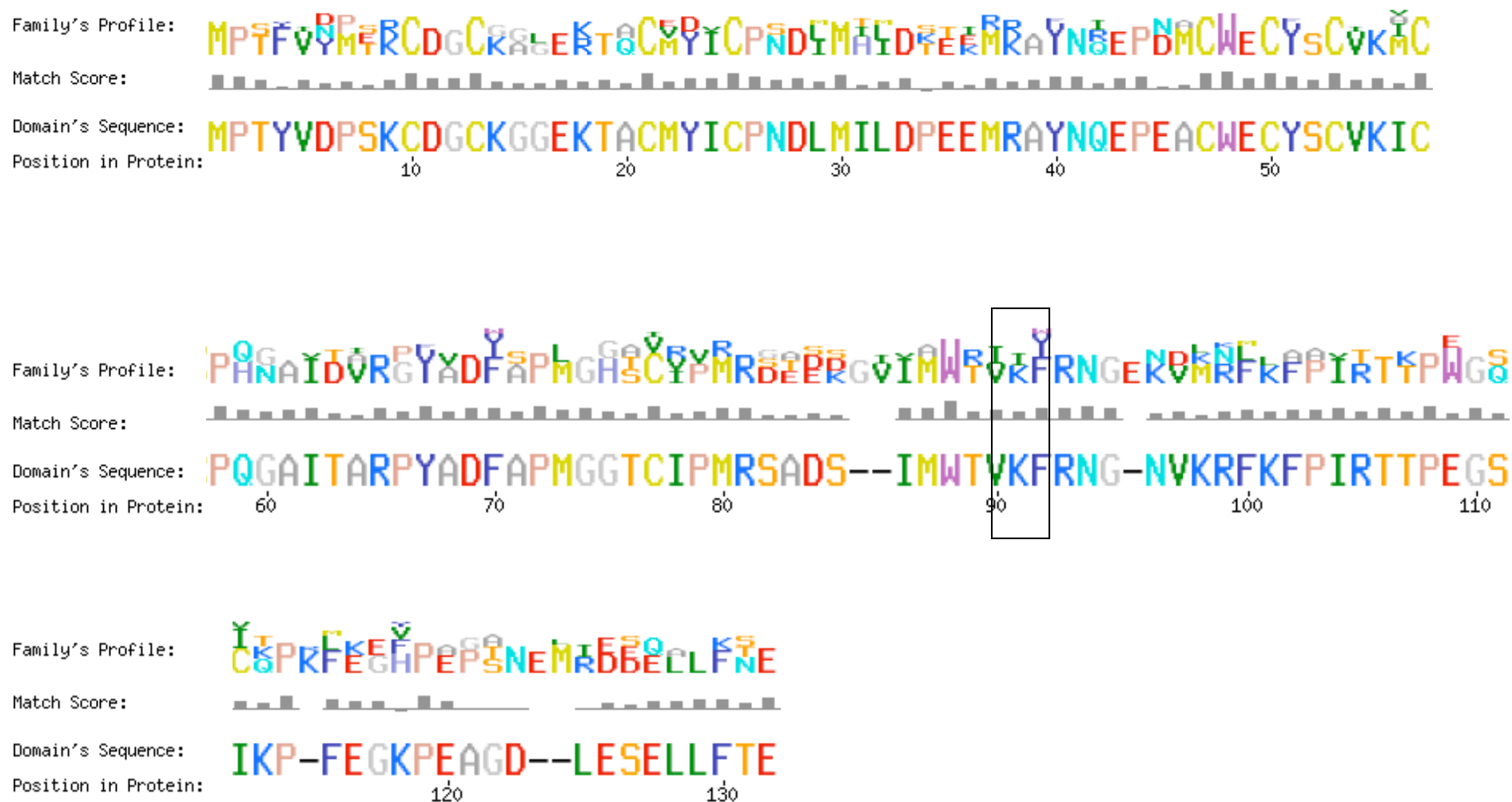


Figure S6: Hidden Markov Model Alignments

S. FIG 6A: Alignment of ApsB (DVU0846) with TIGR02060



S. FIG 6B: Alignment of ApsA (DVU0847) with TIGR02061



Family's Profile:

