

Supplementary Tables and Figures

Table S1. Detailed summary of samples used for tissue collection to construct the transcriptome library. Transcriptome data for *Rana japonica*, *Rana ornativentris*, and *Rana tagoi tagoi* are from our previous study (Lau *et al.* 2017).

Species	Source	Sex	Date of capture/transfer to captivity
<i>Bufo japonicus</i>	Shiwa, Hiroshima 34°47'N, 132°67'E	M	2012/02/23
<i>Dryophytes japonicus</i>	Kurose, Hiroshima 34°33'N, 132°66'E	F	2004/07/02
<i>Fejervarya kawamurai</i>	Mt. Futagami, Hiroshima 34°40'N, 132°70'E	M	Not recorded
<i>Glandirana rugosa</i>	Takayama River, Hiroshima 34°53'N, 132°38'E	M	2011/07/14
<i>Pelophylax nigromaculatus</i>	Kurose, Hiroshima 34°33'N, 132°66'E	F	2009/07/02
<i>Pelophylax porosus porosus</i>	Kawashima-machi, Saitama 35°98'N, 139°49'E	F	2009/06/28
<i>Buergeria buergeri</i>	Uga, Hiroshima	F	2005/08/09
<i>Buergeria japonica</i>	Shirahama, Iriomote 24°37'N, 123°77'E	M	Not recorded

Table S2. Summary of MHC class I supertypes and accession numbers. Bold and bold-italics indicate variants from Japanese frogs collected in our present study and Lau *et al.* (2016), respectively.

Supertype	MHC class I variants/alleles
ST-A	Agca-UA*02/04/05/11-14 [JQ679313/15/16/20/22-25] Bfja-UA*02/03 Buga [KY302832/ KY302833] Bubu-UA*01 Drja-UA*04 Drja* [KY302810/11/16] Espr-UA*05/06/11/12 [JQ679335/36/41/42] Feka-UA*04 Glu-UA*01 Lica-UA*07/10/11 [JQ679349/52/53] Licl-UA*02-06/09/11/16 [JQ679356-60/63/65/70] <u>Liya-UA*01/03/07/08</u> Odma-UA*07-09 [MH784556-58] Peni-UA*05 Poch-UA*05-07,09-10 [KX467508-10/12/13] Pome-UA*02/04/05/07 [KC261638/40/41/43] <u>PSCO</u> [KX372230-34/38; KY072979] <u>Rapi</u> [AF185587.1] Rhom-UA*01-02/04-05/12-13/16-18 [KC261644/45/47/48/55/56/59-61] Smph-UA*01/02/04/06-11 [JQ679380/81/83/85-90]
ST-B	Agca-UA*08 [JQ679319] Bubu-UA*02-05 Buja-UA*01 Espr-UA*07 [JQ679337] Feka-UA*01-03 Glu-UA*02-05 Lica-UA*01-06/08/09/12 [JQ679343-48/50/51/54] Licl-UA*01/07/08/10/12/15 [JQ679355/61/62/64/66-69] <u>Liya-UA*02/04-06/09</u> Odma-UA*01-06 [MH784550-55] Peni-UA*01-04 Pepo-MHCI-UA*01-03 Poch-UA*08 [KX467511] Pome-UA*01/03/04/06 [KC261637/39/40/42] <u>PSCO</u> [KX372241-42] Raja-UA*01-10 Raor-UA*01-03/05-28 Rata-UA*01-22 Rhom-UA*03/06-11/14/15/19 [KC261646/49-54/57-58/62]
ST-C	Agca-UA*16-19 [JQ679327- JQ679330] Espr-UA*01 [JQ679331]
ST-D	Agca-UA*01/03/06/07/10 [JQ679312/14/17/18/21] Bfja-UA*01 Buga [KY302834- KY302858] Drja-UA*01-03,05-08 Drja* [KY302809/12-15/17-31] Espr-UA*02-04,08-10 [JQ679332-4,8-10] Smph-UA*03/05 [JQ679382/84] Xela [AF185580/83; NM_001085732]

