The Open Biochemistry Journal, 2012, *6*, i-xxxvii

SUPPLEMENTAL DATA

ADDITIONAL SUPPORTING INFORMATION MAY BE FOUND IN THE ONLINE VERSION OF THIS ARTICLE

Table S1. Supplementary Data: Listing Primers for Genes Sequences Coding for Identified Proteins in the Carotenoid-protein Complex Used for their Expression Analysis Across Distinct Genotypes of Cassava using RT_PCR

Protein ID	EST ID in ESTIMA Data Base	Primer Name	Strand	Primer Sequence	gc%	Amplicon Size (bp)
Fibrillin	cassava.162.C1.Contig223	CasFibr_432RL	Reverse	CGGCGAGTCAAGAGTGAGCTGCCG	60	
Fibrillin	cassava.162.C1.Contig223	CasFibr_432FL	Forward	TCATGGTTGCTGACCACATACCT	48	107
Or-protein	cassava.695.C1.Contig835	CasDNAj.R	Reverse	CATGAAATCAAACAGCCCACG	48	
Or-protein	cassava.695.C1.Contig835	CasDNAj.F	Forward	ACAACAAGGCCCATGAGTCTGA	50	120
HSP 17.4	cassava.2670.C1.Contig2792	HSP17.4.R1.F	Forward	CACCATTTCCAGGAAAGTTTACCG	46	
HSP 17.4	cassava.2670.C1.Contig2792	HSP17.4.R1.R	Reverse	TGATGAGTGAGGTGCATGGAGA	50	115
HSP 17.6	Cassava.1764.C1.Contig1943	HSP17.6.R1.R	Reverse	CGGCGAGTCAAGAGTGAGCTGCCG	67	
HSP 17.6	Cassava.1764.C1.Contig1943	HSP17.6.R1.F	Forward	TCATGGTTGCTGACCACATACCT	48	89
HSP 18.1	Cassava.388.C1.Contig493	HSP18.1.R1.R	Reverse	CGGCGAGTCAAGAGTGAGCTGCCG	67	
HSP 18.1	Cassava.388.C1.Contig493	HSP18.1.R1.F	Forward	TCATGGTTGCTGACCACATACCT	48	92
HSP21	Cassava.1282.C1.Contig1455	HSP21.F	Reverse	CGGCGAGTCAAGAGTGAGCTGCCG	70	
HSP21	Cassava.1282.C1.Contig1455	HSP21.R	Forward	TCATGGTTGCTGACCACATACCT	48	116

Table S2. Supplementary Data: Listing Peptides Sequences (MASCOT Quality) in the Carotenoid-protein Complex. SDS_PAGE Picture Shows the Gel Zone Fractionation of Separated Proteins used for the LC_MS/MS Analysis

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B2	gi|106778064	286	70.31	592.35	1182.69	1182.71	-0.02	0	70.31	0.00	4	NLQISILLNR
DCP1B1	gi|108897757	382	183.09	651.32	1300.63	1300.65	-0.02	0	71.09	0.00	1	ALEEANADLEVK
DCP1B3	gi|108897757	13	183.09	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|108897757	14	183.09	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|108897757	15	183.09	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B2	gi|108897757	17	183.09	405.22	808.42	808.43	-0.01	0	39.34	5.76	2	LASYLDK
DCP1B3	gi|108897757	128	183.09	497.25	992.48	992.49	-0.02	0	28.12	63.80	3	YENELGLR
DCP1B2	gi|108897757	129	183.09	497.25	992.48	992.49	-0.01	0	38.86	5.52	2	YENELGLR
DCP1B1	gi|108897757	130	183.09	497.25	992.49	992.49	-0.01	0	36.29	10.42	2	YENELGLR
DCP1B1	gi|10943042	26	142.62	421.26	840.50	840.51	-0.01	1	25.22	78.84	5	ADLPGLKK
DCP1B1	gi|10943042	117	142.62	487.77	973.53	973.53	0.00	1	35.74	13.59	2	FRLPENAK
DCP1B1	gi|10943042	567	142.62	586.64	1756.89	1756.90	0.00	1	29.75	26.18	3	VEVEEDRVLQISGER
DCP1B2	gi|10943042	74	142.62	451.25	900.49	900.50	-0.02	0	51.91	0.39	5	VLQISGER
DCP1B3	gi|10943042	75	142.62	451.25	900.49	900.50	-0.01	0	51.07	0.46	5	VLQISGER
DCP1B1	gi|10943042	76	142.62	451.26	900.50	900.50	-0.01	0	45.86	1.51	5	VLQISGER

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Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B1	gi|10943042	77	142.62	451.26	900.51	900.50	0.00	0	51.27	0.41	5	VLQISGER
DCP1B3	gi|110152466	306	57.73	599.28	1196.55	1196.55	0.00	1	9.12	3064.44	7	SARASWCFGR
DCP1B2	gi|110152466	269	57.73	584.85	1167.68	1167.69	-0.01	0	49.38	0.22	3	VLPSIGNEVLK
DCP1B2	gi|112211770	326	212.34	610.80	1219.58	1219.59	-0.02	0	28.03	47.51	1	ASLENSLEETK
DCP1B1	gi|112211770	327	212.34	610.80	1219.59	1219.59	-0.01	0	22.97	175.57	2	ASLENSLEETK
DCP1B2	gi|112211770	431	212.34	681.34	1360.67	1360.68	-0.01	0	50.20	0.34	1	EVATNSELVQSGK
DCP1B3	gi|112211770	432	212.34	681.35	1360.68	1360.68	-0.01	0	53.76	0.15	1	EVATNSELVQSGK
DCP1B1	gi|112211770	433	212.34	681.35	1360.69	1360.68	0.00	0	55.26	0.11	1	EVATNSELVQSGK
DCP1B3	gi|112211770	13	212.34	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|112211770	14	212.34	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|112211770	15	212.34	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B2	gi|112211770	230	212.34	561.79	1121.56	1121.57	-0.01	0	48.43	0.57	1	LEQEIATYR
DCP1B3	gi|112211770	231	212.34	561.79	1121.56	1121.57	-0.01	0	52.59	0.23	1	LEQEIATYR
DCP1B1	gi|112211770	153	212.34	515.30	1028.58	1028.59	0.00	0	42.66	2.00	2	VLDELTLAR
DCP1B2	gi|112211770	154	212.34	515.30	1028.59	1028.59	0.00	0	41.65	2.38	2	VLDELTLAR
DCP1B3	gi|112215081	13	217.98	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|112215081	14	217.98	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|112215081	15	217.98	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B2	gi|112215081	17	217.98	405.22	808.42	808.43	-0.01	0	39.34	5.76	2	LASYLDK
DCP1B1	gi|112215081	449	217.98	695.83	1389.65	1389.67	-0.02	0	52.57	0.15	1	QSLEASLAETEGR
DCP1B3	gi|112215081	450	217.98	695.83	1389.66	1389.67	-0.02	0	40.82	2.24	1	QSLEASLAETEGR
DCP1B3	gi|112215081	41	217.98	424.22	846.43	846.44	-0.02	0	38.38	10.25	6	SEITELR
DCP1B3	gi|112215081	155	217.98	516.30	1030.58	1030.59	-0.01	0	47.39	0.77	1	VLDELTLTK
DCP1B2	gi|112215081	156	217.98	516.30	1030.58	1030.59	-0.01	0	29.62	37.96	1	VLDELTLTK
DCP1B1	gi|112215081	157	217.98	516.30	1030.59	1030.59	0.00	0	53.89	0.11	1	VLDELTLTK
DCP1B2	gi|112745190	219	221.42	554.27	1106.52	1106.54	-0.02	0	47.65	0.57	1	AQYEEIAQR
DCP1B1	gi|112745190	220	221.42	554.27	1106.54	1106.54	0.00	0	48.46	0.55	1	AQYEEIAQR
DCP1B1	gi|112745190	244	221.42	571.26	1140.50	1140.51	-0.01	0	27.05	33.94	1	DYQELMNTK
DCP1B2	gi|112745190	114	221.42	487.26	972.51	972.52	-0.02	0	60.68	0.05	1	IEISELNR
DCP1B3	gi|112745190	115	221.42	487.26	972.51	972.52	-0.02	0	45.11	1.58	2	IEISELNR
DCP1B1	gi|112745190	510	221.42	508.60	1522.77	1522.78	-0.01	1	17.07	751.78	1	LLRDYQELMNTK
DCP1B2	gi|112745190	160	221.42	517.25	1032.49	1032.51	-0.02	0	42.71	2.16	1	TLLEGEESR
DCP1B3	gi|112745190	161	221.42	517.25	1032.49	1032.51	-0.02	0	68.16	0.01	1	TLLEGEESR
DCP1B1	gi|112745190	162	221.42	517.26	1032.50	1032.51	-0.01	0	50.62	0.40	1	TLLEGEESR
DCP1B1	gi|112745190	163	221.42	517.26	1032.50	1032.51	-0.01	0	49.33	0.53	1	TLLEGEESR
DCP1B2	gi|112749711	219	241.32	554.27	1106.52	1106.54	-0.02	0	47.65	0.57	1	AQYEEIAQR

Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B1	gi|112749711	220	241.32	554.27	1106.54	1106.54	0.00	0	48.46	0.55	1	AQYEEIAQR
DCP1B1	gi|112749711	484	241.32	738.39	1474.76	1474.78	-0.02	0	77.38	0.00	1	FLEQQNQVLQTK
DCP1B3	gi|112749711	485	241.32	738.40	1474.78	1474.78	0.00	0	27.99	48.59	3	FLEQQNQVLQTK
DCP1B2	gi|112749711	486	241.32	738.40	1474.78	1474.78	0.00	0	72.05	0.00	1	FLEQQNQVLQTK
DCP1B2	gi|112749711	114	241.32	487.26	972.51	972.52	-0.02	0	60.68	0.05	1	IEISELNR
DCP1B3	gi|112749711	115	241.32	487.26	972.51	972.52	-0.02	0	45.11	1.58	2	IEISELNR
DCP1B2	gi|112749711	448	241.32	692.34	1382.66	1382.68	-0.02	0	54.80	0.09	1	SLNNQFASFIDK
DCP1B3	gi|112758642	13	315.81	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|112758642	14	315.81	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|112758642	15	315.81	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B3	gi|112758642	265	315.81	583.29	1164.56	1164.58	-0.02	0	58.60	0.05	1	LENEIQTYR
DCP1B2	gi|112758642	266	315.81	583.29	1164.56	1164.58	-0.01	0	58.62	0.05	1	LENEIQTYR
DCP1B1	gi|112758642	267	315.81	583.30	1164.58	1164.58	0.00	0	60.25	0.04	1	LENEIQTYR
DCP1B1	gi|112758642	449	315.81	695.83	1389.65	1389.67	-0.02	0	52.57	0.15	1	QSLEASLAETEGR
DCP1B3	gi|112758642	450	315.81	695.83	1389.66	1389.67	-0.02	0	40.82	2.24	1	QSLEASLAETEGR
DCP1B3	gi|112758642	41	315.81	424.22	846.43	846.44	-0.02	0	38.38	10.25	6	SEITELR
DCP1B2	gi|112758642	434	315.81	683.31	1364.61	1364.63	-0.02	0	76.92	0.00	1	SQYEQLAEQNR
DCP1B1	gi|112758642	435	315.81	683.32	1364.62	1364.63	-0.01	0	65.35	0.01	1	SQYEQLAEQNR
DCP1B3	gi|112758642	436	315.81	683.32	1364.63	1364.63	0.00	0	68.15	0.00	1	SQYEQLAEQNR
DCP1B3	gi|112758642	155	315.81	516.30	1030.58	1030.59	-0.01	0	47.39	0.77	1	VLDELTLTK
DCP1B2	gi|112758642	156	315.81	516.30	1030.58	1030.59	-0.01	0	29.62	37.96	1	VLDELTLTK
DCP1B1	gi|112758642	157	315.81	516.30	1030.59	1030.59	0.00	0	53.89	0.11	1	VLDELTLTK
DCP1B1	gi|114214014	391	55.10	656.88	1311.74	1311.75	-0.01	0	55.10	0.07	1	VIQLETAAGAAIR
DCP1B1	gi|114723387	382	220.07	651.32	1300.63	1300.65	-0.02	0	71.09	0.00	1	ALEEANADLEVK
DCP1B1	gi|114723387	604	220.07	701.33	2100.98	2101.01	-0.03	0	10.20	1254.03	3	GQVGGDVNVEMDAALGVDLSR
DCP1B3	gi|114723387	13	220.07	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|114723387	14	220.07	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|114723387	15	220.07	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B2	gi|114723387	17	220.07	405.22	808.42	808.43	-0.01	0	39.34	5.76	2	LASYLDK
DCP1B1	gi|114723387	153	220.07	515.30	1028.58	1028.59	0.00	0	42.66	2.00	2	VLDELTLAR
DCP1B2	gi|114723387	154	220.07	515.30	1028.59	1028.59	0.00	0	41.65	2.38	2	VLDELTLAR
DCP1B2	gi|114723387	210	220.07	545.76	1089.50	1089.52	-0.02	0	22.98	156.65	2	VTMQNLNDR
DCP1B2	gi|114727069	211	124.00	547.26	1092.51	1092.52	-0.01	0	57.13	0.07	1	AQYEEIANR
DCP1B3	gi|114727069	264	124.00	583.29	1164.56	1164.58	-0.02	0	67.64	0.01	1	YEELQVTAGR
DCP1B1	gi|114727069	268	124.00	583.30	1164.58	1164.58	0.00	0	58.41	0.06	1	YEELQVTAGR

Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B3	gi|114747959	13	140.28	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|114747959	14	140.28	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|114747959	15	140.28	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B2	gi|114747959	230	140.28	561.79	1121.56	1121.57	-0.01	0	48.43	0.57	1	LEQEIATYR
DCP1B3	gi|114747959	231	140.28	561.79	1121.56	1121.57	-0.01	0	52.59	0.23	1	LEQEIATYR
DCP1B3	gi|114747959	155	140.28	516.30	1030.58	1030.59	-0.01	0	47.39	0.77	1	VLDELTLTK
DCP1B2	gi|114747959	156	140.28	516.30	1030.58	1030.59	-0.01	0	29.62	37.96	1	VLDELTLTK
DCP1B1	gi|114747959	157	140.28	516.30	1030.59	1030.59	0.00	0	53.89	0.11	1	VLDELTLTK
DCP1B1	gi|117909285	137	100.44	503.75	1005.49	1005.51	-0.02	0	38.78	6.14	1	GPGLYSDIGK
DCP1B1	gi|117909285	524	100.44	521.29	1560.83	1560.85	-0.02	1	61.66	0.02	1	KGELFVADVNTQLK
DCP1B2	gi|119005052	202	101.85	539.79	1077.56	1077.57	-0.01	0	48.39	0.65	1	AENLDYLIK
DCP1B1	gi|119005052	339	101.85	619.31	1236.60	1236.60	0.00	0	38.58	4.74	1	SLGADEVLDYR
DCP1B2	gi|119005052	340	101.85	619.31	1236.60	1236.60	0.00	0	53.46	0.16	1	SLGADEVLDYR
DCP1B2	gi|13264707	49	55.72	428.76	855.51	855.52	-0.01	0	55.72	0.08	2	LATVLSPR
DCP1B2	gi|14489238	50	131.71	429.73	857.45	857.46	-0.01	0	61.40	0.04	6	LLEVDNR
DCP1B2	gi|14489238	286	131.71	592.35	1182.69	1182.71	-0.02	0	70.31	0.00	1	LNQISILVQR
DCP1B2	gi|14924599	206	126.64	541.79	1081.57	1081.59	-0.02	1	9.69	4073.04	8	FASFIDKVR
DCP1B1	gi|14924599	484	126.64	738.39	1474.76	1474.78	-0.02	0	77.38	0.00	1	FLEQQNQVLQTK
DCP1B3	gi|14924599	485	126.64	738.40	1474.78	1474.78	0.00	0	27.99	48.59	3	FLEQQNQVLQTK
DCP1B2	gi|14924599	486	126.64	738.40	1474.78	1474.78	0.00	0	72.05	0.00	1	FLEQQNQVLQTK
DCP1B1	gi|14924599	644	126.64	978.16	2931.45	2931.51	-0.06	1	40.34	0.78	1	FLEQQNQVLQTKWELLQQVDTSTR
DCP1B1	gi|15768669	224	63.70	556.29	1110.56	1110.57	-0.01	0	63.70	0.02	3	LSISTSNSFR
DCP1B2	gi|17312739	397	67.90	659.82	1317.63	1317.65	-0.02	0	67.90	0.01	2	SQLNSLQEASGGK
DCP1B3	gi|17312739	398	67.90	659.84	1317.66	1317.65	0.00	0	63.98	0.01	2	SQLNSLQEASGGK
DCP1B1	gi|21393323	224	63.70	556.29	1110.56	1110.57	-0.01	0	63.70	0.02	2	LSISTSFSNR
DCP1B2	gi|21872084	206	88.41	541.79	1081.57	1081.59	-0.02	1	9.69	4073.04	8	FASFIDKVR
DCP1B2	gi|21872084	114	88.41	487.26	972.51	972.52	-0.02	0	60.68	0.05	2	LEISELNR
DCP1B3	gi|21872084	115	88.41	487.26	972.51	972.52	-0.02	0	45.11	1.58	3	LEISELNR
DCP1B1	gi|21872084	247	88.41	576.78	1151.54	1151.55	-0.01	1	18.04	454.55	4	NKYEDEINK
DCP1B1	gi|21889803	26	167.97	421.26	840.50	840.51	-0.01	1	25.22	78.84	3	ADIPGLKK
DCP1B1	gi|21889803	140	167.97	505.75	1009.48	1009.48	0.00	0	37.19	6.61	1	ENSAFVSTR
DCP1B1	gi|21889803	192	167.97	537.26	1072.50	1072.52	-0.02	0	17.91	433.33	1	ETPESHVFK
DCP1B1	gi|21889803	117	167.97	487.77	973.53	973.53	0.00	1	35.74	13.59	2	FRLPENAK
DCP1B2	gi|21889803	74	167.97	451.25	900.49	900.50	-0.02	0	51.91	0.39	5	VLQISGER
DCP1B3	gi|21889803	75	167.97	451.25	900.49	900.50	-0.01	0	51.07	0.46	5	VLQISGER

Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B1	gi|21889803	76	167.97	451.26	900.50	900.50	-0.01	0	45.86	1.51	5	VLQISGER
DCP1B1	gi|21889803	77	167.97	451.26	900.51	900.50	0.00	0	51.27	0.41	5	VLQISGER
DCP1B2	gi|23844925	195	60.87	537.29	1072.57	1072.57	0.00	0	37.89	7.87	7	LMLQIDNAR
DCP1B2	gi|23844925	210	60.87	545.76	1089.50	1089.52	-0.02	0	22.98	156.65	2	VTMQNLNDR
DCP1B1	gi|24018741	26	131.74	421.26	840.50	840.51	-0.01	1	25.22	78.84	4	ADLPGIKK
DCP1B1	gi|24018741	567	131.74	586.64	1756.89	1756.90	0.00	1	54.61	0.09	1	VEIEDDRVLQISGER
DCP1B2	gi|24018741	74	131.74	451.25	900.49	900.50	-0.02	0	51.91	0.39	5	VLQISGER
DCP1B3	gi|24018741	75	131.74	451.25	900.49	900.50	-0.01	0	51.07	0.46	5	VLQISGER
DCP1B1	gi|24018741	76	131.74	451.26	900.50	900.50	-0.01	0	45.86	1.51	5	VLQISGER
DCP1B1	gi|24018741	77	131.74	451.26	900.51	900.50	0.00	0	51.27	0.41	5	VLQISGER
DCP1B1	gi|24060606	599	140.60	665.01	1992.00	1992.02	-0.02	1	140.60	0.00	1	QIVSSTNEEDKVIVFER
DCP1B2	gi|25038991	59	64.88	436.25	870.48	870.49	-0.01	0	37.74	7.59	2	QAIVDGLR
DCP1B2	gi|25038991	460	64.88	470.25	1407.73	1407.76	-0.03	0	6.86	6966.62	4	SSAVFLPHGPAAVR
DCP1B2	gi|25038991	461	64.88	704.88	1407.75	1407.76	-0.02	0	27.14	61.36	1	SSAVFLPHGPAAVR
DCP1B2	gi|25316734	114	60.68	487.26	972.51	972.52	-0.02	0	60.68	0.05	4	LELSELNR
DCP1B3	gi|25316734	115	60.68	487.26	972.51	972.52	-0.02	0	45.11	1.58	5	LELSELNR
DCP1B2	gi|25510704	230	90.97	561.79	1121.56	1121.57	-0.01	0	48.43	0.57	1	LEQEIATYR
DCP1B3	gi|25510704	231	90.97	561.79	1121.56	1121.57	-0.01	0	52.59	0.23	1	LEQEIATYR
DCP1B3	gi|25510704	41	90.97	424.22	846.43	846.44	-0.02	0	38.38	10.25	6	SEITELR
DCP1B1	gi|27420318	117	76.36	487.77	973.53	973.53	0.00	1	35.74	13.59	2	FRLPENAK
DCP1B1	gi|27420318	567	76.36	586.64	1756.89	1756.90	0.00	1	40.62	2.14	2	VEIEDDSVLQIRGER
DCP1B1	gi|27420379	26	95.32	421.26	840.50	840.51	-0.01	1	25.22	78.84	5	ADLPGLKK
DCP1B1	gi|27420379	487	95.32	739.39	1476.76	1476.73	0.02	0	18.19	483.04	3	ASMENGVLTMTVPK
DCP1B2	gi|27420379	74	95.32	451.25	900.49	900.50	-0.02	0	51.91	0.39	5	VLQISGER
DCP1B3	gi|27420379	75	95.32	451.25	900.49	900.50	-0.01	0	51.07	0.46	5	VLQISGER
DCP1B1	gi|27420379	76	95.32	451.26	900.50	900.50	-0.01	0	45.86	1.51	5	VLQISGER
DCP1B1	gi|27420379	77	95.32	451.26	900.51	900.50	0.00	0	51.27	0.41	5	VLQISGER
DCP1B3	gi|28465823	371	97.03	639.35	1276.68	1276.70	-0.02	0	33.15	17.29	2	LALDIEIATYR
DCP1B1	gi|28465823	247	97.03	576.78	1151.54	1151.55	-0.01	1	18.04	454.55	4	NKYEDEINK
DCP1B2	gi|28465823	107	97.03	486.75	971.49	971.50	-0.01	0	36.89	8.99	2	QEIAELNR
DCP1B3	gi|28465823	108	97.03	486.75	971.49	971.50	-0.01	0	45.84	1.11	1	QEIAELNR
DCP1B1	gi|286630	391	55.10	656.88	1311.74	1311.75	-0.01	0	55.10	0.07	2	VLQLETAAGAAIR
DCP1B2	gi|28911438	262	112.84	581.77	1161.53	1161.54	-0.01	0	63.87	0.01	1	DAVTYTEHAR
DCP1B1	gi|28911438	263	112.84	581.78	1161.54	1161.54	0.00	0	37.47	5.53	1	DAVTYTEHAR
DCP1B1	gi|28911438	283	112.84	590.81	1179.60	1179.61	-0.01	0	48.97	0.53	1	ISGIIYEETR

Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B2	gi|2922036	317	63.10	604.30	1206.58	1206.59	-0.01	0	63.10	0.02	1	VLAPYSSEDAR
DCP1B1	gi|29432310	282	63.67	590.29	1178.57	1178.59	-0.02	0	63.67	0.02	1	YEELQITAGR
DCP1B1	gi|29532161	224	63.70	556.29	1110.56	1110.57	-0.01	0	63.70	0.02	1	ISISTSGGSFR
DCP1B2	gi|29532386	349	77.11	627.80	1253.58	1253.60	-0.02	0	77.11	0.00	1	GFSSGSAVVSGGSR
DCP1B1	gi|29532386	350	77.11	627.80	1253.60	1253.60	0.00	0	37.10	5.78	1	GFSSGSAVVSGGSR
DCP1B3	gi|29532386	351	77.11	627.81	1253.60	1253.60	0.00	0	4.88	9249.04	9	GFSSGSAVVSGGSR
DCP1B1	gi|29532489	484	176.23	738.39	1474.76	1474.78	-0.02	0	77.38	0.00	1	FLEQQNQVLQTK
DCP1B3	gi|29532489	485	176.23	738.40	1474.78	1474.78	0.00	0	27.99	48.59	3	FLEQQNQVLQTK
DCP1B2	gi|29532489	486	176.23	738.40	1474.78	1474.78	0.00	0	72.05	0.00	1	FLEQQNQVLQTK
DCP1B2	gi|29532489	448	176.23	692.34	1382.66	1382.68	-0.02	0	54.80	0.09	1	SLNNQFASFIDK
DCP1B1	gi|29532489	62	176.23	437.75	873.48	873.49	-0.01	0	44.05	2.43	1	SLVNLGGSK
DCP1B2	gi|30161665	119	77.36	488.28	974.54	974.55	-0.01	0	38.73	5.60	1	IGLFGGAGVGK
DCP1B2	gi|30161665	437	77.36	684.38	1366.75	1366.75	0.01	0	38.63	3.33	3	ILNVIGEPIDER
DCP1B1	gi|31015481	189	81.88	533.26	1064.51	1064.51	-0.01	0	42.54	2.09	1	AQYEDLAQK
DCP1B2	gi|31015481	17	81.88	405.22	808.42	808.43	-0.01	0	39.34	5.76	2	LASYLDK
DCP1B3	gi|31423267	13	62.11	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|31423267	14	62.11	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|31423267	15	62.11	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B2	gi|31423267	156	62.11	516.30	1030.58	1030.57	0.02	0	28.31	51.33	2	VLDELTVSR
DCP1B2	gi|31429724	286	70.31	592.35	1182.69	1182.71	-0.02	0	70.31	0.00	3	NIQLSLIINR
DCP1B1	gi|31661492	451	94.90	696.34	1390.66	1390.66	-0.01	0	32.95	14.58	1	FPQPYANEQAAR
DCP1B1	gi|31661492	583	94.90	621.64	1861.89	1861.91	-0.02	1	61.95	0.01	1	ISDRFPQPYANEQAAR
DCP1B1	gi|3248492	360	83.61	633.31	1264.61	1264.63	-0.02	0	67.08	0.01	1	TNAENEFVTIK
DCP1B2	gi|3248492	361	83.61	633.31	1264.62	1264.63	-0.01	0	64.61	0.01	1	TNAENEFVTIK
DCP1B3	gi|3248492	453	83.61	465.24	1392.70	1392.72	-0.02	1	16.53	751.07	1	TNAENEFVTIKK
DCP1B2	gi|3248492	454	83.61	465.24	1392.70	1392.72	-0.02	1	15.46	954.21	3	TNAENEFVTIKK
DCP1B1	gi|32536407	137	79.88	503.75	1005.49	1005.51	-0.02	0	38.78	6.14	1	GPGLYSDIGK
DCP1B1	gi|32536407	524	79.88	521.29	1560.83	1560.85	-0.02	1	41.10	1.99	3	KGEVFLADVNTQLK
DCP1B2	gi|33164780	211	84.86	547.26	1092.51	1092.52	-0.01	0	57.13	0.07	1	AQYEEIANR
DCP1B2	gi|33164780	206	84.86	541.79	1081.57	1081.59	-0.02	1	9.69	4073.04	8	FASFIDKVR
DCP1B1	gi|33164780	247	84.86	576.78	1151.54	1151.55	-0.01	1	18.04	454.55	4	NKYEDEINK
DCP1B2	gi|3326750	50	61.40	429.73	857.45	857.46	-0.01	0	61.40	0.04	1	IIEVDNR
DCP1B2	gi|33405959	397	67.90	659.82	1317.63	1317.65	-0.02	0	67.90	0.01	1	SQLNSIQEASGGK
DCP1B3	gi|33405959	398	67.90	659.84	1317.66	1317.65	0.00	0	63.98	0.01	1	SQLNSIQEASGGK
DCP1B2	gi|33627058	114	56.56	487.26	972.51	972.52	-0.02	0	56.56	0.12	5	IEISEVAGR

Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B3	gi|33627058	115	56.56	487.26	972.51	972.52	-0.02	0	46.40	1.17	1	IEISEVAGR
DCP1B2	gi|37711813	219	135.53	554.27	1106.52	1106.54	-0.02	0	47.65	0.57	1	AQYEEIAQR
DCP1B1	gi|37711813	220	135.53	554.27	1106.54	1106.54	0.00	0	48.46	0.55	1	AQYEEIAQR
DCP1B2	gi|37711813	206	135.53	541.79	1081.57	1081.59	-0.02	1	9.69	4073.04	8	FASFIDKVR
DCP1B1	gi|37711813	484	135.53	738.39	1474.76	1474.78	-0.02	0	77.38	0.00	1	FLEQQNQVLQTK
DCP1B3	gi|37711813	485	135.53	738.40	1474.78	1474.78	0.00	0	27.99	48.59	3	FLEQQNQVLQTK
DCP1B2	gi|37711813	486	135.53	738.40	1474.78	1474.78	0.00	0	72.05	0.00	1	FLEQQNQVLQTK
DCP1B2	gi|3854018	91	75.40	466.73	931.44	931.45	-0.01	0	37.66	7.15	1	AVEDELEK
DCP1B2	gi|3854018	59	75.40	436.25	870.48	870.49	-0.01	0	37.74	7.59	2	QAIVDGLR
DCP1B2	gi|40324499	50	61.40	429.73	857.45	857.46	-0.01	0	61.40	0.04	3	LIEVDNR
DCP1B3	gi|45838141	371	78.38	639.35	1276.68	1276.70	-0.02	0	33.15	17.29	4	LALDLEIATYR
DCP1B3	gi|45838141	194	78.38	537.29	1072.57	1072.59	-0.02	1	34.22	18.49	1	LRSEIDNVK
DCP1B2	gi|45838141	195	78.38	537.29	1072.57	1072.59	-0.02	1	45.23	1.45	4	LRSEIDNVK
DCP1B2	gi|45844527	206	105.11	541.79	1081.57	1081.59	-0.02	1	9.69	4073.04	8	FASFIDKVR
DCP1B1	gi|45844527	484	105.11	738.39	1474.76	1474.78	-0.02	0	77.38	0.00	1	FLEQQNQVLQTK
DCP1B3	gi|45844527	485	105.11	738.40	1474.78	1474.78	0.00	0	27.99	48.59	3	FLEQQNQVLQTK
DCP1B2	gi|45844527	486	105.11	738.40	1474.78	1474.78	0.00	0	72.05	0.00	1	FLEQQNQVLQTK
DCP1B1	gi|45844527	247	105.11	576.78	1151.54	1151.55	-0.01	1	18.04	454.55	4	NKYEDEINK
DCP1B2	gi|46213387	260	57.19	580.78	1159.54	1159.56	-0.02	0	57.19	0.05	2	EEDTTVPLEK
DCP1B3	gi|46213387	261	57.19	580.78	1159.55	1159.56	-0.01	0	20.53	285.93	2	EEDTTVPLEK
DCP1B2	gi|46419503	219	81.61	554.27	1106.52	1106.54	-0.02	0	47.65	0.57	1	AQYEEIAQR
DCP1B1	gi|46419503	220	81.61	554.27	1106.54	1106.54	0.00	0	48.46	0.55	1	AQYEEIAQR
DCP1B3	gi|46419503	371	81.61	639.35	1276.68	1276.70	-0.02	0	33.15	17.29	2	LALDIEIATYR
DCP1B2	gi|47832505	320	61.51	605.31	1208.60	1208.61	-0.02	0	61.51	0.03	1	LQQLENPDPR
DCP1B1	gi|48485734	26	112.87	421.26	840.50	840.51	-0.01	1	25.22	78.84	4	ADLPGIKK
DCP1B1	gi|48485734	117	112.87	487.77	973.53	973.53	0.00	1	35.74	13.59	2	FRLPENAK
DCP1B2	gi|48485734	74	112.87	451.25	900.49	900.50	-0.02	0	51.91	0.39	5	VLQISGER
DCP1B3	gi|48485734	75	112.87	451.25	900.49	900.50	-0.01	0	51.07	0.46	5	VLQISGER
DCP1B1	gi|48485734	76	112.87	451.26	900.50	900.50	-0.01	0	45.86	1.51	5	VLQISGER
DCP1B1	gi|48485734	77	112.87	451.26	900.51	900.50	0.00	0	51.27	0.41	5	VLQISGER
DCP1B1	gi|49014261	26	134.50	421.26	840.50	840.51	-0.01	1	25.22	78.84	5	ADLPGLKK
DCP1B1	gi|49014261	117	134.50	487.77	973.53	973.53	0.00	1	35.74	13.59	2	FRLPENAK
DCP1B1	gi|49014261	567	134.50	586.64	1756.89	1756.90	0.00	1	21.63	169.81	6	IEVEDDRVLQISGER
DCP1B2	gi|49014261	74	134.50	451.25	900.49	900.50	-0.02	0	51.91	0.39	5	VLQISGER
DCP1B3	gi|49014261	75	134.50	451.25	900.49	900.50	-0.01	0	51.07	0.46	5	VLQISGER
DCP1B1	gi|49014261	76	134.50	451.26	900.50	900.50	-0.01	0	45.86	1.51	5	VLQISGER

Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B1	gi|49014261	77	134.50	451.26	900.51	900.50	0.00	0	51.27	0.41	5	VLQISGER
DCP1B3	gi|50366872	13	111.04	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|50366872	14	111.04	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|50366872	15	111.04	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B2	gi|50366872	210	111.04	545.76	1089.50	1089.52	-0.02	0	22.98	156.65	2	VTMQNLNDR
DCP1B3	gi|50366872	128	111.04	497.25	992.48	992.49	-0.02	0	40.19	3.96	1	YENEVALR
DCP1B2	gi|50366872	129	111.04	497.25	992.48	992.49	-0.01	0	54.26	0.16	1	YENEVALR
DCP1B1	gi|50366872	130	111.04	497.25	992.49	992.49	-0.01	0	51.04	0.35	1	YENEVALR
DCP1B2	gi|5042680	119	149.09	488.28	974.54	974.55	-0.01	0	38.73	5.60	1	IGLFGGAGVGK
DCP1B2	gi|5042680	437	149.09	684.38	1366.75	1366.75	0.01	0	38.63	3.33	1	IINVIGEPIDER
DCP1B2	gi|5042680	462	149.09	705.41	1408.80	1408.80	0.00	0	49.56	0.17	1	VLNTGSPITVPVGR
DCP1B2	gi|5042680	277	149.09	587.33	1172.64	1172.66	-0.02	0	22.17	223.60	1	VVDLLAPYQR
DCP1B2	gi|50458206	49	55.72	428.76	855.51	855.52	-0.01	0	55.72	0.08	1	IATVISPR
DCP1B3	gi|50463831	13	114.84	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|50463831	14	114.84	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|50463831	15	114.84	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B3	gi|50463831	41	114.84	424.22	846.43	846.44	-0.02	0	38.38	10.25	6	SEITELR
DCP1B1	gi|50463831	153	114.84	515.30	1028.58	1028.59	0.00	0	42.66	2.00	2	VLDELTLAR
DCP1B2	gi|50463831	154	114.84	515.30	1028.59	1028.59	0.00	0	41.65	2.38	2	VLDELTLAR
DCP1B2	gi|51672597	286	70.31	592.35	1182.69	1182.71	-0.02	0	70.31	0.00	2	LNQLSILLNR
DCP1B1	gi|52582373	478	115.10	731.38	1460.75	1460.75	0.00	0	81.43	0.00	1	SSMENGVLTVTVPK
DCP1B2	gi|52582373	479	115.10	731.39	1460.76	1460.75	0.00	0	115.10	0.00	1	SSMENGVLTVTVPK
DCP1B1	gi|5279974	137	73.64	503.75	1005.49	1005.51	-0.02	0	38.78	6.14	1	GPGLYSDIGK
DCP1B1	gi|5279974	524	73.64	521.29	1560.83	1560.85	-0.02	1	34.86	8.37	6	KGDLFLADVNTQLK
DCP1B2	gi|528491	185	71.25	531.27	1060.53	1060.52	0.01	0	71.25	0.00	1	EFADDVLPR
DCP1B1	gi|53827074	26	58.50	421.26	840.50	840.51	-0.01	1	25.22	78.84	5	ADLPGLKK
DCP1B1	gi|53827074	92	58.50	467.25	932.48	932.47	0.01	0	33.28	26.59	6	MLQISGER
DCP1B1	gi|54535312	382	198.12	651.32	1300.63	1300.65	-0.02	0	71.09	0.00	1	ALEEANADLEVK
DCP1B3	gi|54535312	13	198.12	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|54535312	14	198.12	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|54535312	15	198.12	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B2	gi|54535312	17	198.12	405.22	808.42	808.43	-0.01	0	39.34	5.76	2	LASYLDK
DCP1B3	gi|54535312	155	198.12	516.30	1030.58	1030.59	-0.01	0	47.39	0.77	1	VLDELTLTK
DCP1B2	gi|54535312	156	198.12	516.30	1030.58	1030.59	-0.01	0	29.62	37.96	1	VLDELTLTK
DCP1B1	gi|54535312	157	198.12	516.30	1030.59	1030.59	0.00	0	53.89	0.11	1	VLDELTLTK
DCP1B1	gi|55827991	253	123.12	579.26	1156.51	1156.51	0.00	1	10.28	1388.93	10	AGRXPPQGXPR

Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B2	gi|55827991	262	123.12	581.77	1161.53	1161.54	-0.01	0	63.87	0.01	1	DAVTYTEHAR
DCP1B1	gi|55827991	263	123.12	581.78	1161.54	1161.54	0.00	0	37.47	5.53	1	DAVTYTEHAR
DCP1B1	gi|55827991	283	123.12	590.81	1179.60	1179.61	-0.01	0	48.97	0.53	2	ISGLIYEETR
DCP1B1	gi|56918004	375	54.67	643.81	1285.60	1285.59	0.00	0	54.67	0.09	1	SVSEGGIGFDYR
DCP1B1	gi|56918725	298	150.46	596.81	1191.60	1191.61	-0.01	0	65.50	0.01	1	AVEIYEEIAR
DCP1B1	gi|56918725	345	150.46	622.34	1242.66	1242.66	0.00	0	69.45	0.00	1	GDVVAISNALER
DCP1B1	gi|56918725	457	150.46	700.32	1398.62	1398.64	-0.02	0	15.51	461.74	2	YQDLDPTFSGTR
DCP1B2	gi|56920204	260	249.71	580.78	1159.54	1159.56	-0.02	0	57.19	0.05	1	EEDTTVPIEK
DCP1B3	gi|56920204	261	249.71	580.78	1159.55	1159.56	-0.01	0	20.53	285.93	1	EEDTTVPIEK
DCP1B3	gi|56920204	377	249.71	644.83	1287.64	1287.66	-0.02	1	42.54	2.12	2	KEEDTTVPIEK
DCP1B2	gi|56920204	378	249.71	644.83	1287.64	1287.66	-0.02	1	73.61	0.00	1	KEEDTTVPIEK
DCP1B2	gi|56920204	646	249.71	788.87	3151.46	3151.52	-0.06	0	9.22	527.13	1	KPEEVATPPPPPPPTEHVHAESASHEGEAK
DCP1B3	gi|56920204	169	249.71	522.76	1043.50	1043.51	-0.01	0	27.72	54.22	1	VQVSEPEEK
DCP1B2	gi|56920204	482	249.71	734.31	1466.60	1466.62	-0.01	0	74.18	0.00	1	YEEAEAANQADEK
DCP1B2	gi|56920204	535	249.71	532.57	1594.68	1594.71	-0.03	1	7.79	1480.99	2	YEEAEAANQADEKK
DCP1B1	gi|56920981	26	226.18	421.26	840.50	840.51	-0.01	1	25.22	78.84	5	ADLPGLKK
DCP1B1	gi|56920981	192	226.18	537.26	1072.50	1072.52	-0.02	0	17.91	433.33	1	ETPESHVFK
DCP1B1	gi|56920981	117	226.18	487.77	973.53	973.53	0.00	1	35.74	13.59	2	FRLPENAK
DCP1B3	gi|56920981	501	226.18	755.85	1509.69	1509.71	-0.02	0	26.96	38.08	1	SELANETSAFANTR
DCP1B2	gi|56920981	502	226.18	755.86	1509.70	1509.71	-0.01	0	95.40	0.00	1	SELANETSAFANTR
DCP1B2	gi|56920981	74	226.18	451.25	900.49	900.50	-0.02	0	51.91	0.39	5	VLQISGER
DCP1B3	gi|56920981	75	226.18	451.25	900.49	900.50	-0.01	0	51.07	0.46	5	VLQISGER
DCP1B1	gi|56920981	76	226.18	451.26	900.50	900.50	-0.01	0	45.86	1.51	5	VLQISGER
DCP1B1	gi|56920981	77	226.18	451.26	900.51	900.50	0.00	0	51.27	0.41	5	VLQISGER
DCP1B1	gi|56921806	474	156.66	726.37	1450.72	1450.72	0.00	0	61.76	0.02	1	DLVGVAYTEEEVK
DCP1B1	gi|56921806	451	156.66	696.34	1390.66	1390.66	-0.01	0	32.95	14.58	1	FPQPYANEQAAR
DCP1B1	gi|56921806	583	156.66	621.64	1861.89	1861.91	-0.02	1	61.95	0.01	2	LSDRFPQPYANEQAAR
DCP1B3	gi|56924004	342	58.00	620.30	1238.58	1238.59	-0.02	0	34.68	9.40	1	EPAFFTGSEVR
DCP1B2	gi|56924004	212	58.00	548.78	1095.54	1095.56	-0.01	0	23.32	173.27	1	HEEVVEQVK
DCP1B3	gi|56927029	42	121.23	426.73	851.45	851.45	0.00	0	52.44	0.26	1	FVFAGPSK
DCP1B2	gi|56927029	570	121.23	888.98	1775.94	1775.92	0.02	0	68.79	0.00	2	YIAPEQVPVQYGGLSR
DCP1B2	gi|58121190	50	61.40	429.73	857.45	857.46	-0.01	0	61.40	0.04	4	LLEVDGGR
DCP1B1	gi|58208336	26	91.89	421.26	840.50	840.51	-0.01	1	25.22	78.84	5	ADLPGLKK
DCP1B1	gi|58208336	117	91.89	487.77	973.53	973.53	0.00	1	35.74	13.59	2	FRLPENAK
DCP1B2	gi|58208336	502	91.89	755.86	1509.70	1509.71	-0.01	0	30.93	17.08	2	SELSNETAAFANTR

Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B2	gi|58600440	119	107.29	488.28	974.54	974.55	-0.01	0	38.73	5.60	1	IGLFGGAGVGK
DCP1B3	gi|58600440	101	107.29	478.77	955.53	955.55	-0.01	0	46.39	0.92	1	VLNTGSPIR
DCP1B2	gi|58600440	277	107.29	587.33	1172.64	1172.66	-0.02	0	22.17	223.60	1	VVDLLAPYQR
DCP1B2	gi|61962850	206	75.06	541.79	1081.57	1081.59	-0.02	1	9.69	4073.04	8	FASFIDKVR
DCP1B3	gi|61962850	371	75.06	639.35	1276.68	1276.70	-0.02	0	33.15	17.29	2	LALDIEIATYR
DCP1B1	gi|61962850	247	75.06	576.78	1151.54	1151.55	-0.01	1	18.04	454.55	4	NKYEDEINK
DCP1B1	gi|61962850	555	75.06	572.61	1714.80	1714.79	0.01	1	14.18	732.61	4	TAAESRAAEAAAAASTXR
DCP1B2	gi|62844198	211	92.48	547.26	1092.51	1092.52	-0.01	0	26.16	85.43	3	AQYEDIAQR
DCP1B2	gi|62844198	206	92.48	541.79	1081.57	1081.59	-0.02	1	9.69	4073.04	8	FASFIDKVR
DCP1B1	gi|62844198	319	92.48	604.80	1207.59	1207.61	-0.02	0	56.63	0.08	1	TAAENDFVTLK
DCP1B2	gi|62873293	235	61.90	563.27	1124.52	1124.53	-0.02	0	23.95	111.79	1	AEAESVYQTK
DCP1B1	gi|62873293	236	61.90	563.27	1124.53	1124.53	0.00	0	26.05	79.43	1	AEAESVYQTK
DCP1B2	gi|62873293	211	61.90	547.26	1092.51	1092.52	-0.01	0	26.16	85.43	3	AQYEDIAQR
DCP1B2	gi|62873293	206	61.90	541.79	1081.57	1081.59	-0.02	1	9.69	4073.04	8	FASFIDKVR
DCP1B1	gi|62895721	26	77.13	421.26	840.50	840.51	-0.01	1	25.22	78.84	5	ADLPGLKK
DCP1B2	gi|62895721	74	77.13	451.25	900.49	900.50	-0.02	0	51.91	0.39	2	VIQISGER
DCP1B3	gi|62895721	75	77.13	451.25	900.49	900.50	-0.01	0	51.07	0.46	2	VIQISGER
DCP1B1	gi|62895721	76	77.13	451.26	900.50	900.50	-0.01	0	45.86	1.51	2	VIQISGER
DCP1B1	gi|62895721	77	77.13	451.26	900.51	900.50	0.00	0	51.27	0.41	2	VIQISGER
DCP1B2	gi|67056530	114	60.68	487.26	972.51	972.52	-0.02	0	60.68	0.05	3	LELSEINR
DCP1B3	gi|67056530	115	60.68	487.26	972.51	972.52	-0.02	0	45.11	1.58	4	LELSEINR
DCP1B1	gi|67208610	140	179.45	505.75	1009.48	1009.48	0.00	0	37.19	6.61	1	ENSAFVSTR
DCP1B1	gi|67208610	117	179.45	487.77	973.53	973.53	0.00	1	35.74	13.59	2	FRLPENAK
DCP1B1	gi|67208610	567	179.45	586.64	1756.89	1756.90	0.00	1	54.61	0.09	1	VEIEDDRVLQISGER
DCP1B2	gi|67208610	74	179.45	451.25	900.49	900.50	-0.02	0	51.91	0.39	5	VLQISGER
DCP1B3	gi|67208610	75	179.45	451.25	900.49	900.50	-0.01	0	51.07	0.46	5	VLQISGER
DCP1B1	gi|67208610	76	179.45	451.26	900.50	900.50	-0.01	0	45.86	1.51	5	VLQISGER
DCP1B1	gi|67208610	77	179.45	451.26	900.51	900.50	0.00	0	51.27	0.41	5	VLQISGER
DCP1B1	gi|67211137	520	97.61	772.85	1543.68	1543.69	-0.01	0	97.61	0.00	1	SEFANETSAFANTR
DCP1B3	gi|67211197	364	66.03	635.33	1268.65	1268.67	-0.02	0	21.30	278.40	1	VLAEDAYYVVK
DCP1B1	gi|67211197	365	66.03	635.34	1268.66	1268.67	0.00	0	66.03	0.01	1	VLAEDAYYVVK
DCP1B1	gi|68328510	382	93.32	651.32	1300.63	1300.65	-0.02	0	21.14	244.96	2	ALEDANAELEVK
DCP1B3	gi|68328510	13	93.32	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|68328510	14	93.32	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|68328510	15	93.32	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR

Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B3	gi|68328510	41	93.32	424.22	846.43	846.44	-0.02	0	38.38	10.25	6	SEITELR
DCP1B2	gi|71568401	211	65.50	547.26	1092.51	1092.52	-0.01	0	26.16	85.43	4	AQYEDLAQR
DCP1B2	gi|71568401	17	65.50	405.22	808.42	808.43	-0.01	0	39.34	5.76	2	LASYLDK
DCP1B1	gi|71865472	298	65.50	596.81	1191.60	1191.61	-0.01	0	65.50	0.01	2	GIEIYEEIAR
DCP1B1	gi|7233578	26	167.48	421.26	840.50	840.51	-0.01	1	25.22	78.84	3	ADIPGLKK
DCP1B1	gi|7233578	117	167.48	487.77	973.53	973.53	0.00	1	35.74	13.59	2	FRLPENAK
DCP1B1	gi|7233578	567	167.48	586.64	1756.89	1756.90	0.00	1	54.61	0.09	1	VEIEDDRVLQISGER
DCP1B2	gi|7233578	74	167.48	451.25	900.49	900.50	-0.02	0	51.91	0.39	5	VLQISGER
DCP1B3	gi|7233578	75	167.48	451.25	900.49	900.50	-0.01	0	51.07	0.46	5	VLQISGER
DCP1B1	gi|7233578	76	167.48	451.26	900.50	900.50	-0.01	0	45.86	1.51	5	VLQISGER
DCP1B1	gi|7233578	77	167.48	451.26	900.51	900.50	0.00	0	51.27	0.41	5	VLQISGER
DCP1B2	gi|7238484	570	68.79	888.98	1775.94	1775.96	-0.02	1	68.79	0.00	1	YIAPEQVPVKYGGLSR
DCP1B1	gi|7284912	26	95.32	421.26	840.50	840.51	-0.01	1	25.22	78.84	3	ADIPGLKK
DCP1B1	gi|7284912	487	95.32	739.39	1476.76	1476.73	0.02	0	18.19	483.04	3	ASMENGVLTMTVPK
DCP1B2	gi|7284912	74	95.32	451.25	900.49	900.50	-0.02	0	51.91	0.39	5	VLQISGER
DCP1B3	gi|7284912	75	95.32	451.25	900.49	900.50	-0.01	0	51.07	0.46	5	VLQISGER
DCP1B1	gi|7284912	76	95.32	451.26	900.50	900.50	-0.01	0	45.86	1.51	5	VLQISGER
DCP1B1	gi|7284912	77	95.32	451.26	900.51	900.50	0.00	0	51.27	0.41	5	VLQISGER
DCP1B1	gi|7325689	189	63.88	533.26	1064.51	1064.51	-0.01	0	30.08	36.89	2	AQYDELAQK
DCP1B3	gi|7325689	13	63.88	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|7325689	14	63.88	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR
DCP1B2	gi|7325689	15	63.88	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B1	gi|74115952	94	71.93	472.77	943.53	943.52	0.01	0	22.96	262.72	5	AGLQFPVGR
DCP1B1	gi|74115952	283	71.93	590.81	1179.60	1179.61	-0.01	0	48.97	0.53	2	ISGLIYEETR
DCP1B2	gi|78335658	50	61.40	429.73	857.45	857.46	-0.01	0	61.40	0.04	2	ILEVDNR
DCP1B1	gi|8172498	26	167.48	421.26	840.50	840.51	-0.01	1	25.22	78.84	5	ADLPGLKK
DCP1B1	gi|8172498	117	167.48	487.77	973.53	973.53	0.00	1	35.74	13.59	2	FRLPENAK
DCP1B1	gi|8172498	567	167.48	586.64	1756.89	1756.90	0.00	1	54.61	0.09	1	VEIEDDRVLQISGER
DCP1B2	gi|8172498	74	167.48	451.25	900.49	900.50	-0.02	0	51.91	0.39	5	VLQISGER
DCP1B3	gi|8172498	75	167.48	451.25	900.49	900.50	-0.01	0	51.07	0.46	5	VLQISGER
DCP1B1	gi|8172498	76	167.48	451.26	900.50	900.50	-0.01	0	45.86	1.51	5	VLQISGER
DCP1B1	gi|8172498	77	167.48	451.26	900.51	900.50	0.00	0	51.27	0.41	5	VLQISGER
DCP1B1	gi|82971987	382	225.21	651.32	1300.63	1300.65	-0.02	0	71.09	0.00	1	ALEEANADLEVK
DCP1B3	gi|82971987	417	225.21	669.83	1337.65	1337.66	0.00	0	15.34	926.64	3	APSAYGGLSVSSSR
DCP1B3	gi|82971987	13	225.21	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|82971987	14	225.21	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR

Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B2	gi|82971987	15	225.21	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B2	gi|82971987	17	225.21	405.22	808.42	808.43	-0.01	0	39.34	5.76	2	LASYLDK
DCP1B1	gi|82971987	153	225.21	515.30	1028.58	1028.59	0.00	0	42.66	2.00	2	VLDELTLAR
DCP1B2	gi|82971987	154	225.21	515.30	1028.59	1028.59	0.00	0	41.65	2.38	2	VLDELTLAR
DCP1B2	gi|82971987	210	225.21	545.76	1089.50	1089.52	-0.02	0	22.98	156.65	2	VTMQNLNDR
DCP1B2	gi|82972689	219	143.83	554.27	1106.52	1106.54	-0.02	0	47.65	0.57	1	AQYEEIAQR
DCP1B1	gi|82972689	220	143.83	554.27	1106.54	1106.54	0.00	0	48.46	0.55	1	AQYEEIAQR
DCP1B2	gi|82972689	206	143.83	541.79	1081.57	1081.59	-0.02	1	9.69	4073.04	8	FASFIDKVR
DCP1B1	gi|82972689	247	143.83	576.78	1151.54	1151.55	-0.01	1	18.04	454.55	4	NKYEDEINK
DCP1B3	gi|82972689	264	143.83	583.29	1164.56	1164.58	-0.02	0	67.64	0.01	1	YEELQVTAGR
DCP1B1	gi|82972689	268	143.83	583.30	1164.58	1164.58	0.00	0	58.41	0.06	1	YEELQVTAGR
DCP1B2	gi|82973417	206	121.21	541.79	1081.57	1081.59	-0.02	1	9.69	4073.04	8	FASFIDKVR
DCP1B3	gi|82973417	194	121.21	537.29	1072.57	1072.59	-0.02	1	34.22	18.49	1	LRSEIDNVK
DCP1B2	gi|82973417	195	121.21	537.29	1072.57	1072.59	-0.02	1	45.23	1.45	4	LRSEIDNVK
DCP1B1	gi|82973417	247	121.21	576.78	1151.54	1151.55	-0.01	1	18.04	454.55	4	NKYEDEINK
DCP1B3	gi|82973417	299	121.21	597.78	1193.55	1193.57	-0.01	0	48.25	0.41	1	YEELQQTAGR
DCP1B2	gi|82974719	219	292.92	554.27	1106.52	1106.54	-0.02	0	47.65	0.57	1	AQYEEIAQR
DCP1B1	gi|82974719	220	292.92	554.27	1106.54	1106.54	0.00	0	48.46	0.55	1	AQYEEIAQR
DCP1B1	gi|82974719	244	292.92	571.26	1140.50	1140.51	-0.01	0	27.05	33.94	1	DYQELMNTK
DCP1B1	gi|82974719	484	292.92	738.39	1474.76	1474.78	-0.02	0	77.38	0.00	1	FLEQQNQVLQTK
DCP1B3	gi|82974719	485	292.92	738.40	1474.78	1474.78	0.00	0	27.99	48.59	3	FLEQQNQVLQTK
DCP1B2	gi|82974719	486	292.92	738.40	1474.78	1474.78	0.00	0	72.05	0.00	1	FLEQQNQVLQTK
DCP1B1	gi|82974719	510	292.92	508.60	1522.77	1522.78	-0.01	1	17.07	751.78	1	LLRDYQELMNTK
DCP1B2	gi|82974719	448	292.92	692.34	1382.66	1382.68	-0.02	0	54.80	0.09	1	SLNNQFASFIDK
DCP1B2	gi|82974719	160	292.92	517.25	1032.49	1032.51	-0.02	0	42.71	2.16	1	TLLEGEESR
DCP1B3	gi|82974719	161	292.92	517.25	1032.49	1032.51	-0.02	0	68.16	0.01	1	TLLEGEESR
DCP1B1	gi|82974719	162	292.92	517.26	1032.50	1032.51	-0.01	0	50.62	0.40	1	TLLEGEESR
DCP1B1	gi|82974719	163	292.92	517.26	1032.50	1032.51	-0.01	0	49.33	0.53	1	TLLEGEESR
DCP1B1	gi|82976817	382	293.16	651.32	1300.63	1300.65	-0.02	0	71.09	0.00	1	ALEEANADLEVK
DCP1B2	gi|82976817	326	293.16	610.80	1219.58	1219.59	-0.02	0	28.03	47.51	1	ASLENSLEETK
DCP1B1	gi|82976817	327	293.16	610.80	1219.59	1219.59	-0.01	0	22.97	175.57	2	ASLENSLEETK
DCP1B2	gi|82976817	431	293.16	681.34	1360.67	1360.68	-0.01	0	50.20	0.34	1	EVATNSELVQSGK
DCP1B3	gi|82976817	432	293.16	681.35	1360.68	1360.68	-0.01	0	53.76	0.15	1	EVATNSELVQSGK
DCP1B1	gi|82976817	433	293.16	681.35	1360.69	1360.68	0.00	0	55.26	0.11	1	EVATNSELVQSGK
DCP1B3	gi|82976817	13	293.16	404.20	806.39	806.39	0.00	0	25.50	135.78	5	LAADDFR
DCP1B1	gi|82976817	14	293.16	404.20	806.39	806.39	0.00	0	31.97	28.05	2	LAADDFR

Table S2. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
DCP1B2	gi|82976817	15	293.16	404.21	806.40	806.39	0.01	0	33.80	18.52	2	LAADDFR
DCP1B2	gi|82976817	17	293.16	405.22	808.42	808.43	-0.01	0	39.34	5.76	2	LASYLDK
DCP1B1	gi|82976817	153	293.16	515.30	1028.58	1028.59	0.00	0	42.66	2.00	2	VLDELTLAR
DCP1B2	gi|82976817	154	293.16	515.30	1028.59	1028.59	0.00	0	41.65	2.38	2	VLDELTLAR
DCP1B2	gi|82976817	210	293.16	545.76	1089.50	1089.52	-0.02	0	22.98	156.65	2	VTMQNLNDR
DCP1B1	gi|83708557	189	57.48	533.26	1064.51	1064.51	-0.01	1	29.75	39.80	3	AQYEDSPKK
DCP1B2	gi|83708557	206	57.48	541.79	1081.57	1081.59	-0.02	1	9.69	4073.04	8	FASFIDKVR
DCP1B1	gi|83708557	247	57.48	576.78	1151.54	1151.55	-0.01	1	18.04	454.55	4	NKYEDEINK
DCP1B2	gi|83916608	18	78.95	406.22	810.42	810.44	-0.02	0	23.22	189.05	8	IPGYHPK
DCP1B3	gi|83916608	377	78.95	644.83	1287.64	1287.62	0.02	0	32.86	19.67	3	QEDETTVPIEK
DCP1B2	gi|83916608	378	78.95	644.83	1287.64	1287.62	0.02	0	55.73	0.10	2	QEDETTVPIEK
DCP1B1	gi|86171718	127	59.50	495.76	989.51	989.52	-0.01	0	21.88	371.45	2	GPGLFSDIGK
DCP1B1	gi|86171718	524	59.50	521.29	1560.83	1560.85	-0.02	1	37.62	4.43	4	KGELFVGDLNTQLK
DCP1B2	gi|86238712	50	61.40	429.73	857.45	857.45	0.00	0	61.40	0.04	5	LLEVDNGV
DCP1B1	gi|87148168	345	56.47	622.34	1242.66	1242.66	0.00	0	56.47	0.09	2	GDVVAVTNALER
DCP1B2	gi|87210283	172	111.27	523.28	1044.54	1044.56	-0.02	0	48.82	0.68	1	LSSPATLNSR
DCP1B1	gi|87210283	173	111.27	523.28	1044.55	1044.56	-0.01	0	61.15	0.04	1	LSSPATLNSR
DCP1B1	gi|87210283	32	111.27	421.75	841.49	841.50	-0.02	0	45.36	0.96	2	VATVSLPR
DCP1B2	gi|87210283	33	111.27	421.75	841.49	841.50	-0.01	0	42.29	2.05	2	VATVSLPR
DCP1B1	gi|87210283	35	111.27	421.76	841.51	841.50	0.01	0	50.12	0.25	2	VATVSLPR
DCP1B2	gi|89226389	211	108.32	547.26	1092.51	1092.52	-0.01	0	57.13	0.07	1	AQYEEIANR
DCP1B3	gi|89226389	371	108.32	639.35	1276.68	1276.70	-0.02	0	33.15	17.29	2	LALDIEIATYR
DCP1B1	gi|89226389	247	108.32	576.78	1151.54	1151.55	-0.01	1	18.04	454.55	4	NKYEDEINK
DCP1B1	gi|90644699	333	55.96	616.33	1230.64	1230.63	0.01	1	55.96	0.11	1	WGVLKGCNAAR
DCP1B3	gi|9960131	573	54.72	892.93	1783.84	1783.86	-0.02	0	54.72	0.06	1	VQLDSQPEEIDNLER

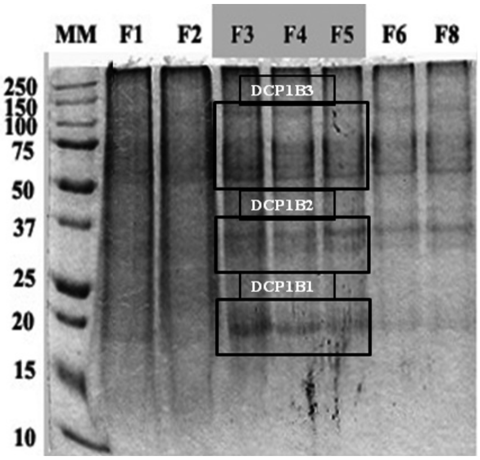

Image complement to Table S2: Proteins from Carotenoid-Protein Complex (CPC) separated in SDS_PAGE. Showing is the shaded area of fractions of the gel zone harvested for in gel tripityc digestion and MS/MS analysis. Label gel zone is coded as DCP1/DCP2/DCP3 in table discrimination.

