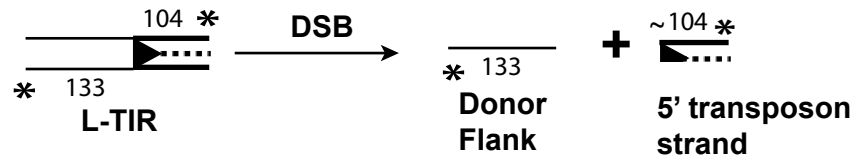
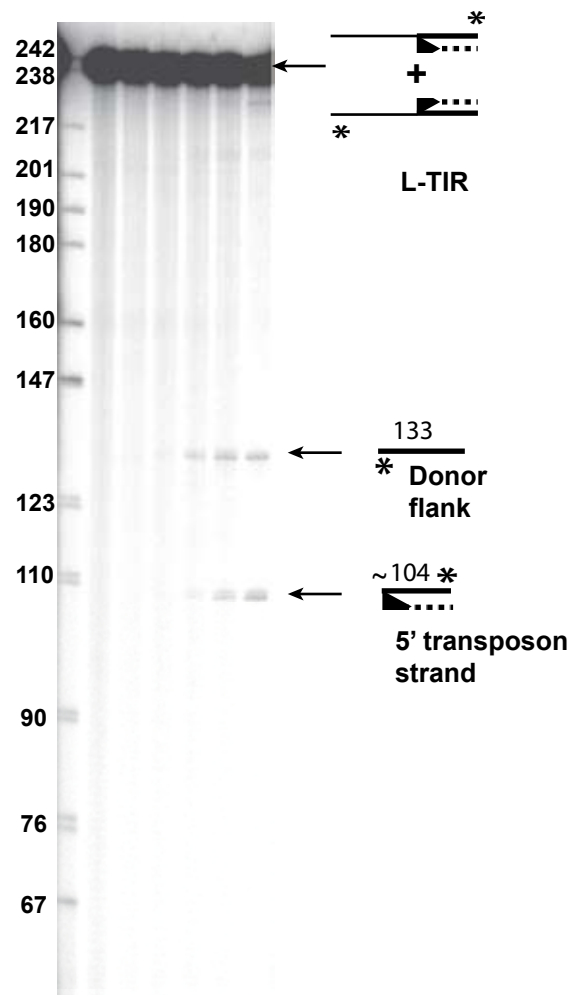


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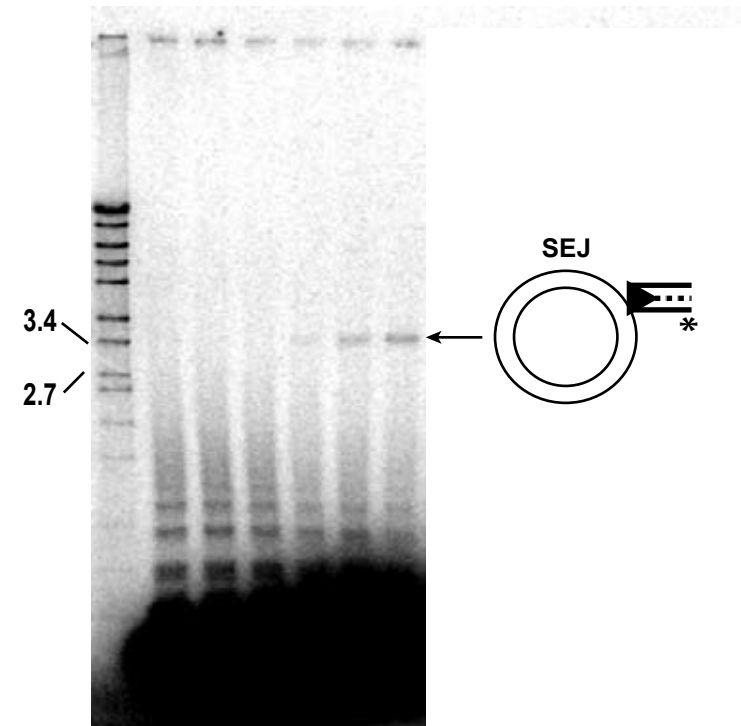


