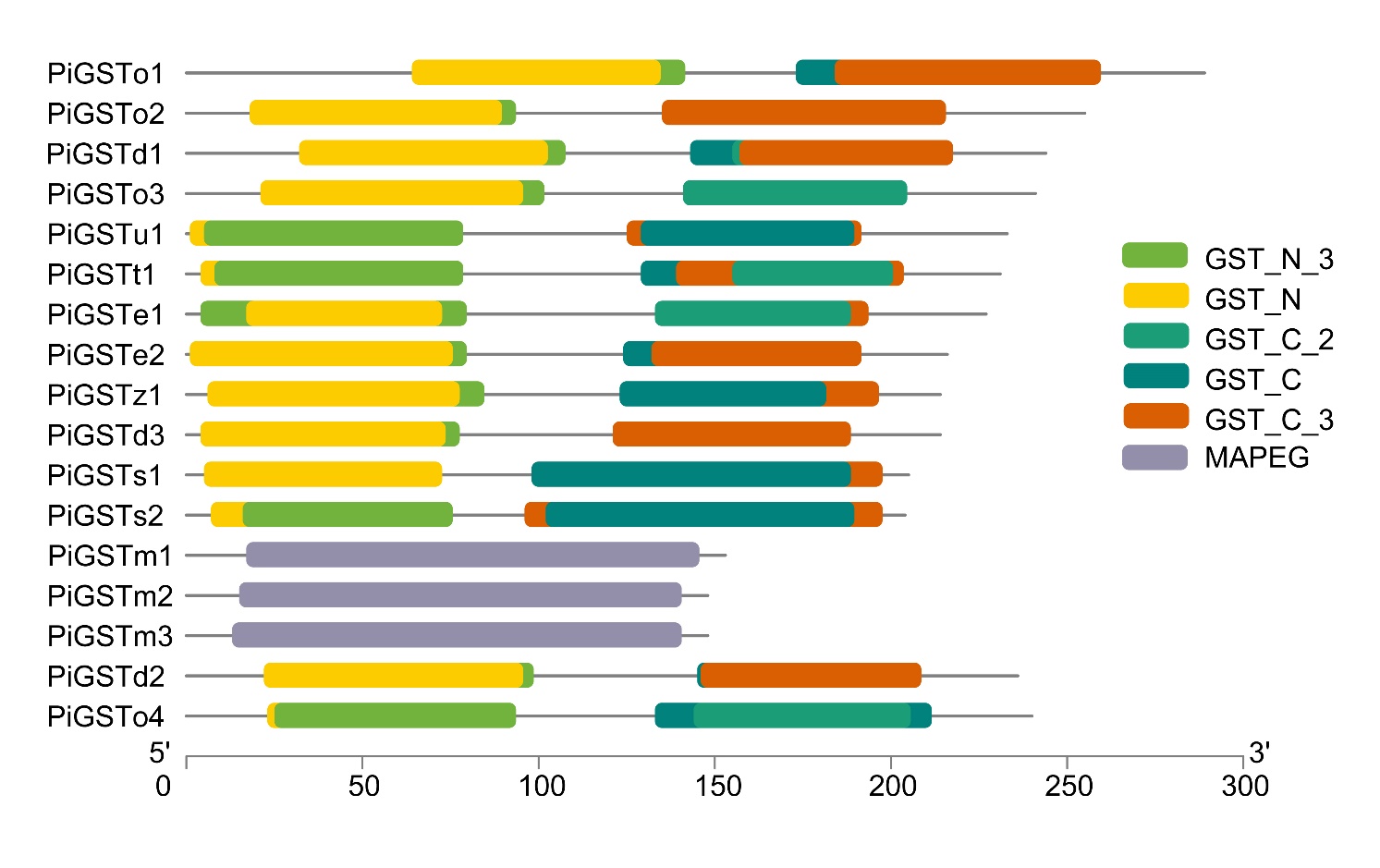
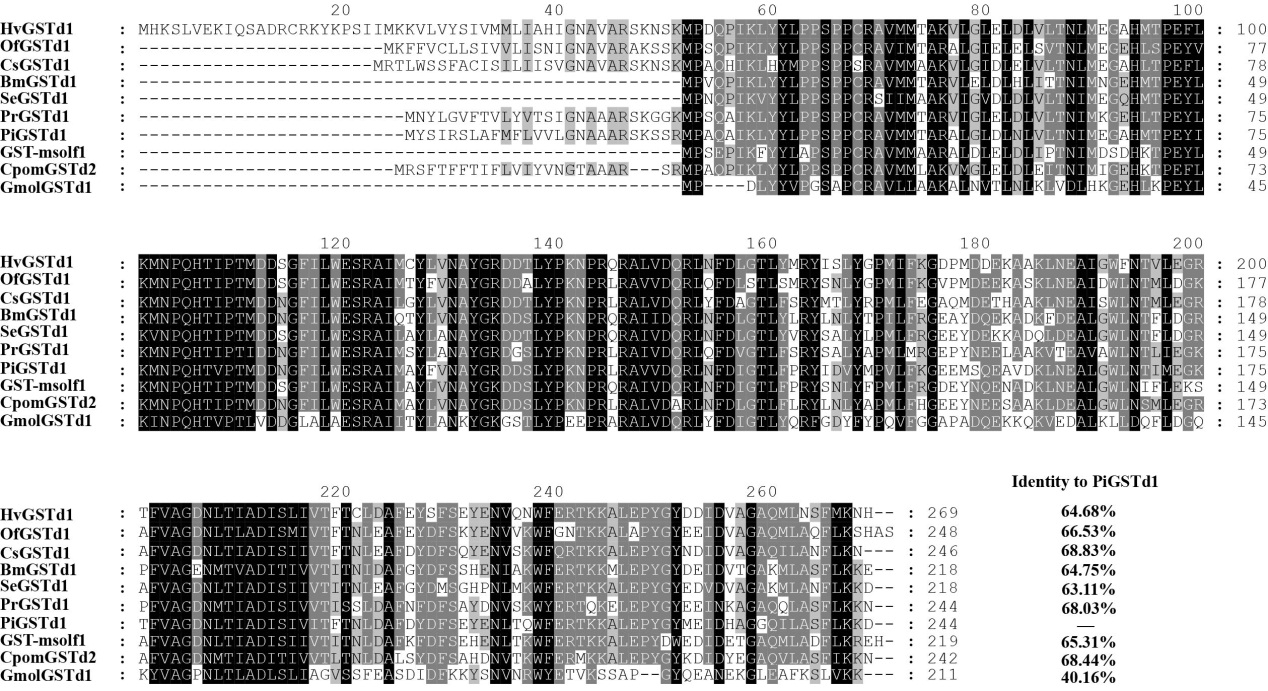
Supplementary Material



