Appendix A Primers used in quantitative RT-PCR of *DlAGO* genes.

	Genes ID/Accession number	**Gene Name**		**Primers used in quantitative RT-PCR (5′→3′)**	**Tm (℃）**
1	EU330204	*Fe-SOD*	Forwards：	GGTCAGATGG TGAAGCCGTA GAG	**58**
			Reverse：	GTCTATGCCACCGATACAACAAACCC	
2	AK073620	*eIF-4a*	Forwards：	TTGTGCTGGATGAAGCTGATG	**58**
			Reverse：	GGAAGGAGCTGGAAGATATCATAGA	
3	DQ471426	*EF-1a*	Forwards：	GATGATTCCCACCAAGCCCAT	**58**
			Reverse：	GGGTCCTTCT TCTCAACACT CT	
4	_	*UBQ*	Forwards：	GCCGACTACAACATCCAGAAG	**53**
			Reverse：	GCTTGGTGTA GGTCTTCTTC TT	
5	Dlo031503	*DlAGO1*	Forwards：	GAACATCATTCGAGTGGGGC	**58**
			Reverse：	CCATATCCTCCACGGCCTC	
6	Dlo022883	*DlAGO2*	Forwards：	GAACTGCTGGTGGTGGTAATG	**59**
			Reverse：	GGGTGGAGGAGAAGAAGAAGA	
7	Dlo025430	*DlAGO4*	Forwards：	AAGAAGGAAATGGAGCGGAG	**58**
			Reverse：	GCCACGCCTAGACATTAGAAC	
8	Dlo026081	*DlAGO5-1*	Forwards：	GCCGGAAGAGGTAGAGGATC	**57**
			Reverse：	GCCAATGTAAGTTTCTGCGC	
9	Dlo027040	*DlAGO6*	Forwards：	ATCATGAGTAGGCGTGGAGT	**60**
			Reverse：	GCATCCTGAGCTTTAACCGA	
10	Dlo018449	*DlAGO7*	Forwards：	TCTCCACAAACCCTCTTCCA	**59**
			Reverse：	AATCAGGTCTCTTTGCAGCC	
11	Dlo002921	*DlAGO10*	Forwards：	AAACCCCACTTGCAAAACAC	**58**
			Reverse：	TGGTGAAGTTTGGTTGTGGT	
12	Dlo029681	*DlAGOMEL1*	Forwards：	GGTCTCACTCTCCAAACTCAG	**57**
			Reverse：	TTGAAGAAGCAGCTGTCTCC	

Appendix B RNA-seq data of the *DlAGO* family that were used in this study.

Gene ID	EC	IcpEC	GE
Dlo031503	230.30	259.47	201.41
Dlo022883	21.67	20.36	19.29
Dlo025430	321.52	294.69	392.05
Dlo026081	24.13	21.44	11.04
Dlo010130	0.17	0.17	0.01
Dlo010241	0	0	0
Dlo027040	81.12	81.37	38.44
Dlo018449	0.20	0.12	0.08
Dlo002921	8.78	12.65	33.78
Dlo029681	2.65	2.61	0.53

Appendix C The information for each conserved domain of DlAGOs

Protein Name	Gly-rich_Ago1		ArgoN		DUF1785		PAZ		ArgoL2		ArgoMid		Piwi	
	Start	End	Start	End	Start	End	Start	End	Start	End	Start	End	Start	End
DlAGO1	81	189	201	336	345	397	402	534	538	584	594	674	687	1008
DlAGO2			138	274	283	335	340	474					632	930
DlAGO4			67	229	239	291	295	427	436	482	489	571	579	887
DlAGO5-1			126	259	268	320	325	455	459	506	516	596	613	915
DlAGO5-2			84	220	229	281	286	418	421	468	478	558	575	882
DlAGO5-3			81	201			316	377	365	406			472	779
DlAGO6			55	214	231	283	284	419	420	466			563	855
DlAGO7			162	309	318	370	378	509					666	979
DlAGO10			149	284	293	345	350	482	486	532	542	622	634	956
DlAGOMEL1			97	231	240	292	297	430	456	499	509	588	598	843