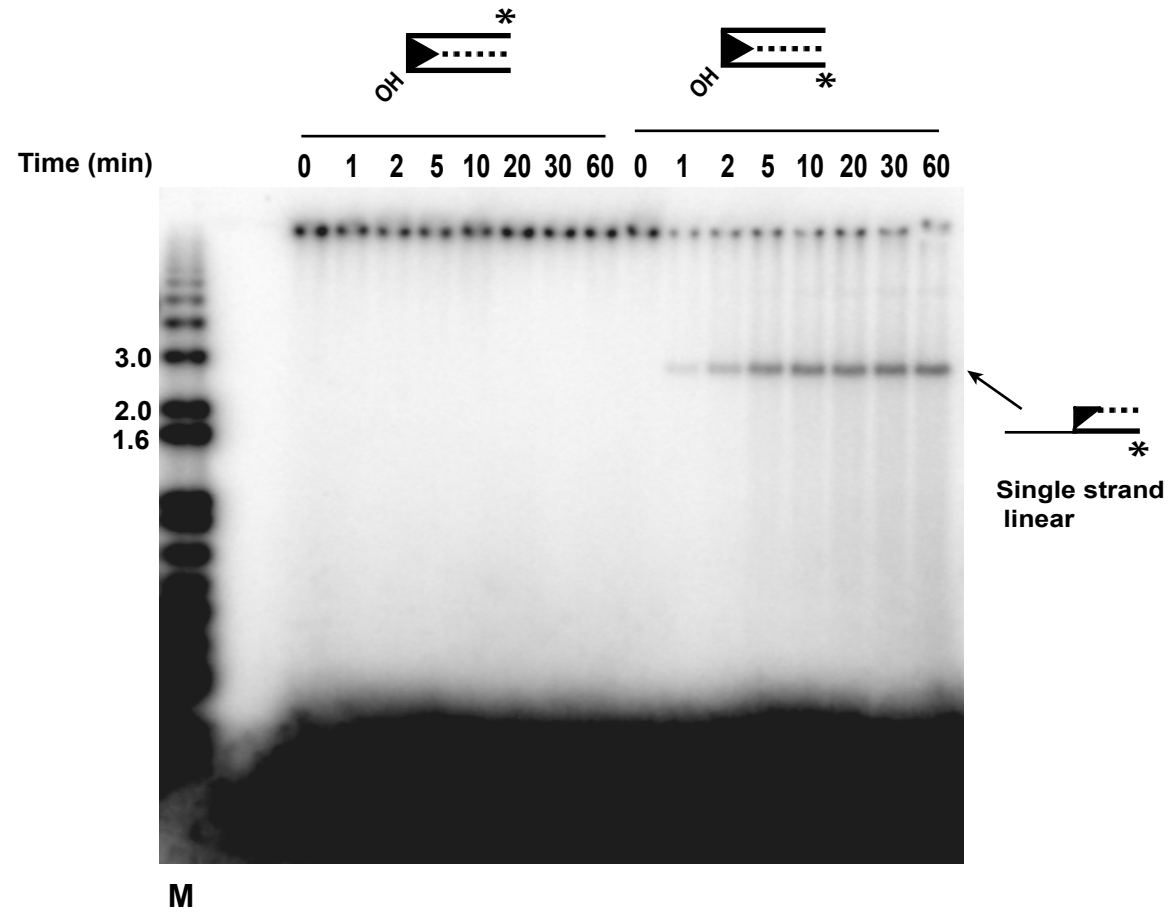
Time (min) 0 1 2 5 10 20



B

Time (min) 0 1 2 5 10 20





Total number of transposition reactions	4
No of colonies sequenced from each transposition reactions	5
Total number of colonies sequenced	20