**Supplementary Figure S1** Conserved domains of PiGSTs



**Supplementary Figure S2** Sequence alignment of the conserved motifs logo of PiGSTs



**Supplementary Figure S3** Multiple alignment of PiGSTd1 with delta GSTs from other moths, including HvGSTd1 (AWX68884.1), OfGSTd1 (QIC35737.1), CsGSTd1 (AKS40338.1), SeGSTd1 (ASN63930.1), BmGSTd1 (NP\_001037183.1) and PrGSTd1 (APW77568.1), as well as three antennae-specific delta GSTs: GmolGSTD1 (MG696891), GST-msolf1 (AF133268) and CpomGSTd2 (KX500029)

**Supplementary Table S1**. Primers used in RNA interference and qRT-PCR.

|  |  |  |
| --- | --- | --- |
| **Primers** | **Sequence (5'-3')**  **Forward** | **Sequence (5'-3')**  **Reverse** |
| *β-actin* | GTATCAACGGATTTGGTCG | CACCTTCCAAGTGAGCAGAT |
| PiGSTo1 | CACCTTGCTTGCTCTCATC | CATGAATAGGACCCGTAGC |
| PiGSTo2 | GCCGACTTATCCTGGTAAAC | CAGACTGAGCAGAAGCAAAG |
| PiGSTd1 | GCTCAAGCCATCAAACTG | CGTTCACGAAGTAAGCCA |
| PiGSTo3 | CCAGCATAAATCATCGGAGG | GTTCTGCGGGTACCTCTCGT |
| PiGSTu1 | CTGGATGACGAGGGATTC | TGATGAGTTGGAAGTCCG |
| PiGSTt1 | CCATCTACAAATACCTGTCTCG | GGTCTGCTCTGGAGTGTTCT |
| PiGSTe1 | CCTTTACCCTGACGACATC | CTCAAGCATCTGATAGGCG |
| PiGSTe2 | GGCGTGGATTATGTCAATG | GAAACTCTCTGTGAAGCCG |
| PiGSTz1 | GCAATGAGTATCGGGATGTC | CACTCCTTCTTCTTCTCCTCG |
| PiGSTd3 | GCTCTCAACCTCAACCTGAAC | TAGCAGCCTTCTCCTTGTCG |
| PiGSTs1 | ATGGTGGGCATAACTTCG | CTTCTCAAACCGTGACAGG |
| PiGSTs2 | GCTGCTGCTGTCTTATGG | CGTCTTCCTCGTATTGGACT |
| PiGSTm1 | CCTGATGTTGAAAGAGTAAGGC | AATGGTATGCCGTATGCG |
| PiGSTm2 | GAGTGAAGACTGACGATAGGG | GCAGAACGGGATAGATAGC |
| PiGSTm3 | CAAGAGCTCGGTACAGCAAG | GAGGCATCGGCTTTATTG |

