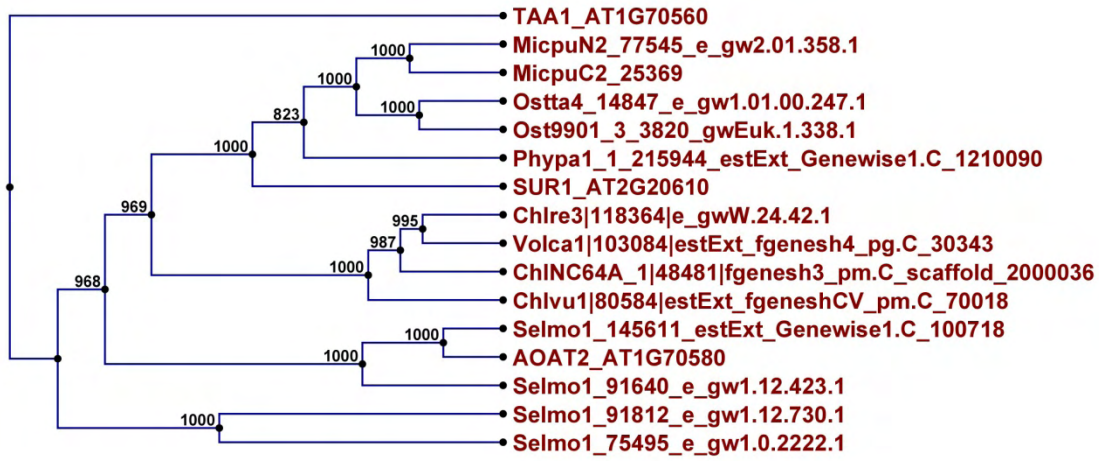


Figure S10 – UPGMA tree for UGT74B1 and UGT84B1

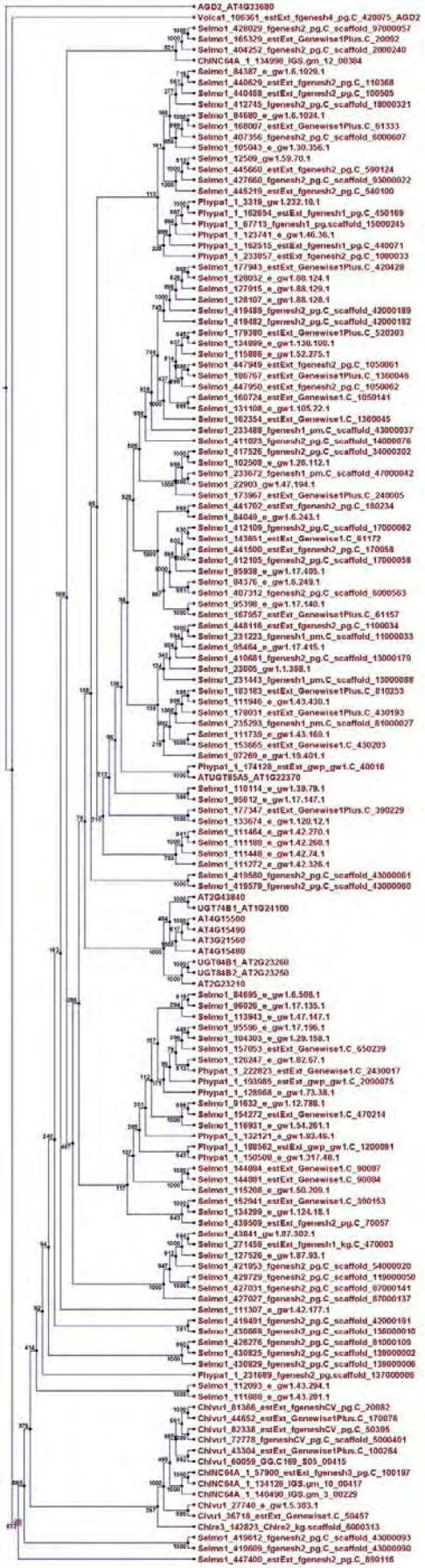


Figure S11 – UPGMA tree for ST5A orthologs

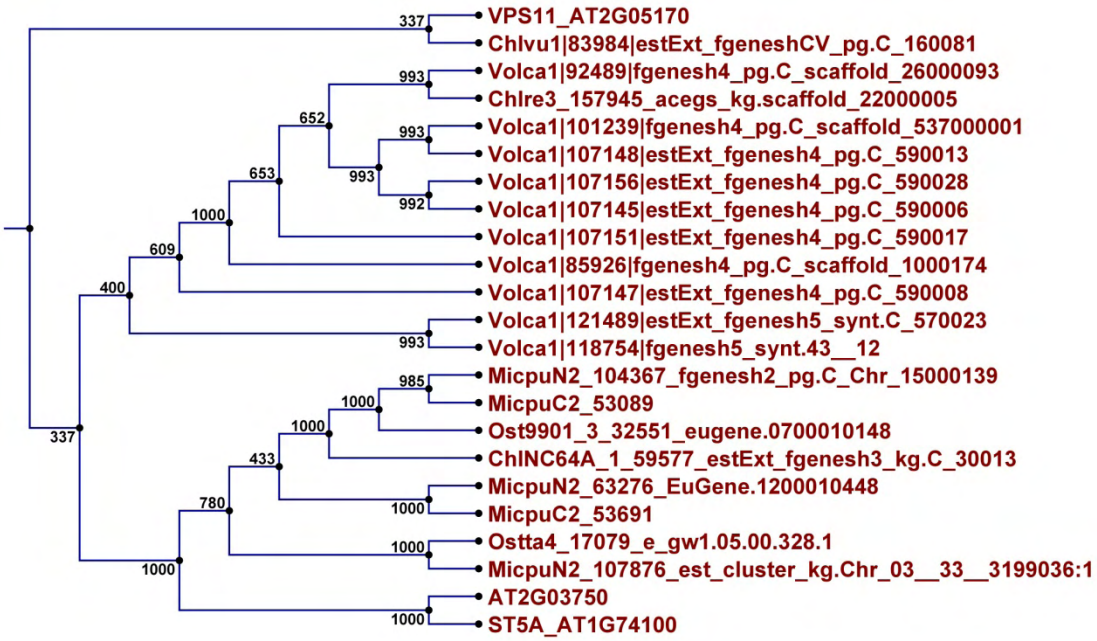


Figure S12 – UPGMA tree for TGG1-TGG2 orthologs

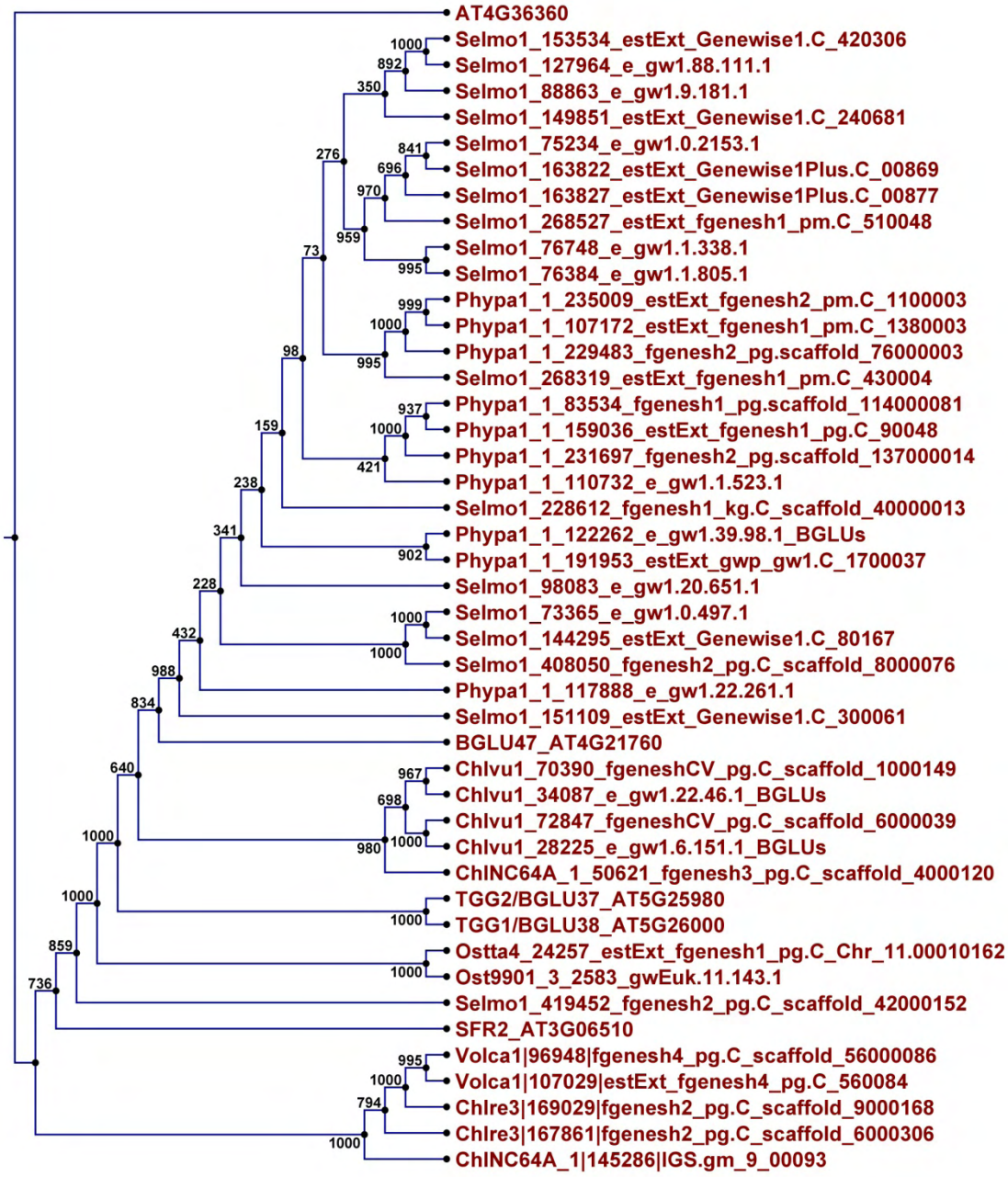


Figure S13 – UPGMA tree for ESP orthologs

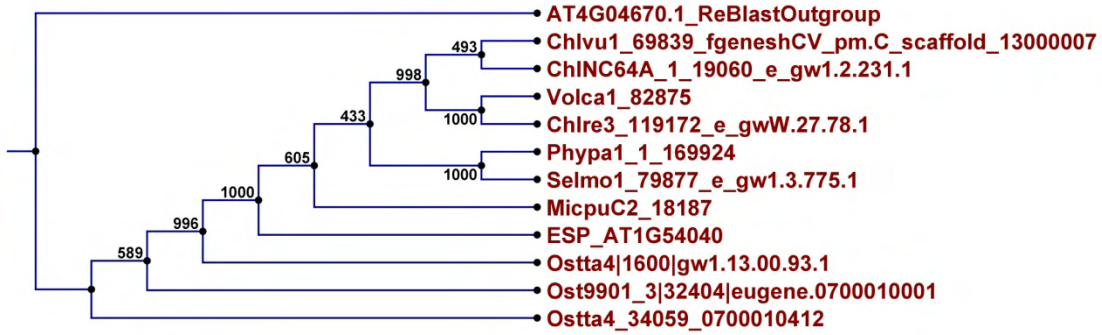


Figure S14 – UPGMA tree for ESM1 orthologs

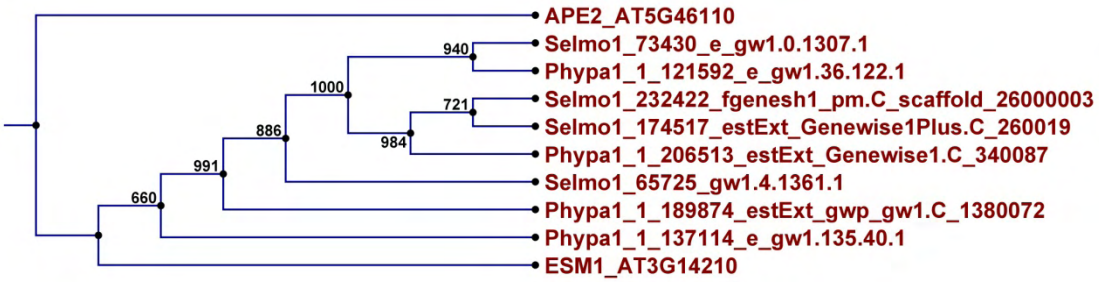


Figure S15 – UPGMA tree for YUCCA orthologs

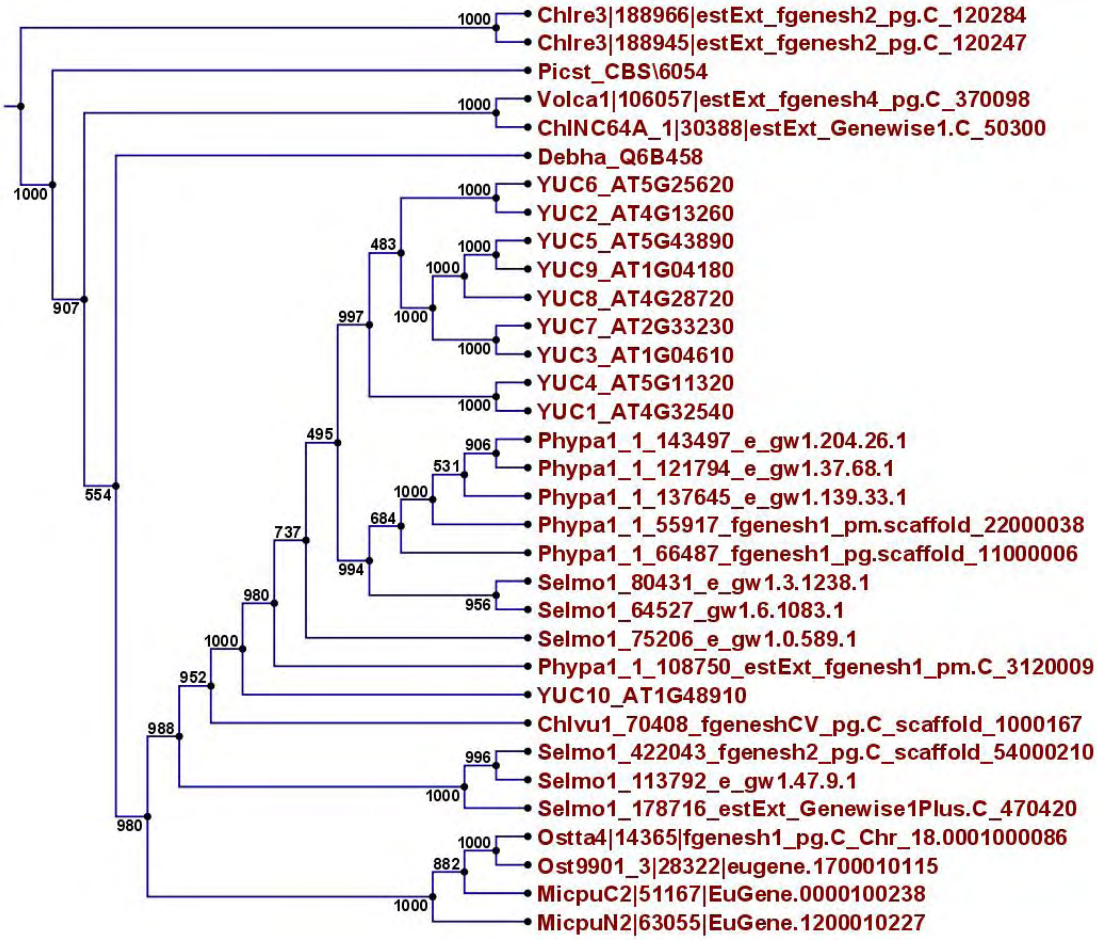


Figure S16 – UPGMA tree for AMI1 orthologs

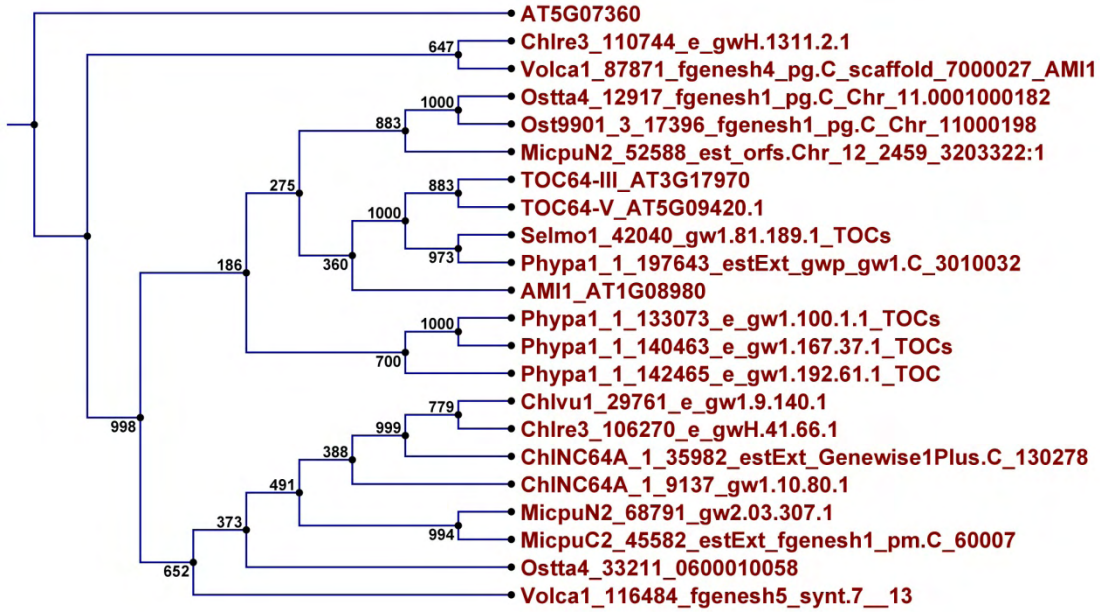


Figure S17 – UPGMA tree for NITRILASES orthologs

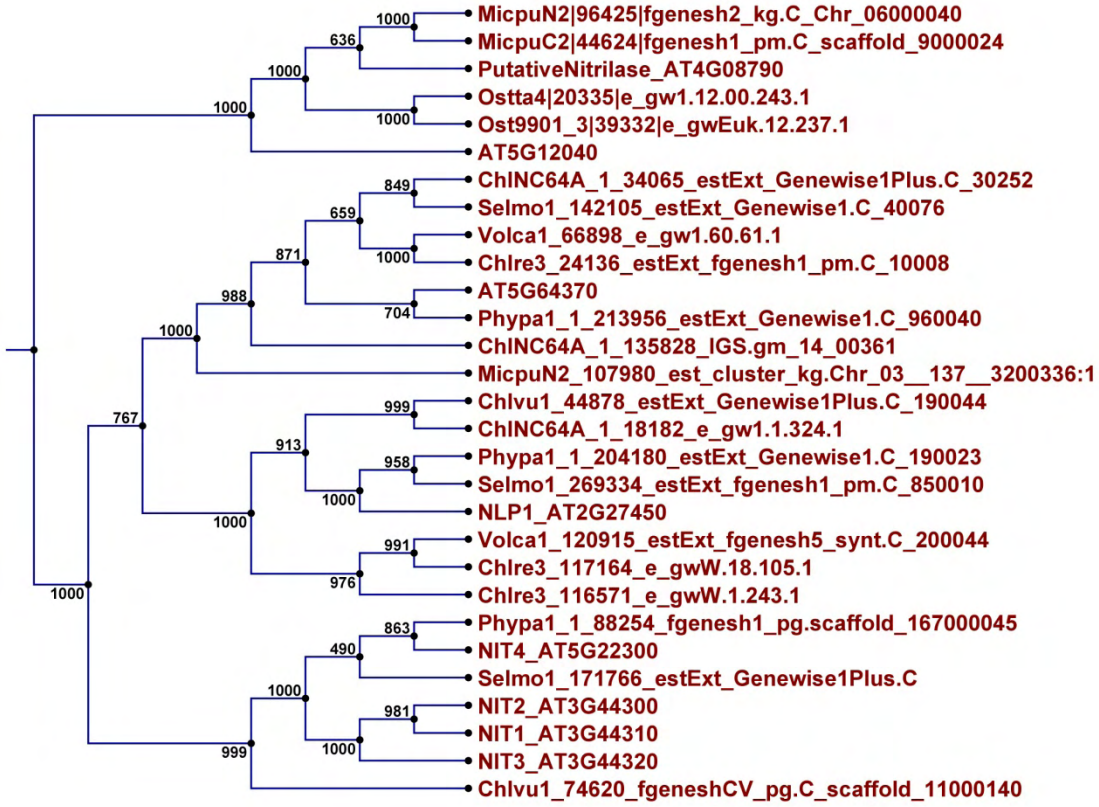


Figure S18 – UPGMA tree for ILL1-6-ILR1-IAR3 orthologs

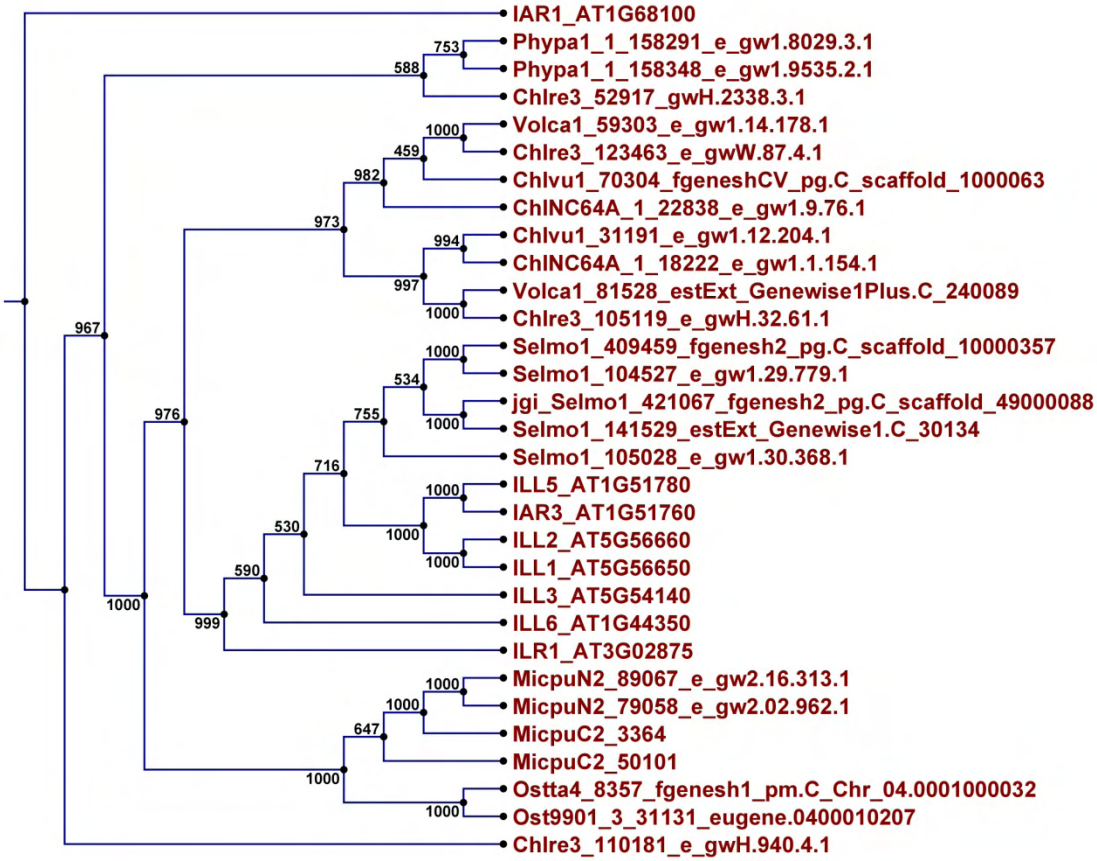


Figure S19 – UPGMA tree for GH3s

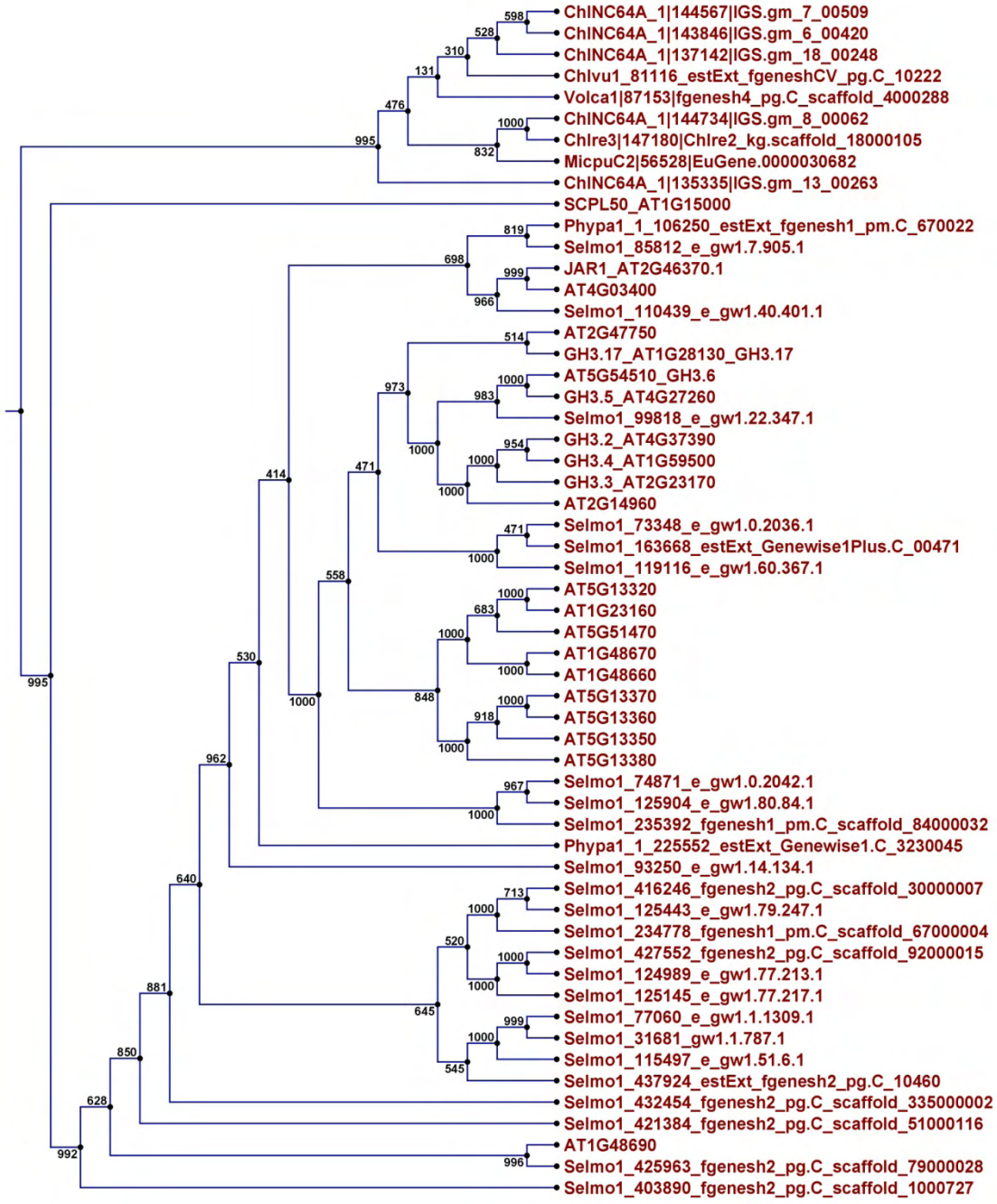


Figure S20 – UPGMA tree for IAR4 orthologs

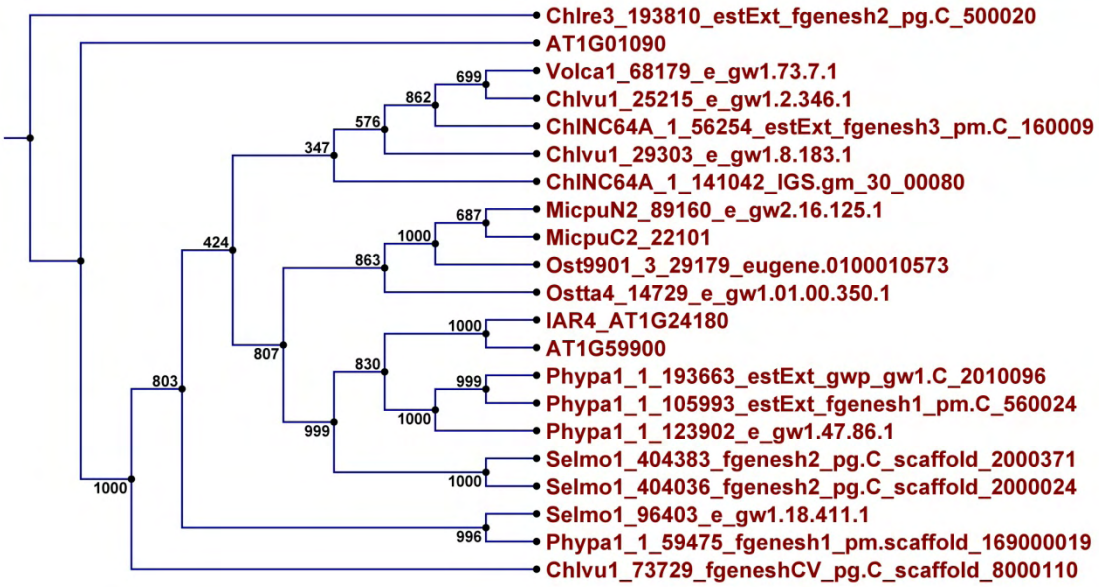


Figure S21 – UPGMA tree for IAMT1 orthologs

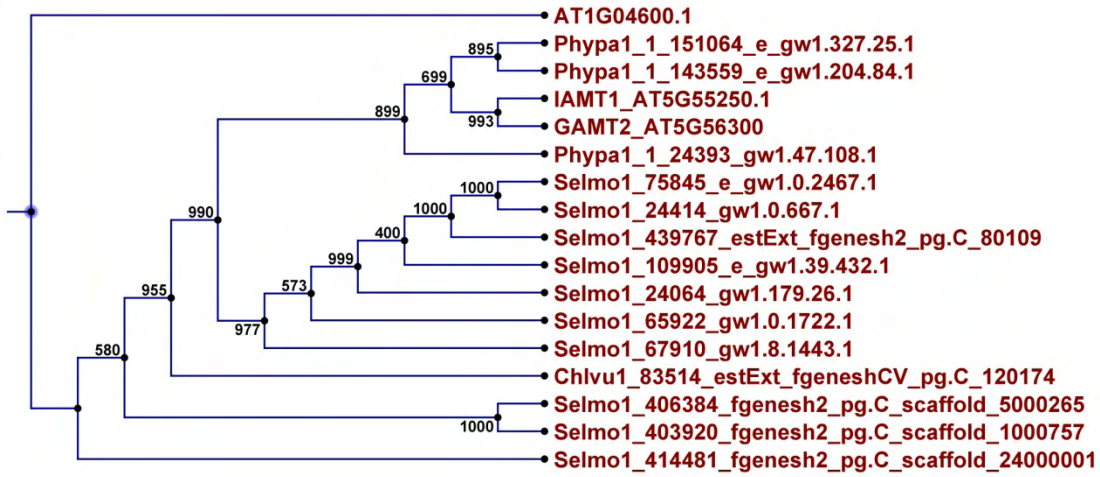
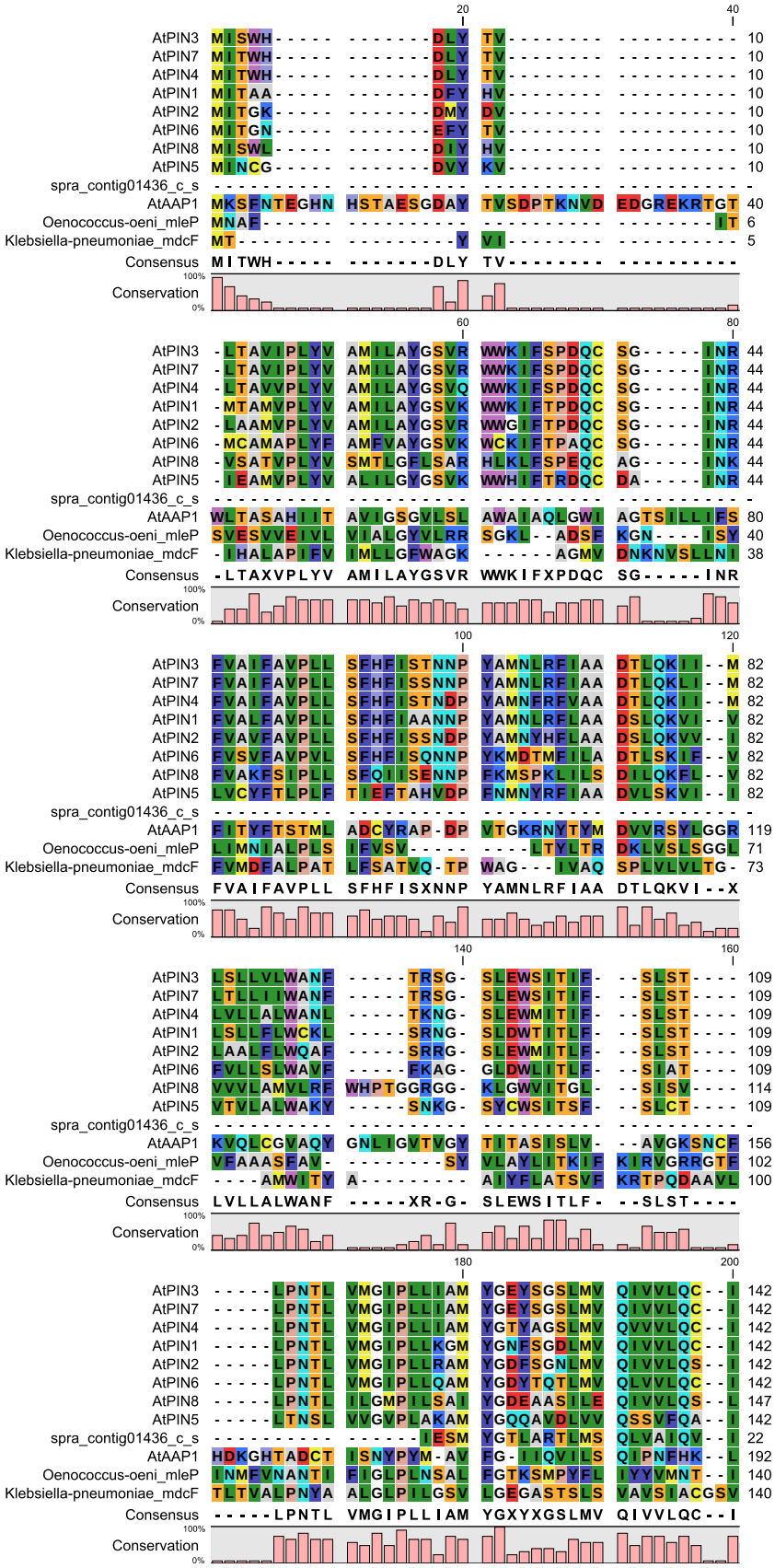
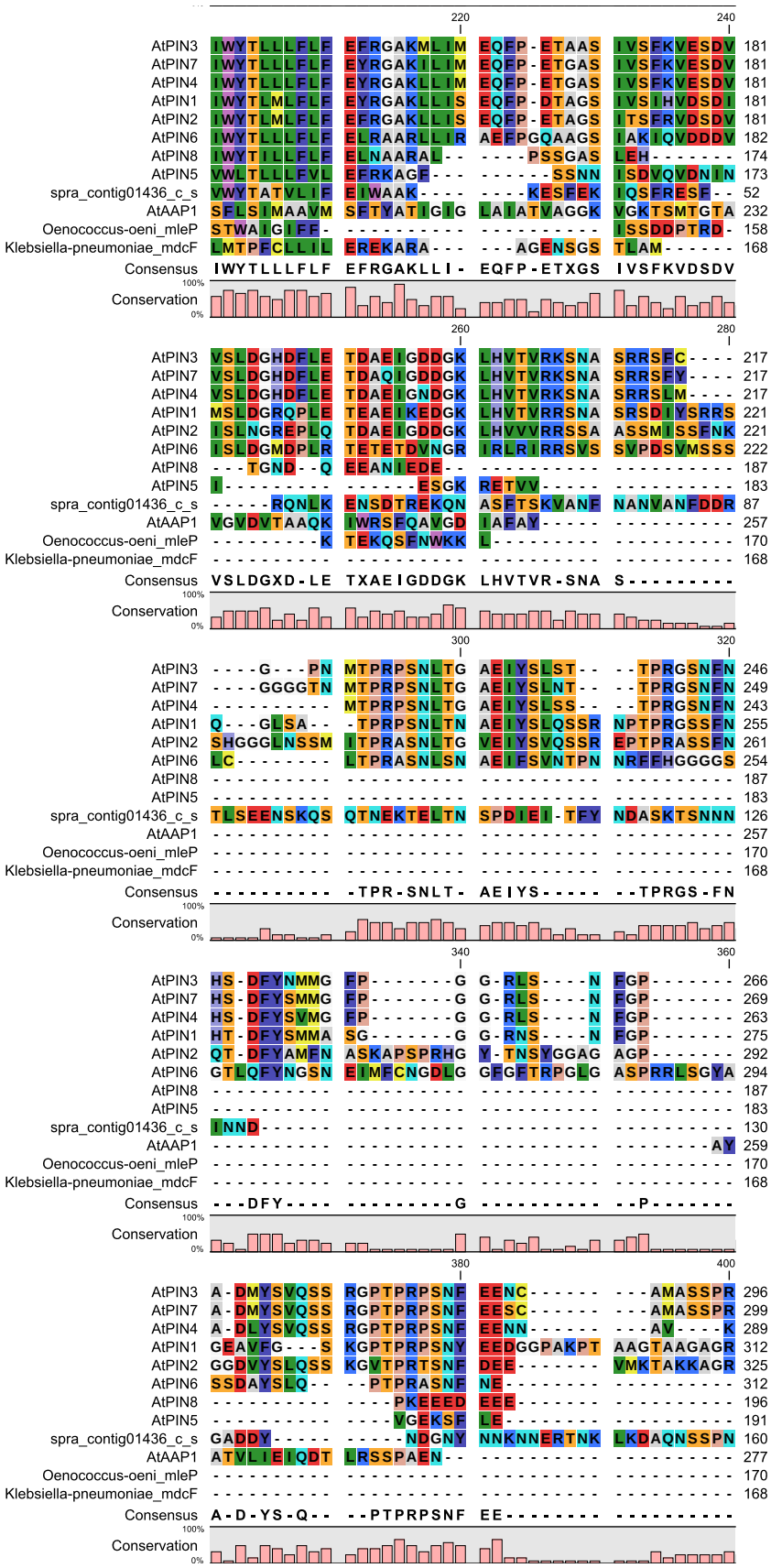
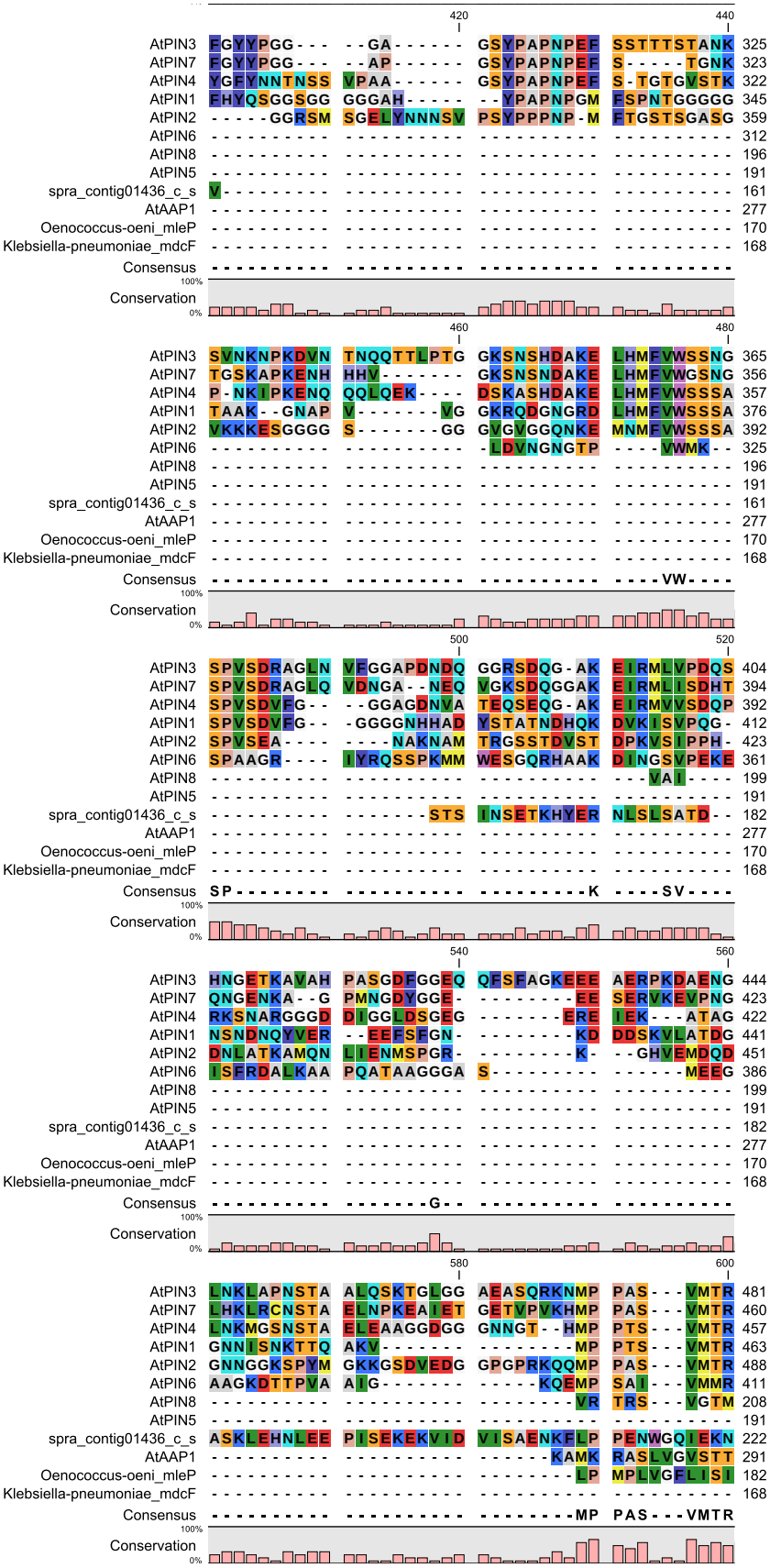
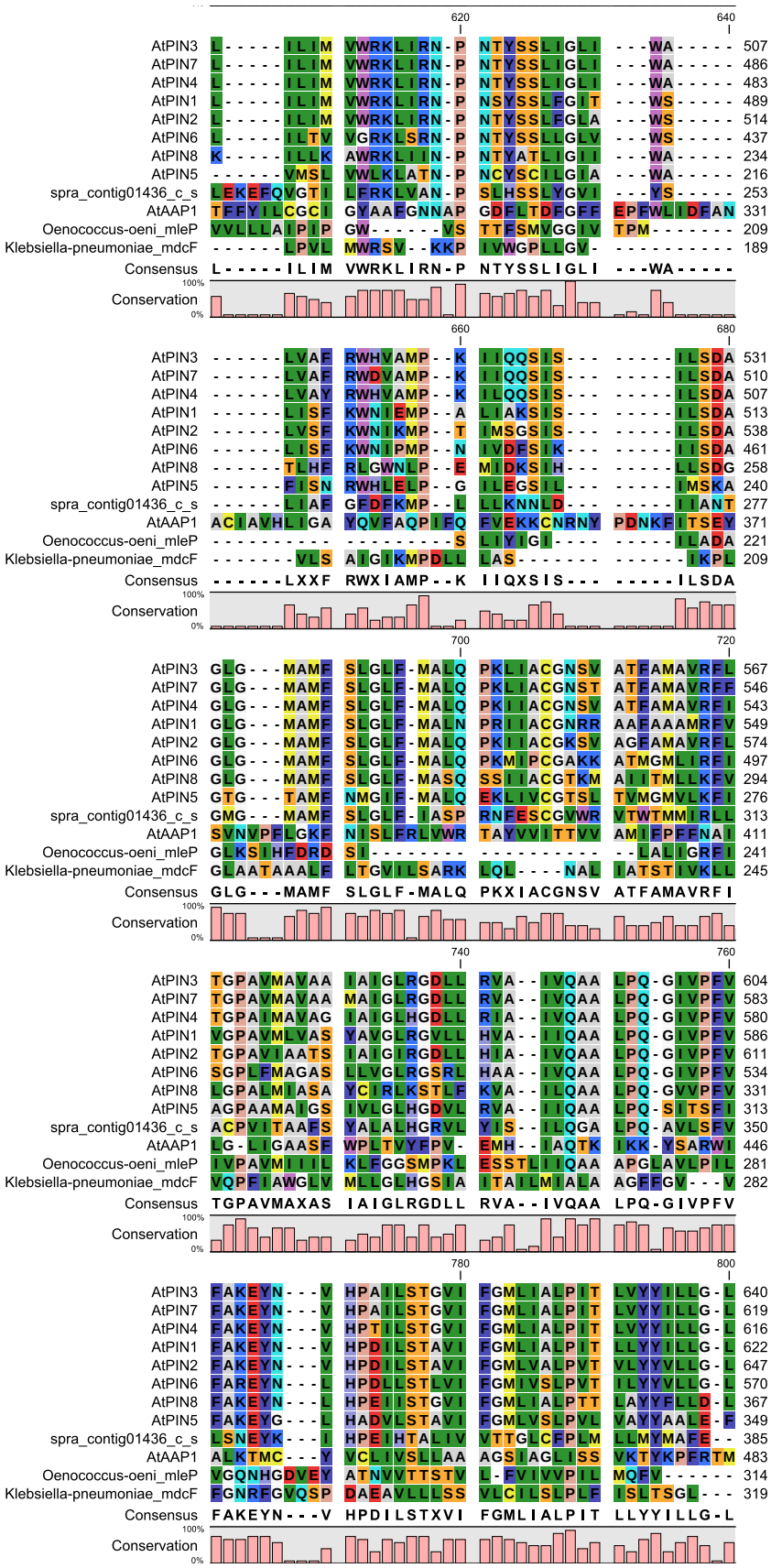


Figure S22 – Alignment of AtPIN proteins and putative orthologs


AtPIN3
AtPIN7
AtPIN4
AtPIN1
AtPIN2
AtPIN6
AtPIN8
AtPIN5
spra_contig01436_c_s
AtAAP1
Oenococcus-oeni_mleP
Klebsiella-pneumoniae_mdcF
Consensus
Conservation
100%
0%


220
240
AtPIN3 IWYTLLLFLF EFRGAKMLIM EQFP-ETAAS IVSFKVESDV 181
AtPIN7 IWYTLLLFLF EYRGAKILIM EQFP-ETGAS IVSFKVESDV 181
AtPIN4 IWYTLLLFLF EYRGAKLLIM EQFP-ETGAS IVSFKVESDV 181
AtPIN1 IWYTLMLFLF EYRGAKLLIS EQFP-DTAGS IVSIHVDSDI 181
AtPIN2 IWYTLMLFLF EFRGAKLLIS EQFP-ETAGS ITSFRVDSDV 181
AtPIN6 IWYTLLLFLF ELRAARLLIR AEFPGQAAGS IAKIQVDDDV 182
AtPIN8 IWYTILLFLF ELNAARAL--- ----PSSGAS LEH------- 174
AtPIN5 VWLTLLLFVL EFRKAGF--- ------SSNN ISDVQVDNIN 173
spra_contig01436_c_s VWYTATVLIF EIWAAK---- ----KESFEK IQSFRESF-- 52
AtAAP1 SFLSIMAAVM SFTYATIGIG LAIATVAGGK VGKTSMTGTA 232
Oenococcus-oeni_mleP STWAIGIFF- ---------- ---------- ISSDDPTRD- 158
Klebsiella-pneumoniae_mdcF LMTPFCLLIL EREKARA--- ---AGENSGS TLAM------ 168
Consensus IWYTLLLFLF EFRGAKLLI- EQFP-ETXGS IVSFKVDSDV
100%
Conservation
0%
260
280
AtPIN3 VSLDGHDFLE TDAEIGDDGK LHVTVRKSNA SRRSFC---- 217
AtPIN7 VSLDGHDFLE TDAQIGDDGK LHVTVRKSNA SRRSFY---- 217
AtPIN4 VSLDGHDFLE TDAEIGNDGK LHVTVRKSNA SRRSLM---- 217
AtPIN1 MSLDGRQPLE TEAEIKEDGK LHVTVRRSNA SRSDIYSRRS 221
AtPIN2 ISLNGREPLQ TDAEIGDDGK LHVVVRRSSA ASSMISSFNK 221
AtPIN6 ISLDGMDPLR TETETDVNGR IRLRIRRSVS SVPDSVMSSS 222
AtPIN8 ---TGND--Q EEANIEDE-- ---------- ---------- 187
AtPIN5 I--------- ------ESGK RETVV----- ---------- 183
spra_contig01436_c_s -----RQNLK ENSDTREKQN ASFTSKVANF NANVANFDDR 87
AtAAP1 VGVDVTAAQK IWRSFQAVGD IAFAY----- ---------- 257
Oenococcus-oeni_mleP ---------K TEKQSFNWKK L--------- ---------- 170
Klebsiella-pneumoniae_mdcF ---------- ---------- ---------- ---------- 168
Consensus VSLDGXD-LE TXAEIGDDGK LHVTVR-SNA S---------
100%
Conservation
0%
300
320
AtPIN3 ----G---PN MTPRPSNLTG AEIYSLST-- --TPRGSNFN 246
AtPIN7 ----GGGGTN MTPRPSNLTG AEIYSLNT-- --TPRGSNFN 249
AtPIN4 ---------- MTPRPSNLTG AEIYSLSS-- --TPRGSNFN 243
AtPIN1 Q---GLSA-- -TPRPSNLTN AEIYSLQSSR NPTPRGSSFN 255
AtPIN2 SHGGGLNSSM ITPRASNLTG VEIYSVQSSR EPTPRASSFN 261
AtPIN6 LC-------- LTPRASNLSN AEIFSVNTPN NRFFHGGGGS 254
AtPIN8 ---------- ---------- ---------- ---------- 187
AtPIN5 ---------- ---------- ---------- ---------- 183
spra_contig01436_c_s TLSEENSKQS QTNEKTELTN SPDIEI-TFY NDASKTSNNN 126
AtAAP1 ---------- ---------- ---------- ---------- 257
Oenococcus-oeni_mleP ---------- ---------- ---------- ---------- 170
Klebsiella-pneumoniae_mdcF ---------- ---------- ---------- ---------- 168
Consensus ----------TPR-SNLT- AEIYS----- --TPRGS-FN
100%
Conservation
0%
340
360
AtPIN3 HS-DFYNMMG FP-------G G-RLS----N FGP------- 266
AtPIN7 HS-DFYSMMG FP-------G G-RLS----N FGP------- 269
AtPIN4 HS-DFYSVMG FP-------G G-RLS----N FGP------- 263
AtPIN1 HT-DFYSMMA SG-------G G-RNS----N FGP------- 275
AtPIN2 QT-DFYAMFN ASKAPSPRHG Y-TNSYGGAG AGP------- 292
AtPIN6 GTLQFYNGSN EIMFCNGDLG GFGFTRPGLG ASPRRLSGYA 294
AtPIN8 ---------- ---------- ---------- ---------- 187
AtPIN5 ---------- ---------- ---------- ---------- 183
spra_contig01436_c_s INND------ ---------- ---------- ---------- 130
AtAAP1 ---------- ---------- ---------- --------AY 259
Oenococcus-oeni_mleP ---------- ---------- ---------- ---------- 170
Klebsiella-pneumoniae_mdcF ---------- ---------- ---------- ---------- 168
Consensus ---DFY---- ----------G ---------- --P-------
100%
Conservation
0%
380
400
AtPIN3 A-DMYSVQSS RGPTPRPSNF EENC------ ---AMASSPR 296
AtPIN7 A-DMYSVQSS RGPTPRPSNF EESC------ ---AMASSPR 299
AtPIN4 A-DLYSVQSS RGPTPRPSNF EENN------ ---AV----K 289
AtPIN1 GEAVFG---S KGPTPRPSNY EEDGGPAKPT AAGTAAGAGR 312
AtPIN2 GGDVYSLQSS KGVTPRTSNF DEE------- VMKTAKKAGR 325
AtPIN6 SSDAYSLQ-- --PTPRASNF NE-------- ---------- 312
AtPIN8 ---------- ----PKEEED EEE------- ---------- 196
AtPIN5 ---------- ----VGEKSF LE-------- ---------- 191
spra_contig01436_c_s GADDY----- -----NDGNY NNKNNERTNK LKDAQNSSPN 160
AtAAP1 ATVLIEIQDT LRSSPAEN-- ---------- ---------- 277
Oenococcus-oeni_mleP ---------- ---------- ---------- ---------- 170
Klebsiella-pneumoniae_mdcF ---------- ---------- ---------- ---------- 168
Consensus A-D-YS-Q-- --PTPRPSNF EE-------- ----------
100%
Conservation
0%


420
440
AtPIN3 FGYYPGG - - - - - GA - - - - - - GSYPAPNPEF SSTTTSTANK 325
AtPIN7 FGYYPGG - - - - - AP - - - - - - GSYPAPNPEF S - - - - - TGNK 323
AtPIN4 YGFYNNTNSS VPAA - - - - - - GSYPAPNPEF S - TGTGVSTK 322
AtPIN1 FHYQSGGSGG GGGAH - - - - - - - - YPAPNPGM FSPNTGGGGG 345
AtPIN2 - - - - - GGRSM SGELYNNNSV PSYPPPNP - M FTGSTSGASG 359
AtPIN6 - 312
AtPIN8 - 196
AtPIN5 - 191
spra_contig01436_c_s V - 161
AtAAP1 - 277
Oenococcus-oeni_mleP - 170
Klebsiella-pneumoniae_mdcF - 168
Consensus -
100%
Conservation
0%
460
480
AtPIN3 SVNKNPKDVN TNQQTTLPTG GKSNSHDAKE LHMFVWSSNG 365
AtPIN7 TGSKAPKENH HHV - - - - - - - GKSNSNDAKE LHMFVWGSNG 356
AtPIN4 P - NKIPKENQ QQLQEK - - - - DSKASHDAKE LHMFVWSSSA 357
AtPIN1 TAAK - - GNAP V - - - - - - - VG GKRQDGNGRD LHMFVWSSSA 376
AtPIN2 VKKKESGGGG S - - - - - - - GG GVGVGGQNKE MNMFVWSSSA 392
AtPIN6 - 325
AtPIN8 - 196
AtPIN5 - 191
spra_contig01436_c_s - 161
AtAAP1 - 277
Oenococcus-oeni_mleP - 170
Klebsiella-pneumoniae_mdcF - 168
Consensus -
100%
Conservation
0%
500
520
AtPIN3 SPVSDRAGLN VFGGAPDNDQ GGRSDQG - AK EIRMLVPDQS 404
AtPIN7 SPVSDRAGLQ VDNGA - - NEQ VGKSDQGGAK EIRMLISDHT 394
AtPIN4 SPVSDVFG - - - GGAGDNVA TEQSEQG - AK EIRMVVSDQP 392
AtPIN1 SPVSDVFG - - - GGGGNHHAD YSTATNDHQK DVKISVPQG - 412
AtPIN2 SPVSEA - - - - - - - - NAKNAM TRGSSTDVST DPKVSIPPH - 423
AtPIN6 SPAAGR - - - - IYRQSSPKMM WESGQRHAAK DINGSVPEKE 361
AtPIN8 - 199
AtPIN5 - 191
spra_contig01436_c_s - 182
AtAAP1 - 277
Oenococcus-oeni_mleP - 170
Klebsiella-pneumoniae_mdcF - 168
Consensus -
100%
Conservation
0%
540
560
AtPIN3 HNGETKAVAH PASGDFGGEQ QFSFAGKEEE AERPKDAENG 444
AtPIN7 QNGENKA - - G PMNGDYGGE - - - - - - - - - - EE SERVKEVPNG 423
AtPIN4 RKSNARGGGD DIGGLDSGEG - - - - - - - - ERE IEK - - - ATAG 422
AtPIN1 NSNDNQYVER - - EEFSFGN - - - - - - - - - KD DDSKVLATDG 441
AtPIN2 DNLATKAMQN LIENMSPGR - - - - - - - - - K - - - - GHVEMDQD 451
AtPIN6 ISFRDALKAA PQATAAGGGA S - - - - - - - - - - - - - - - - - MEEG 386
AtPIN8 - 199
AtPIN5 - 191
spra_contig01436_c_s - 182
AtAAP1 - 277
Oenococcus-oeni_mleP - 170
Klebsiella-pneumoniae_mdcF - 168
Consensus - - - - - - - - - - - - - - - - G -
100%
Conservation
0%
580
600
AtPIN3 LNKLAPNSTA ALQSKTGLGG AEASQRKNMP PAS - - - VMTR 481
AtPIN7 LHKLRCNSTA ELNPKEAIET GETVPVKHMP PAS - - - VMTR 460
AtPIN4 LNKMGSNSTA ELEAAGGDGG GNNGT - - HMP PTS - - - VMTR 457
AtPIN1 GNNISNKTTQ AKV - - - - - - - - - - - - - - - MP PTS - - - VMTR 463
AtPIN2 GNNGGKSPYM GKKGSDVEDG GPGPRKQQMP PAS - - - VMTR 488
AtPIN6 AAGKDTTPVA AIG - - - - - - - - - - - - - KQEMP SAI - - - VMMR 411
AtPIN8 - 208
AtPIN5 - 191
spra_contig01436_c_s ASKLEHNLEE PISEKEKVID VISAENKFLP PENWGQIEKN 222
AtAAP1 - 291
Oenococcus-oeni_mleP - 182
Klebsiella-pneumoniae_mdcF - 168
Consensus -
100%
Conservation
0%