CAACGCAATTAA CCC GGG TTAATGTGCGTT
GTTGCGTTAATT GGG CCC AATTACACTCAA

CCGCATAGTTAA CCC GGG TTAAGCCAGCCC
GGCGTATCAATT GGG CCC AATTCTGGTCGGG

TTTATAGGTTAA CCC GGG TTAATGTCATGA
AATTATCCAATT GGG CCC AATTACAGTACT

CCGATTCATTAA CCC GGG TTAATGCAGCTG
GGCTAAGTAATT GGG CCC AATTACGTTCGAC

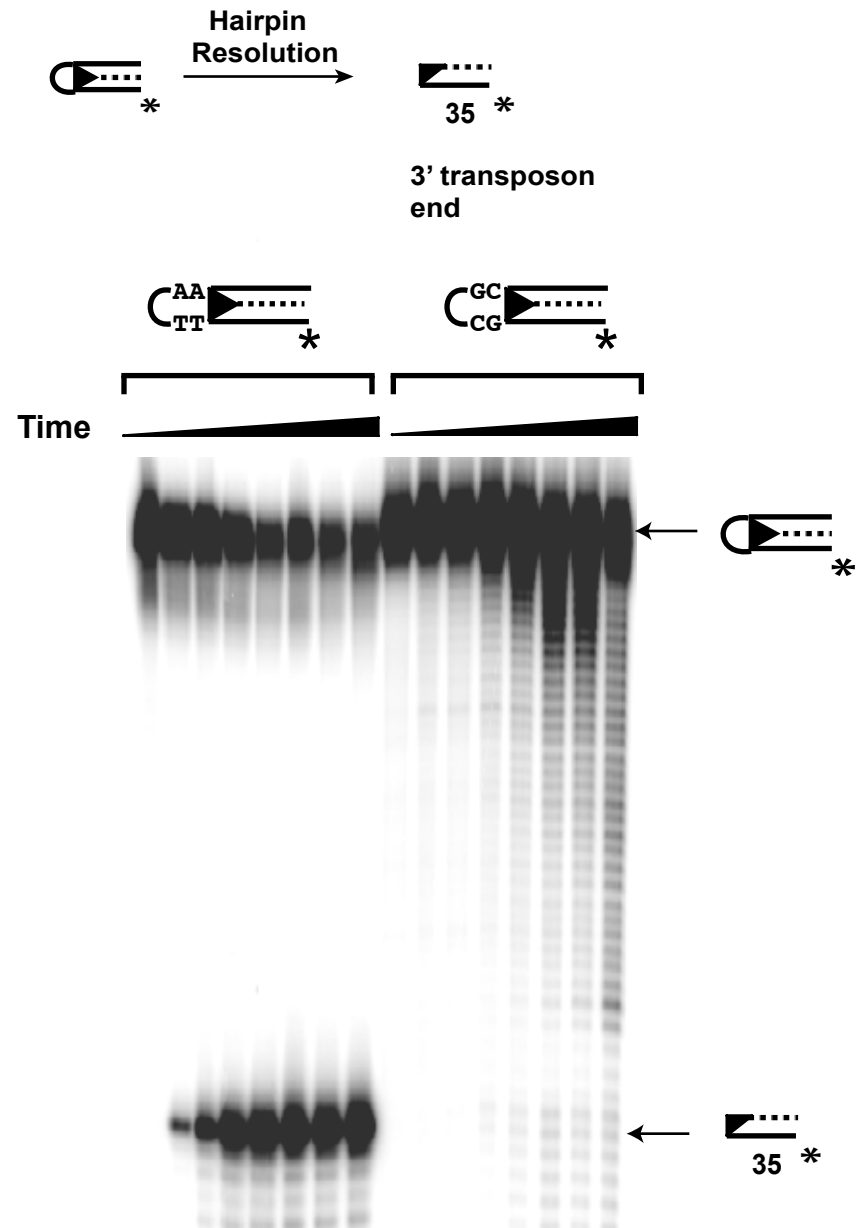
AAAATCCCTTAA CCC GGG TTAACGTGAGTT
TTTTAGGGAATT GGG CCC AATTGCACTCAA

AAAATCCCTTAA CCC GGG TTAACGTGAGTT
TTTTAGGGAATT GGG CCC AATTGCACTCAA

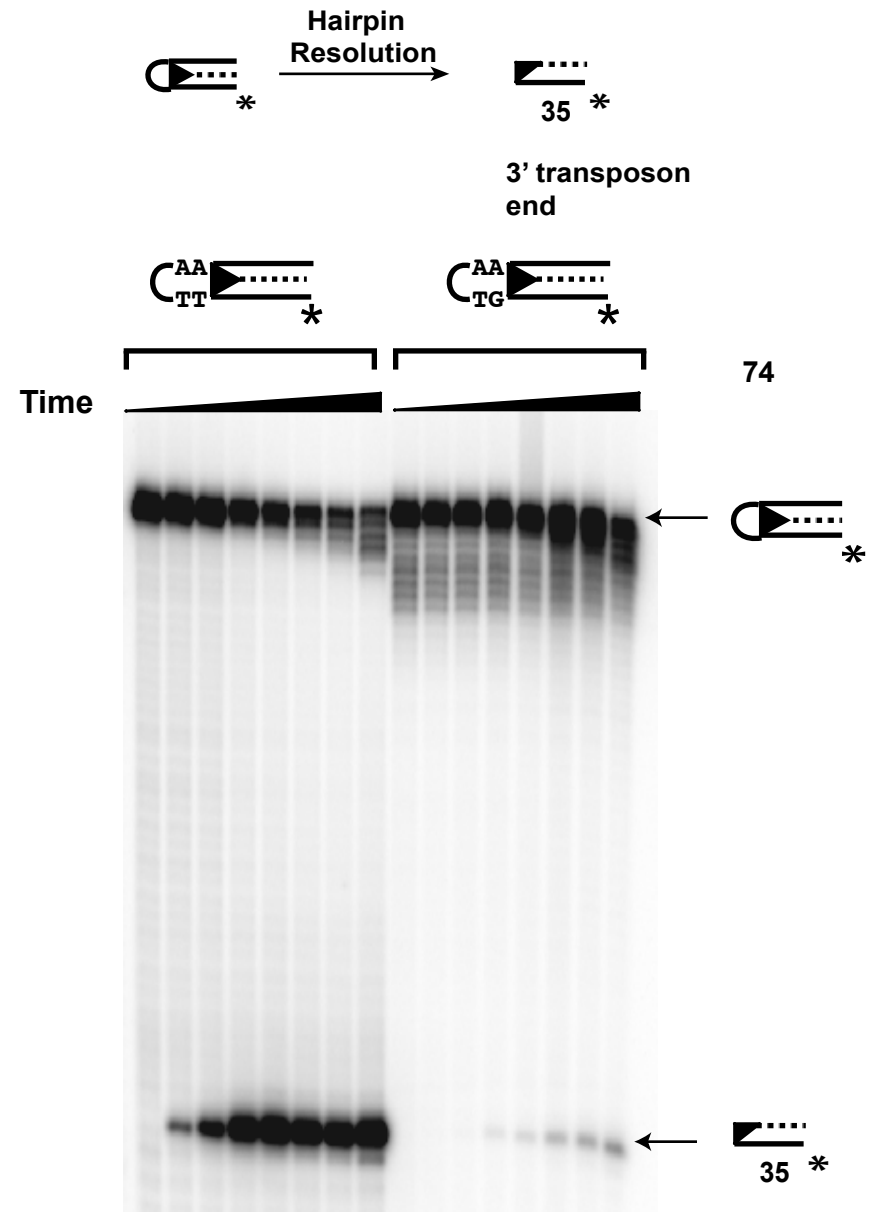
AGATTGATTTAA CCC GGG TTAAACTTTCAT
TCTAACTAAATT GGG CCC AATTTTGAAGTA

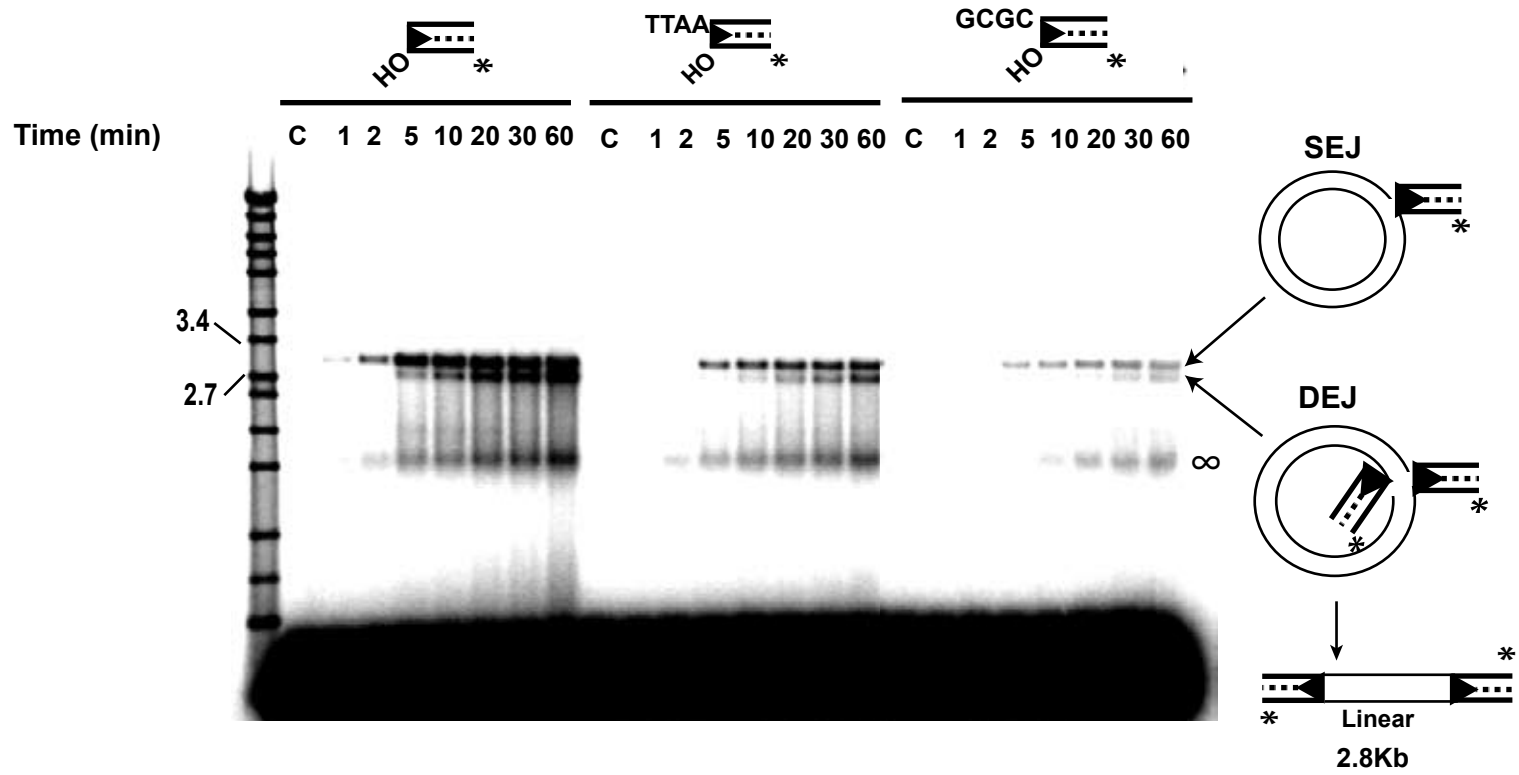
TTTTTAATTTAA CCC GGG TTAAAAGGATCT
AAAAATTAAATT GGG CCC AATTTTCCTAGA

