Transcriptomic-proteomic correlation in the predation-evoked venom of the cone snail, *Conus imperialis*

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List of supporting information provided

Supplementary Table 1: 62 sequences common between two *C. imperialis* specimens.

Supplementary Table 2: Sequences validated by MS/MS.

Supplementary Table 3: Assembly of *C imperialis* venom duct for specimen 1 (S1) and specimen 2 (S2).

Supplementary Table 4: Comparison of assembled and raw data from two assemblers.

Supplementary Report: AGRF RNA quality measurement (2100 expert_mRNA Pico_DE54700697).

Supplementary Table 1: 62 sequences identified in both *C. imperialis* specimens.

Name by superfamily	**Precursor sequence**	**S1***	**S2***
A_1	MGMRMMFTVFLLVVLATTVVPITLASATDGRNAAADARMSPLISKFKKDYCHKYGYTIG	360	1689
A_2	MGMRMMFTVFLLVVLATTVVPITLASATDGRNAAANARVSPVISKFSKKWCHPNPYTVG	437	1665
A_3_Bn1.3	MGMRMMFTVFLLVVLATAVLPVTLDRASDGRNAAANAKTPRLIAPFIRDYCCHRGPCMVWCG	245	516
A_4	MGMRMMFTVFLLVVLATAVLPVTLDRASDGRNAAANAKTARLIAPFIRDYCCHRGPCMVWCG	2	526
A_5	MGMRMMFTVFLLVVLATTVVSITLDRASDGRNATVDNQLSALIGSPLSVWWKLHLLKHPLNHDKSPSA	52	47
A_6	MGMRMMFTVFLLVVLATTVVPITLASATDGRNAAADARMSPLISKFKRIIVISMVTLLGK	10	34
A_7	MGMRMMFTVFLLVVLATTVVPITLASATDGRNAAANARVSPVISKFSKNGVIRILTLWGK	9	28
A_8	MGMRMMFTVFLLVVLATTVVPITLASATDGRNAAADARMSPLISKFKKGLLS	3	16
A_9	MGMRMMFTVFLLVVLATTVVPITLASATDGRNAAANARVSPVISKFSKKWCHPNPYTVGK	2	14
A_10	MGMRMMFTVFLLVVLATTVVPITLASATDGRNAAANARVSPVISKFSRNGVIRILTLWGK	2	14
A_11	MGMRMMFTVFLLVVLATAVLPVTLDRASDEECSSQRQNASPDRAIHQGLLLS	2	9
A_12	MGMRMMFTVFLLVVLATTVVPITLASATDGRNAAADARMSPLISKLQKGLLS	2	6
A_13	MGMRMMFTVFLLVVLATTVVPITLASATDGRNAAADARMSPLISKFKKDYVISMVTLLGK	3	3
A_14	MGMRMMFTVFLLVVLATTVVPITLASATDGRNAAADARMSPLISKIQKRIIVISMVTLLGK	2	3
A_15	MGMRMMFTVFLLVVLATTVVPITLASATDGRNAAANARVSPVISKFSRNGVIRILTLWGNKAAAAAGPSEPRPAALCLTCFTFCLFVPLELNNLIH	2	3
D_1_Lt15.5	MPKLEMMLLVLLILPLCYIDAVGPPPPWNMEDEIIEHWQKLHCHEISDLTPWILCSPEPLCGGKGCCAQEVCDCSGPVCTCPPCL	438	1856
D_2	MPKLEMMLLVLLILPLCYIDAGPPPPWNMEDEIIEHWQKLHCHEISDLTPWILCSPEPLCGGKGCCAQEVCDCSGPVCTCPPCL	6	32