Table S3. Supplementary Data: Listing Identified Proteins in the Carotenoid-protein Complex Assigned to Cassava EST Data Bases (NCBI, ESTIMA, EMBRAPA, CIAT, and RIKEN) and *Arabidopsis* Loci Data Base

SDS_PAGE Zone Code	Peptide Sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Protein Abreviation
DCP1B2	VAPEEHPVLLTEAPLN	scaff_7813_1	AT5G09812.1	310	2.0e-84	ACT7	ACT7
DCP1B1	AVEIYEEIAR	rni.05.I9.5 MBra685	AT3G56190.1	284	3.0e-77	ALPHA-SNAP2, ASNAP | alpha-soluble	ASNAP2
DCP1B1	GDVVAISNALER	rni.05.I9.5 MBra685	AT3G56190.1	284	3.0e-77	ALPHA-SNAP2, ASNAP | alpha-soluble	ASNAP2
DCP1B1	GIEIYEEIAR	rni.05.I9.5 MBra685	AT3G56190.1	284	3.0e-77	ALPHA-SNAP2, ASNAP | alpha-soluble	ASNAP2
DCP1B1	YQDLDPTFSGTR	rni.05.I9.5 MBra685	AT3G56190.1	284	3.0e-77	ALPHA-SNAP2, ASNAP | alpha-soluble	ASNAP2
DCP1B2	YYIGEIDASTVPAIR	scaff_9241_1	AT5G09810.1	348	4.0e-96	ATB5-A	ATB5-A
DCP1B2	DAIEGMNGQDLDGRNITVNEAQSR	scaff_7404_1	AT2G21660	146	2.0e-35	ATGRP7	ATGRP7
DCP1B2	GFGFVTFNSEK	scaff_7485_2	AT2G21660	89	1.0e-18	ATGRP7	ATGRP7
DCP1B2	GFGFVTFSNEK	CAS017_B22	ATMG01190.1	370	e-103	ATPase	ATPase
DCP1B2	IGLFGGAGVGK	31706rsicef_13335.y1	AT5G08690.1	265	1.0e-71	ATP synthase alpha/beta family protein	ATPase
DCP1B2	ILNVIGEPIDER	ABA1_32_D07.g1_A012	AT5G08690.1	211	3.0e-55	ATP synthase alpha/beta family protein	ATPase
DCP1B2	ITNYYTNFQVDEIGR	CAS017_B22	ATMG01190.1	370	e-103	ATPase	ATPase
DCP1B2	QISELGIYPAVDPLDSTSR	scaff_6888_1	AT5G08690.1	288	9.0e-78	ATPase	ATPase
DCP1B2	TAIAIDTILNQK	scaff_6888_1	AT5G08690.1	288	9.0e-78	ATPase	ATPase
DCP1B2	VLNTGSPIR	31706rsicef_13335.y1	AT5G08690.1	265	1.0e-71	ATP synthase alpha/beta family protein	ATPase
DCP1B2	VVDLLAPYQR	31706rsicef_13335.y1	AT5G08690.1	265	1.0e-71	ATP synthase alpha/beta family protein	ATPase
DCP1B2	VVSVGDGISR	scaff_8296_1	ATCG00120.1	405	e-113	ATPase	ATPase
DCP1B1	QIVSSTNEEDKVIVFER	CAA54308.1	AT2G36390.1	826	0.0	SBE2.1, BE3 | starch branching enzymy	BE3
DCP1B3	AGRXPPQGXPR	c.10.J1.5 CM523-7	AT3G27240.1	286	7.0e-78	Cytochrome C1 family	Cyt_c1
DCP1B3	ALEDANAELEVK	c.10.J1.5 CM523-7	AT3G27240.1	286	7.0e-78	Cytochrome C1 family	Cyt_c1
DCP1B3	DLVGVAYTEEEVK	c.10.J1.5 CM523-7	AT3G27240.1	286	7.0e-78	Cytochrome C1 family	Cyt_c1
DCP1B3	EPAFFTGSEVR	c.05.G19.5 CM523-7	AT3G27240.1	286	7.0e-78	Cytochrome C1 family	Cyt_c1
DCP1B3	FPQPYANEQAAR	Cassava.419.C1.Contig536	AT5G40810.1	373	7.9e-104	Cytochrome C1 family	Cyt_c1
DCP1B3	HEEVVEQVK	c.05.G19.5 CM523-7	AT3G27240.1	286	7.0e-78	Cytochrome C1 family	Cyt_c1
DCP1B3	LSDRFPQPYANEQAAR	Cassava.419.C1.Contig536	AT5G40810.1	370	e-103	Cytochrome C1 family	Cyt_c1
DCP1B3	LSISTSFSNR	Cassava.419.C1.Contig536	AT5G40810.1	370	e-103	Cytochrome C1 family	Cyt_c1
DCP1B3	LLEVDNR	C024P63U	ATMG00160.1	91	1.0e-35	Ctochrome oxidase 2	Cyt_c2

Table S3. Contd…..

SDS_PAGE Zone Code	Peptide Sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Protein Abreviation
DCP1B3	LNQISILVQR	C024P63U	ATMG00160.1	91	1.0e-35	Ctochrome oxidase 2	Cyt_c2
DCP1B3	SQLNSIQEASGGK	CGF1000749_A02	AT1G54220.2	2409	0.0e-115	Dihydrolipoamide acetyltransferase	Dihy
DCP1B3	EEDTTVPIEK	si.02.O23.5 MCol1522	AT1G20450.2	41	4.0e-04	LTI29, LTI45, ERD10 | dehydrin protein family	ERD10
DCP1B3	KEEDTTVPIEK	si.02.O23.5 MCol1522	AT1G20450.2	41	4.0e-04	LTI29, LTI45, ERD10 | dehydrin protein family	ERD10
DCP1B2	KPEEVATPPPPPPPTEHVHAESASHEGEAK	si.02.O23.5 MCol1522	AT1G20450.2	41	4.0e-04	LTI29, LTI45, ERD10 | dehydrin protein family	ERD10
DCP1B3	VQVSEPEEK	si.02.O23.5 MCol1522	AT1G20450.2	41	4.0e-04	LTI29, LTI45, ERD10 | dehydrin protein family	ERD10
DCP1B2	YEEAEAANQADEK +	si.02.O23.5 MCol1522	AT1G20450.2	41	4.0e-04	LTI29, LTI45, ERD10 | dehydrin protein family	ERD10
DCP1B3	DAIEGMNGQDLDGRNITVNEAQSR	scaff_9887_1	AT5G52840.1	275	6.0e-74	NADH-ubiquinone oxidoreductase-related	NADH
DCP1B2	AVEDELEK	A022P66U	AT5G62740.1	151	1.0e-70	HIR1, ATHIR1 | SPFH/Band 7/PHB domain	HIR1
DCP1B2	QAIVDGLR	KS12045C05 KS12	AT5G62740.1	258	1.0e-69	HIR1, ATHIR1 | SPFH/Band 7/PHB domain	HIR1
DCP1B2	SSAVFLPHGPAAVR	KS12045C05 KS12	AT5G62740.1	258	1.0e-69	HIR1, ATHIR1 | SPFH/Band 7/PHB domain	HIR1
DCP1B2	AGLQFPVGR	AU065163	AT5G59970.1	167	2.0e-42	Histone superfamily protein	Histone
DCP1B2	DAVTYTEHAR	AU065163	AT5G59970.1	167	2.0e-42	Histone superfamily protein	Histone
DCP1B1	ASMENGVLTVTVPK	scaff_6675_1	AT5G37670.1	154	4.0e-38	HSP15.7	HSP_15.7
DCP1B1	ACMENGVLTVTVPK	Cassava.2670.C1.Contig2792	AT3G46230.1	197	7.2e-051	ATHSP17.4 (Arabidopsis thaliana heat shock protein 17.4)	HSP_17.4I
DCP1B1	ASMENGVLTVTVPKEEVQKPDVK	CAS035_D18	AT3G46230.1	126	2.0e-47	sHSP_17.4 kDa class I	HSP_17.4I
DCP1B1	FRLPENANMDQIR	scaff_8565_1	AT3G46230	142	1.0e-34	sHSP_17.4 kDa class I	HSP_17.4I
DCP1B1	SSMENGVLTVTVPK	CAS037_L03.f	AT3G46230	192	1.0e-49	sHSP_17.4 kDa class I	HSP_17.4I
DCP1B1	VELEDGRVLQISGER	CAS035_D18	AT3G46230.1	126	2.0e-47	sHSP_17.4 kDa class I	HSP_17.4I
DCP1B1	VEVEEGRILQVSGER	CAS035_D18	AT3G46230.1	126	2.0e-47	sHSP_17.4 kDa class I	HSP_17.4I
DCP1B1	ASMENGVLTVTVPKEEVNKPEVK	Cassava.859.C1.Contig1017	AT2G29500.1	146	1.6e-035	sHSP_17.6 kDa class I	HSP_17.6I
DCP1B1	ASMENGVLTVTVPKEEVQKPDVK	Cassava.1764.C1.Contig1943	AT2G29500.1	146	1.6e-035	17.6 kDa class I small heat shock protein (HSP17.6B-CI)	HSP_17.6I
DCP1B1	ETPEAHVFEADLPGLK	Cassava.859.C1.Contig1017	AT2G29500	146	1.6e-035	sHSP_17.6 kDa class I	HSP_17.6I
DCP1B1	FRLPENANMDQIR	scaff_6764_1	AT2G29500.1	211	3.0e-55	sHSP_17.6 kDa class I	HSP_17.6I
DCP1B1	IDWKETPEAHVFQADLPGLR	Cassava.1764.C1.Contig1943	AT2G29500	146	1.6e-035	sHSP_17.6 kDa class I	HSP_17.6I

Table S3. Contd…..

SDS_PAGE Zone Code	Peptide Sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Protein Abreviation
DCP1B1	IEVEDDRVLQISGER	Cassava.859.C1.Contig1017	AT2G29500.1	146	1.6e-035	17.6 kDa class I small heat shock protein (HSP17.6B-CI)	HSP_17.6I
DCP1B1	SVSEGGIGFDYR	Cassava.859.C1.Contig1017	AT2G29500.1	146	1.6e-035	17.6 kDa class I small heat shock protein (HSP17.6B-CI)	HSP_17.6I
DCP1B1	VEIEDDRVLQISGER	Cassava.1764.C1.Contig1943	AT2G29500.1	146	1.6e-035	17.6 kDa class I small heat shock protein (HSP17.6B-CI)	HSP_17.6I
DCP1B1	VEVEEGRILQVSGER	scaff_6764_1	AT2G29500.1	211	3.0e-55	sHSP_17.6 kDa class I	HSP_17.6I
DCP1B1	VEWKETPEAHVFK	Cassava.1764.C1.Contig1943	AT2G29500.1	146	1.6e-035	sHSP_17.6 kDa class I	HSP_17.6I
DCP1B2	ASMENGVLTVTVPKEEVQKPDVK	Cassava.388.C1.Contig493	AT5G59720	217	6.3e-057	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	ETPESHVFKADLPGLK	Cassava.388.C1.Contig493	AT5G59720	217	6.3e-057	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	ETSAFINAR	Cassava.388.C1.Contig493	AT5G59720	217	6.3e-057	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	FPSTALSAPR	CAS037_M18.f	AT5G59720.1	112	3.0e-35	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	FRLPENAQVDQVK	Cassava.388.C1.Contig493	AT5G59720	217	6.3e-057	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	IDWKETPESHVFK	Cassava.388.C1.Contig493	AT5G59720	217	6.3e-057	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	IEVEDGRVLQISGER	CAS010_O01.f	AT5G59720	171	3.0e-43	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	LPENANMDQIR	Cassava.388.C1.Contig493	AT5G59720	217	6.3e-057	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	PFQDFPFPSTALSAPR	CAS010_O01.f	AT5G59720.1	171	3.0e-43	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	SSMENGVLTVTVPK	scaff_8870_1	AT5G59720.1	220	7.0e-58	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	VEIEDGRVLQISGER	scaff_7380_1	AT5G59720.1	194	7.0e-50	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	VEVEEGRILQVSGER	scaff_8870_1	AT5G59720.1	220	7.0e-58	sHSP_18.1 kDa class I	HSP_18.1I
DCP1B2	ACMENGVLTVTVPK	scaff_7380_1	AT5G59720.1	194	7.0e-50	HSP18.2	HSP_18.2
DCP1B2	ASMENGVLTVTVPKEEVQKPDVK	Cassava.388.C1.Contig493	AT5G59720.1	217	6.3e-057	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP_18.2
DCP1B2	FPSTALSAPR	CAS037_M18.f	AT5G59720.1	112	3.0e-35	HSP18.2 | heat shock protein 18.2 |	HSP_18.2
DCP1B2	FRLPENANMDQIR	scaff_7380_1	AT5G59720.1	194	7.0e-50	Symbols: HSP18.2 | heat shock protein 18.2	HSP_18.2
DCP1B2	PFPSTALSAPR	Cassava.388.C1.Contig493	AT5G59720.1	217	6.3e-057	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP_18.2
DCP1B2	PFQDFPFPSTALSAPR	CAS010_O01.f	AT5G59720.1	171	3.0e-43	HSP18.2 (heat shock protein 18.2)	HSP_18.2
DCP1B2	SELANETSAFANTR	CAS010_O01.f	AT5G59720.1	171	3.0e-43	HSP18.2 (heat shock protein 18.2)	HSP_18.2
DCP1B2	SELSNETAAFANTR	CAS010_O01.f	AT5G59720.1	171	3.0e-43	HSP18.2 (heat shock protein 18.2)	HSP_18.2
DCP1B2	VEIEDGRVLQISGER	scaff_7380_1	AT5G59720.1	194	7.0e-50	HSP18.2 | heat shock protein 18.2	HSP_18.2
DCP1B2	VELEDGRVLQISGER	Cassava.388.C1.Contig493	AT5G59720.1	217	6.3e-057	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP_18.2
DCP1B2	VEVEEGRVLQISGER	scaff_7380_1	AT5G59720.1	194	7.0e-50	HSP18.2 | heat shock protein 18.2	HSP_18.2

Table S3. Contd…..

SDS_PAGE Zone Code	Peptide Sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Protein Abreviation
DCP1B1	ACMENGVLTVTVPK	CAS037_L20	AT2G29500.1	162	2.0e-40	HSP20-like chaperones superfamily	HSP_20
DCP1B1	ADLPGLKK	si.05.K16.5 MCol1522	AT1G07400.1	64	2.0e-09	HSP20-like chaperones superfamily	HSP_20
DCP1B1	AQYEDSPKK	CAST023F09	AT2G29500.1	107	2.0e-43	HSP20-like chaperones superfamily	HSP_20
DCP1B1	ASMENGVLTMTVPK	CAST023F09	AT2G29500.1	107	2.0e-43	HSP20-like chaperones superfamily	HSP_20
DCP1B1	ENSAFVSTR	CAST023F09	AT2G29500.1	107	2.0e-43	HSP20-like chaperones superfamily	HSP_20
DCP1B1	ETPESHVFK	si.05.K16.5 MCol1522	AT1G07400.1	64	2.0e-09	HSP20-like chaperones superfamily	HSP_20
DCP1B1	FRLPENAK	si.05.K16.5 MCol1522	AT1G07400.1	64	2.0e-09	HSP20-like chaperones superfamily	HSP_20
DCP1B1	FRLPENANMDQIR	scaff_6764_1	AT2G29500.1	211	3.0e-55	HSP20-like chaperones superfamily	HSP_20
DCP1B1	GPGLYSDIGK	saq58h07.y1 Gm-c1076	AT2G29500.1	241	3.0e-64	HSP20-like chaperones superfamily	HSP_20
DCP1B1	ISGLIYEETR	si.05.K16.5 MCol1522	AT1G07400.1	64	2.0e-09	HSP20-like chaperones superfamily	HSP_20
DCP1B1	KGDLFLADVNTQLK	si.05.K16.5 MCol1522	AT1G07400.1	64	2.0e-09	HSP20-like chaperones superfamily	HSP_20
DCP1B1	SEFANETSAFANTR	CAST050D04	AT1G07400.1	53	4.0e-08	HSP20-like chaperones superfamily	HSP_20
DCP1B3	SELANETSAFANTR	si.05.K16.5 MCol1522	AT1G07400.1	64	2.0e-09	HSP20-like chaperones superfamily	HSP_20
DCP1B1	SSMENGVLTVTVPK	CAS037_L20	AT2G29500.1	162	2.0e-40	HSP20-like chaperones superfamily	HSP_20
DCP1B1	VELEDGRVLQISGER	CAS037_L20	AT2G29500.1	162	2.0e-40	HSP20-like chaperones superfamily	HSP_20
DCP1B1	VEVEEGRVLQISGER	CAS037_L20	AT2G29500.1	162	2.0e-40	HSP20-like chaperones superfamily	HSP_20
DCP1B2	VLQISGER	si.05.K16.5 MCol1522	AT1G07400.1	64	2.0e-09	HSP20-like chaperones superfamily	HSP_20
DCP1B2	AELKNGVLFISIPK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP_21
DCP1B2	APWDIKEDENEFK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP_21
DCP1B2	FDMPGLSKEDVK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP_21
DCP1B2	IFEDAMTLPGSR	scaff_6656_1	AT4G27670.1	131	1.0e-30	HSP21	HSP_21
DCP1B2	KVIDVEIQ +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP_21

Table S3. Contd…..

