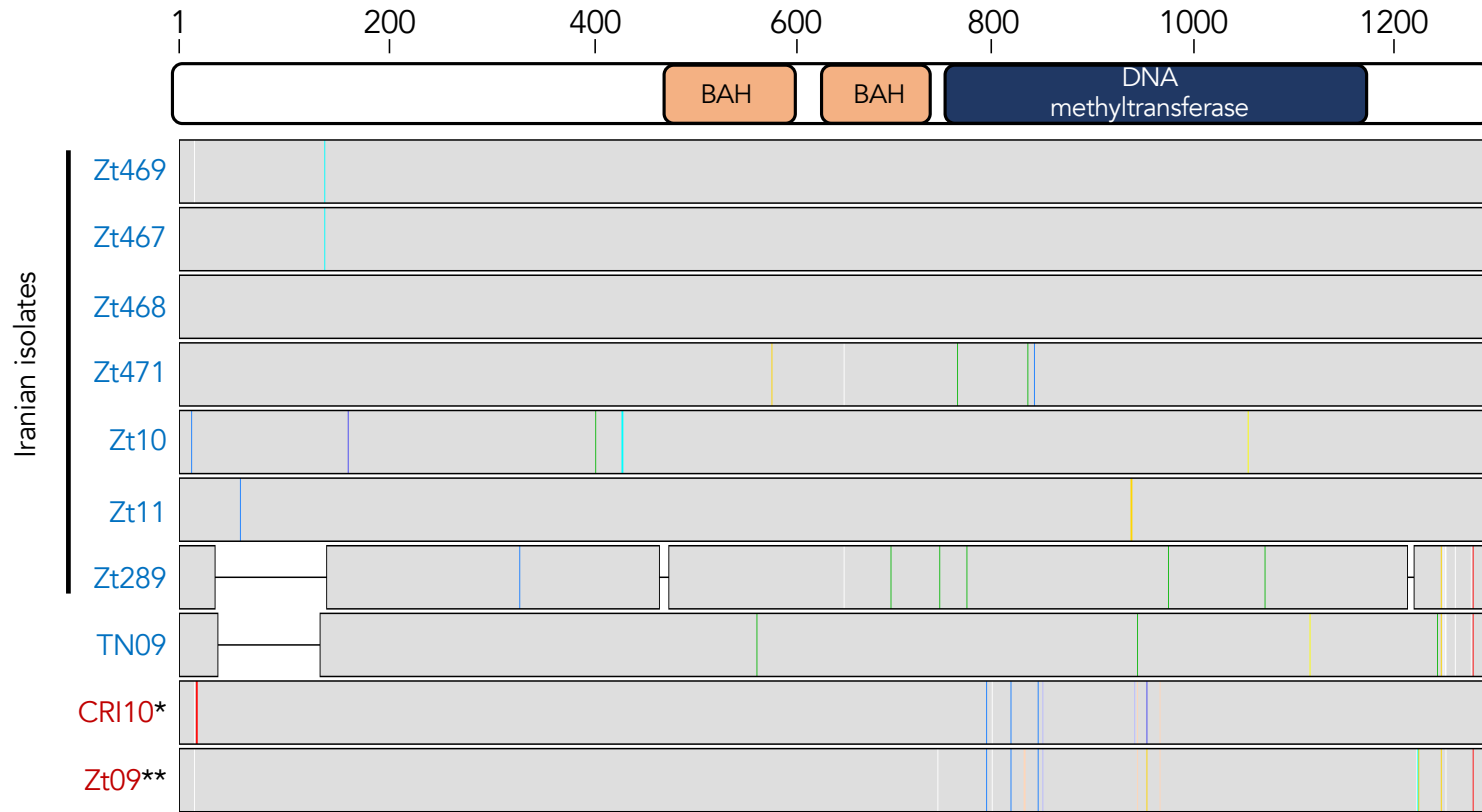


A



\*de-RIPed native allele

\*\*de-RIPed transversion allele (chr 5)