620
640
AtPIN3 L - - - - - I L I M V W R K L I R N - P N T Y S S L I G L I - - - W A - - - - - 507
AtPIN7 L - - - - - I L I M V W R K L I R N - P N T Y S S L I G L I - - - W A - - - - - 486
AtPIN4 L - - - - - I L I M V W R K L I R N - P N T Y S S L I G L I - - - W A - - - - - 483
AtPIN1 L - - - - - I L I M V W R K L I R N - P N S Y S S L F G I T - - - W S - - - - - 489
AtPIN2 L - - - - - I L I M V W R K L I R N - P N T Y S S L F G L A - - - W S - - - - - 514
AtPIN6 L - - - - - I L T V V G R K L S R N - P N T Y S S L L G L V - - - W S - - - - - 437
AtPIN8 K - - - - - I L L K A W R K L I I N - P N T Y A T L I G I I - - - W A - - - - - 234
AtPIN5 - - - - - - V M S L V W L K L A T N - P N C Y S C I L G I A - - - W A - - - - - 216
spra_contig01436_c_s L E K E F Q V G T I L F R K L V A N - P S L H S S L Y G V I - - - Y S - - - - - 253
AtAAP1 T F F Y I L C G C I G Y A A F G N N A P G D F L T D F G F F E P F W L I D F A N 331
Oenococcus-oeni_mleP V V L L L A I P I P G W - - - - - - V S T T F S M V G G I V T P M - - - - - - - 209
Klebsiella-pneumoniae_mdcF - - - - - - L P V L M W R S V - - K K P I V W G P L L G V - - - - - - - - - - 189
Consensus L - - - - - I L I M V W R K L I R N - P N T Y S S L I G L I - - - W A - - - - -
100%
Conservation
0%
660
680
AtPIN3 - - - - - - L V A F R W H V A M P - - K I I Q Q S I S - - - - - - - - - I L S D A 531
AtPIN7 - - - - - - L V A F R W D V A M P - - K I I Q Q S I S - - - - - - - - - I L S D A 510
AtPIN4 - - - - - - L V A Y R W H V A M P - - K I L Q Q S I S - - - - - - - - - I L S D A 507
AtPIN1 - - - - - - L I S F K W N I E M P - - A L I A K S I S - - - - - - - - - I L S D A 513
AtPIN2 - - - - - - L V S F K W N I K M P - - T I M S G S I S - - - - - - - - - I L S D A 538
AtPIN6 - - - - - - L I S F K W N I P M P - - N I V D F S I K - - - - - - - - - I I S D A 461
AtPIN8 - - - - - - T L H F R L G W N L P - - E M I D K S I H - - - - - - - - - L L S D G 258
AtPIN5 - - - - - - F I S N R W H L E L P - - G I L E G S I L - - - - - - - - - I M S K A 240
spra_contig01436_c_s - - - - - - L I A F G F D F K M P - - L L L K N N L D - - - - - - - - - I I A N T 277
AtAAP1 A C I A V H L I G A Y Q V F A Q P I F Q F V E K K C N R N Y P D N K F I T S E Y 371
Oenococcus-oeni_mleP - S L I Y I G I - - - - - - - - - I L A D A 221
Klebsiella-pneumoniae_mdcF - - - - - - - V L S A I G I K M P D L L L A S - - - - - - - - - - - - - I K P L 209
Consensus - - - - - - L X X F R W X I A M P - - K I I Q X S I S - - - - - - - - - I L S D A
100%
Conservation
0%
700
720
AtPIN3 G L G - - - M A M F S L G L F - M A L Q P K L I A C G N S V A T F A M A V R F L 567
AtPIN7 G L G - - - M A M F S L G L F - M A L Q P K L I A C G N S T A T F A M A V R F F 546
AtPIN4 G L G - - - M A M F S L G L F - M A L Q P K I I A C G N S V A T F A M A V R F I 543
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AtPIN6 G L G - - - M A M F S L G L F - M A L Q P K M I P C G A K K A T M G M L I R F I 497
AtPIN8 G L G - - - M A M F S L G L F - M A S Q S S I I A C G T K M A I I T M L L K F V 294
AtPIN5 G T G - - - T A M F N M G I F - M A L Q E K L I V C G T S L T V M G M V L K F I 276
spra_contig01436_c_s G M G - - - M A M F S L G L F - I A S P R N F E S C G V W R V T W T M M I R L L 313
AtAAP1 S V N V P F L G K F N I S L F R L V W R T A Y V V I T T V V A M I F P F F N A I 411
Oenococcus-oeni_mleP G L K S I H F D R D S I - L A L I G R F I 241
Klebsiella-pneumoniae_mdcF G L A A T A A A L F L T G V I L S A R K L Q L - - - - N A L I A T S T I V K L L 245
Consensus G L G - - - M A M F S L G L F - M A L Q P K X I A C G N S V A T F A M A V R F I
100%
Conservation
0%
740
760
AtPIN3 T G P A V M A V A A I A I G L R G D L L R V A - - I V Q A A L P Q - G I V P F V 604
AtPIN7 T G P A V M A V A A M A I G L R G D L L R V A - - I V Q A A L P Q - G I V P F V 583
AtPIN4 T G P A I M A V A G I A I G L H G D L L R I A - - I V Q A A L P Q - G I V P F V 580
AtPIN1 V G P A V M L V A S Y A V G L R G V L L H V A - - I I Q A A L P Q - G I V P F V 586
AtPIN2 T G P A V I A A T S I A I G I R G D L L H I A - - I V Q A A L P Q - G I V P F V 611
AtPIN6 S G P L F M A G A S L L V G L R G S R L H A A - - I V Q A A L P Q - G I V P F V 534
AtPIN8 L G P A L M I A S A Y C I R L K S T L F K V A - - I L Q A A L P Q - G V V P F V 331
AtPIN5 A G P A A M A I G S I V L G L H G D V L R V A - - I I Q A A L P Q - S I T S F I 313
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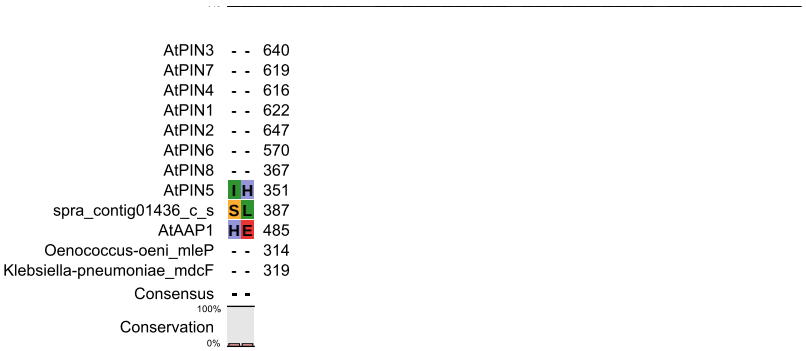
AtAAP1 L G - L I G A A S F W P L T V Y F P V - E M H - - I A Q T K I K K - Y S A R W I 446
Oenococcus-oeni_mleP I V P A V M I I I L K L F G G S M P K L E S S T L I I Q A A A P G L A V L P I L 281
Klebsiella-pneumoniae_mdcF V Q P F I A W G L V M L L G L H G S I A I T A I L M I A L A A G F F G V - - - V 282
Consensus T G P A V M A X A S I A I G L R G D L L R V A - - I V Q A A L P Q - G I V P F V
100%
Conservation
0%
780
800
AtPIN3 F A K E Y N - - - V H P A I L S T G V I F G M L I A L P I T L V Y Y I L L G - L 640
AtPIN7 F A K E Y N - - - V H P A I L S T G V I F G M L I A L P I T L V Y Y I L L G - L 619
AtPIN4 F A K E Y N - - - V H P T I L S T G V I F G M L I A L P I T L V Y Y I L L G - L 616
AtPIN1 F A K E Y N - - - V H P D I L S T A V I F G M L I A L P I T L L Y Y I L L G - L 622
AtPIN2 F A K E Y N - - - V H P D I L S T A V I F G M L V A L P V T V L Y Y V L L G - L 647
AtPIN6 F A R E Y N - - - L H P D L L S T L V I F G M I V S L P V T I L Y Y V L L G - L 570
AtPIN8 F A K E Y N - - - L H P E I I S T G V I F G M L I A L P T T L A Y Y F L L D - L 367
AtPIN5 F A K E Y G - - - L H A D V L S T A V I F G M L V S L P V L V A Y Y A A L E - F 349
spra_contig01436_c_s L S N E Y K - - - I H P E I H T A L I V V T T G L C F P L M L L M Y M A F E - - 385
AtAAP1 A L K T M C - - - Y V C L I V S L L A A A G S T A G L I S S V K T Y K P F R T M 483
Oenococcus-oeni_mleP V G Q N H G D V E Y A T N V V T T S T V L - F V I V V P I L M Q F V - - - - - - 314
Klebsiella-pneumoniae_mdcF F G N R F G V Q S P D A E A V L L L S S V L C I L S L P L F I S L T S G L - - - 319
Consensus F A K E Y N - - - V H P D I L S T X V I F G M L I A L P I T L L Y Y I L L G - L
100%
Conservation
0%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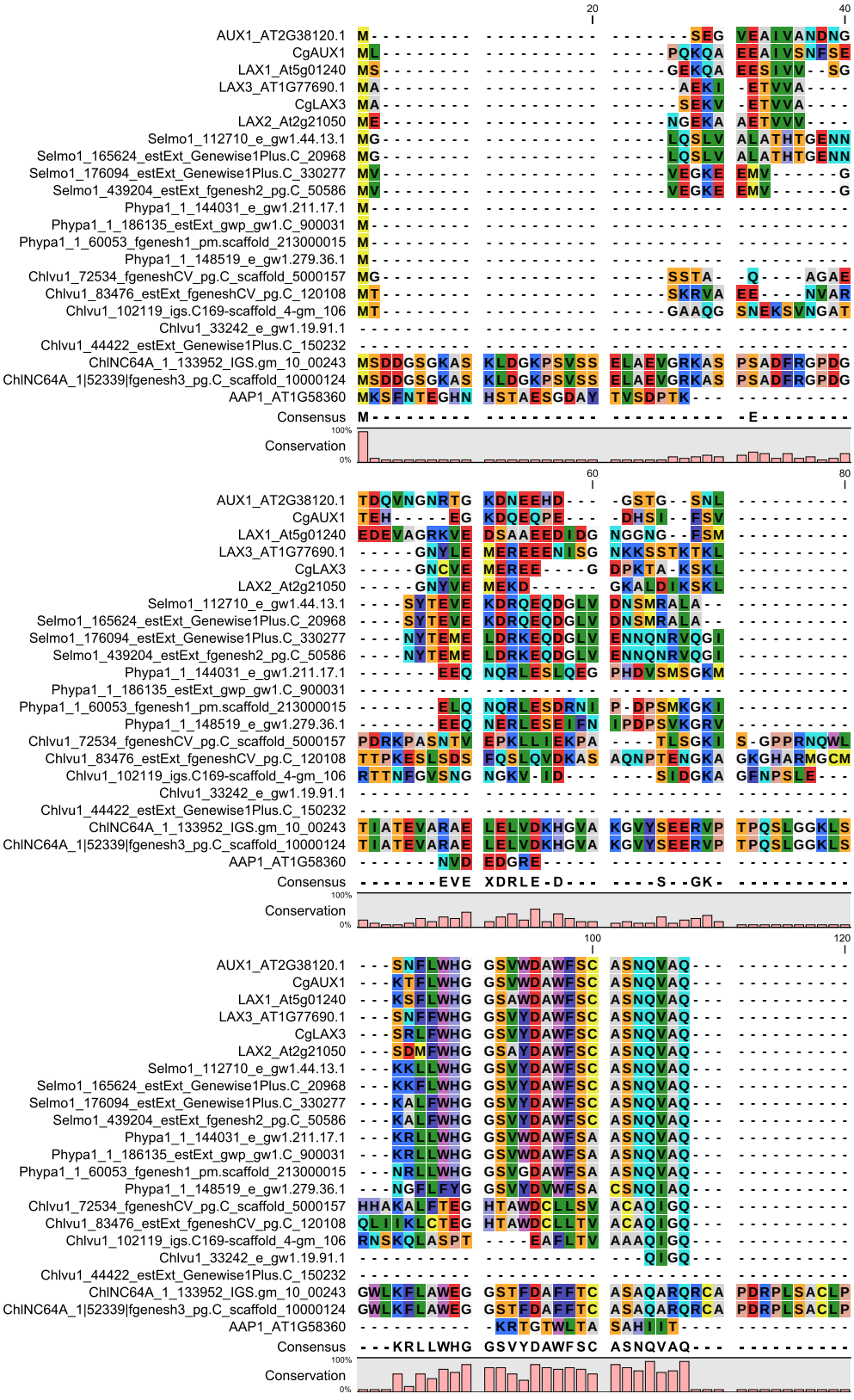
AtPIN8 - - 367
AtPIN5 I H 351
spra_contig01436_c_s S L 387
AtAAP1 H E 485
Oenococcus-oeni_mleP - - 314
Klebsiella-pneumoniae_mdcF - - 319
Consensus
100%
Conservation
0%

Figure S23 – alignment of AUX1-LAXs and putative orthologs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LAX1_At5g01240 15
LAX3_AT1G77690.1 11
CgLAX3 11
LAX2_At2g21050 13
Selmo1_112710_e_gw1.44.13.1 17
Selmo1_165624_estExt_Genewise1Plus.C_20968 17
Selmo1_176094_estExt_Genewise1Plus.C_330277 11
Selmo1_439204_estExt_fgenesh2_pg.C_50586 11
Phypa1_1_144031_e_gw1.211.17.1 1
Phypa1_1_186135_estExt_gwp_gw1.C_900031 1
Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 1
Phypa1_1_148519_e_gw1.279.36.1 1
Chlvu1_72534_fgeneshCV_pg.C_scaffold_5000157 11
Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 13
Chlvu1_102119_igs.C169-scaffold_4-gm_106 17
Chlvu1_33242_e_gw1.19.91.1 -
Chlvu1_44422_estExt_Genewise1Plus.C_150232 -
ChlNC64A_1_133952_IGS.gm_10_00243 40
ChlNC64A_1|52339|fgenesh3_pg.C_scaffold_10000124 40
AAP1_AT1G58360 27
Consensus
100%
Conservation
0%
60
80
AUX1_AT2G38120.1 38
CgAUX1 36
LAX1_At5g01240 43
LAX3_AT1G77690.1 36
CgLAX3 31
LAX2_At2g21050 32
Selmo1_112710_e_gw1.44.13.1 41
Selmo1_165624_estExt_Genewise1Plus.C_20968 41
Selmo1_176094_estExt_Genewise1Plus.C_330277 37
Selmo1_439204_estExt_fgenesh2_pg.C_50586 37
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Phypa1_1_186135_estExt_gwp_gw1.C_900031 1
Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 23
Phypa1_1_148519_e_gw1.279.36.1 24
Chlvu1_72534_fgeneshCV_pg.C_scaffold_5000157 46
Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 53
Chlvu1_102119_igs.C169-scaffold_4-gm_106 46
Chlvu1_33242_e_gw1.19.91.1 -
Chlvu1_44422_estExt_Genewise1Plus.C_150232 -
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AAP1_AT1G58360 35
Consensus
100%
Conservation
0%
100
120
AUX1_AT2G38120.1 62
CgAUX1 60
LAX1_At5g01240 67
LAX3_AT1G77690.1 60
CgLAX3 55
LAX2_At2g21050 56
Selmo1_112710_e_gw1.44.13.1 65
Selmo1_165624_estExt_Genewise1Plus.C_20968 65
Selmo1_176094_estExt_Genewise1Plus.C_330277 61
Selmo1_439204_estExt_fgenesh2_pg.C_50586 61
Phypa1_1_144031_e_gw1.211.17.1 48
Phypa1_1_186135_estExt_gwp_gw1.C_900031 25
Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 47
Phypa1_1_148519_e_gw1.279.36.1 48
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Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 80
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Consensus
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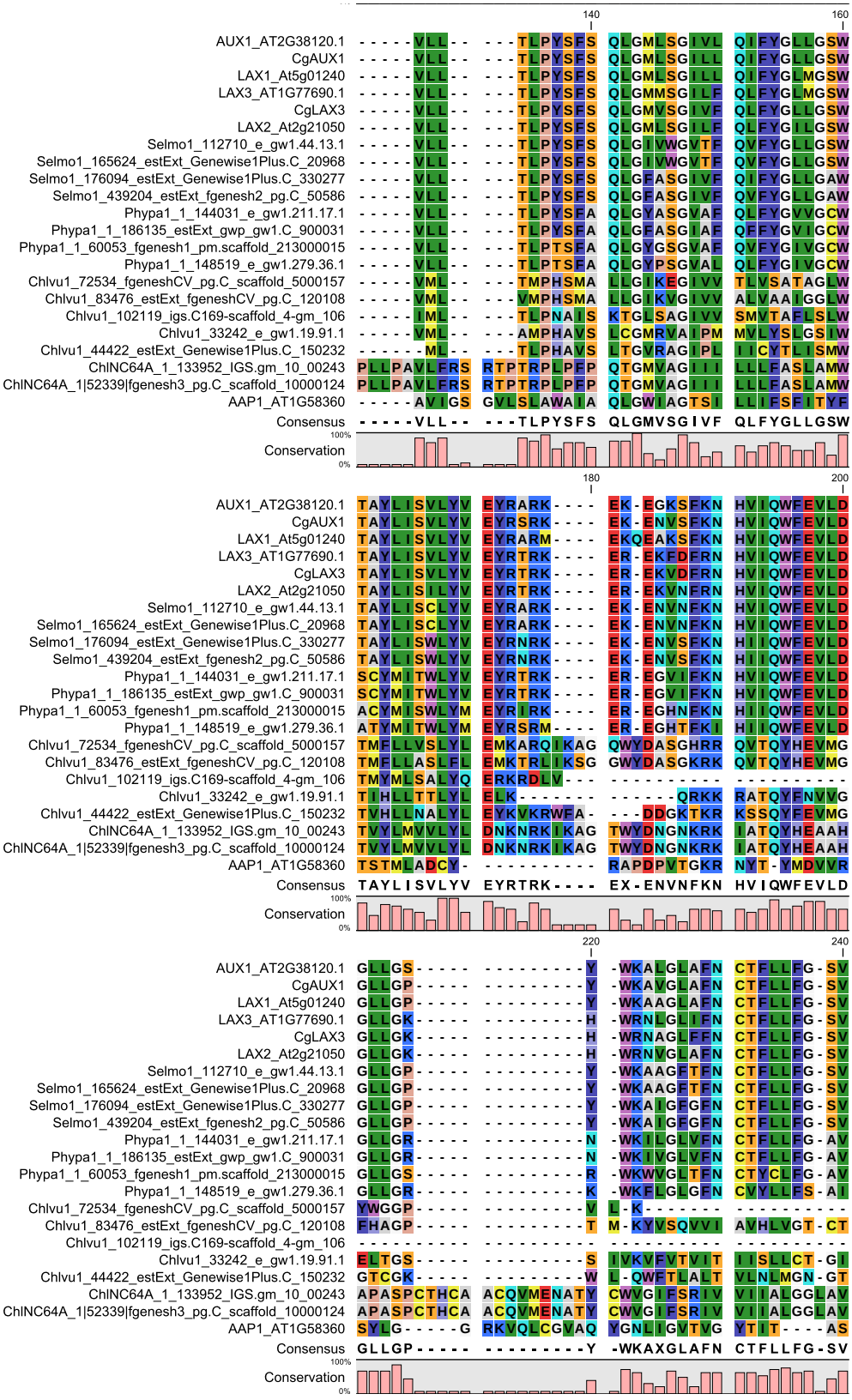
Conservation
0%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Selmo1_112710_e_gw1.44.13.1 95
Selmo1_165624_estExt_Genewise1Plus.C_20968 95
Selmo1_176094_estExt_Genewise1Plus.C_330277 91
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Phypa1_1_186135_estExt_gwp_gw1.C_900031 55
Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 77
Phypa1_1_148519_e_gw1.279.36.1 78
Chlvu1_72534_fgeneshCV_pg.C_scaffold_5000157 103
Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 110
Chlvu1_102119_igs.C169-scaffold_4-gm_106 99
Chlvu1_33242_e_gw1.19.91.1 34
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AAP1_AT1G58360 85
Consensus
100%
Conservation
0%
180
200
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CgAUX1 125
LAX1_At5g01240 133
LAX3_AT1G77690.1 125
CgLAX3 120
LAX2_At2g21050 121
Selmo1_112710_e_gw1.44.13.1 130
Selmo1_165624_estExt_Genewise1Plus.C_20968 130
Selmo1_176094_estExt_Genewise1Plus.C_330277 126
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Chlvu1_33242_e_gw1.19.91.1 61
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Consensus
100%
Conservation
0%
220
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AUX1_AT2G38120.1 151
CgAUX1 149
LAX1_At5g01240 157
LAX3_AT1G77690.1 149
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Selmo1_112710_e_gw1.44.13.1 154
Selmo1_165624_estExt_Genewise1Plus.C_20968 154
Selmo1_176094_estExt_Genewise1Plus.C_330277 150
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Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 174
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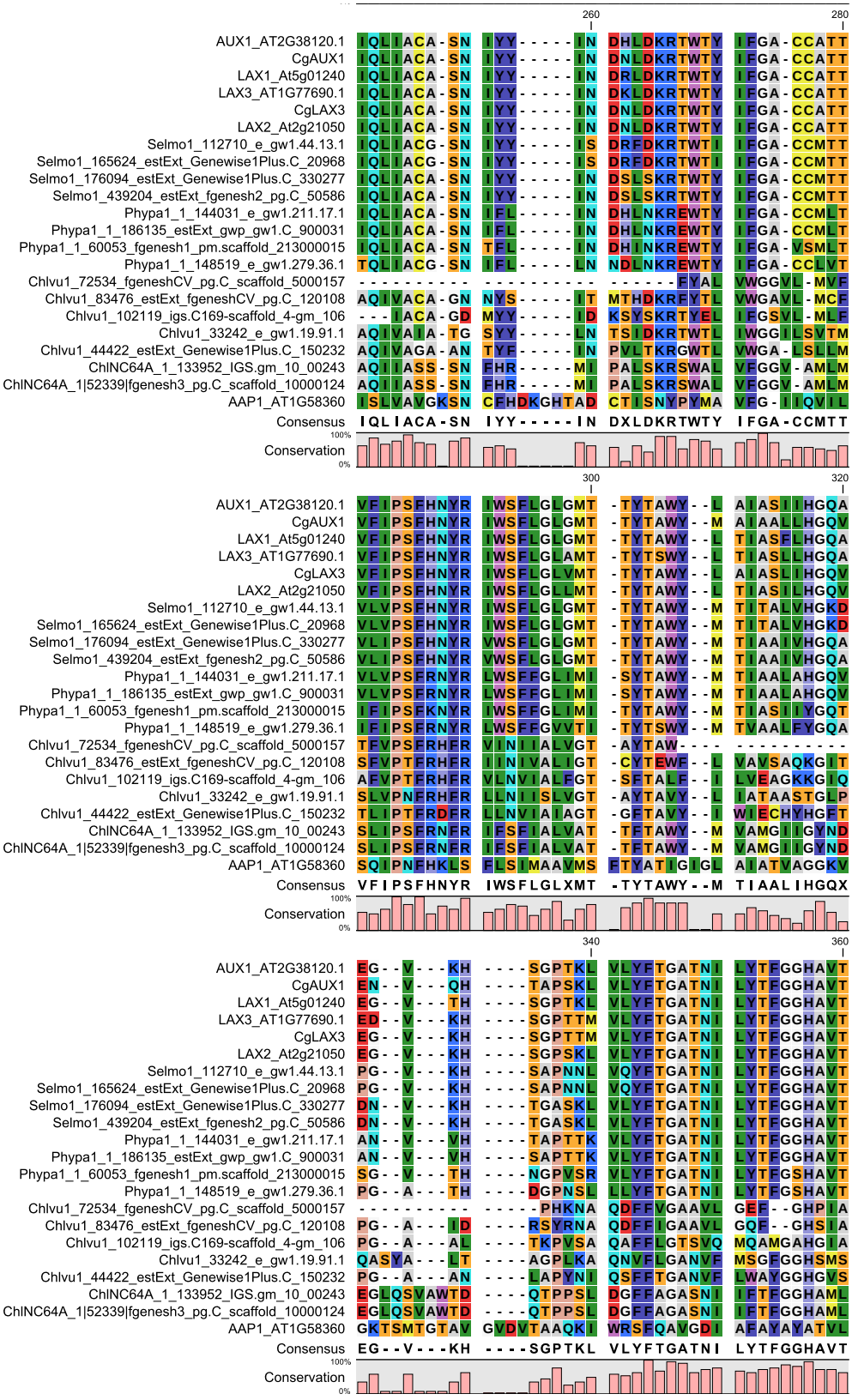
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LAX3_AT1G77690.1 IQLIACA-SN IYY-----IN DKLDKRTWTY IFGA-CCATT 182
CgLAX3 IQLIACA-SN IYY-----IN DNLDKRTWTY IFGA-CCATT 177
LAX2_At2g21050 IQLIACA-SN IYY-----IN DNLDKRTWTY IFGA-CCATT 178
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100%
Conservation
0%
300
320
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100%
Conservation
0%
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360
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LAX3_AT1G77690.1 ED--V---KH ----SGPTTM VLYFTGATNI LYTFGGHAVT 250
CgLAX3 EG--V---KH ----SGPTTM VLYFTGATNI LYTFGGHAVT 245
LAX2_At2g21050 EG--V---KH ----SGPSKL VLYFTGATNI LYTFGGHAVT 246
Selmo1_112710_e_gw1.44.13.1 PG--V---KH ----SAPNNL VQYFTGATNI LYTFGGHAVT 255
Selmo1_165624_estExt_Genewise1Plus.C_20968 PG--V---KH ----SAPNNL VQYFTGATNI LYTFGGHAVT 255
Selmo1_176094_estExt_Genewise1Plus.C_330277 DN--V---KH ----TGASKL VLYFTGATNI LYTFGGHAVT 251
Selmo1_439204_estExt_fgenesh2_pg.C_50586 DN--V---KH ----TGASKL VLYFTGATNI LYTFGGHAVT 251
Phypa1_1_144031_e_gw1.211.17.1 AN--V---VH ----TAPTTK VLYFTGATNI LYTFGGHAVT 238
Phypa1_1_186135_estExt_gwp_gw1.C_900031 AN--V---VH ----SAPTTK VLYFTGATNI LYTFGGHAVT 215
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Chlvu1_102119_igs.C169-scaffold_4-gm_106 PG--A---AL ----TKPVSA QAFFLGTSVQ MQAMGAHGIA 214
Chlvu1_33242_e_gw1.19.91.1 QASYA---LT ----AGPLKA QNVFLGANVF MSGFGGHSMS 190
Chlvu1_44422_estExt_Genewise1Plus.C_150232 PG--A---AN ----LAPYNI QSFFTGANVF LWAYGGHGVS 190
ChlNC64A_1_133952_IGS.gm_10_00243 EGLQSVAWTD ----QTPPSL DGFFAGASNI IFTFGGHAML 346
ChlNC64A_1|52339|fgenesh3_pg.C_scaffold_10000124 EGLQSVAWTD ----QTPPSL DGFFAGASNI IFTFGGHAML 346
AAP1_AT1G58360 GKTSMTGTAV GVDVTAAQKI WRSFQAVGDI AFAYAYATVL 263
Consensus EG--V---KH ----SGPTKL VLYFTGATNI LYTFGGHAVT
100%
Conservation
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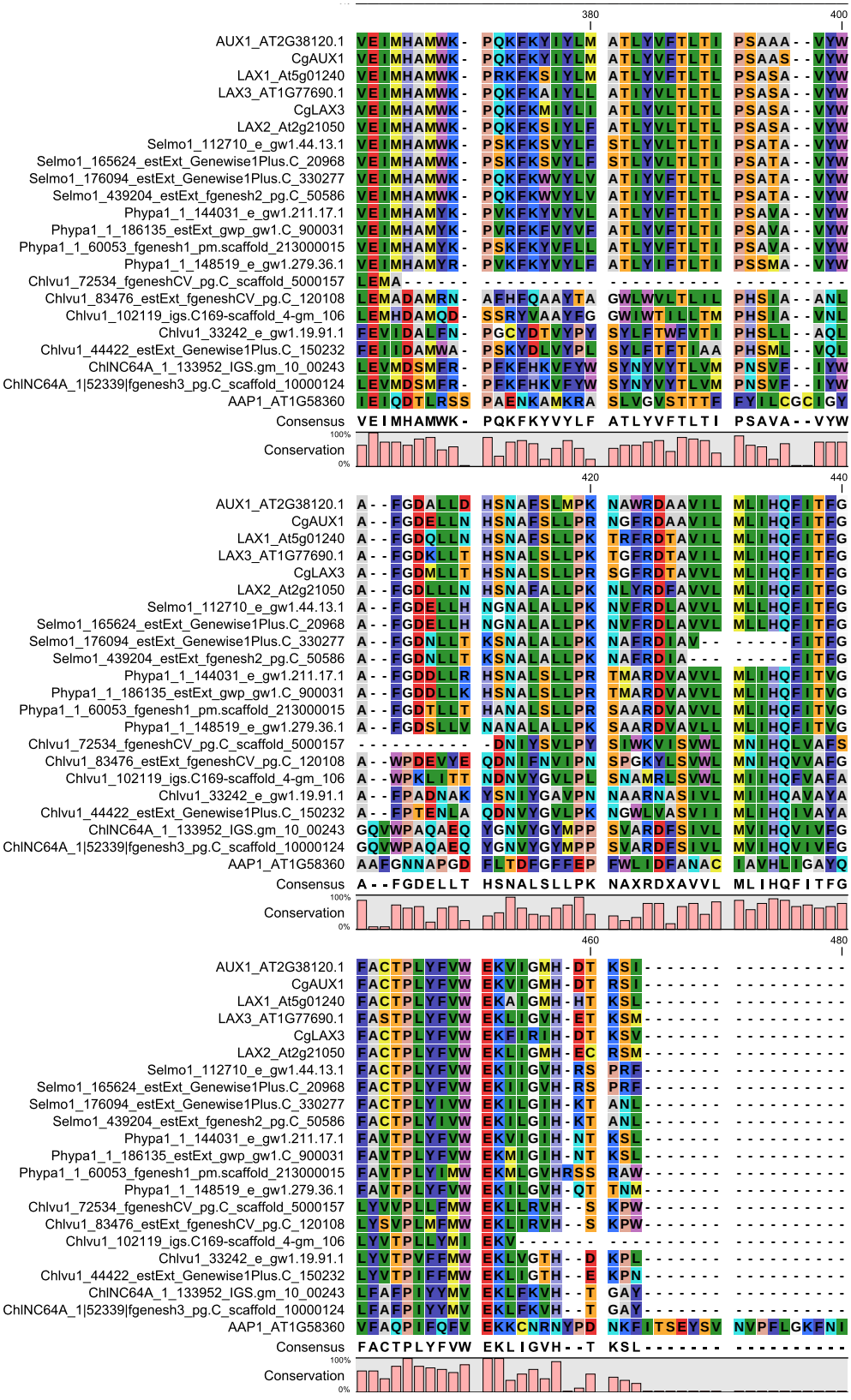
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LAX1_At5g01240 VEIMHAMWK- PRKFKSIYLM ATLYVFTLTL PSASA--VYW 295
LAX3_AT1G77690.1 VEIMHAMWK- PQKFKAIYLL ATIYVLTLTL PSASA--VYW 287
CgLAX3 VEIMHAMWK- PQKFKMIYLI ATLYVLTLTL PSASA--VYW 282
LAX2_At2g21050 VEIMHAMWK- PQKFKSIYLF ATLYVLTLTL PSASA--VYW 283
Selmo1_112710_e_gw1.44.13.1 VEIMHAMWK- PSKFKSVYLF STLYVLTLTI PSATA--VYW 292
Selmo1_165624_estExt_Genewise1Plus.C_20968 VEIMHAMWK- PSKFKSVYLF STLYVLTLTI PSATA--VYW 292
Selmo1_176094_estExt_Genewise1Plus.C_330277 VEIMHAMWK- PQKFKWVYLV ATIYVFTLTL PSATA--VYW 288
Selmo1_439204_estExt_fgenesh2_pg.C_50586 VEIMHAMWK- PQKFKWVYLV ATIYVFTLTL PSATA--VYW 288
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Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 VEIMHAMYK- PSKFKYVFLL ATLYVFTLTI PSAVA--VYW 274
Phypa1_1_148519_e_gw1.279.36.1 VEIMHAMYR- PVKFKYVYLF ATLYIFTLTI PSSMA--VYW 275
Chlvu1_72534_fgeneshCV_pg.C_scaffold_5000157 LEMA------ ---------- ---------- ---------- 216
Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 LEMADAMRN- AFHFQAAYTA GWLWVLTLIL PHSIA--ANL 310
Chlvu1_102119_igs.C169-scaffold_4-gm_106 LEMHDAMQD- SSRYVAAYFG GWIWTILLTM PHSIA--VNL 251
Chlvu1_33242_e_gw1.19.91.1 FEVIDALFN- PGCYDTVYPY SYLFTWFVTI PHSLL--AQL 227
Chlvu1_44422_estExt_Genewise1Plus.C_150232 FEIIDAMWA- PSKYDLVYPL SYLFTFTIAA PHSML--VQL 227
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ChlNC64A_1|52339|fgenesh3_pg.C_scaffold_10000124 LEVMDSMFR- PFKFHKVFYW SYNYVYTLVM PNSVF--IYW 383
AAP1_AT1G58360 IEIQDTLRSS PAENKAMKRA SLVGVSTTTF FYILCGCIGY 303
Consensus VEIMHAMWK- PQKFKYVYLF ATLYVFTLTI PSAVA--VYW
100%
Conservation
0%
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440
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LAX1_At5g01240 A--FGDQLLN HSNAFSLLPK TRFRDTAVIL MLIHQFITFG 333
LAX3_AT1G77690.1 A--FGDKLLT HSNALSLLPK TGFRDTAVIL MLIHQFITFG 325
CgLAX3 A--FGDMLLT HSNALSLLPR SGFRDTAVVL MLIHQFITFG 320
LAX2_At2g21050 A--FGDLLLN HSNAFALLPK NLYRDFAVVL MLIHQFITFG 321
Selmo1_112710_e_gw1.44.13.1 A--FGDELLH NGNALALLPK NVFRDLAVVL MLLHQFITFG 330
Selmo1_165624_estExt_Genewise1Plus.C_20968 A--FGDELLH NGNALALLPK NVFRDLAVVL MLLHQFITFG 330
Selmo1_176094_estExt_Genewise1Plus.C_330277 A--FGDNLLT KSNALALLPK NAFRDIAV-- ------FITFG 319
Selmo1_439204_estExt_fgenesh2_pg.C_50586 A--FGDNLLT KSNALALLPK NAFRDIA--- -----FITFG 318
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Phypa1_1_186135_estExt_gwp_gw1.C_900031 A--FGDDLLK HSNALSLLPR TMARDVAVVL MLIHQFITVG 290
Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 A--FGDTLLT HANALSLLPR SAARDVAVVL MLIHQFITVG 312
Phypa1_1_148519_e_gw1.279.36.1 A--FGDSLLV NANALALLPK SAARDVAVLL MLIHQFITVG 313
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Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 A--WPDEVYE QDNIFNVIPN SPGKYLSVWL MNIHQVVAFG 348
Chlvu1_102119_igs.C169-scaffold_4-gm_106 A--WPKLITT NDNVYGVLPL SNAMRLSVWL MIIHQFVAFA 289
Chlvu1_33242_e_gw1.19.91.1 A--FPADNAK YSNIYGAVPN NAARNASIVL MIIHQAVAYA 265
Chlvu1_44422_estExt_Genewise1Plus.C_150232 A--FPTENLA QDNVYGVLPK NGWLVASVII MLIHQIVAYA 265
ChlNC64A_1_133952_IGS.gm_10_00243 GQVWPAQAEQ YGNVYGYMPP SVARDFSIVL MVIHQVIVFG 423
ChlNC64A_1|52339|fgenesh3_pg.C_scaffold_10000124 GQVWPAQAEQ YGNVYGYMPP SVARDFSIVL MVIHQVIVFG 423
AAP1_AT1G58360 AAFGNNAPGD FLTDFGFFEP FWLIDFANAC IAVHLIGAYQ 343
Consensus A--FGDELLT HSNALSLLPK NAXRDXAVVL MLIHQFITFG
100%
Conservation
0%
460
480
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CgAUX1 FACTPLYFVW EKVIGMH-DT RSI---------- ---------- 347
LAX1_At5g01240 FACTPLYFVW EKAIGMH-HT KSL---------- ---------- 355
LAX3_AT1G77690.1 FASTPLYFVW EKLIGVH-ET KSM---------- ---------- 347
CgLAX3 FACTPLYFVW EKFIRIH-DT KSV---------- ---------- 342
LAX2_At2g21050 FACTPLYFVW EKLIGMH-EC RSM---------- ---------- 343
Selmo1_112710_e_gw1.44.13.1 FACTPLYFVW EKIIGVH-RS PRF---------- ---------- 352
Selmo1_165624_estExt_Genewise1Plus.C_20968 FACTPLYFVW EKIIGVH-RS PRF---------- ---------- 352
Selmo1_176094_estExt_Genewise1Plus.C_330277 FACTPLYIVW EKILGIH-KT ANL---------- ---------- 341
Selmo1_439204_estExt_fgenesh2_pg.C_50586 FACTPLYIVW EKILGIH-KT ANL---------- ---------- 340
Phypa1_1_144031_e_gw1.211.17.1 FAVTPLYFVW EKVIGIH-NT KSL---------- ---------- 335
Phypa1_1_186135_estExt_gwp_gw1.C_900031 FAVTPLYFVW EKMIGIH-NT KSL---------- ---------- 312
Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 FAVTPLYIMW EKMLGVHRSS RAW---------- ---------- 335
Phypa1_1_148519_e_gw1.279.36.1 FAVTPLYFVW EKILGVH-QT TNM---------- ---------- 335
Chlvu1_72534_fgeneshCV_pg.C_scaffold_5000157 LYVVPLLFMW EKLLRVH--S KPW---------- ---------- 266
Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 LYSVPLMFMW EKLIRVH--S KPW---------- ---------- 369
Chlvu1_102119_igs.C169-scaffold_4-gm_106 LYVTPLLYMI EKV---------- ---------- ---------- 302
Chlvu1_33242_e_gw1.19.91.1 LYVTPVFFMW EKLVGTH--D KPL---------- ---------- 286
Chlvu1_44422_estExt_Genewise1Plus.C_150232 LYVTPIFFMW EKLIGTH--E KPN---------- ---------- 286
ChlNC64A_1_133952_IGS.gm_10_00243 LFAFPIYYMV EKLFKVH--T GAY---------- ---------- 444
ChlNC64A_1|52339|fgenesh3_pg.C_scaffold_10000124 LFAFPIYYMV EKLFKVH--T GAY---------- ---------- 444
AAP1_AT1G58360 VFAQPIFQFV EKKCNRNYPD NKFITSEYSV NVPFLGKFNI 383
Consensus FACTPLYFVW EKLIGVH--T KSL---------- ----------
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Conservation
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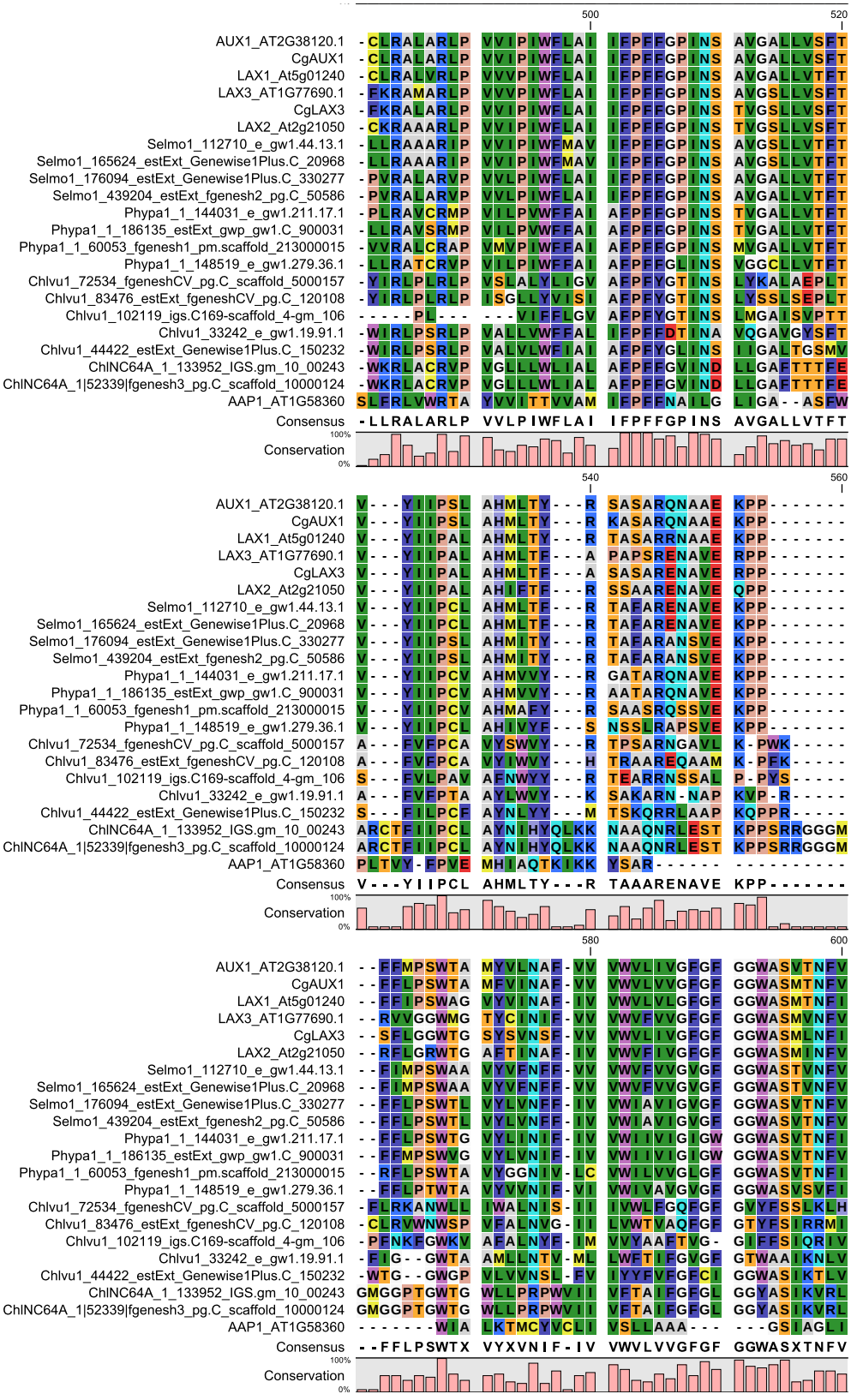
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LAX1_At5g01240 394
LAX3_AT1G77690.1 386
CgLAX3 381
LAX2_At2g21050 382
Selmo1_112710_e_gw1.44.13.1 391
Selmo1_165624_estExt_Genewise1Plus.C_20968 391
Selmo1_176094_estExt_Genewise1Plus.C_330277 380
Selmo1_439204_estExt_fgenesh2_pg.C_50586 379
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Phypa1_1_186135_estExt_gwp_gw1.C_900031 351
Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 374
Phypa1_1_148519_e_gw1.279.36.1 374
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Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 408
Chlvu1_102119_igs.C169-scaffold_4-gm_106 331
Chlvu1_33242_e_gw1.19.91.1 325
Chlvu1_44422_estExt_Genewise1Plus.C_150232 325
ChlNC64A_1_133952_IGS.gm_10_00243 483
ChlNC64A_1|52339|fgenesh3_pg.C_scaffold_10000124 483
AAP1_AT1G58360 421
Consensus
100%
Conservation
0%
540
560
AUX1_AT2G38120.1 415
CgAUX1 413
LAX1_At5g01240 421
LAX3_AT1G77690.1 413
CgLAX3 408
LAX2_At2g21050 409
Selmo1_112710_e_gw1.44.13.1 418
Selmo1_165624_estExt_Genewise1Plus.C_20968 418
Selmo1_176094_estExt_Genewise1Plus.C_330277 407
Selmo1_439204_estExt_fgenesh2_pg.C_50586 406
Phypa1_1_144031_e_gw1.211.17.1 401
Phypa1_1_186135_estExt_gwp_gw1.C_900031 378
Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 401
Phypa1_1_148519_e_gw1.279.36.1 401
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Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 436
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Chlvu1_33242_e_gw1.19.91.1 352
Chlvu1_44422_estExt_Genewise1Plus.C_150232 354
ChlNC64A_1_133952_IGS.gm_10_00243 523
ChlNC64A_1|52339|fgenesh3_pg.C_scaffold_10000124 523
AAP1_AT1G58360 444
Consensus
100%
Conservation
0%
580
600
AUX1_AT2G38120.1 452
CgAUX1 450
LAX1_At5g01240 458
LAX3_AT1G77690.1 450
CgLAX3 445
LAX2_At2g21050 446
Selmo1_112710_e_gw1.44.13.1 455
Selmo1_165624_estExt_Genewise1Plus.C_20968 455
Selmo1_176094_estExt_Genewise1Plus.C_330277 444
Selmo1_439204_estExt_fgenesh2_pg.C_50586 443
Phypa1_1_144031_e_gw1.211.17.1 438
Phypa1_1_186135_estExt_gwp_gw1.C_900031 415
Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 438
Phypa1_1_148519_e_gw1.279.36.1 438
Chlvu1_72534_fgeneshCV_pg.C_scaffold_5000157 371
Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 474
Chlvu1_102119_igs.C169-scaffold_4-gm_106 396
Chlvu1_33242_e_gw1.19.91.1 388
Chlvu1_44422_estExt_Genewise1Plus.C_150232 390
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Consensus
100%
Conservation
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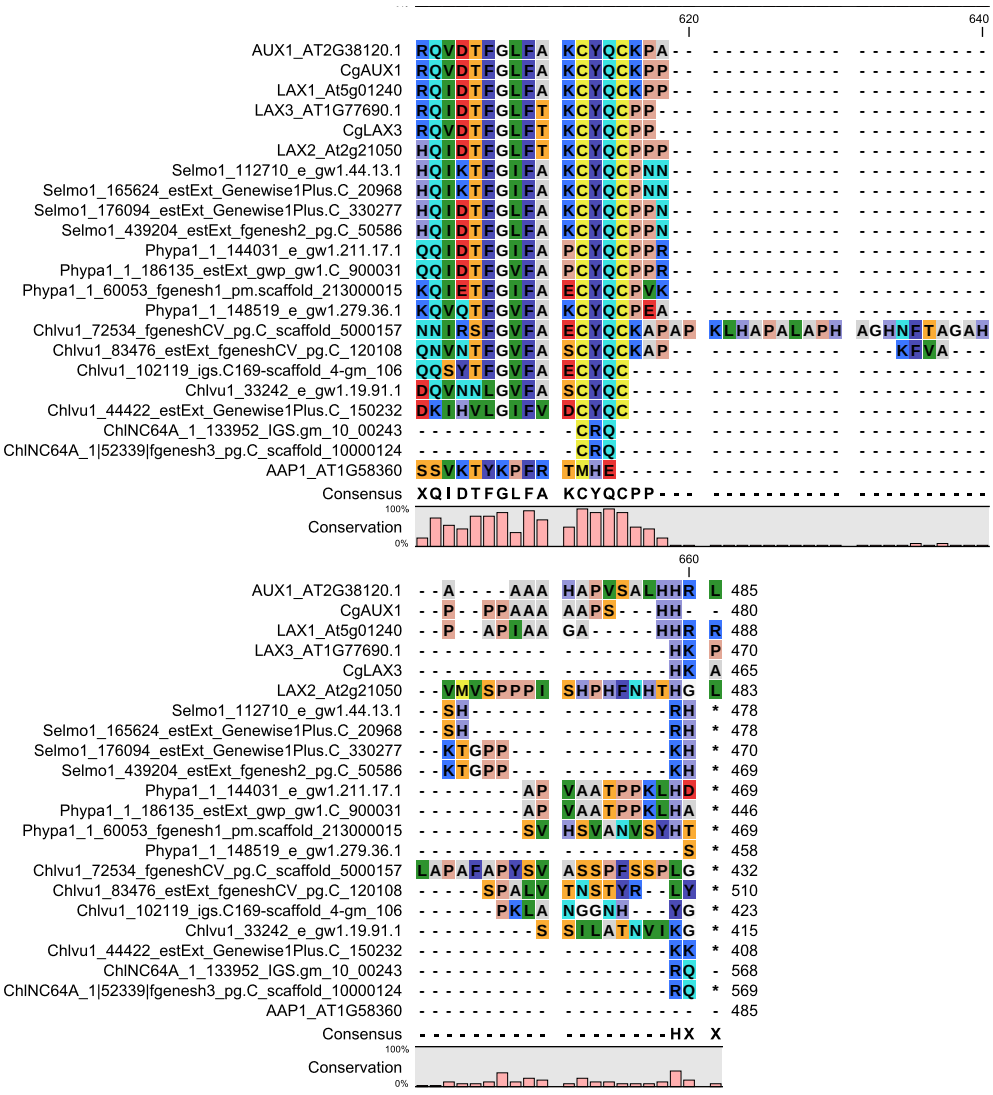
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CgAUX1 RQVDTFGLFA KCYQCKPP 468
LAX1_At5g01240 RQIDTFGLFA KCYQCKPP 476
LAX3_AT1G77690.1 RQIDTFGLFT KCYQCPP 467
CgLAX3 RQVDTFGLFT KCYQCPP 462
LAX2_At2g21050 HQIDTFGLFT KCYQCPPP 464
Selmo1_112710_e_gw1.44.13.1 HQIKTFGIFA KCYQCPNN 473
Selmo1_165624_estExt_Genewise1Plus.C_20968 HQIKTFGIFA KCYQCPNN 473
Selmo1_176094_estExt_Genewise1Plus.C_330277 HQIDTFGLFA KCYQCPPN 462
Selmo1_439204_estExt_fgenesh2_pg.C_50586 HQIDTFGLFA KCYQCPPN 461
Phypa1_1_144031_e_gw1.211.17.1 QQIDTFGIFA PCYQCPPR 456
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Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 KQIETFGIFA ECYQCPVK 456
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Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 QNVNTFGVFA SCYQCKAP KFVA 496
Chlvu1_102119_igs.C169-scaffold_4-gm_106 QQSYTFGVFA ECYQC 411
Chlvu1_33242_e_gw1.19.91.1 DQVNNLGVFA SCYQC 403
Chlvu1_44422_estExt_Genewise1Plus.C_150232 DKIHVLGIFV DCYQC 405
ChlNC64A_1_133952_IGS.gm_10_00243 CRQ 566
ChlNC64A_1|52339|fgenesh3_pg.C_scaffold_10000124 CRQ 566
AAP1_AT1G58360 SSVKTYKPFR TMHE 485
Consensus XQIDTFGLFA KCYQCPP
100%
Conservation
0%
660
AUX1_AT2G38120.1 A AAA HAPVSALHHR L 485
CgAUX1 P PPAAA AAPS HH L 480
LAX1_At5g01240 P APIAA GA HHR R 488
LAX3_AT1G77690.1 HK P 470
CgLAX3 HK A 465
LAX2_At2g21050 VMVSPPPI SHPHFNHTHG L 483
Selmo1_112710_e_gw1.44.13.1 SH RH * 478
Selmo1_165624_estExt_Genewise1Plus.C_20968 SH RH * 478
Selmo1_176094_estExt_Genewise1Plus.C_330277 KTGPP KH * 470
Selmo1_439204_estExt_fgenesh2_pg.C_50586 KTGPP KH * 469
Phypa1_1_144031_e_gw1.211.17.1 AP VAATPPKLHD * 469
Phypa1_1_186135_estExt_gwp_gw1.C_900031 AP VAATPPKLHA * 446
Phypa1_1_60053_fgenesh1_pm.scaffold_213000015 SV HSVANVSYHT * 469
Phypa1_1_148519_e_gw1.279.36.1 S * 458
Chlvu1_72534_fgeneshCV_pg.C_scaffold_5000157 LAPAFAPYSV ASSPFSSPLG * 432
Chlvu1_83476_estExt_fgeneshCV_pg.C_120108 SPALV TNSTYR LY * 510
Chlvu1_102119_igs.C169-scaffold_4-gm_106 PKLA NGGNH YG * 423
Chlvu1_33242_e_gw1.19.91.1 S SILATNVIKG * 415
Chlvu1_44422_estExt_Genewise1Plus.C_150232 KK * 408
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ChlNC64A_1|52339|fgenesh3_pg.C_scaffold_10000124 RQ * 569
AAP1_AT1G58360 - 485
Consensus HX X
100%
Conservation
0%

