

Supplemental material

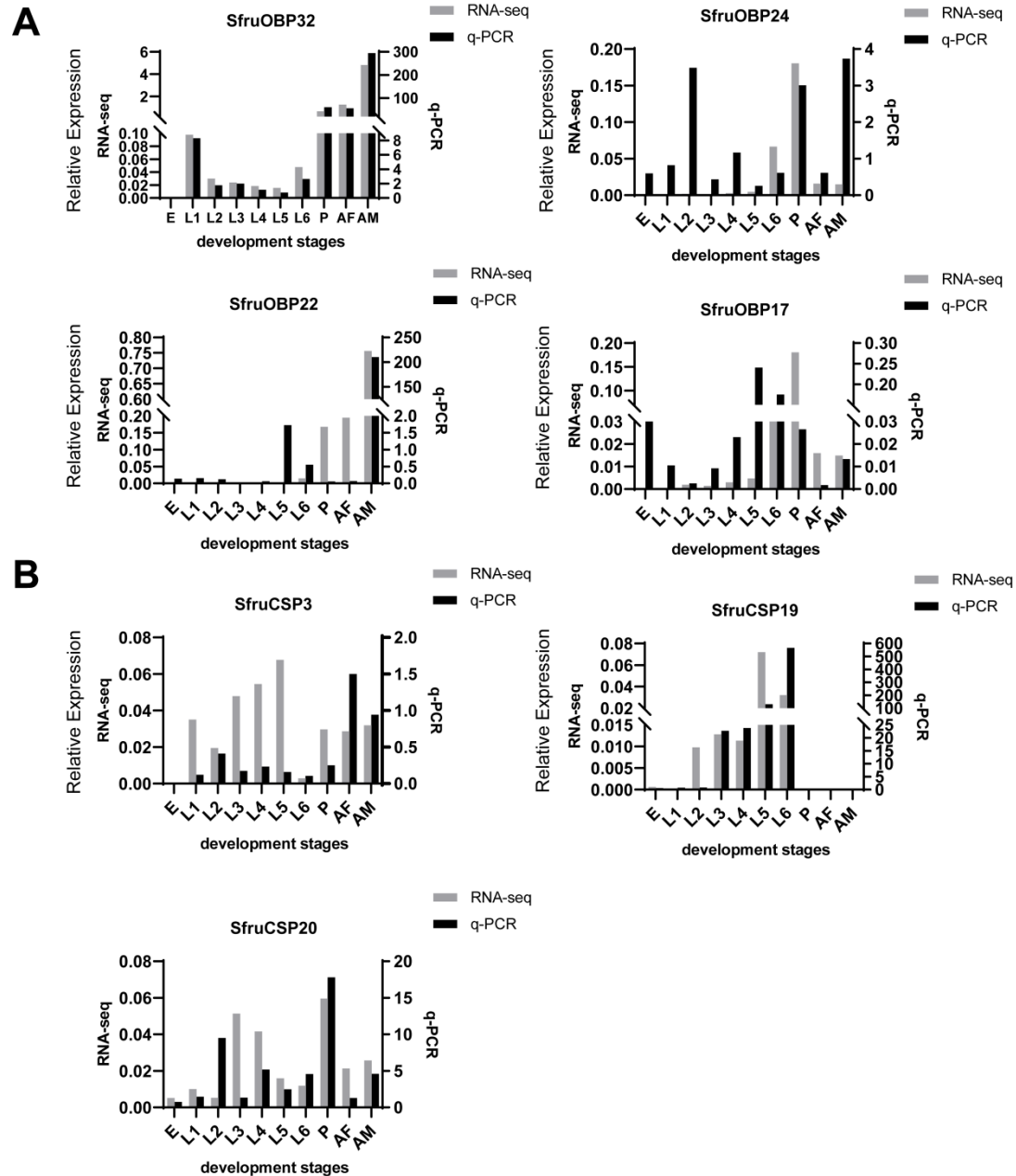


Figure S1. Measurements of relative expression levels of selected *SfruOBPs* and *SfruCSPs* by RNA-seq and q-RT-PCR. Expression level of each gene was calculated relative to reference genes of Rp132. (A) expression levels of OBPs. (B) expression levels of CSPs. Expression levels were measured across different developmental stages from eggs to adults (E: eggs; L: larvae; P: pupae; A: adult, where F: females and M: males).