**Supplementary Table S2**. Substrate compounds used for degradation evaluation of PiGSTd1

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **No.** | **Compounds** | **CAS No.** | **Source** | **Purity(%)** | **Clarification** |
| 1 | 9Z-Dodecenyl acetate  (Z9-12:Ac) | 16974-11-1 | J&K | 93 | Sex pheromone |
| 2 | 8Z- Dodecenyl acetate  (Z8-12:Ac) | 28079-04-1 | J&K | 93 | Sex pheromone analogue |
| 3 | (+)-α-Pinene | 7785-70-8 | J&K | 98 | Green leaf volatile |
| 4 | (*Z*)-3-Hexenol | 928-96-1 | aladdin | 98 | Green leaf volatile |
| 5 | (*Z*)-3-Hexenyl acetate | 3681-71-8 | aladdin | 98 | Green leaf volatile |
| 6 | Isopentanol | 123-51-3 | aladdin | >99 | Grain volatile |
| 7 | Hexanal | 66-25-1 | aladdin | ≥99 | Grain volatile |
| 8 | Heptanal | 111-71-7 | aladdin | ≥99 | Grain volatile |
| 9 | Octanal | 124-13-0 | aladdin | 99 | Grain volatile |
| 10 | (*E*)-2-Octenal | 2548-87-0 | aladdin | ≥95 | Grain volatile |
| 11 | Nonanal | 124-19-6 | aladdin | 96 | Grain volatile |
| 12 | (*E*)-2-Nonenal | 18829-56-6 | J&K | >95 | Grain volatile |
| 13 | Decanal | 112-31-2 | aladdin | 97 | Grain volatile |
| 14 | (*E*)-2-Decenal | 3913-81-3 | aladdin | 95 | Grain volatile |
| 15 | Benzaldehyde | 100-52-7 | aladdin | ≥99 | Floral volatile |
| 16 | 2-Phenylethanal | 122-78-1 | aladdin | 95 | Floral volatile |

**Supplementary Table S3** Comparison of antennal GST repertoire of various insect species

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Insect species** | **Delta** | **Epsilon** | **Omega** | **Sigma** | **Theta** | **Zeta** | **Unclassified** | **Microsomal** | **Total** | **References** |
| *Spodoptera littoralis* | 3 | 15 | 3 | 4 | 1 | 2 | 2 | 3 | **33** | Legeai et al., 2011 |
| Chilo suppressalis | 4 | 3 | 4 | 2 | 1 | 1 | 1 | 0 | **16** | Liu et al., 2015 |
| *Cydia pomonella* | 1 | 1 | 2 | 1 | 1 | 1 | 1 | 1 | **10** | Huang et al., 2017 |
| *Epiphyas postvittana* | 3 | 5 | 3 | 6 | 1 | 0 | 2 | 0 | **20** | Jordan et al., 2008 |
| *Drosophila melanogaster* | 8 | 12 | 3 | 1 | 4 | 2 | 1 | 0 | **31** | Younus et al., 2014 |
| *Plodia interpunctella* | 3 | 2 | 4 | 2 | 1 | 1 | 1 | 3 | **17** | Present study |

**Supplementary Table S4** Sequences used in the phylogenetic tree

>PiGSTd1

MYSIRSLAFMFLVVLGNAAARSKSSRMPAQAIKLYYLPPSPPCRAVMMTARALGLDLNLVLTNIMEGAHMTPEYIKMNPQHTVPTMDDNGFILWESRAIMAYFVNAYGRDDSLYPKNPRLRAVVDQRLNFDIGTLFPRYIDVYMPVLFKGEEMSQEAVDKLNEALGWLNTIMEGKTFVAGDNLTIADISIVITFTNLDAFDYDFSEYENLTQWFERTKKALEPYGYMEIDHAGGQILASFLKKD

>PiGSTd2

YTPVASHFNFFINVKTQTDRMPIDFYYTPGSPPCRSVLLTAKALGLELNLKTLDLHHGEHMKPEFIKLNPQHCVPTLVDGDLVLWESRAIIVYLAQAYGKDDSLLPKDPKKQALVNQRLQFDVSTLYPAFSDQYYPWIFAGVPKSDDKEKKIHDALGFLDIFLGSSTWAAGDSVTVADLALVASISTIEAVGVDLSKYANVSKWFEKCKTTLVGYQEFNQKGIDGFKIMVANLTKK

>PiGSTd3

MPDLYYVPGSAPCRAVLLTAKALNLNLNLKLVDLHHGEHLKPEYLKLNPQHTVPTLVDDGFSIWESRAIITYLVNKYGKGSTLYPEEPKARALVDQRLYFDIGTLYQRFADYFYPQVFGGAPADKEKAAKIEESLKLLDQFLEGQKYVAGPNLTVADLSLIAGVSSFEASDIDFKKYNNIKRWYETVRATAPGYQEANEKGLEAFKALVNSMKK

>PiGSTe1

MPVLYKSDASPPARTVLMVSELLGVVLELRELNPVLREQDAPPYRQKNPMRTVPVLDEGDFSLADSHAIVLYLIAKYGKPEHMYLYPDDIRIRARIHLILFFDCGVLFPRLRTVMAPTYGGKLGELSKRMIHNIDDAYQMLEEYLNDGSYLAGDAMTIADLSVLTTTSSLHGLHPVDEKRFPKLTRWLENMNQKEVCQRINAPGSQLHVEGLKALMAHHRENQKSKL