*Korean population. Species that are reportedly susceptible to Bd are underlined. Species abbreviations: Agca - *Agalychnis callidryas*; Bfja - *Bufo japonicus*; Bubu - *Buergeria buergeri*; Buja - *Buergeria japonica*; Buga - *Bufo gargarizans*; Drja - *Dryophytes japonicus*; Espr - *Espadarana prosoblepon*; Feka - *Fejervarya kawamurai*; Glru - *Glandirana rugosa*; Lica - *Lithobates catesbeianus*; Licl - *Lithobates clamitans*; Odma - *Odorrana margaretae*; Peni - *Pelophylax nigromaculata*; Pepo - *Pelophylax porosus porosus*; Poch - *Rhacophorus chenfui*; Pome - *Polypedates megacephalus*; PSCO - *Pseudophryne corroboree*; Raja - *Rana*

japonica; Raor - *Rana ornativentris*; Rata - *Rana tagoi tagoi*; Rapi - *Rana pipiens*; Rhom - *Zhangixalus omeimontis*; Smph - *Smilisca phaeota*; Xela - *Xenopus laevis*.

Table S3. Summary of MHC class II supertypes and accession numbers. Bold and bold-italics indicate variants from Japanese frogs collected in our present study and previous study (Lau *et al.* 2017), respectively.

Supertype	MHC class II variants/alleles
ST-1	Bfja-01 – 03 Bfja [LC065651] Boor-05 [KJ679329] Buga-01 - 08 [KJ679317-24] Buja-01/02 Bubu-01/02 Drja-01/04 Epca [HQ388288] Feka-01/02 Glu-01/02 Lica [BT081564; transcriptome data from DRA accession number SRP051787] Livea-1*/2*/3/3b*/11*/12/17/19/23 [KJ679288-91/304/05/10/12/16] Napa-DRB1*15 [XM_018558121] Peni-03 Pepo-01/02 Raja-01/02/04-06/08 Raor-04/07/08/11 Rata-01 -03/05 -11/13 RhmaDAB01/DBB01/DCB01 [KP995700/04/06]
ST-2	Boor-02/06 [KJ679326/30] Drja-02/03 Livea-4/6/7a/7b/9/10/15/18/20 [KJ679292/97/98/99/302/03/08/11/13] Raja-03/07/09 Raor-01-03/05/06/09/10 Rata-04/12 Xetr [NP001039259], Xela [D13684, D13688]
ST-3	Rhom(Zhom) [KT276421/23/25/28/34/35/43/44/52/53/62/64/72/75/83/84] Ly1-32/40-42/79-80 [KU877031-62/70-72/107-108]
ST-4	Boor-01/03/04/07 [KJ679325/27/28/31] Livea-5a*/5b*/5c/5d/8a/8b/13*/14*/16/21/22 [KJ679293-96/300/01/06/07/09/14/15] Ly33-39/43-78 [KU877064-69/73-106] Peni-01/02 Rhom [KT276499/505/08/10]
ST-5	Qusp [KJ082083] Rhom(Zhom) [KT276411-20/22/24/26/29-33/36-38/40/41/45-51/54-61/63/65-71/73/74/76-82/85-98/500-04/06/07/09/11/12]

Additional abbreviations: Qusp - *Quasipaa spinosa*, Boor - *Bombina orientalis*, Rhma - *Rhinella marina*, Napa - *Nanorana parkeri*, Livea - *Litoria verreauxii alpina*, Epca - *Epidalea calamita*. *MHC-II alleles from Livea suggested to be ‘resistant’ to Bd (Bataille *et al.* 2015). See Table S2 for other species abbreviations. Ly is equivalent to Liya [*Lithobates yavapaiensis*].

Table S4. List of peptides used for MHC binding prediction. A combined set of Bd-related proteins were analyzed (A), including three Bd-related antigens [70 kDa heat shock protein 3, 26S protease regulatory subunit 6A-B, and JEL423 surface antigen], and proteins of M36, S41, ASP, adhesion, CRN, and lipase3 genes with increased expression after Bd was inoculated in frog skin (Rosenblum *et al.* 2012). In addition, as a control, we examined (B) a set of 13 immunogenic antigens from human fungal pathogen, *Aspergillus fumigatus* (Bacher *et al.* 2014) (i.e. non-Bd-related antigens) and (C) a set of 7 antigens from *Escherichia coli* bacteria (i.e. non-fungal antigens). Full list of compiled peptide sequences (before and after protein cleavage) is available upon request.