Figure S24 – UPGMA tree for PGP orthologs

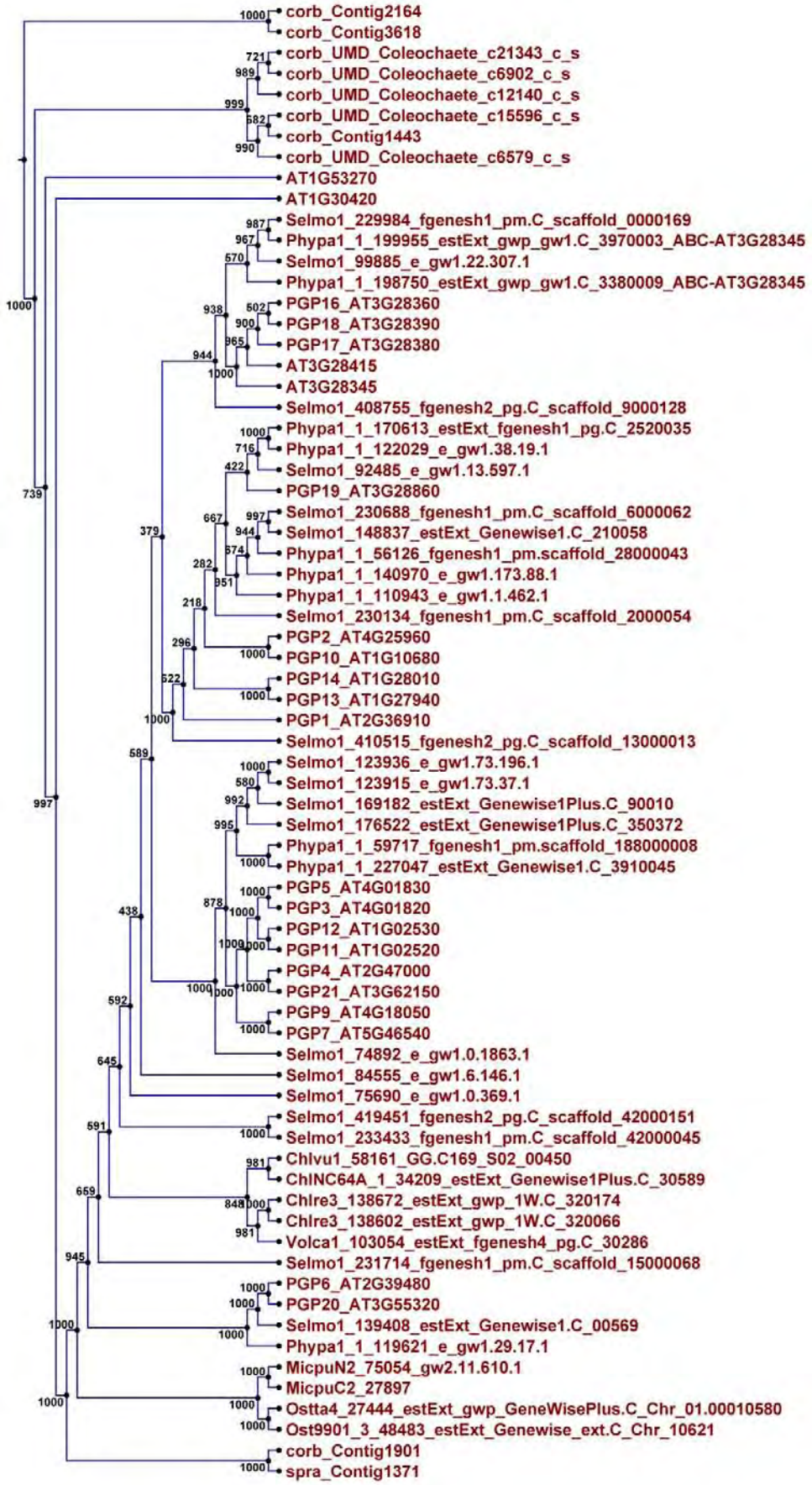


Figure S25 – UPGMA tree for TPL-TPR1,2,3,4 orthologs

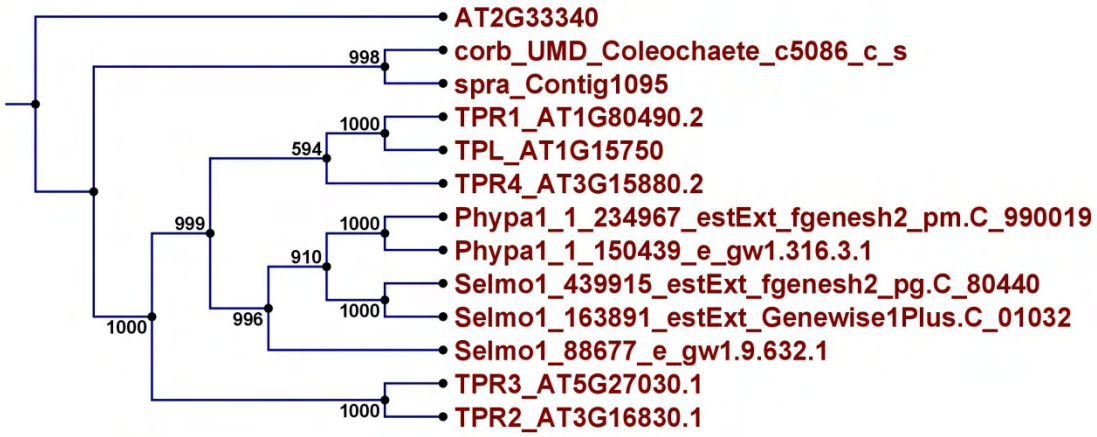


Figure S26 – UPGMA tree for IBR5 orthologs

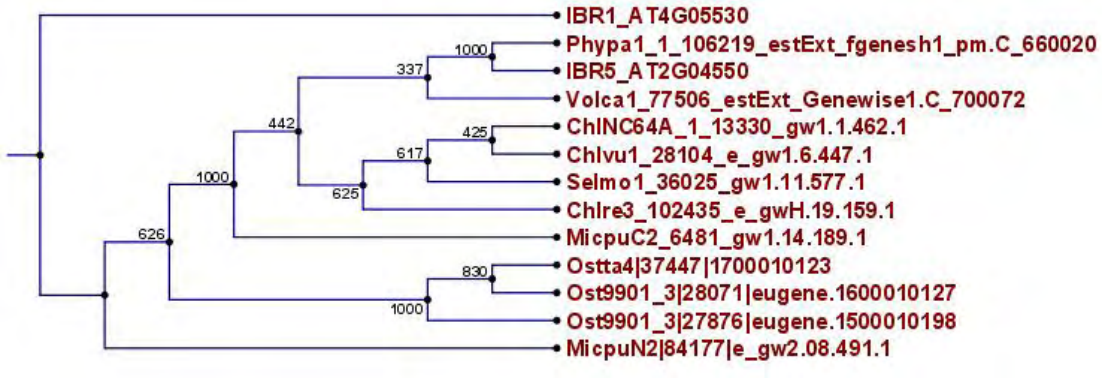


Figure S27 – UPGMA tree for ABP1 orthologs

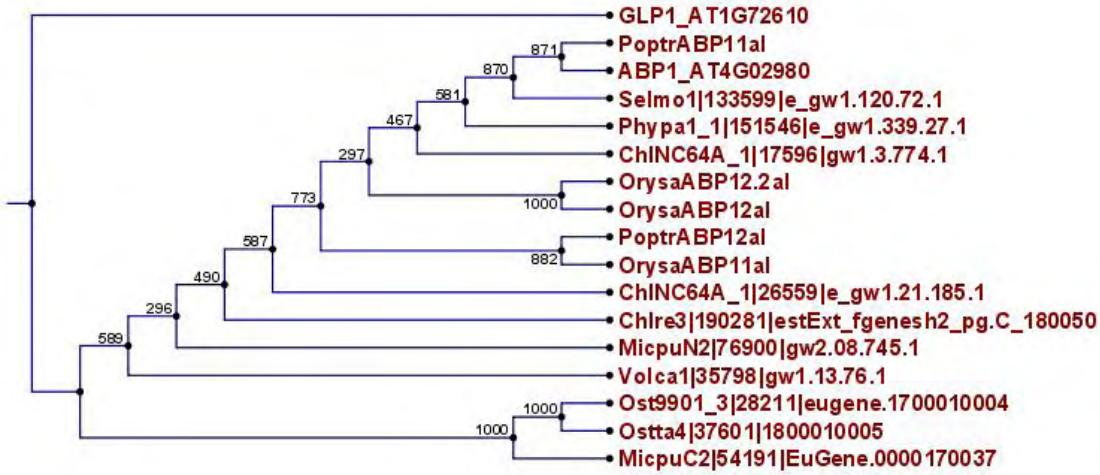
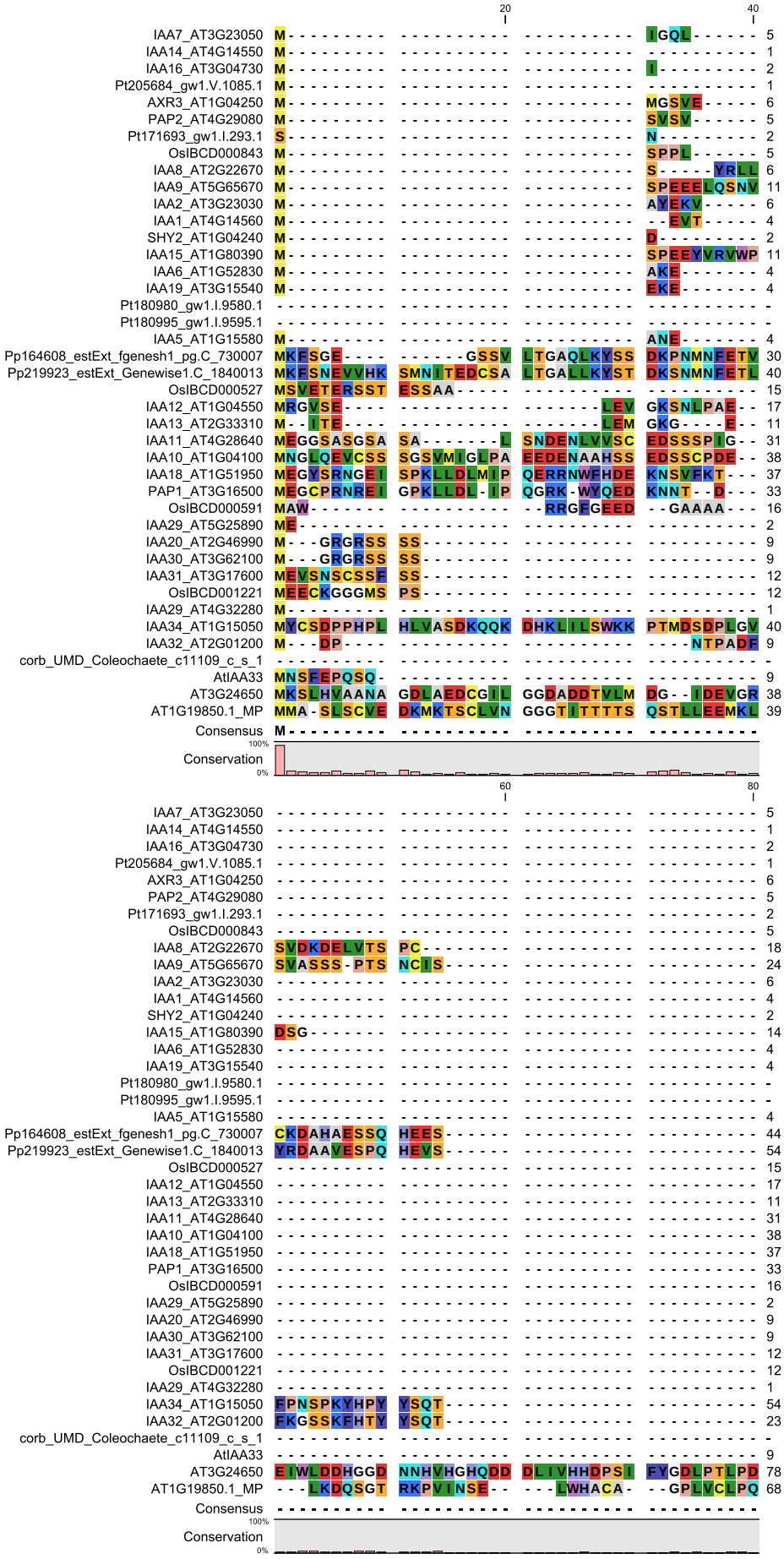