Appendix D The sequences of conserved domain of DlAGO proteins

Protein Name	Conserved domain						
	Piwi	ArgoN	PAZ	DUF1785	ArgoL2	ArgoMid	Gly-rich_Ago1
DlAGO1	LIVILPDNNGSLYGDLKRICETDLGLVSQCCLTKHVFRMSKQYLANVALKINVKVGGRNTVLLDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEVTKYAGLVCAQAHRQELIQDLYKTWQDPVRGQVTGGMIKELLISFRRATGQKPQRIIFYRDGVSEGQFYQVLLYELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHHDRNTIDRSGNILPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENKFTADGLQSLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYM	RCIVKANHFFAELPDKDLHQYDVTITPEVTSRGVNRAVMEQLVKQHRESHLGKRLPAYDGRKSLYTAGPLPFISKEFRINLLDEDDGQGGQRRERDFRVVIKLAARADLHHLGLFLQGRQADAPQEALQVLDIVL	DFVAQLLNRDVSARPLSDADRVKIKKALRGVKVEVTHRGNMRRKYRISGLTSQTTGELTFPVDESGTLKSVVEYFYETYGFVIQHSQWPCLQVGNQQRPNYLPMEVCKIVEGQRYSKRLNERQITA	PVGRSFYSPDLGRRQPLGEGLESWRGFYQSIRPTQMGLSLNIDMSSTAFI	ERELDIMQTVHHNAYHNDPYAKEFGIKISERLASVEARILPAPWLKY	PQVGQWNMMNKKMVNGGTVNHWICINFSRNVQDSVARGFCYELAQMCYVSGMAFNPEPVLPPISSRPEQVERVLKA	GGPSEYQGRGRGASPQQGGRGGYTPARGSAGMGGGGTSGGRGGPSFGGQPRSSPIPELYQAQPASYPSGVTPQASSSEAGSSSQIVEH

DlAGO2	ILLCVMDKKHSGYKYLKWISETRVGVVTQC CLSSHANSARDQYLANLSIKINAKLGGSNVE LFDRLPYFEDEGHVMFVGADVNHPASRDTTS PSMAAVVATVNWPGANRYVARVRPQSHRT EKILNFGDMCMELIDSYARLNKVKPAKIVIFR DGVSEGQFDMVLNEELVPLKRAFRQRDYSPT ITLIVAQKRHQTRLFPESRRDGGATGNVPPGT VVDTTIVHPFEFDFYLCSHYGSLGTSKPTHYH VLWDDHKFTSDQLQKLIYNMCFTFARCTKP VSLVPPVYYADLVAYRGR	TARLCVNHFPVKFNPN SIIRHYDVDVKPVVPSK HGRPSKLSKSLLAMIR NKLFEDDPAQFPLPMT AYDGEKNIFSAVELPT GNFNVKLEEEDGRVQS FIFTIKLVNELRLGKLK DYLTGNLSTIPRDILQG MDVVM	DFLSEHIRYFGQRNFRD WGKVESALKGLKVTVT HRRTKQKFIIGGLTKQIT RQLSFLIEDPEEKAPPRQ VRIIDYFREKYHTDIMW KDFPCLDLGRNGRKNY VPMEFCELVEGQIYQKD K	SVGRSFHPVHPYEE DDLGFGLTASRGFQ QGLKATSQGLALCL DYSVLAFRK		
DlAGO4	LLCLLPERKNCDIYGPWKRKNLADFGIVTQCI APTRVNDQYLTNVLLKINAKLGGLNQLLAIE RSPSIPIVSKAPTIILGMDVSHGSPGQSDVPSIA AVVSSRHWPLISRYRAAVRTQSPKVEMIDSL FKKVSDTEDEGIVRELLLDFYTSSGKRKPEQII IFRDGVSESQFNQVMNIELDQMIEACKFLDE KWNPKFVIIVAQKNHHTKFFQSGSPDNVPPG TVIDNRICHPKNNDFYLCAHAGMIGTTRPTH YHVLYDEIGISADDLQELVHSLSYVYQRSTT AISVVAPICYAHLAATQMGTFMK	QKIPLLTNHFKVNVTN VEGHFFHYSVSICYED GRPVDGKGVGRRVIDR VHETYKAELDGKDFA YDGEKSLFTVGSLPRN KLEFTVVLEDVSSNRN NNGNASPDGQGSPNW GDRKRVRRPYQSKSYR VEISFAAKIPMQAIANA LRGQESENSQEALRVL DIIL	DFLIANQNVRDPFSIDW AKAKRVLKNLRIKTMPS NQEYKITGLSEKSCKEQ MFSLKQKNVKDDDGES QNLEISVYDYFVNHRNI ELRYSGDLPCMNVGKP KRPTYIPLELCSLVSLQR YTKALSTLQRASL	VRQSFFHNDPKNY ADVGGGVLGCRGF HSSFRTTQGGLSLNI DVSTTMII	ERMSALSNALKNSK YDAEPMLRSCGISIST NFAQVEGRVLSAPR LK	PRNGRWNFNNKKLVEP TKIERWAVVNFSARCDI RSLVRDLVKCGDMKGI QIDQ