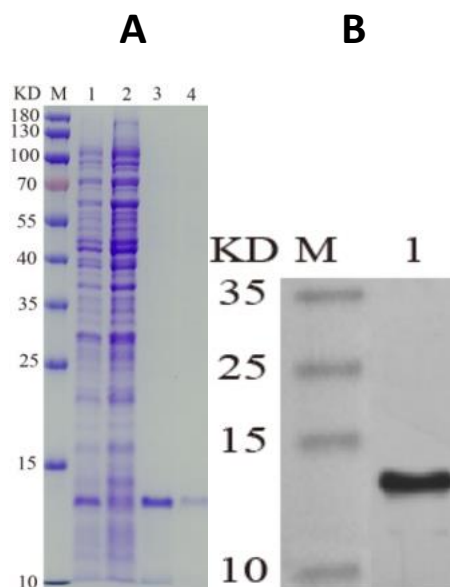


Figure S2. SfruOBP31 protein expression and purification. (A) SDS-PAGE analysis of SfruOBP31 protein. M: Protein marker. 1. Induced protein products. 2. Flow through. 3-4. Purified SfruOBP31 protein. (B) Western blot analysis of SfruOBP31 protein. M. Protein marker. 1. Purified SfruOBP31 protein.

Supplemental Table S1. Results of all *SfruOBPs* and *SfruCSPs* blastx in NCBI

Name	Description	Insect species	Max Score	Total Score	Query Cover	E Value	Per. Ident	Acc. Len	Accession	No. of conserved Cys residues
OBPs										
OBP1	OBP 1	<i>Sesamia inferens</i>	202	202	80%	9E-65	88.68%	106	AGS36743.1	6
OBP2	OBP 2	<i>Spodoptera exigua</i>	318	318	99%	3E-109	94.44%	162	AGH70098.1	6
OBP3	OBP 3	<i>Spodoptera exigua</i>	273	273	93%	5E-91	85.80%	170	AGH70099.1	6
OBP4	OBP 4	<i>Spodoptera exigua</i>	283	283	99%	2E-95	81.71%	164	AGH70100.1	6
OBP5	OBP 5	<i>Spodoptera litura</i>	224	224	95%	1E-72	85.50%	147	AKI87966.1	6
OBP6	OBP 6	<i>Spodoptera exigua</i>	230	620	92%	2E-69	92.00%	147	AGH70102.1	6
OBP7	OBP 7	<i>Spodoptera exigua</i>	195	473	99%	2E-58	97.92%	142	AGH70103.1	6
OBP8	OBP 8	<i>Spodoptera exigua</i>	272	272	48%	5E-89	99.31%	149	AGH70104.1	6
OBP9	OBP 9	<i>Spodoptera litura</i>	319	319	99%	5E-107	98.08%	339	ALD65883.1	5
OBP10	OBP 10	<i>Spodoptera exigua</i>	309	309	99%	6E-106	95.54%	157	AGH70106.1	5
OBP11	OBP 11	<i>Apocheima cinerarius</i>	120	120	62%	3E-30	46.62%	155	QOV03027.1	6
OBP12	OBP 12	<i>Corythucha ciliata</i>	193	193	88%	8E-60	56.85%	160	AYP30811.1	6
OBP13	OBP 13	<i>Corythucha ciliata</i>	87	87	69%	2E-17	35.81%	167	AYP30812.1	6
OBP14	SexiOBP 14	<i>Spodoptera exigua</i>	206	206	57%	7E-65	88.18%	139	AGP03460.1	6
OBP15	OBP 15	<i>Corythucha ciliata</i>	227	227	33%	3E-69	72.73%	177	AYP30814.1	7
OBP16	OBP 16	<i>Carposina sasakii</i>	268	268	98%	2E-89	78.18%	166	AYD42191.1	5
OBP17	OBP 17	<i>Spodoptera exigua</i>	258	258	94%	8E-86	91.85%	148	AKT26495.1	4
OBP18	OBP 18	<i>Spodoptera exigua</i>	317	317	99%	4E-108	79.03%	186	AKT26496.1	1
OBP19	OBP 19	<i>Spodoptera exigua</i>	224	342	54%	1E-66	65.16%	216	AKT26497.1	5
OBP20	OBP 20	<i>Spodoptera exigua</i>	228	228	68%	5E-73	78.91%	146	AKT26498.1	5
OBP21	GOBP 69a-like isoform X1	<i>Spodoptera frugiperda</i>	320	320	99%	3E-110	100.00%	154	XP_035437860.1	6