D_3	MPKLEMMLLVLLILPLCYIDAVGPPHHGTWKMKLLNIGKSFIVMKFQISHHGYCAARNHFAVEKAAVPRKSATALDQFVHARHVYSCSAHSPFSFPHDLALRKEPIKEQLQALRHI	4	12
D_4	MPKLEMMLLVLLILPLCYIDAVGPRHHGTWKMKLLNIGKSFIVMKFQISHHGYCAARNHFAVEKAAVPRKSATALDQFVHARHVYSCSAHSPFSFPHDLALRKEPIKEQLQALRHI	2	4
E_1	MMMRVFIAMFFLLALVEAGWPRLYDKNCKKNILRTYCSNKICGEATKNTNGELQCTMYCRCANGCFRGQYIDWPNQQTNLLFC	65	103
E_2	MMMRVFIAMFFLLALVEAGWPRLYDKNCRKTYCAPTAQIRYVERQRRIRMGNFSAPCTVGVQTAVFAVNTSIGPISRPISSSARPGFDHCLRRRERKWLM	7	12
E_3	MMMRVFIAMFFLLALVEAGWPRLYDKNCKKTYCAPTAQIRYVERQRRIRMGNFSAPCTVGVQTAVFAVNTSIGPISRPISSSARPGFDHCLRRRERKWLM	7	10
I1_1	MKLALTFLLILMILPLMTGEKTSDDLELRGVESLRAIFRDRRCSDNIGATCSDRFDCCGSMCCIGGQCVVTFAECS	6	28
I2_1	MFRVTSVLLVIVLLNLVVLTNACHMDCSKMTCCSGICCFYCGRPMCPGTRRALLQRLVGHQR	141	740
I2_2	MFRLTSVGCILLVIAFLNLVGLTNACTSEGYSCSSDSNCCKNVCCWNVCESHCRHPGKRTRLQGFFKHRR	161	257
I2_3	MFRVTSVLLVIVLLNLVVLTNACHMDCSKMTCCSGICCFTADVLCVLALGGRYSKD	17	85
I2_4	MFRLTSVGCILLVIAFLNLVGLTNACTSEGYSCSSDSNCCKMCAVGMYAKVTVDILERGRDSKDSLNIDVDMLPRGLLLFVVNGR	7	4
K_1_Im23b	MIMRMTLTLFVLVVMTAASASGDALTEAKRIPYCGQTGAECYSWCIKQDLSKDWCCDFVKTIARLPPAHICSQ	155	348
K_2_Im23a	MIMRMTLTLFVLVVMTAASASGDALTEAKRIPYCGQTGAECYSWCIKQDLSKDWCCDFVKDIRMNPPADKCP	105	174
K_3	MIMRMTLTLFVLVVMTAASASGDALTEAKRVPYCGQTGAECYSWCKEQHLIRCCDFVKYVGMNPPADKCR	60	109
K_4	MIMRMTLTLFVLVVMTAASASGDALTEAKRIPYCGQTGAECYSWCIKQDLSKDWCCDFVKDIRMNPRLTNVRNDCCSMP	12	12
K_5	MIMRMTLTLFVLVVMTAASASGDALTEAKRVPYCGQTGAECYSWCKEQHLIRCCDFVKYVGMNPRLTNVGNDCCSMP	7	11
K_6	MIMRMTLTLFVLVVMTAASASGDALTEAKRIPYCGQTGAECYSWCIKQDLSKAGVVISSRL	2	2
M_1	MMSTLVVLLTICLLMLPLTARQLDADQLADQLAERMEDISADQNRWFDPVKRCCMRPICMCPCCVNG	238	343
M_2_Eu3.3	MMSKLGVLLAICLLMLPLTALPLDGDQPQERKEDGKSAALQPWFDPVKRCCQAACSPWLCLPCCG	19	43
M_3_Bt3.1	MMSTLGVLLTIGLLLFPLTALPLDGDQPADQPAERLQDISPKEIPGSDPFKRCCHAPYCTPPHLGCPCCGK	41	25
M_4	MSKVGVVPLIFLVLLSIAALQNGDDPRRQRDEKQSPQGDILRSTLTKYSYNIQRRCWAGGSPCHLCSSSQVCIAPTGHPAIMCGRCVPILT	2	9
M_5	MSKVGVVPLIFLVLLSIAALQNGDDPRRQRDEKQSPQGDILRSTLTKYSYNIQRRCWAGAHPATCAAAVKFASRRLDTQQ	5	5
N_1	MSTLGMMLLILLLLVPLATFADDGPTMRGHRSAKLLAHTTRDSCPSGTNCPSKICCNGNCCSKSSCRCETNQATKERVCVC	16	6