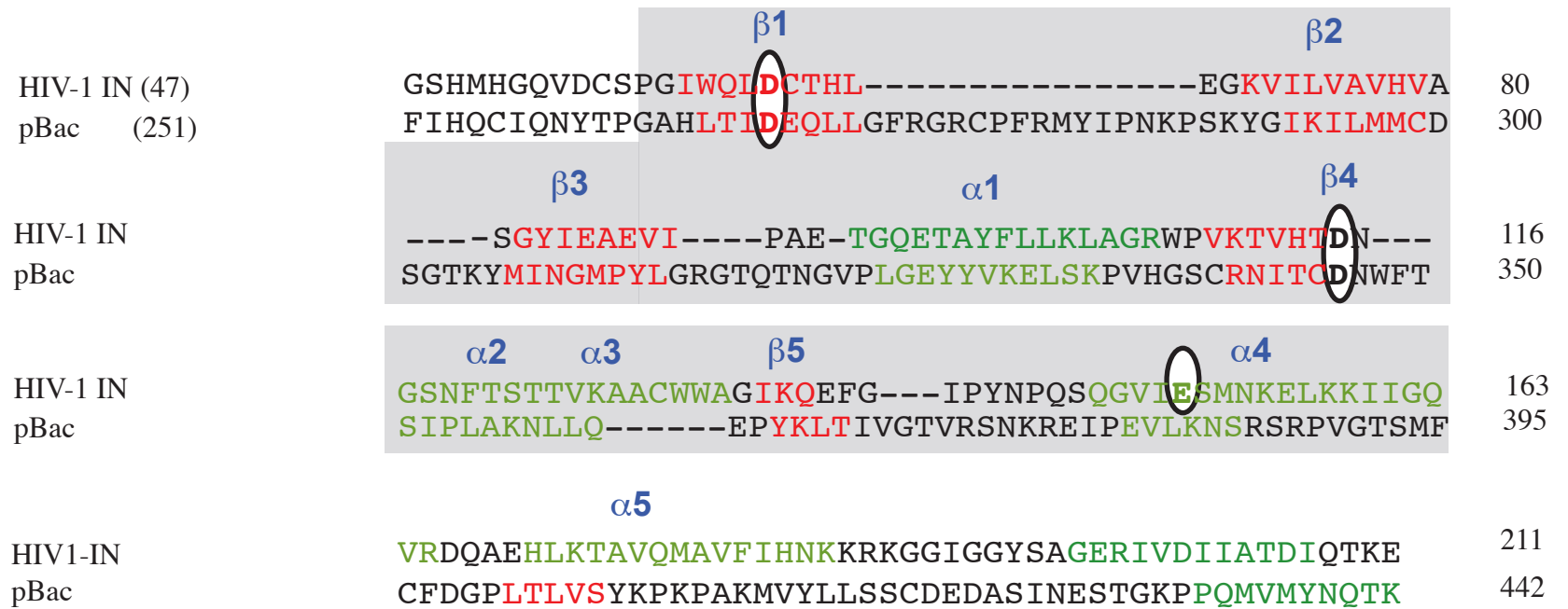
A



B







D227 D228 D239

Adineta --GWINEKSRKILIFV--NRSPLESPNIQSYHVKNRFETI ISSIQFDNKTAREERKRTDKF 209
Adineta_1 LAGLLGRLRSDLHSLW--RTSPLESPIFKDTISKSRFDKIIACLRFDKSTREERKKADKF 202
Anopheles IRGATESKGMIDLW--SEKYGLPFCKNVMSRNRFRIMKFLRFDEKSTRSQRLOTDKF 240
Bombyx LAGLIKSNRQSLKDLW--RTDGTGVDIFRRTMSLQRFQFLQNNIRFDDKSTRDERKQTDNM 258
Ciona LTGVVHKRG--KLESYWIKNSMIETPYFGKMSRNRQAITGFLHFNDNEKLAENIDNDKL 211
Heliothis MSGVLRSSHLNFKDLW--ATDGTGIEFFQNTMSFNRF LFISRCVRFDDKNTKSERLKTDKL 232
Takifugu LAGVFRSKGESAESLW--DAE--TGREIFRATMSLENFHIISRIIRFDNZDDRRPARWORDKL 237
T.ni MTAVRKDNHMSTDDL F---DRSLSMVYVSVMSRDRFDFLIRCLRMDDKSIRPTLRENDVF 241