OBP22	OBP 22	<i>Spodoptera exigua</i>	289	289	99%	9E-98	94.87%	156	AKT26499.1	4
OBP23	OBP 23	<i>Spodoptera exigua</i>	479	479	99%	5E-170	94.19%	252	AKT26500.1	0
OBP24	OBP 24	<i>Spodoptera exigua</i>	324	324	99%	2E-111	100.00%	184	AKT26501.1	6
OBP25	OBP 25	<i>Spodoptera litura</i>	195	195	98%	6E-61	68.67%	154	ALD65899.1	7
OBP26	OBP 26	<i>Spodoptera exigua</i>	201	310	53%	2E-58	90.08%	149	AKT26503.1	6
OBP27	OBP 9	<i>Cnaphalocrocis medinalis</i>	281	281	75%	5E-93	77.50%	204	ALT31639.1	5
OBP28	OBP 59a	<i>Spodoptera frugiperda</i>	227	227	85%	3E-72	97.69%	244	XP_035435754.2	5
OBP29	OBP 29	<i>Spodoptera litura</i>	255	357	99%	1E-82	95.38%	156	ALD65903.1	7
OBP30	OBP 1	<i>Carposina sasakii</i>	171	171	78%	4E-52	71.30%	107	AYD42176.1	5
OBP31	OBP 31	<i>Plutella xylostella</i>	171	171	76%	7E-52	72.64%	136	ANG08529.1	6
OBP32	OBP 32	<i>Plutella xylostella</i>	216	216	99%	7E-70	78.95%	136	ANG08535.1	4
OBP33	OBP 33	<i>Helicoverpa armigera</i>	171	171	64%	3.00E-52	82.83%	99	ASA40071.1	6
CSPs										
CSP1	CSP 1	<i>Mythimna separata</i>	248	248	95%	1.00E-78	70.80%	290	AWT22249.1	0
CSP2	CSP 2	<i>Pieris rapae</i>	162	162	95%	2.00E-49	76.70%	100	QDW65468.1	4
CSP3	CSP 3	<i>Spodoptera frugiperda</i>	224	224	99%	3.00E-73	98.43%	127	QXT24549.1	4
CSP4	CSP 4	<i>Spodoptera exigua</i>	190	190	99%	9.00E-60	82.93%	123	AKT26481.1	4
CSP5	CSP 5	<i>Spodoptera exigua</i>	124	124	87%	2.00E-34	90.77%	131	AKT26482.1	4
CSP6	CSP 6	<i>Spodoptera exigua</i>	129	129	81%	8.00E-36	59.57%	111	AKF42439.1	4
CSP7	CSP 7	<i>Spodoptera exigua</i>	212	212	99%	3.00E-68	89.84%	128	AKT26484.1	4
CSP8	CSP 8	<i>Conogethes punctiferalis</i>	183	183	98%	5.00E-57	70.59%	120	AHX37222.1	4
CSP9	CSP 9	<i>Spodoptera exigua</i>	253	253	99%	7.00E-85	97.56%	123	AVC68635.1	4
CSP10	CSP 10	<i>Spodoptera exigua</i>	230	230	73%	6.00E-75	100.00%	122	AKT26486.1	4
CSP11	CSP 11	<i>Spodoptera exigua</i>	208	208	85%	7.00E-67	94.29%	122	AKT26487.1	4