SDS_PAGE Zone Code	Peptide Sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Protein Abreviation
DCP1B2	LRFDMPGLSK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP_21
CP1B2	NGVLFISIPK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP_21
DCP1B2	QLAVDVSPFGLLDPLSPMR +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP_21
DCP1B2	QMMDTMDRIFEDAMTLPGSR +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP_21
DCP1B2	VFVEEDVLVIK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP_21
DCP1B2	ASMENGVLTVTVPK-EEVQKPDVK	scaff_6708_1	AT4G10250	125	1e-28	ATHSP22.0	HSP_22.0
DCP1B2	FRLPENANMDQIR	scaff_9075_1	AT4G10250	139	1.0e-33	ATHSP22.0	HSP_22.0
DCP1B2	IEVEDGRVLQISGER	scaff_9075_1	AT4G10250	139	1.0e-33	ATHSP22.0	HSP_22.0
DCP1B2	VEIEDGRVLQISGER	scaff_6708_1	AT4G10250.1	125	1.0e-28	ATHSP22.0	HSP_22.0
DCP1B2	VIDIAEQGSSGQDIK	scaff_6708_1	AT4G10250.1	125	1.0e-28	ATHSP22.0	HSP_22.0
DCP1B2	ASMENGVLTVTVPK-EEVQKPDV	scaff_9466_1	AT4G25200.1	186	1.0e-47	ATHSP23.6	HSP_23.6
DCP1B2	SSMENGVLTVTVPK	scaff_8927_1	AT4G25200.1	226	2.0e-59	ATHSP23.6-MITO, HSP23.6-MITO, MITOCHONDRION-LOCALIZED	HSP_23.6
DCP1B2	ASMENGVLTVTVPKEEVQKPDVK	CAS011_L20	AT1G52560	141	6.0e-34	HSP26.5	HSP_26.5
DCP1B2	AVFPSIVGRPR	scaff_6671_1	AT3G11500.1	150	8.0e-37	Small nuclear ribonucleoprotein family protein	snRNP
DCP1B2	VLAPYSSEDAR	CLF20	AT5G50850.1	263	1.0e-70	MAB1 | Transketolase family protein	MAB1
	QTTGIVGLDVVPNAR	scaff_8720_1	AT4G27670.1	210	1.0e-54	NADH	NADH
DCP1B3	VLAEDAYYVVK	CAST051C10	AT2G28900.1	165	2.0e-41	OEP16	OEP16
DCP1B2	AENLDYLIK +	CV01021A2C07.f1 CV01	AT4G13010.1	321	3.0e-88	Oxidoreductase, zinc-binding dehydrogenase family protein	Oxireductase
DCP1B2	SLGADEVLDYR +	CV01021A2C07.f1 CV01	AT4G13010.1	54	2.1e-008	Oxidoreductase, zinc-binding dehydrogenase family protein	Oxireductase
DCP1B2	YIAPEQVPVKYGGLSR	CV01023A2D03.f1	AT1G72150.1	168	3.9e-042	PATL1 (PATELLIN 1)	PATL1
DCP1B2	VLPSIGNEVLK		AT3G27280.2			ATPHB4, PHB4, PROHIBITIN	PHB4
DCP1B2	AEVLGLDPR	Cassava.661.C1.Contig800	AT5G09660.1	601	5.3e-172	PMDH2 (PEROXISOMAL NAD-MALATE DEHYDROGENASE 2); malate dehydrogenase	PMDH2
DCP1B2	LKLIPERGVSEPTEDG	Cassava.661.C1.Contig800	AT5G09660.1	601	5.3e-172	PMDH2 (PEROXISOMAL NAD-MALATE DEHYDROGENASE 2); malate dehydrogenase	PMDH2

Table S3. Contd…..

SDS_PAGE Zone Code	Peptide Sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Protein Abreviation
DCP1B3	FVFAGPSK	m.04.H15.5 MPer183	AT4G09160.1	233	5.0e-62	SEC14 cytosolic factor family protein	SEC14
DCP1B2	IIEVDNR	coau0004K06	AT1G29310.1	194	3.0e-50	SecY protein transport family protein	SecY
DCP1B3	GNSVVTVEALEPVNRAM	CAS008_G02	AT4G24770.1	136	3.0e-32	RBP31	RBP31
DCP1B1	VLQLETAAGAAIR		AT5G17310.2			UDP-glucose pyrophosphorylase 2 (UGP2)	UGP2

Table S4. Supplementary Data: Listing Peptides Sequences (MASCOT Quality) in Non-carotenoid-protein Complex. SDS_PAGE Picture Shows the Gel Zone Fractionation of Separated Proteins Used for the LC_MS/MS Analysis

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B2	gi|13928270	787	49.01	600.28	1198.54	1198.55	-0.01	0.00	8.08	443.28	2	AAAEDTMLSYK +
M2B7	gi|1771261	1124	564.8	707.37	1412.73	1412.75	-0.02	0.00	71.11	0.00	1	AAQPSLIADDIATK +
M2B7	gi|120666	1151	263.1	717.87	1433.73	1433.75	-0.02	0.00	22.01	32.28	1	AASFNIIPSSTGAAK +
M2B7	gi|74419004	1151	247.4	717.87	1433.73	1433.75	-0.02	0.00	22.01	32.28	1	AASFNIIPSSTGAAK +
M2B7	gi|462137	1151	141	717.87	1433.73	1433.75	-0.02	0.00	22.01	32.28	1	AASFNIIPSSTGAAK +
M2B7	gi|15228683	304	191.3	499.76	997.50	997.52	-0.02	0.00	42.75	0.16	1	AFATYVQAK +
M2B7	gi|629646	304	190.1	499.76	997.50	997.52	-0.02	0.00	42.75	0.16	1	AFATYVQAK +
M2B7	gi|13195430	304	128.3	499.76	997.50	997.52	-0.02	0.00	42.75	0.16	1	AFATYVQAK +
M2B7	gi|130172	304	121.3	499.76	997.50	997.52	-0.02	0.00	42.75	0.16	1	AFATYVQAK +
M2B7	gi|1730557	304	118.3	499.76	997.50	997.52	-0.02	0.00	42.75	0.16	1	AFATYVQAK +
M2B7	gi|34305475	304	101.3	499.76	997.50	997.52	-0.02	0.00	42.75	0.16	1	AFATYVQAK +
M2B7	gi|120666	721	263.1	581.31	1160.60	1160.62	-0.02	0.00	36.26	1.26	1	AGIALNDNFVK +
M2B7	gi|74419004	721	247.4	581.31	1160.60	1160.62	-0.02	0.00	36.26	1.26	1	AGIALNDNFVK +
M2B7	gi|120642	721	100	581.31	1160.60	1160.62	-0.02	0.00	36.26	1.26	1	AGIALNDNFVK +
M2B7	gi|10120773	721	99.24	581.31	1160.60	1160.62	-0.02	0.00	36.26	1.26	1	AGIALNDNFVK +
M2B4	gi|120666	722	263.1	581.80	1161.59	1161.60	-0.01	0.00	61.33	0.00	1	AGIALNDNFVK + Deamidation (NQ)
M2B4	gi|74419004	722	247.4	581.80	1161.59	1161.60	-0.01	0.00	61.33	0.00	1	AGIALNDNFVK + Deamidation (NQ)
M2B4	gi|120642	722	100	581.80	1161.59	1161.60	-0.01	0.00	61.33	0.00	1	AGIALNDNFVK + Deamidation (NQ)
M2B4	gi|10120773	722	99.24	581.80	1161.59	1161.60	-0.01	0.00	61.33	0.00	1	AGIALNDNFVK + Deamidation (NQ)
M2B4	gi|34099812	744	192.2	588.31	1174.62	1174.63	-0.02	0.00	48.78	0.07	1	AGIALNENFVK +
M2B4	gi|48142692	722	104	581.80	1161.59	1161.60	-0.01	0.00	61.33	0.00	2	AGIALNNNFVK + 2 Deamidation (NQ)
M2B7	gi|48142692	721	104	581.31	1160.60	1160.62	-0.02	0.00	36.26	1.26	2	AGIALNNNFVK + Deamidation (NQ)
M2B4	gi|56481797	1148	168.5	717.84	1433.66	1433.68	-0.02	0.00	93.50	0.00	1	ALDMNTAEDAIVR + Oxidation (M)
M2B4	gi|2213867	1619	115.1	704.86	2815.42	2815.45	-0.03	0.00	32.72	2.38	1	ALNDHHVLLEGTLLKPNMVTPGSESK + Oxidation (M)

Table S4. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B1	gi|550544	583	52.17	553.30	1104.58	1104.58	0.00	0.00	52.17	0.03	1	AMQLLESGLK + Oxidation (M)
M2B4	gi|77745483	181	110.8	451.25	900.49	900.50	-0.01	0.00	38.24	0.77	1	ANSLAQLGK +
M2B4	gi|15226185	181	88.55	451.25	900.49	900.50	-0.01	0.00	38.24	0.77	1	ANSLAQLGK +
M2B2	gi|68422636	769	57.52	594.82	1187.62	1187.61	0.00	1.00	57.52	0.01	1	AQLLNSQEKR + 2 Deamidation (NQ)
M2B2	gi|57106334	484	81.57	533.26	1064.50	1064.51	-0.02	0.00	35.58	1.18	2	AQYDELAQK +
M2B2	gi|74009044	484	48.38	533.26	1064.50	1064.51	-0.02	0.00	35.58	1.18	2	AQYDELAQK +
M2B3	gi|57106334	485	81.57	533.26	1064.50	1064.51	-0.02	0.00	28.78	5.63	2	AQYDELAQK +
M2B3	gi|74009044	485	48.38	533.26	1064.50	1064.51	-0.02	0.00	28.78	5.63	2	AQYDELAQK +
M2B4	gi|57106334	483	81.57	533.25	1064.49	1064.51	-0.02	0.00	21.34	29.23	2	AQYDELAQK +
M2B4	gi|74009044	483	48.38	533.25	1064.49	1064.51	-0.02	0.00	21.34	29.23	2	AQYDELAQK +
M2B7	gi|57335398	1087	77.82	695.84	1389.66	1389.67	-0.02	0.00	31.83	3.25	2	ASLENTLAETEGR +
M2B1	gi|123534	1184	155.3	731.87	1461.73	1461.74	-0.01	0.00	88.19	0.00	1	ASMENGVLTVTVPK + Deamidation (NQ); Oxidation (M)
M2B1	gi|123534	1183	155.3	731.37	1460.73	1460.75	-0.02	0.00	106.43	0.00	1	ASMENGVLTVTVPK + Oxidation (M)
M2B7	gi|6911553	1406	308.8	559.24	1674.70	1674.72	-0.03	0.00	35.89	0.35	1	ATAGDTHLGGEDFDNR +
M2B7	gi|425194	1406	215.9	559.24	1674.70	1674.72	-0.03	0.00	35.89	0.35	1	ATAGDTHLGGEDFDNR +
M2B7	gi|8918240	1406	145.4	559.24	1674.70	1674.72	-0.03	0.00	35.89	0.35	1	ATAGDTHLGGEDFDNR +
M2B7	gi|51012459	1406	130.8	559.24	1674.70	1674.72	-0.03	0.00	35.89	0.35	1	ATAGDTHLGGEDFDNR +
M2B7	gi|17647515	1406	109.5	559.24	1674.70	1674.72	-0.03	0.00	35.89	0.35	1	ATAGDTHLGGEDFDNR +
M2B4	gi|6272285	530	53.18	541.26	1080.50	1080.51	-0.01	0.00	53.18	0.02	1	AYSDDEIIR +
M2B4	gi|388261	530	53.18	541.26	1080.50	1080.51	-0.01	0.00	53.18	0.02	2	AYSDDELIR +
M2B4	gi|8918240	843	145.4	616.32	1230.62	1230.64	-0.02	0.00	16.75	116.50	1	DAGVIAGLNVMR + Oxidation (M)
M2B7	gi|6911553	842	308.8	616.32	1230.62	1230.64	-0.02	0.00	22.89	29.45	1	DAGVIAGLNVMR + Oxidation (M)
M2B7	gi|8918240	842	145.4	616.32	1230.62	1230.64	-0.02	0.00	22.89	29.45	1	DAGVIAGLNVMR + Oxidation (M)
M2B4	gi|120666	945	263.1	653.32	1304.62	1304.64	-0.02	0.00	51.84	0.03	1	DAPMFVVGVNEK +
M2B4	gi|74419004	945	247.4	653.32	1304.62	1304.64	-0.02	0.00	51.84	0.03	1	DAPMFVVGVNEK +
M2B4	gi|34099812	945	192.2	653.32	1304.62	1304.64	-0.02	0.00	51.84	0.03	1	DAPMFVVGVNEK +
M2B4	gi|120666	976	263.1	661.32	1320.62	1320.64	-0.02	0.00	82.70	0.00	1	DAPMFVVGVNEK + Oxidation (M)
M2B4	gi|74419004	976	247.4	661.32	1320.62	1320.64	-0.02	0.00	82.70	0.00	1	DAPMFVVGVNEK + Oxidation (M)
M2B4	gi|34099812	976	192.2	661.32	1320.62	1320.64	-0.02	0.00	82.70	0.00	1	DAPMFVVGVNEK + Oxidation (M)
M2B7	gi|15228683	1128	191.3	708.31	1414.60	1414.61	0.00	0.00	31.36	1.43	1	DFPSYIECQEK + Carbamidomethyl (C)
M2B7	gi|13195430	1128	128.3	708.31	1414.60	1414.61	0.00	0.00	31.36	1.43	1	DFPSYIECQEK + Carbamidomethyl (C)
M2B7	gi|130172	1128	121.3	708.31	1414.60	1414.61	0.00	0.00	31.36	1.43	1	DFPSYIECQEK + Carbamidomethyl (C)
M2B7	gi|34305475	1128	101.3	708.31	1414.60	1414.61	0.00	0.00	31.16	1.49	2	DFPSYIECQQK + Carbamidomethyl (C); Deamidation (NQ)
M2B4	gi|77745483	278	110.8	492.77	983.52	983.53	-0.01	0.00	30.22	2.37	1	DQNIVPGIK + Deamidation (NQ)
M2B1	gi|50420223	460	47.84	530.77	1059.52	1059.54	-0.02	1.00	47.84	0.09	1	DVLDLNKNK + 2 Deamidation (NQ)