D268

Adineta AVSREIWTDFSRKFKEMYNPGSHGTIDERLLGFRGKCPFRQYIPSKPKDYAIKFWFCVDV 269
Adineta_1 AAIREIWLDFQDKLKTCTYTPGLNITIDEQLLGFGRGKCPFRQFIPTKPKDYGLKFWLCVDA 262
Anopheles ALISDVFSRFSVNCQNTYVPGPHISVDEQLFPSKTRCPFTQFMASKPKDYGQKYWMAVDV 300
Bombyx AAFRSIFDQFVQCCQNAYSPEFLTIDEMLLSFRGRCLFRVYIPNPKPAKYGIKILALVDA 318
Ciona YKVRPVYDLIVARWKALYNLGEHISIDEGMMKWRGRLGFRVYNKDKPIKYGIKSYILADS 271
Heliothis AAVREFTDLMNNNF INNYCASENVTLDEQLPAFRGRFSGVVYMPNKPTKYGIKHYALVDS 292
Takifugu GVIRTVWDKVVRRLLPLYNPGPNVTIDEQLMPFRGRCPFLQYLPSKPAKNGIKIWAACDA 297
T.ni TPVRKIWDLFIHQCIQNYTPGAHLTIDEQLLGFGRGCPFRMYIPNPKPSKYGIKILMMCD 301

D346

Adineta NSYYIFDAFPYIERQP--NEHRQRFVGPVNVLELMKPMYGSNRNVTIDNFFTSIHLAKEL-- 327
Adineta_1 ESYVVLNAFPYIGRQP--GOEKQAHVGESVLELLRPFYGSNRNVTIDNFFTSVPLARNL-- 320
Anopheles DSKYVVNIIPYLGKND--ERPAEERLGDFVVKLVDPYLNRRNVTCDNFFTSLELAKFL-- 358
Bombyx KNFYVVNLEVYAGKQPSGPYAVSNRPFVVERLIQPVARSHRNVTFDNWF TGYELMLHLL 378
Ciona HSHYCWNLDMYH-----RVQKTLKETVSQILTSKCHFLWHSLYMDNFYNSVMSQML-- 323
Heliothis ATFYLLKFEIYAGVQPEGPYRMPNDTVSLVKRMTEPIWGTGRNVTMDNWF TSVPLANILL 352
Takifugu TSSYAWNLOVYTGKPD--GGAPEKNPRNESCPRHVSGTQWTQHH--MRHFF TSHKLGQEL-- 353
T.ni GTKYMINGMPYLGRGTQ--TNGVPLGEYVVKELSKPVHGSCRNITCDNWF TSIPLAKNLL 359

Adineta -HSGKLTLVGTLRKNKPEIPIEFQSNKNRDVGSSIFGFS--DNLTLVSYVPKKNKAVILLS 385
Adineta_1 -QTKNLTLIGTLRKNKPEIPIEFLLSSKIREIGSSFLGFE--DNLALVSFVPKKNKAVLLLS 378
Anopheles -KSKKTSLVGTINKARREVPICVKKVKEKLYFTKAFK--S--DDTTLTVYQGTKKNVLLS 415
Bombyx -NEYRLTSVGTVRKNKRQIPESFIRTD--RQPNSSVFGFQ--KDITLVSYAPKKNKVVVMS 435
Ciona -LAFQIHSVGTLSRNGEP--REIRTPPNQMKKGDIIARQNSVTVLAW---KDKRVVKAI 378
Heliothis -KDHQLTMVGTIRKNKPEIPTCFQPKRTRTEHSSFLGFGQ--EDVTLCSYVPKKS KAVLLIS 410
Takifugu -LKRKLTIVGTIRKNRSELPPQLLTSKNRPVKSSQFAYT--ADTSLVSYVPKKGKNVVLMS 411
T.ni QEPYKLTIVGTVRSNKREIPEVLKNSRSPVGTSMFCFD--GPLTLVSYKPKPAKMVYLLS 418

D447**D450****W465**

Adineta SMHHD SKV--DI-----GTGKPNIVLDYNSKSGAVDTIDEMCHKYSVCRGTRRWP 433
Adineta_1 SKHHDNHV--DN-----KTGKPVII LDYNTKKGAVDTVDQMCHKYTVKRGTKRWP 426
Anopheles SMHRDIRTGND-----KSKPETVAFYNSTKYGVVDVDMCRKYSLSASRRWS 464
Bombyx TMHHDNSIDEST-----G--EKQKPEITFYNSTKAGVDVDEL CANYNVSRNSKRWP 486
Ciona STKHDASVTTITRRQRRGGEXESVEKPVCIADYNLHMSGVDQVDMISYYPCHRKSLKWT 438
Heliothis SMHNDNNIVES-----EKKKPEIILYINSTKGGVDTNDQMCANYNVRRTKRWP 459
Takifugu TLHRDGRMCDQ-----EHHKPEIIMDYNATKGGVDNMDKLVTAYSCKRRTL RWP 460
T.ni SCDEDASI--NE-----STGKQPVMYYNQTKGGVDTLDQMCSVMTC SRKTNRWP 466