CSP12	CSP 12	<i>Spodoptera exigua</i>	187	187	86%	2.00E-58	80.00%	125	AKT26488.1	4
CSP13	CSP 13	<i>Spodoptera exigua</i>	223	223	99%	5.00E-73	92.68%	123	AKT26489.1	4
CSP14	CSP 14	<i>Heortia vitessoides</i>	147	147	86%	1.00E-42	62.26%	128	UVB79217.1	4
CSP15	CSP 15	<i>Adelphocoris lineolatus</i>	206	206	79%	3.00E-65	79.37%	126	AXS78221.1	4
CSP16	CSP 16	<i>Spodoptera exigua</i>	234	234	80%	2.00E-76	91.80%	122	AKT26491.1	4
CSP17	CSP 17	<i>Spodoptera exigua</i>	199	199	99%	3.00E-63	93.44%	122	AVC68636.1	4
CSP18	CSP CSP18	<i>Lobesia botrana</i>	148	148	86%	3.00E-43	63.21%	127	AXF48714.1	4
CSP19	CSP 19	<i>Spodoptera exigua</i>	195	195	86%	9.00E-62	86.79%	122	AKT26493.1	4
CSP20	putative CSP 23	<i>Conopomorpha sinensis</i>	174	174	73%	1.00E-48	93.02%	557	QGN03668.1	4
CSP21	putative CSP 9	<i>Corcyra cephalonica</i>	218	218	99%	1.00E-69	62.75%	154	UDM59702.1	4
CSP22	CSP 4	<i>Athetis dissimilis</i>	239	239	85%	6.00E-78	76.87%	151	AND82446.1	4

Supplemental Table S2. Orthologues of *OBP* between *S. frugiperda* and *S. litura* that are located in the same subclades with highest similarities

<i>S. frugiperda</i>	<i>S. litura</i>
<i>SfruOBP19</i>	<i>SlitOBP13</i>
<i>SfruOBP29</i>	<i>SlitOBP30</i>
<i>SfruOBP5</i>	<i>SlitOBP5</i>
<i>SfruOBP25</i>	<i>SlitOBP25</i>
<i>SfruOBP26</i>	<i>SlitOBP22</i>
<i>SfruOBP6</i>	<i>SlitOBP6</i>
<i>SfruOBP14</i>	<i>SlitOBP28</i>
<i>SfruOBP21</i>	<i>SlitOBP26</i>
<i>SfruOBP17</i>	<i>SlitOBP27</i>
<i>SfruOBP18</i>	<i>SlitOBP18</i>
<i>SfruOBP22</i>	<i>SlitOBP33</i>
<i>SfruOBP32</i>	<i>SlitOBP12</i>
<i>SfruOBP8</i>	<i>SlitOBP21</i>
<i>SfruOBP31</i>	<i>SlitOBP3</i>
<i>SfruOBP7</i>	<i>SlitOBP17</i>
<i>SfruOBP27</i>	<i>SlitOBP31</i>
<i>SfruOBP20</i>	<i>SlitOBP19</i>
<i>SfruOBP30</i>	<i>SlitOBP20</i>
<i>SfruOBP16</i>	<i>SlitOBP32</i>
<i>SfruOBP28</i>	<i>SlitOBP1</i>
<i>SfruOBP9</i>	<i>SlitOBP9</i>
<i>SfruOBP24</i>	<i>SlitOBP10</i>
<i>SfruOBP2</i>	<i>SlitGOBP2</i>
<i>SfruOBP15</i>	<i>SlitGOBP1</i>

Supplemental Table S3. Orthologues of CSP between *S. frugiperda* and *S. litura* that are located in the same subclades with highest similarities

<i>S. frugiperda</i>	<i>S. litura</i>
<i>SfruCSP21</i>	<i>SlitCSP23</i>
<i>SfruCSP8</i>	<i>SlitCSP13</i>
<i>SfruCSP6</i>	<i>SlitCSP11</i>
<i>SfruCSP2</i>	<i>SlitCSP4</i>
<i>SfruCSP20</i>	<i>SlitCSP3</i>
<i>SfruCSP10</i>	<i>SlitCSP12</i>
<i>SfruCSP16</i>	<i>SlitCSP10</i>
<i>SfruCSP19</i>	<i>SlitCSP6</i>
<i>SfruCSP4</i>	<i>SlitCSP7</i>
<i>SfruCSP5</i>	<i>SlitCSP8</i>
<i>SfruCSP17</i>	<i>SlitCSP14</i>
<i>SfruCSP13</i>	<i>SlitCSP5</i>
<i>SfruCSP12</i>	<i>SlitCSP1</i>
<i>SfruCSP11</i>	<i>SlitCSP9</i>
<i>SfruCSP9</i>	<i>SlitCSP17</i>
<i>SfruCSP7</i>	<i>SlitCSP16</i>
<i>SfruCSP14</i>	<i>SlitCSP18</i>
<i>SfruCSP18</i>	<i>SlitCSP21</i>
<i>SfruCSP3</i>	<i>SlitCSP20</i>
<i>SfruCSP22</i>	<i>SlitCSP22</i>
<i>SfruCSP15</i>	<i>SlitCSP15</i>