O1_1_Conotoxin3	MKLRCMMIVAVLFLTASIFITADNSRNGIENLPRMRRHEMKKPKASKLNKRGCLPDEYFCGFSMIGALLCCSGWCLGICMT	6	18
O2_1_im6.2	MKLTILLLVAALLVLTQARTERRRVKSRKTSSTYDDEMATFCWSYWNEFQYSYPYTYVQPCLTLGKACTTNSDCCSKYCNTKMCKINWEG	188	481
O2_2	MKLTILLLVAALLVLTQARTERRRVKSRKTSSTYDDEMATFCGLIGMNFNIHIHIHMYNHALLWARLVRRTRIVVPSTVTPRCARLIGRDEPQTIRHHHSSLQRLQRLLFSV	3	17
O2_3	MEKLTILLLVTAVLMSTQALMQSGIEKRQRAKIKFFSKRKTTAERWWEGECYDWLRQCSSPAQCCSGNCGAHCKAW	8	9
P_1	MHLSLASSAALMLLLLFALGNFVGVQPGQIRDLNKGQLKDNRRNLQSQRKQMSLLKSLHDRNGCNGNTCSNSPCPNNCYCDTEDDCHPDRREH	38	56
P_2	MHLSTASSVALMFFLLFAFYGVQPELMTRDVDNGQLTDNRRNLRSRVKPTGLFKSRKPSEDCGKTCETAENCPDDCSSCLSVEGTYRCA	39	23
P_3	MHRSLAGSAVLMLLLLFALGNFVGVQPGLVTRDADNGQLMDNRRNLRLERKTMSLFKSLDKRADCSTYCFGMGICQSGCYCGPGHACMPNGR	15	20
P_4	MHLSLASSAALMLLLLFALGNFVGVQPGQIRDLNKGQLKDNRRNLQSQRKQMSLLKSLHDRNGCNGNTCSNTPLP	2	3
T_1_Im5.4	MRCLPVVVFLLLLLSAAAAPGVGSKTERLPGLTSSGDSDESLPFLNTICCWSGACCGG	494	1027
T_2	MCCIPVFFILLLLIPSAPSILAQPTTKGDVALASSYDDAKRTLQRLSIKYSCCPGIVSCCVIP	42	199
T_3	MRCLPVFIILLLLIPSAPSLTAQIKVKTNSSEASSHGNAKRTLQRLSTRIERCCPMEDRP	5	31
T_4	MRCLPVVVFLLLLLSAAAAPGVGSKTERLPGLTSSGDSDESLPFLNTILLLVRRLLWWLT	7	20
T_5	MRCLPVVVFLLLLLSAAAAPGVGSKTERLPGLTSSGDSDESLPFFEYNLLLVRRLLWWLT	16	19
T_6	MRCLPVVVFLLLLLSAAAAPGGRIENRKASRAHIIRRFRRESPLFEYNLLLVRRLLWWLT	2	7
T_7	MRCLPVVVFLLLLLSAAAAPGVGSKNRKASRAHIIRRFRRESPLFEYNLLLVRRLLWWLT	2	5
T_8	MRCLPVVVFLLLLLSAAAAPGVGSKTEGFQGSHHPEIPTRVSPFEYNLLLVRRLLWWLT	4	5
T_9	MRCLPVVVFLLLLLSAAAAPGSDRNRKASRAHIIRRFRRESPLFEYNLLLVRRLLWWLT	2	3
T_10	MRCLPVVVFLLLLLSAAAAPGVGSKPKASRAHIIRRFRRESPLLNTICCWSGACCGG	2	3
SF-im1_1	MARFLSILLCFAMATGLAAGIRYPDRVLGRCSTHDLSKMEIDTNLDGVYSPHRSFCTCGSGEVYFTAKDRRNHSNYRVYVCGMPTEFCTAENPVRDPKKGNRWLQCRCRQYKMVIYRDWLVLCE	7	25
SF-im2_1	MRLTTMHSVILMLLLVFAFDNVDGDEPGQTARDVDNRNFMSILRSEGKPVHFLRAIKKRDCTGQACTTGDNCPSECVCNEHHFCTGKCCYFLHA	14	31
SF-im3_1	MSKSGMLLFVLLLLLPLAIPELAPAGRSVTHHFRDFGAKRSVPISCVNPSTPNLQGSWQDKKCCSTKLCSPTNCCESSTCSCVEGSCQCL	4	55
SF-im4_1	MKFFTCLLLLLVVLTVVFDNVDACDRSCTGVMGHPSCATCCACFTSAGKRHADGQHSRMKVRTGAKNLLKRMPLH	5	27
SF-im5_1	MKTGMIICLLLIAFMDADGSPGDTLYSQKTADTDSGMKRFQKTFQKRRCVFCPKEPCCDGDQCMTAPGTGPFCG	2	10