Dataset/proteins	Accession number/ Locus tag	Original length (aa)	No. of 15-24 amino acid-long peptides after protein cleavage
(A) Bd-related proteins and proteins with increased expression when Bd was grown in frog skin			Total =644
70 kDa heat shock protein 3	XP_006675784	647	6
26S protease regulatory subunit 6A-B	XP_006680816	434	3
JEL423 surface antigen	OAJ39392	449	4
M36 (metallo-proteases)	BATDEDRAFT_11205	450	2
	BATDEDRAFT_1502	300	0
	BATDEDRAFT_16613	289	3
	BATDEDRAFT_1489	300	1
	BATDEDRAFT_1469	300	0
	BATDEDRAFT_12637	413	1
	BATDEDRAFT_1639	404	3
S41 (serine-proteases)	BATDEDRAFT_85649	883	11
	BATDEDRAFT_36653	100	0
	BATDEDRAFT_23534	640	6
	BATDEDRAFT_23310	883	12
	BATDEDRAFT_23544	705	8
	BATDEDRAFT_24207	843	9
	BATDEDRAFT_24208	322	3
	BATDEDRAFT_24156	885	11
	BATDEDRAFT_87928	571	8
	BATDEDRAFT_24985	928	10
	BATDEDRAFT_25462	629	6
	BATDEDRAFT_35365	885	10
	BATDEDRAFT_90146	883	10
	BATDEDRAFT_26287	643	6
	BATDEDRAFT_27937	882	8
	BATDEDRAFT_92476	577	8
ASP (aspartyl-proteases)	BATDEDRAFT_21660	480	5
	BATDEDRAFT_22611	503	5
	BATDEDRAFT_22623	476	3
	BATDEDRAFT_86720	475	4
	BATDEDRAFT_23192	491	5
	BATDEDRAFT_23275	525	6
	BATDEDRAFT_87177	423	5
	BATDEDRAFT_87185	476	8
	BATDEDRAFT_87250	475	10
	BATDEDRAFT_23765	503	7
	BATDEDRAFT_87859	389	3
	BATDEDRAFT_87892	472	7
	BATDEDRAFT_88273	481	4
	BATDEDRAFT_24300	476	7

	BATDEDRAFT_24380	492	6
	BATDEDRAFT_24760	490	5
	BATDEDRAFT_24767	487	3
	BATDEDRAFT_25148	477	4
	BATDEDRAFT_25666	491	6
	BATDEDRAFT_36999	302	3
	BATDEDRAFT_89345	469	6
	BATDEDRAFT_25259	509	6
	BATDEDRAFT_89380	431	5
	BATDEDRAFT_25355	541	7
	BATDEDRAFT_89821	477	2
	BATDEDRAFT_25680	384	6
	BATDEDRAFT_25784	418	2
	BATDEDRAFT_89959	458	5
	BATDEDRAFT_26088	379	5
	BATDEDRAFT_26151	476	6
	BATDEDRAFT_26132	482	9
	BATDEDRAFT_90236	179	2
	BATDEDRAFT_90237	241	3
	BATDEDRAFT_26134	476	4
	BATDEDRAFT_90267	476	3
	BATDEDRAFT_26425	477	7
	BATDEDRAFT_90625	478	4
	BATDEDRAFT_26741	477	5
	BATDEDRAFT_35725	441	6
	BATDEDRAFT_90888	375	4
	BATDEDRAFT_26762	473	9
	BATDEDRAFT_26758	464	5
	BATDEDRAFT_26748	452	5
	BATDEDRAFT_90978	400	6
	BATDEDRAFT_91075	405	7
	BATDEDRAFT_27277	475	7
	BATDEDRAFT_27069	484	3
	BATDEDRAFT_27286	399	7
	BATDEDRAFT_92020	471	5
	BATDEDRAFT_27966	488	5
	BATDEDRAFT_28166	469	5
	BATDEDRAFT_28328	487	8
	BATDEDRAFT_28256	490	4
	BATDEDRAFT_92488	442	6
	BATDEDRAFT_92592	475	2
	BATDEDRAFT_28513	478	5
	BATDEDRAFT_92740	212	4
	BATDEDRAFT_28541	559	7
	BATDEDRAFT_28537	400	6
	BATDEDRAFT_28684	484	9
Adhesin genes	BATDEDRAFT_84886	149	0
	BATDEDRAFT_22355	363	5
	BATDEDRAFT_21697	569	4
	BATDEDRAFT_85835	303	2
	BATDEDRAFT_85893	302	6
	BATDEDRAFT_22768	376	0
	BATDEDRAFT_87248	379	6
	BATDEDRAFT_87422	284	1
	BATDEDRAFT_23878	345	6
	BATDEDRAFT_87864	324	3
	BATDEDRAFT_87929	340	1
	BATDEDRAFT_11071	328	3
	BATDEDRAFT_90520	323	6