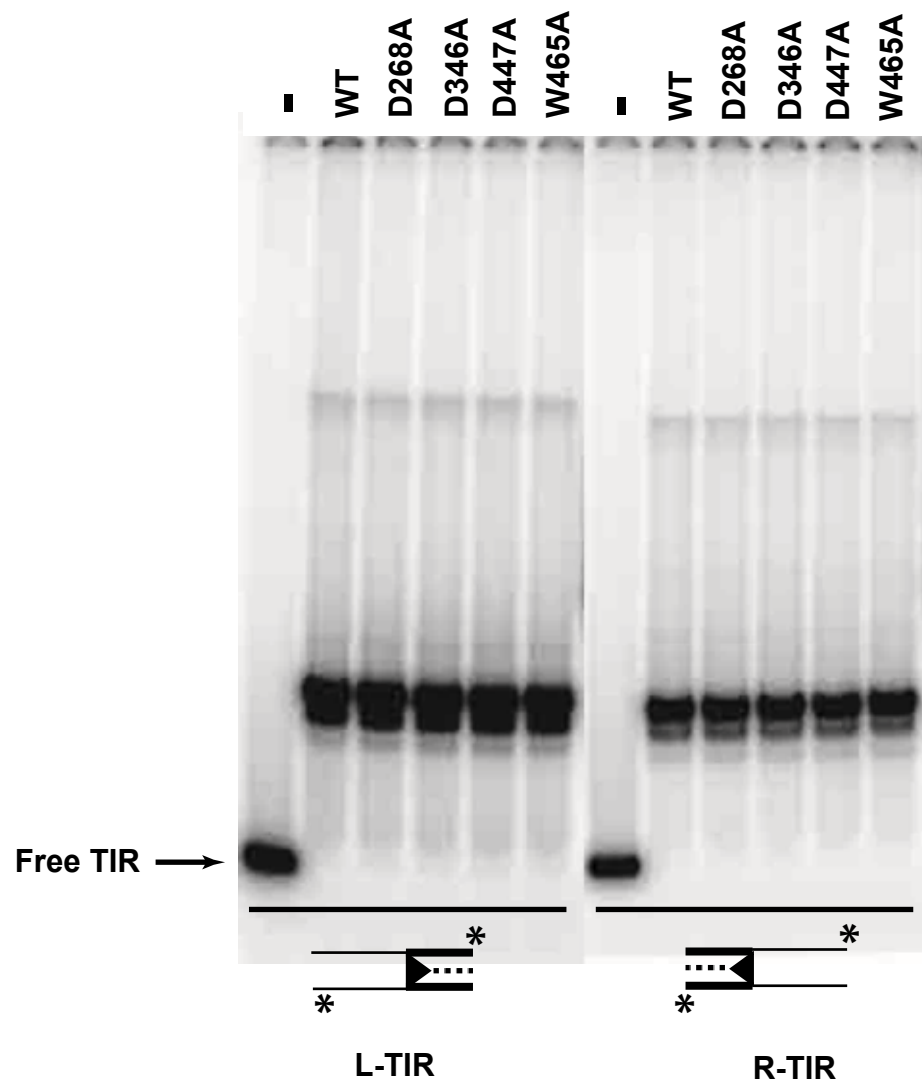
Adineta LCVFYGMIDAAA INAMSLWKKKNPNWNANKKYKRRLFLEELGTLT SYLLDFRIKNSS-- 491
Adineta_1 LCIFYGMIDMAALNAFILWKSKNPVWNNENKRYQRRLFLEELRLSLVTPLLDFRSKTSN-- 484
Anopheles VHSFFNILDLAGINAWVLYKELT-----KENISRRDFLFLKGEELAE EYVENKSANAN-- 517
Bombyx MTLFYGVNLMAAINACIIYRTN-----KNVTIKRTEFIRSLGLSMIYEHLSRNKKKN-- 539
Ciona KKVFFYFMTISVHNAYILYKSKS-----SA--KSCKTLYSFI LTLVSQLCQODRLOPO-- 489
Heliothis MVIFYHLLNVAGINAYVIFKNK-----IDHGISRREFLKH LAVDLVKVHQQTRSNIPO-- 512
Takifugu LVIFFDMLDISAYNAFVIWMALNPEWKRVKLQKRRLFLEDLGKALVRPQIERRKHIPRTP 520
T.ni MALLYGMINIACINSFIIYSH--NVSSKGEKVQSRKKFMRNLYMSLTSSFMKRLEAPT-- 523