DlAGO5-1	LIVILPDVSGSYGRIKRVCETELGIVTQCCQPRQASRLNMQYFENVALKINVKVGGRNTVLNDAIQRKIPHVSDHPTIIIGADVTHPQPGEDSSPSIAAVVASMDWPEVTKYRGIVSAQTHREEIIKDLYTTHQDAQRGVIHGGMIRELLRAFRMSTGHKPHRIIFYRDGVSEGQFSQVLLHEVDAIRQACTSLEAEYMPPITFVVVQKRHHTRLFPVDHRNRQMTDKSGNILPGTVVDTKICHPTEFDFYLNSHAGIQGTSRPTHYHVLFDENKFSADELQVLTNNLCYTYARCTRSVSI	RPCMVRANHFLVEVADRDIHHYDVTISPEITSKKINREVMAQVTRLYGESHLGRRIPAYDGRKSLYTAGPFPFDSKEFVVDLEQDAGARTRRDRKFKVTIKLASKPDLFTLQQFLRGRVLDSPQEVIQVLDVVL	NMLSNALSDQDRVKVKKALRGIKVALNHMEfvKSYKITGITSEPLSQLTFPLDDNVRTSVVKYFRDKYRIVLKYTALPALLAGSEARPVYLPMELSRIVEGQRYSKKLNERQVTAL	VGRSFFSPQLGPKGELGDGIEFWRGFYQSLRPAQMGLSFNIDISARGFYE	DRENNIKRMVLSNNYNRDKLANEEFGIHVGDDLTLCEARILPSPMLNY	PSFGQWNMINKRMINGGRVEFWTCVCFSTRVSRELPSQFCEQLANMCTSKGMAFNPRPVIPIITANPNQIERALTDVN
DlAGO5-2	VGGCYGRIKRVCETELGIVTQCCRPQQALKLNMQYFENVALKINVKRRIPHVSDHPTIIIGAAITHPHPGEDSSASIAAVVASMDWPEVTKYRCTVSAQPPRLEIIKDLYKTHQDAQRGVVHGGMIRELLAAFKMSTGCKPHRIIFYRDGVSEGQFSKVLLHEVDAIRQACASLEAEYMPPITFVVVQKRHHTRLFPADHQNEQMTDRSGNILPGTVVDTKICHPKEFDFYLNSHAVSQGTSRPTHYHVLFDENRFTADELQLLTNNLCYTYARCTRSVSVVPPAYYAHLAAIRACYY	KKCLVRANHFLVQVADRDIHHYHVTITPWAAEKIKRDVMAQVTRMYGESYLGKRIIAYDGRKSLYTAGPFPFDSKEFIVNLEQDFRGSSSTGTRIERKFEVAIKLASKLDFIGLQQFLRQGHLDFRQEVIQVL	FVKKYMYNKNLSNPLSNQDLVKVKKALRGVKVAPTHMEYVKSYRITGISNQPLSQMTFMLNDKVAKSYVVQYYREKYGIVLKYTALPALQAGSEAKPIYLPMELSRIVEGQQYSKRLNEGQEIA	VRRSFFSPHLGPKGELGDGIEFWRGFYQNLRLTQMGLSLNIDVSARGFYE	DRESNITRVVLSNNYNQVKLANEEFGIHVGDDLKLCDARILPSPMLNY	PSFGQWNMINKKMINGGRVEFWTCVCFSKRVNGELPSLFCEQLVNMCKSKGVEFSPHPVIPIITANPCQMEKALTDVHR