Table S4. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B7	gi|50420223	462	47.84	530.77	1059.53	1059.54	-0.01	1.00	39.91	0.59	1	DVLDLNKNK + 2 Deamidation (NQ)
M2B7	gi|130172	347	121.3	509.25	1016.49	1016.50	-0.01	0.00	20.43	36.47	2	EAWNITQR +
M2B7	gi|33326375	977	157.3	662.30	1322.59	1322.60	0.00	0.00	13.81	138.08	2	EDQLEYLEER +
M2B7	gi|1708314	977	133.2	662.30	1322.59	1322.60	0.00	0.00	13.81	138.08	2	EDQLEYLEER +
M2B2	gi|6984140	313	90.02	500.78	999.55	999.56	-0.01	0.00	57.23	0.01	1	EEAVQLALK +
M2B1	gi|40646966	942	73.65	651.82	1301.62	1301.65	-0.02	1.00	44.52	0.17	2	EEVKVQVEEGR + Deamidation (NQ)
M2B7	gi|1771261	470	564.8	531.26	1060.50	1060.52	-0.02	0.00	34.96	1.36	1	EFADDVLPR +
M2B7	gi|1771261	471	564.8	531.26	1060.50	1060.52	-0.02	0.00	45.76	0.12	1	EFADDVLPR +
M2B7	gi|109715750	470	176.3	531.26	1060.50	1060.52	-0.02	0.00	34.96	1.36	1	EFADDVLPR +
M2B7	gi|109715750	471	176.3	531.26	1060.50	1060.52	-0.02	0.00	45.76	0.12	1	EFADDVLPR +
M2B7	gi|76496236	470	79.87	531.26	1060.50	1060.52	-0.02	0.00	34.96	1.36	2	EFADNVLPR + Deamidation (NQ)
M2B7	gi|76496236	471	79.87	531.26	1060.50	1060.52	-0.02	0.00	45.76	0.12	2	EFADNVLPR + Deamidation (NQ)
M2B7	gi|4586236	470	66.73	531.26	1060.50	1060.52	-0.02	0.00	34.96	1.36	2	EFADNVLPR + Deamidation (NQ)
M2B7	gi|4586236	471	66.73	531.26	1060.50	1060.52	-0.02	0.00	45.76	0.12	2	EFADNVLPR + Deamidation (NQ)
M2B4	gi|10334493	348	45.07	509.26	1016.50	1016.52	-0.01	0.00	45.07	0.14	1	EFAPSIPEK +
M2B4	gi|113621	131	77.41	435.25	868.48	868.50	-0.02	0.00	49.14	0.02	1	EGGVLPGIK +
M2B4	gi|786178	131	58.08	435.25	868.48	868.50	-0.02	0.00	49.14	0.02	1	EGGVLPGIK +
M2B4	gi|33326375	902	157.3	638.32	1274.63	1274.64	0.00	0.00	80.77	0.00	1	EIISNASDALDK +
M2B4	gi|21536853	1086	272.4	694.87	1387.72	1387.73	-0.01	0.00	73.14	0.00	1	ELDYLVGAVANPK +
M2B4	gi|115469436	1086	191.5	694.87	1387.72	1387.73	-0.01	0.00	73.14	0.00	1	ELDYLVGAVANPK +
M2B4	gi|23100613	902	98.66	638.32	1274.63	1274.64	0.00	0.00	80.77	0.00	2	ELISNASDAIDK +
M2B7	gi|111063883	631	67.42	561.78	1121.55	1121.56	-0.01	0.00	33.11	2.17	1	ELQQIAQYK + 2 Deamidation (NQ)
M2B1	gi|3582434	494	77.93	536.27	1070.53	1070.54	-0.01	0.00	29.02	4.18	2	ETPEAHIFK +
M2B1	gi|40646966	494	73.65	536.27	1070.53	1070.54	-0.01	0.00	29.13	4.08	1	ETPQAHIFK + Deamidation (NQ)
M2B3	gi|47212110	79	84.1	414.21	826.42	826.42	-0.01	0.00	52.09	0.01	1	FASFIDK +
M2B3	gi|47604942	79	78.73	414.21	826.42	826.42	-0.01	0.00	52.09	0.01	1	FASFIDK +
M2B4	gi|115496454	78	113.8	414.21	826.41	826.42	-0.01	0.00	13.85	107.58	2	FASFIDK +
M2B4	gi|47212110	78	84.1	414.21	826.41	826.42	-0.01	0.00	13.85	107.58	2	FASFIDK +
M2B7	gi|116004057	77	153.5	414.21	826.41	826.42	-0.01	0.00	37.29	0.47	1	FASFIDK +
M2B7	gi|6980088	77	134.2	414.21	826.41	826.42	-0.01	0.00	37.29	0.47	1	FASFIDK +
M2B7	gi|47212110	77	84.1	414.21	826.41	826.42	-0.01	0.00	37.29	0.47	1	FASFIDK +
M2B3	gi|109071958	79	67.73	414.21	826.42	826.42	-0.01	0.00	52.09	0.01	2	FASFINK + Deamidation (NQ)
M2B7	gi|109071958	77	67.73	414.21	826.41	826.42	-0.01	0.00	37.29	0.47	2	FASFINK + Deamidation (NQ)
M2B4	gi|629646	272	190.1	490.72	979.43	979.44	-0.01	0.00	30.95	2.00	1	FCNPDLSK + Carbamidomethyl (C)
M2B4	gi|92887207	957	160.3	655.82	1309.63	1309.63	-0.01	0.00	26.87	9.62	1	FDMGGSAAVLGAAK + Oxidation (M)
M2B1	gi|15234240	189	56.44	455.71	909.41	909.43	-0.01	0.00	26.41	6.32	1	FDMPGLSK + Oxidation (M)

Table S4. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B7	gi|6911553	990	308.8	665.30	1328.59	1328.61	-0.01	0.00	10.04	268.97	1	FEELNMDLFR + Oxidation (M)
M2B7	gi|425194	990	215.9	665.30	1328.59	1328.61	-0.01	0.00	10.04	268.97	1	FEELNMDLFR + Oxidation (M)
M2B7	gi|116504654	990	104.9	665.30	1328.59	1328.61	-0.01	0.00	10.04	268.97	1	FEELNMDLFR + Oxidation (M)
M2B4	gi|4733946	289	208.4	496.26	990.51	990.51	-0.01	0.00	25.55	14.35	1	FQEIGLER +
M2B4	gi|13160142	289	191.4	496.26	990.51	990.51	-0.01	0.00	25.55	14.35	1	FQEIGLER +
M2B4	gi|22331535	289	182.9	496.26	990.51	990.51	-0.01	0.00	25.55	14.35	1	FQEIGLER +
M2B4	gi|80973758	289	177	496.26	990.51	990.51	-0.01	0.00	25.55	14.35	1	FQEIGLER +
M2B4	gi|37790792	289	159.4	496.26	990.51	990.51	-0.01	0.00	25.55	14.35	1	FQEIGLER +
M2B7	gi|4733946	288	208.4	496.26	990.50	990.51	-0.01	0.00	37.05	0.96	1	FQEIGLER +
M2B7	gi|13160142	288	191.4	496.26	990.50	990.51	-0.01	0.00	37.05	0.96	1	FQEIGLER +
M2B7	gi|22331535	288	182.9	496.26	990.50	990.51	-0.01	0.00	37.05	0.96	1	FQEIGLER +
M2B7	gi|80973758	288	177	496.26	990.50	990.51	-0.01	0.00	37.05	0.96	1	FQEIGLER +
M2B7	gi|37790792	288	159.4	496.26	990.50	990.51	-0.01	0.00	37.05	0.96	1	FQEIGLER +
M2B7	gi|6056373	169	51.05	445.75	889.49	889.50	-0.01	0.00	32.53	1.92	1	FSVSPVVR +
M2B7	gi|1705587	128	121.2	430.72	859.42	859.42	-0.01	0.00	28.53	5.69	1	FVEYFR +
M2B7	gi|92874670	128	62.93	430.72	859.42	859.42	-0.01	0.00	28.53	5.69	1	FVEYFR +
M2B4	gi|1100223	1064	68.36	686.35	1370.69	1370.72	-0.02	0.00	16.96	89.02	1	GAGQNIIPSSTGAAK +
M2B4	gi|87303442	1064	55.64	686.35	1370.69	1370.72	-0.02	0.00	16.96	89.02	1	GAGQNIIPSSTGAAK +
M2B3	gi|62526587	204	227.5	459.24	916.46	916.46	0.00	0.00	25.66	13.30	2	GCAPLMLR + Carbamidomethyl (C)
M2B7	gi|6056373	241	51.05	478.26	954.51	954.52	-0.02	0.00	18.52	39.74	1	GGGQVIPTAR +
M2B4	gi|115434198	1170	176.5	724.85	1447.68	1447.70	-0.01	0.00	51.08	0.04	1	GILAIDESNATCGK + Carbamidomethyl (C)
M2B4	gi|15226185	1170	88.55	724.85	1447.68	1447.70	-0.01	0.00	51.08	0.04	1	GILAIDESNATCGK + Carbamidomethyl (C)
M2B4	gi|6911142	848	51.55	616.80	1231.59	1231.58	0.01	1.00	25.29	14.11	2	GSGGGGGGGGFRGPR +
M2B7	gi|6911142	846	51.55	616.79	1231.57	1231.58	-0.01	1.00	51.55	0.03	2	GSGGGGGGGGFRGPR +
M2B4	gi|113624	1572	63.32	764.03	2289.08	2289.11	-0.03	0.00	63.32	0.00	1	GTVELAGTNGETTTQGLDGLAQR + Deamidation (NQ)
M2B4	gi|21536853	1321	272.4	787.41	1572.81	1572.84	-0.03	0.00	73.68	0.00	1	GVTTIIGGGDSVAAVEK +
M2B4	gi|115469436	1321	191.5	787.41	1572.81	1572.84	-0.03	0.00	73.68	0.00	1	GVTTIIGGGDSVAAVEK +
M2B4	gi|1022805	1321	86.85	787.41	1572.81	1572.84	-0.03	0.00	73.68	0.00	1	GVTTIIGGGDSVAAVEK +
M2B7	gi|21536853	1322	272.4	787.42	1572.82	1572.84	-0.02	0.00	46.21	0.12	1	GVTTIIGGGDSVAAVEK +
M2B7	gi|115469436	1322	191.5	787.42	1572.82	1572.84	-0.02	0.00	46.21	0.12	1	GVTTIIGGGDSVAAVEK +
M2B7	gi|1022805	1322	86.85	787.42	1572.82	1572.84	-0.02	0.00	46.21	0.12	1	GVTTIIGGGDSVAAVEK +
M2B3	gi|62526587	1489	227.5	615.30	1842.87	1842.91	-0.03	0.00	19.37	60.07	1	HAAEQGHAANNGLDIAVR +
M2B4	gi|62526587	1488	227.5	615.30	1842.87	1842.91	-0.04	0.00	32.96	2.62	1	HAAEQGHAANNGLDIAVR +

Table S4. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B3	gi|62526587	1493	227.5	615.64	1843.88	1843.89	-0.01	0.00	43.98	0.21	1	HAAEQGHAANNGLDIAVR + Deamidation (NQ)
M2B2	gi|2511588	693	61.2	578.80	1155.59	1155.60	-0.02	0.00	61.20	0.00	1	HITIFSPEGR +
M2B1	gi|83649448	56	45.99	404.20	806.38	806.39	-0.01	0.00	27.59	7.04	1	IAADDFR +
M2B3	gi|83649448	57	45.99	404.20	806.39	806.39	0.00	0.00	37.61	0.75	1	IAADDFR +
M2B4	gi|83649448	55	45.99	404.20	806.38	806.39	-0.01	0.00	45.99	0.11	1	IAADDFR +
M2B1	gi|29839257	557	65.8	546.80	1091.58	1091.60	-0.02	0.00	65.80	0.00	1	IAEYVTQLR +
M2B2	gi|29839257	556	65.8	546.80	1091.58	1091.60	-0.02	0.00	57.60	0.01	1	IAEYVTQLR +
M2B3	gi|62526587	1028	227.5	449.89	1346.65	1346.66	-0.01	0.00	43.14	0.27	1	IAWHSAGTYDVK +
M2B1	gi|1173201	1164	58.74	722.38	1442.74	1442.73	0.01	0.00	58.74	0.01	1	IEDVTPIPTDSTR +
M2B3	gi|13539964	365	70.39	513.30	1024.59	1024.60	-0.02	0.00	61.39	0.00	2	IGGIGTVPVGR +
M2B4	gi|13539964	366	70.39	513.30	1024.59	1024.60	-0.02	0.00	54.47	0.01	2	IGGIGTVPVGR +
M2B4	gi|111053717	366	65.88	513.30	1024.59	1024.60	-0.02	0.00	54.47	0.01	1	IGGIGTVPVGR +
M2B4	gi|3410705	366	65.83	513.30	1024.59	1024.60	-0.02	0.00	54.47	0.01	1	IGGIGTVPVGR +
M2B4	gi|58615198	366	65.83	513.30	1024.59	1024.60	-0.02	0.00	54.47	0.01	1	IGGIGTVPVGR +
M2B4	gi|56377850	366	65.31	513.30	1024.59	1024.60	-0.02	0.00	54.47	0.01	1	IGGIGTVPVGR +
M2B3	gi|120666	90	263.1	417.23	832.44	832.46	-0.01	0.00	42.70	0.24	1	IGINGFGR +
M2B3	gi|74419004	90	247.4	417.23	832.44	832.46	-0.01	0.00	42.70	0.24	1	IGINGFGR +
M2B3	gi|462137	90	141	417.23	832.44	832.46	-0.01	0.00	42.70	0.24	1	IGINGFGR +
M2B3	gi|48142692	90	104	417.23	832.44	832.46	-0.01	0.00	42.70	0.24	1	IGINGFGR +
M2B3	gi|118351869	90	97.06	417.23	832.44	832.46	-0.01	0.00	42.70	0.24	1	IGINGFGR +
M2B3	gi|15602789	90	81.38	417.23	832.44	832.46	-0.01	0.00	42.70	0.24	1	IGINGFGR +
M2B3	gi|21672565	90	81.38	417.23	832.44	832.46	-0.01	0.00	42.70	0.24	1	IGINGFGR +
M2B3	gi|30248344	90	81.38	417.23	832.44	832.46	-0.01	0.00	42.70	0.24	1	IGINGFGR +
M2B3	gi|1100223	90	68.36	417.23	832.44	832.46	-0.01	0.00	42.70	0.24	1	IGINGFGR +
M2B3	gi|3023812	90	67.27	417.23	832.44	832.46	-0.01	0.00	42.70	0.24	1	IGINGFGR +
M2B3	gi|113476798	90	63.54	417.23	832.44	832.46	-0.01	0.00	42.70	0.24	1	IGINGFGR +
M2B4	gi|113621	1539	77.41	1040.02	2078.03	2078.06	-0.03	0.00	28.27	8.09	1	IGPNEPSQLAIDLNAQGLAR + 2 Deamidation (NQ)
M2B7	gi|21672507	1191	46.21	735.40	1468.78	1468.80	-0.02	0.00	46.21	0.08	1	IHNITNQGLIFAK + Deamidation (NQ)
M2B4	gi|429116	1471	96.93	596.66	1786.95	1786.98	-0.03	1.00	9.58	573.69	1	IINEPTAAAIAYGIDKK +
M2B7	gi|429116	1470	96.93	596.66	1786.95	1786.98	-0.03	1.00	96.93	0.00	1	IINEPTAAAIAYGIDKK +
M2B4	gi|425194	1471	215.9	596.66	1786.95	1786.98	-0.03	1.00	9.58	573.69	2	IINEPTAAAIAYGLDKK +
M2B4	gi|50259091	1471	193.5	596.66	1786.95	1786.98	-0.03	1.00	9.58	573.69	2	IINEPTAAAIAYGLDKK +
M2B4	gi|3114993	1471	174	596.66	1786.95	1786.98	-0.03	1.00	9.58	573.69	2	IINEPTAAAIAYGLDKK +
M2B4	gi|112819494	1471	142.6	596.66	1786.95	1786.98	-0.03	1.00	9.58	573.69	2	IINEPTAAAIAYGLDKK +
M2B7	gi|6911553	1470	308.8	596.66	1786.95	1786.98	-0.03	1.00	96.93	0.00	2	IINEPTAAAIAYGLDKK +