Figure S28 – alignment of AUX/IAAs and putative orthologs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IAA14_AT4G14550 1
IAA16_AT3G04730 2
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AXR3_AT1G04250 6
PAP2_AT4G29080 5
Pt171693_gw1.I.293.1 2
OsIBCD000843 5
IAA8_AT2G22670 6
IAA9_AT5G65670 11
IAA2_AT3G23030 6
IAA1_AT4G14560 4
SHY2_AT1G04240 2
IAA15_AT1G80390 11
IAA6_AT1G52830 4
IAA19_AT3G15540 4
Pt180980_gw1.I.9580.1
Pt180995_gw1.I.9595.1
IAA5_AT1G15580 4
Pp164608_estExt_fgenesh1_pg.C_730007 30
Pp219923_estExt_Genewise1.C_1840013 40
OsIBCD000527 15
IAA12_AT1G04550 17
IAA13_AT2G33310 11
IAA11_AT4G28640 31
IAA10_AT1G04100 38
IAA18_AT1G51950 37
PAP1_AT3G16500 33
OsIBCD000591 16
IAA29_AT5G25890 2
IAA20_AT2G46990 9
IAA30_AT3G62100 9
IAA31_AT3G17600 12
OsIBCD001221 12
IAA29_AT4G32280 1
IAA34_AT1G15050 40
IAA32_AT2G01200 9
corb_UMD_Coleochaete_c11109_c_s_1
AtIAA33 9
AT3G24650 38
AT1G19850.1_MP 39
Consensus
100%
Conservation
0%
60
80
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IAA14_AT4G14550 1
IAA16_AT3G04730 2
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PAP2_AT4G29080 5
Pt171693_gw1.I.293.1 2
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IAA9_AT5G65670 24
IAA2_AT3G23030 6
IAA1_AT4G14560 4
SHY2_AT1G04240 2
IAA15_AT1G80390 14
IAA6_AT1G52830 4
IAA19_AT3G15540 4
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IAA10_AT1G04100 38
IAA18_AT1G51950 37
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IAA32_AT2G01200 23
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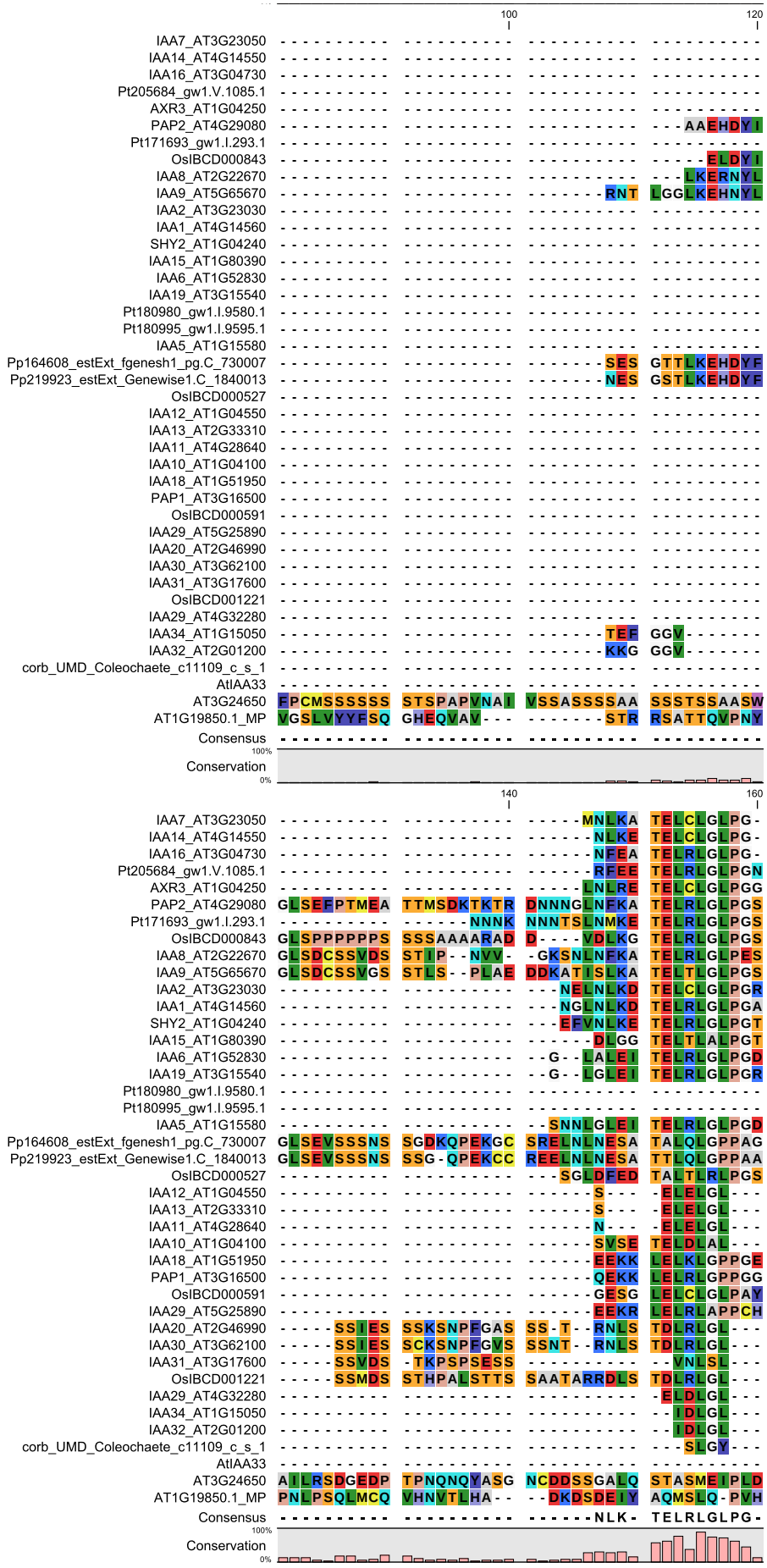
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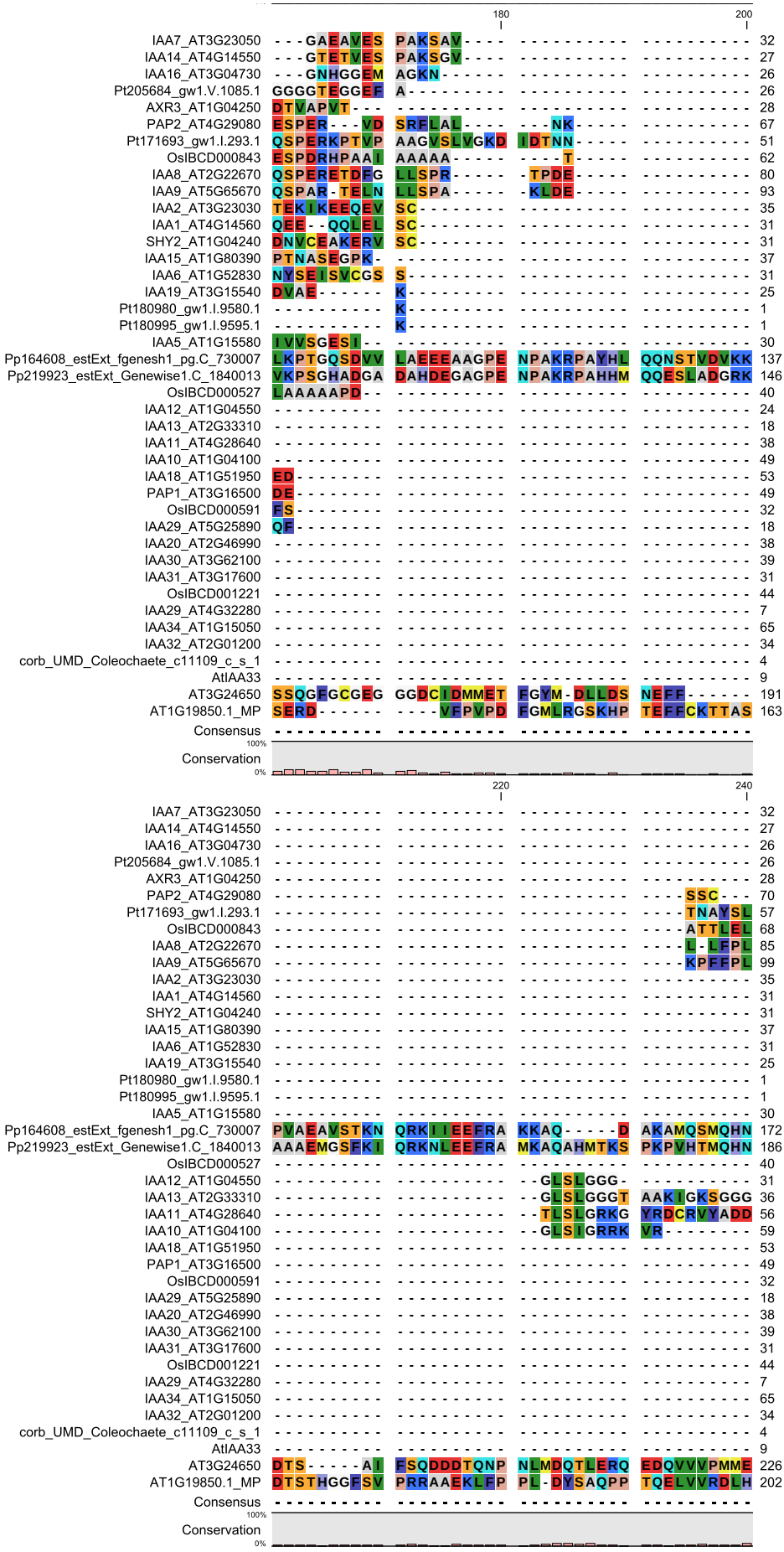
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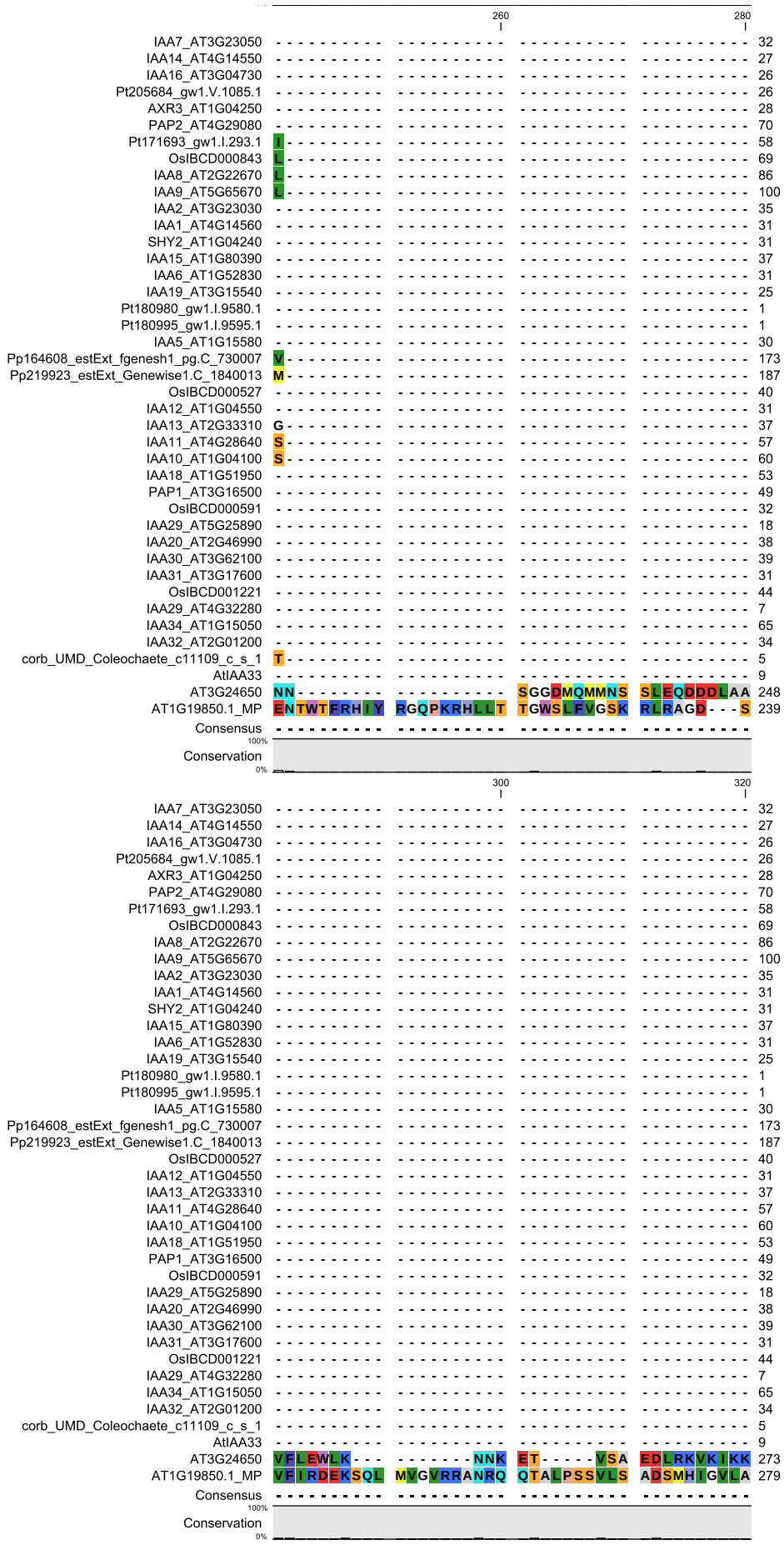
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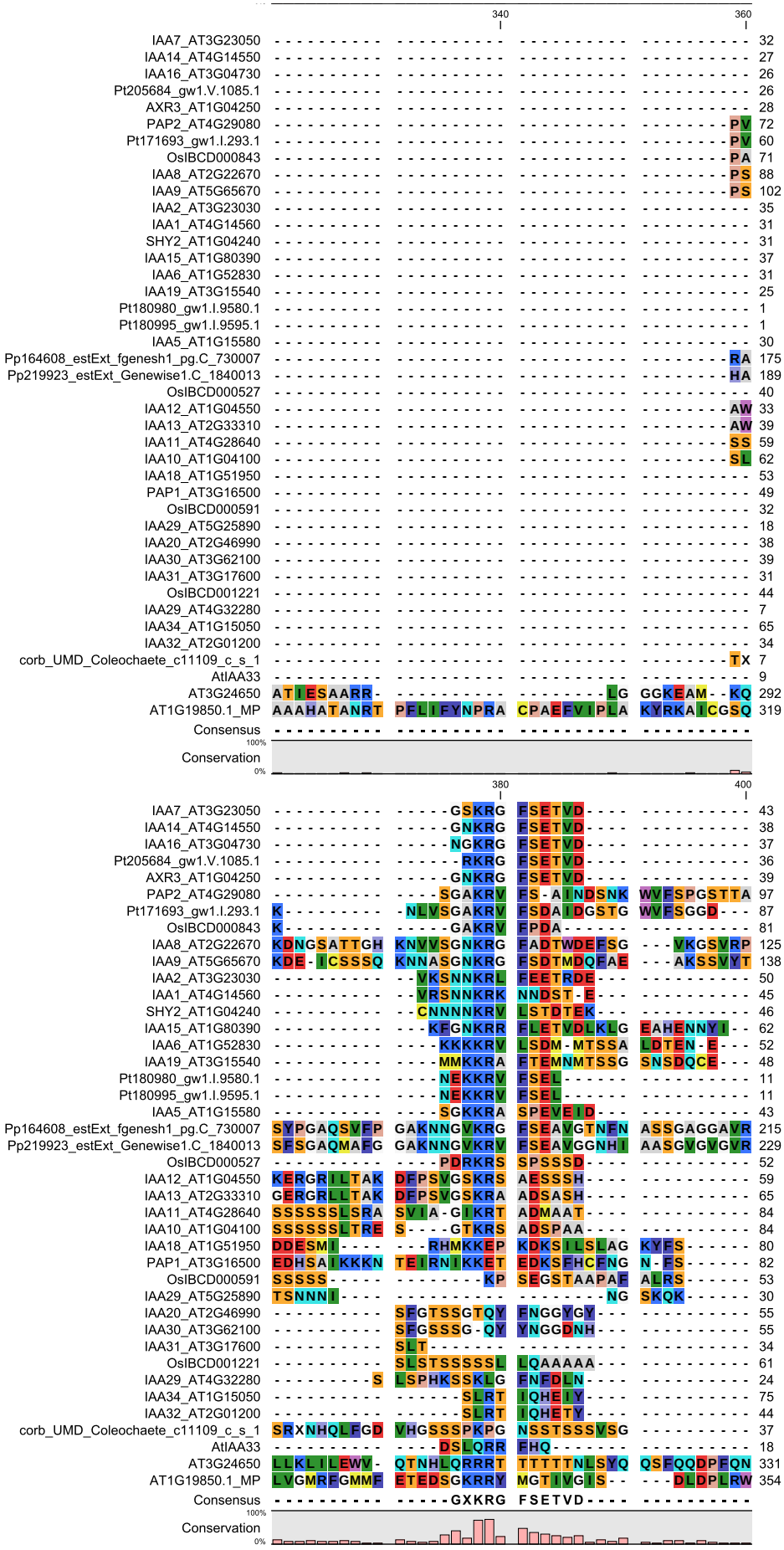
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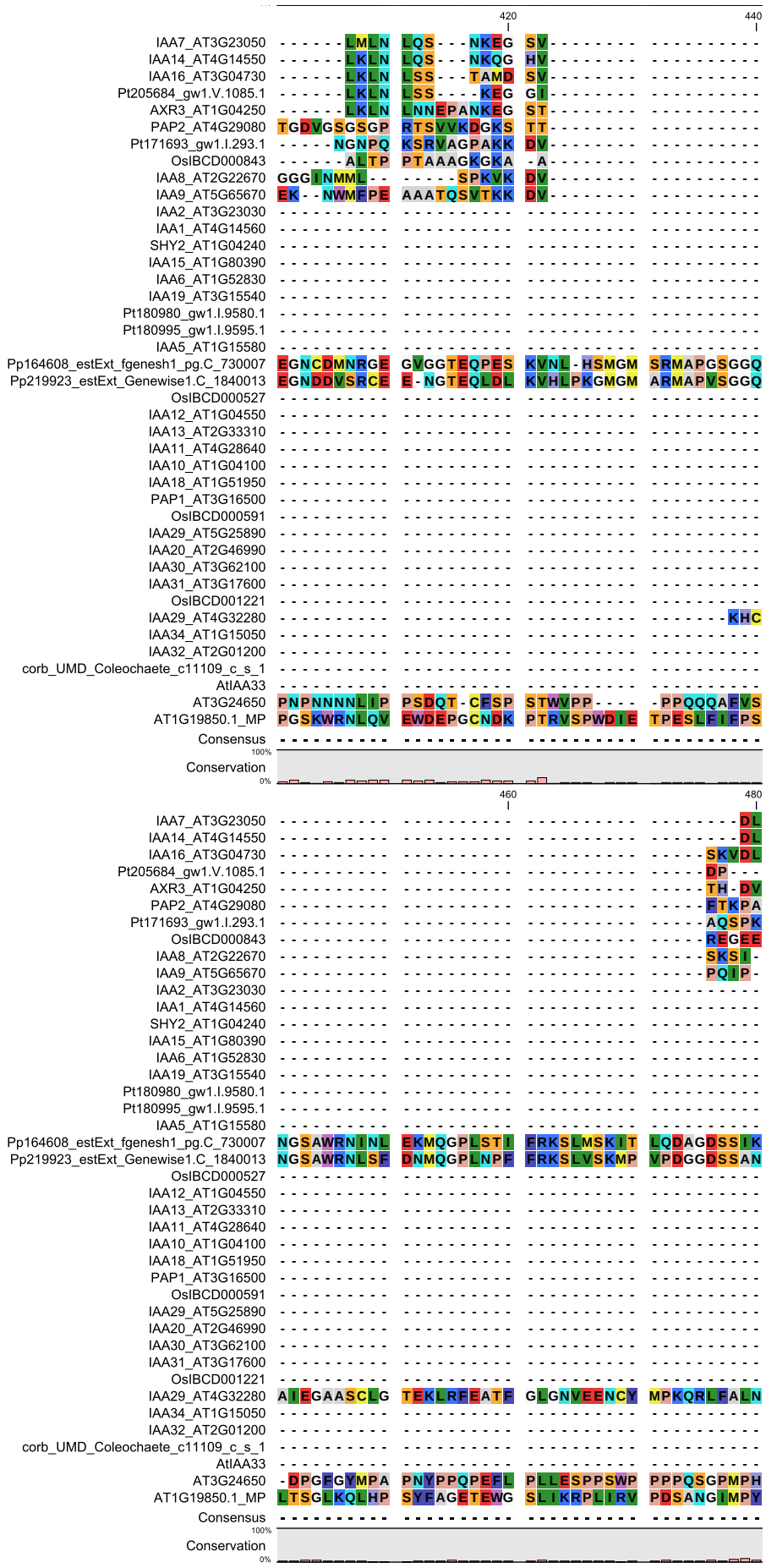
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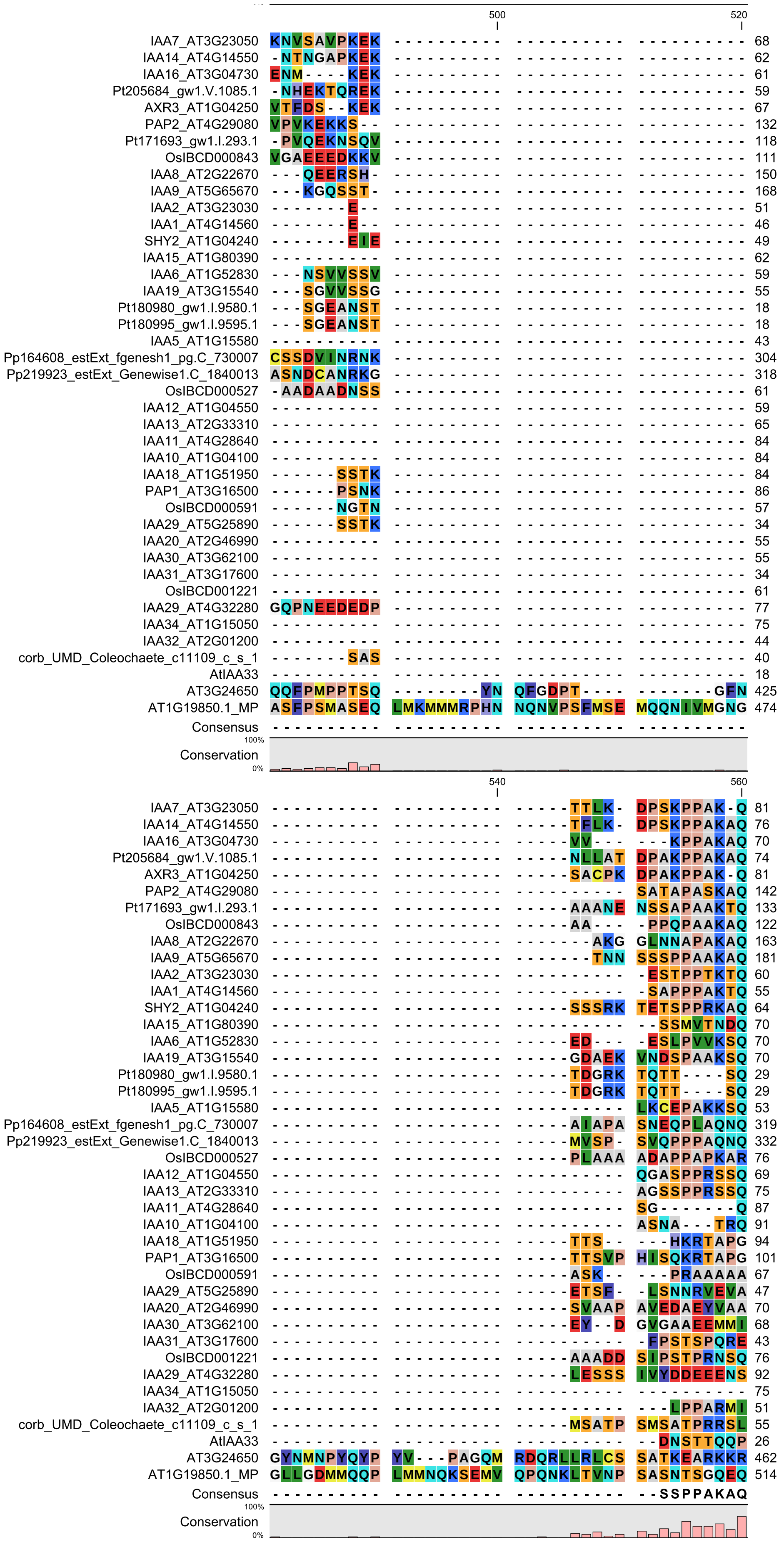
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IAA1_AT4G14560 -------E-- ---------- ---------- ----------- 46
SHY2_AT1G04240 -------EIE ---------- ---------- ----------- 49
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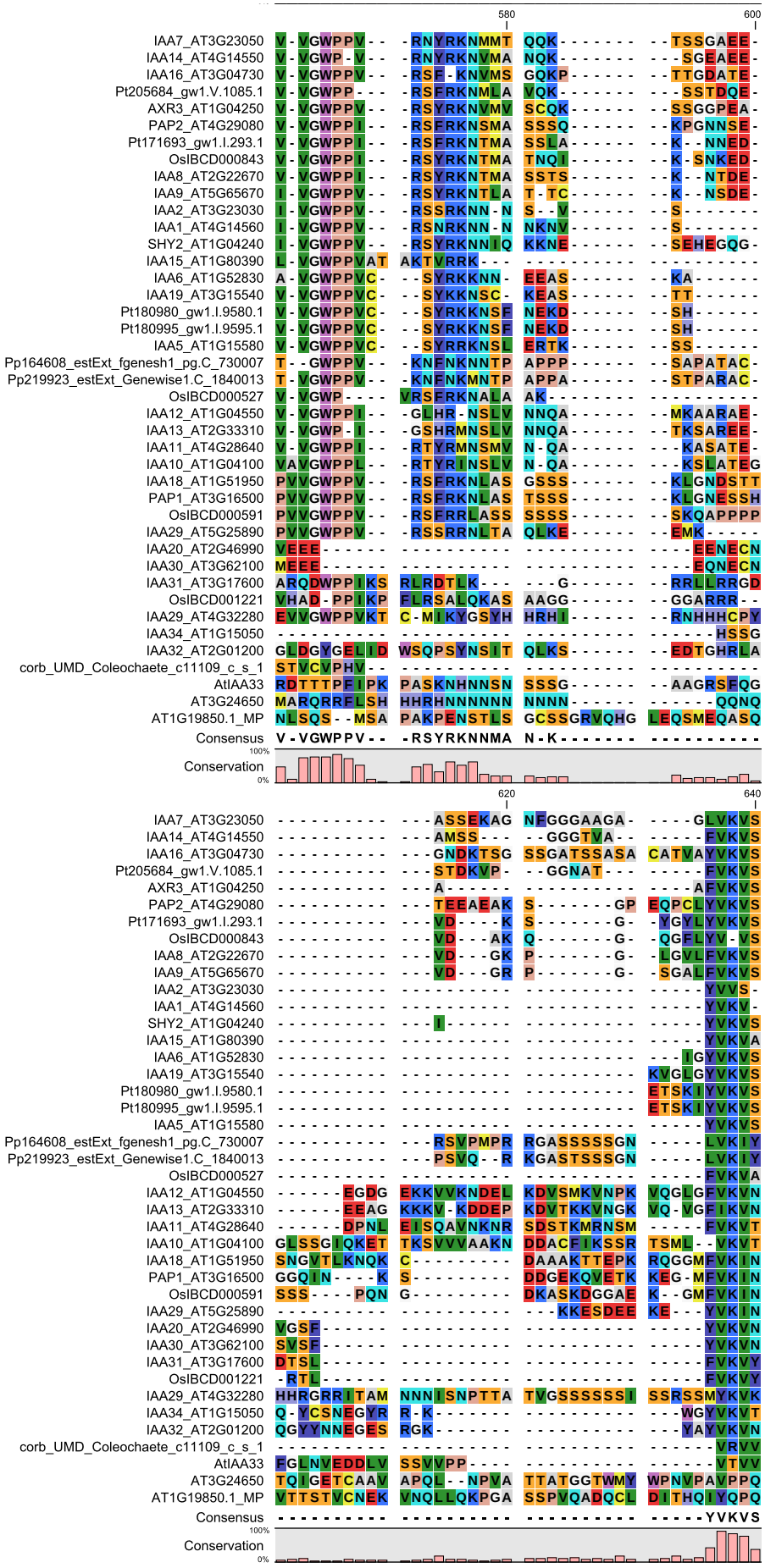
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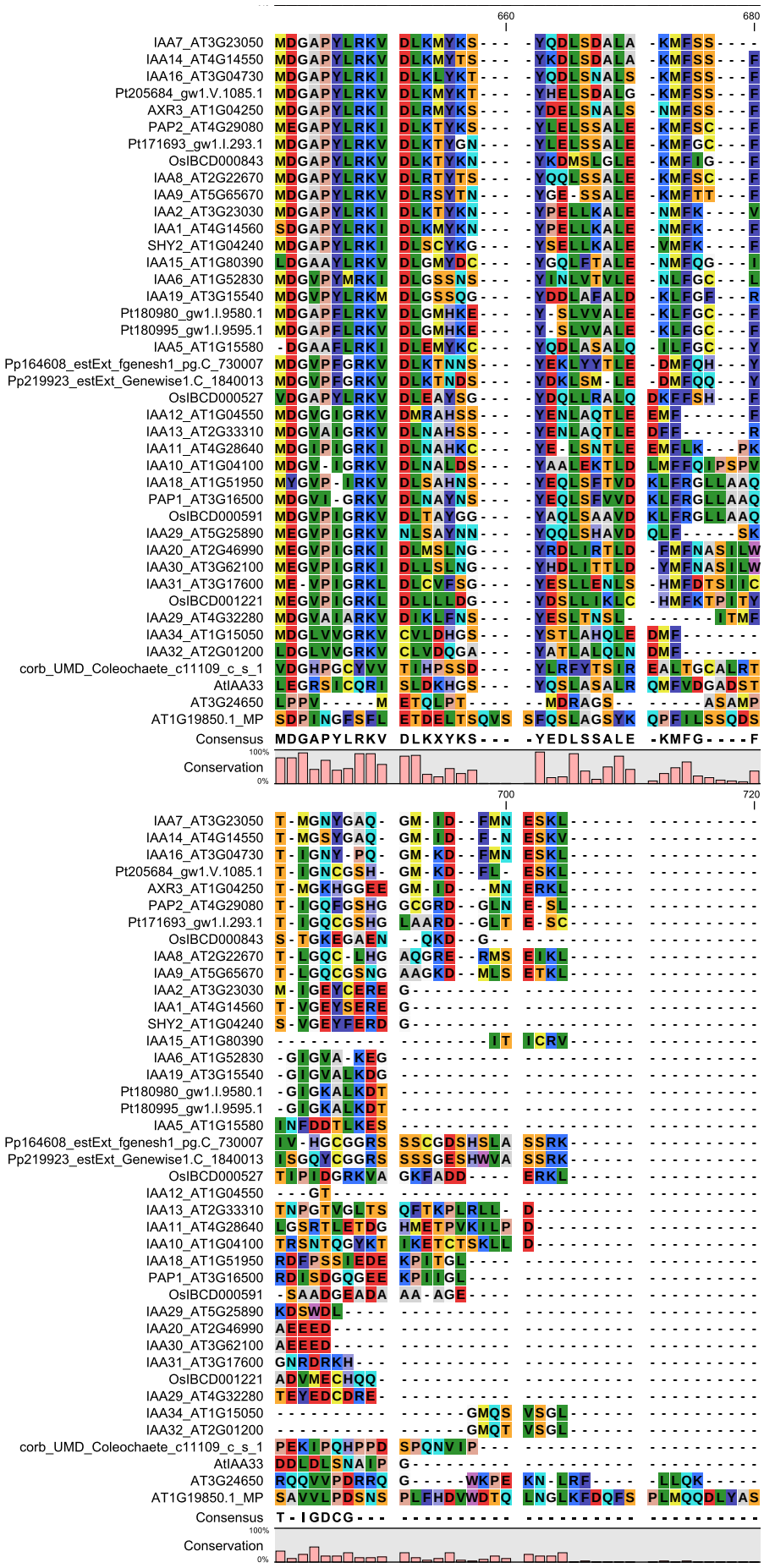
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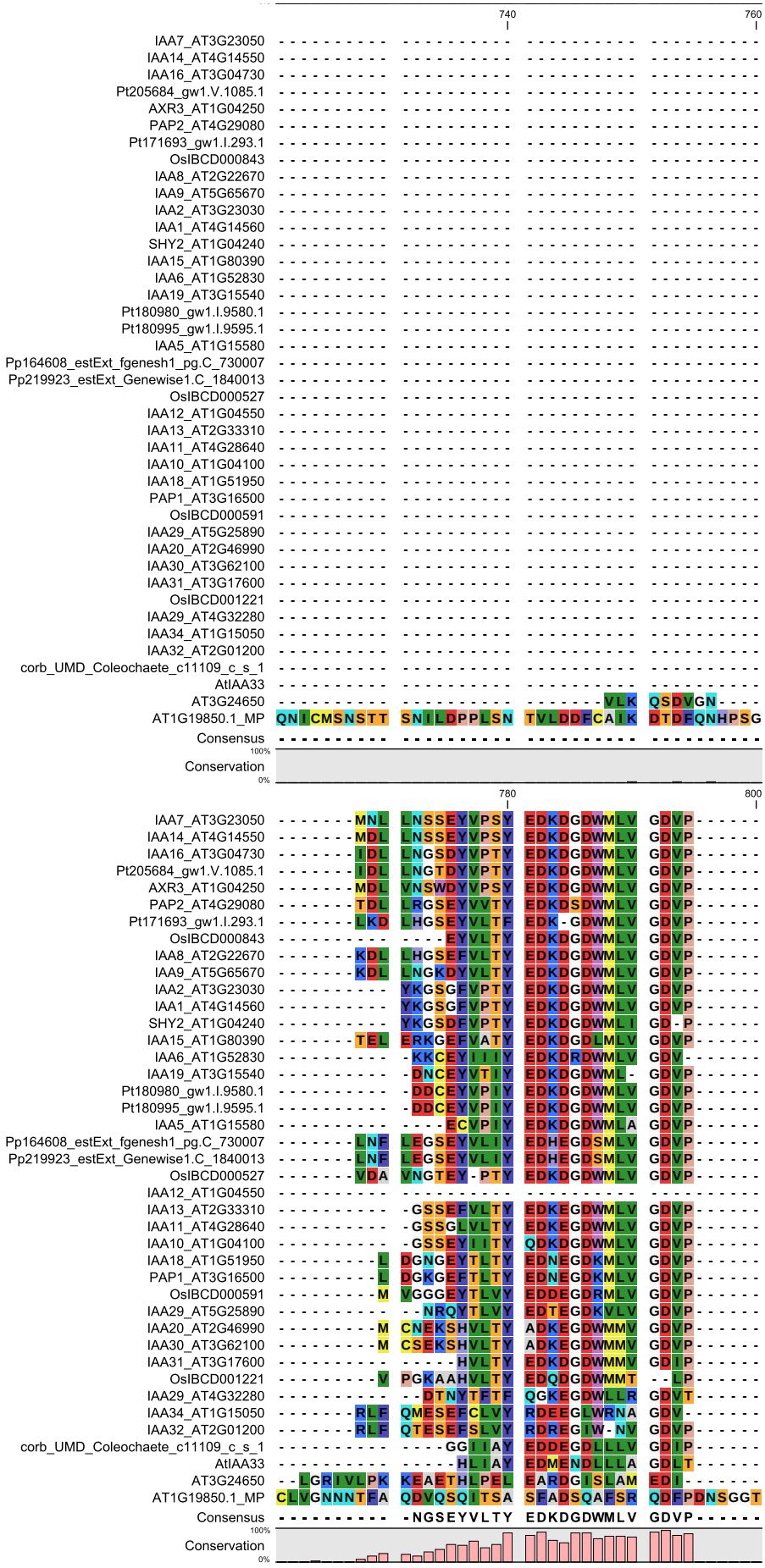
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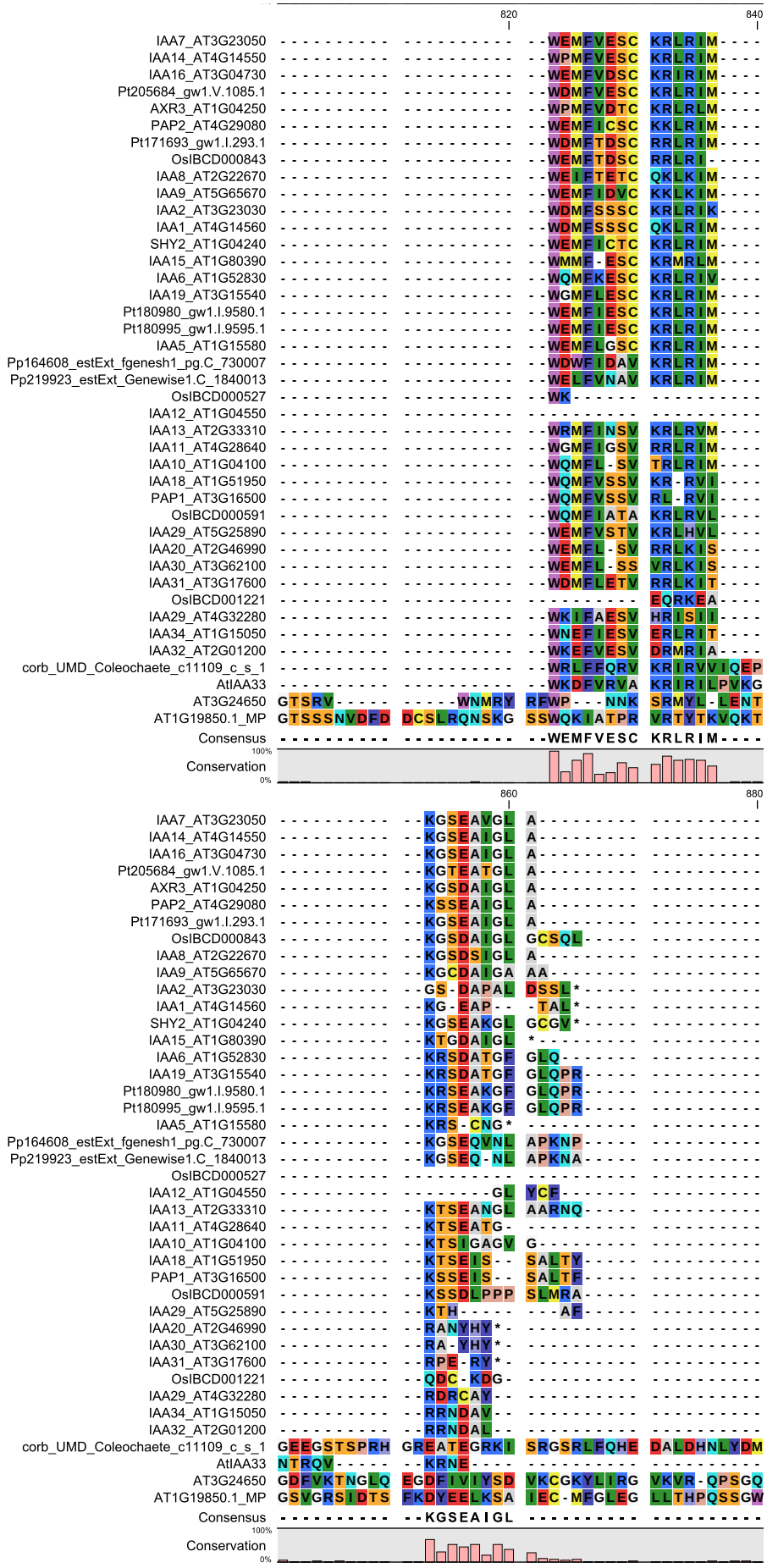
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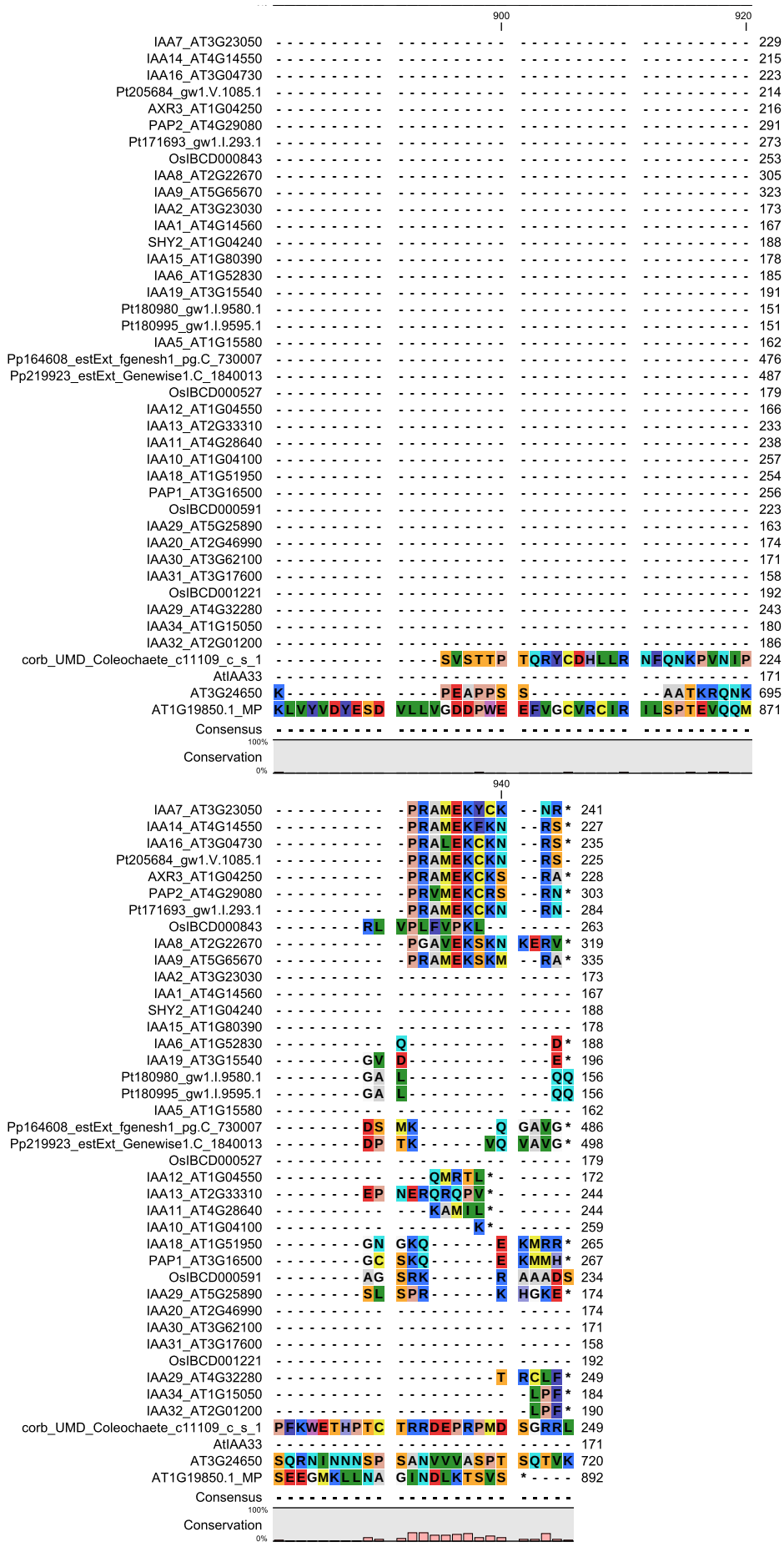
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corb_UMD_Coleochaete_c11109_c_s_1 249
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Consensus
100%
Conservation
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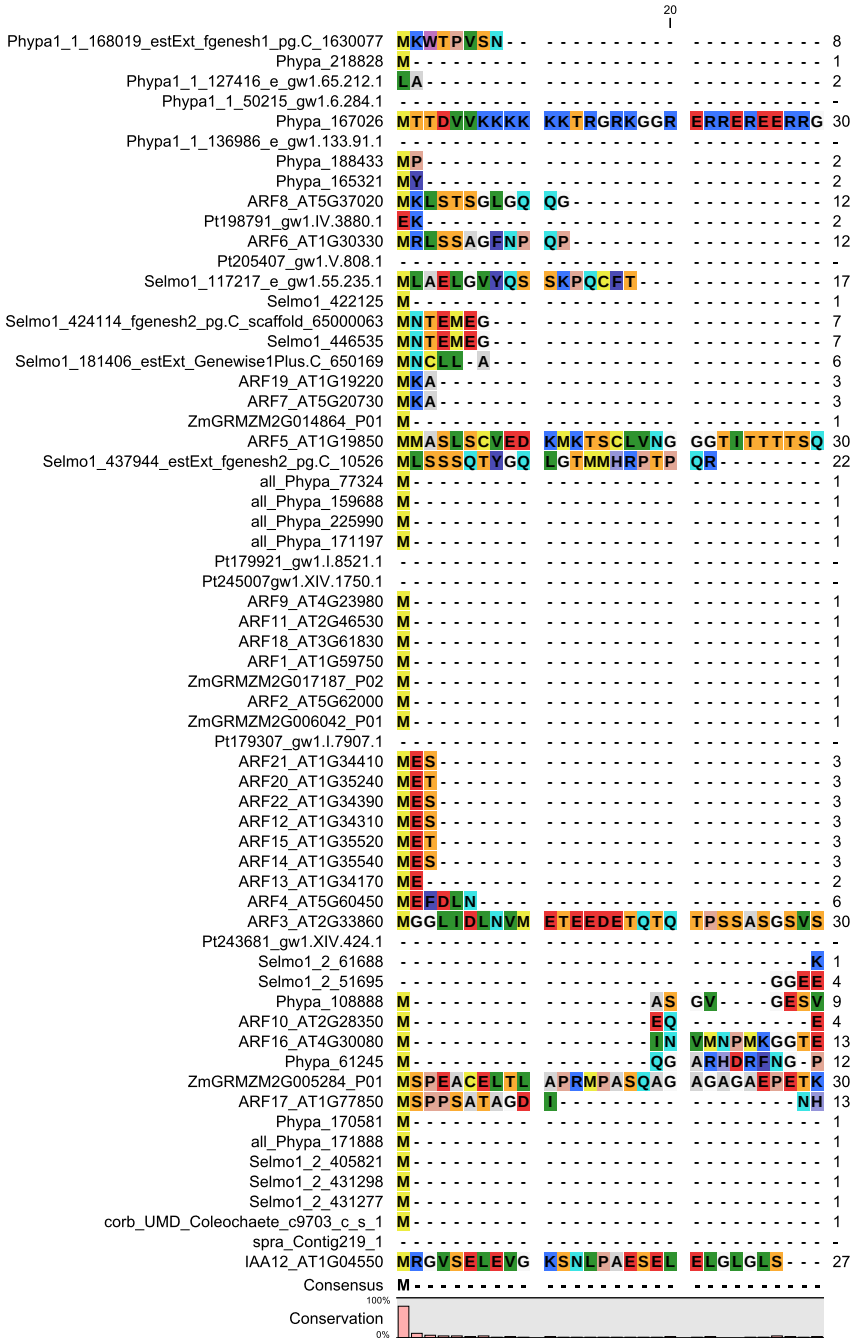