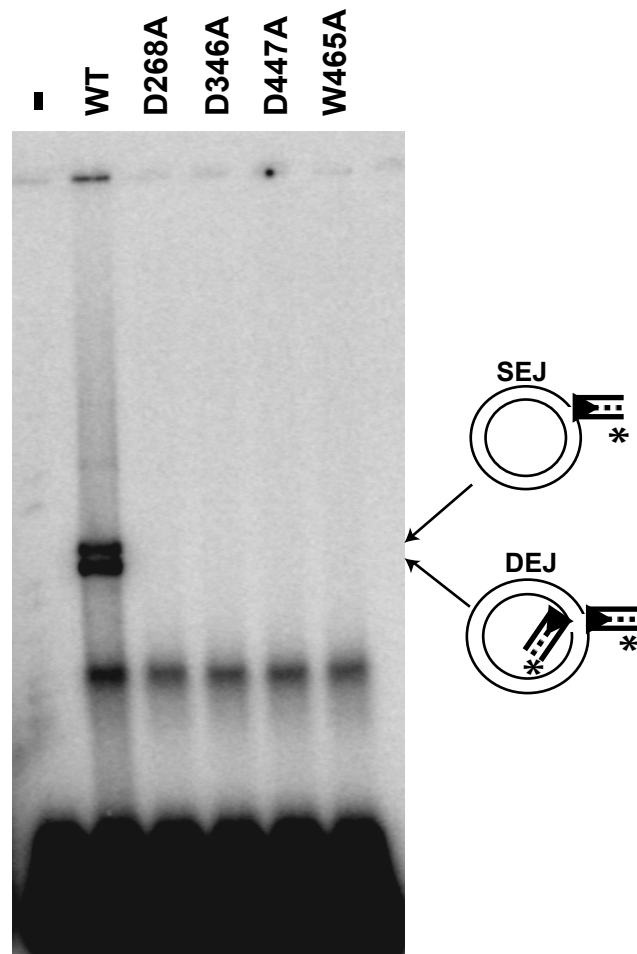
C558**C561**

Adineta ---TLHKDIQ--NALVRFVGYPRIETELE---TFVTDSARSKRKRCSLCDYSSDRKVSNT 542
Adineta_1 ---FLHKDIQ--NALLIVGHPVSKRDSQ---KSDEDSAQSKRKRCSICETS KDRKTSNK 535
Anopheles ---LPM-----TNAGGSRRRYKVQTSCHEGKSANE 544
Bombyx ---IPTYL RQ--RIEQQLGEPSP-----RHVNVPGRYVRCQDCPYKKDRKTKRS 583
Ciona ---IDD-----ENLAGPPP KSPRIDS---TKRLKGGFKKHVIALYPP TKKKAAAQRP 535
Heliothis ---LP--RAVQ--KRLKR---NAEVQDPG---STSRGGPSTSYKRCHICPRSKDKKIRFM 559
Takifugu ASAAMVRRIQKENAGALSTQPTQPQSAEPEVNVZ XVVNSSNKKKRCEVCGPKMDRKTQYT 580
T.ni ---LKRYLRD--NISNILPNEV--PGTSD---DSTEEMPV MKRRTYCTYCP SKIRRKANAS 573

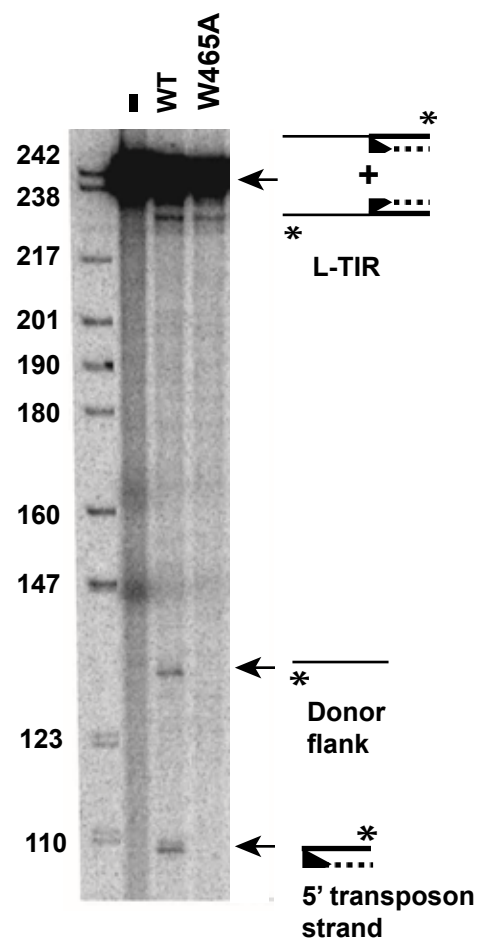
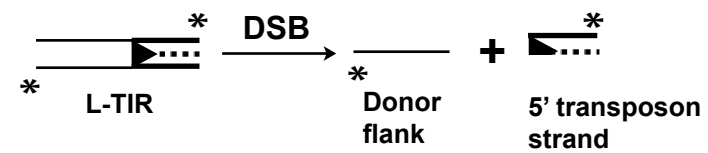
C574 C577 C582 H585 C590 C593

Adineta CYKCSEPICKQHSMK--RVFRINCSK----- 566
Adineta_1 CYNCSAFVCS EHCVK--QIFCINCSK----- 559
Anopheles CFTCNRPVCKCKTKRISYVCV SCEPGSDEAM 575
Bombyx CNACAKPICMEHAK---FLCENCAE--LDSSL 610
Ciona CRACMKNGCRKDTIL---L----- 551
Heliothis CAKCHHHICH DHST---MICDKCID----- 581
Takifugu CIKCKKYICNTHTVK---LWPSCVV----- 602
T.ni CKKCKKVICREHNID---MCQSC--F----- 594