>PiGSTe2

MVLTLYKIDASPPVRAVFMTIEALNIPGVDYVNVNLLEREHLKDDFVKINPQHTVPTLKDDDFVLWDSHAIAGYLVAKYGADDSLYPNDPKRRALVDQRLHFDTGILFPSLRGTVEPIFFWGEKSPRPENLEKIEKAYGFTESFLTSPWLVGGEVTLADICCVATISSMNEVLPIDGNKYPNLVGWLERCEKEIFYKKGNESGLLQFRQLLKSKLQ

>PiGSTo1

MITSTLTFAVHVIMSSFRVLAPVARLLENAFPDRNMASKAVKGKVNFNSKHLRRGDPMPPYTGKLRVYNMRYCPYAQRTLLALIAKDIDFEVVNIHLMDKPEWFLARSAFGKVPALEVADGVTIYESLVTVEYLDDAYPQRPLLPKDPVTKAYDKIIIEATGPIHGLFYRILRTPESVTNEHVEAYHKALKFIEDQIKARGNKFLGGSKPGYADYMVWPWFERIINSDLDGRLKIDGQKFKVLSEYINHMLQDPVVSQYIVPKEVMSQFIIPYRSGDFANINYDIMIEE

>PiGSTo2

MSEKHLQTGDALPTYPGKLRLFAMRFCPYAERSVLVLNAKKLSYELVFINLDHKPEWIFKYSPKGTVPALEYEEGKAIFDSNIINVYLDEKYPDISLQSADPLRRAQDKMLVENFASAQSAYYTAAFNSQALQPSNVENYHKGLELLQKEIETRGTKFLNGDEPGLVDYTLWPFLERFEALPLIGKSEFAFDKDKYAALIAYMNVMKSAPAVQAYRLAPETHAKFTESRAKGDPDYNMLDSSDTVCCMRPRKKKE

>PiGSTo3

MSYYQHKSSEAPPPPPLPPGQLRLYHVHMNPYAHRVRLVLEAKRVPYELHALDPLRLPDWFREKNPRLKIPVLEVPTPQGDRCLFESIVICDYLDERYPQNPLHSSDPLVKAQDRLLIERFNELIKGSLECFDTNFTFGGDQILQTVDVFEKELAARGTPYFGGSSAGMLDYMVWPWLERLCLLRCLRPRAFDAKRDAFPHMSQWGHAMQCEAVVKQLASSPERYLQYYRSARAHAMGYCL

>PiGSTo4

NILPVIKVIENLSVAMATNQEHVKLLGATGSPFVCRVQIALKLKGIEYEFVEENLATKSEQLLKYNPVHKKVPVFVHNEKPISESLVILEYIDEVWKQNPILPSDPHQRALARFWSKFIDDKIVSTSFKSVFSLDEKEREKNIEEATEALHFLENELKDKYFGGEEFNFVDIAAVFVAFWVPLVQDITELQLFTAEKFPKLYNWSQEFLDHPVVKETLPPREPLFAFFKGRYESLLAASK

>PiGSTs1

MSKKLLYFSIGGIAEYIRYMLHYGGHNFEDVRFDYKKWPIKEVKDSLPYGQLPLYEEGDRKLNQSIAISRYIASQTGLLPSDPWEQAILDAAVLNVNDFRLKSYSYFIEKDETKKEQIKKEFLTDSVDFYLSRFEKELKDNNGHFGGKLSWADFYLVGMLEGINLAMNVQLEKNYPSITALMKEIPSLPGVKEYVAKRGPYVFPA

>PiGSTs2

MSKVEFYYFPIKALGEPVRLLLSYGGQEFEDNRVVPEKWPEFKPKTPFGQMPFLVINGKQYAQCTPICRYLGRKYGLAGADLEEDFEIDQNVELVHDLRAKAAQVQYEEDAATKAKRHEKYTREIYPNLLTKLDEIIRKNNGHLALGKLTWGDFIFAGIYEYLKVMLQAPDLDEKFPSLRALEQAVLNLPKVKEYVAKAPKCDY

>PiGSTt1

MGKMTLKLYYDLMSQPSRALYILLKTVNCKFESKYVDLRKGEHYSDEFTKVNRIQRVPVIDHNGFVLTESVAIYKYLSREGIVPESLFPKESQQQARVEEFLEWHHIGLRLHTAMYFRAVYLDPIIFNRKNTPEQTVGYQRRMETCLEDFSTKWLGRGHAFVVGDKVTVADLVAACELEQPRMAGYDPREKFSNIAEWYERVRSYFNPHYDEAHVIVNKVIAKNNKTNAKL

>PiGSTz1

MAKPVLYSYWRSSCSWRVRIALNLKEIPYDIKAVSLIKGGGEQHCNEYRDVNPMEQVPSLCIDGHTFIESLSIMHYLEETRPQRPLMPQDCFKRAKVREICEVISSSIQPLQNLIVLIYVGEEKKKEWAQHWITRGFRAVEKLLSASAGKYCVGDEITLADCCLVPQVFNARRFHVDLRPFPIILRIDRELEQHPAFRAAHPSAQPDCPPEVAK