Supplemental Table S4. Homologous *SfruOBPs* and *SfruCSPs* in this paper and previous report

Gene name in previous (Legeai et al., 2014)	Sf_TR2012b ID	Gene name in this paper	Annotation of inconsistent genes	identity of between two papers
OBPs				
GOBP1	c7994		Select seq ref XP_035439875.2 partner of Y14 and mago [<i>Spodoptera frugiperda</i>] <i>Spodoptera frugiperda</i>	
GOBP2	joint2_rep_c3475	OBP2		98.77%
OBP1	rep_c2034	OBP18		100%
OBP2	joint2_rep_c9255	OBP24		99.36%
OBP3	rep_c490		Select seq ref XP_035458708.2 GPI mannosyltransferase 3 [<i>Spodoptera frugiperda</i>] <i>Spodoptera frugiperda</i>	
OBP4	rep_c877	OBP32		99.25%
OBP5	rep_c2055	OBP10		96.18%
OBP6	c15965	OBP1		100%
OBP7	rep_c571	OBP8		100%
OBP8	joint2_rep_c7287	OBP23		99.59%
OBP9	Not found			
OBP10	c11418	OBP28		97.95%
OBP11	joint2_rep_c104	OBP6		98.4%
OBP12	rep_c504		Select seq ref XP_035454964.2 armadillo repeat-containing protein 6 homolog isoform X2 [<i>Spodoptera frugiperda</i>] <i>Spodoptera frugiperda</i>	
OBP13	c32728	OBP19		98.65%
OBP14	joint2_c2406	OBP7		77.27%

OBP15	joint2_rep_c3798	OBP7	100%
OBP16	Not found		
OBP17	rep_c44968		97.87%
		Select seq ref XP_050560119.1 titin isoform X1 [<i>Spodoptera frugiperda</i>] <i>Spodoptera frugiperda</i>	
OBP18	rep_c2988		
OBP19	Not found		
OBP20	Not found		
OBP22	joint2_rep_c1191		89.23%
OBP23	rep_c3716	OBP6	99.17%
OBP24	joint2_c2045	OBP6	91.3%
OBP25	joint2_c2317		72.8%
OBP26	rep_c2960	OBP21	100%
OBP27	c28274	OBP33	92.16%
OBP28	joint2_c6322	OBP28	99.07%
OBP29	joint2_rep_c3596	OBP29	95.65%
		Select seq gb AEA76329.1 chitin binding domain 3 protein [<i>Mamestra configurata</i>] <i>Mamestra configurata</i>	
OBP30	rep_c4239		
OBP31	Not found		
PBP1	joint2_c4216	OBP4	99.39%
PBP2	rep_c1860	OBP3	99.42%
PBP3	rep_c5672	OBP12	99.39%
CSPs			
CSP1	joint2_rep_c612	CSP7	99.22%
CSP2	joint2_rep_c3099	CSP8	100%
CSP3	Not found		
CSP4	joint2_c3581	CSP22	94.38%
CSP5	rep_c3130	CSP18	94.81%
CSP6	joint2_rep_c2279	CSP9	99.19%
CSP7	joint2_c1683	CSP20	98.1%
CSP8	rep_c4613	CSP3	96.06%
CSP9	rep_c23815	CSP14	99.17%
CSP10	c10036	CSP1	77.88%
CSP11	joint2_c9626	CSP6	99.12%
CSP12	joint2_c1394	CSP4	100%

CSP13	rep_c3399	CSP17	99.18%
CSP14	joint2_c3078	CSP15	94.25%
CSP15	rep_c4149	CSP5	96%
CSP16	joint2_c2765	CSP19	96.72%
CSP17	rep_c28057	CSP10	85.16%
		<i>Gossypium</i>	
		<i>herbaceum</i> isolate	
		GPA1alz	
CSP17	rep_c475	chromosome 5	
		<i>Gossypium</i>	
		<i>herbaceum</i>	
CSP18	joint2_c9032	CSP16	98.55%
CSP19	rep_c601	CSP13	99.19%