*** The values in these couloumns refer to the read numbers of each paralog found in the transcriptomic analysis for each specimen**

Supplementary Table 2: Sequences validated by MSMS (99% confidence)

Name by superfamily	**Seq number**	**MS/MS (> 99% conf)**	**Fixed modification**	**Enzyme Digestion**	**PTMs**	**Prec MW**	**z**
A_3_Bn1.3	>im003	DYCCHR	Ethanolyl	Trypsin		883.34	2
D_1_Lt15.5	>im004	ILCSPEPLCGGK	Ethanolyl	Trypsin		1303.66	2
E_1	>im005	NTNGELQCTMYCR	Ethanolyl	Trypsin		1619.69	2
I1_1	>im006	CSDNIGATCSDR	Ethanolyl	Trypsin		1328.54	2
I2_1	>im007	MTCCSGICCFYCGR	Ethanolyl	Trypsin		1765.69	2
I2_2	>im008	NVCCWNVCESHCR	Ethanolyl	Trypsin		1727.7	3
K_1_Im23b	>im009	LPPAHICSQ	Ethanolyl	Trypsin		1008.52	2
K_2_Im23a	>im010	MNPPADKCP	Ethanolyl	Trypsin		1015.47	2
K_3	>im011	YVGMNPPADK		Trypsin		1090.54	2
M_1	>im012	CCMRPICMCPCCVN	Ethanolyl	Trypsin	Hyp@10, Amidated@C-term	1853.85	2
M_4	>im015	CWAGGSPCHLCSSSQVCIAPTGHPAIMCGR	Ethanolyl	Trypsin	Hyp@7, HyP@20	2181	3
N_1	>im016	ICCNGNCCSKSSCR	Ethanolyl	Trypsin		1724.69	2
O2_1_im6.2	>im018	ACTTNSDCCSK	Ethanolyl	Trypsin		1263.49	2
O2_3	>im019	QCSSPAQCCSGNCGAHCK	Ethanolyl	Trypsin	Hyp@5	2018.78	3
P_3	>im022	ADCSTYCFGMGICQSGCYCGPGHACMPN	Ethanolyl	Trypsin	M(oxi)@26, Amidated@C-term	3154.23	3
T_1_Im5.4	>im023	FLNTICCWSGACCG	Ethanolyl	Trypsin	Amidated@C-term	1651.79	2
SF-im1_1	>im025	VYVCGMPTEFCTAENPVRDPK	Ethanolyl	Trypsin		2443.33	2
SF-im2_1	>im026	EHHFCTGK	Ethanolyl	Trypsin	PyroGlu@N-term	983.45	2
SF-im4_1	>im028	CDRSCTGVMGHPSCATCCACFTSA	Ethanolyl	Trypsin	Hyp@12, Amidated@C-term	2689.09	3
SF-im5_1	>im029	CVFCPK	Ethanolyl	Trypsin		783.37	2
SF-im6_1	>im031	TGECDKNPGYMVNH	Ethanolyl	Trypsin		1607.68	3

Supplementary Table 3: Assembly of *C imperialis* venom duct for specimen 1 (S1) and specimen 2 (S2).

IMP S1 (Total De-multiplexed 249,349 and total assembled 198,889)

	Raw Reads	***Newbler Contigs***	***Newbler Isotigs***	***Trinity***
# Sequences	220,516	703	473	1,594
Length Interval	24-770	1-3,060	58-3,060	101-3,075
Average Length	396.70	436.81	709.57	481.38
N50	459	700	770	502
N75	504	1,197	1,301	818
N90	528	1,690	1,723	1,387
%GC	52.41	47.67	47.04	46.30
%N	0	0	0	0
Total # bases	87,478,648	307,076	335,626	767,323

IMP S2 (Total De-multiplexed 379,998 and total assembled 281,952)