>PiGSTu1

MVLKLYAVSDGPPSLSVRQALARLQIPYELIDVNFNAGDHMTPQYALMNPQKEIPVLDDEGFFLSESNAILQYVCDKFQPGGPLYPADPKDRAIVNHRLCFNLSTYYANISAYTMAPIFFDYERTPFGLKRVNMALDVFETYMERLGTSHAAGDHLTIADFQLINSTMTLEAVDIDFSKYKRITKWYNDFKSNYPDLWKISADAMKIIQHFAANPPDLSHLNHPIHKARKTNK

>PiGSTm1

MSSFIFSFDDPAVQSYAFYSGVLALKTLGMSVLTAKVRHSKKVVANEEDAKLDKKAVIKFDDPDVERVRRAHLNDLENIPAFWLLGGLYLTTGPPASTAINLFRVYTAGRIVHTLVYAIKPLPQPARGIAYGIPFFIMVFMGVKVIIYYSKSL

>PiGSTm2

MAAIPFDNPAVQSFILYSAILAIKLLILSPITGFTRIIKRSFANPEDSKFLGGRVKTDDRVERFRRAHLNDLENIPAFWILGALYLTTGPNVVWATQLFRVYAAARVSHTIFHAIYPVLQIRGLSFTTALLINAYMSVQVILQYITAL

>PiGSTm3

MVSLSDPAVQSYALYSTILALKVLAMAFLTARARYSKKVFANEEDAVATKGKVKYDDPDVERVRRAHRNDLENIPAFWILGALYLTTGPAASTAANLFRAYTAGRLIHTFVYAIKPMPQPARGIAFGVPLFIMIFMGFKVITFYASAL

>PxGSTd1

MPVEPIKLYYFPPSPPCRAVMMAAKAMGIELEMVLTNIIEGEHMTPEFLKMNPQHTIPTIDDNGFILWESRAIIQYLANAYGRDDSLYPKNPRLRAMGDQRLNFDLGTLVSRYLNLYSPVLHGEPFSDDMDAKLKEALGWFNTMLEGRAFSAGDNLTVADISIVVVFSNLEAFGYDFTAYDNVSKWFERTKKALEPHGYKEIDQAGAQMLASFIKKD

>PxGSTd2

MPDLYYVPGSAPCRAVLLTAKALNLNLNLKLVDLHHGEQMKPEYLKLNPQHTVPTLVDDGLAIAESRAILTYLVNKYGKGSTLYPEDPKARAIVDQRLYFDIGTLYQRFGDYFYPQLFGGAPEDKEKLAKVDEALKFLDTFLEGQKYVAGNNLTVADLSLVASVSSFEAANIDFLKYGNVKRWYETVKATAPGYEEANGKGLEAFKGLVNSIMKK

>PxGSTd3

MAIDLYLTPGSAPCRLVLLTAAALNIQLNLNHVDLRAGEQFSPDFLKLNPQHTIPTIVDQGFALWESRAISRYLVNKYGHGSTLYPEDPQSRALVDQRLDFDLGTLYPKFADYFYPQVFGSAPADPEKLKKLHEVLGFLDIFLGDEKYAAGSDLTIADLSLVATVSTIDAAGISLDDFPNIHRWFELVKSTAPDYENANGKGIKAFKELVAQLNAKTEL

>PxGSTd4

MPAIDLYEMPSSAPCRAVKLTARALGVPVKLHLVDLMAGEHLKPEFTKINPQHTIPTIVDDGFTLWESRTIMRYLVNKYGKGSSLYPEEPKARALVDQRLDFDLGTLYDRYAVYFYPQIFGTAPENPELLKKLHEALAHLNHFLGESKYAAGPNLTIADLTLVVTVSTIDLWEIIDFKQYPNIDKWYEHLKSSVEGYEEENLAGLGKFRAFIKEFKAKKAAAK

>PxGSTd5

MPAIELYEMQGSAPCRAVRLTARALGKPLTVHHLDLMAGEHLKPEFVKINPQHTIPTIVDDGFALWESRTIMRYLVNKYGKGSSLYPEEPKARALVDQRLDFDLGTLYAKYAVYFYPQVFGTAPENAEDLKKLNEALAHLNTFLGESKYAAGSNLTIADFSLVATISTIDVSDIVDLKQYPNIVKWYEHLQSSVEGYEEENLAGLENFRSFIKEFKAKKAAAK

>PxGSTe1

MMRKLLFRNSPTDLVRCKSITLYGDEISPPVRFVQMTADLLGIQYKFKKVDLFKQENKQDFFKKINPLQKVPALKVGDTVITDSHAIAMFLCENSDGQTLYPDDPIIRPIVQQMMFFNSSTLFNIDSTIYSNFFAGSESIDANLVKDWTLALDYLEYQLRKHEWLAYDKMSLCDLCCGATVSTLQLLIPPTEKHKKVNRWIKRLEEIPCHSINKIGLDRLQFLIDQIKDVAH

>PxGSTe2

MSKLLLYKVDGSPPSNSILMIAHLLNLDMDYKEPDLLRLEHRSPEFKKINPMGTIPVLKDGNFVLAESHSILKYIVEKYGGPPRSTLYPCARRPRAAVDERMHFDTGVLFISLSSVVKASIFGDQPAVTPEQLASIESSYATLELYLERSRFVAADHLTIADFGVLSTTLALRHILPIDANKFPKISAWLSQLEEEAFVKNVGAPNMEKFKAILYSSWERNKSKMAR