QMEHRFVTPARFKDGYGPVGAWFLHFKCKATNSNGGEEYCRTWAWMLQKYKEDYAGDPAGS

HRTHRPIIP

Match Score:

Domain's Sequence:

MMENRFVTPARFKDGYGPVGAWFLLFKAKATNYKGEDYCATNRAMLKPYEDRGYAKGHV-----IP

Position in Protein:

280

290

300

310

320

330

Family's Profile:

TCLRNHMMMLREMRGRGPIYMDTKTALQSTFANMTPEQQKHLESEAWEDFLDMCVGQANLWACTNY

Match Score:

Domain's Sequence:

TCLRNHMMMLREMRGRGPIYMDTKTALQSTFANMTPEQQKHLESEAWEDFLDMCVGQANLWASMN

Position in Protein:

340

350

360

370

380

390

Family's Profile:

DPKNEEESSEIMPTPEPYLLGSHSGCCGIWVSGPDEKWPEDYKVRASNGKIYNRMTTVEGLFTCADGVG

Match Score:

Domain's Sequence:

QPEERNGSEIMPTPEPYLLGSHSGCCGIWVSGPDEKWPEDYKVRASNGKIYNRMTTVEGLWTCADGVG

Position in Protein:

400

410

420

430

440

450

460

Family's Profile:

ASGPHRFSSGSFTEGRMAAKAMCRWCLDGHKREKRYPDAYEELRKRKYRPMERFMQYRNESTADSV

Match Score:

Domain's Sequence:

ASGHKFSSSGSHAEGRICGKQMVWRWCLD-HKDYKPAIKESADELVKLIYRPYYNYMEGKAASTDPVV

Position in Protein:

470

480

490

500

510

520

530

Family's Profile:

NPNYINPKWOGMMRLKYKCMDEYCGGVSTYTSMTNERMLRDTAEERLKMMKEEDEEKLAARDEHELLARCWEN

Match Score:



Domain's Sequence:

NPSYITPKNFMMRLVKCTDEYGGGVGYTYSAAALDTGFSLLGMLEEDSLKLAARDLHELLRCWEN

Position in Protein:

540 550 560 570 580 590

Family's Profile:

YHRLWTSELHMAHSMFRRESRWPGYFYSRYSDFMRELDDEPWKVCFVCSKYDPBTGEWTKFEFKPYQII

Match Score:



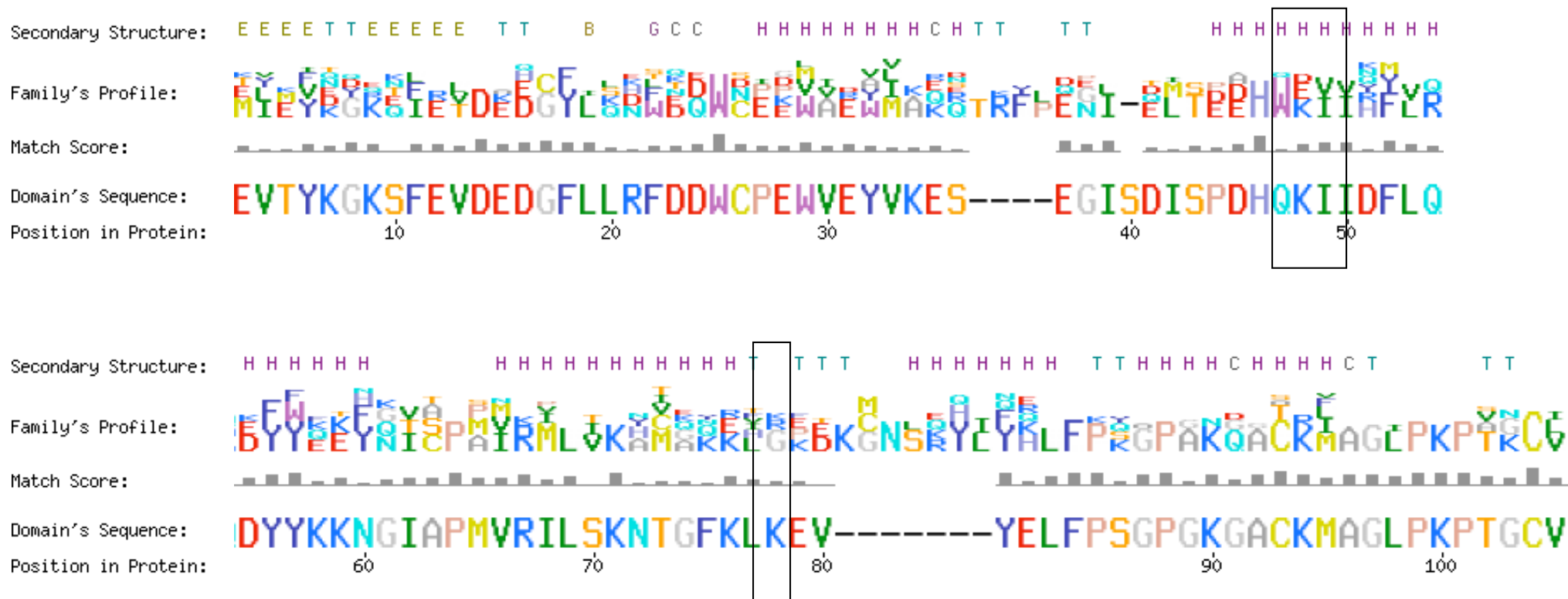
Domain's Sequence:

YHRLWTVRLHMQHIRFREESRYPGFYRADFMGLDDSKWKCFVNSKYDPATGETKIFKKAYYQII

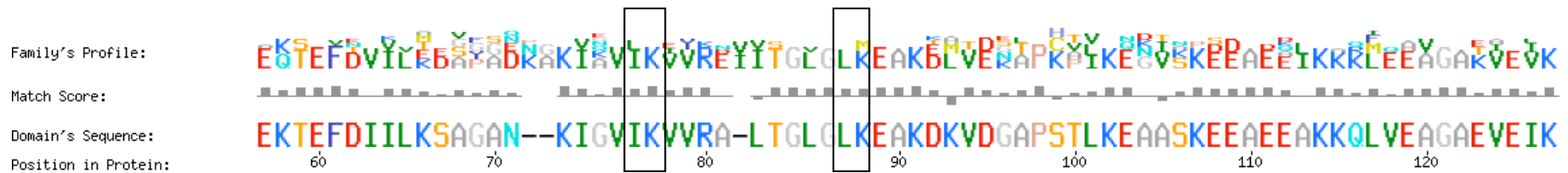
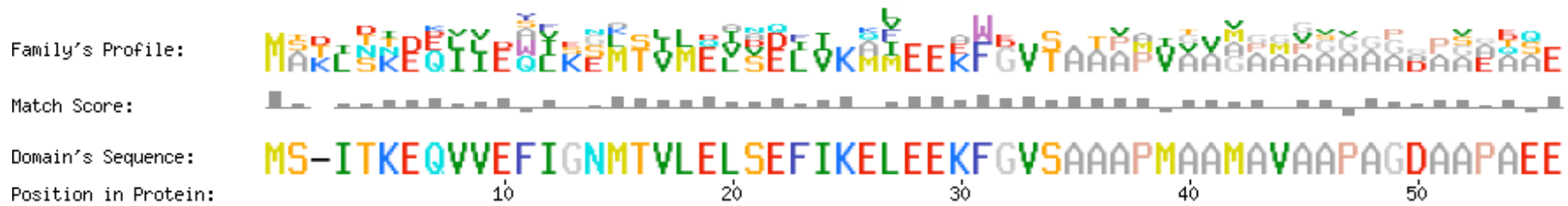
Position in Protein:

600 610 620 630 640 650 660

S. FIG 6C: Alignment of DsrC (DVU2776) with PF04358



S. FIG 6D: Alignment of RplL (DVU2927) with TIGR0855



Note: Boxed region indicates position of methylated lysine residue observed in this study.