	BATDEDRAFT_27092	457	0
	BATDEDRAFT_27091	663	3
	BATDEDRAFT_28554	993	9
	BATDEDRAFT_93124	563	2
CRN (crinkler-like effectors)	BATDEDRAFT_84882	596	6
	BATDEDRAFT_85109	603	6
	BATDEDRAFT_86517	222	1
	BATDEDRAFT_31422	673	9
	BATDEDRAFT_23217	281	1
	BATDEDRAFT_87221	806	9
	BATDEDRAFT_87524	769	8
	BATDEDRAFT_24811	671	6
	BATDEDRAFT_37012	765	9
	BATDEDRAFT_26085	458	4
	BATDEDRAFT_26137	671	7
	BATDEDRAFT_90343	561	6
	BATDEDRAFT_90726	354	2
	BATDEDRAFT_26749	780	8
	BATDEDRAFT_28183	721	8
Lipase-3 encoding genes	BATDEDRAFT_86691	407	4
	BATDEDRAFT_86693	323	3
	BATDEDRAFT_89307	261	2
	BATDEDRAFT_26489	250	2
	BATDEDRAFT_26490	376	6
	BATDEDRAFT_26491	470	7
	BATDEDRAFT_93190	284	3
	BATDEDRAFT_93191	375	3
(B) Single <i>A. fumigatus</i> proteins			Total: 49
Scw4 (Cell wall glucanase)	AFUA_6G12380	369	2
Gel1 (1,3- β -glucanosyltransferase)	AFUA_2G01170	452	7
Crf1/Aspf9 (Cell wall glucanase)	AFUA_1G16190	395	2
Pst1 (GPI-anchored cell wall protein)	AFUA_6G10290	406	8
Sod3/Aspf6 (Manganese superoxide dismutase)	AFUA_1G14550	210	3
Shm2 (Serine hydroxymethyltransferase)	AFUA_3G09320	471	2
Aspf2 (Allergen, expressed in zinc-limiting conditions)	AFUA_4G09580	310	3
	AFUA_4G13170	316	5
CpcB (RACK1 ortholog)	AFUA_5G13450	256	3
TpiA (Triosephosphate isomerase)	AFUA_6G02280	438	3
Aspf3 (Peroxiredoxin family reductase)	AFUA_6G09740	334	3
GliT (Gliotoxin oxidase)	AFUA_3G02270	728	3
CatB (Catalase B)	AFUA_1G04130	307	5
FG-GAP (FG-GAP repeat protein)			
(C) <i>E. coli</i> proteins			Total: 24
Surface antigen	SYX50777.1	179	1
clpG surface antigen	AAA23585.1	278	1
Surface antigen	EFX23024.1	577	7
Capsular polysaccharide	ALY13557.1	540	8
Capsular polysaccharide	GCO29334.1	248	4
Lipopolysaccharide 1,2-glucosyltransferase RfaJ	WP_032226820.1	338	3

Table S5. Nucleotide lengths of mitochondrial gene sequence collated from published and transcriptomic data. These sequences were concatenated to generate the species phylogeny shown in Figure 3.