Figure S29 - alignment of ARFs and putative orthologs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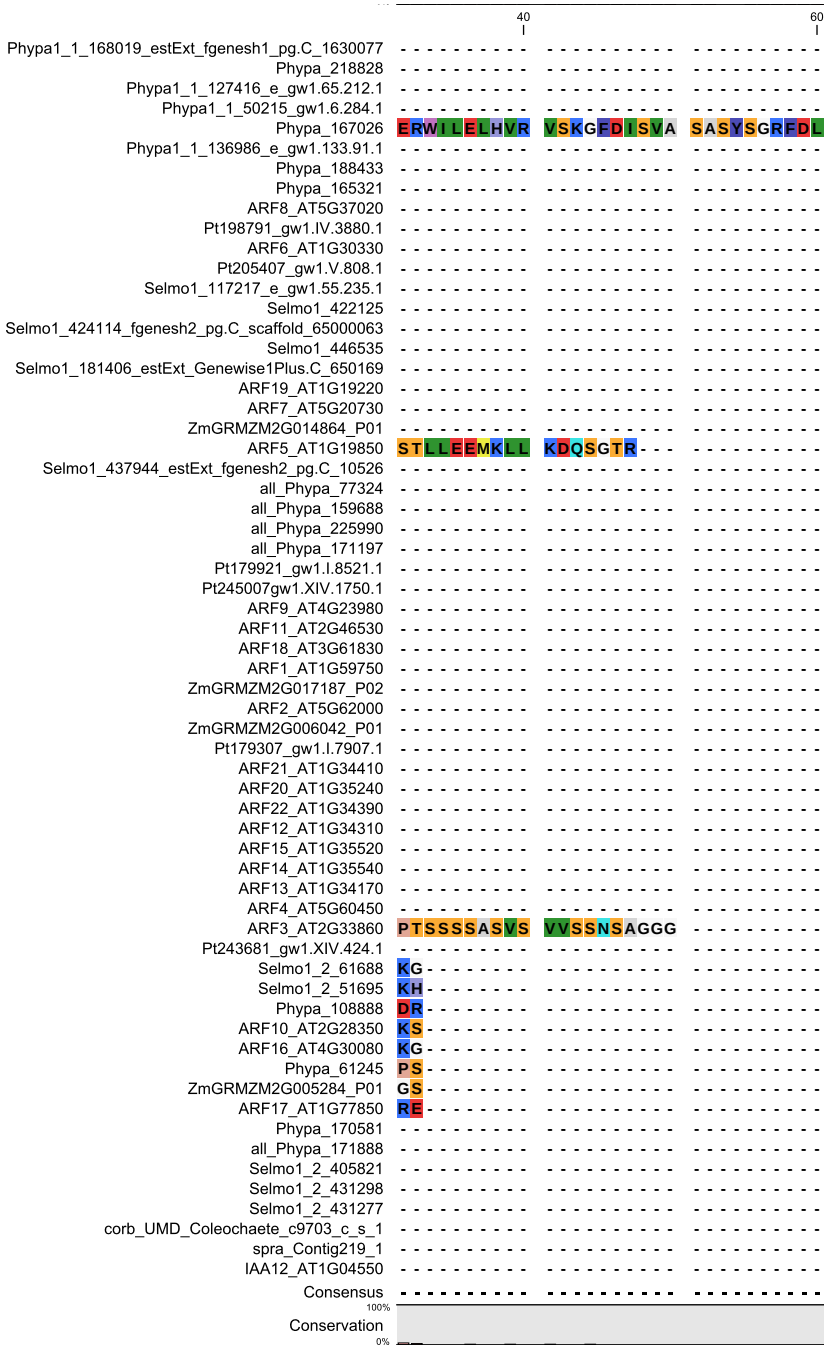
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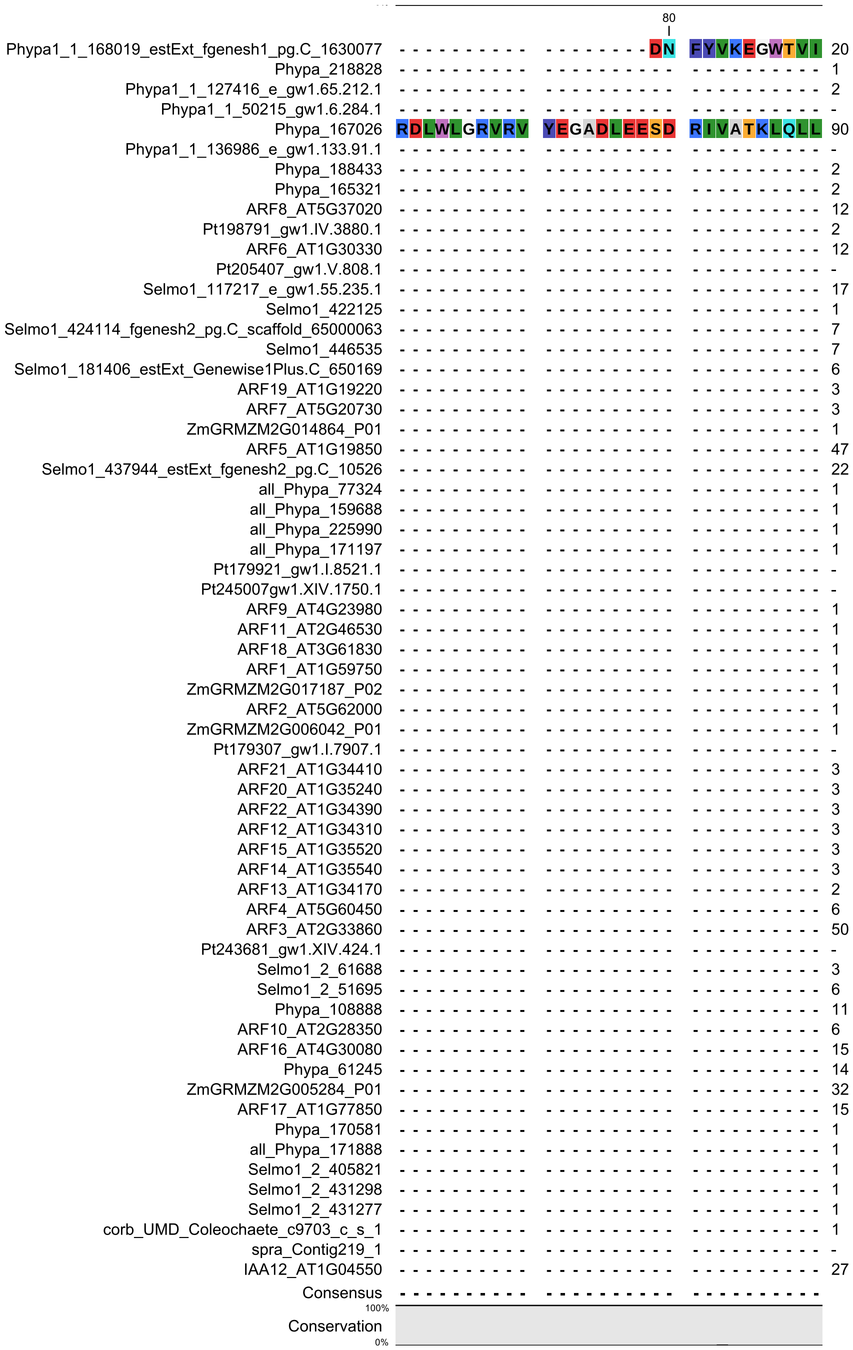
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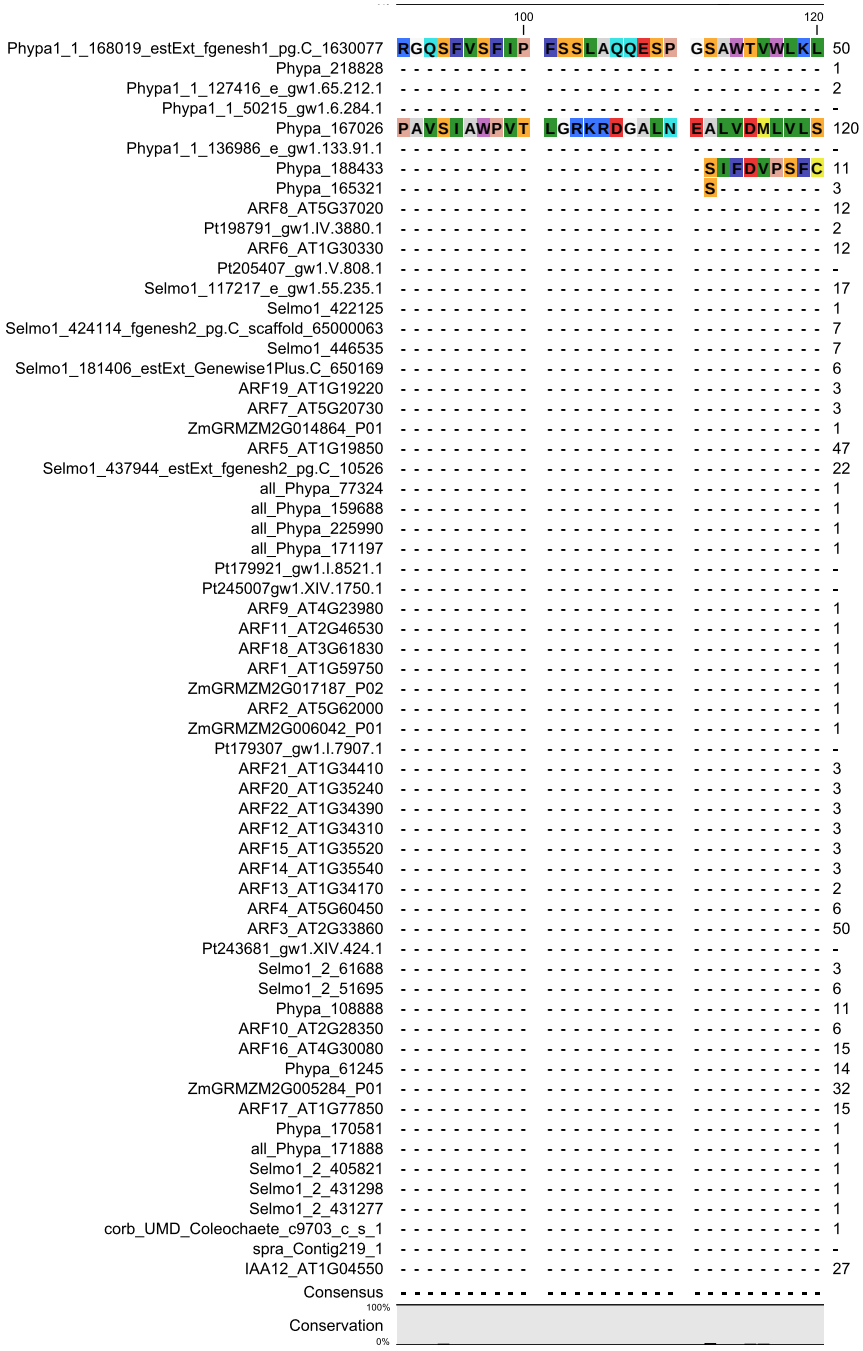
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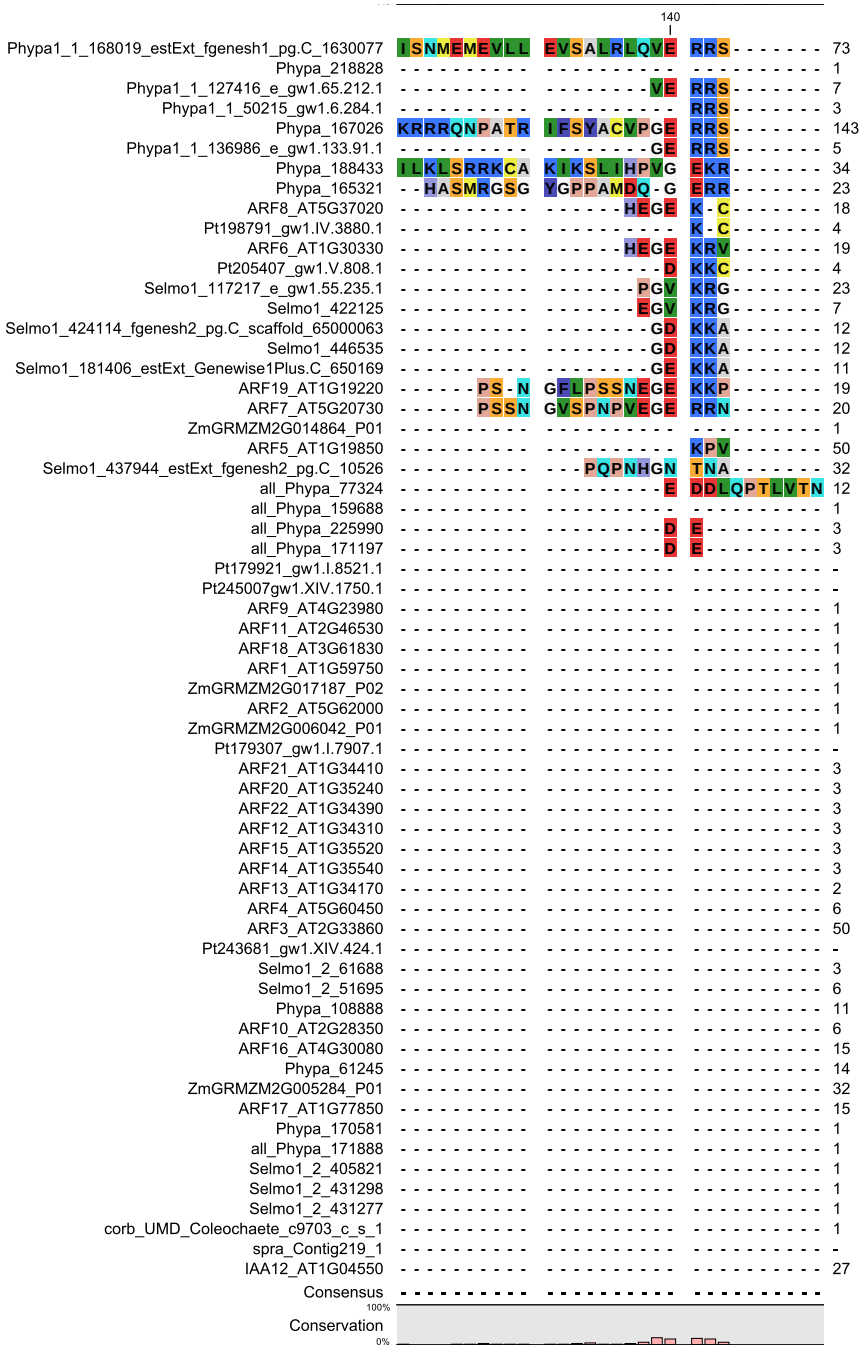
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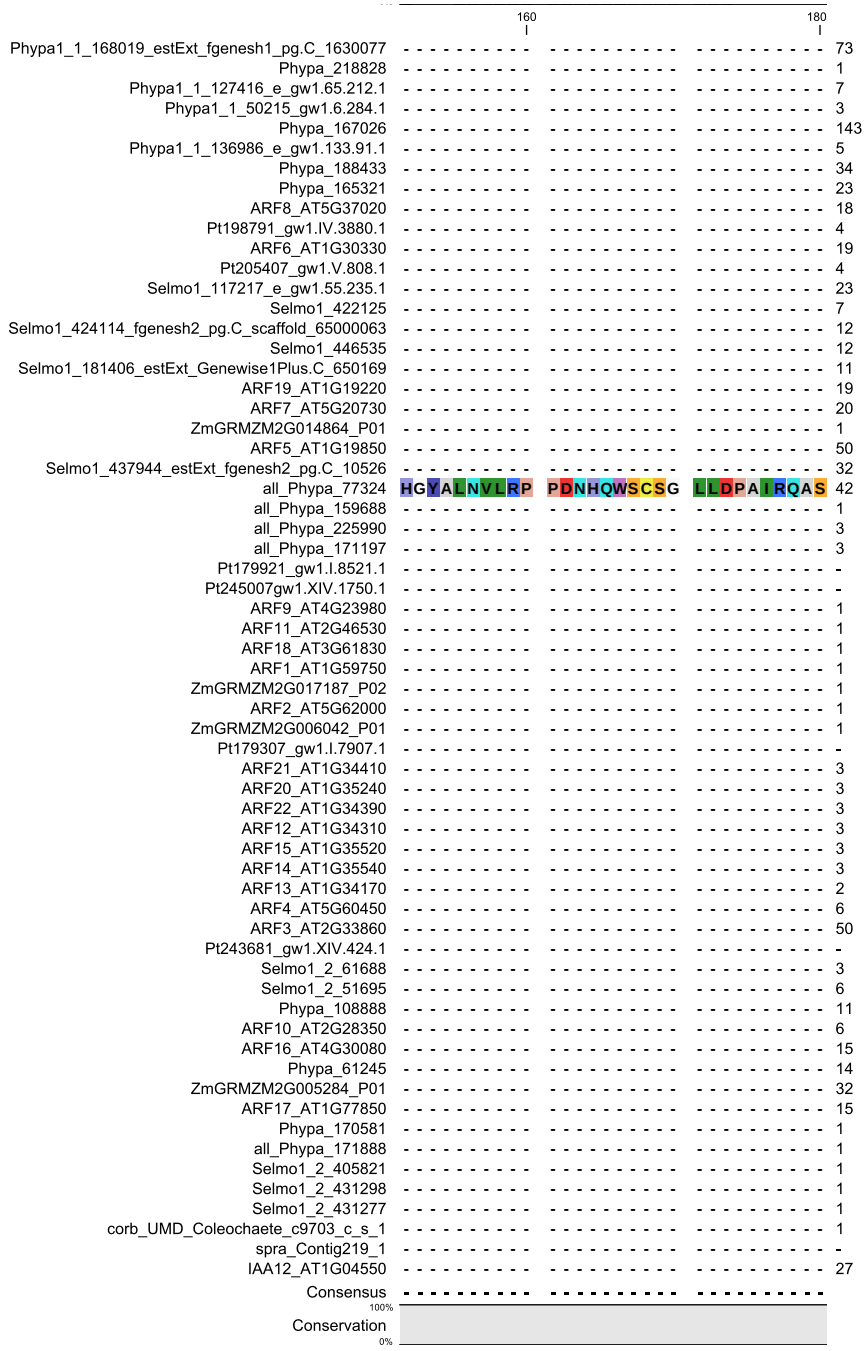
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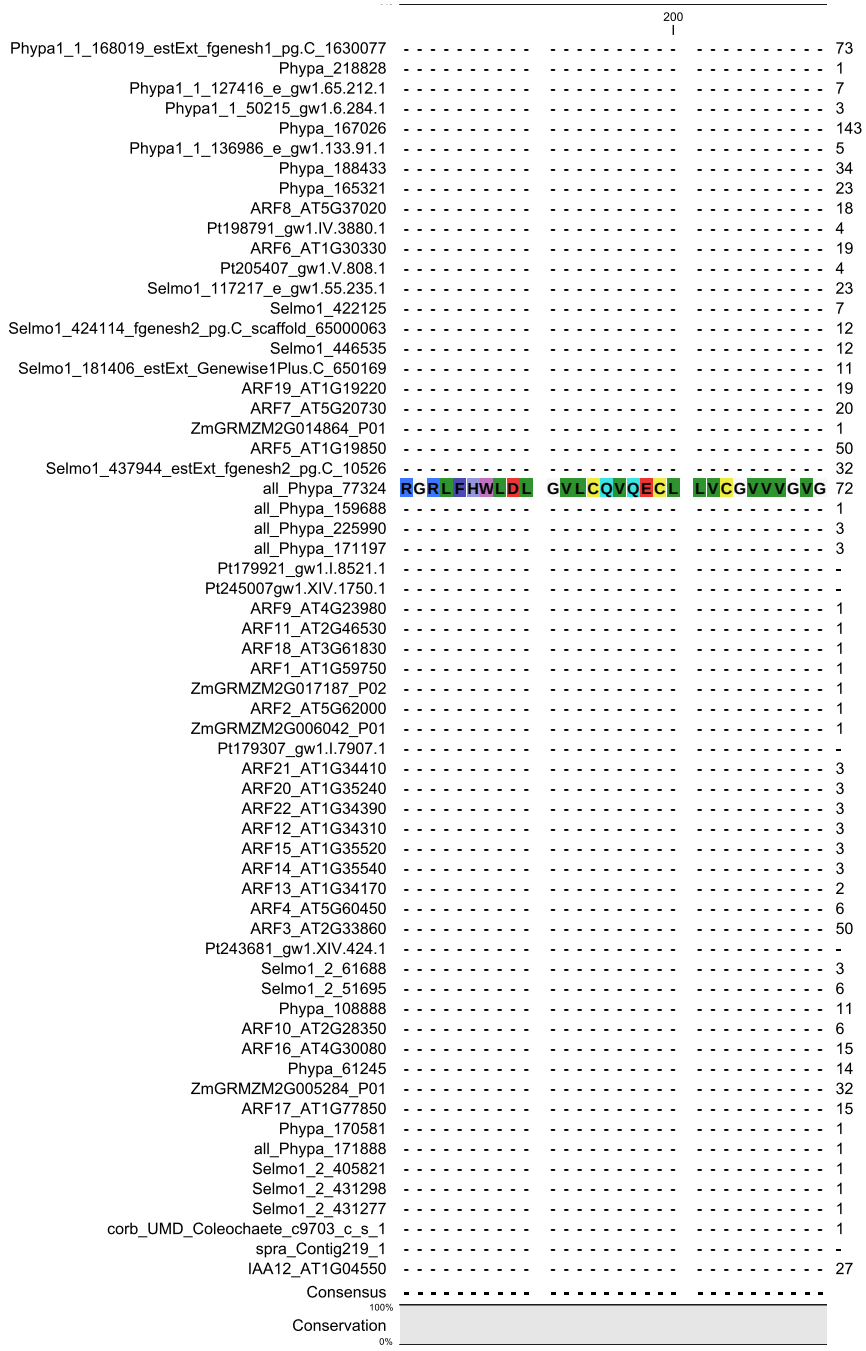
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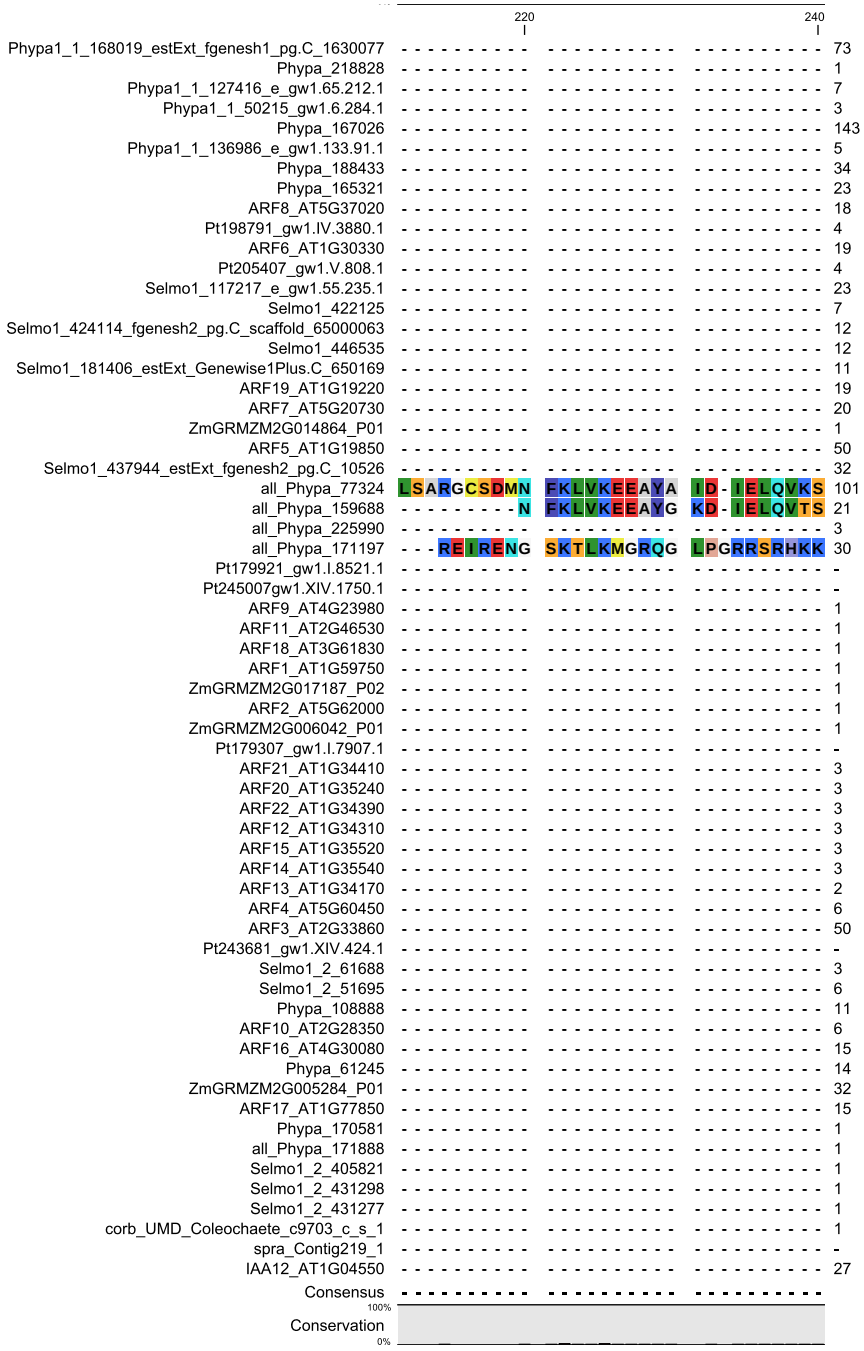
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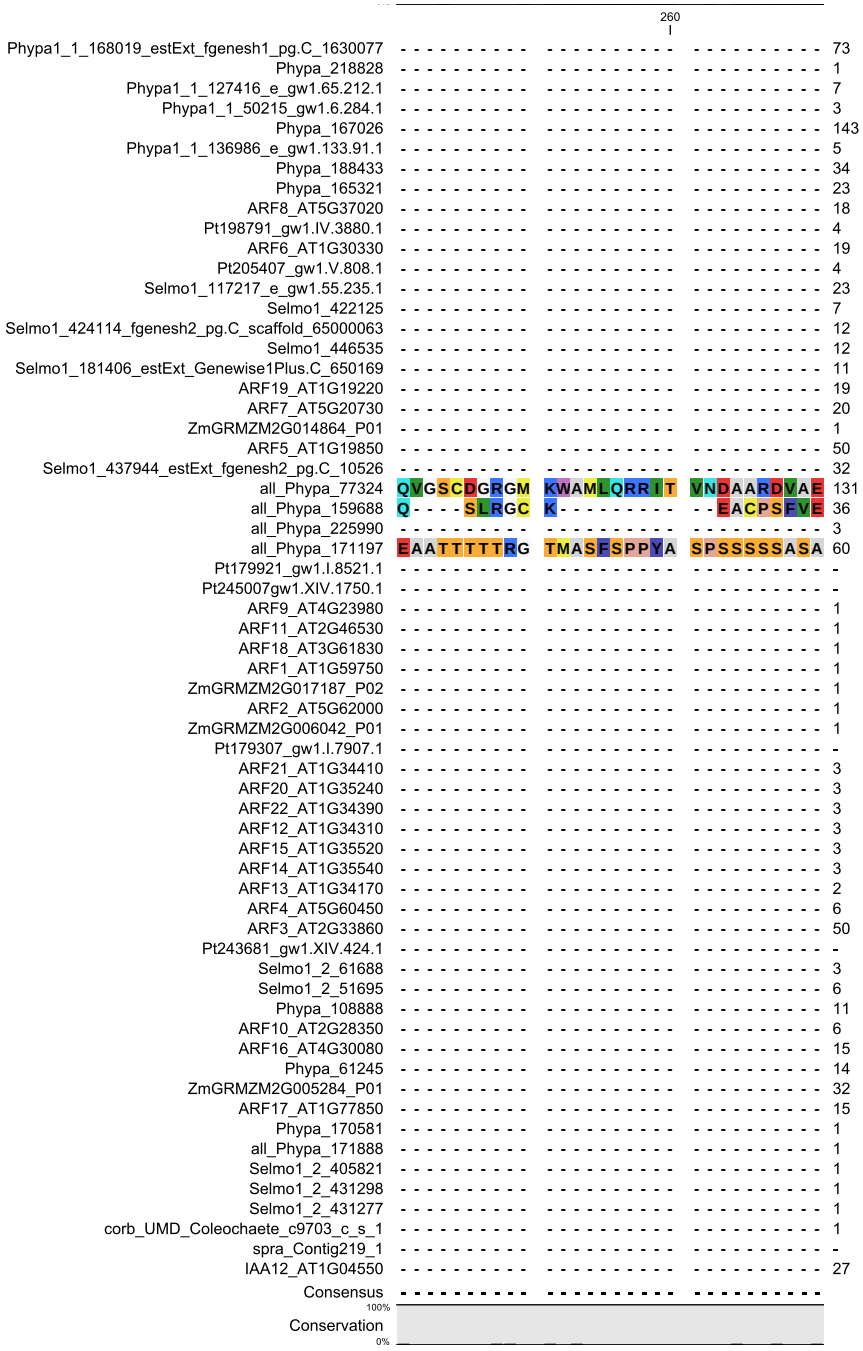
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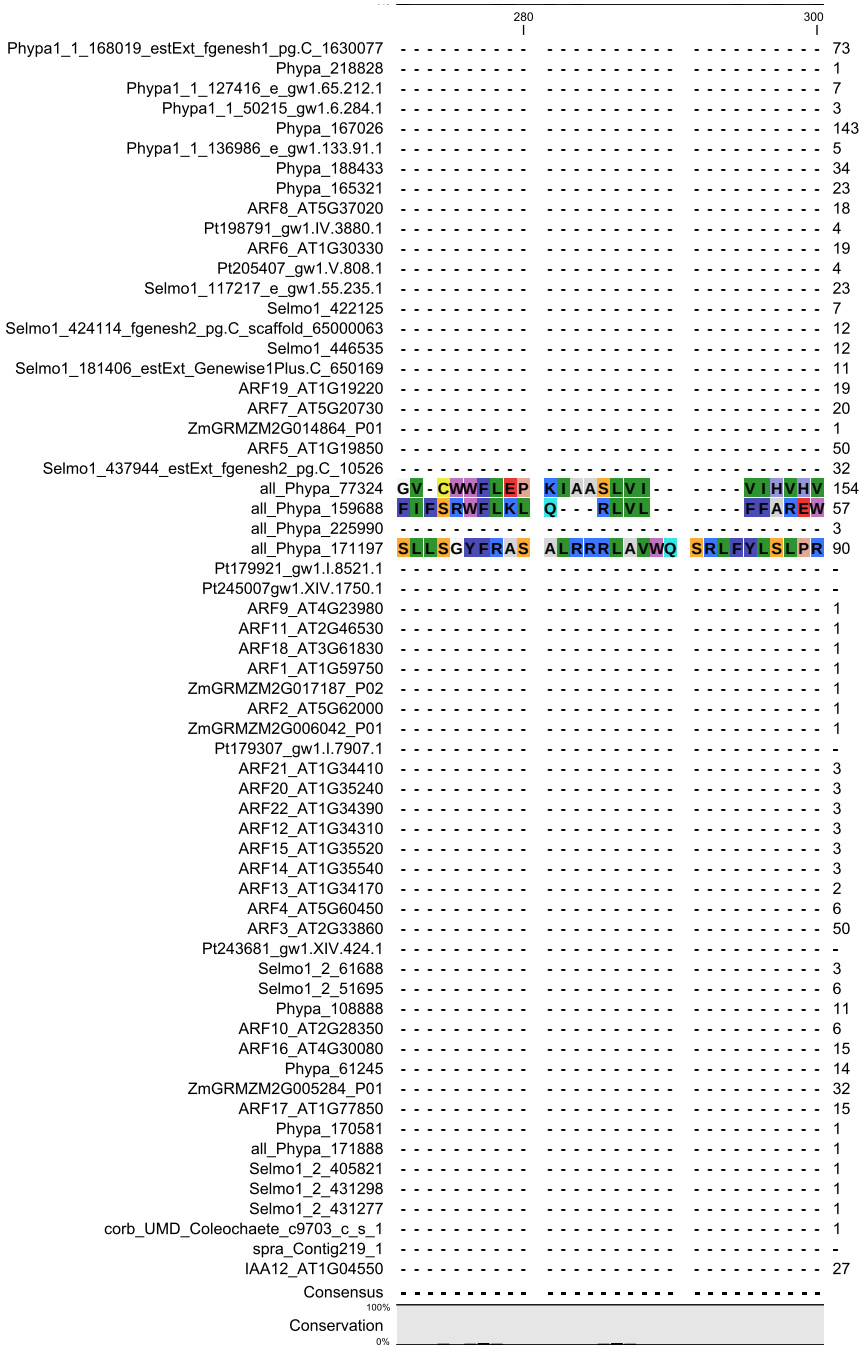
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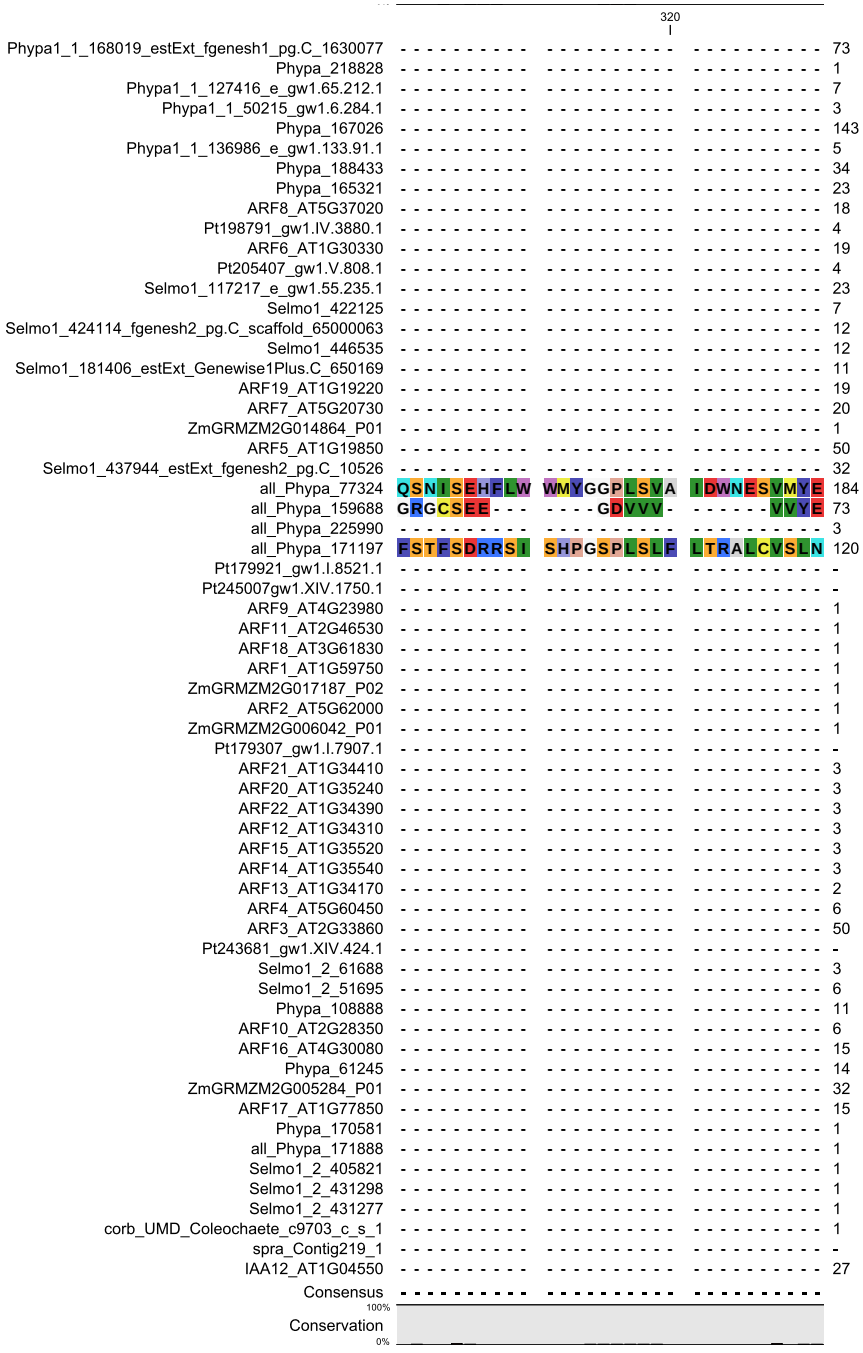
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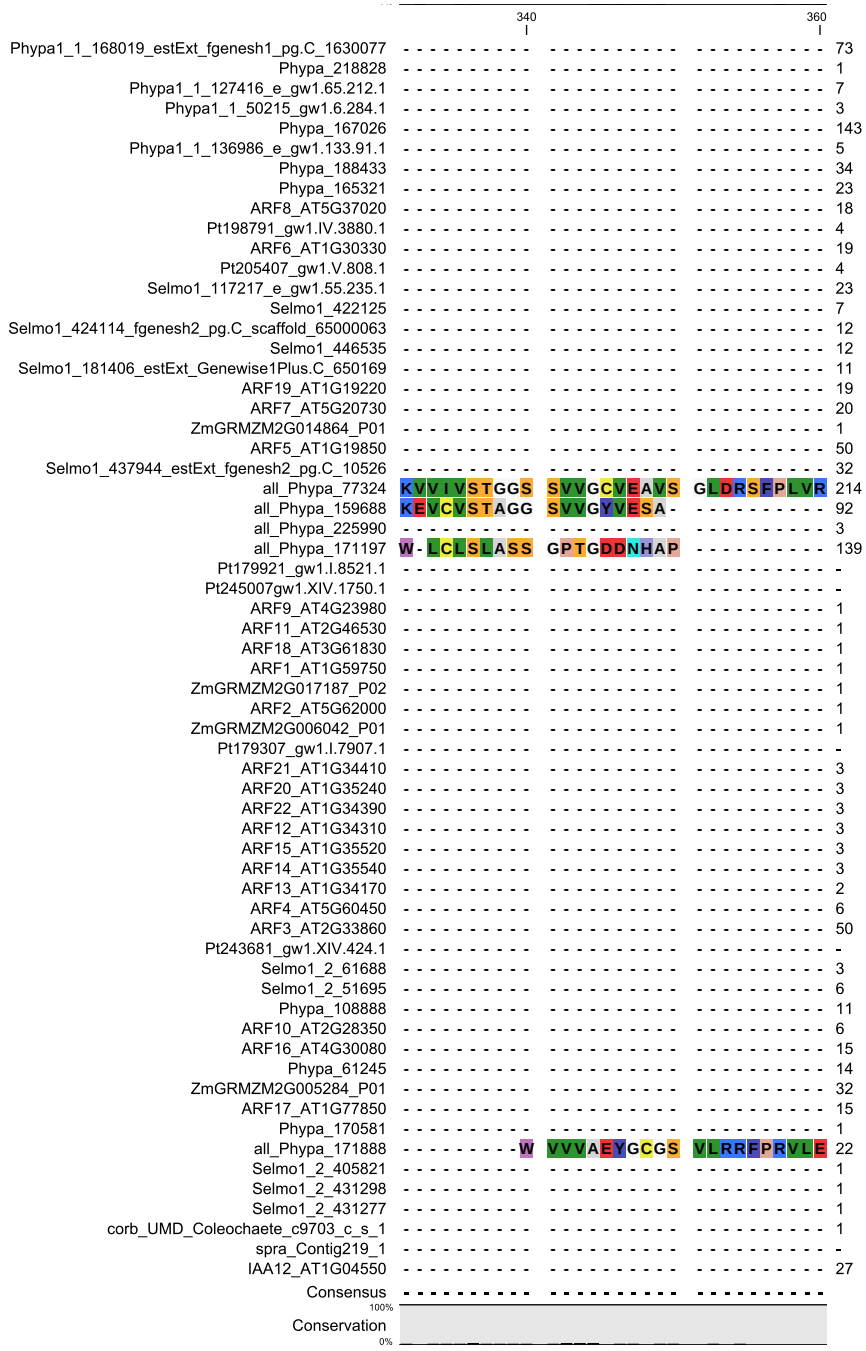
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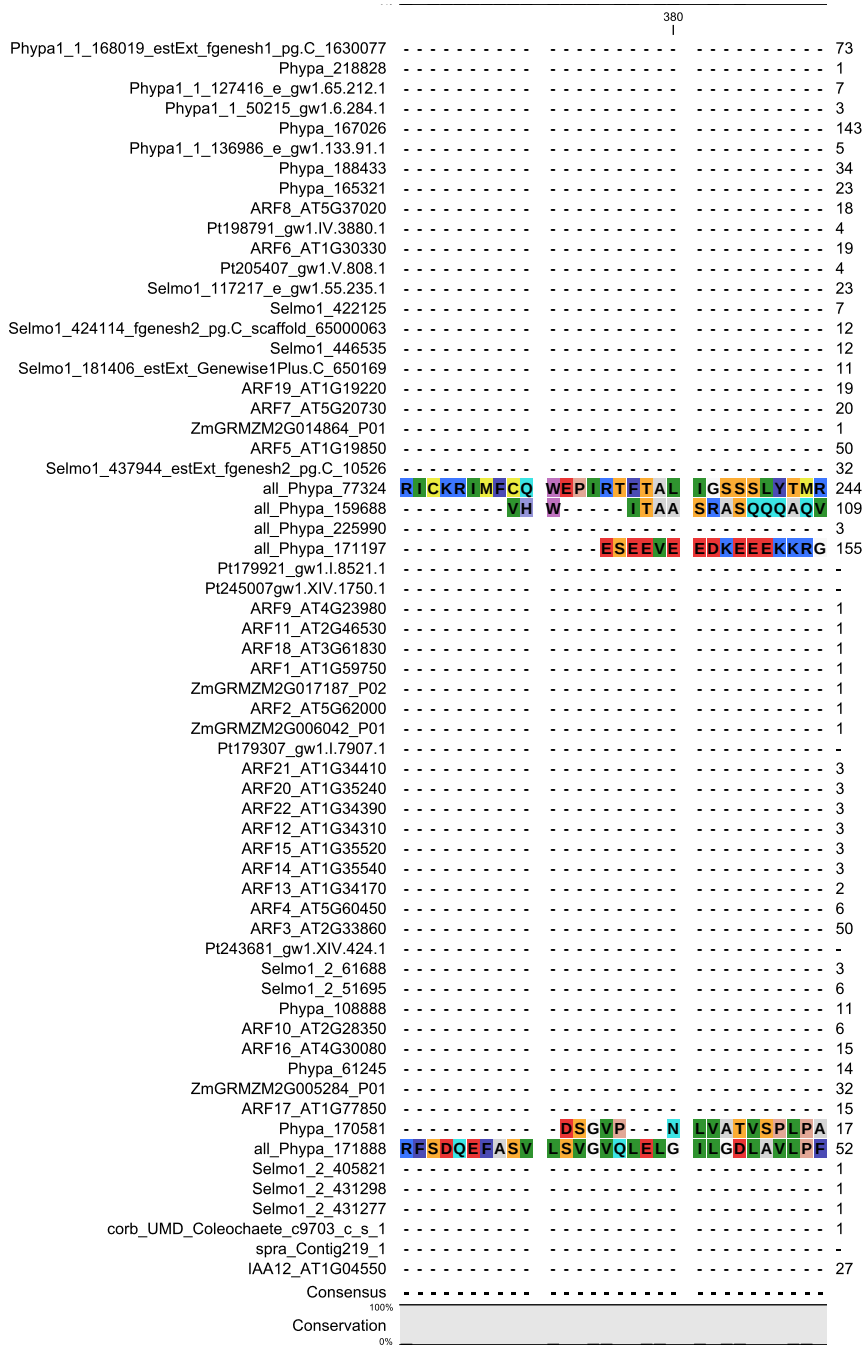
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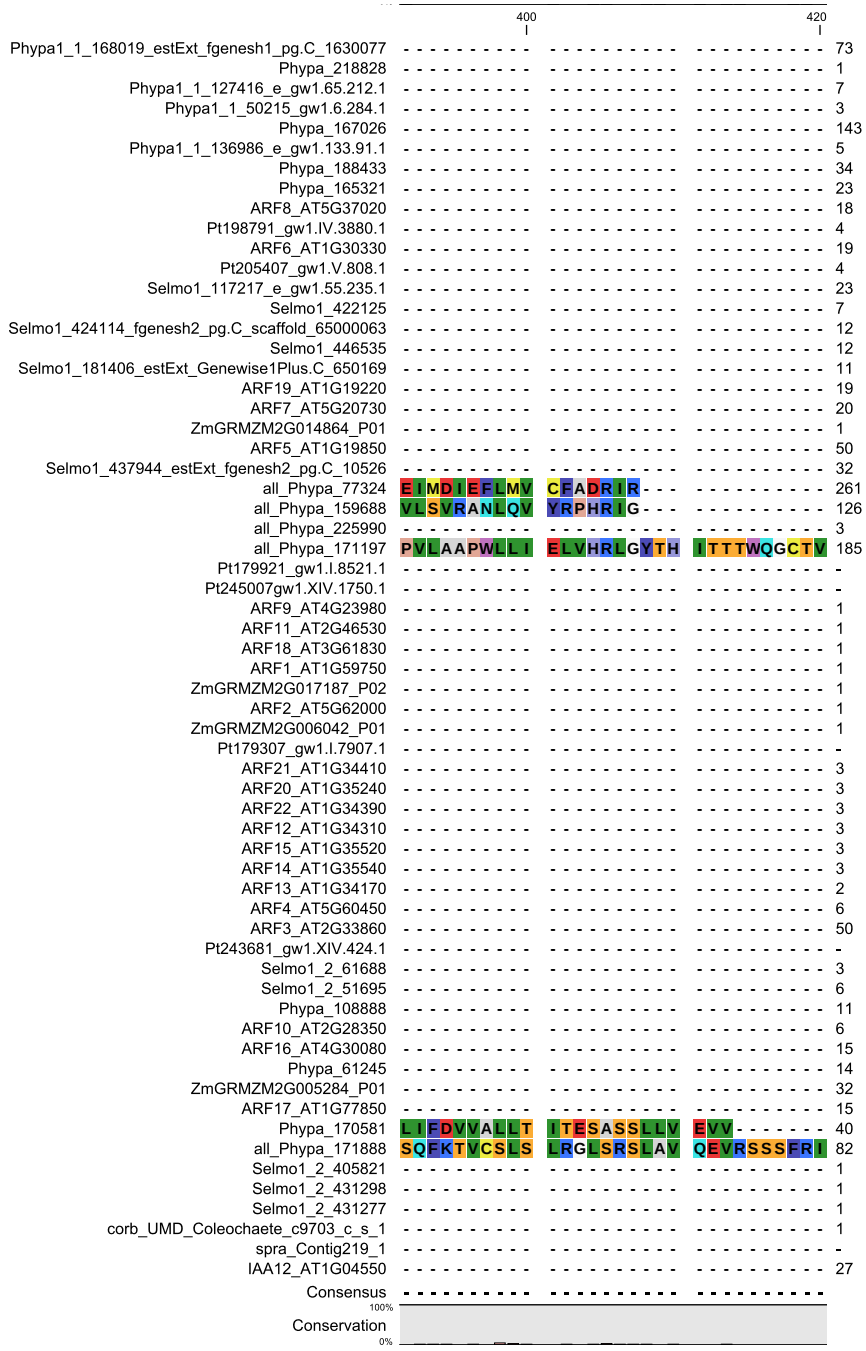
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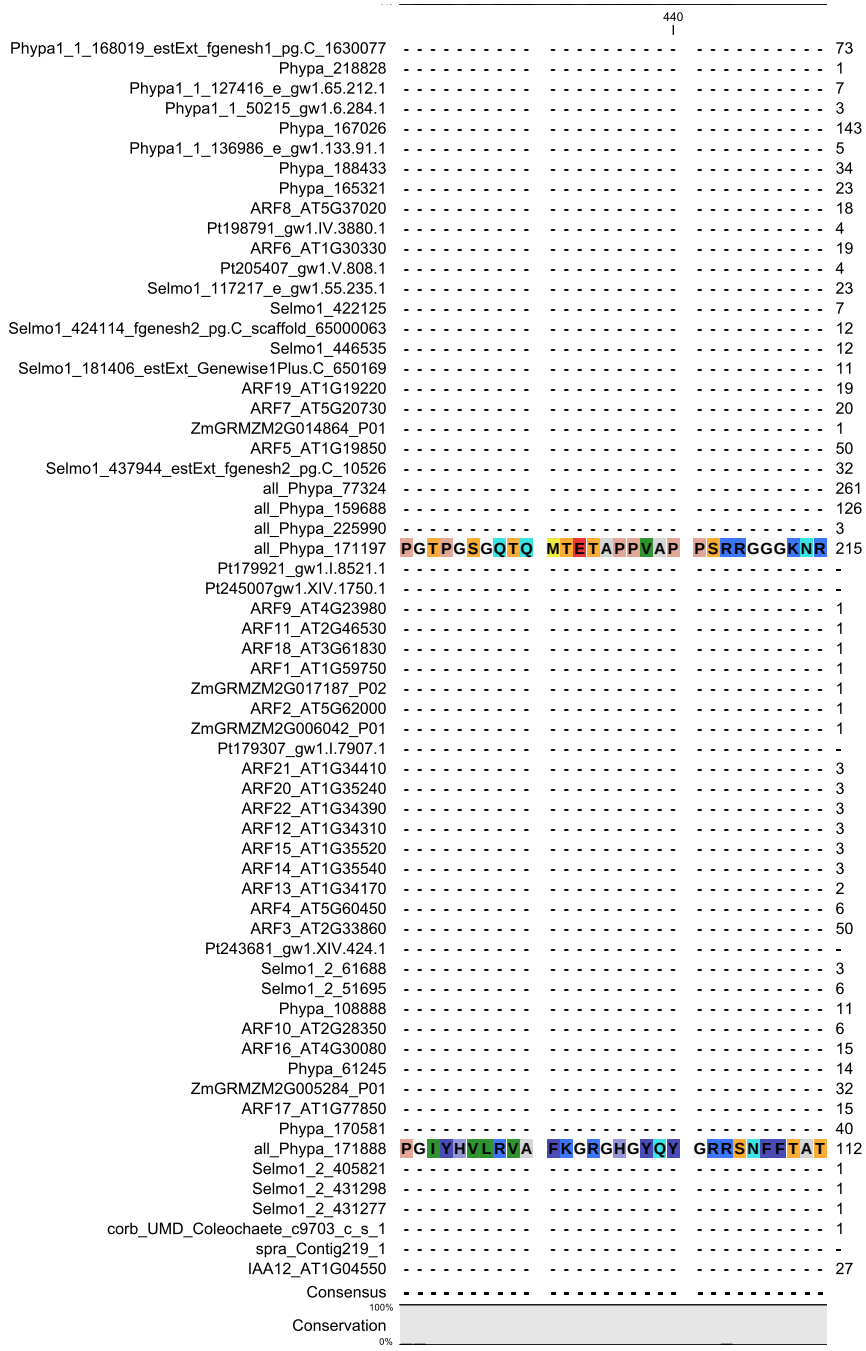
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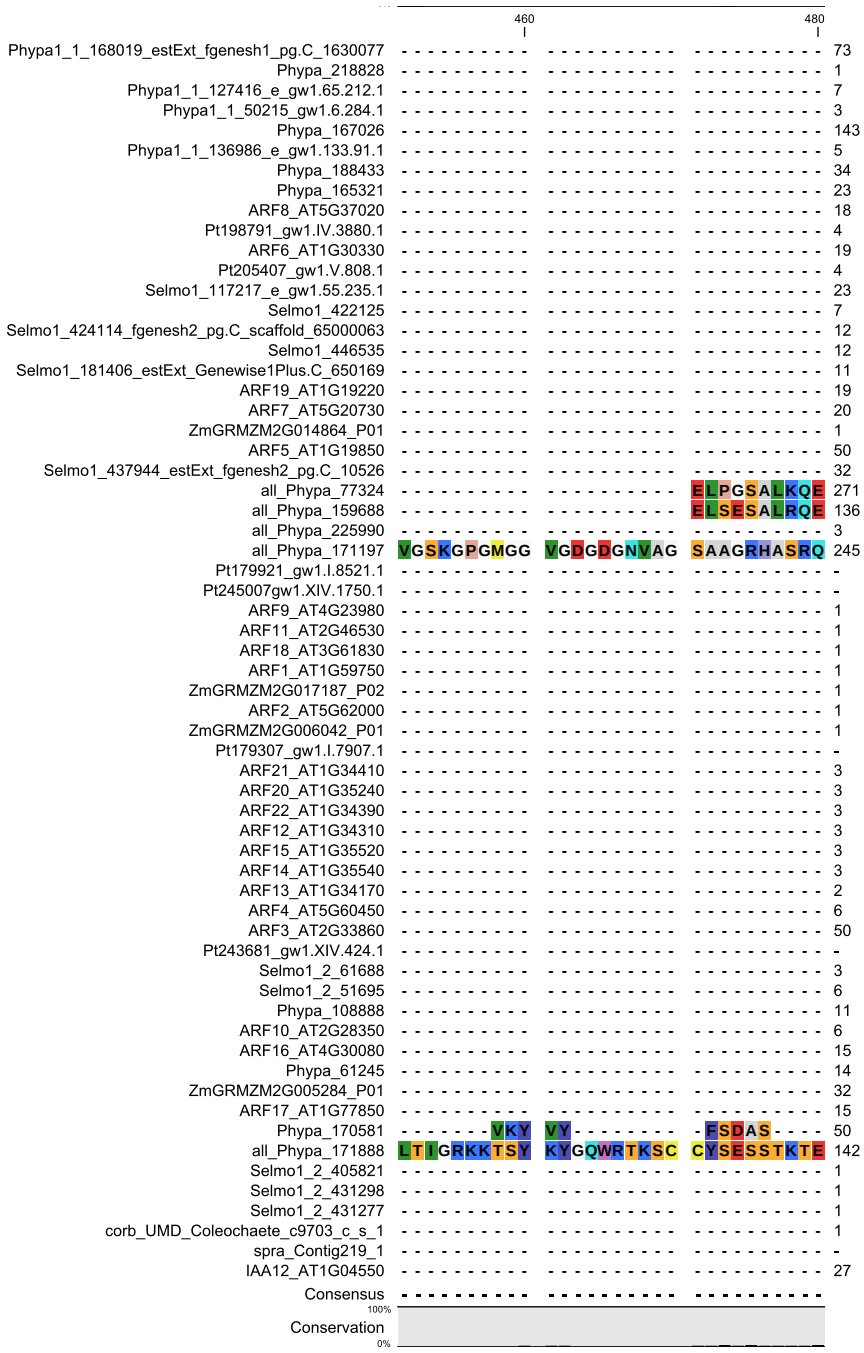
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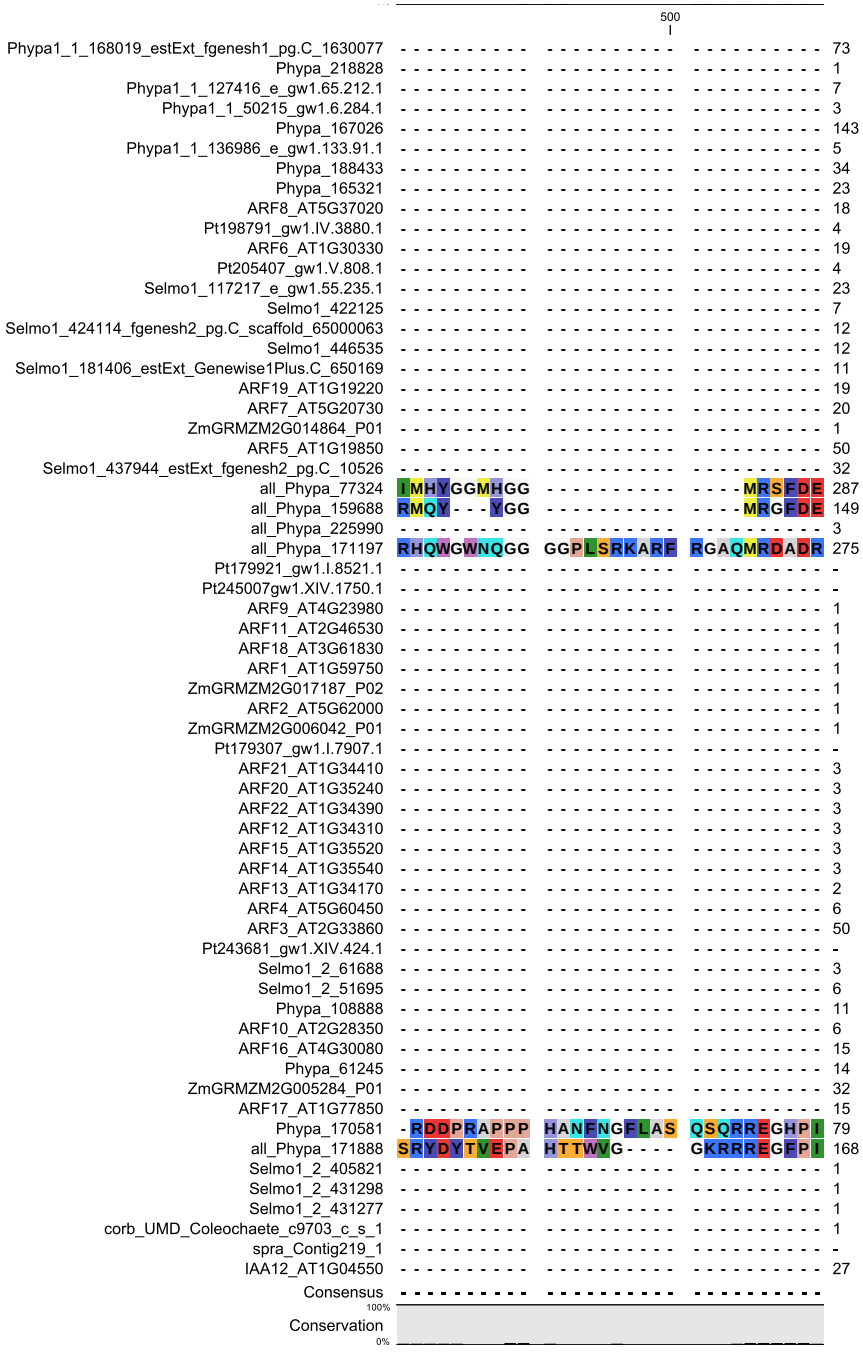
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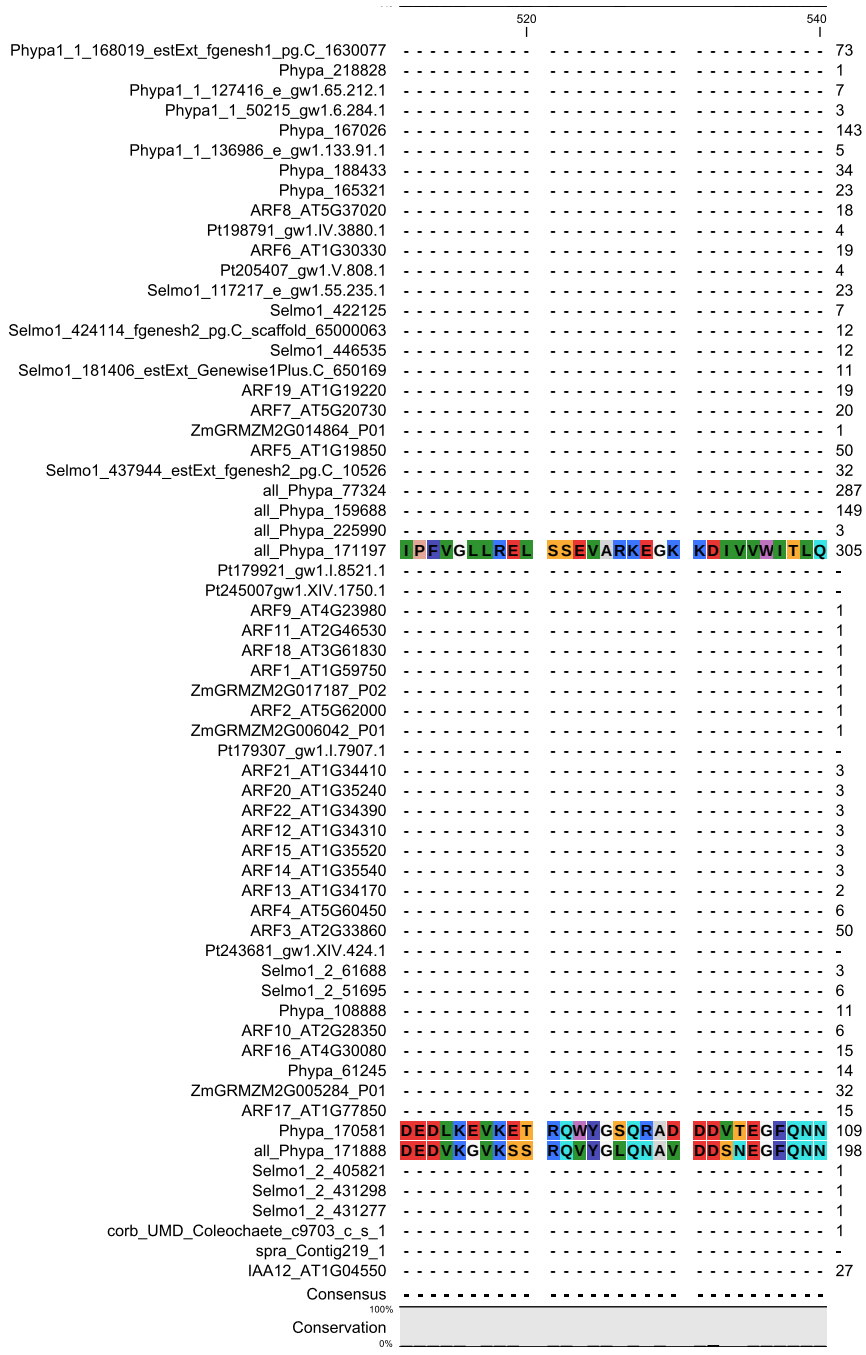
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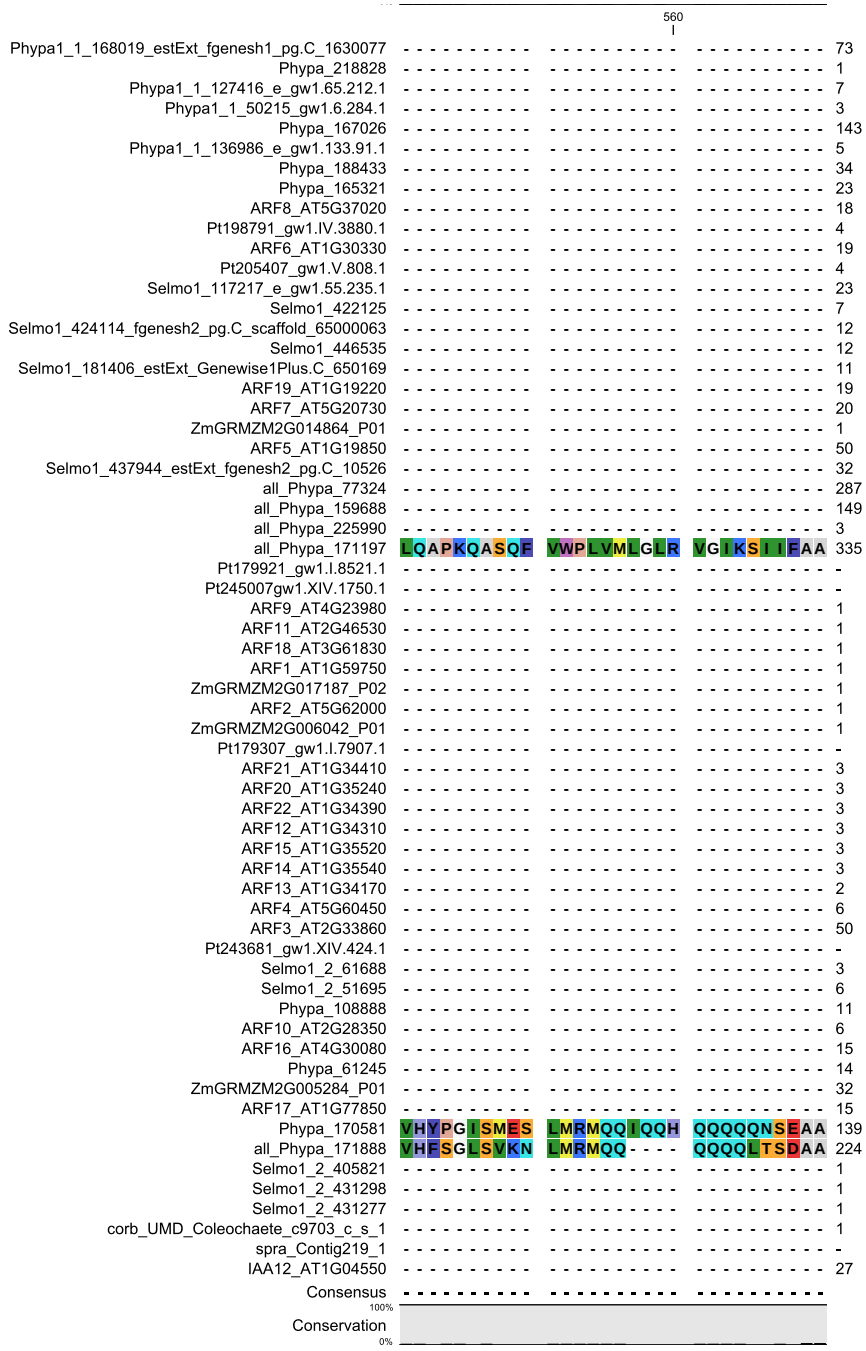
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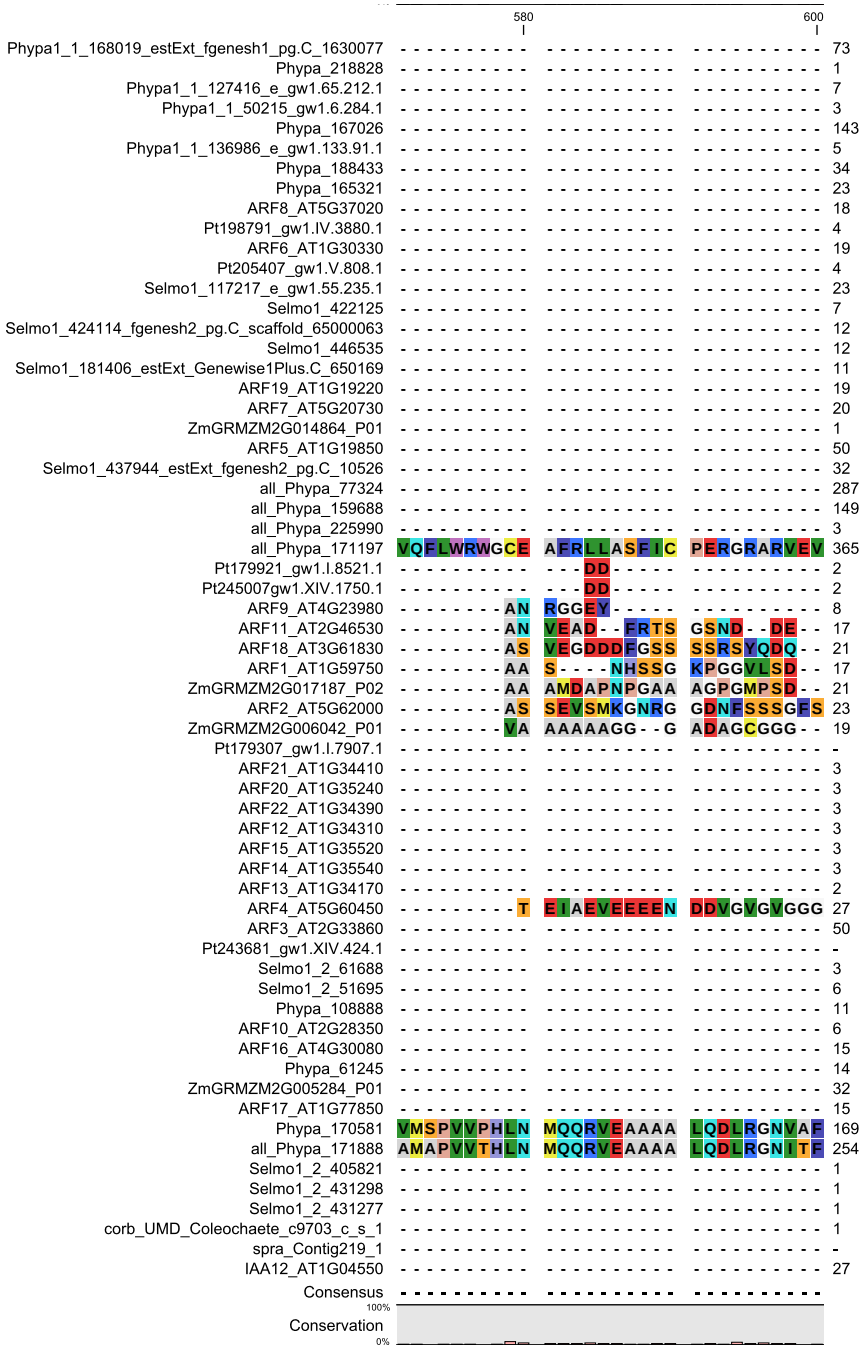
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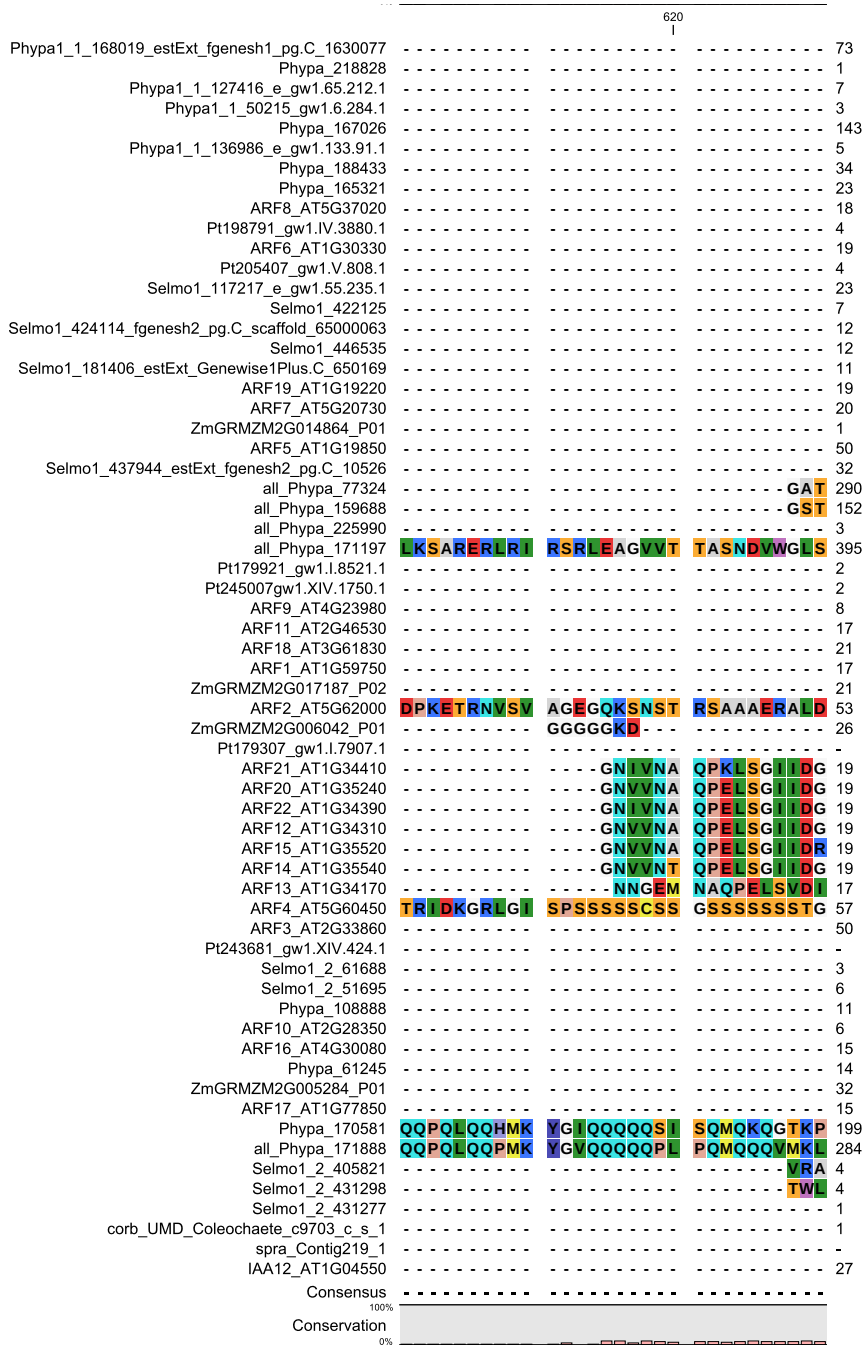
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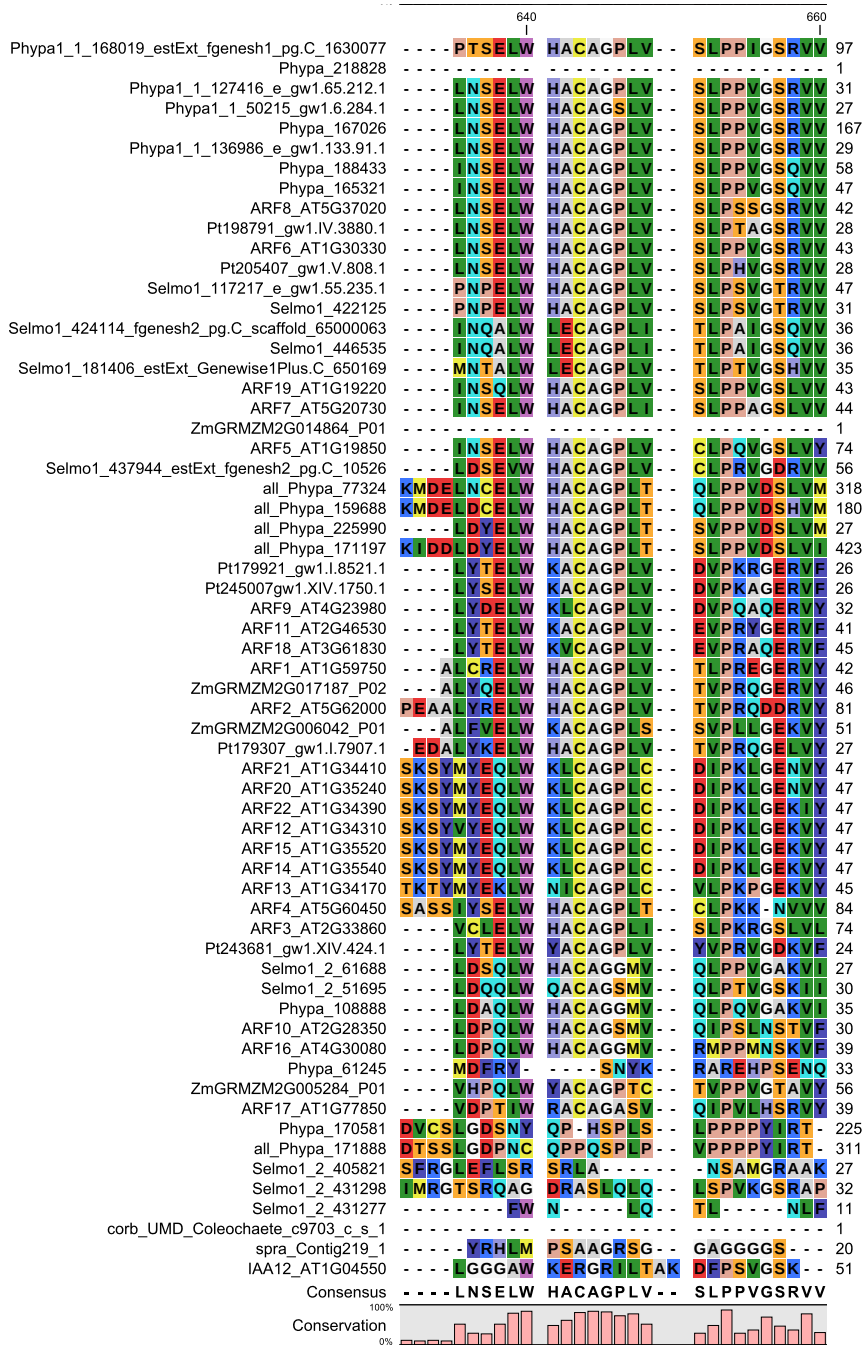
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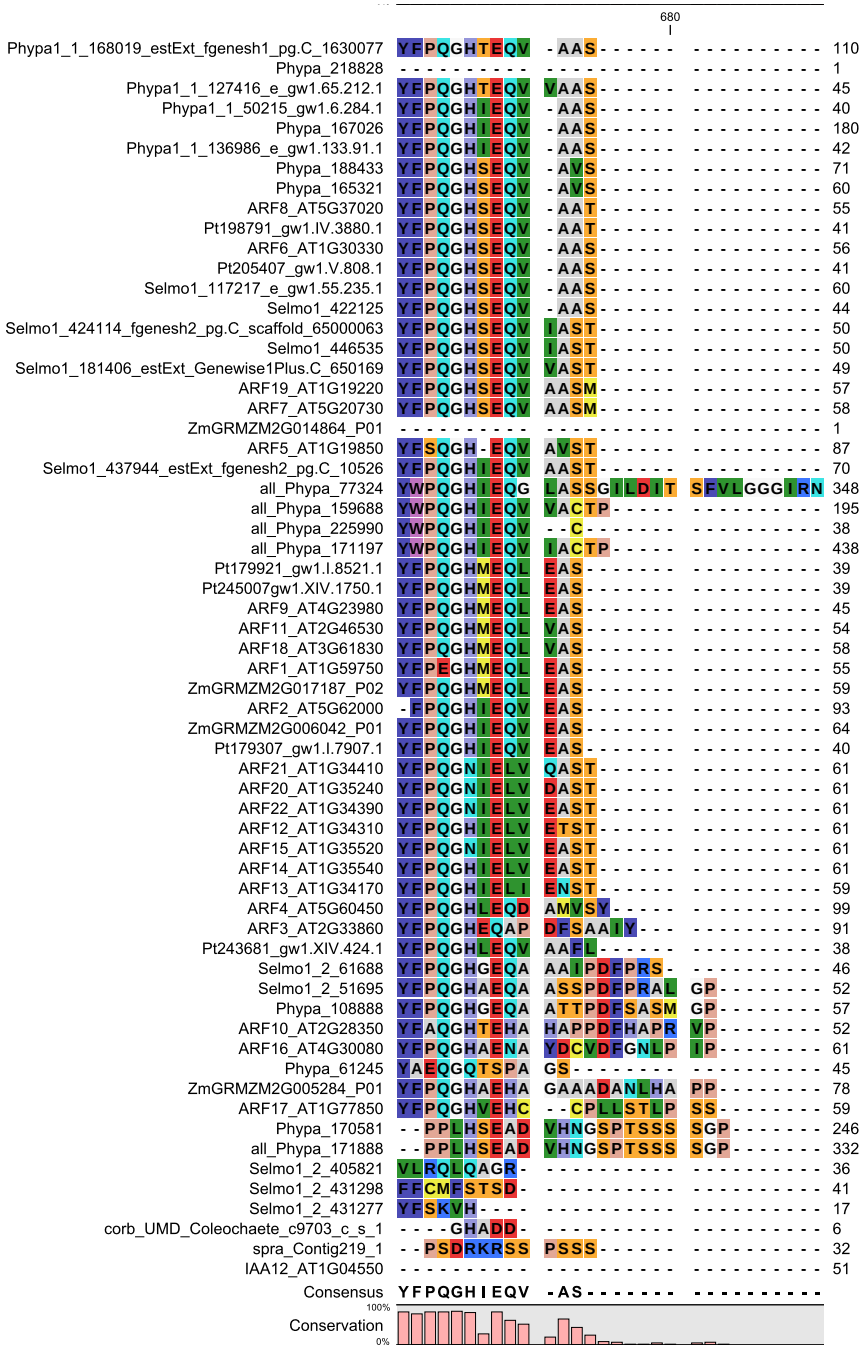
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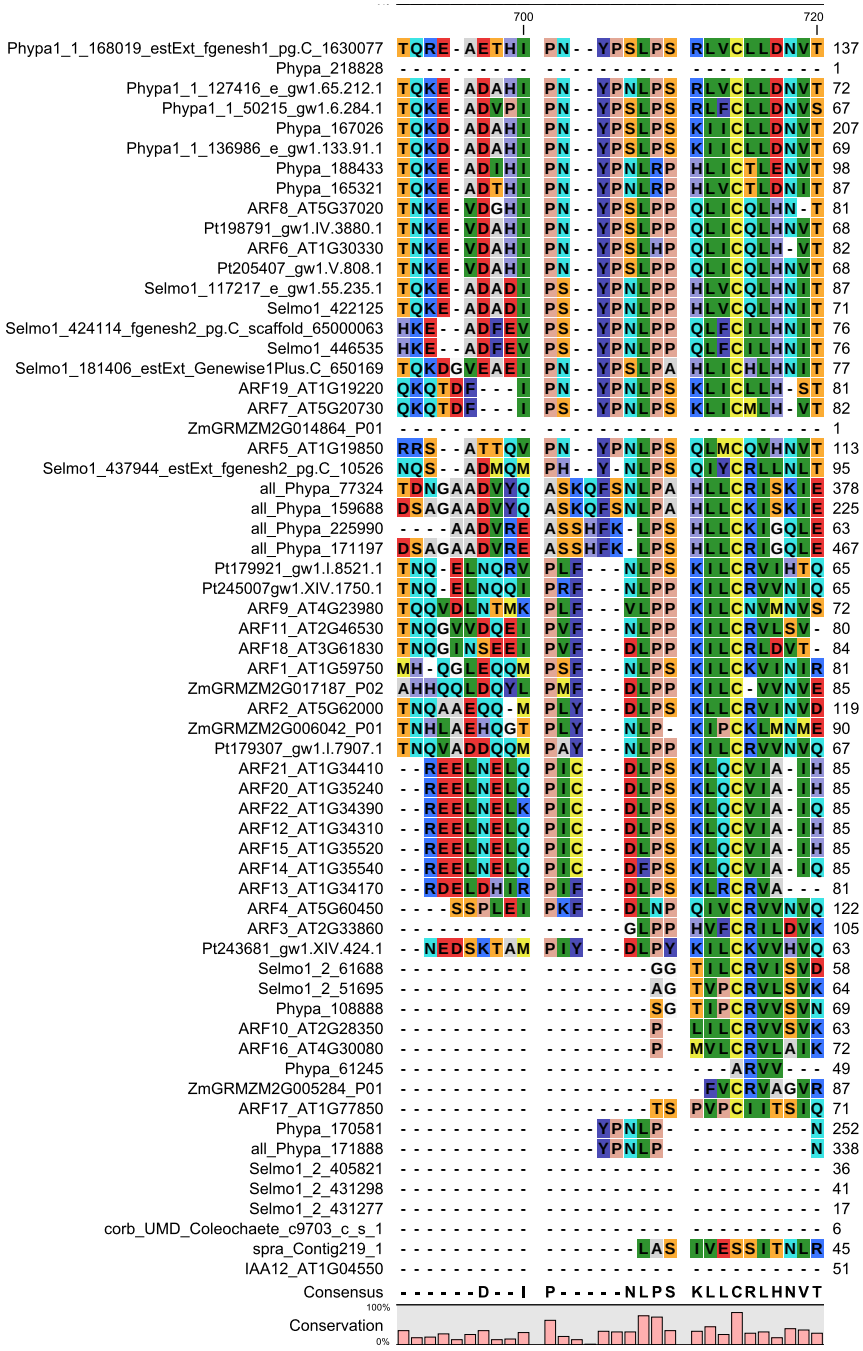
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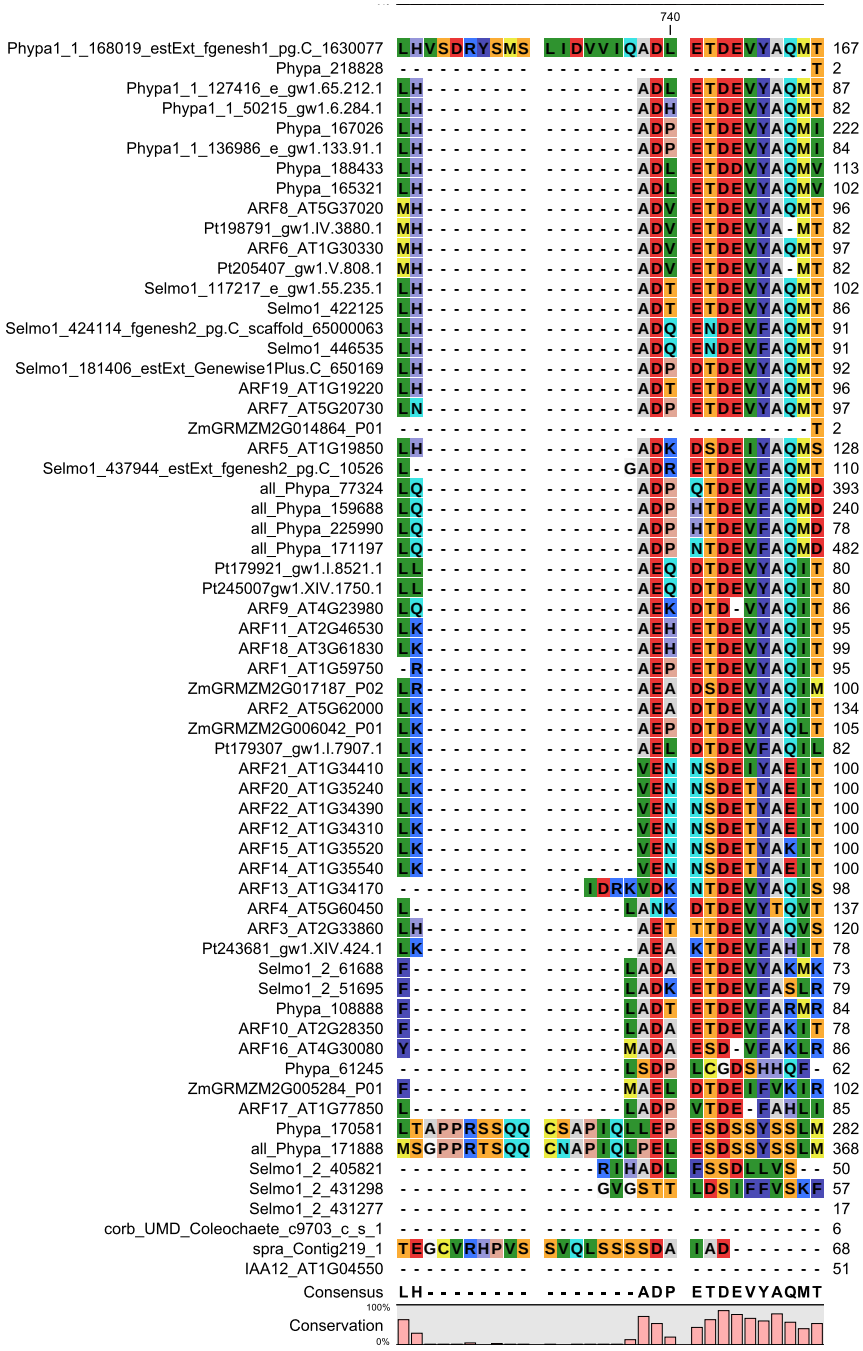
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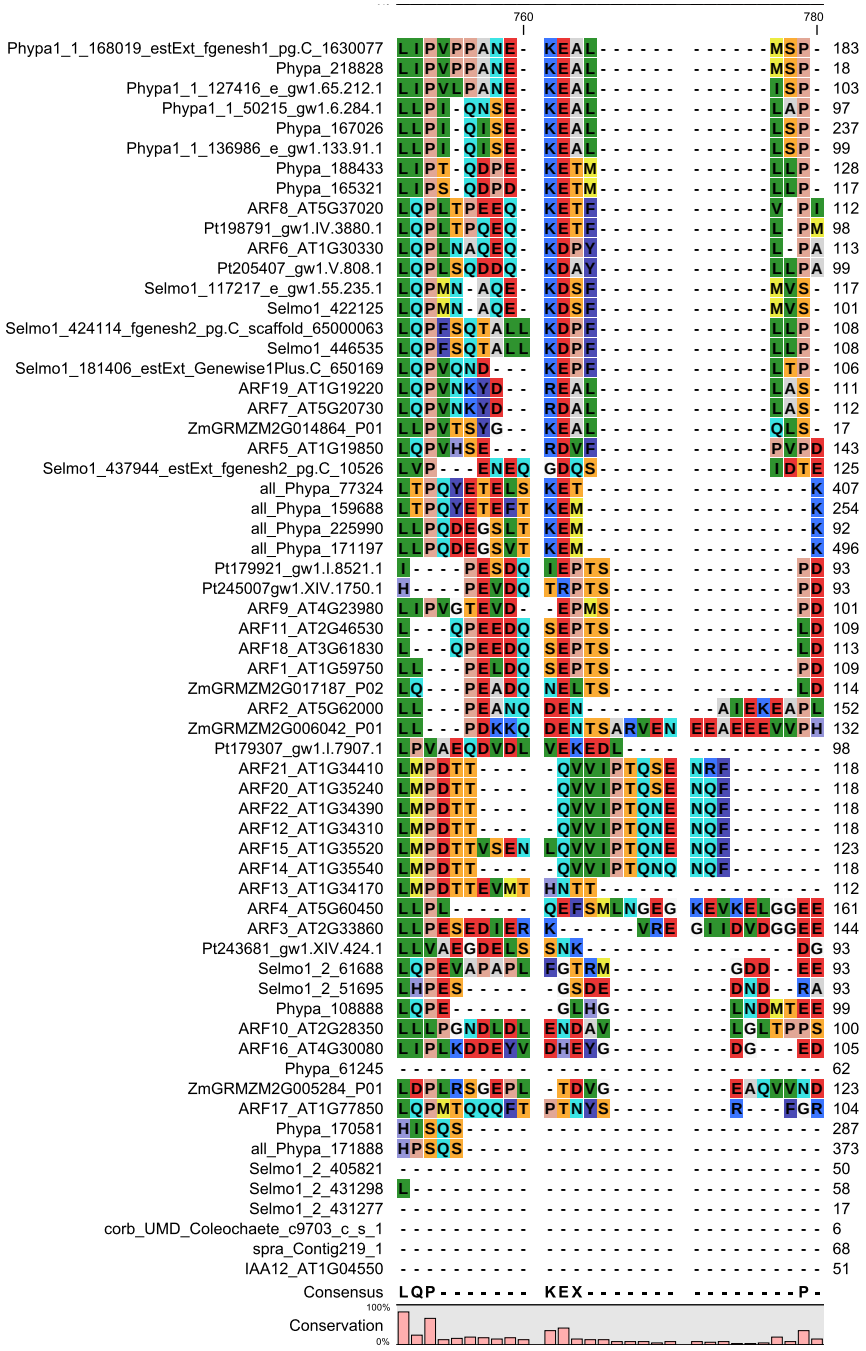
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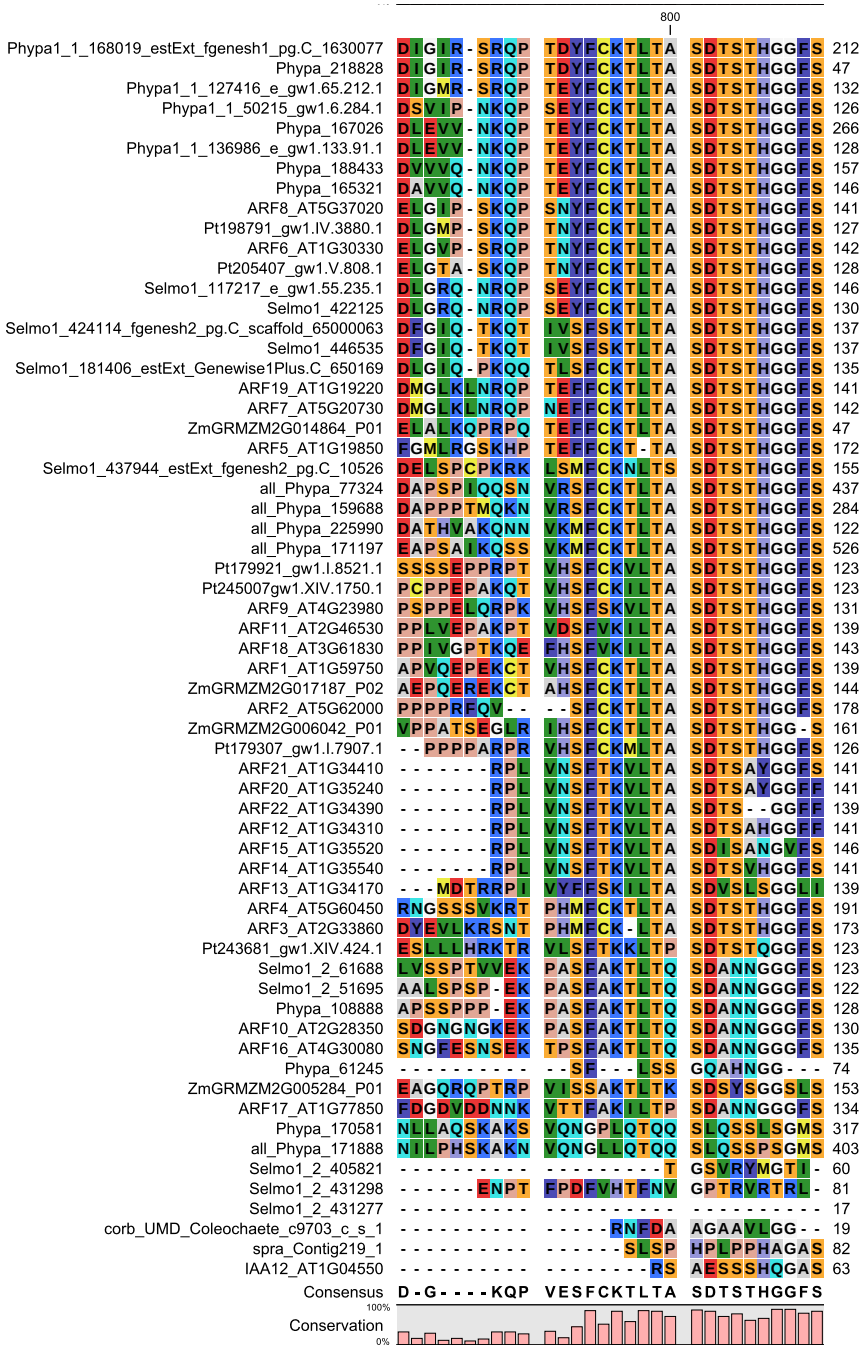
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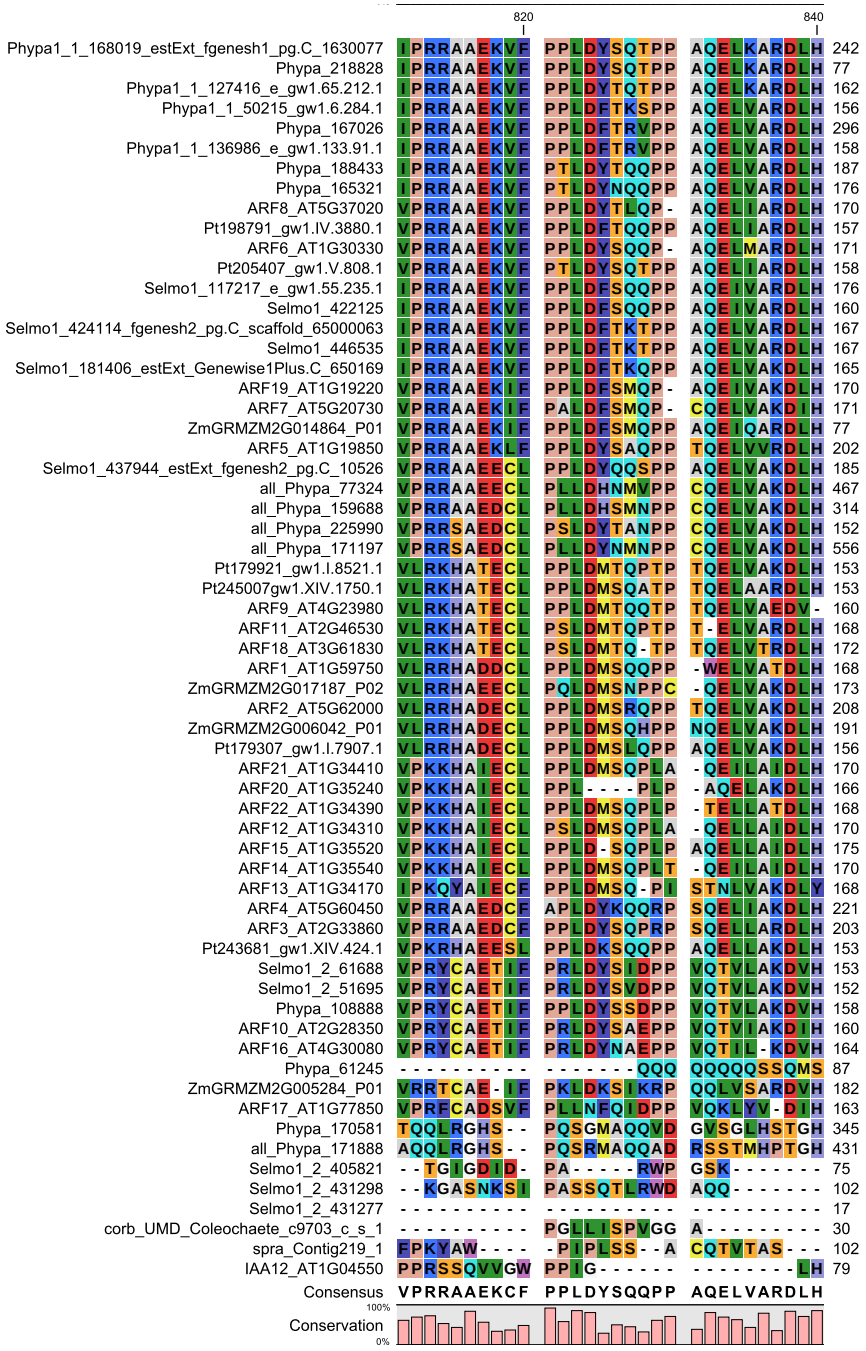
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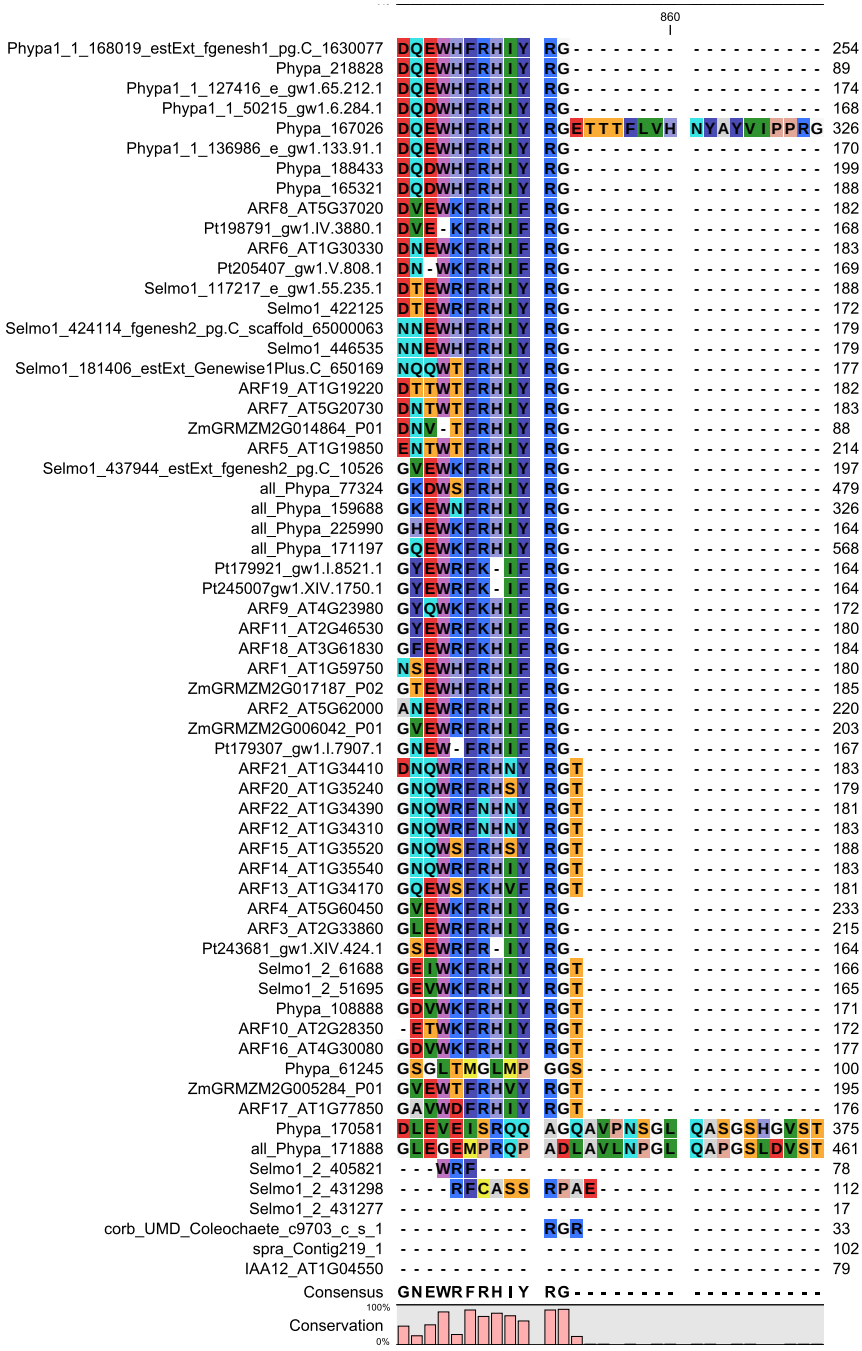
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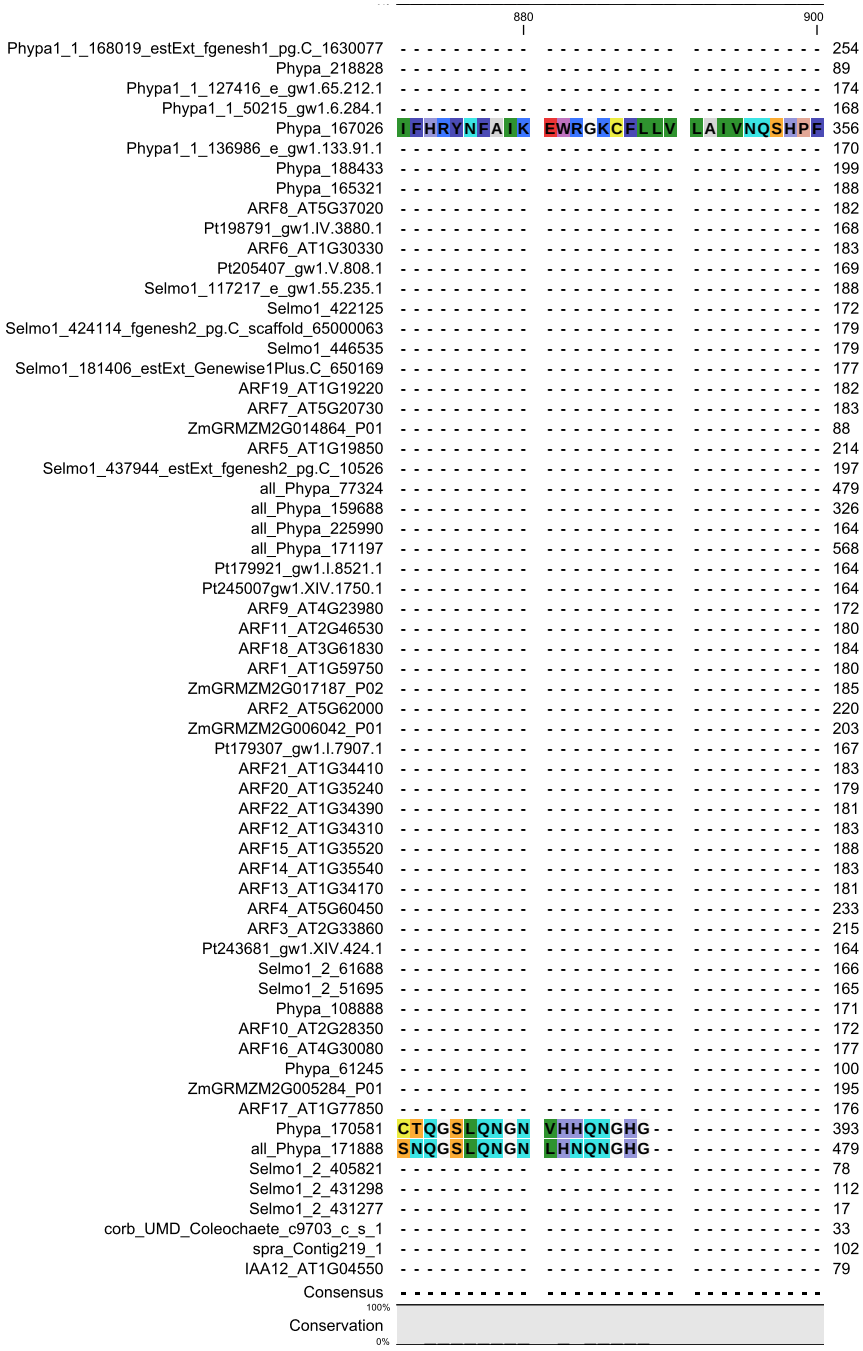
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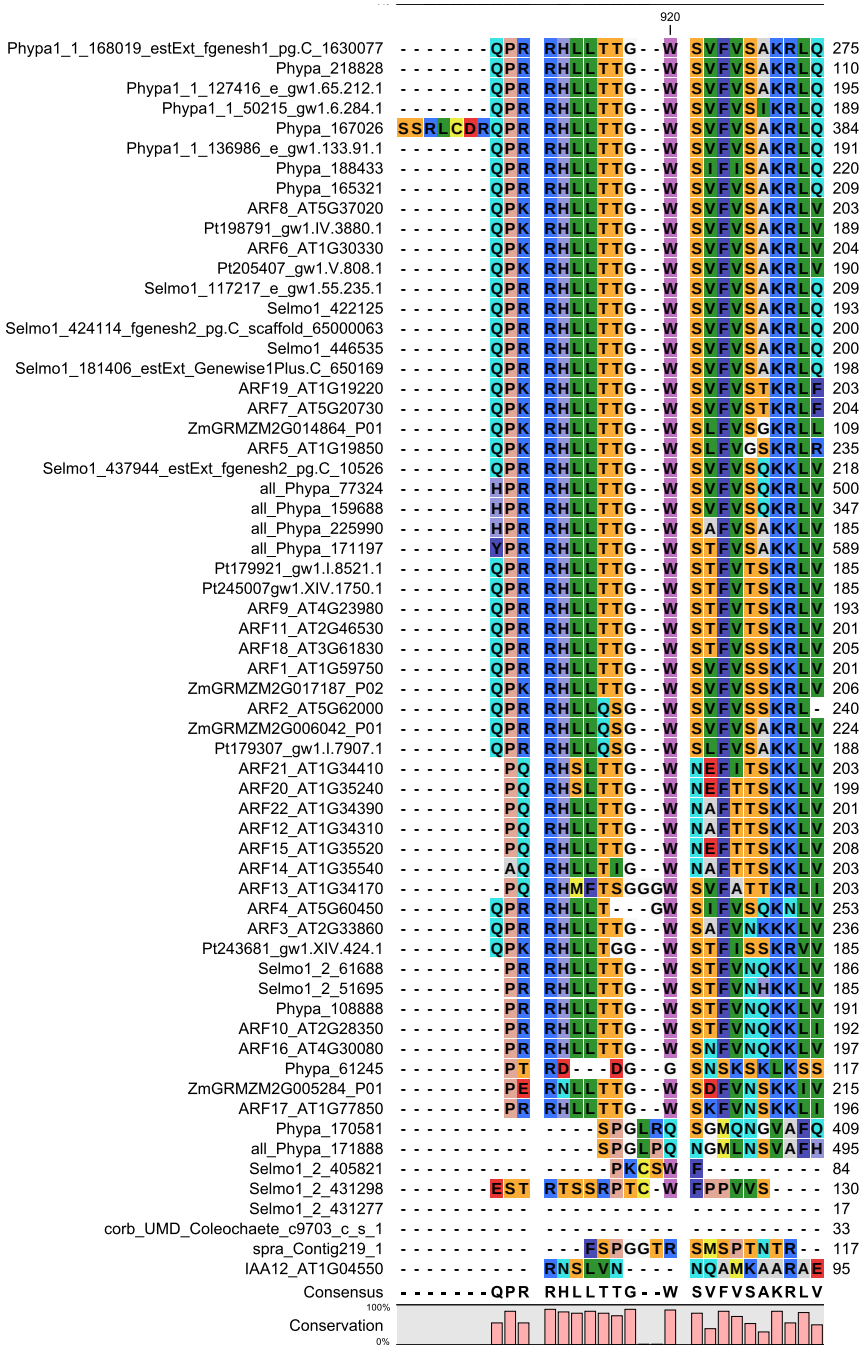
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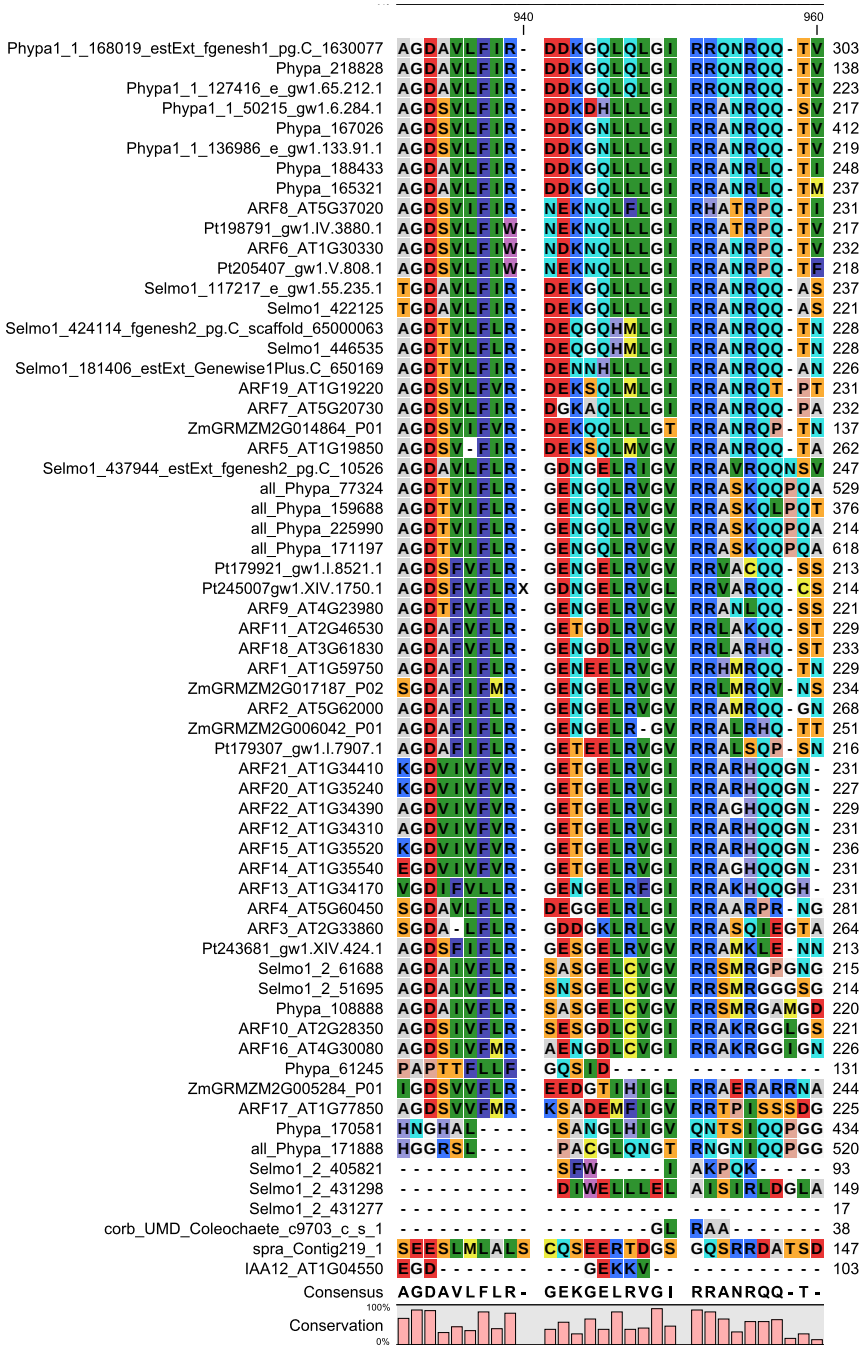