>PxGSTe3

MPLILYVSDASPPARAVLMLAEILQLEFDKQYINPVLREQDSPEMTQKNPMRTVPTLEDGEFCLADSHAIILYLMEKYGQNHRNLYPEDLRVRSTIHQRLFFDCSILFPRLRAIMAPTFLGKLSQPSGSMVTNIEDAYRTLEAYLSQSKYLAGPEMTIADISAVATVSGLDGLHPIDEKRYPNTREWLVNMSRKTFYRKCNAQGNEMLISLLKSSMENNKQNDKKAKL

>PxGSTe4

MGLTVYKIDWSPPARAVIMTLEALNITDAELVDVSLLDGKHMSEEYLKMNPQHTVPVIKDGDFVLWDSHAICAYLVDKYGKDDSLYPKDLQKRAVVDQRLHFDTGILFPSVRGAAEPVLFDWEPTFNPEKLKVIQSGYDFLEKFLDHSYLAGDHLTIADICAGATVSSMNVIVPIAANRYPKISAWLDRLNSIEYFSRINGNGIKIITALFESKLNKSKK

>PxGSTe5

MVLTLYKLDASPPARAVMMTLEALGIRDVEMVDVNLFEGAQFTEEYVKMNPQHTIPALKDDDFAIWDSHAICPYLVSKYGQDDSLYPQDPQRRAVIDQRLHFDSGILFPSLRATVAPVLFLGERSFKPEGLQAIKAGYDFLEKFLDKPYCAGDQLSIADICTSATVSSMSAALPIDADTYPNITAWLDRLSKEEFYTKVNLPGLQQFSGALKSKLL

>PxGSTo1

MSEKHLQTGDALPPFGGKLRLFAMRFCPYAERSVLVLNAKNIPYDLVFINLDQKPEWIFNFSPRGAVPALEYEQGKGIFDSNVINVYLDEKYPEVPLQAADPLRRAQDKLIVENFSAAQSAYYTAAFNAQALQPSHLENYHKGLELLQKELETRGTKFLHGDQAGLVDYTLWPFLERFEALPLLGKSEYAIDKSKYDILLTYMESMKQVPAVKTYYLSADMHAKFTESRVKGDPNYNMLDSSAEVCCFRPRKKKE

>PxGSTo2

MSTRGIKFNTKHLRKGDPLPPYNGKLRLYNMRYCPFAQRTVLALNAKDIDYEVVNINLFEKPEWLTSKSAFGKVPSLEIKEGLSIYESLVTVEYLDEVYPQRPLLPKDPVQRALDKIIVEACTPIQGLFIKLIKFPESISEDTVAAYHKALHFLQEQLQSRGTRFFGGDQPGFVDYMIWPWFERVLPYQKVESRVQIDAGKFKLLLEYLQNLKQDPVVKQYLIEDEVLFKFLEPYKTGGEPNYDLLLEA

>PxGSTo3

MSFYYQERPAGPTPPGPLSNKLRLYHVDMNPYGHRVLLILDAKKVPYEVCKLDPLRLPEWFREKNPRLKIPVLEIPTDQGDKYLFESIVICDYLDERYTRNPLHSRDPFVKAQDRLLIERFNELIKGSLECFDTNFAFGNEQIIQTVNIFEKELESRGTVYFGGDRPGMLDYMIWPWIERLYMLRCLNPTKFDEKRHIFPNFADWGDQMQLDEVVKKHASSPEDNFEYYKNARAHSMGYYL

>PxGSTo4

MSTRGIKFNTKHLRKGDPLPPYNGKLRLYNMRYCPFAQRTVLALNAKNIDYEVININLFDKPAWLTSKSAFGKVPSLEIKEGLSIYESLVTVEYIDEVYPQRPLLSKDPVQRALDKIIVEACTPIQNLYIKLIRFPKTFTEDTVTAYNKALEFLQEQLKIRGTKFFGGAEPGFVDYMIWPWFEQVLSYQKIDSRAKIDAEKFKTLLDYLQHLKQDPVVKQYLIEEDVLFKFLEPYKTGGEPNYDLMLDA

>PxGSTo5

MTEKHLQTGDALPPYNGRLRLFAMRFCPYAGRCVLVLNAKNIPYDVVYINLTKKPEWIFNFSPKGAVPALEYEQGKALFDSNVINTYLDEEYPEVPLQASDPLRKAEDQLVVENFNTVITAYFTAAYNPQGLQPSHPEIFHRGLEQLQKELETRGTEFLHGEEVGMVDYTLWPFLERFNTLPLGNAEFALDKSNYETLLTYMESMKQLPAVMSNYLPPDIYAKFTDSFVTGDPDYNMLLSNDEGC

>PxGSTs1

MAKKLHYFDVNGIGESIRYILHYGGQKFEDVRYQISGWPDKKVKDALPFGQLPLYEEGDRSLHQSLAIARYVASQSKLLPNDLWEQAVVDSYVMTIYDFWFTKVIPFVKETDAAKKATLKKEILDESIHFFFSRFDKVLKEHNGFFIGKLTWAEFILVGIIEAGNLFLDYEIEKNYPHVKAAVQKVLTLPGVKEYIAKRKVYAL