	Raw Reads	***Newbler Contigs***	***Newbler Isotigs***	***Trinity***
# Sequences	332,390	2,256	1,386	6,021
Length Interval	22-737	1-6,389	26-6,389	101-6,994
Average Length	393.38	463.77	816.63	497.22
N50	459	824	953	521
N75	503	1,382	1,619	868
N90	527	2,218	2,513	1,428
%GC	50.62	46.59	46.36	45.34
%N	0	0	0	0
Total # bases	130,754,372	1,046,266	1,131,845	2,993,735

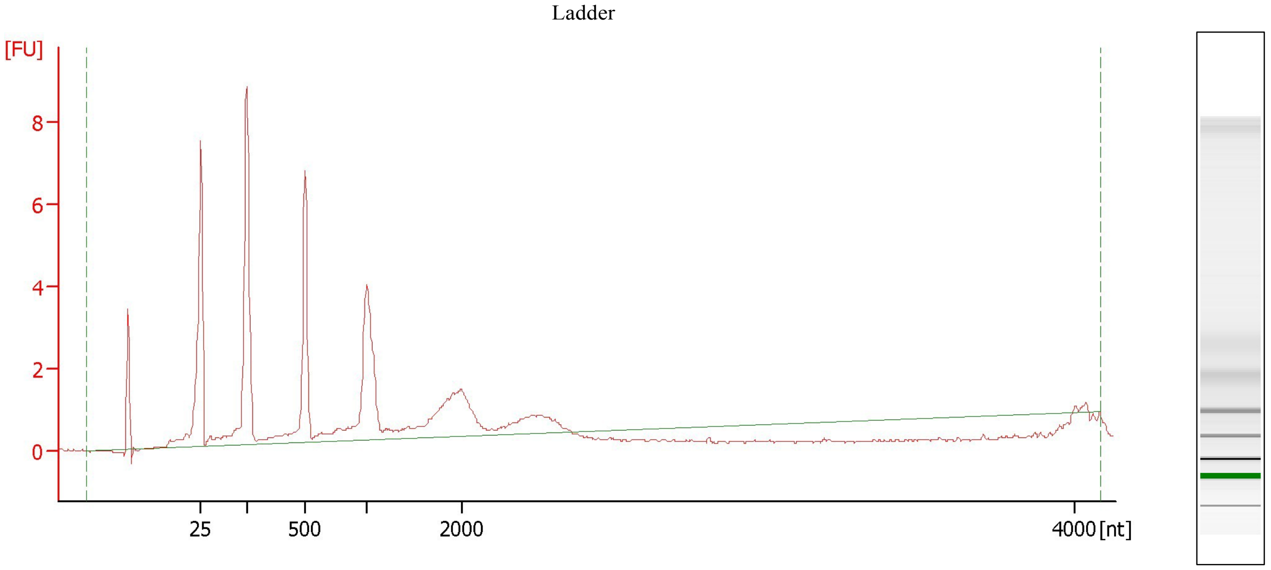
Supplementary Table 4: Comparison of assembled raw data from two assemblers. Detected sequences (Y) and undetected sequences (N) have been highlighted along with their subsequent detection in the MSMS spectra.