DlAGO5-3	VGGCYGRIKRVCETQLGIVSQCCRPQQALKL NMQYFENVALKINVKRRIPHVSDHPTIIIGAAI THPQPGEDSSPSIAAVVASMDWPEVTKYRCT VSAQPHRLEIIKDLYKTHQDAQRGVVHGGMI RELLAAFKMSTGCKPHRIIFYRDGVSEGQFSK VLLHEVDAIRQACGSLEAEYMPPITFVVVQK RHHTRLFPADHKNEQMTDRSGNILPGTVVDT KICHPKEFDFYLNSHAASQGTSRPTHYHVLF DENRFTSDELQLLTNTLCYTYARCTRSVSVV PPAYYARLAAIRARYYM	AAEKIKRDVMVQVIR MYGESYLGKRIIAYDG GESLYTAGPFPFYSKEF VVNLEQDFHASSSTGT RKERKFEVAIKLASKL DFIGLQQFLRQGHLDF HQEVIQVL	MVKKVLRGVKVAPTH MEFVKSYRITGISNQPLS QITIFEDFRGQGIDELWK KVRFWGSVWASISINFK NTYLSLRTSPALRRLGV PLTSMVYMFMLNDKVA KKSVIQYYREKYGIALK YTALPALQAGSEANIYL PMEVV		VLSNNYNEVKQANE EFGIHVGDDLTLCDA RILPSPMLNY
DlAGO6	FILCVLAERKNSDIYGPWKKICLTDMGIPTQC ISPTRINDQYLTNVLLKINSKLGGINSLLAME HSSHIPLIKDTPTLILGMDVSHGSPGRSDASIA AAVRTQSSKMEMIDALYKPLADGTDDGIIRE LLMDFYQTSNQRKPRQIIVFRDGVSESQFSQV LNIELDQIVKAYQHLGEADVPKFTVVVAQKN HHTKLFQSNGTENVPPGTVVDTKVVHPRNY DFYMCAQAGMIGTSRPAHYHVLLDEIGFSPD ILQNLIHSLSYVYQRSTTAIAIVAPICYAHLAA AQMGQFIK	RIGLLTNHFKVSVKAQ DAVFYQYTVTISGDDK RGVEGKGIGRKLLDRL YQMYSAELAHKKFAY DGEKSLYTVGALPQNN LEFIVVLDESRAKPKN GSPSADDSASDAGKRS KVSFRSKTFKVDISYSA KIPLKSIALALKGSEVD SGTQDALRVLDIAL	IDFLTLNQNVQDPRHID WAKAKKMLKNLRVKP RHRNMEFKIIGLSERPCN QQLFTMKKEGDTVEITV YDYFKNHCGIELTRSAY LPCLDVGKPNRPIYLPLE LCSLISLQRYTKSLSLMQ RASL	VRQSFFHDDSKNFV DVGGGVTGVRGFH SSFRPTQGGLSLNM DTSTTMIV	ERMRTLTDAVRNYH YDEDPVLSACGISIE KQLAQVDGRVLETP KLK

DlAGO7	LICIMERKHKGYADLKRIAETSVGVVSQCCL YSNLGKLSSQFLANLALKINAKVGGCTVALY NSLPSQIPRLFRPDEPVIFMGADVTHPHPLDD FSPSVAAVVGSMNWPAANKYVSRMRSQTHR QEIIQDLGAMVGELLDDFYNEENKLPKRIIFF RDGVSETQFYKVLQEELQAIKEACSRFPGYSP PITFAVVQKRHHTRLFPFENNDPSSTQNQNQF LDENIPPGTVVDTVITHPREFDFYLCSHWGV KGTSRPTHYHILWDENHFTSDELQKLVYNLC YTFVRCTKPVSLVPPAYYAHLAAYRGR ISLLANHFLVQFDSSQR IFQYNVEITPNPSKEVA RKIKQKLVGNNSVVLS GADPAYDGRKNLYSP VEFQNDRLEFFISLPITT NKSLLPHGEVNESKEK HQQHKLFRINIKLVSKF DGKDLNSYLSKEGDD WIPLPQDYLHALDVVL LEFLKDLLQRKTRGLSG EERKEVEKALKNMRIFV CHRETVQRYRVYGLTEE ATENLWFPDRDGKSLRL VSYFKDHYNYNIQFRNL PCLQISRSKPCYLPMELC MICEGQKFLGKLSDDQT ARI PVGRSLYSSSMEGT KEIGGGVVGLRGYF QSLRPTQQGLALNV DSSVSAFH
DlAGO10	LLAILPDNNGSLYGDLKRICETDLGLISQCCL TKHVFRISKQYLANVSLKINVKMGGRNTVLL DAISCRIPLVSDIPTIIFGADVTHPENGEDSSPSI AAVVASQDWPEVTKYAGLVCAQAHRQELIQ DLYKTWHDPVRGTGSGGMIRDLLISFRKATG QKPLRIIFYRDGVSEGQFYQVLLYELDAIRKA CASLEPNYQPPVTFIVVQKRHHTRLFANNHR DRSSTDSKSGNVLPGTVVDSKICHPTEFDFYL CSHAGIQGTSRPAHYHVLWDENNFTADGIQS LTNNLCYTYARCTRSVSVVPPAYYAHLAAFR ARFY KCIVKANHFFAELPDK DLNQYDVTITPEVASR TVNRAIMAELVRLYKE SDLGMRLPAYDGRKSL YTAGELPFAWKEFKIK LVDEDDGINGPKRERE YKVVIKFVARANMHH LGQFLAGKRADAPQE ALQILDIVL CRTLSDSDRVKIKKALR GVKVEVTHRGNVRRKY RVSGLTSQPTRELVFPV DDNSTMKSVVEYFQEM YGFTIQHTHLPCLQVGN QKKANYLPMEACKIVE GQRYTKRLNERQITA PIGRSFFSPDIRTPQ RLGDGLESWCGFY QSIRPTQMGLSLNI DMASAAFI DRENDILQTVQHNA YDQDPYAKEFGIKIS EKLASVEARILPAPW LKY PQVGQWNMMNKKMIN GMTVNRWACINFSRSV QESVARGFCNELAQMC QVSGMEFNPDPVIPIYN ARPEQVEKALKHVY