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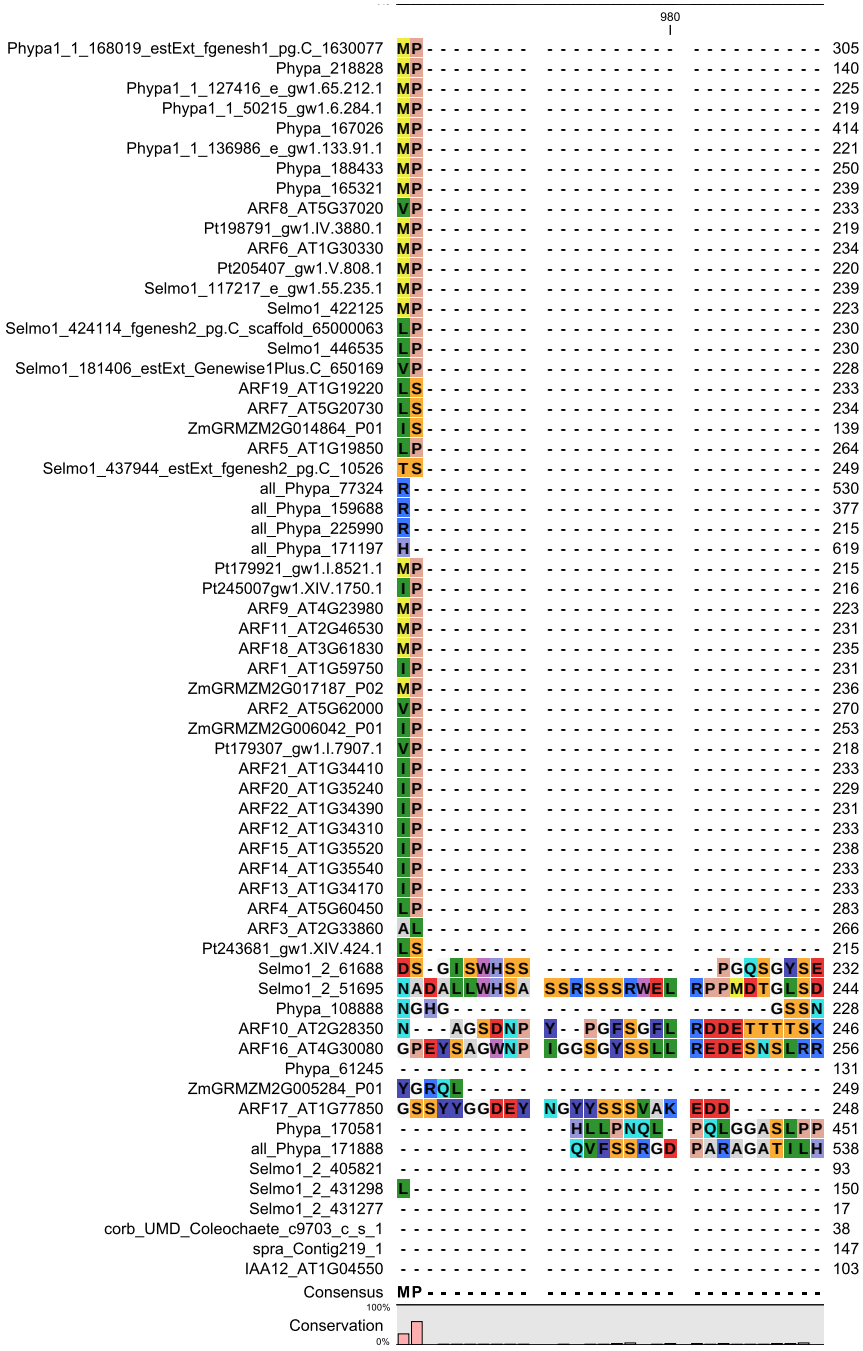
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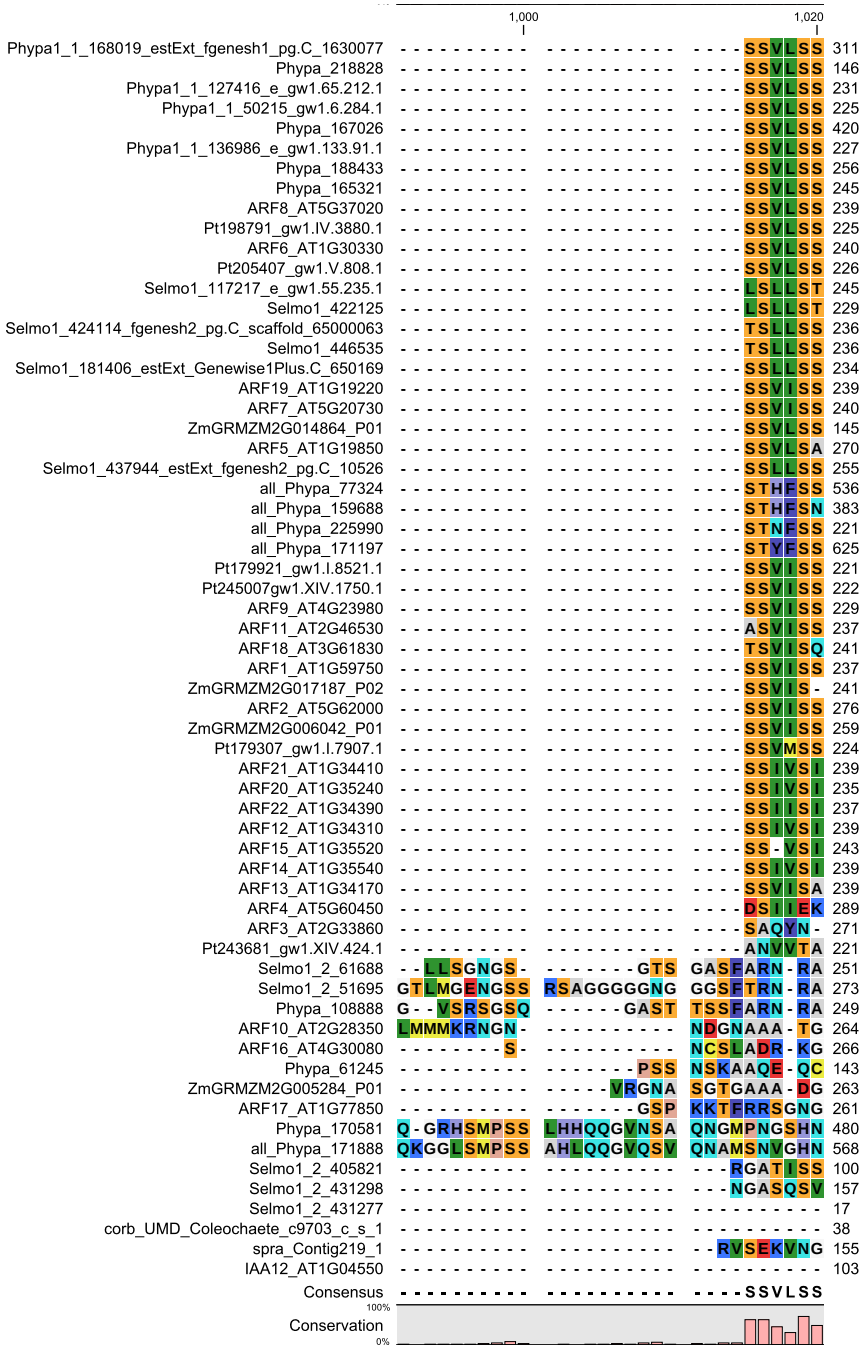
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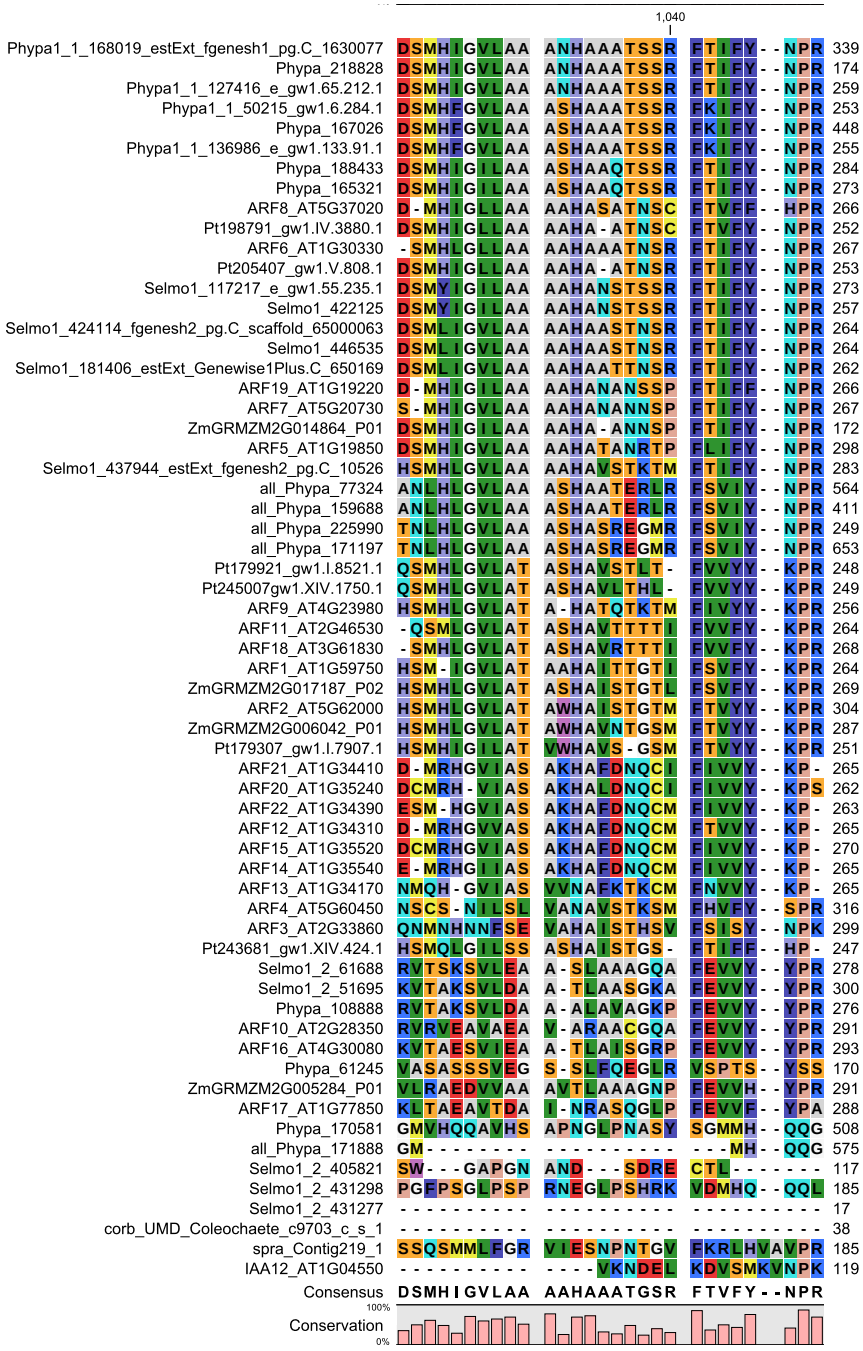
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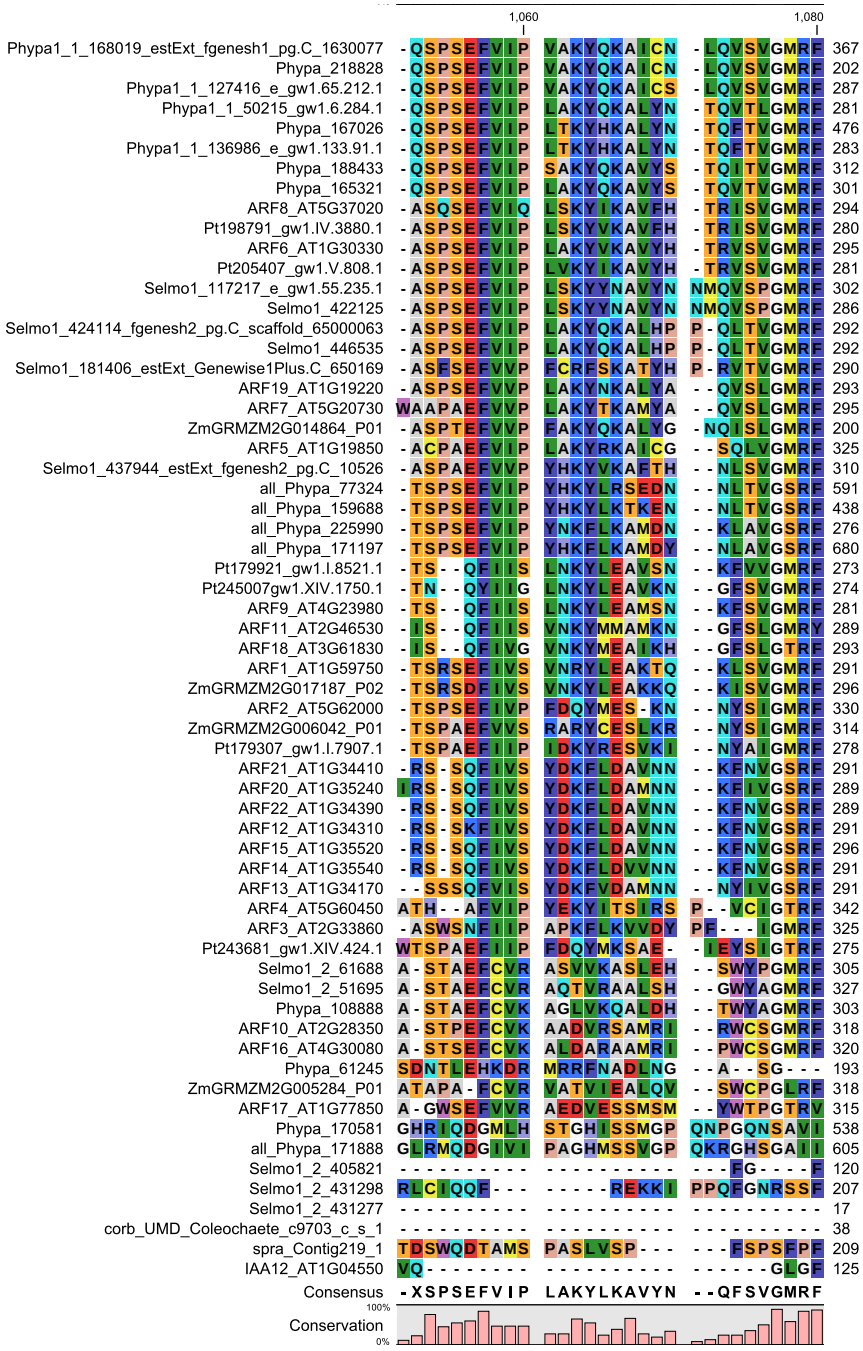
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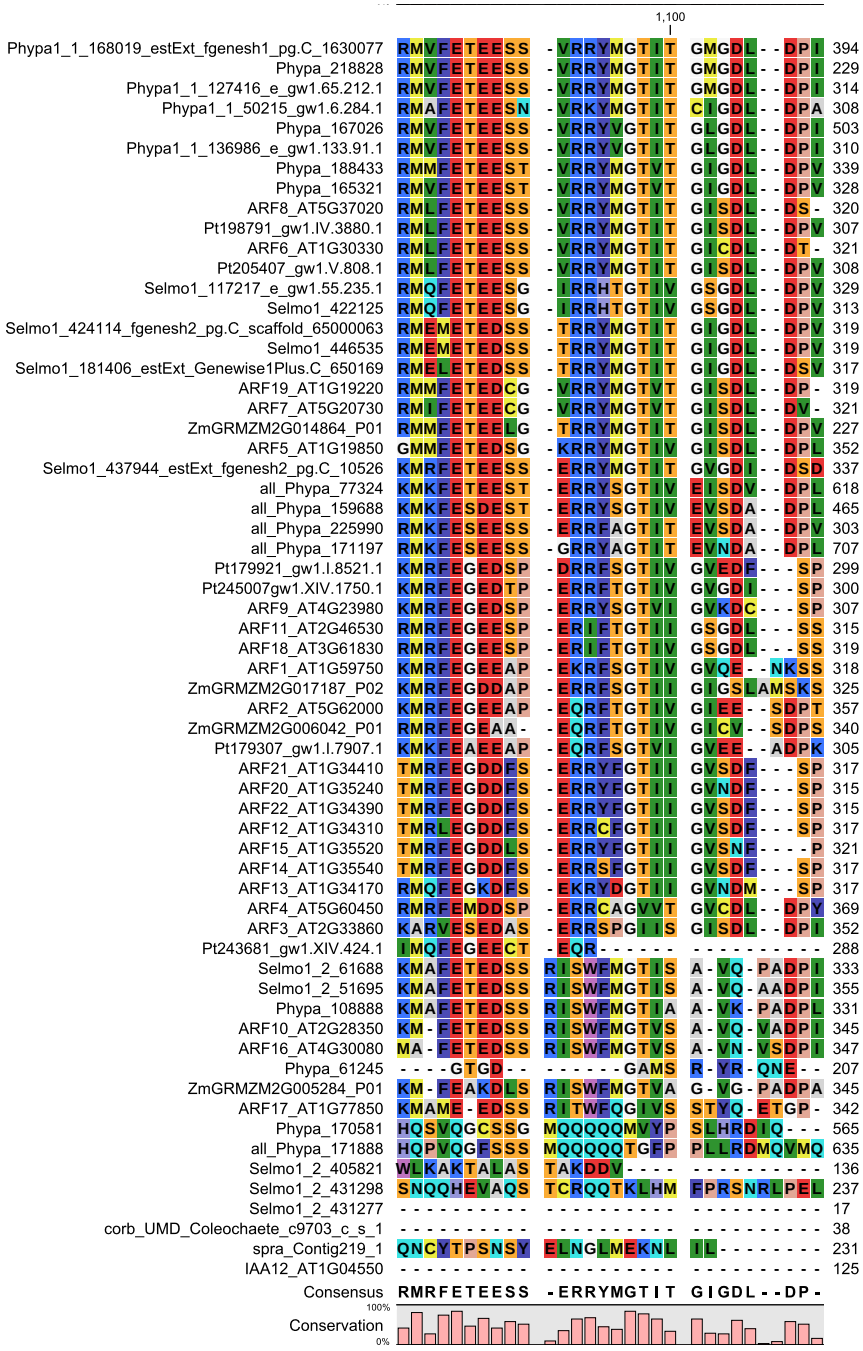
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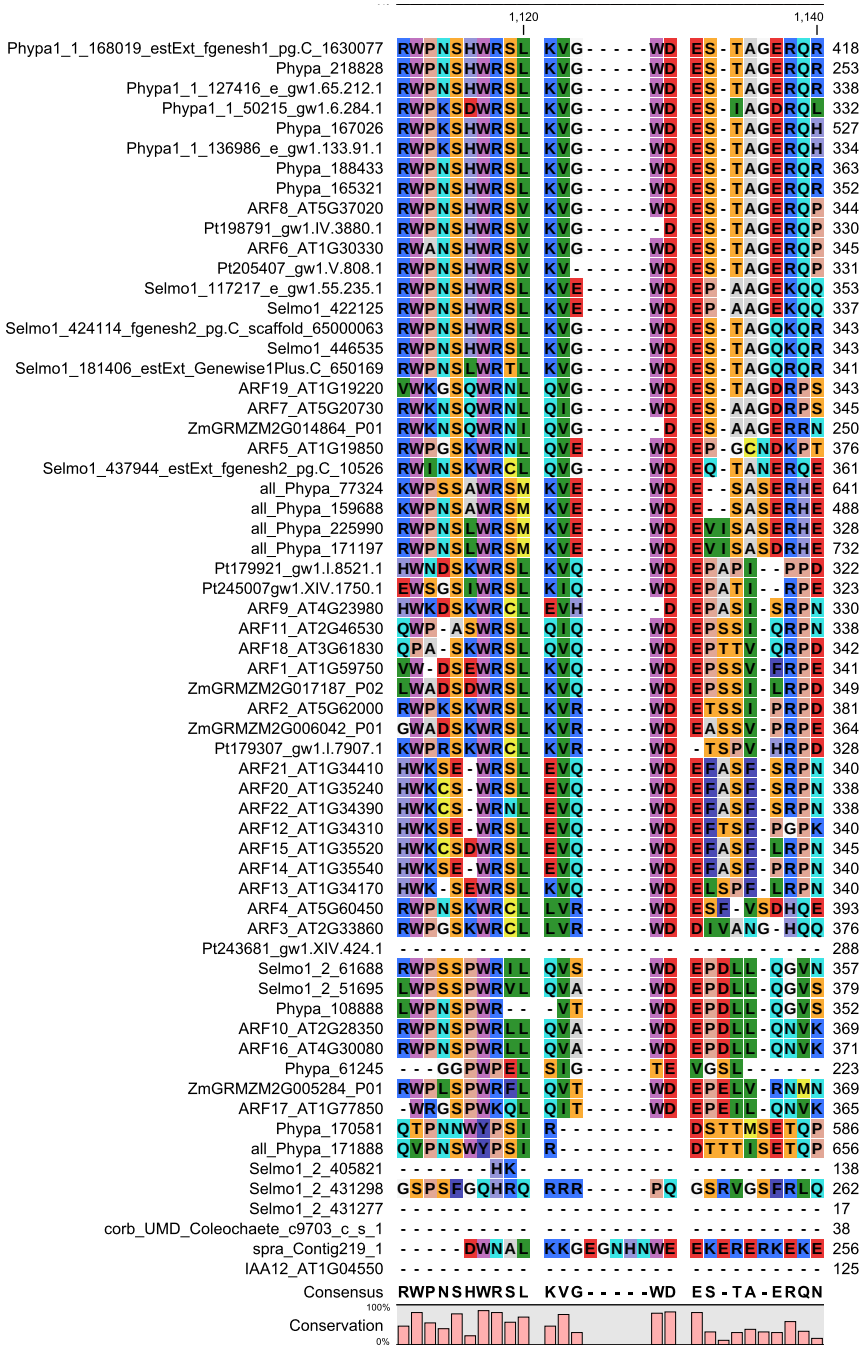
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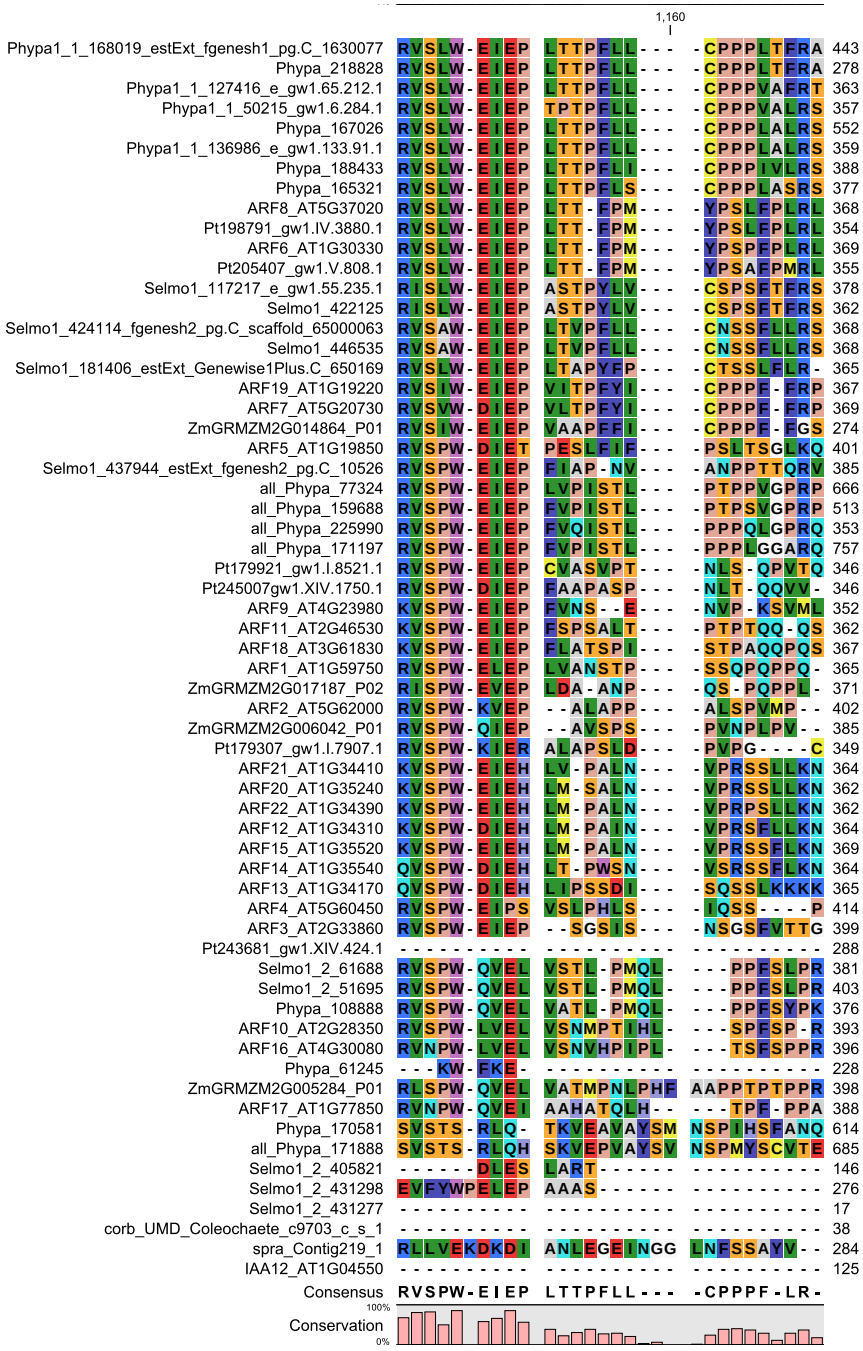
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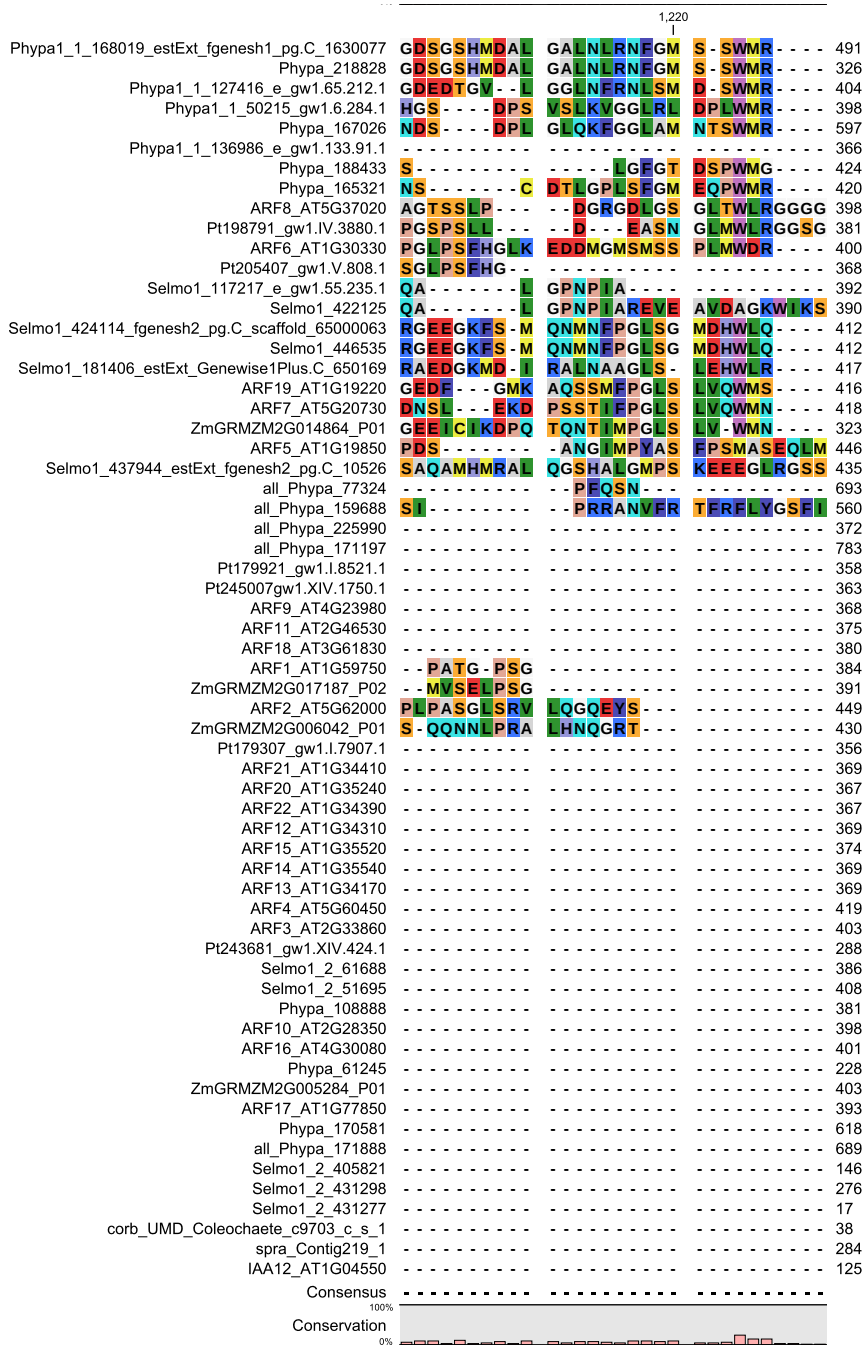
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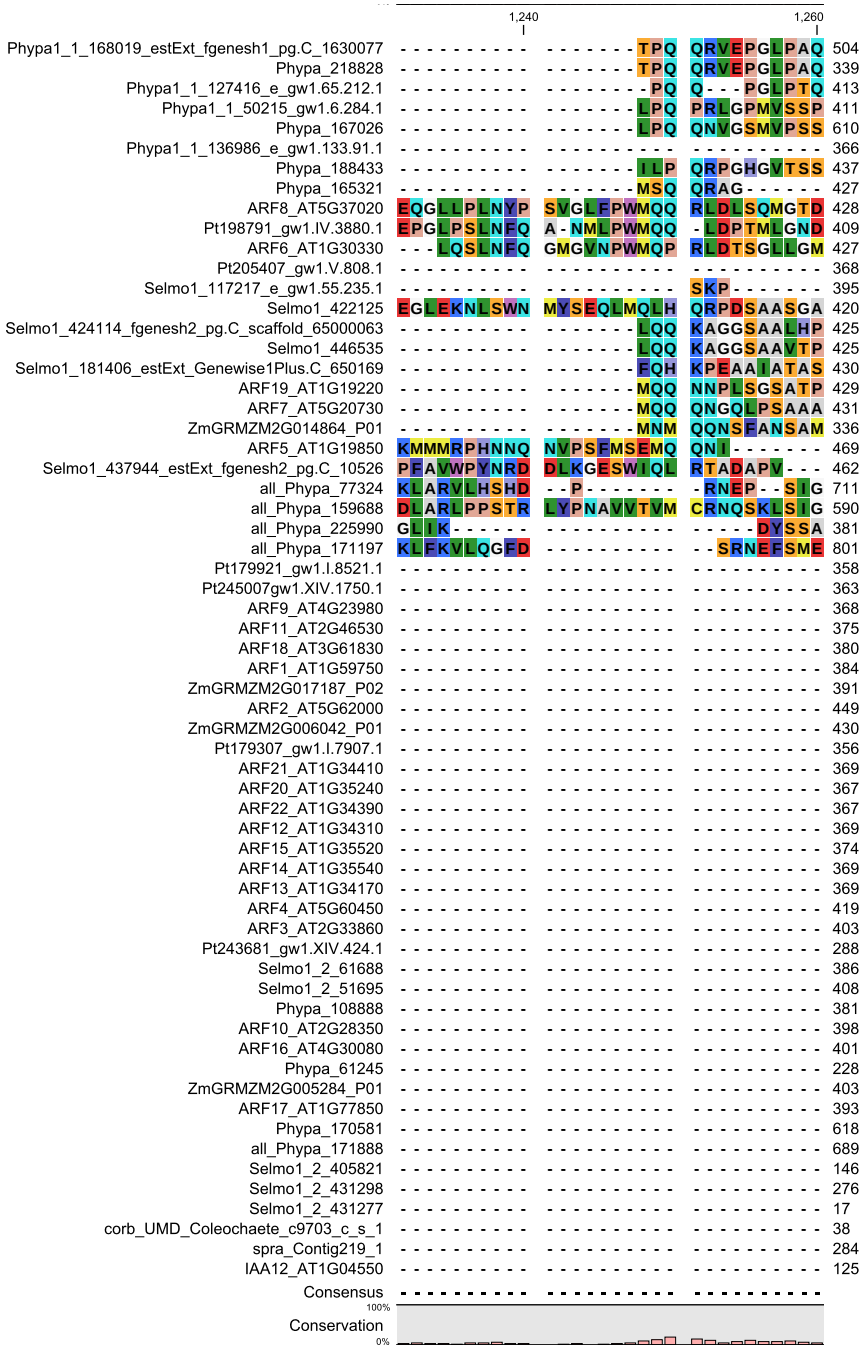
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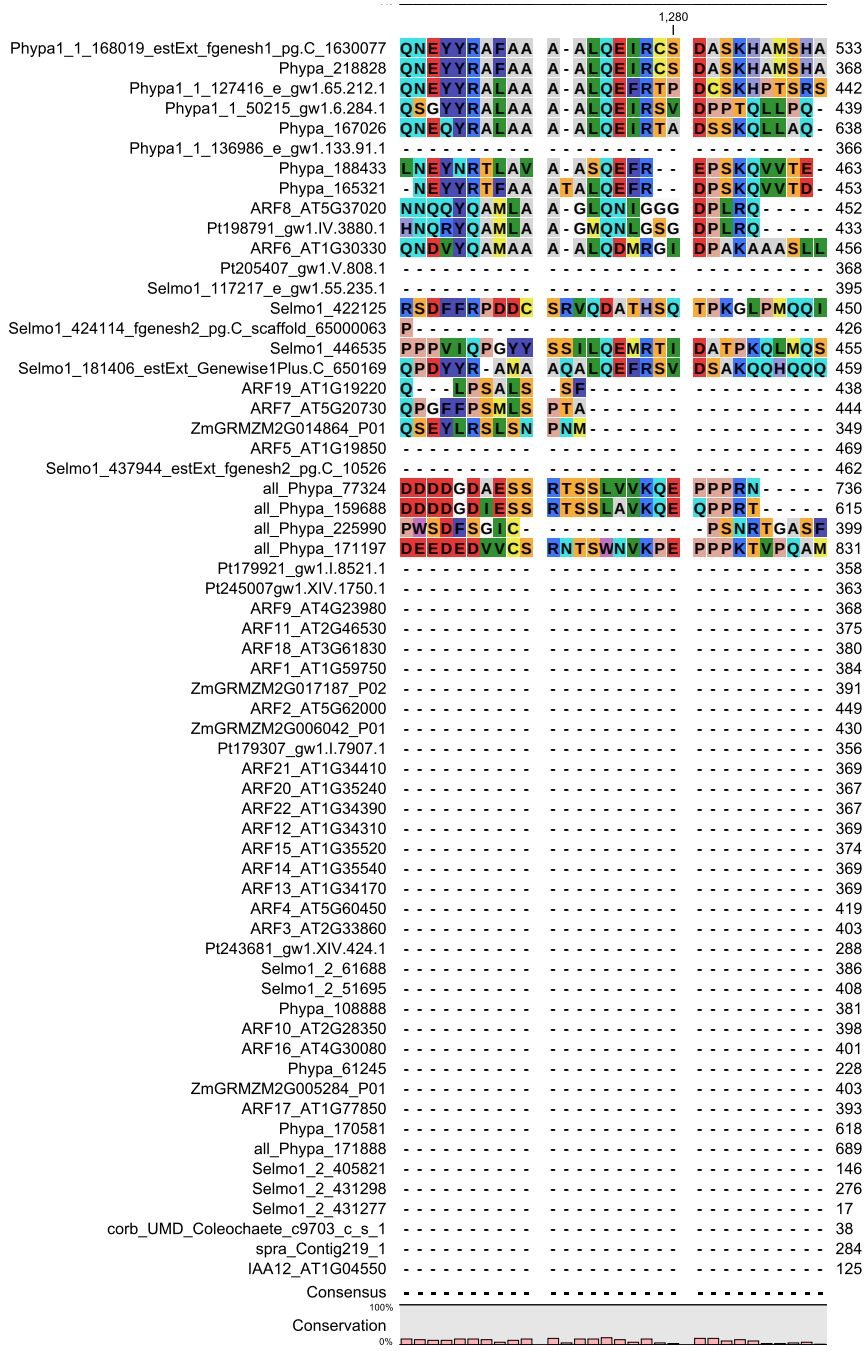
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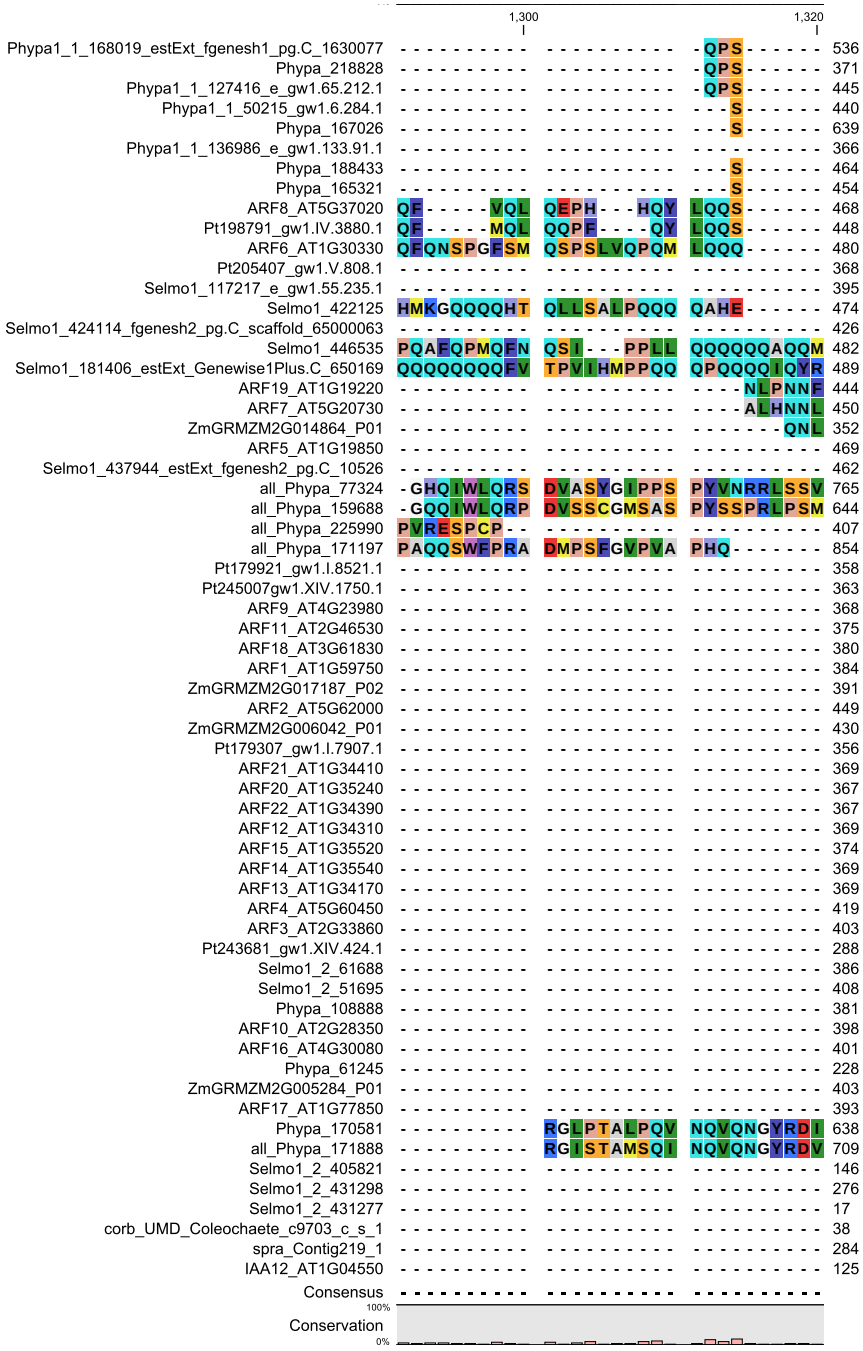
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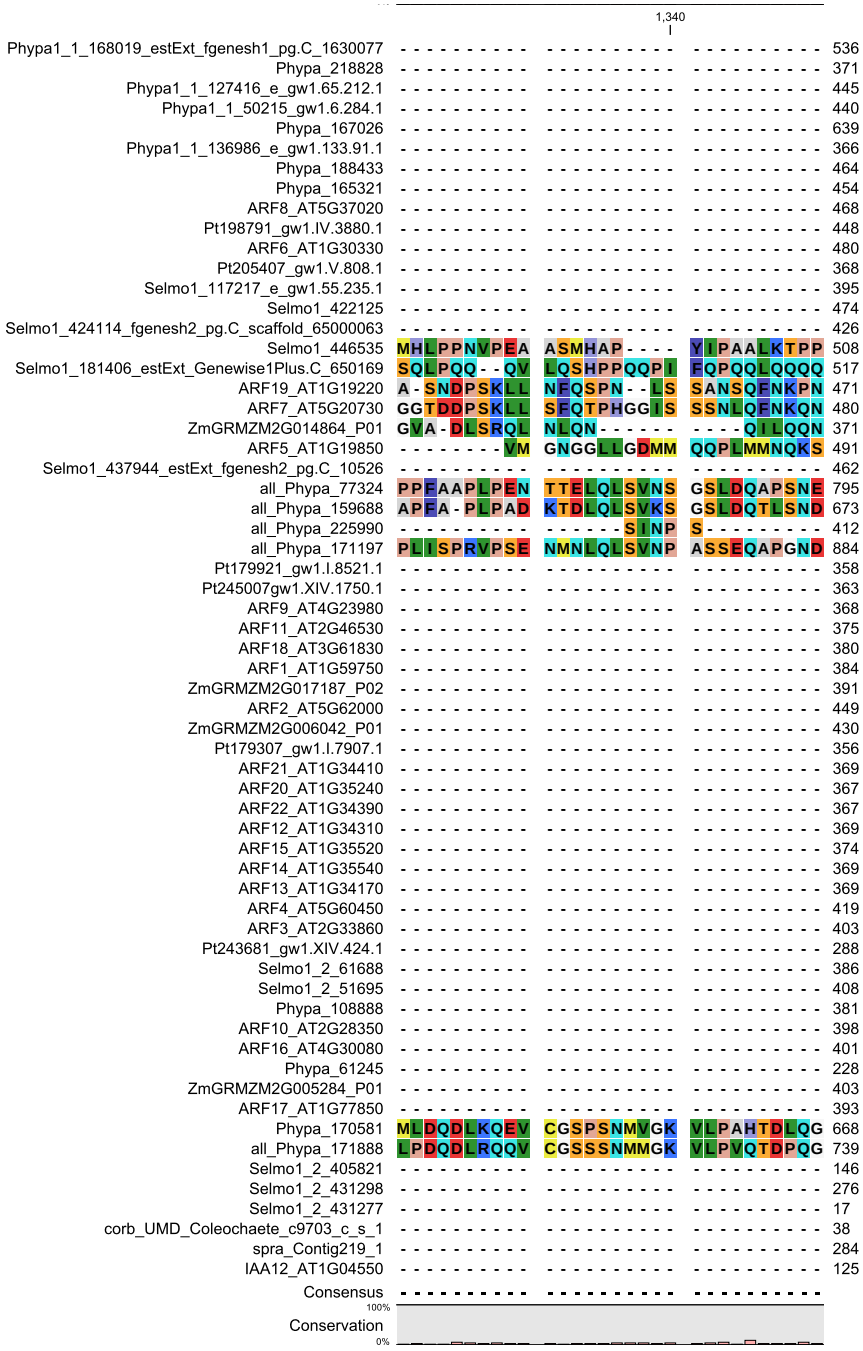
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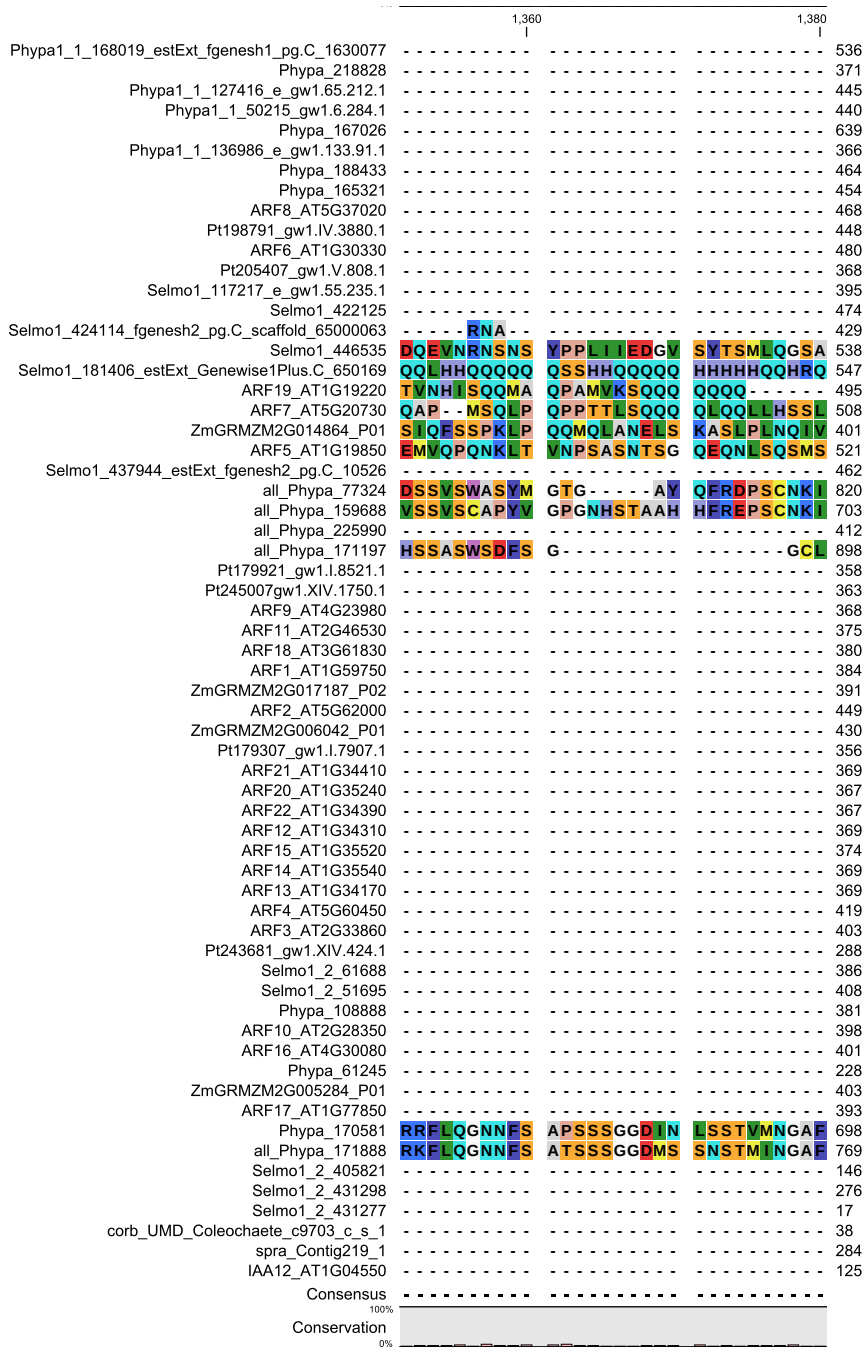
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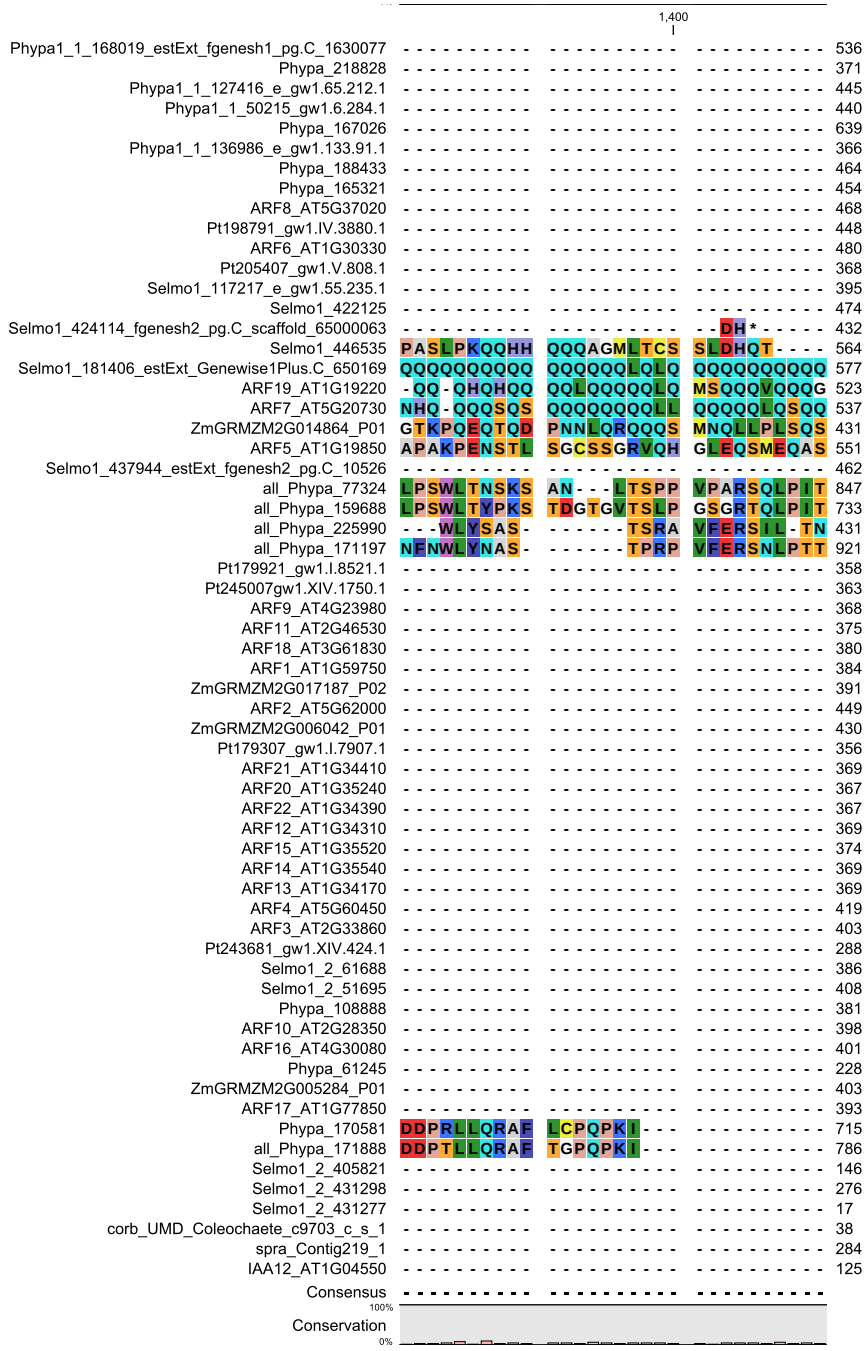
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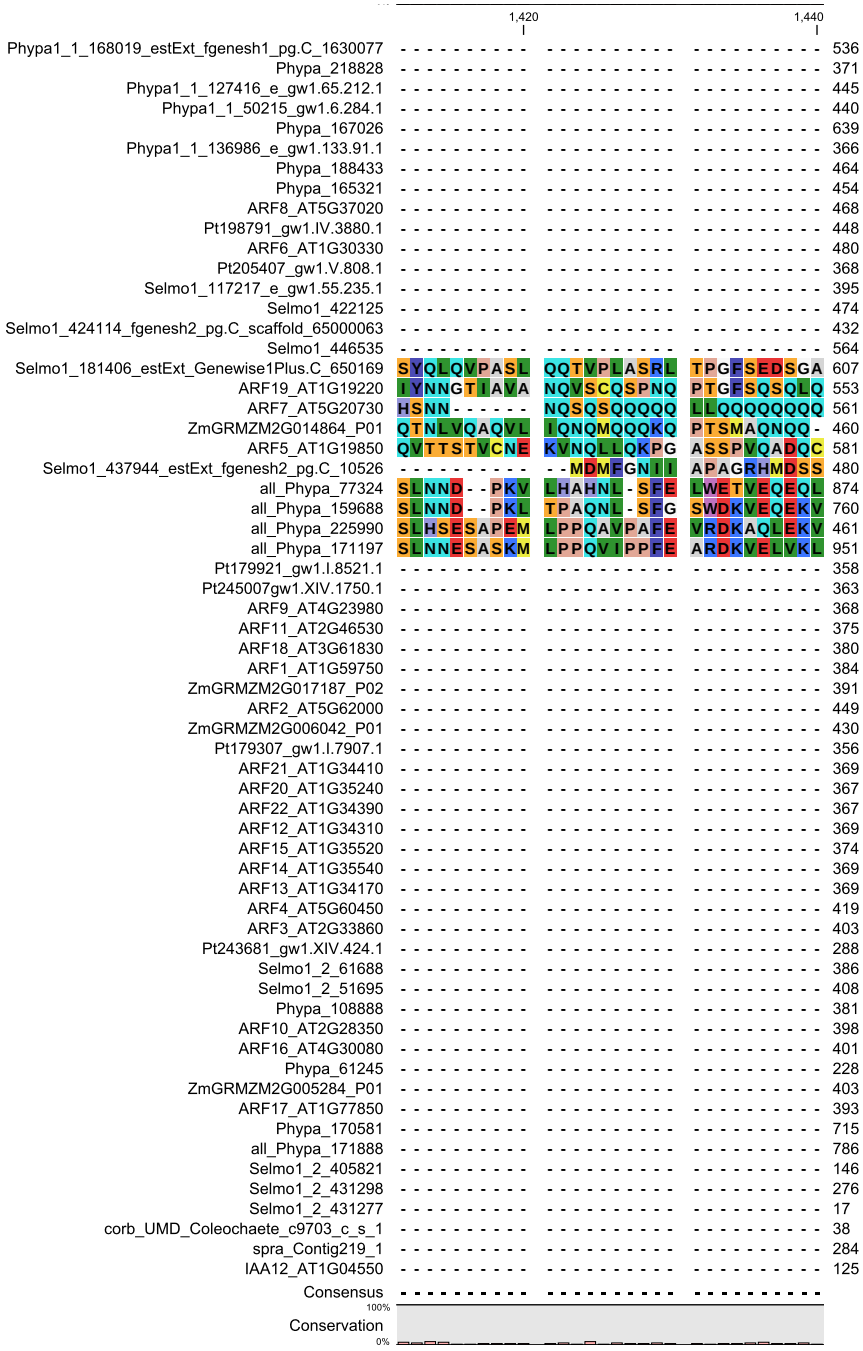
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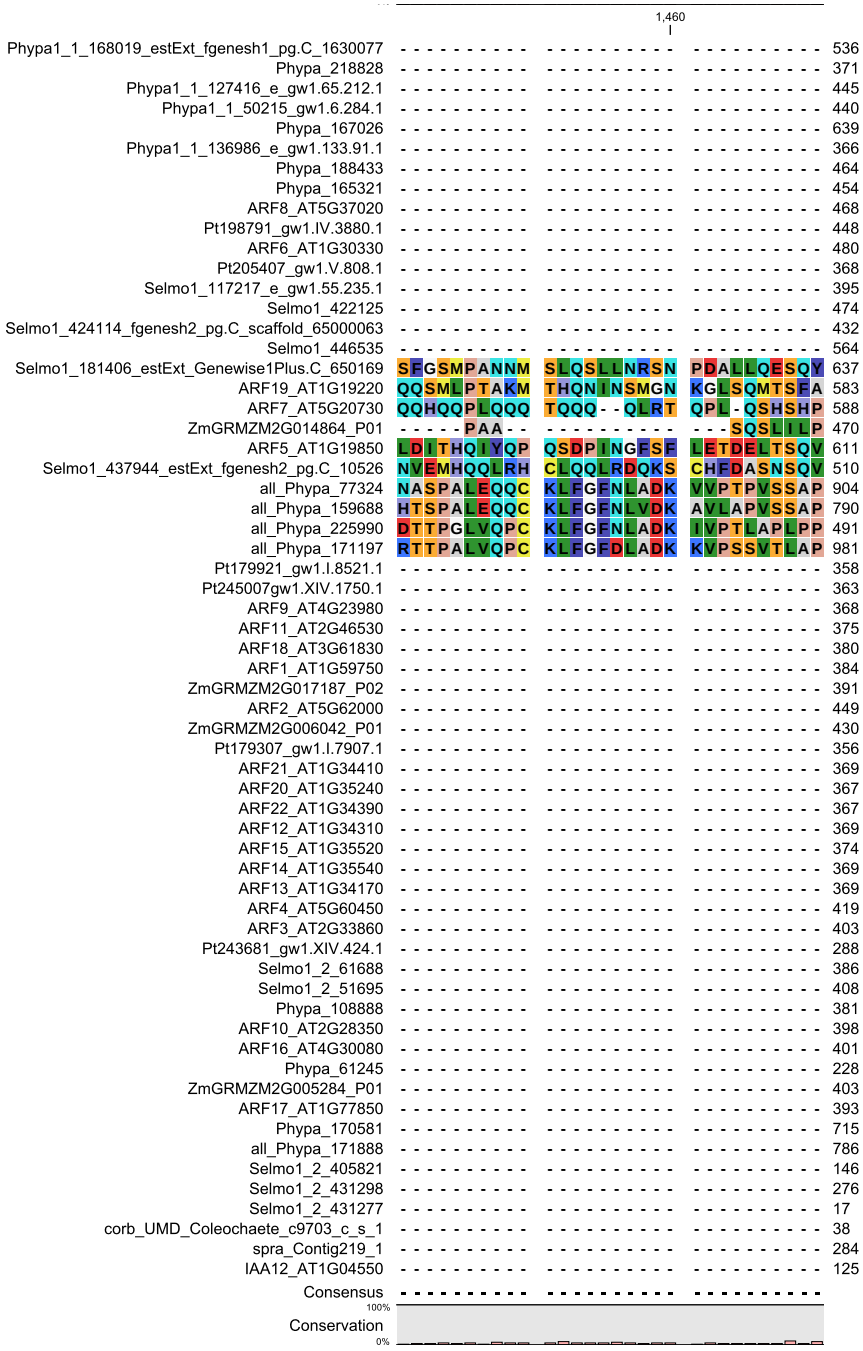
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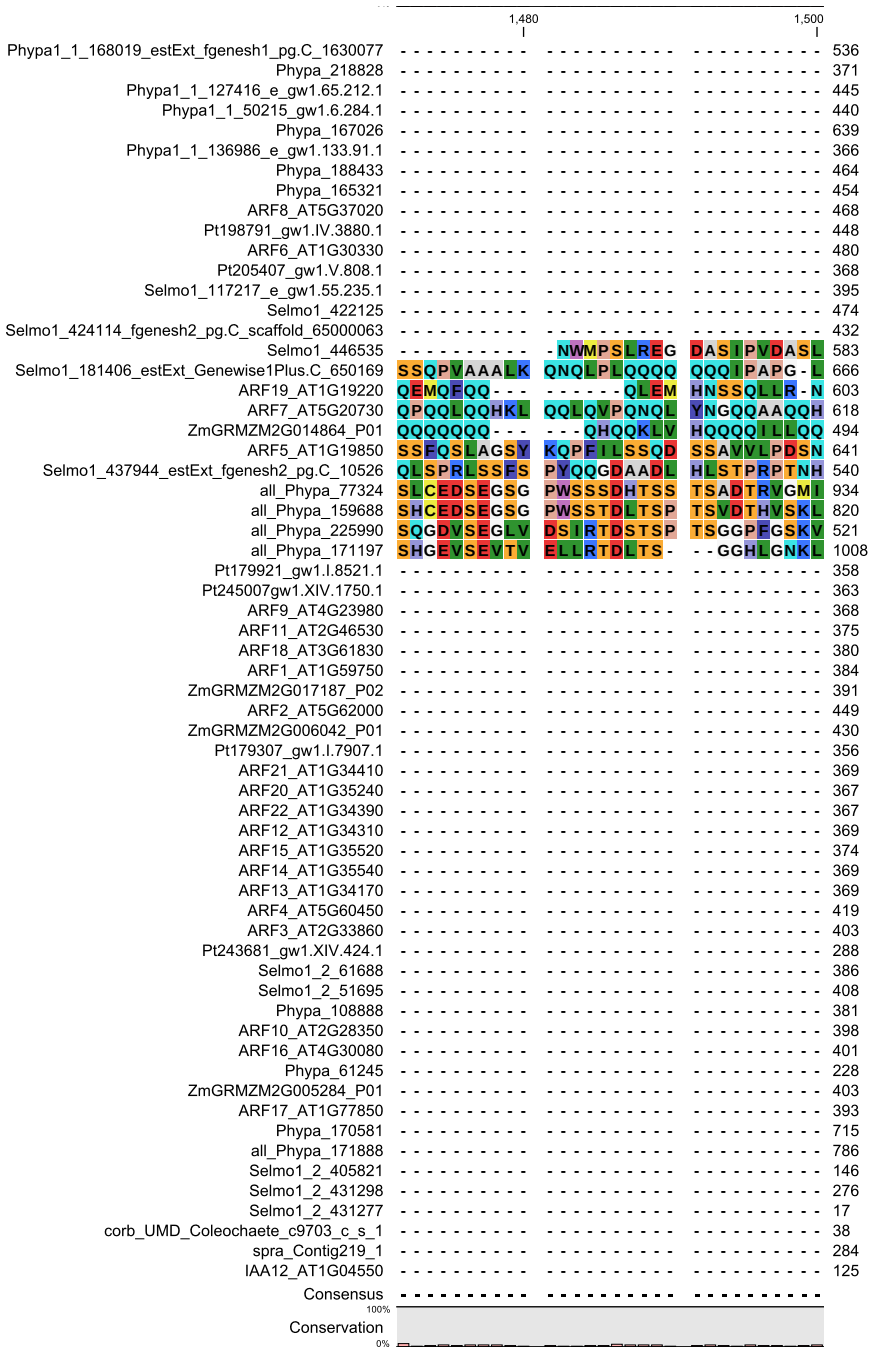
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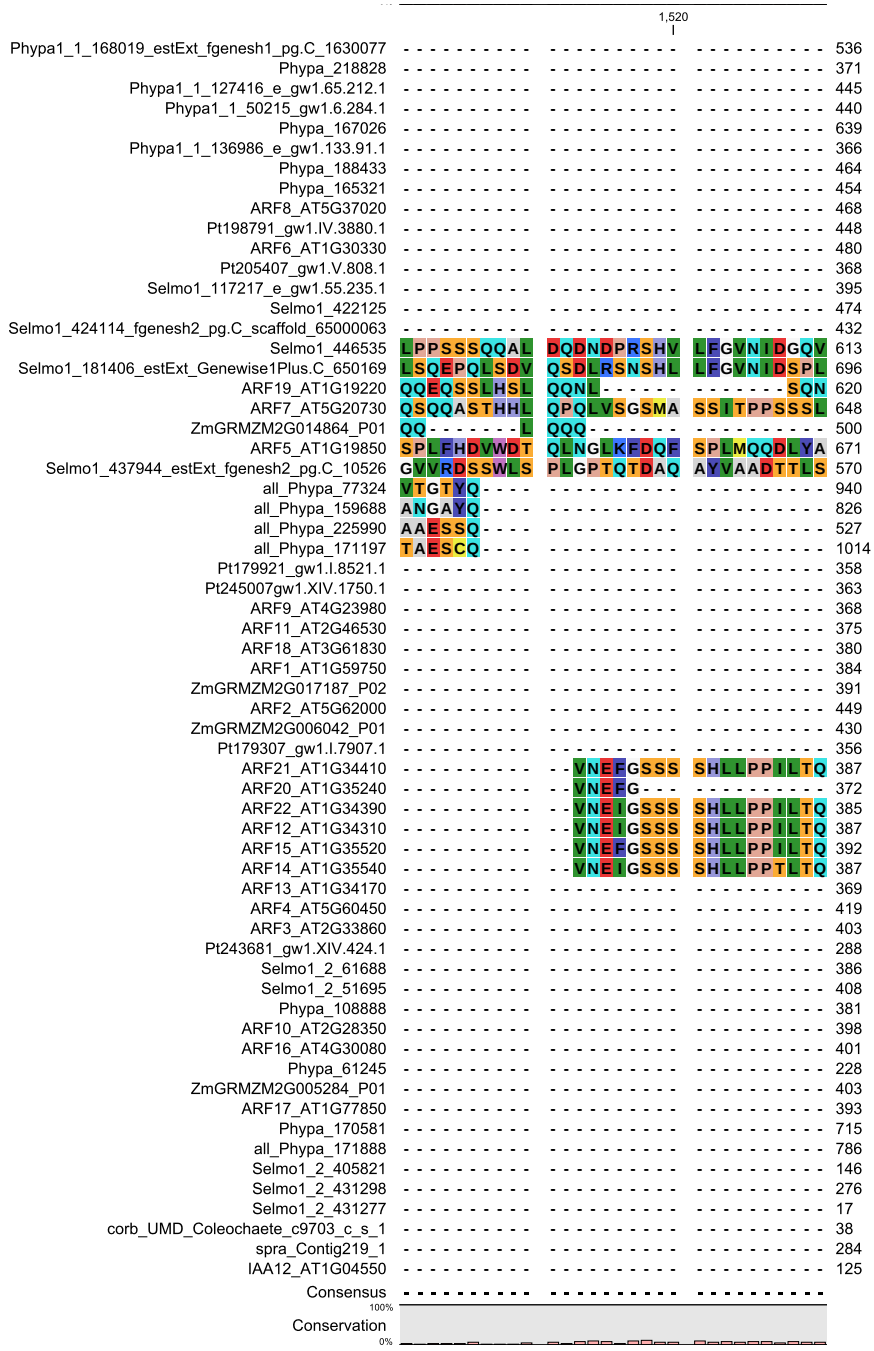
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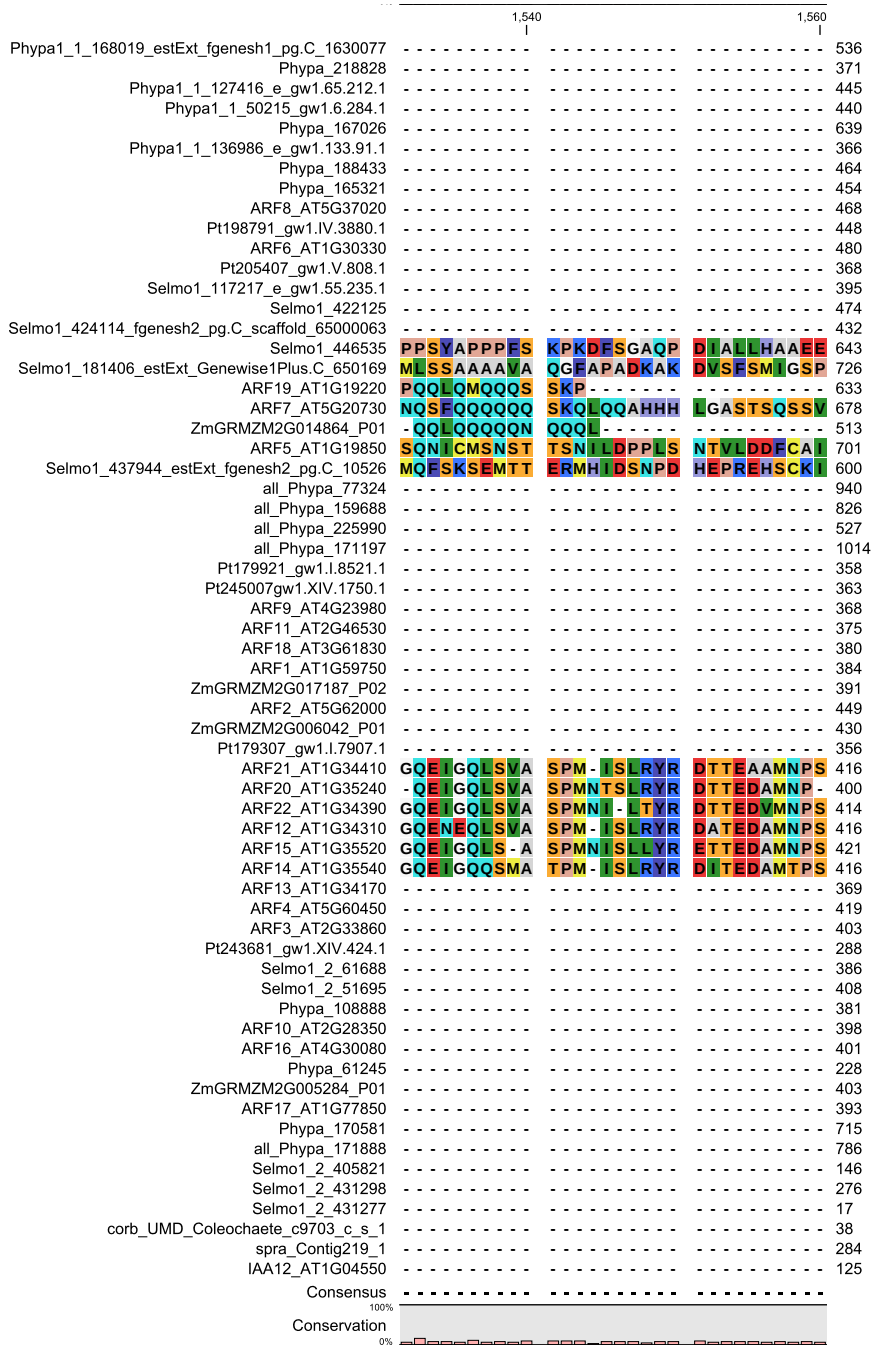
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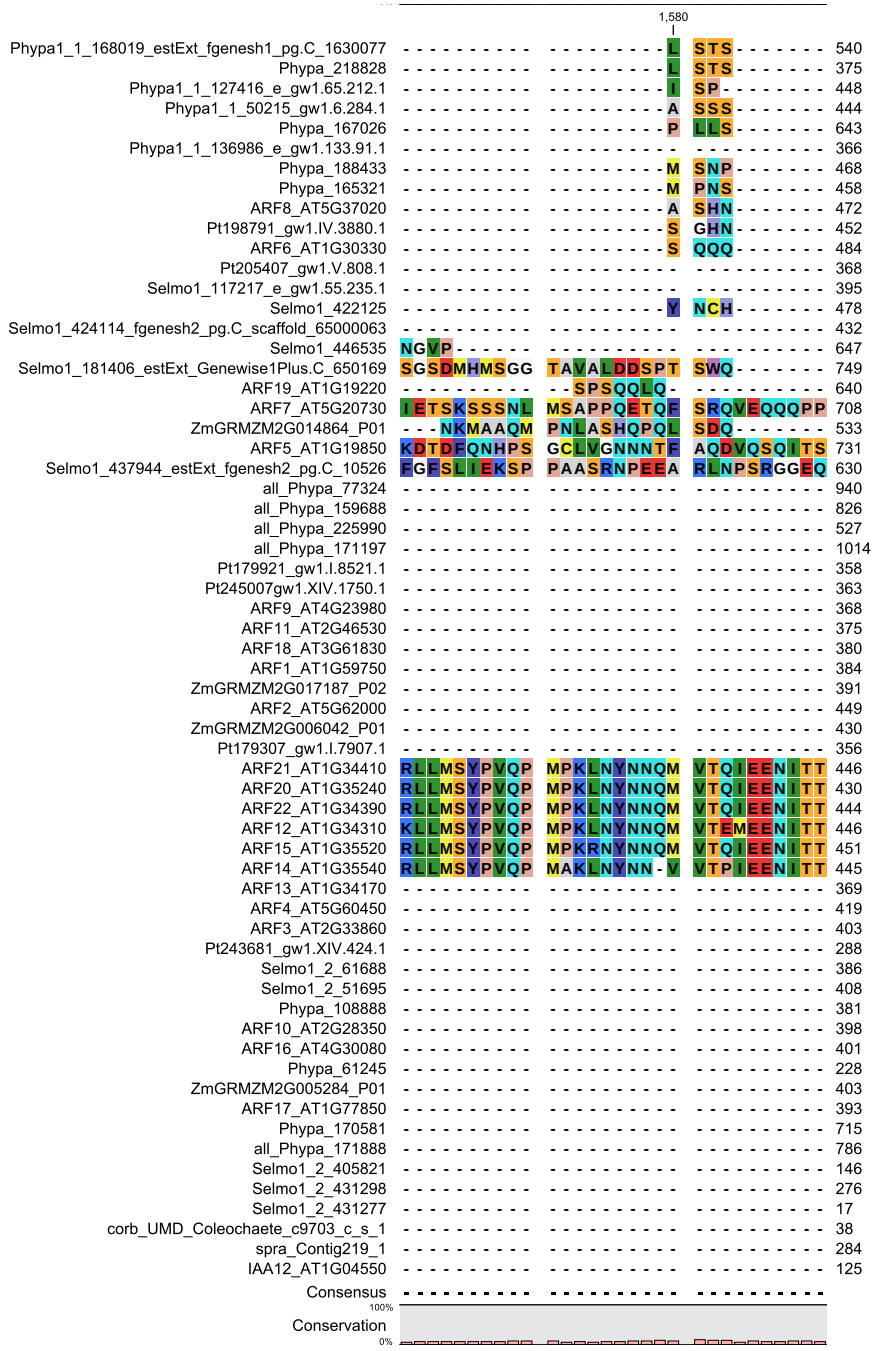
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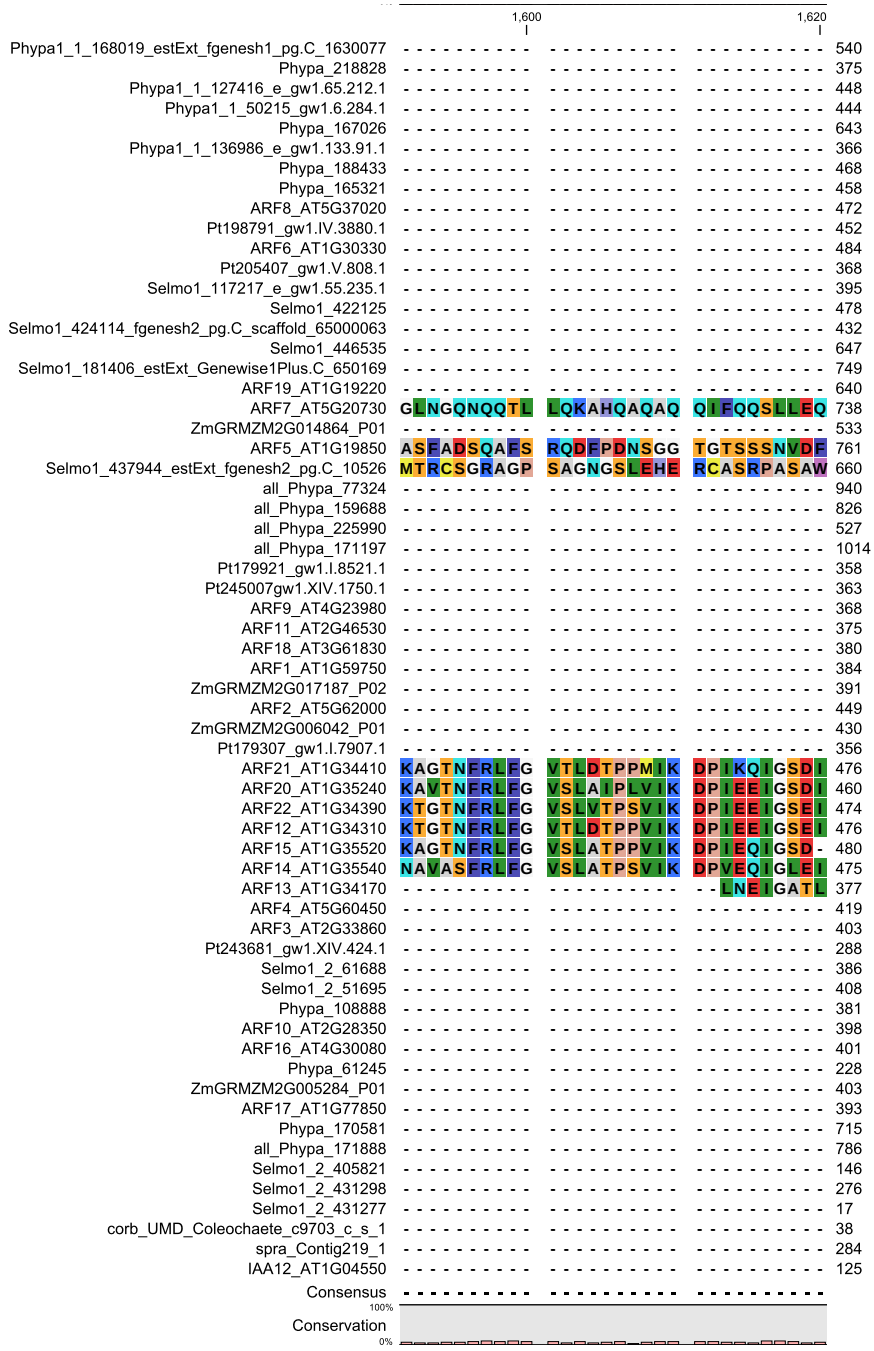
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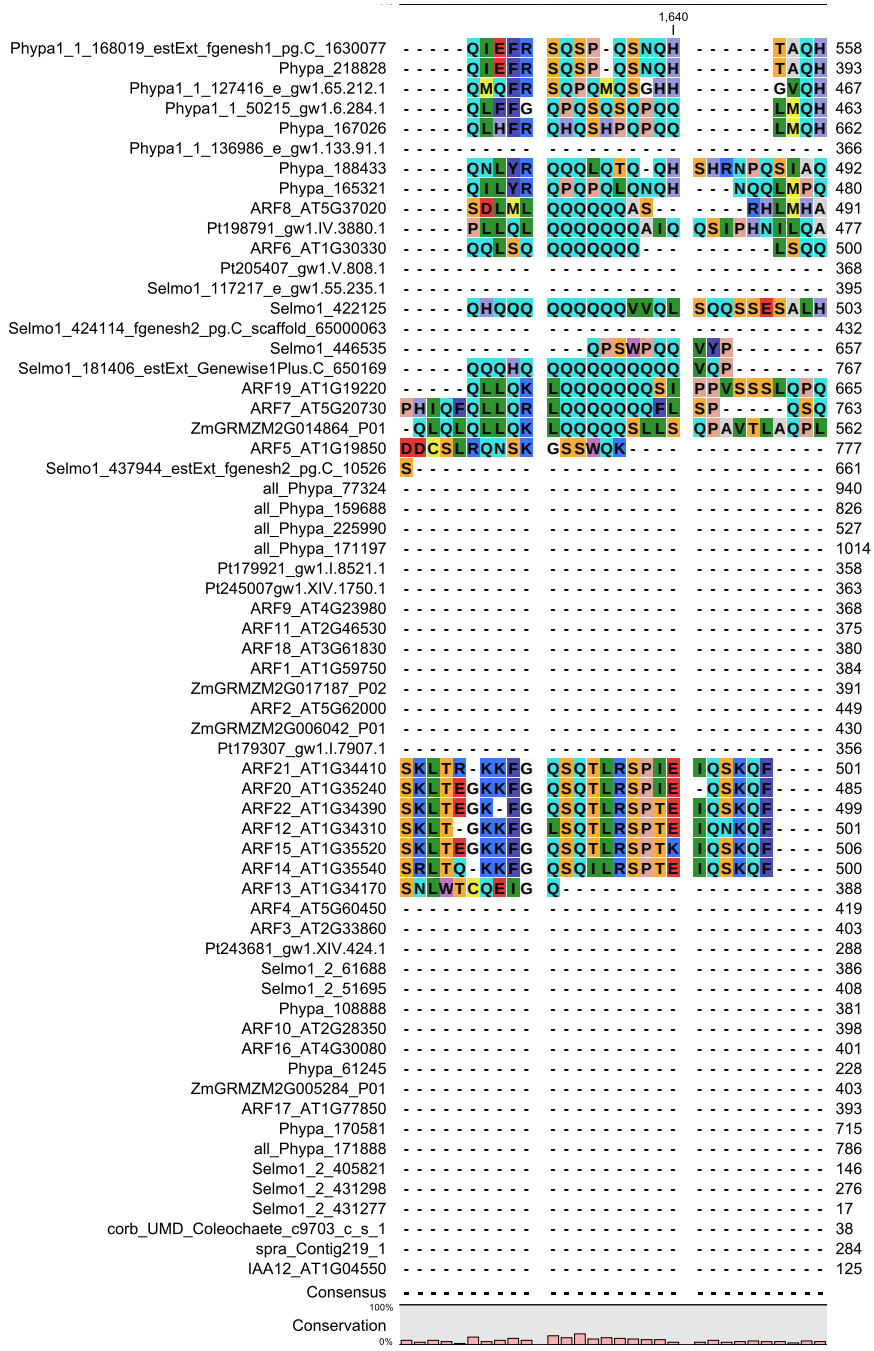
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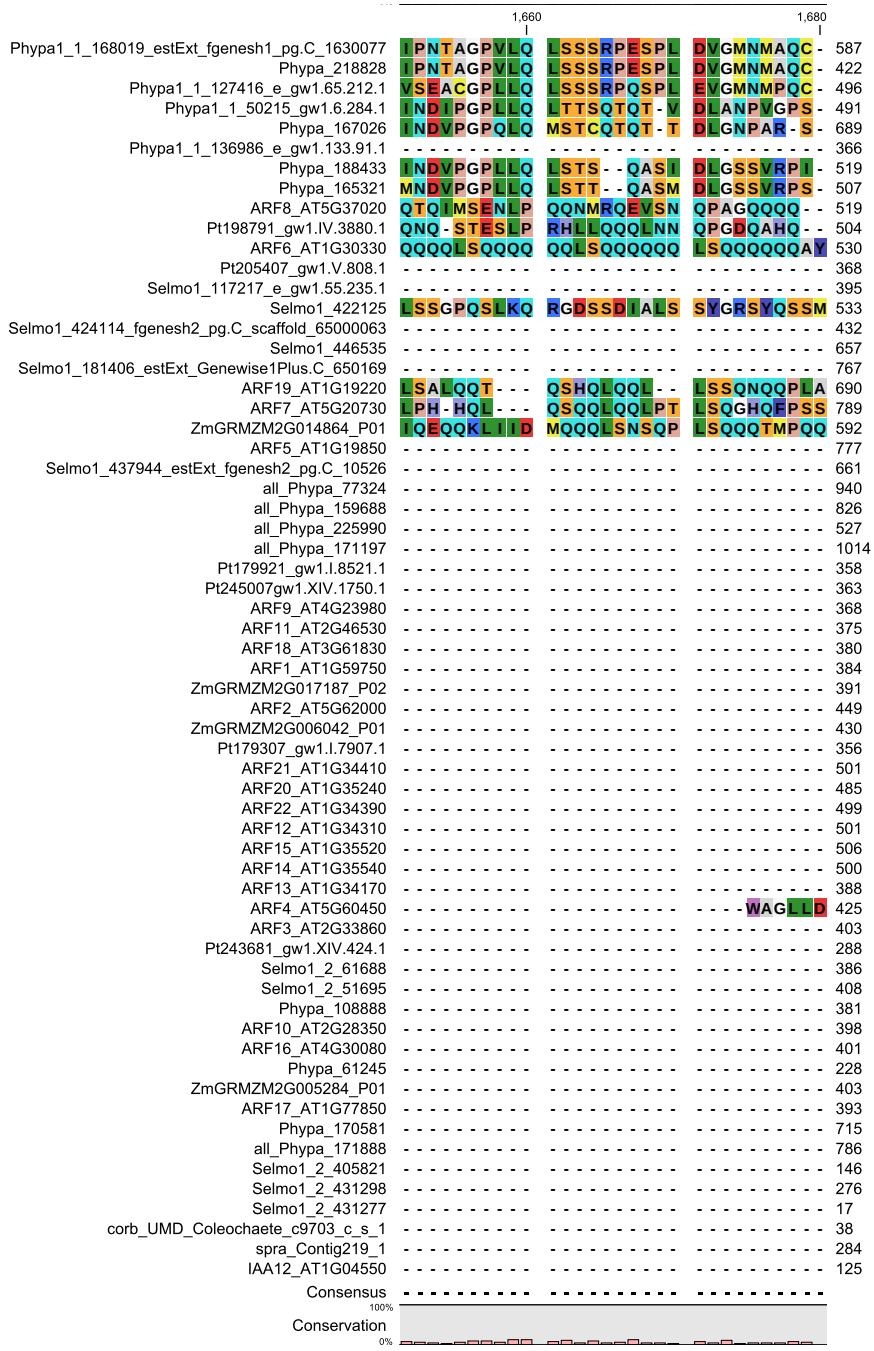
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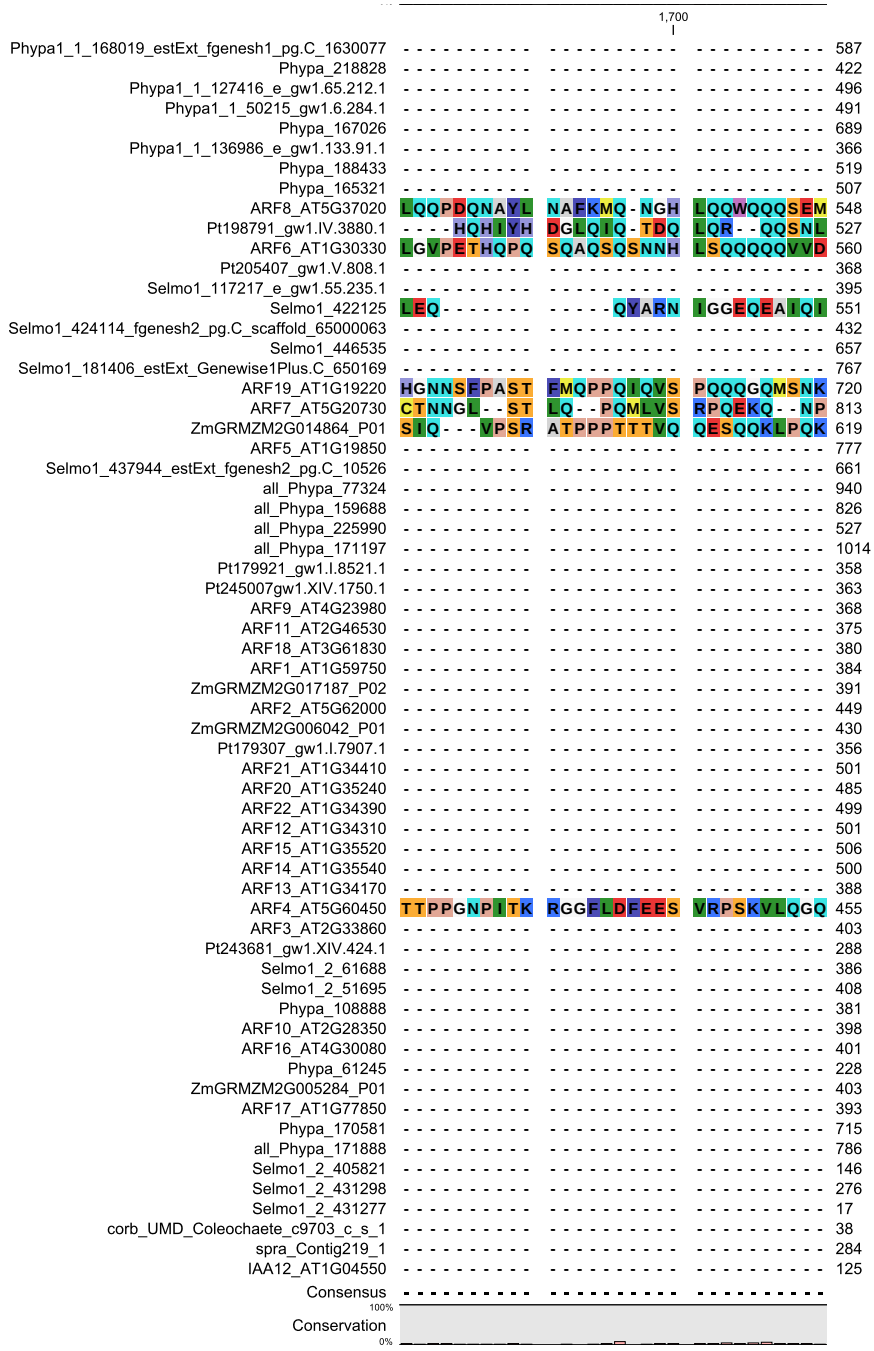
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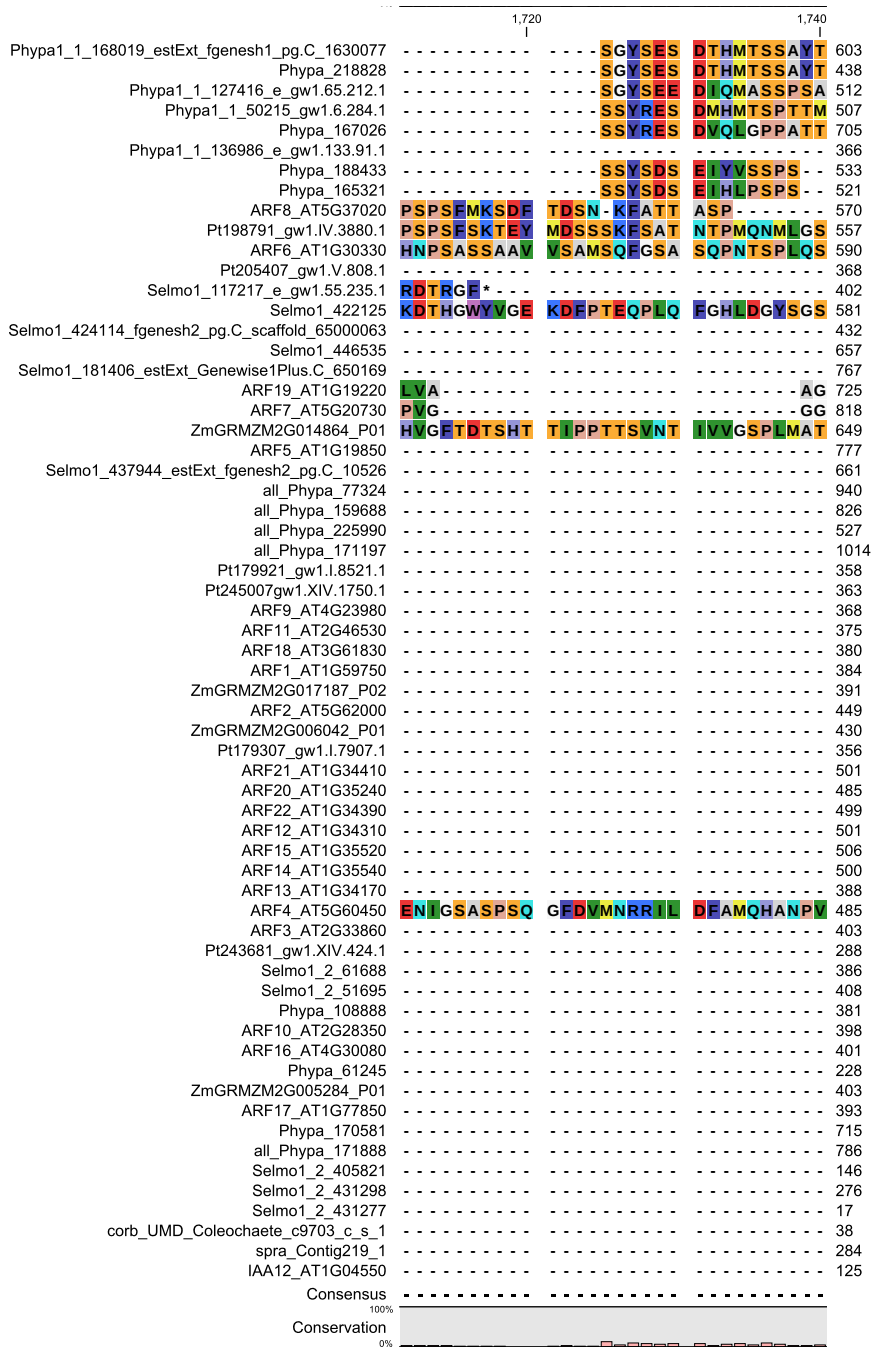
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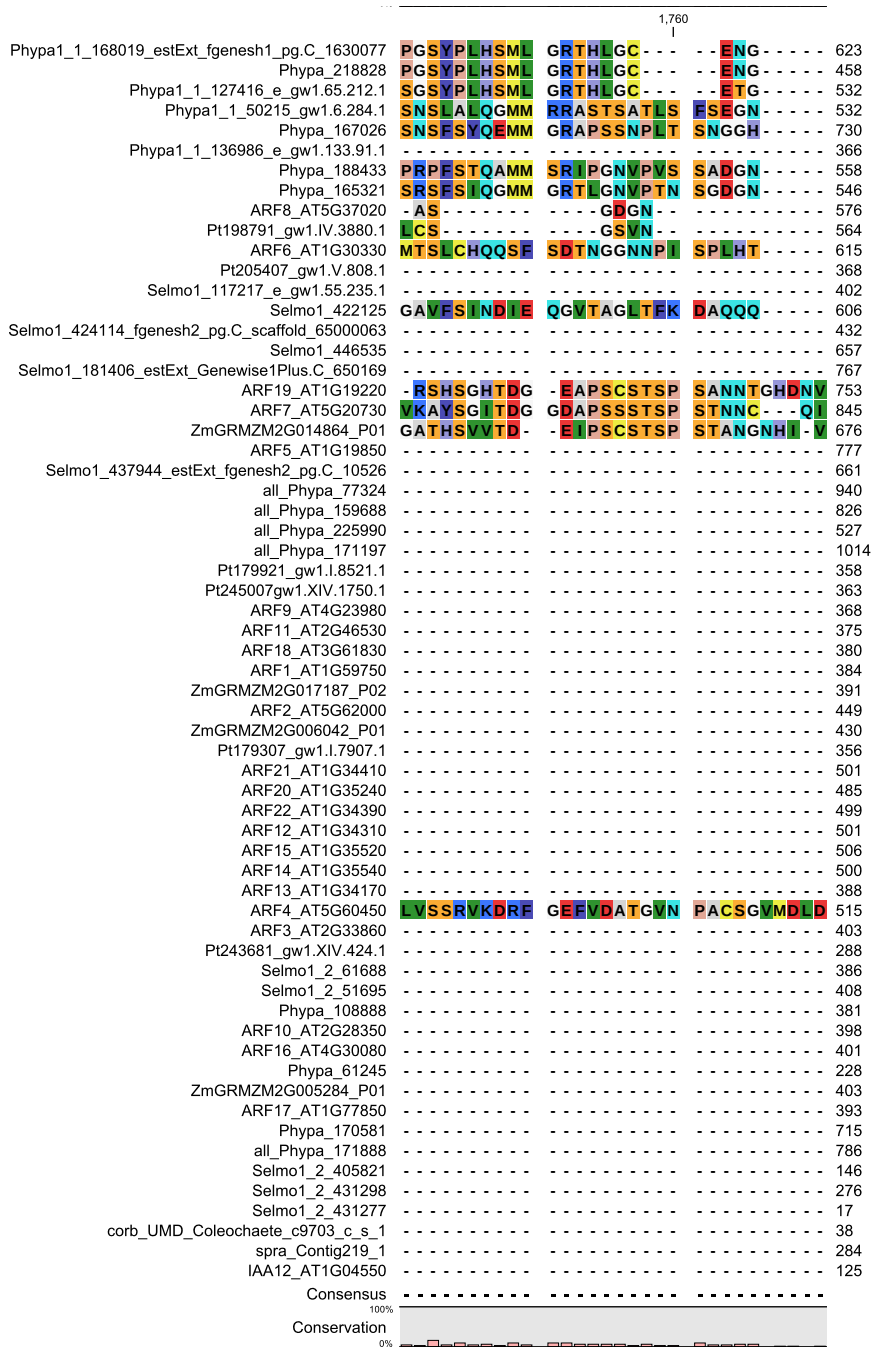
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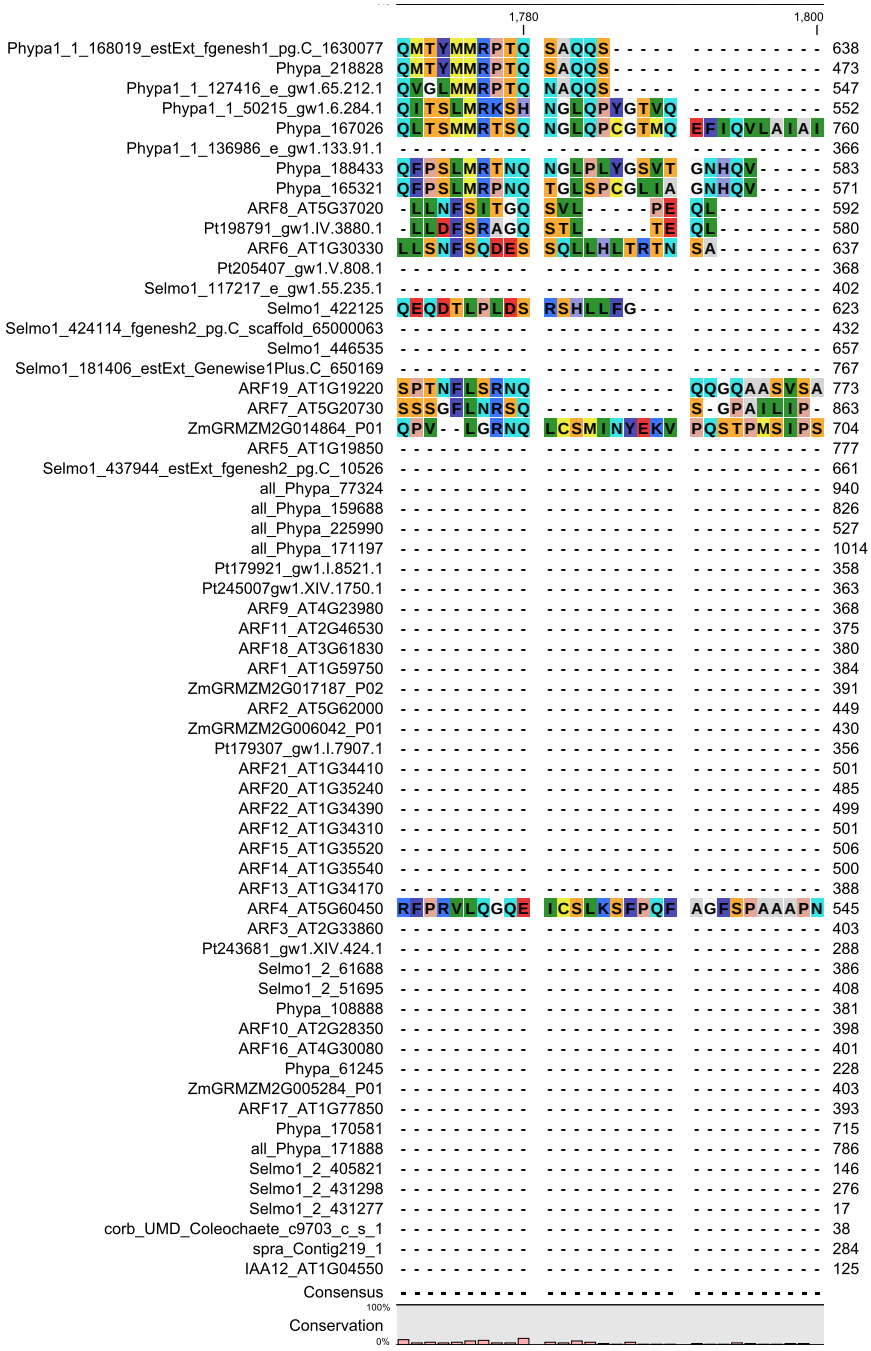
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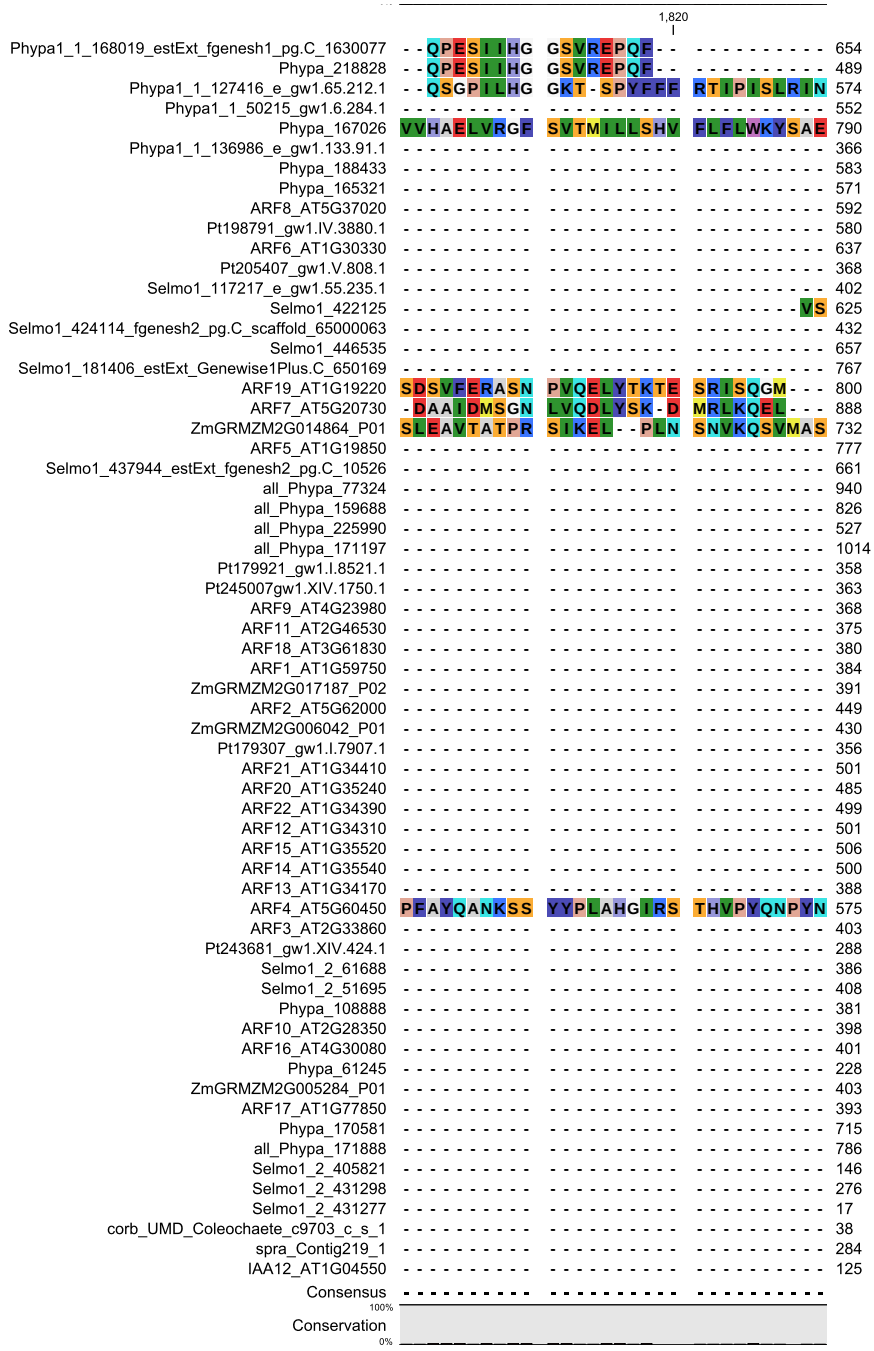
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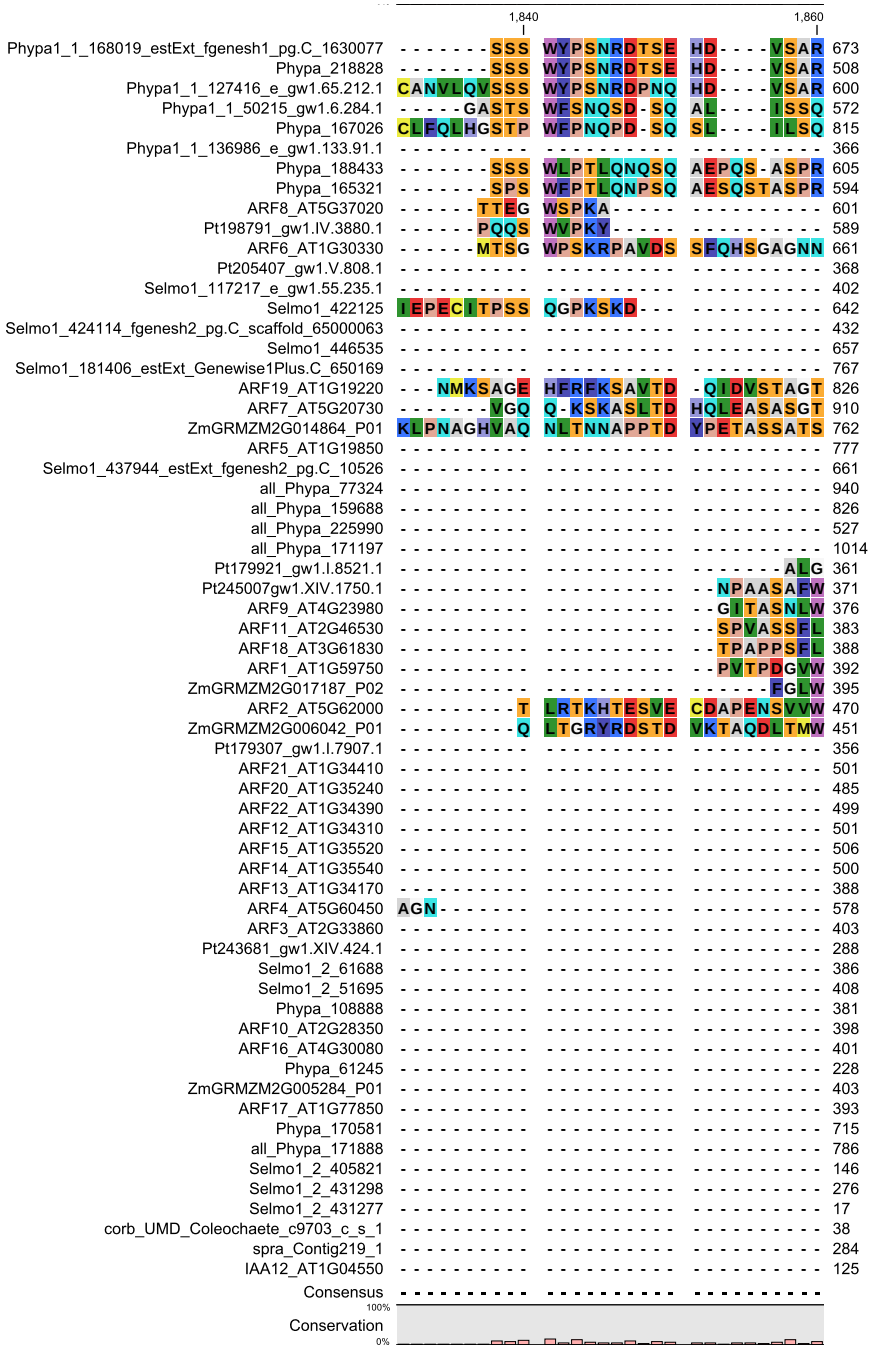
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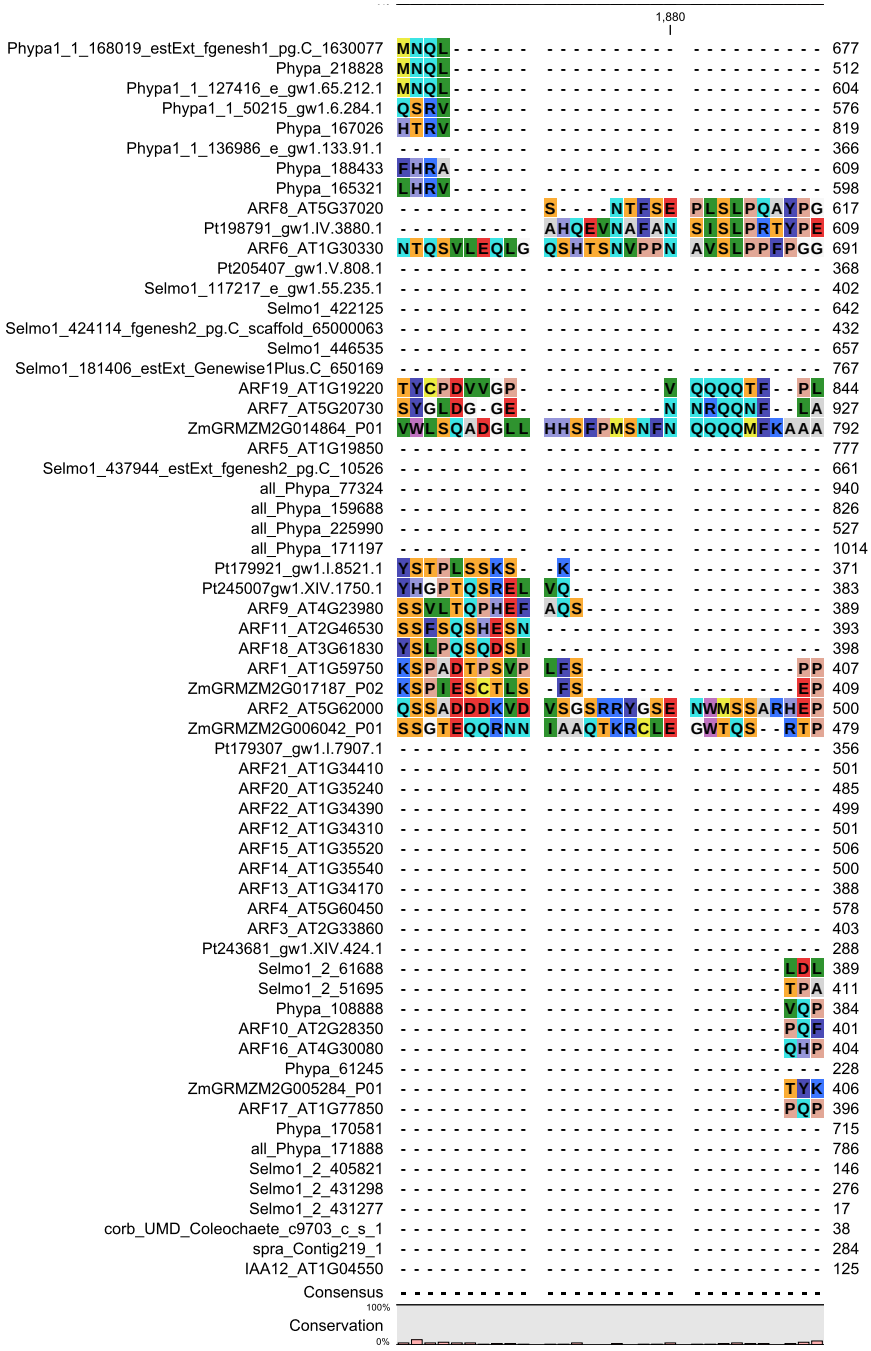
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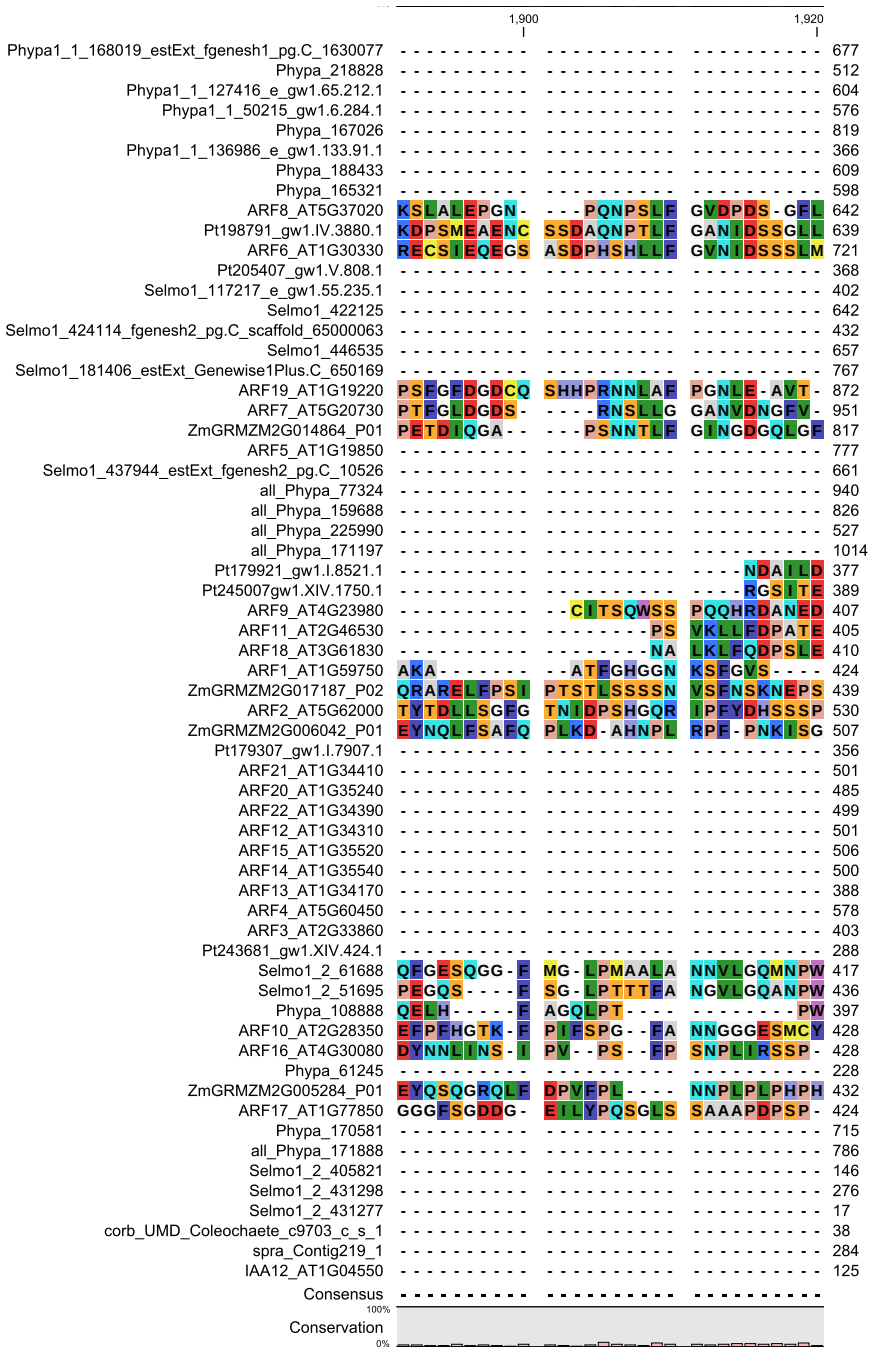