	Newbler assmebly		**Trinity assembly**		**Raw reads**		
Name by superfamily	**S1**	**S2**	**S1**	**S2**	**S1**	**S2**	**MSMS**
A_1	N	N	Y	Y	360	1689	
A_2	Y	N	N	N	437	1665	
A_3_Bn1.3	Y	N	N	Y	245	516	Y
A_4	N	N	N	N	2	526	
A_5	Y	N	N	N	52	47	
A_6	N	N	N	N	10	34	
A_7	N	N	N	N	9	28	
A_8	N	N	N	N	3	16	
A_9	N	N	N	N	2	14	
A_10	N	N	N	N	2	14	
A_11	N	N	N	N	2	9	
A_12	N	N	N	N	2	6	
A_13	N	N	N	N	3	3	
A_14	N	N	N	N	2	3	
A_15	N	N	N	N	2	3	
D_1_Lt15.5	Y	Y	Y	Y	438	1856	Y
D_2	N	N	N	N	6	32	
D_3	N	N	N	N	4	12	
D_4	N	N	N	N	2	4	
E_1	Y	Y	Y	N	65	103	Y
E_2	N	N	N	N	7	12	
E_3	N	N	N	N	7	10	
I1_1	Y	Y	Y	Y	6	28	Y
I2_1	Y	Y	Y	Y	141	740	Y
I2_2	N	N	Y	Y	161	257	Y
I2_3	N	N	N	N	17	85	
I2_4	N	N	N	N	7	4	
K_1_Im23b	Y	Y	Y	Y	155	348	Y
K_2_Im23a	Y	Y	N	N	105	174	Y
K_3	Y	Y	N	N	60	109	Y
K_4	N	N	N	N	12	12	
K_5	N	N	N	N	7	11	
K_6	N	N	N	N	2	2	
M_1	Y	Y	Y	Y	238	343	Y
M_2_Eu3.3	N	Y	N	N	19	43	
M_3_Bt3.1	N	Y	N	N	41	25	
M_4	N	N	N	Y	2	9	Y
M_5	N	N	N	N	5	5	
N_1	Y	N	Y	N	16	6	Y
O1_1_Conotoxin3	N	N	N	Y	6	18	
O2_1_im6.2	Y	Y	Y	Y	188	481	Y
O2_2	N	N	N	N	3	17	
O2_3	Y	N	Y	Y	8	9	Y
P_1	Y	Y	Y	Y	38	56	
P_2	N	N	Y	N	39	23	
P_3	Y	Y	Y	Y	15	20	Y
P_4	N	N	N	N	2	3	
T_1_Im5.4	Y	N	Y	Y	494	1027	Y
T_2	N	N	Y	N	42	199	
T_3	N	Y	N	N	5	31	
T_4	N	N	N	N	7	20	
T_5	N	N	N	N	16	19	
T_6	N	N	N	N	2	7	
T_7	N	N	N	N	2	5	
T_8	N	N	N	N	4	5	
T_9	N	N	N	N	2	3	
T_10	N	N	N	N	2	3	
SF-im1_1	Y	N	N	N	7	25	Y
SF-im2_1	N	N	N	Y	14	31	Y
SF-im3_1	N	Y	Y	Y	4	55	
SF-im4_1	N	N	N	N	5	27	Y
SF-im5_1	N	Y	N	Y	2	10	Y
	18	16	15	18			
S2 only							

S_1	N	N	N	N	0	10	
SF-im6_1	N	Y	N	N	0	6	Y
S1 only							
T-**S1**	N	N	N	N	41	0	Y

Note: Absent sequences after assembly had been unambiguously confirmed by MSMS, highlighting a major issue with current assembly algorithms, as this approach can eliminate valid sequences.