Species name	GenBank ID of mitochondrial genome	Nucleotide length												Concatenated nucleotide length
		ND1	ND3	ND4	ND4L	ND5	ND6	COX1	COX2	COX3	ATP6	ATP8	CYTB	
<i>Alytes obstetricans pertinax</i>	NC_006688.1	960	342	1377	294	1806	507	1548	687	783	681	165	1140	10290
<i>Andrias davidianus</i>	NC_004926.1	969	348	1374	294	1809	516	1548	687	783	681	165	1140	10314
<i>Ascaphus truei</i>	AJ871087.1	969	348	1371	294	1800	507	1548	687	783	681	165	1140	10293
<i>Bombina fortinuptialis</i>	NC_006402.1	960	342	1377	294	1806	507	1551	687	783	681	165	1140	10293
<i>Bombina maxima</i>	NC_011049.1	960	339	1377	294	1806	546	1551	687	783	681	165	1140	10329
<i>Bombina orientalis</i>	NC_006689.1	960	342	1377	294	1806	507	1551	687	783	681	165	1140	10293
<i>Bombina variegata</i>	NC_009258.1	960	342	1377	294	1806	507	1551	687	783	681	165	1140	10293
<i>Buergeria buergeri</i>	AB127977.1	963	342	1365	282	1788	489	1548	684	783	681	162	1167	10254
<i>Bufo gargarizans</i>	NC_008410.1	960	339	1362	297	1788	492	1539	687	783	681	162	1143	10233
<i>Bufo melanostictus</i>	NC_005794.2	960	339	1362	297	1788	492	1539	687	783	681	162	1143	10233
<i>Discoglossus galganoi</i>	NC_006690.1	963	342	1377	294	1815	507	1551	687	783	681	165	1140	10305
<i>Euphylyctis hexadactylus</i>	NC_014584.1	960	339	1353	279	1845	483	1548	678	783	681	159	1140	10248
<i>Fejervarya cancrivora</i>	NC_012647.1	954	342	1359	276	1803	486	1533	681	783	681	162	1134	10194
<i>Fejervarya limnocharis</i>	NC_005055.1	957	342	1350	276	1800	486	1533	681	783	681	159	1134	10182
<i>Glandirana emeljanovi</i>	KF771343.1	960	339	1359	282	1788	495	1548	687	783	681	162	1140	10224
<i>Glandirana rugosa</i>	KF771341.1	960	339	1359	282	1788	495	1548	687	783	681	162	1140	10224
<i>Glandirana tientaiensis</i>	KF771342.1	960	339	1359	282	1788	492	1548	687	783	681	162	1140	10221
<i>Bufo japonicus</i>	NC_009886.1	960	339	1362	297	1800	492	1539	687	783	681	162	1143	10245
<i>Hoplobatrachus tigerinus</i>	NC_014581.1	960	339	1356	279	1824	483	1548	681	783	681	159	1143	10236
<i>Hymenochirus boettgeri</i>	NC_015615.1	966	342	1377	294	1815	513	1545	687	783	657	165	1140	10284
<i>Hyla chinensis</i>	NC_006403.1	960	339	1362	300	1788	495	1539	687	783	681	162	1146	10242
<i>Dryophytes japonicus</i>	NC_010232.1	960	339	1362	300	1800	495	1539	687	783	681	162	1146	10254
<i>Kaloula pulchra</i>	NC_006405.1	957	339	1359	282	1791	501	1548	687	783	681	162	1140	10230
<i>Leiopelma archeyi</i>	NC_014691.1	966	348	1377	294	1824	507	1548	687	783	681	162	1140	10317
<i>Limnonectes fujianensis</i>	AY974191.2	954	324	1365	282	1824	489	1536	684	783	681	159	1239	10320
<i>Mantella madagascariensis</i>	NC_007888.1	960	339	1362	279	1794	486	1548	687	783	681	162	1140	10221
<i>Microhyla heymonsi</i>	NC_006406.1	957	339	1359	282	1761	498	1548	687	783	681	162	1143	10200
<i>Microhyla okinavensis</i>	NC_010233.1	957	339	1362	282	1803	498	1548	687	783	681	162	1140	10242
<i>Microhyla ornata</i>	NC_009422.1	957	339	1362	282	1791	501	1548	687	783	681	162	1143	10236
<i>Nanorana pleskei</i>	NC_016119.1	957	357	1362	282	1821	495	1548	684	783	681	159	1143	10272
<i>Occidozyga martensii</i>	NC_014685.1	960	342	1365	276	1806	489	1545	687	783	681	159	1134	10227
<i>Odorrana ishikawae</i>	NC_015305.1	960	339	1365	282	1800	498	1548	687	783	675	165	1137	10239
<i>Amolops tormotus</i>	NC_009423.1	960	309	1365	282	1788	498	1551	687	783	675	165	1143	10206
<i>Pelophylax chosonicus</i>	NC_016059.1	960	339	1359	282	1791	498	1536	687	783	681	162	1140	10218
<i>Pelobates cultripes</i>	AJ871086.1	972	342	1377	294	1818	507	1551	681	783	681	165	1140	10311
<i>Pelophylax nigromaculatus</i>	NC_002805.1	960	339	1359	282	1794	498	1536	687	783	681	162	1140	10221
<i>Pelophylax plancyi</i>	NC_009264.1	960	339	1359	282	1794	498	1536	687	783	681	162	1140	10221