# B

```

Zt469 1 MKRRISGDTIVIEDDGDNIIVVGPTSRPSKKPRLQNGQLQMDILRAGASLSNAIVISPAASEQDRGESKQEEEDGAQRAVQYEMESGEEQTSQTVGDREVEDQGPLRTPRQRRLRTALTPP 120
Zt467 1 .....
Zt468 1 .....
Zt471 1 .....
Zt10 1 .....K.....
Zt11 1 .....K.....
Zt289 1 .....
TN09 1 .....
CRI10 1 .....G.D.....
Zt09 1 .....G.....
***** ** * *****

```

```

Zt469 121 ATETEPGDEPAARAEPGATARSGNRRQLRYLSHISIAGPAFPRSAYHGYPPLQPVNEVEASLDLSAGFFAAAKSAGTETPECATFKLDQFSVYMDGRRASDLVTLEKLRQSNYAEFCF 240
Zt467 121 .....N.....
Zt468 121 .....K.....
Zt471 121 .....K.....
Zt10 121 .....K.....Y.....
Zt11 121 .....K.....
Zt289 37 .....
TN09 40 .....K.....
CRI10 121 .....K.....
Zt09 121 .....K.....
*****

```

### N-terminal RFD-like motif in Dim2

```

Zt469 241 DGILSAGNEKRYVQGVRFEILAISGYGLDFTDFAGSICIQSKLQSKASALFGHWYELGTPAPEYRRFYEPFLWLARFGKHFDYLLSNQQVTLGHFRRRFYQWLTGLYGGDTSFNQWLA 360
Zt467 241 .....
Zt468 241 .....
Zt471 241 .....
Zt10 241 .....
Zt11 241 .....
Zt289 132 .....R.....
TN09 142 .....
CRI10 241 .....
Zt09 241 .....
*****

```

### short conserved motif

### NLS

```

Zt469 361 ECKLKDFRTTIAANVGFLWKECWDIDDKESGLCRQPIWGEVDPYNLTAIPAQPNKELRTIVTFFVYQCFRHMVYFGDQLEERTITDRNVLKKSDELKARLRLTPRRASPSAPPMTLTPRS 480
Zt467 361 .....
Zt468 361 .....
Zt471 361 .....
Zt10 361 .....L.....N.....
Zt11 361 .....
Zt289 252 .....
TN09 262 .....
CRI10 361 .....
Zt09 361 .....
*****

```

BAH domain 1

Zt469 481 MSRSSEQEGNKAVTVNTGDVVCVAPDVSTKWGIKAHAWYAYVQNVHTRKDRTSLDVLWLYEPKDTTLGKAYYPFANELFLSDNCSCGTSALDLDLDCVLDKADVCWYAKDPYQQGGHFVROK 600
Zt467 481
Zt468 481
Zt471 481
Zt10 481
Zt11 481
Zt289 364
TN09 382
CRI10 481
Zt09 481
\*\*\*\*\*

BAH domain 2

Zt469 601 FRTVHEQDITYDFVAIQASDFRCQCKHDVPIFDECRSKYAIGDITVLVREWNDDLDEDLRQPAQIIEFDTQKRRVVLRLQFLRKSEQQTGAKARPNELVLTDDVDFDKACDKIIRKCHVRCFRQ 720
Zt467 601
Zt468 601
Zt471 601
Zt10 601
Zt11 601
Zt289 483
TN09 502
CRI10 601
Zt09 601
\*\*\*\*\*

motif I (SAM-binding)

Zt469 721 DQIDSGDIVTPYDRDGTGDFFFLAEDLSAARDGFPMPKEGWNPNMHGKEMVGMSLFCGGGTFDRGLEEAGIAKFKYAVDWNHALHSHRANVRRPDQMEYFLGSVNDLLARAMAGDKPK 840
Zt467 721
Zt468 721
Zt471 721
Zt10 721
Zt11 721
Zt289 603
TN09 622
CRI10 721
Zt09 721
\*\*\*\*\*

motif IV (catalytic site)

motif V

motif VI

motif VII

motif VIII

Zt469 841 NIAQPGDIQILAGGSPCPGFSMLQLFLKLESEQKQNASLIVASIVSFVDFYVPRYFLENNVTMTAGMGPNKDQNVFSQIVAALVALGYVQQFLGDAWSYGSSQQRSRVFIVASAPGLPPL 960
Zt467 841
Zt468 841
Zt471 841
Zt10 841
Zt11 841
Zt289 723
TN09 742
CRI10 841
Zt09 841
\*\*\*\*\*