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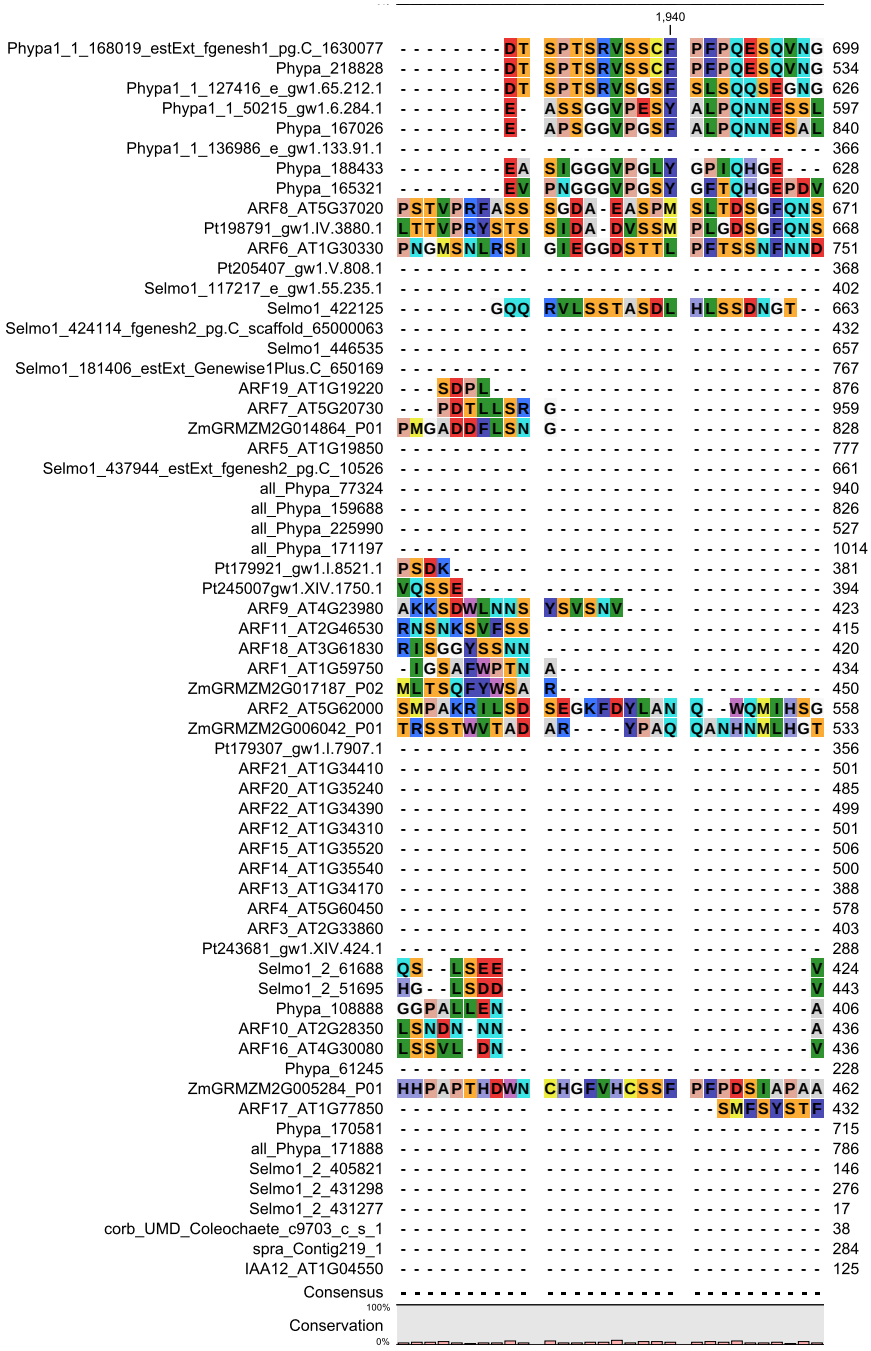
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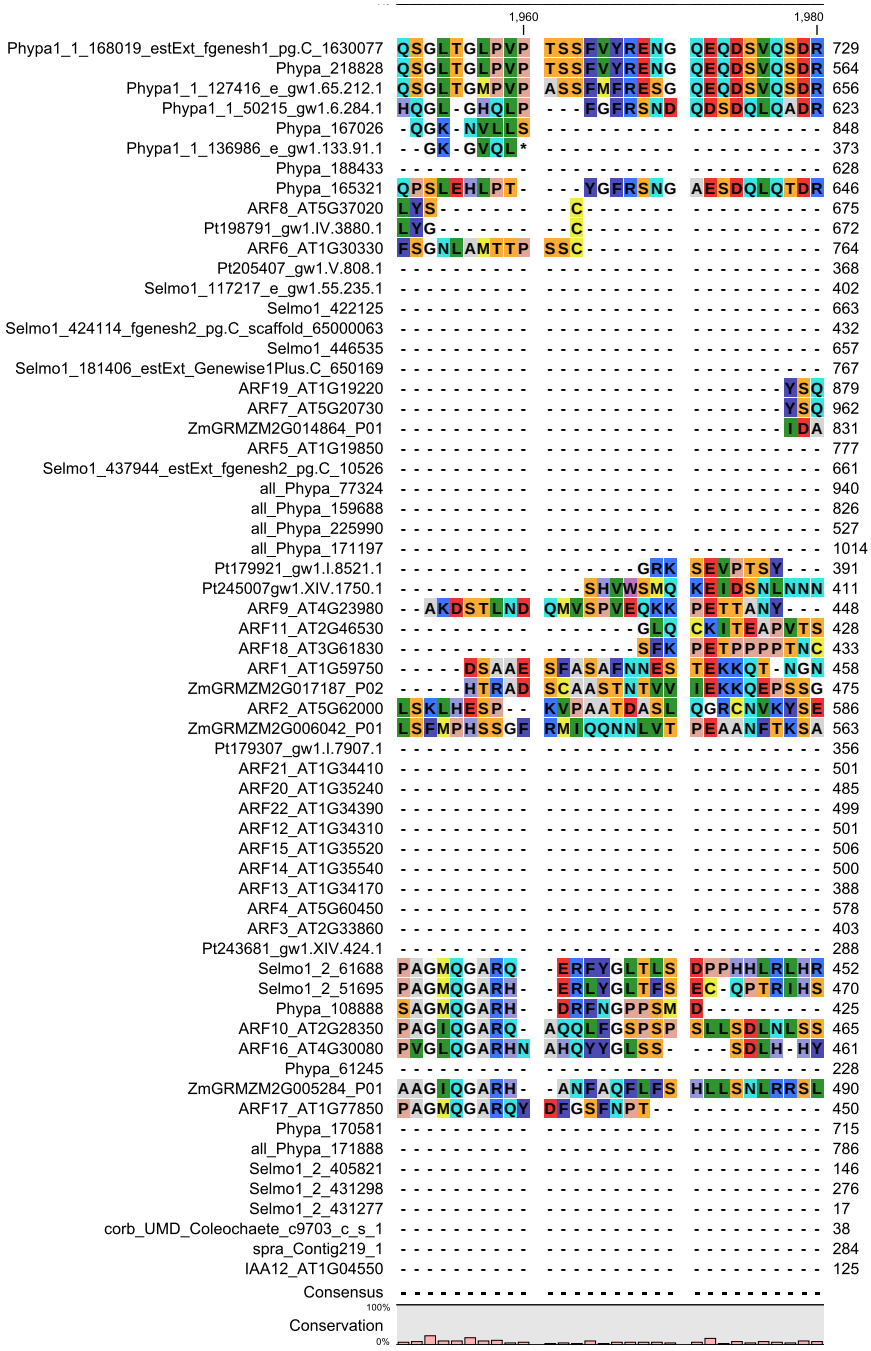
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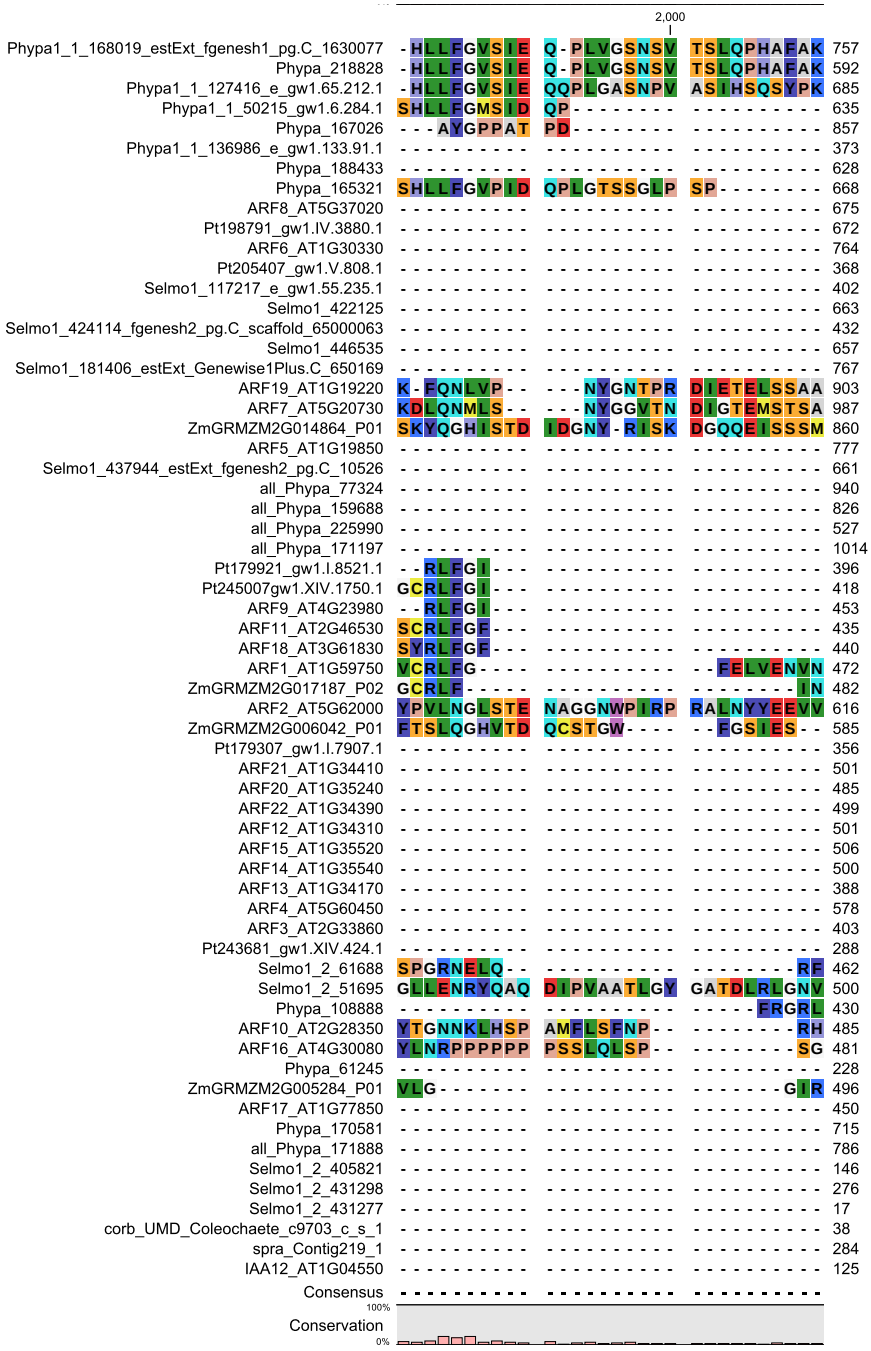
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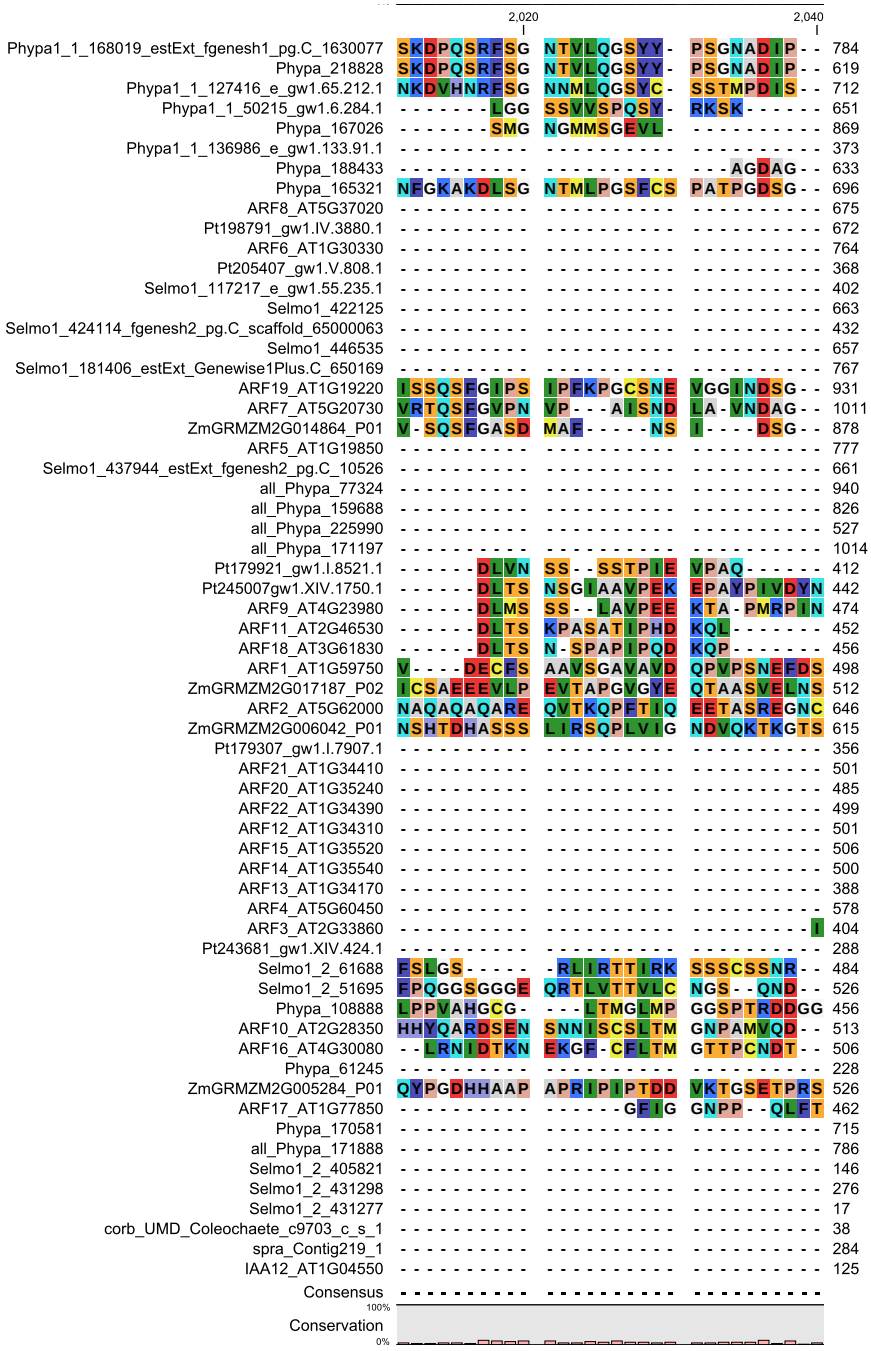
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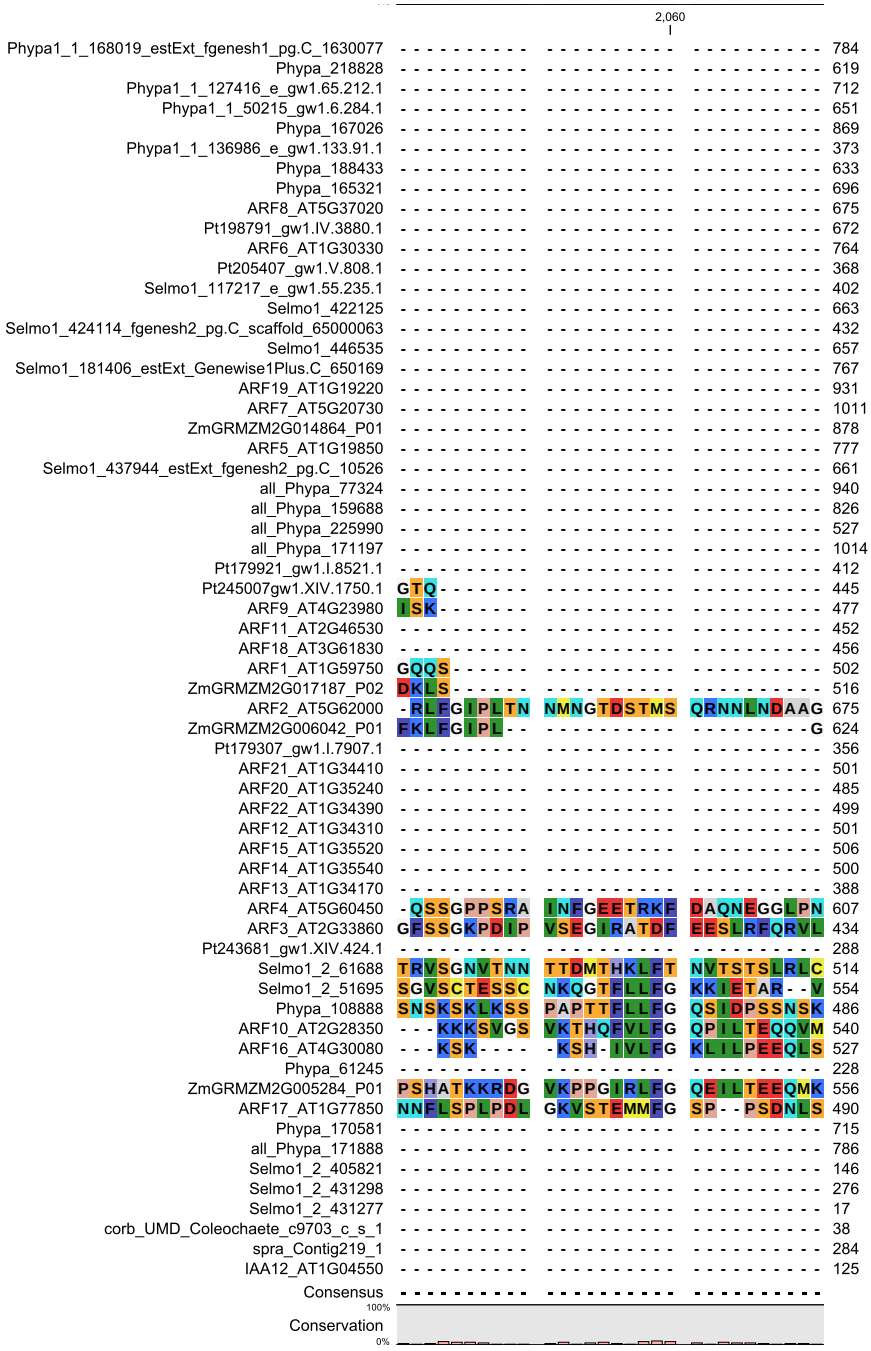
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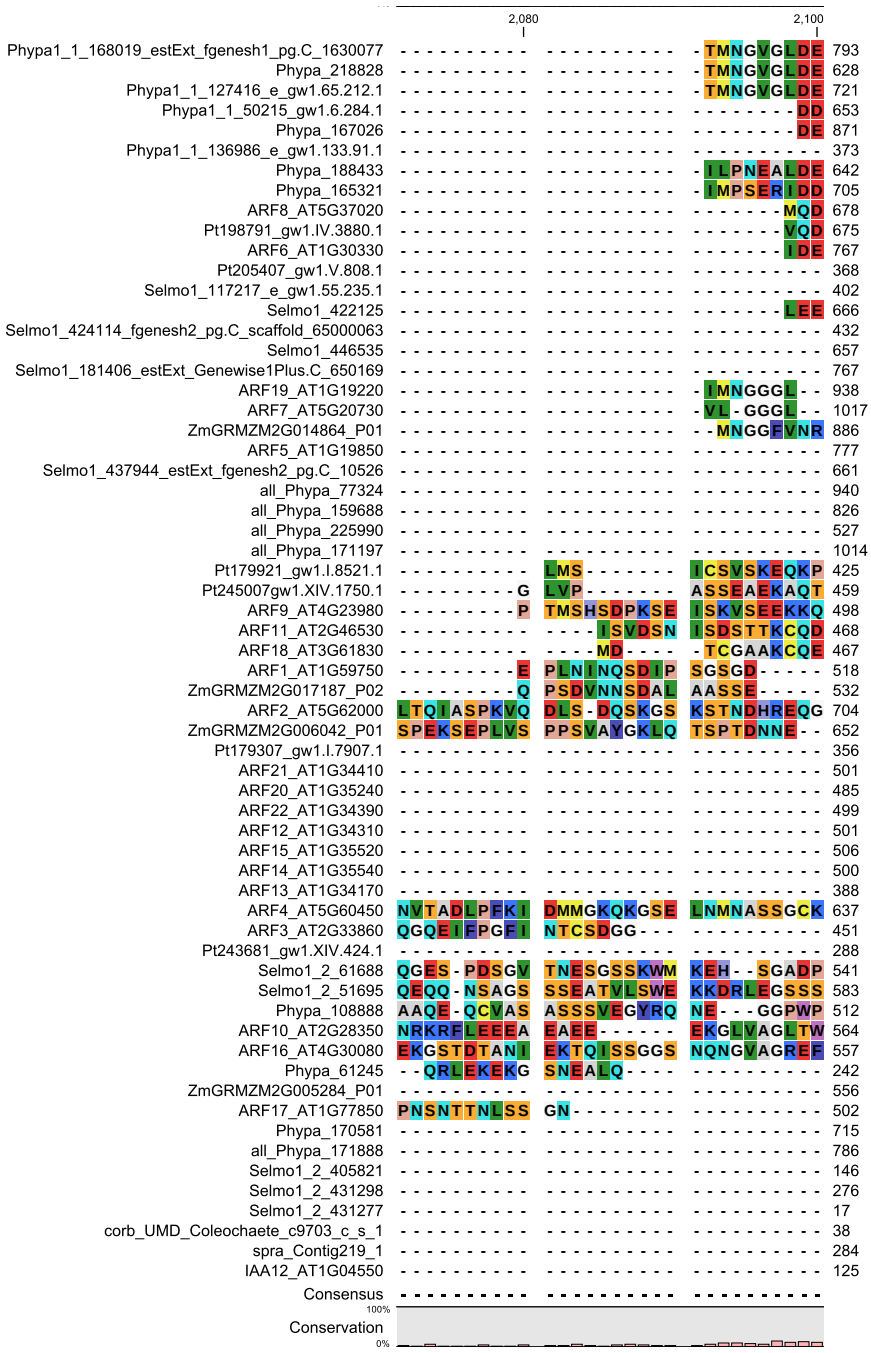
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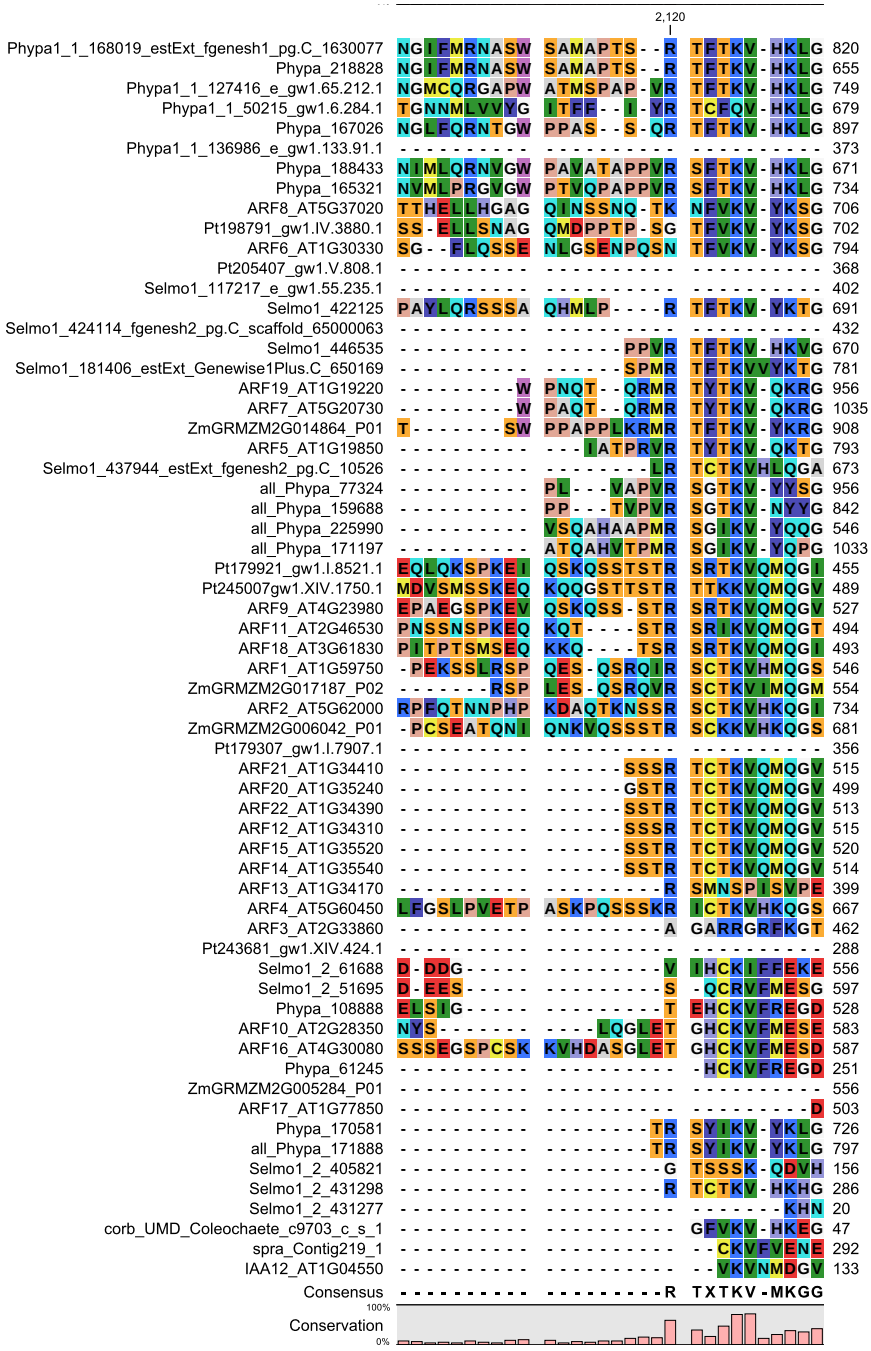
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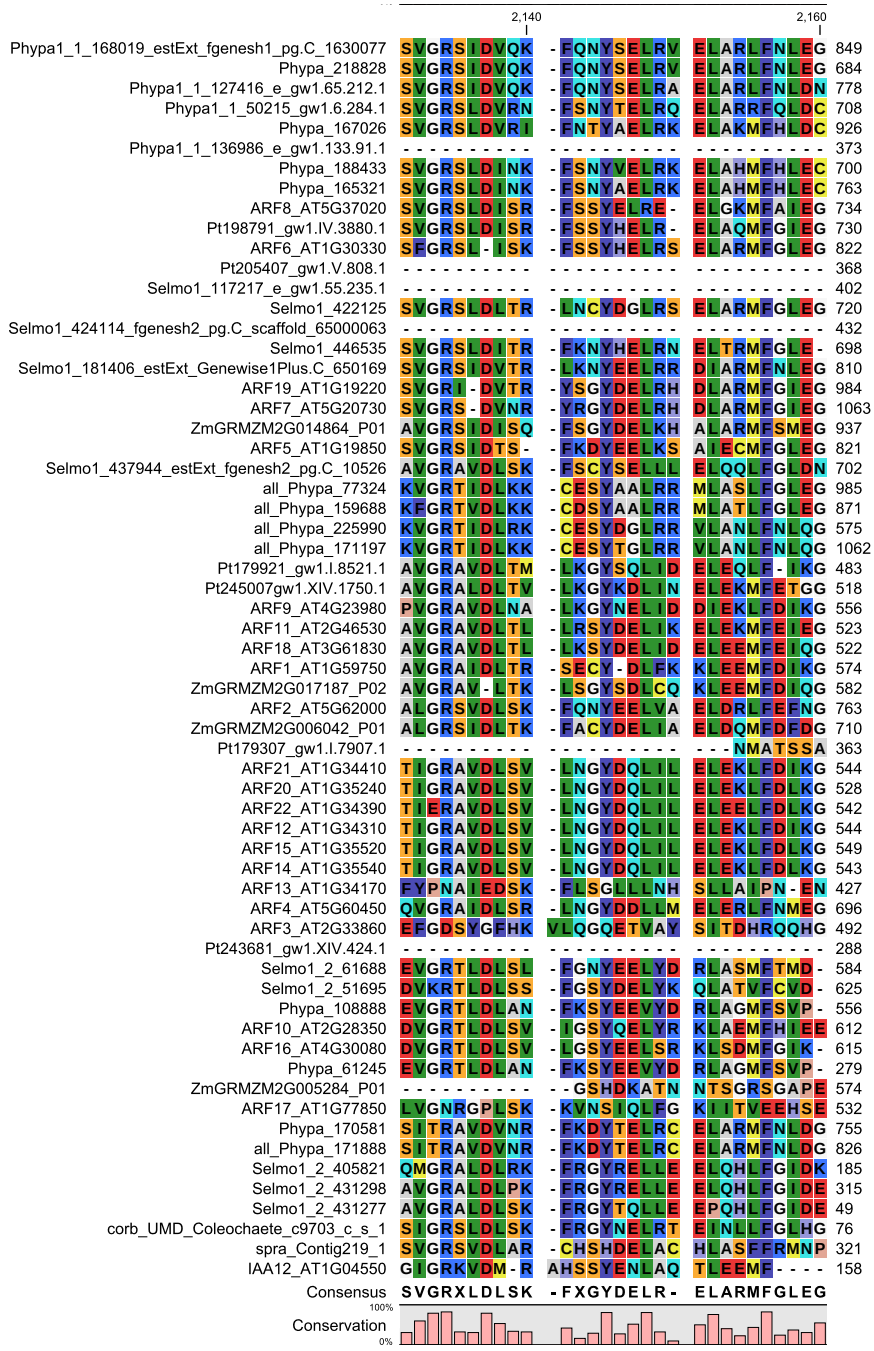
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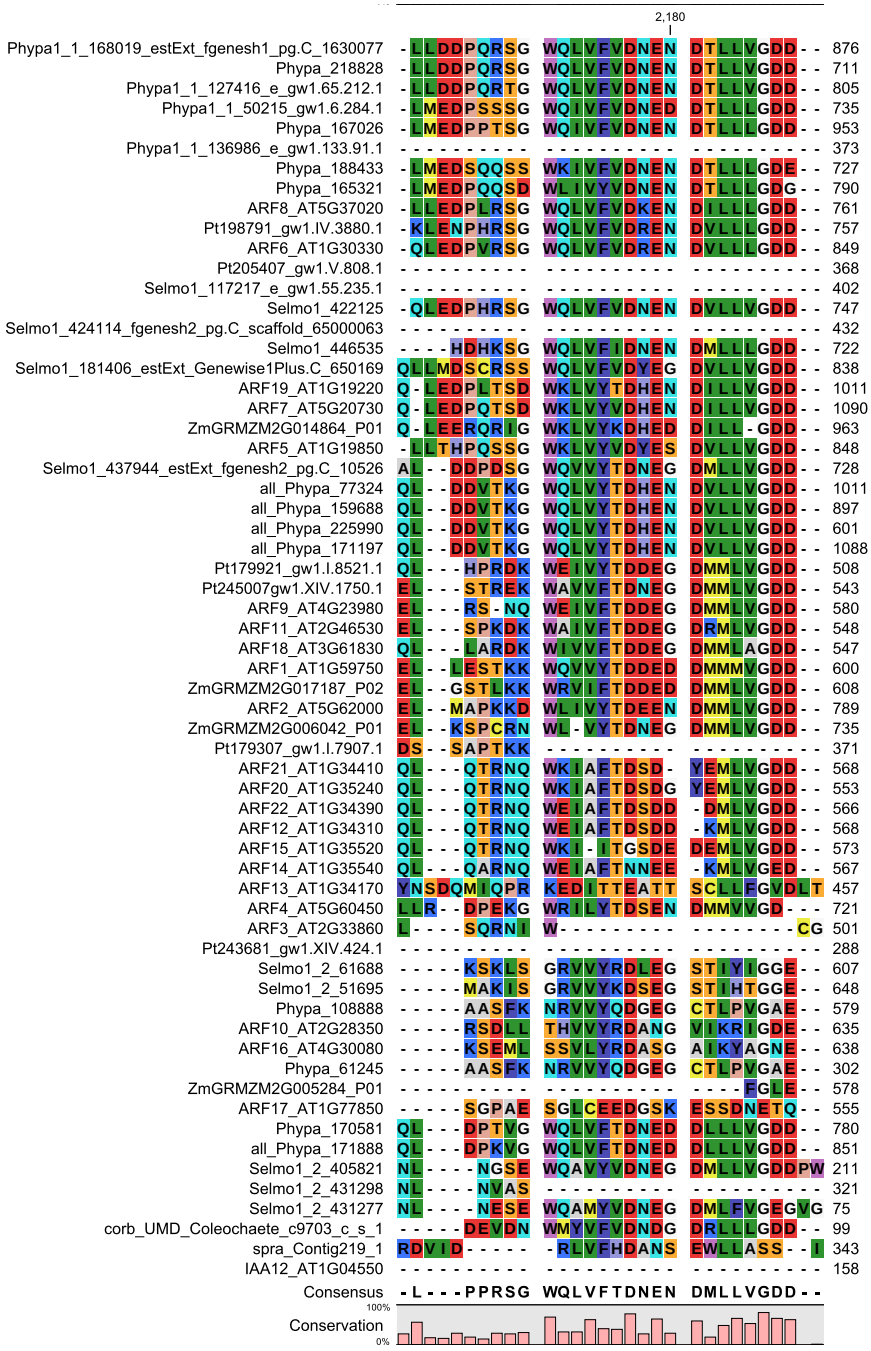
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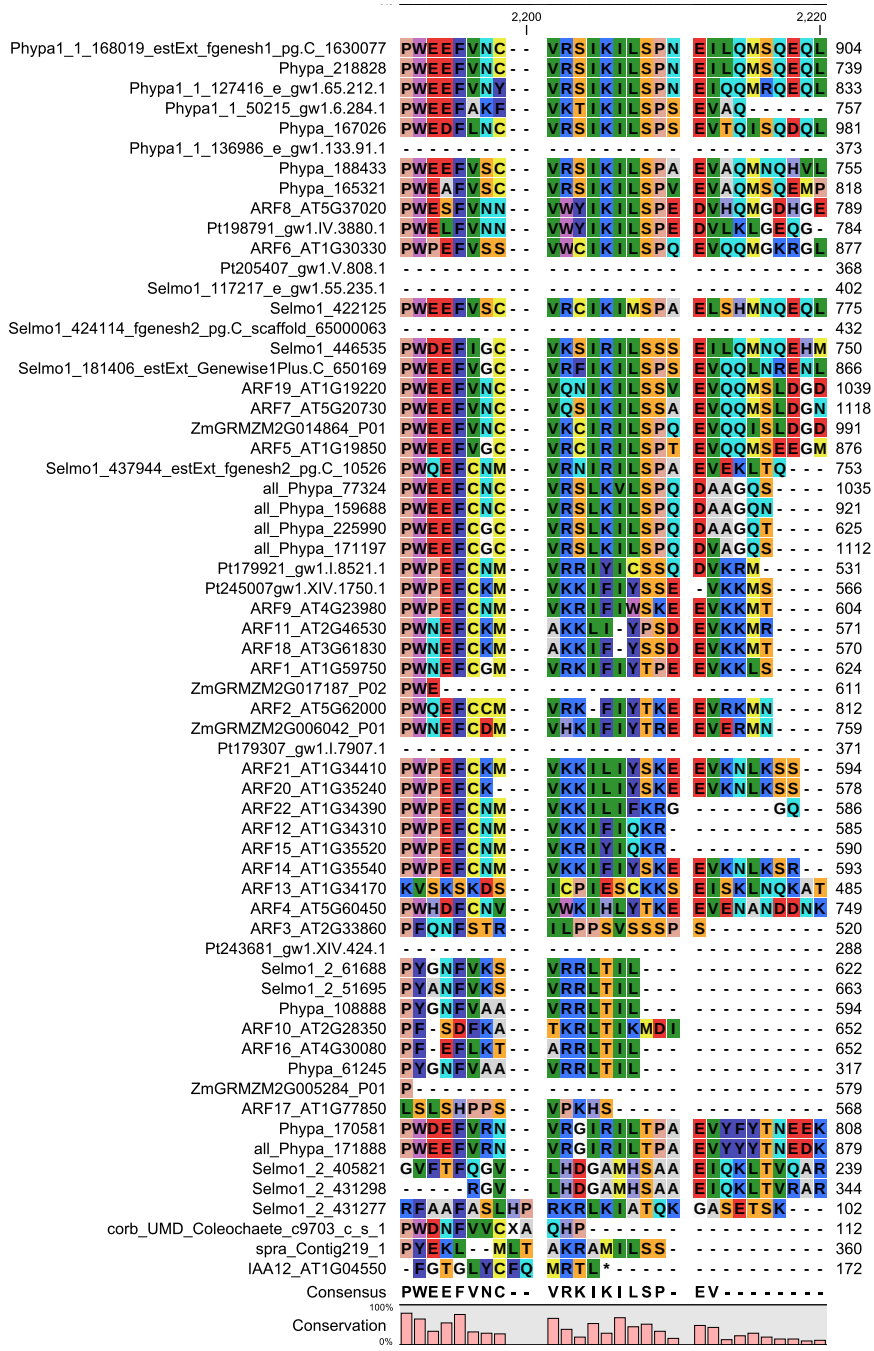
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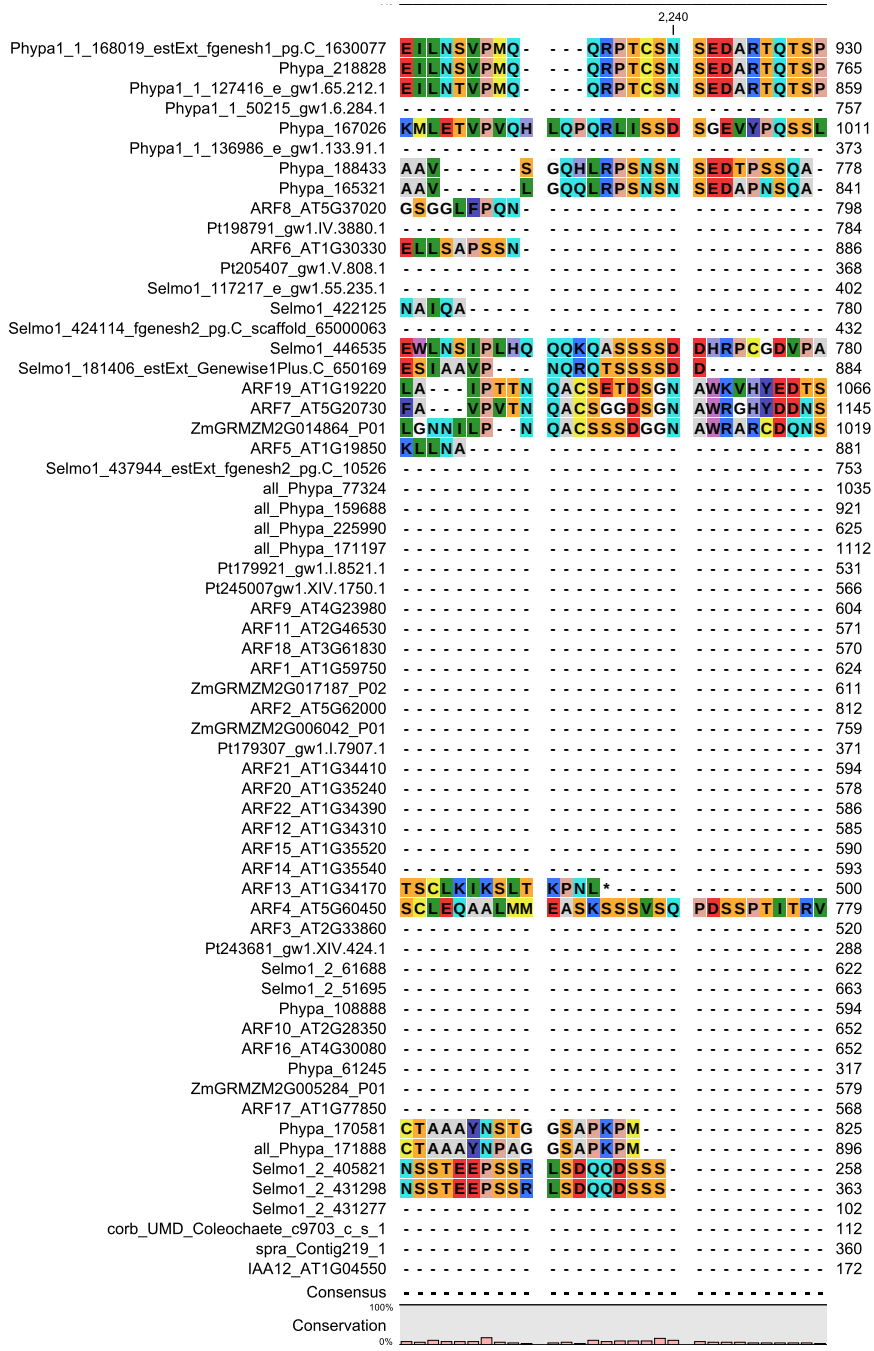
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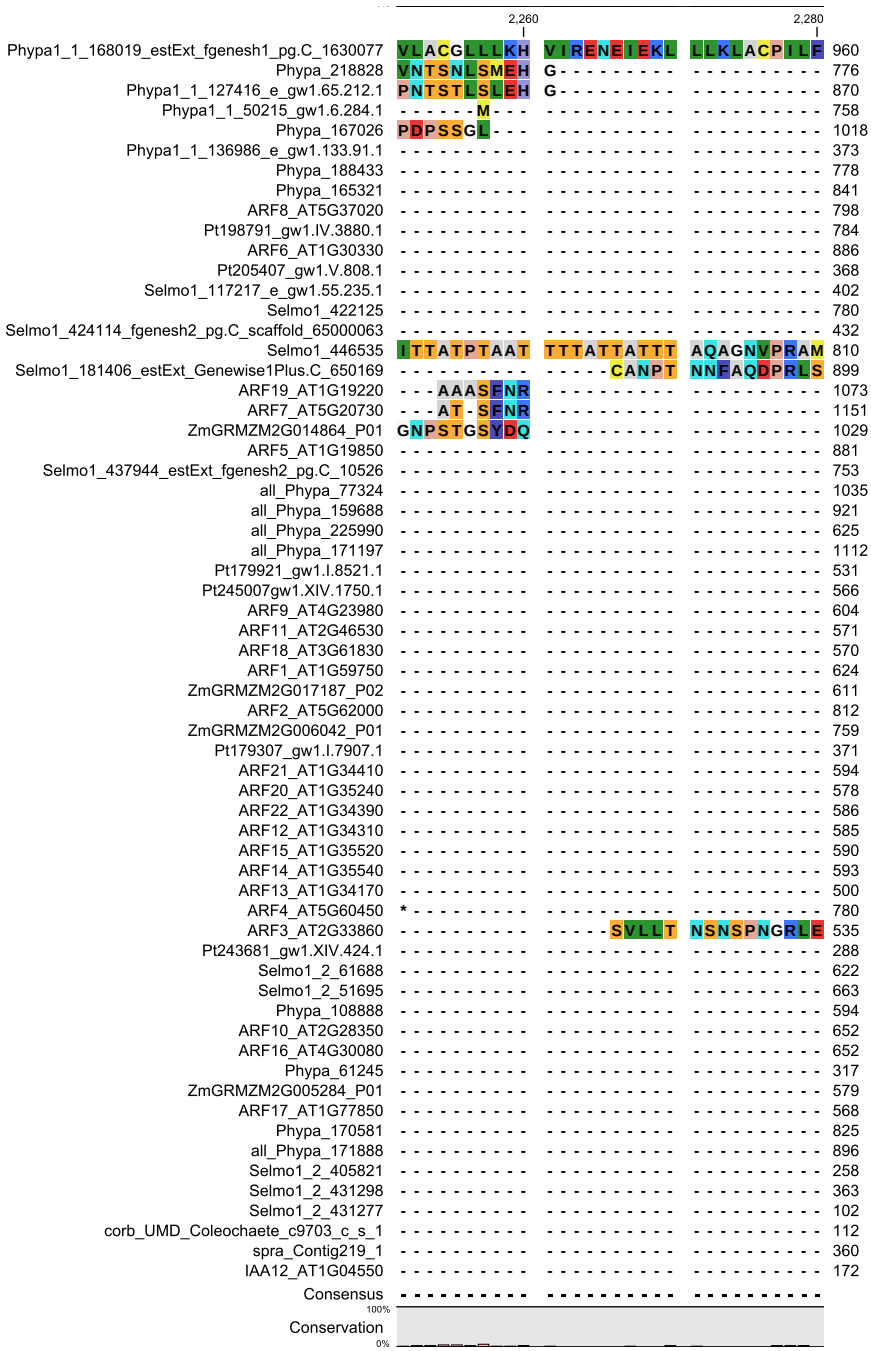
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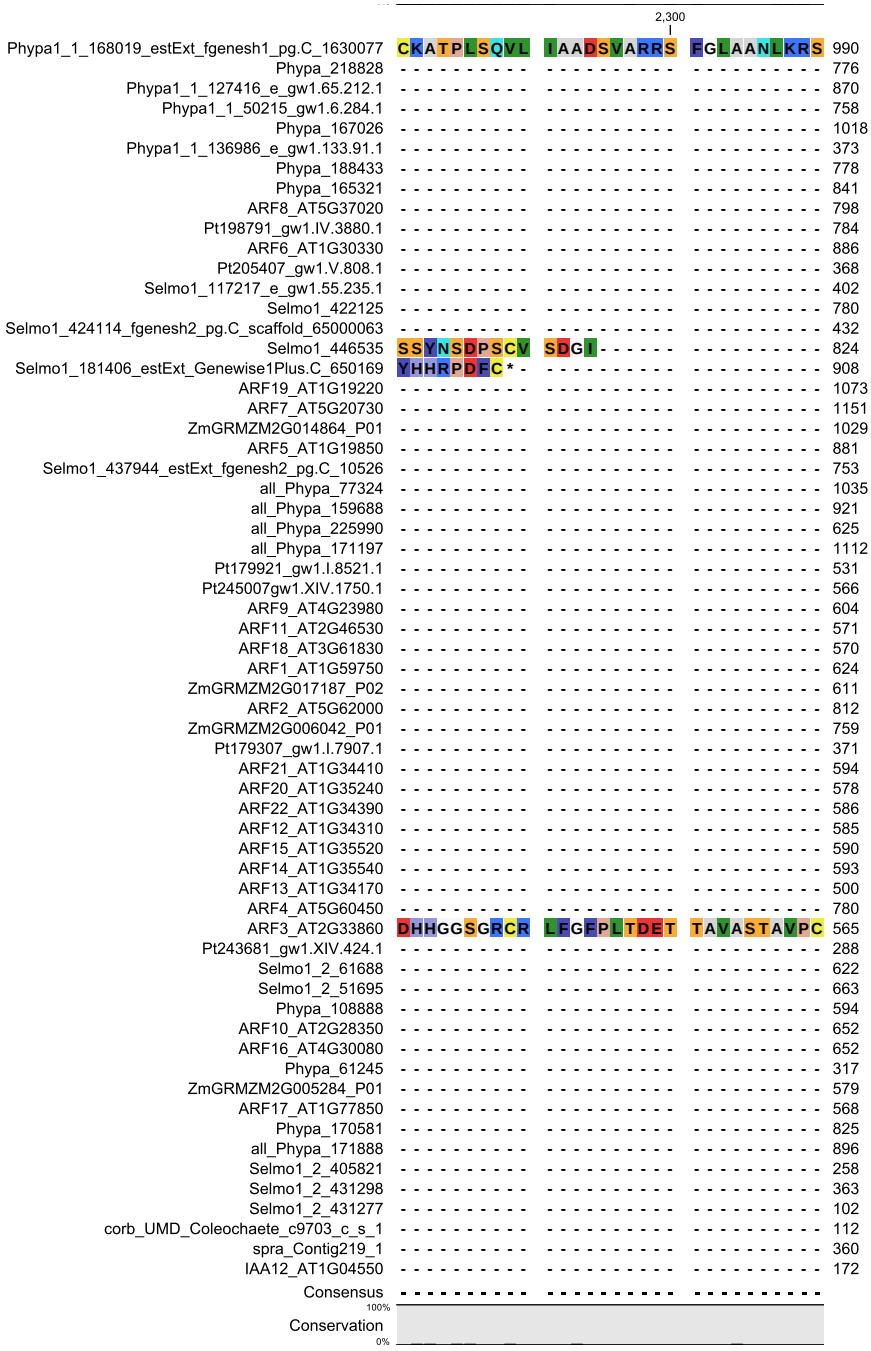
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all_Phypa_159688	---------- ---------- ----------	921
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all_Phypa_171197	---------- ---------- ----------	1112
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Pt245007gw1.XIV.1750.1	---------- ---------- ----------	566
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ARF12_AT1G34310	---------- ---------- ----------	585
ARF15_AT1G35520	---------- ---------- ----------	590
ARF14_AT1G35540	---------- ---------- ----------	593
ARF13_AT1G34170	---------- ---------- ----------	500
ARF4_AT5G60450	---------- ---------- ----------	780
ARF3_AT2G33860	VEGNSMKGAS AVQSNHHHSQ GRDIYAMRDM	595
Pt243681_gw1.XIV.424.1	---------- ---------- ----------	288
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Selmo1_2_51695	---------- ---------- ----------	663
Phypa_108888	---------- ---------- ----------	594
ARF10_AT2G28350	---------- ---------- ----------	652
ARF16_AT4G30080	---------- ---------- ----------	652
Phypa_61245	---------- ---------- ----------	317
ZmGRMZM2G005284_P01	---------- ---------- ----------	579
ARF17_AT1G77850	---------- ---------- ----------	568
Phypa_170581	---------- ---------- ----------	825
all_Phypa_171888	---------- ---------- ----------	896
Selmo1_2_405821	---------- ---------- ----------	258
Selmo1_2_431298	---------- ---------- ----------	363
Selmo1_2_431277	---------- ---------- ----------	102
corb_UMD_Coleochaete_c9703_c_s_1	---------- ---------- ----------	112
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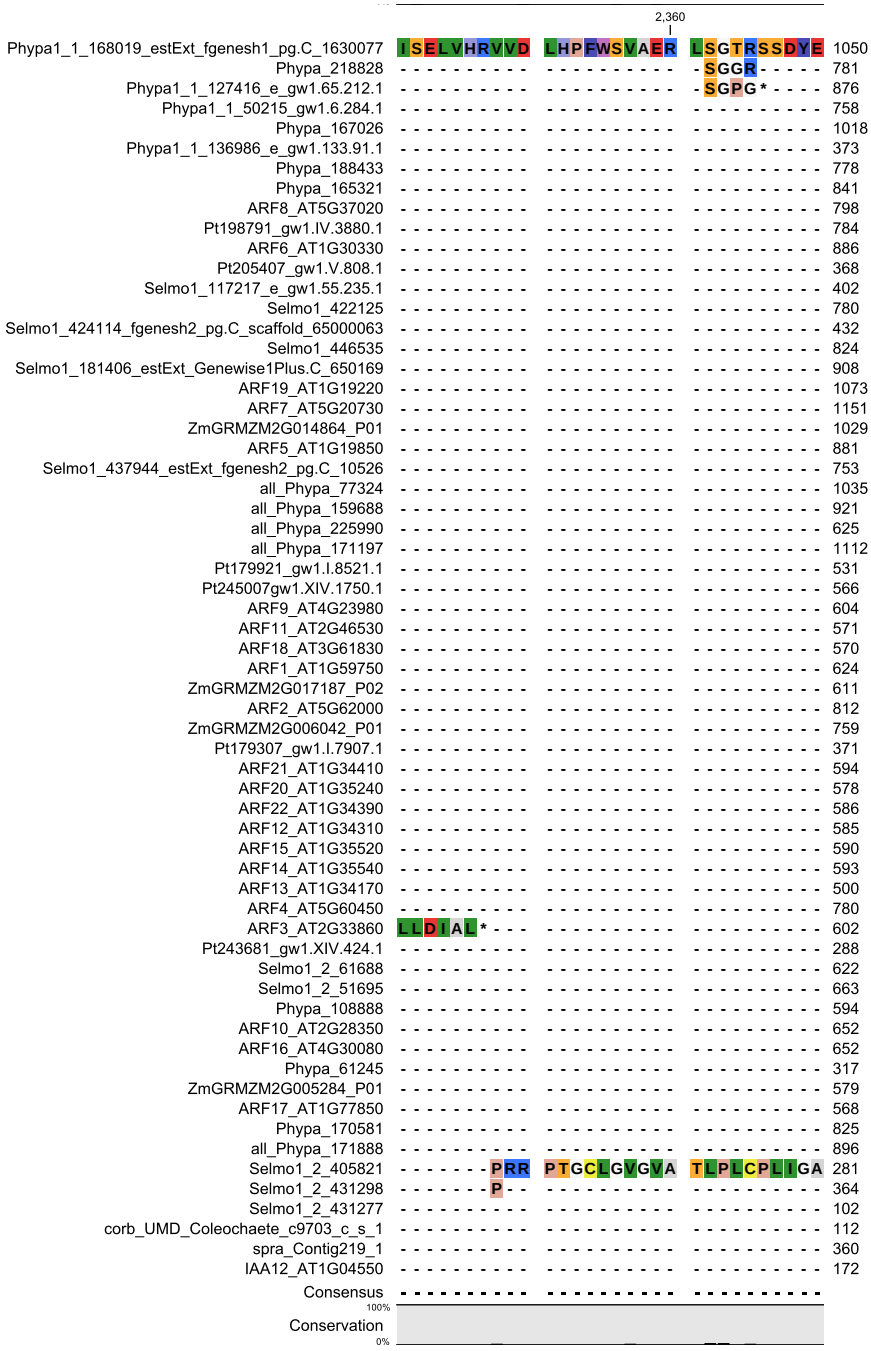
IAA12_AT1G04550	---------- ---------- ----------	172
Consensus	---------- ---------- ----------	