<i>Pipa carvalhoi</i>	NC_015617.1	963	342	1377	294	1809	510	1548	687	783	681	165	1140	10299
<i>Pipa pipa</i>	GQ244477.1	963	342	1377	294	1809	504	1545	687	783	681	165	1140	10290
<i>Pseudhymenochirus merlini</i>	NC_015618.1	963	342	1374	294	1809	516	1545	684	783	681	165	1137	10293
<i>Quasipaa spinosa</i>	NC_013270.1	954	339	1362	282	1821	495	1548	684	783	681	159	1143	10251
<i>Rana adenopleura</i>	JX033120.1	960	339	1362	282	1797	498	1548	687	783	675	162	1140	10233
<i>Lithobates catesbeianus</i>	KF049927.1	960	339	1359	282	1809	498	1551	687	783	678	159	1140	10245
<i>Rana kunyuensis</i>	KF840516.1	957	339	1359	282	1809	492	1551	684	783	681	159	1140	10236
<i>Rana dybowskii</i>	KF898355.1	957	339	1359	282	1791	492	1548	687	783	681	159	1140	10218
<i>Rana sylvatica</i>	KP222281.1	960	339	1359	282	1791	498	1551	687	783	681	159	1140	10230
<i>Rhinophrynus dorsalis</i>	NC_015620.1	963	342	1377	294	1821	507	1551	687	783	681	165	1140	10311
<i>Rhacophorus schlegelii</i>	NC_007178.1	960	342	1362	282	1794	486	1551	681	783	621	162	1143	10167
<i>Xenopus laevis</i>	NC_001573.1	969	342	1383	294	1812	510	1554	687	780	678	165	1137	10311
<i>Xenopus tropicalis</i>	NC_006839.1	966	342	1377	294	1815	516	1554	687	783	681	165	1140	10320
PRESENT STUDY:														
<i>Bufo japonicus</i>		969	342	1374	300	1798	495	1555	688	786	684	165	1143	10299
<i>Fejervarya kawamurai</i>		960	342	1362	279	1820	363	1548	682	786	684	165	1139	10130
<i>Hyla japonica</i>		969	339	1374	303	1812	498	1554	688	786	684	165	1143	10315
<i>Glandirana rugosa</i>		966	342	1370	285	1798	498	1558	495	626	684	165	1036	9823
<i>Rana japonica</i>		966	342	1368	294	1789	495	1557	572	772	684	165	705	9709
<i>Rana ornativentris</i>		966	342	1368	294	1800	495	1551	688	786	524	165	1143	10122
<i>Rana tagoi tagoi</i>		966	342	1364	294	1792	495	1557	657	786	684	165	1143	10245
<i>Pelophylax nigromaculatus</i>		966	342	1345	285	1792	501	1040	688	786	684	165	1142	9736
<i>Pelophylax porosa</i>		969	342	1353	300	1798	495	1554	688	786	684	165	1143	10277
<i>Buergeria buergeri</i>		960	342	1369	285	1800	492	1557	688	786	684	165	1143	10271
<i>Buergeria japonica</i>		960	342	1372	279	1789	492	1525	688	786	606	165	1141	10145

Species names in bold indicate overlap between publically available mitochondrial genome sequences and the present study. Nucleotide lengths in bold indicate incompletely mapped genes from our transcriptome data.

Table S6. Chi-square analyses of MHC class I supertypes and assumed/reported Bd susceptibility.

Observed no. of alleles				
MHC-I				
supertype	Susceptible	Tolerant	Resistant	Total
ST-A	11	32	35	78
ST-B	7	19	100	126
ST-C	0	5	0	5
ST-D	0	13	56	69
Total	18	69	191	278
Expected no. of alleles				
MHC-I				
supertype	Susceptible	Tolerant	Resistant	Total
ST-A	5.05	19.36	53.59	78
ST-B	8.16	31.27	86.57	126
ST-C	0.32	1.24	3.44	5
ST-D	4.47	17.13	47.41	69
Total	18	69	191	278
Chisq p-value	3.044E-09			