Supplemental Table S5. Protein and nucleic acid sequences of *SfruOBPs* and *SfruCSPs*

Protein sequences of *SfruOBPs*

>*SfruOBP1*

MTLIKKKSKFGEIVKRTVIATAHTCMDHVNATTKDLEHLRDEPPYPETSACIVKCLLEKIGVVKS
NRYSKMGFMTAVTPLVFANKKKMEHMKTVSENCDEKVNHHKHETPCQLGNEVTTCIFKYAPELHFK
S

>*SfruOBP2*

MTSKCCLLLVVMATVTSSVMATAEVM SHVTAHF GKALEECREESGLSAEVLEE FQHFWREDFEVV
HRELGCAIICMSNKFSLQDDSRMHVNMHDYVKSFPNGHVLSEKLVELIHNCEKKFDSMTDDCE
RVVKVAACFKVDAKAAGIAPEVAMIEAVMEKY

>*SfruOBP3*

MTLRQSGTMSVRVALVVALVVAASLLVVQASQDVMKNLAINFAKPLDDCRKEMDLPDSVTTDFYN
FWKEGYELTNRTGCAILCLSSKLEILDQELNLHHGRAQEFAMKHGADEAMAKQIVDMIHTCAQS
TPDVAADPCMKTNLVAKCFKDKIHELNWAPSMELVVGEVLAEV

>*SfruOBP4*

MADARWRVVCVVCALCLTSAVLASQDLMVKMTKGFSKVVDCKTELNIGDHIMQDMYNYWREEYQ
LINRDMGCMVLCMAKKLDLMEDQKMHGKAEEFAKSHGADDDVAKKLVSI IHECEQQHAGVADEC
MRALVAKCFRTKIHELKWAPSMEVIMEEMMTAV

>*SfruOBP5*

MFVVRCSFVVALFCLVSVYAQSDEEAGIKEALRPFVEECADEFGITEEQFEEAKKKGNAADIDP
CFMSCFLKKAGFFDSQGKFDVDSTMAFAKDHVSSEPAMKFVEAVGDECVKINDEDVSDGDKGCDR
AKLLFDCIGETKKKME

>*SfruOBP6*

MSKFACLVLCVAVSLSGVHATAE EKA AFIEAVKPHIQECSKEHGVTPEEIKSAKAAGNADGINS
CFLSCVYKKA EVINDKGEYDADKALEKLKKFVSNEDDYAKFAEIGKKCASVNEKSVSDGDAGCER
AALLTTCFLEHKSEIPA

>*SfruOBP7*

MTRQQLKNSGKLMKKSCMPKNDVTEDEVGDIEKGKFIESRNVMCYIACVYTMTQVVKNKLSYEA
VIKQVDVMFPAEMRDAVKAAATHCKETTKKYKDLCESSYWTAKCMYDYDAENFVFP

>*SfruOBP8*

MARRQRGAMFTETLPLFVILVAVTHGGKDKPVFSDEIKEIIQTVHDECVAKTGVAEEDITNCENG
IFKEDAKLKCVMFCLLEEASLVDDDDTVDYDMLVSLIPDEYYERTTKMIFACKHLDTDPDKRCQR
AFEVHKCSYEKDPDLYFLF

>*SfruOBP9*

MGQYNNNYSTTQSSRRYKRERRPSNSGQRSQYNPN SHKISGYEDNFRSDERNNTENNSSKETDN
KSCALHCFLENLEMTGEDGMPDRYLVTHAITKDVKNEDLRDFLQESIEECFQILDNENTEDKCEF
SKNLLICLSEKGRANCDDWKDDLTF

>*SfruOBP10*

MTKVLFAIVLTMITFAVALSASTKEAQTTMSDQVNSIEVDVLAVMDMCNDSYRIDPTYLQALNE
SGSFIDETDKTPKCFIRC VFENVGIVSE DGKQFNPARAAVIFAGERNGKPMEDIADMTALCATDR
QETCPCDRSYKFLRCLMSMEIEREYKS

>*SfruOBP11*

MCKFRVLLLGFVAVVYF SHVNCLYDEDKKILRDGLESIAHDC LHGCGIDETEIENIEADDNVDQ

CFKKCVMTDAGFALSDREKSTIQKELTTVGLQCIQQHPLSLSDIRSFNKMIPDGKKPKCFVACL
FKKIGVMDDMGMISPMKAEENAKKVFKDNEEHKHKVNEIMEKCSSVNHQNTSDGNKGCDRAKLAF
NCFTENADRYGDFDF