Conservation (100% – 0%)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Phypa1_1_50215_gw1.6.284.1 758
Phypa_167026 1018
Phypa1_1_136986_e_gw1.133.91.1 373
Phypa_188433 778
Phypa_165321 841
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ARF6_AT1G30330 886
Pt205407_gw1.V.808.1 368
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Selmo1_422125 780
Selmo1_424114_fgenesh2_pg.C_scaffold_65000063 432
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Selmo1_437944_estExt_fgenesh2_pg.C_10526 753
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all_Phypa_159688 921
all_Phypa_225990 625
all_Phypa_171197 1112
Pt179921_gw1.I.8521.1 531
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ARF9_AT4G23980 604
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ARF1_AT1G59750 624
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ZmGRMZM2G006042_P01 759
Pt179307_gw1.I.7907.1 371
ARF21_AT1G34410 594
ARF20_AT1G35240 578
ARF22_AT1G34390 586
ARF12_AT1G34310 585
ARF15_AT1G35520 590
ARF14_AT1G35540 593
ARF13_AT1G34170 500
ARF4_AT5G60450 780
ARF3_AT2G33860 LLDIAL* 602
Pt243681_gw1.XIV.424.1 288
Selmo1_2_61688 622
Selmo1_2_51695 663
Phypa_108888 594
ARF10_AT2G28350 652
ARF16_AT4G30080 652
Phypa_61245 317
ZmGRMZM2G005284_P01 579
ARF17_AT1G77850 568
Phypa_170581 825
all_Phypa_171888 896
Selmo1_2_405821 PRR PTGCLGVGVA TLPLCPLIGA 281
Selmo1_2_431298 P 364
Selmo1_2_431277 102
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Consensus
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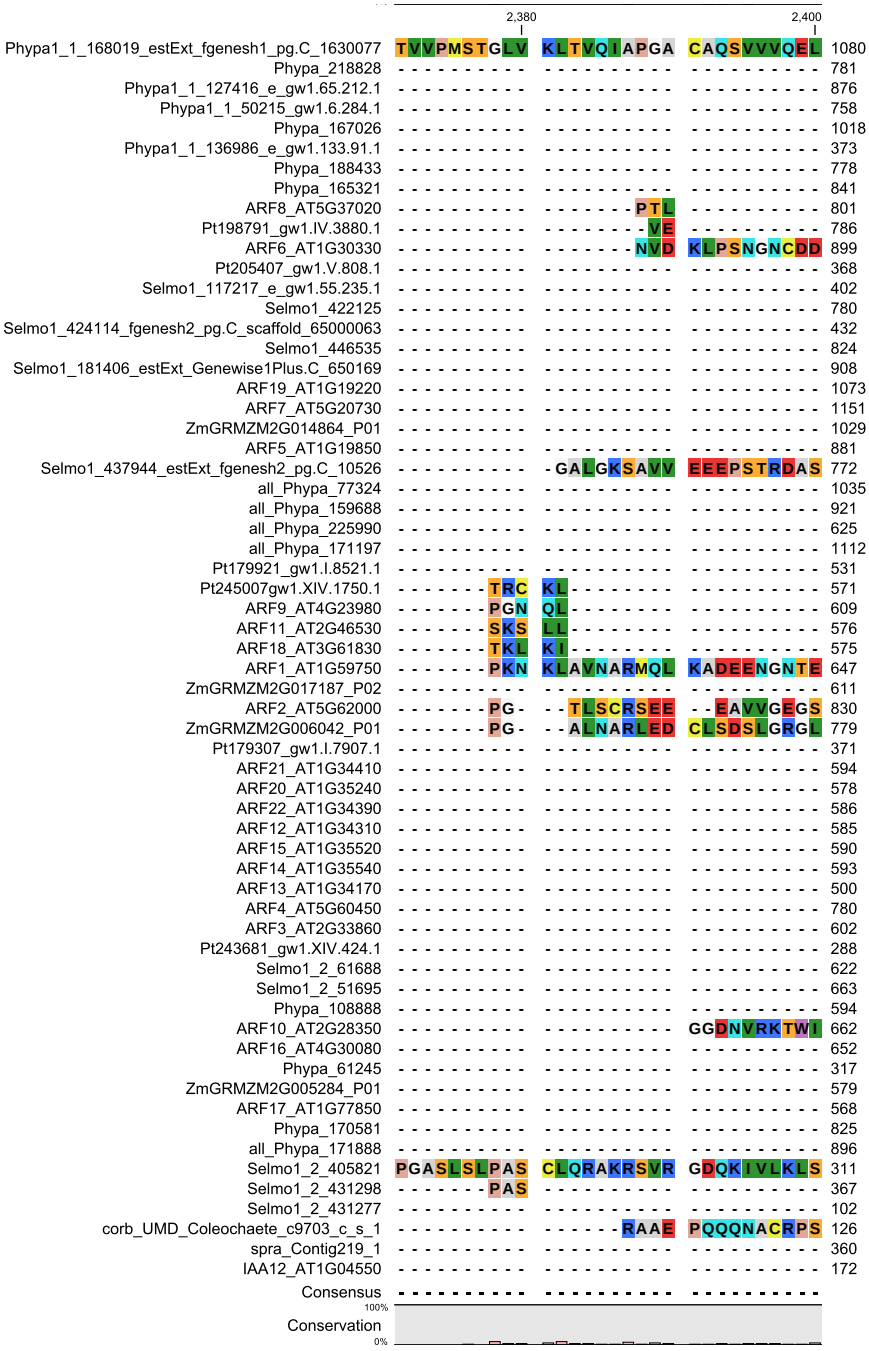
Conservation
0%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Phypa1_1_50215_gw1.6.284.1 758
Phypa_167026 1018
Phypa1_1_136986_e_gw1.133.91.1 373
Phypa_188433 778
Phypa_165321 841
ARF8_AT5G37020 PTL 801
Pt198791_gw1.IV.3880.1 VE 786
ARF6_AT1G30330 NVD KLPSNGNCDD 899
Pt205407_gw1.V.808.1 368
Selmo1_117217_e_gw1.55.235.1 402
Selmo1_422125 780
Selmo1_424114_fgenesh2_pg.C_scaffold_65000063 432
Selmo1_446535 824
Selmo1_181406_estExt_Genewise1Plus.C_650169 908
ARF19_AT1G19220 1073
ARF7_AT5G20730 1151
ZmGRMZM2G014864_P01 1029
ARF5_AT1G19850 881
Selmo1_437944_estExt_fgenesh2_pg.C_10526 GALGKSAVV EEEPSTRDAS 772
all_Phypa_77324 1035
all_Phypa_159688 921
all_Phypa_225990 625
all_Phypa_171197 1112
Pt179921_gw1.I.8521.1 531
Pt245007gw1.XIV.1750.1 TRC KL 571
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ARF11_AT2G46530 SKS LL 576
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ZmGRMZM2G017187_P02 611
ARF2_AT5G62000 PG TLSCRSEE EAVVGEGS 830
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Pt179307_gw1.I.7907.1 371
ARF21_AT1G34410 594
ARF20_AT1G35240 578
ARF22_AT1G34390 586
ARF12_AT1G34310 585
ARF15_AT1G35520 590
ARF14_AT1G35540 593
ARF13_AT1G34170 500
ARF4_AT5G60450 780
ARF3_AT2G33860 602
Pt243681_gw1.XIV.424.1 288
Selmo1_2_61688 622
Selmo1_2_51695 663
Phypa_108888 594
ARF10_AT2G28350 GGDNVRKTWI 662
ARF16_AT4G30080 652
Phypa_61245 317
ZmGRMZM2G005284_P01 579
ARF17_AT1G77850 568
Phypa_170581 825
all_Phypa_171888 896
Selmo1_2_405821 PGASLSLPAS CLQRAKRSVR GDQKIVLKLS 311
Selmo1_2_431298 PAS 367
Selmo1_2_431277 102
corb_UMD_Coleochaete_c9703_c_s_1 RAAE PQQQNACRPS 126
spra_Contig219_1 360
IAA12_AT1G04550 172
Consensus
100%
Conservation
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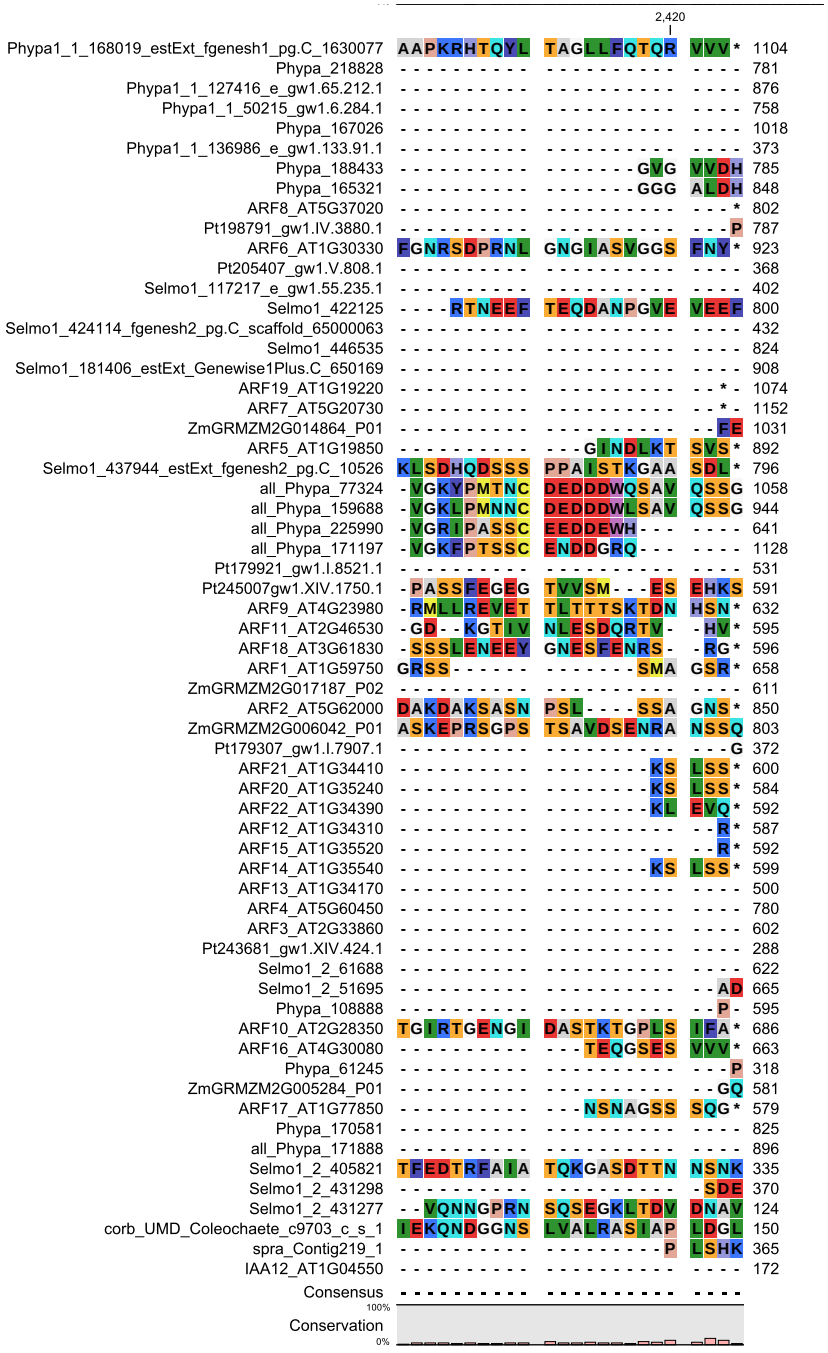
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Phypa_167026 1018
Phypa1_1_136986_e_gw1.133.91.1 373
Phypa_188433 785
Phypa_165321 848
ARF8_AT5G37020 802
Pt198791_gw1.IV.3880.1 787
ARF6_AT1G30330 923
Pt205407_gw1.V.808.1 368
Selmo1_117217_e_gw1.55.235.1 402
Selmo1_422125 800
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Selmo1_446535 824
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all_Phypa_77324 1058
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Pt179921_gw1.I.8521.1 531
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Selmo1_2_61688 622
Selmo1_2_51695 665
Phypa_108888 595
ARF10_AT2G28350 686
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Phypa_61245 318
ZmGRMZM2G005284_P01 581
ARF17_AT1G77850 579
Phypa_170581 825
all_Phypa_171888 896
Selmo1_2_405821 335
Selmo1_2_431298 370
Selmo1_2_431277 124
corb_UMD_Coleochaete_c9703_c_s_1 150
spra_Contig219_1 365
IAA12_AT1G04550 172
Consensus
100%
Conservation
0%

Figure S30 - alignment of IAA33 and putative ortholog