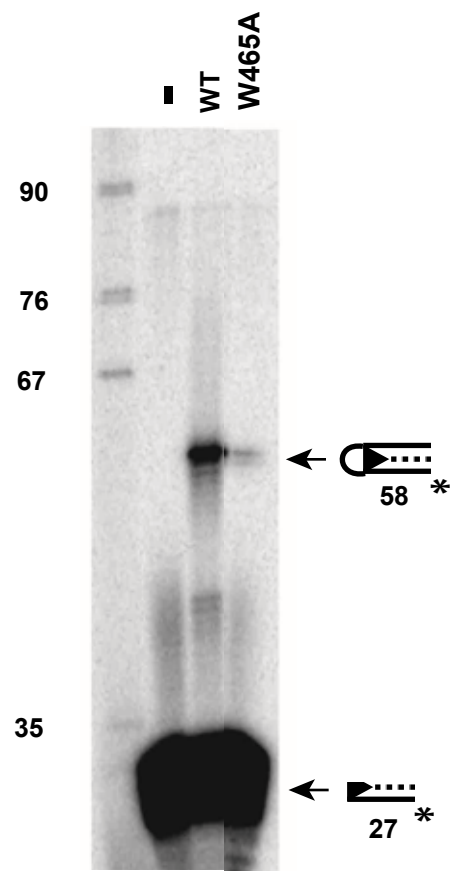




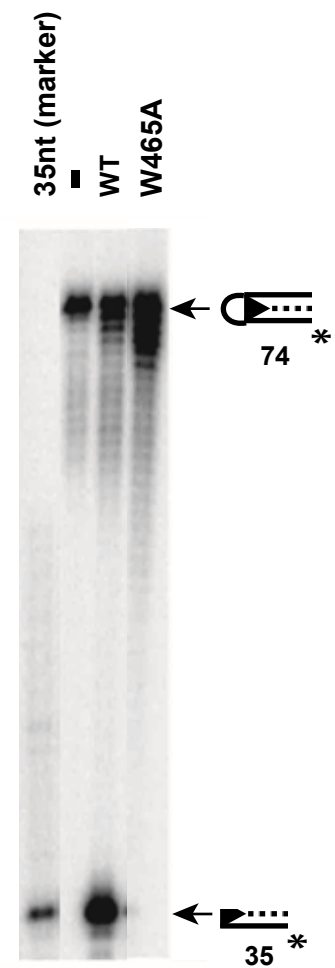
A



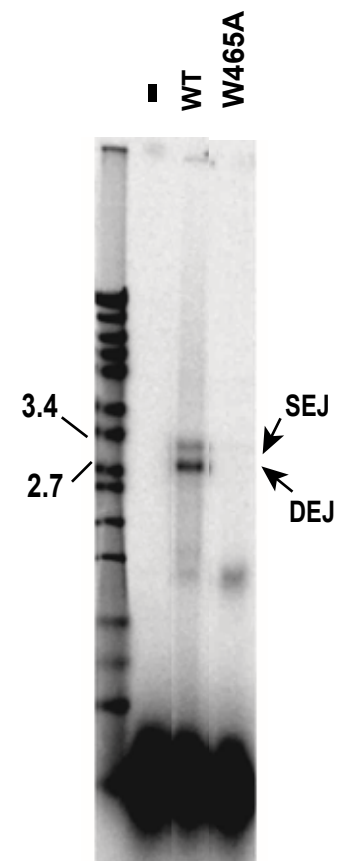
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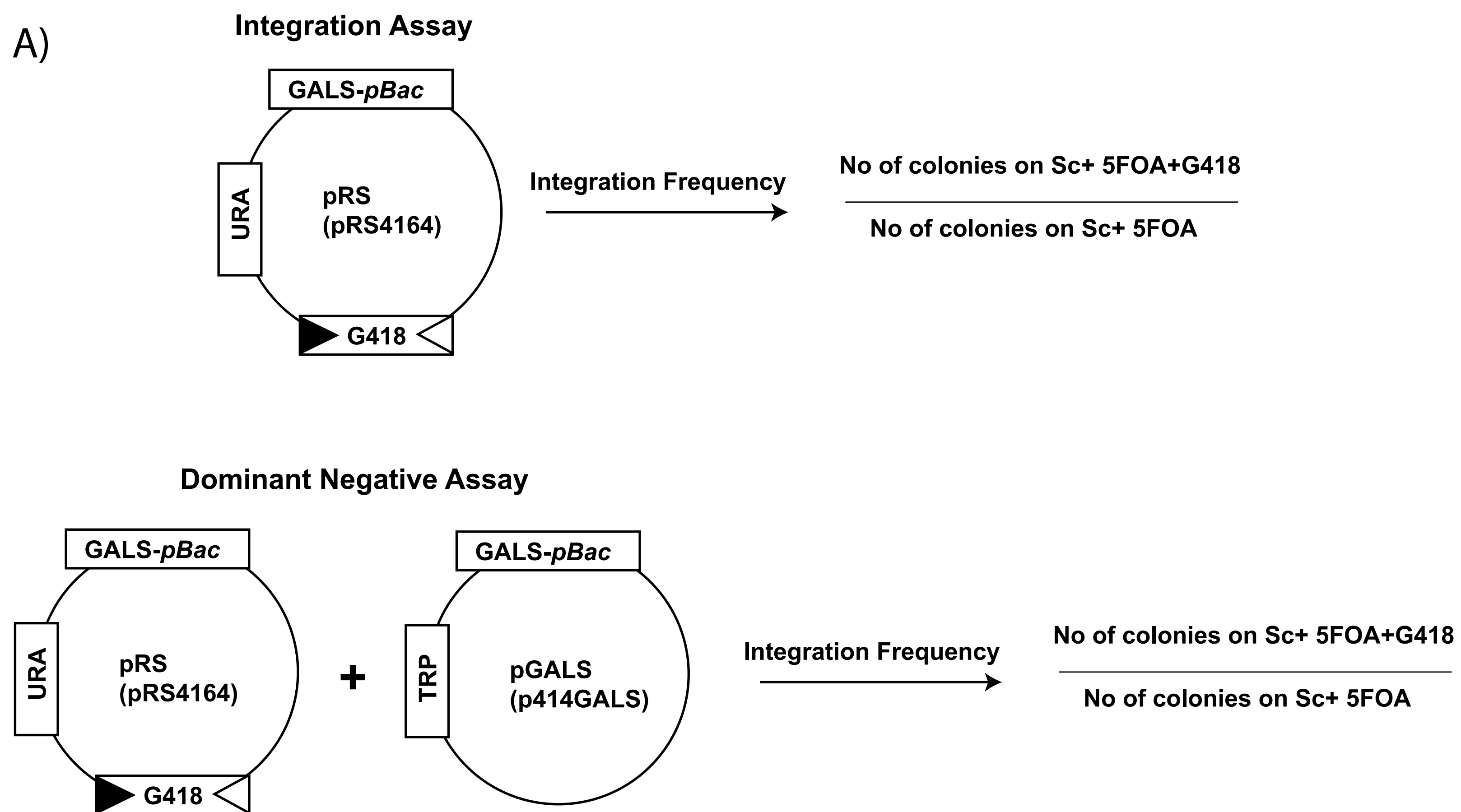


C



D





B)

Transposase plasmid	Galactose induction	Integration frequency <i>G418^R</i> colonies
pRS(no transposase)	+	$<1.0 \times 10^{-7}$
pRS-TnspWT	+	2.4×10^{-2}
pRS-TnspWT+ pGALS-Tnsp WT	+	8.1×10^{-3}
pRS-TnspWT+ pGALS-Tnsp D268A	+	6.6×10^{-3}
pRS-TnspWT+ pGALS-Tnsp D346A	+	1.2×10^{-3}
pRS-TnspWT+ pGALS-Tnsp D447A	+	3.3×10^{-3}
pRS-TnspWT+ pGALS-Tnsp W465A	+	6.5×10^{-3}