>SfruOBP12

MGSCNVFVALVVLTVGVREIEPSKDAMKYITSGFVKVLEECKQELNMNDHIIADLFHYWKLEYTL
LNRDTGCAIICMSKKLELLDANGRMHHGNAQEFAKKHGAGDEVASKIVQIIHECEKKHERDDDEC
LRVLEVAKCFRTGIHELWDWQPKVEVIVEEVLTEM

>SfruOBP13

MLGMKTIVVLCLIVYEAGLVHGEHEVSVLRALSTSIGDTLLECQTELDIKNEVIQSFLNFWDLKN
PADTKEWGCALDCVQKNAFLTPDGKTVISANVREFCKAAGADELMSVRMVDLFEMCKDGAKKII
SKCDNALEVTKCFRHGIVQLDWAPEHNFWRNRTREHPDNI PVQRTDIVKIPLPQRHSSLNVWRRRF
GYRRLASILRRSFC

>SfruOBP14

MMRKTCPKNNVEDEKIDPIADGVFIDEKEVKCYMACIMKMANTIKNGKLNVDAAIKQADLLLDP
DIKEPAKEAITACRKVGMDCNIEHPITPKEMLELKDNKIPDTNNAKCFVACVFKKTGMLDSKGM
DAENSIAMTQKDFANDPKRLEGSKKLETCCKVND EAVSDGEKGCERSVLLHKCFVETAPQ

>SfruOBP15

MLLLLRLALPLLA AVLPLRADVNVMKDVTLGFGQALDKCRQESQLTEEKMEEFFHFWRDDFKFEHR
ELGCAIQCMSRHFNLLTDSSRMHHENTEQFIQSFPNGEVLARHMVELIHACEKQHDHEEDHCWRI
LHVAECFKQACVQRGVAPSMEMMMTEFIMEAEAR

>SfruOBP16

MEKILIFTTFLSLAVVNSFKTKFFSQSLDSEPPVSILYARDKKSDKVTDDCLTEMYPRNLYKYP
LRIDRNDIPCI IHCVLKKFGIMTNDGYINIKNYRRVQAIHRYDPRILISDVGETCAQNINGMNL
DHDVCKKAKVFNDCTQLYAVSYKDPDEWK

>SfruOBP17

MAQHCCNASHADVQTPTKRETRASLKPLSVCCDIPELADERQLSKCSPKPPGPCEDVQCIFEAS
GFLTDKNTLNKAAYRSHLQKWEKSNPGWTD AIYKAITDCVDNDPRQHLDVACKAYDVFTCTGIAM
LKKCPETAWKC

>SfruOBP18

MFKFCVFLALGFVACHGAPNTNPGTYCGATPDNMFRC LNNPRVVTPEVAAKCGSQVTECERMTCI
FRELKWSKKGAI DAKAVRAYFEQYETEHPDWAQAVQHVKSFCLVPELRAQGVFLNCPAYDIMQCI
LSSFIKHASPSVWSNATDCDYPKAFAAACPVCPSDCYSPQIPFGSCNACYSQPRTV

>SfruOBP19

MITSSSLVLAAVVQVLFAQEPAFESGPPEPWGPPEKQTPRLAPRI PRNCWAPPQRINVYKCCP
IPSLYPDEAMQSCGFEKLPEGEAPKAVYRPEGTCKEGYCVMKFNLL LANKSVDYEFKGNYLDS
WAEANPEFAKPIKLAKEECAKDEGPKGPPICDPDRIFLCLTSII FWNCDLRDGEGCSALQEHMNE
CRQYYTR

>SfruOBP20

MFRRALLFLSVIYSLQYCNGQTEAPEKNRMMGIDAVHDNNVKIDKDTI ITRNLKLEKRN RGPKSD
SNKNVDEKEPDWSYASFPKEISEHVENFKNMSECLKEVQSSDKRPVKRLSPKMESPVHGECLIA
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Protein sequences of SfruCSPs

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Nucleic acid sequences of SfruOBPs

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Nucleic acid sequences of SfruCSPs