>PxGSTs2

MPVVKFYYFPIKALGEGPRLLLAYGGQEFQDIRVDKESWPEFKPKTKYGQMPILEIDGKQYAQSAAICRYLASRYGLTGADAEQNFEIDEAVDFFNDIRAKAAQVHYEEDEKVKEKRHETYSQTVYPDLLGKLHDIVQRNNGHLAANKLTWADFYFAGVYDYMKVMLRRPDLDQQYPGFAKVYETVYSLPKVKAFADAAPKTDF

>PxGSTt1

MSQPSRAVYILLKKSNINFEPKYVDLRKGVHYTDEYSNNINRFKKVPVIDHNGFILTESVAIIRYLGRENVLPEALFPRADKVLNTRLDEFLEWQHLGLRAPLAMYFRVVMFSPDSEKIPSYQKRMETALDEFSTLWLGRGNQYILGDTATVADLLAACEVEQPRMTGYDCTANYPVIREWMDRVRSYFNPHYAEASSIVEKIAAKRIPMKKPTAKL

>PxGSTu1

MVLKLYAVSDGPPSLSVRQTLAALQLPHELVSVNYGAGEHLTEGYAQMNPQKEIPVLDDDGFFLSESNAIMQYLCDKYKRDSPLYPTEAKARAIINQRMCFNLASYYANISAYTLAPIFFDYERSSLGLKKVHLVLEVFDTYLARLGARHAAADHLTIADFPLVNSTMTLEAINVDFSKYERVRKWYNDFKRNYPDLWKISEDAMKELKQFSAHPPDLSNLNHPFHPIRH

>PxGSTz1

MAKPVLYSYWRSSCSWRVRIALNLKEIPYDIKAVSLIKGGGEQHCNEYREVNPMEQVPSLCIDGHTLIESLSILHYLEETRPQRPLMPQDCYKRAKVREICEVISSGIQPLQNLVVLIYVGEEKKKEWAAHWMTRGFRAVERLLSGSAGKYCVGDEITLADCCLVPQVFNARRFHVDLRPFPIILRIDRELEHHPAFRAAHPSTQPDCPPEAAK

>PxGSTz2

MASPAVLHGFFASSCTWRVRAALVLKSIPFEERHVDIVQLKTHLSDQYQAVHPAQKVPALEIDGTTLVESMAILQYLEDTRPRPALAPAAPLPRARMREIVETIVSGIQPLQNVGVRGLLGSDEEYSAFSRGAARRALQTLEALLARSAGQYCVGDQLSMADLCFVPQLFNAVGRLKLDISDLPTISKLYAKLSKEEIFMKTHPRTVKHLSET

>CpGSTd2

MRSFTFFTIFLVIYVNGTAAARSRMPAQPIKLYYLPPSPPCRAVMMLAKVMGLELDLEITNIMIGEHKTPEFLKMNPQHTIPTMDDNGFILWESRAIMAYLVNAYGRDDSLYPKNPRLRALVDARLNFDLGTLFLRYLNLYAPMLFHGEEYNEESAAKLDEALGWLNSMLEGRAFVAGDNMTIADITIVVTLTNLDALSYDFSAHDNVTKWFERMKKALEPYGYKDIDYEGAQVLASFIKKN

>CpGSTd3

MPIDLYYLPYSPPCRPVLVLADALKLKLNLKELNTRAGEHLTPEFKKINPQHCLPTLVDDDLTLWESRAILTYLASKYGDGSLYPADHKLRAAVDQRLYFDMGTLYQTFTDYLYPQLFGNQPADEEKLKKLEEALEFLNIFLEGKPWVAGSTLTVADYSIICTVNSIIALDVDVYKYPNIKEWYERAKSSMPGFNVSEQVIELLKKLFQDFKAKNTSV

>CpGSTd4

MDLYYTPGSAPCRLVLLVAAALDIQLNLKELNLQAGEHMTTEFLELNPQHTVPTLVDDGFALWESHAICRYLIRKYNNRELYPEDIQIRALIDQRLDFDLGTLYPRFRNFFYPQVFAGKPANESLFRNLKESLDIFNSFLKGHKYAVGDTLTLADLSLVATVSTLEAAGVSLESYPRVERWFELVKSTAPAYEEANEKGLIKFKALVANFKAKTEL

>CpGSTe1

MVLTLYKLDASPPVRAVKMVIAAINLPDVEYVDVNLLQGDHLKEDYIKINPQHTVPTLADDDFVIWDSHVIATYLINMYADNDSLYPSDPKTRALIDQRMHFDCSILFPPIREAVGPVIFGNDKAFQPEVLHKIQSGYEFTEKFLTGEWLAGDDLSVADICCVATISTSNEILPIDETLFPKLAEWMKRCSELEIYKNENEPGLNIFSQILKSKLA