DlAGOMEL1	IIILPDLTGSYGRIKRVCETELGIVSQCCQPKHARKCSPQYLENVALKINVKAGGQNTVLEDAFYRRIPLLSDIPTIIFGADVTHPPPGEDSSPSIAAVVASMDWPVVTTYRGQVYAQKHRQEIIQDLYKEKGLVGAGMVRELLIAFKRATNQKPQRIIFYRDGISEGQFSQVLHCEMDAIH	RCMIRANHFLVELSDRDLHHYDISITPEVTSRGLNRAVMRELLDKEGKTVFDERKPAYDGRKGFYTAGALPFTSKDFVVKLIDRDKKGSTIKQRDFKVTIKLASRTDLKHLKEFLTSRQEEAPHETIQVLDVVL	ASRPLSEQDLIKLKKVLRGVKVEVCHGEAKRYKVTGITSAPTNQLKFLAEGKKEKLVIQYFREKYNISLRYASWPSLQSGNDSKPIFLPMELCTIVEGQRYSKKLNEKQVAA	VGRSFFSAGLDTKTEIGSGVECWRGFYQSLRPTQMGMSLNMDVSATSFYE	QIAQFNNYQNDSLAKEFGVNVKSELVCIDGRVLPPPVLKY	PRVGQWNMINAKMYHGAKVKFWTCLNFSTVSRQMAAGFCQDLINMCRNKGMDVNPSPTFPVWSSNSSQIERALSDVHR

Appendix E The information for each motif of DlAGOs.

Motif	E-value	Sites	Width	Best possible match
Motif1	3.3E-277	10	50	EFDFYLCSHAGIQGTSRPTHYHVLWDENKFTADELQKLTNNLCYTYARCT
Motif2	3.2E-196	9	50	GADVTHPHPGEDSSPSIAAVVASMDWPEVTKYRGLVSAQSHRQEIIQDLY
Motif3	1.6E-118	9	29	RIIFYRDGVSEGQFSQVLLHELDAIRKAC
Motif4	8.1E-85	10	22	YGRJKRICETDLGIVSQCCLPK
Motif5	1.7E-125	9	41	GDGVEGWRGFYQSLRPTQMGLSLNIDVSATAFYEPJPVIDF
Motif6	3.1E-81	6	33	EPEYMPPITFVVVQKRHHTRLFPADHRBRQMTD
Motif7	1.4E-97	6	41	DARILPSPMLKYHETGKEKRVNPSVGQWNMINKKMINGGRV
Motif8	1.8E-83	9	27	RSVSVVPPAYYAHLAAYRARYYMEGET
Motif9	5.3E-88	10	29	SELGKRIPAYDGRKSLYTAGPLPFBSKEF
Motif10	1.7E-76	10	21	NDQYLENVALKINVKLGGRNT