Electropherogram Summary



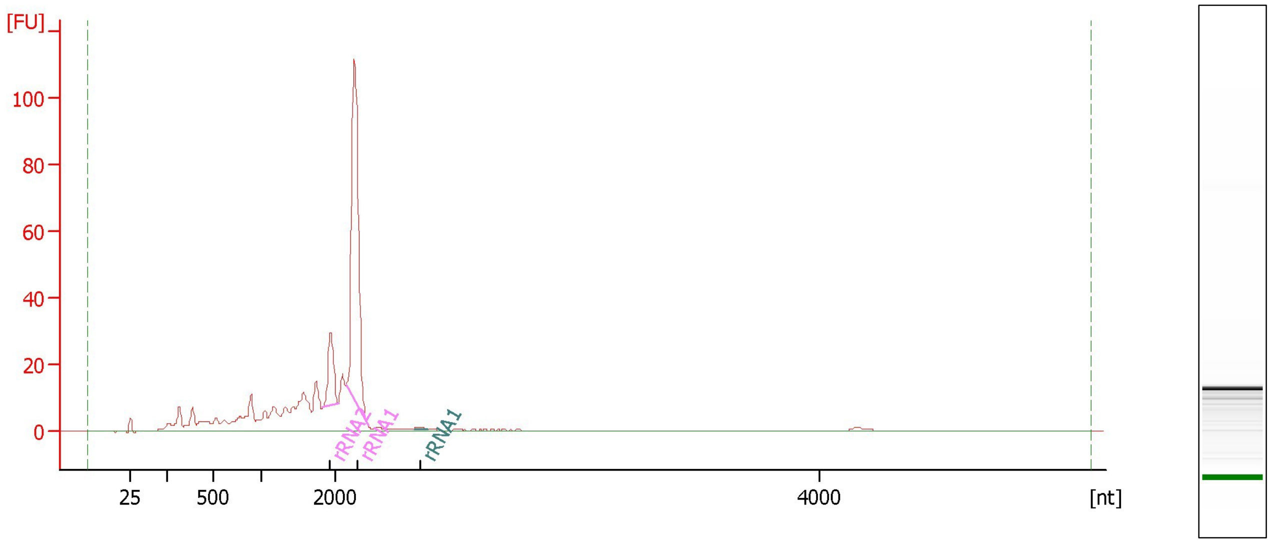
Overall Results for Ladder

RNA Area:	52.0	RNA Concentration:	1,000 pg/µl

Assay Class:	mRNA Pico	Created:	1/16/2013 2:44:32 PM
Data Path:	C:\...16\2100 expert_mRNA Pico_DE54700697_2013-01-16_14-44-32.xad	Modified:	1/16/2013 3:08:43 PM

Electropherogram Summary Continued ...

SDIMPSMA - 1:10



Overall Results for sample 3 : **SDIMPSMA - 1:10**

RNA Area:	498.8	rRNA Contamination:	38.4 %
RNA Concentration:	9,600 pg/µl		

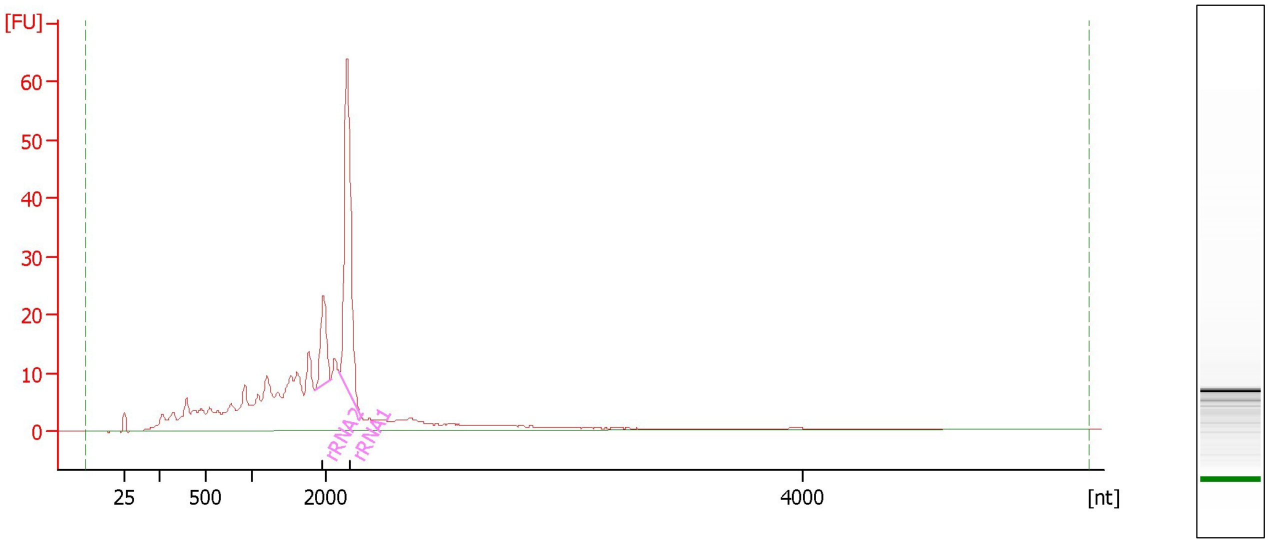
Fragment table for sample 3 : **SDIMPSMA - 1:10**

Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	1,830	2,011	29.7	6.0
rRNA1	2,045	2,136	161.0	32.3
rRNA1	2,324	2,379	0.6	0.1

Assay Class:	mRNA Pico	Created:	1/16/2013 2:44:32 PM
Data Path:	C:\...16\2100 expert_mRNA Pico_DE54700697_2013-01-16_14-44-32.xad	Modified:	1/16/2013 3:08:43 PM

Electropherogram Summary Continued ...

SDIMPMED - 1:10



Overall Results for sample 4 : SDIMPMED-1:10

RNA Area:	435.2	rRNA Contamination:	24.9 %
RNA Concentration:	8,377 pg/µl		

Fragment table for sample 4 : SDIMPMED-1:10

Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	1,862	2,022	22.3	5.1
rRNA1	2,056	2,146	85.9	19.7