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GAAAATACTTTGCCAAATTCGAAGCGTCTGTTACCGGATTTTAA

>SfruCSP20

ATGGGTAAATTGCTGTTCTAAATTACCTACTATGATCAAATACGCGTTGCTGTTATGTTGTGTGGC
CGCGGTGTCCGTGGCGCAGTCCCAAAGGCCTCCAGTCTCCGACACAGCCCTTGATGATGCCCTAC
AAGACAAACGTTTCATTTCAGAGACAGCTAAAGTGCAGCTGGGGGAAGGACCTTGTGATCCCATC
GGGAAAAGACTTAAACACTAGCACCCCTGGTACTTCGAGGAGCCTGTCCCCAGTGACAGCCACA
AGAAACCAAGCAAATCCAACGCACTCTATCGTACGTGCAAAGAAATTATCCGCAGCAGTGGGCGA
AAATAGTGCGCCAATACGCAGGATAG

>SfruCSP21

ATGTGGGCTCAGGCGATTCCATACCTGATCGTAGTACATGTGGCGATGGGAGAACAAAAAGTGCC
AGGGTTCTCTAGAGAAATGAGCGACGGAGTAGAAAGCAGAGGCTTTAAGATCATTTACGGCGATG
AAGACATGACCATCATCAACCAAGTGGTCAGTGAAGCCGAAAAAGGCAGTGCTTTTAAAGAAGAGA
GTACGTTTGAATGAAGCTATTAAACCCTTACCGGCGCAAGATGTCAAGTGCTTGATGTCTGTGCA
CCGGTACTGTAGCAAGGAGATGGGCATGATGAAAAGTGTATTGATACAAGCTGTAAAAGATGACT
GCGCGAAATGTTTCAGTGGAGCAGAAGGATCAAGCTGGGAAAAGTAATTGCATCCATGATGGCTCAT
GATCCAGTCGCGTGGAAGTTTTCTCACCAGGTACGACGGCATCAAAAAAGTCCAAAGGATACT
AGGATAG

>SfruCSP22

ATGGCTTCCTCATACTATTTCAGTGCTCACTGTGAACGAGACTGTTATTTCTTCTGCTGTTCTTG

AATGATGAAGAACTCGTATAAAACAATGATACTCTTAGTATACCTGACAATTCAGAGCAACGCGA
CAGAGACTTCCACATACACGACCAAATATGATGGCATCGATCTCGACGAAATACTAGACAACGAC
CGTCTACTGACTGGGTATGTCAACTGTCTGATGGATCTTGGTCCTTGCACGGCTGATGGAAAGGA
ATTGAAAAAGAACCTTCCGGATGCTATAGACAATGACTGTAAGAAGTGCACTGAGAGACAGCGTG
AGGGCGCTGACCGTGTCTGTCATTACCTCATCGACAACAGACCTGAAGACTGGACCAAACCTTGAG
GAGAAATACAAATCTGATGGAAGCTATAGAGCTAAATATTTAGCCAGTAAGCAGACTAAAGATGA
GAAGGAATCAAATGCCACAAAATCCAGTGAGGATACAAATAATGTATCTAAAGAATAA

Supplemental Table S6. qRT-PCR primers of selected *SfruOBPs* and *SfruCSPs*

Gene	Forward primer (5'→3')	Reverse primer (5'→3')
<i>Rpl32</i>	TACAATCGTCAAAAAGAGGACGA	AAACCATTGGGTAGCATGTGA
<i>OBP17</i>	AATGTTCCCCAAAACCTCC	GCTTCTGTATGCAGCCTTAT
<i>OBP22</i>	CTACTGCGTGCTGCTCAAG	TGTCGCCCCGTCTGGTCTGC
<i>OBP24</i>	TCACGCACGATGAGAAGAG	CAGGACCGCCATGAAGTAG
<i>OBP32</i>	ACCGCTCCGAATGTCTGACTGA	CGTCCTTCTTGAACTTGCCATCCT
<i>CSP3</i>	TTCCGACAAACCTGTAACCAACCT	GCTTCCCTGATGTGTTCTGTGTGA
<i>CSP19</i>	AGCCCTTGATGATGCCCTAC	CGCACTATTTTCGCCCCACT
<i>CSP20</i>	CCTTTGCGGTGGTAATGGC	TCGCTAGGTGCTTCTGTGC