>CpGSTe2

MVKLYKLDGSPPARACMIACELFNVPVELIDVNLMAGEHLTPEFLKKNLLHTVPTLEDGSLVIHDSHAALMYLADVYGKQESFYPKETKQRAHVNQKLFFNSTILFPRMRNTTYPIFMEGMTEIPQKNLDAIEEAYGFVEEFLSRTKYLAGDNITIADIAAYPTVTSLLIFLELNAQKYPKTQAWLKDLEKLPYVQKGNAKGLEDLSNFIKSKLG

>CpGSTe3

MRAILYHSNSSPPSRAVKMVAGILKVQLEERYLNPVARDQDTPELIEKNPMRSIPMLDEGDYWIADSHAIIVYLFEKYAKPEHQHLYPSDIRKRATINQRMYFECGILFPRLRSVMAPTFWGKLTELSKSMKSNIEDAYRTLEAYLSRNLYVADDVLTLADISIVTTVSTMDGIYSVDGKRYPKLKQWLQTMSQKDFCQKYNEPGREELVTVLVTMMDNNKHNQRAKL

>CpGSTz1

MAKPVLYSYWRSSCSWRVRIALNLKEIPYDIKAVSLIKGGGEQHCNEYREVNPMEQVPSLCIDGHTLVESLSIMHYLEETRPQRPLMPQDCFKRAKVREICEVISSGIQPLQNLIVLIYVGEEKKKEWAGHWITRGFRAVEKLLSASAGKYCVGDEITLADCCLVPQVFNARRFHVDLRPFPIILRIDRELENHPAFRAAHPSSQPDCPPEVAK

>CpGSTt1

MTLKLYFDLMSQPSRALYILLKNIKCNFTPVPVDLREAEHYSEEYTKINRFQRVPVIDHNGFVLTESVAILKYLSREGIIPDSLYPKDSKQAARVEEFLEWQHAGLRLHCAMFFRVKALDPIITGKTPDPKTLQGYERRMENALGTFNDLWLGQGKPFVAGDHISVADLLAACEVEQPRMAGYDAIAKYPNIAEWMGRVRDHFNPHYDEGHVILNKIVRNKSKMAPKL

>CpGSTs1

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>CpGSTo1

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>CpGSTo2

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>CpGSTu1

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>CpGSTm1

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>CpGSTm2

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>BmGSTd1

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>BmGSTd2

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>BmGSTd3

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>BmGSTe1

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>BmGSTe2

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>BmGSTe3

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>BmGSTe4

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>BmGSTe5

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>BmGSTe6

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>BmGSTe7

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>BmGSTo1

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>BmGSTo2

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>BmGSTo3

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>BmGSTo4

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>BmGSTs1

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>BmGSTs2

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>BmGSTt1

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>BmGSTz1

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>BmGSTz2

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>BmGSTu1

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>CsGSTd1

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>CsGSTd2

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>CsGSTd3

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>CsGSTd4

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>CsGSTe1

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>CsGSTe2

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>CsGSTe3

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>CsGSTo1

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>CsGSTo2

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>CsGSTo3

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>CsGSTo4

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>CsGSTs1

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>CsGSTs2

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>CsGSTt1

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>CsGSTz1

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>CsGSTu1

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>ApGSTd1

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>ApGSTd3

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>ApGSTd7

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>ApGSTd8

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>ApGSTd11

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>ApGSTd15

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>ApGSTo1

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>ApGSTs1

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>ApGSTs2

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>ApGSTs3

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>ApGSTs4

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>ApGSTs6

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>ApGSTt1

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>ApGSTt2

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>ApGSTm1

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>ApGSTm2

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>DmGSTd1

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>DmGSTd2

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>DmGSTd3

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>DmGSTd4

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>DmGSTd5

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>DmGSTd6

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>DmGSTd7

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>DmGSTd8

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>DmGSTd9

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>DmGSTd10

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>DmGSTe1

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>DmGSTe2

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>DmGSTe3

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>DmGSTe4

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>DmGSTe5

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>DmGSTe6

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>DmGSTe7

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>DmGSTe8

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>DmGSTe10

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>DmGSTs1

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>DmGSTm1

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>DmGSTm3

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>AgGSTd3

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>AgGSTd4

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>AgGSTd5

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>AgGSTd6

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>AgGSTd7

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>AgGSTd10

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>AgGSTd12

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>AgGSTd15

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>AgGSTd16

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>AgGSTd17

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>AgGSTe1

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>AgGSTe2

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>AgGSTe4

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>AgGSTe5

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>AgGSTe6

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>AgGSTe7

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>AgGSTo1

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>AgGSTs1

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>AgGSTt1

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>AgGSTt2

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>AgGSTz1

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>AgGSTm1

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>AgGSTm2

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>AgGSTm3

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>AgGSTu1

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>TcGSTd1

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>TcGSTo1

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>TcGSTo2

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>TcGSTo3

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>TcGSTs1

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>TcGSTs2

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>TcGSTs3

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>TcGSTs4

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>TcGSTs5

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>TcGSTs6

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>TcGSTs7

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>TcGSTt1

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>TcGSTz1

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>TcGSTm1

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>TcGSTm3

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>TcGSTm4

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>TcGSTu1

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