Table S4. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B7	gi|425194	1470	215.9	596.66	1786.95	1786.98	-0.03	1.00	96.93	0.00	2	IINEPTAAAIAYGLDKK +
M2B7	gi|3114993	1470	174	596.66	1786.95	1786.98	-0.03	1.00	96.93	0.00	2	IINEPTAAAIAYGLDKK +
M2B7	gi|112819494	1470	142.6	596.66	1786.95	1786.98	-0.03	1.00	96.93	0.00	2	IINEPTAAAIAYGLDKK +
M2B7	gi|249262	1447	78.52	877.91	1753.81	1753.83	-0.02	0.00	78.52	0.00	1	ILDGSNGDVAVDFYNR +
M2B4	gi|20599	248	162.6	481.77	961.52	961.53	-0.02	0.00	59.51	0.00	1	INLGVGAYR +
M2B4	gi|13516907	1426	82.87	570.28	1707.83	1707.86	-0.03	1.00	47.58	0.10	1	INTYAEFRDDVLPR +
M2B7	gi|13516907	1427	82.87	570.28	1707.83	1707.86	-0.03	1.00	60.61	0.00	1	INTYAEFRDDVLPR +
M2B7	gi|1771261	1427	564.8	570.28	1707.83	1707.86	-0.03	1.00	60.61	0.00	2	INTYREFADDVLPR +
M2B7	gi|92872649	668	71.82	571.82	1141.63	1141.65	-0.02	0.00	39.88	0.34	1	ISANIAANVAAK +
M2B3	gi|15792899	523	50.61	539.79	1077.56	1077.58	-0.02	0.00	50.61	0.04	2	ISEYGLQLR +
M2B4	gi|15792899	524	50.61	539.80	1077.58	1077.58	-0.01	0.00	32.61	2.45	2	ISEYGLQLR +
M2B3	gi|21027	523	66.56	539.79	1077.56	1077.58	-0.02	0.00	66.56	0.00	1	ISEYVAQLR +
M2B4	gi|21027	524	66.56	539.80	1077.58	1077.58	-0.01	0.00	49.00	0.06	1	ISEYVAQLR +
M2B4	gi|50256615	1611	61.38	680.81	2719.23	2719.21	0.02	1.00	22.70	23.92	1	KDYDSSMSVVSNASCTTNCLAPLAK + 2 Carbamidomethyl (C); Deamidation (NQ)
M2B4	gi|7288201	511	48.83	537.80	1073.59	1073.59	0.00	0.00	48.83	0.06	1	KPMAAIVGGSK + Oxidation (M)
M2B1	gi|1168193	1389	52.24	549.93	1646.76	1646.77	-0.01	1.00	12.08	274.97	1	KVTEQGQELSNEER + Deamidation (NQ)
M2B4	gi|74419004	214	247.4	464.79	927.58	927.58	0.00	1.00	38.68	0.16	2	KVVISAPSK +
M2B4	gi|34099812	214	192.2	464.79	927.58	927.58	0.00	1.00	38.68	0.16	2	KVVISAPSK +
M2B4	gi|86130515	214	81.38	464.79	927.58	927.58	0.00	1.00	38.68	0.16	2	KVVISAPSK +
M2B4	gi|50256615	214	61.38	464.79	927.58	927.58	0.00	1.00	38.68	0.16	2	KVVISAPSK +
M2B1	gi|119912330	56	117.7	404.20	806.38	806.39	-0.01	0.00	27.59	7.04	2	LAADDFR +
M2B1	gi|12852628	56	117.6	404.20	806.38	806.39	-0.01	0.00	27.59	7.04	2	LAADDFR +
M2B1	gi|57106334	56	81.57	404.20	806.38	806.39	-0.01	0.00	27.59	7.04	2	LAADDFR +
M2B1	gi|57335398	56	77.82	404.20	806.38	806.39	-0.01	0.00	27.59	7.04	2	LAADDFR +
M2B1	gi|29335504	56	60.4	404.20	806.38	806.39	-0.01	0.00	27.59	7.04	2	LAADDFR +
M2B4	gi|119912330	55	117.7	404.20	806.38	806.39	-0.01	0.00	45.99	0.11	2	LAADDFR +
M2B4	gi|12852628	55	117.6	404.20	806.38	806.39	-0.01	0.00	45.99	0.11	2	LAADDFR +
M2B4	gi|57106334	55	81.57	404.20	806.38	806.39	-0.01	0.00	45.99	0.11	2	LAADDFR +
M2B4	gi|57335398	55	77.82	404.20	806.38	806.39	-0.01	0.00	45.99	0.11	2	LAADDFR +
M2B4	gi|29335504	55	60.4	404.20	806.38	806.39	-0.01	0.00	45.99	0.11	2	LAADDFR +
M2B7	gi|92874670	911	62.93	641.35	1280.69	1280.71	-0.02	0.00	34.40	1.04	1	LADLEAAPAAIAR +
M2B7	gi|1705587	911	121.2	641.35	1280.69	1280.71	-0.02	0.00	34.40	1.04	2	LADLEAAPAALAR +
M2B7	gi|1771261	1415	564.8	564.96	1691.86	1691.90	-0.03	1.00	34.11	2.00	1	LAMAIPDKWIDYLK + Oxidation (M)
M2B7	gi|76496236	1415	79.87	564.96	1691.86	1691.90	-0.03	1.00	34.11	2.00	1	LAMAIPDKWIDYLK + Oxidation (M)

Table S4. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B4	gi|115434198	1109	176.5	701.36	1400.71	1400.73	-0.02	0.00	83.08	0.00	1	LASIGLDNTEVNR +
M2B3	gi|62122767	60	86.25	405.22	808.43	808.43	-0.01	0.00	37.10	0.47	2	LASYLDK +
M2B7	gi|54873534	1221	53.29	747.92	1493.83	1493.86	-0.03	0.00	18.05	27.10	1	LATIPITGTGINPAR +
M2B7	gi|1705587	677	121.2	574.79	1147.57	1147.59	-0.02	0.00	58.31	0.01	1	LATPELEYGR +
M2B3	gi|2754860	1028	68.8	449.89	1346.65	1346.66	-0.01	0.00	43.14	0.27	2	LAWHSAGTYDVK +
M2B3	gi|74483945	1028	68.8	449.89	1346.65	1346.66	-0.01	0.00	43.14	0.27	2	LAWHSAGTYDVK +
M2B7	gi|33326375	792	157.3	601.32	1200.63	1200.65	-0.02	0.00	31.61	3.16	1	LDAQPELFIR +
M2B7	gi|1708314	792	133.2	601.32	1200.63	1200.65	-0.02	0.00	31.61	3.16	1	LDAQPELFIR +
M2B7	gi|1771261	1485	564.8	917.44	1832.86	1832.88	-0.02	0.00	11.70	349.43	1	LGDFEGINETSPADAVAK +
M2B4	gi|136429	1554	176.5	737.70	2210.08	2210.10	-0.01	0.00	38.58	0.74	1	LGEHNIDVLEGNEQFINAAK +
M2B7	gi|136429	1550	176.5	737.70	2210.07	2210.10	-0.02	0.00	61.62	0.00	1	LGEHNIDVLEGNEQFINAAK +
M2B7	gi|136429	1551	176.5	737.70	2210.08	2210.10	-0.02	0.00	54.37	0.02	1	LGEHNIDVLEGNEQFINAAK +
M2B7	gi|136429	1552	176.5	737.70	2210.08	2210.10	-0.01	0.00	32.21	3.23	1	LGEHNIDVLEGNEQFINAAK +
M2B4	gi|6981420	1554	46.99	737.70	2210.08	2210.10	-0.01	0.00	17.48	95.56	2	LGEHNINVLEGDEQFINAAK +
M2B7	gi|6981420	1550	46.99	737.70	2210.07	2210.10	-0.02	0.00	46.99	0.11	2	LGEHNINVLEGDEQFINAAK +
M2B7	gi|6981420	1551	46.99	737.70	2210.08	2210.10	-0.02	0.00	36.14	1.30	2	LGEHNINVLEGDEQFINAAK +
M2B7	gi|6981420	1552	46.99	737.70	2210.08	2210.10	-0.01	0.00	26.15	13.03	2	LGEHNINVLEGDEQFINAAK +
M2B4	gi|16973318	719	62.33	581.29	1160.56	1160.58	-0.02	0.00	62.33	0.00	1	LGTDEWALTR +
M2B7	gi|37790792	1261	159.4	514.60	1540.77	1540.79	-0.02	0.00	11.89	292.51	2	LGVTECTIAHALEK + Carbamidomethyl (C)
M2B7	gi|4733946	1261	208.4	514.60	1540.77	1540.79	-0.02	0.00	13.15	218.84	1	LGVTQCTIAHALEK + Carbamidomethyl (C); Deamidation (NQ)
M2B7	gi|13160142	1261	191.4	514.60	1540.77	1540.79	-0.02	0.00	13.15	218.84	1	LGVTQCTIAHALEK + Carbamidomethyl (C); Deamidation (NQ)
M2B7	gi|22331535	1261	182.9	514.60	1540.77	1540.79	-0.02	0.00	13.15	218.84	1	LGVTQCTIAHALEK + Carbamidomethyl (C); Deamidation (NQ)
M2B7	gi|80973758	1261	177	514.60	1540.77	1540.79	-0.02	0.00	13.15	218.84	1	LGVTQCTIAHALEK + Carbamidomethyl (C); Deamidation (NQ)
M2B7	gi|135061	1261	105	514.60	1540.77	1540.79	-0.02	0.00	13.15	218.84	1	LGVTQCTIAHALEK + Carbamidomethyl (C); Deamidation (NQ)
M2B7	gi|115310620	1261	74.04	514.60	1540.77	1540.79	-0.02	0.00	13.15	218.84	1	LGVTQCTIAHALEK + Carbamidomethyl (C); Deamidation (NQ)
M2B7	gi|530207	1046	132.7	679.88	1357.75	1357.76	-0.02	0.00	74.53	0.00	1	LIALDMGALVAGAK + Oxidation (M)
M2B4	gi|168324	1256	168.8	765.89	1529.77	1529.78	-0.01	0.00	85.28	0.00	1	LIFGADSPAIQENR +
M2B4	gi|20599	1256	162.6	765.89	1529.77	1529.78	-0.01	0.00	85.28	0.00	1	LIFGADSPAIQENR +
M2B7	gi|114566045	1046	47.39	679.88	1357.75	1357.76	-0.02	0.00	47.39	0.06	2	LLALDMGSLVAGAK +
M2B7	gi|4733946	1084	208.4	694.35	1386.69	1386.69	-0.01	0.00	81.66	0.00	1	LLPDAVGTTCGQR + Carbamidomethyl (C)

Table S4. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B7	gi|13160142	1084	191.4	694.35	1386.69	1386.69	-0.01	0.00	81.66	0.00	1	LLPDAVGTTCGQR + Carbamidomethyl (C)
M2B7	gi|1351138	1084	181.7	694.35	1386.69	1386.69	-0.01	0.00	81.66	0.00	1	LLPDAVGTTCGQR + Carbamidomethyl (C)
M2B7	gi|37790792	1084	159.4	694.35	1386.69	1386.69	-0.01	0.00	81.66	0.00	1	LLPDAVGTTCGQR + Carbamidomethyl (C)
M2B7	gi|135061	1084	105	694.35	1386.69	1386.69	-0.01	0.00	81.66	0.00	1	LLPDAVGTTCGQR + Carbamidomethyl (C)
M2B7	gi|80973758	1084	177	694.35	1386.69	1386.69	-0.01	0.00	67.20	0.00	2	LLPDAVGTTCNQR +
M2B7	gi|42525587	1063	46.44	686.35	1370.68	1370.69	-0.02	1.00	46.44	0.09	1	LNDLENHFNKK +
M2B4	gi|168324	248	168.8	481.77	961.52	961.53	-0.02	0.00	59.51	0.00	2	LNLGVGAYR +
M2B4	gi|531555	248	102.4	481.77	961.52	961.53	-0.02	0.00	59.51	0.00	2	LNLGVGAYR +
M2B1	gi|118742193	632	69.87	561.78	1121.56	1121.57	-0.02	0.00	58.47	0.01	2	LQQQIATYR + 2 Deamidation (NQ)
M2B4	gi|118742193	633	69.87	561.79	1121.56	1121.57	-0.02	0.00	69.87	0.00	2	LQQQIATYR + 2 Deamidation (NQ)
M2B1	gi|41619832	488	48.55	533.75	1065.49	1065.49	-0.01	1.00	48.55	0.04	2	MEMEKVQR + Oxidation (M)
M2B3	gi|119192758	529	45.27	541.25	1080.49	1080.48	0.01	1.00	41.53	0.23	2	MGMAGERASR + Oxidation (M)
M2B4	gi|119192758	528	45.27	541.25	1080.48	1080.48	0.00	1.00	45.27	0.08	2	MGMAGERASR + Oxidation (M)
M2B1	gi|42561108	1198	45.21	738.38	1474.74	1474.73	0.00	0.00	45.21	0.18	1	MINNVGIDIVENK + Deamidation (NQ); Oxidation (M)
M2B7	gi|42561108	1200	45.21	738.38	1474.75	1474.73	0.02	0.00	21.79	38.32	2	MINNVGIDIVENK + Deamidation (NQ); Oxidation (M)
M2B4	gi|115623569	1256	66.13	765.89	1529.77	1529.79	-0.02	1.00	66.13	0.00	2	MLLGADSPALKENR + Oxidation (M)
M2B4	gi|115469436	1476	191.5	601.63	1801.85	1801.89	-0.03	0.00	14.77	175.49	1	MSHISTGGGASLELLEGK + Oxidation (M)
M2B1	gi|16124126	583	52.17	553.30	1104.58	1104.58	0.00	0.00	52.17	0.03	2	MSQLIESAVK +
M2B4	gi|115401362	192	50.63	457.19	912.37	912.37	0.01	0.00	50.63	0.01	1	MTIDDMR + 2 Oxidation (M)
M2B7	gi|115401362	193	50.63	457.20	912.38	912.37	0.01	0.00	34.84	0.55	1	MTIDDMR + 2 Oxidation (M)
M2B4	gi|109898422	192	50.63	457.19	912.37	912.37	0.01	0.00	50.63	0.01	2	MTLDDMR + 2 Oxidation (M)
M2B7	gi|109898422	193	50.63	457.20	912.38	912.37	0.01	0.00	34.84	0.55	2	MTLDDMR + 2 Oxidation (M)
M2B7	gi|92871836	1409	51.43	840.91	1679.82	1679.83	-0.01	0.00	51.43	0.04	2	NAVISVPAYFNDSQR +
M2B7	gi|6911553	1409	308.8	840.91	1679.82	1679.83	-0.01	0.00	66.01	0.00	1	NAVVTVPAYFNDSQR +
M2B7	gi|425194	1409	215.9	840.91	1679.82	1679.83	-0.01	0.00	66.01	0.00	1	NAVVTVPAYFNDSQR +
M2B7	gi|92871811	1409	101.9	840.91	1679.82	1679.83	-0.01	0.00	66.01	0.00	1	NAVVTVPAYFNDSQR +

Table S4. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B4	gi|1730557	222	118.3	468.24	934.46	934.48	-0.01	0.00	33.51	1.99	1	NDISYPVK +
M2B5	gi|1730557	221	118.3	468.24	934.46	934.48	-0.01	0.00	48.79	0.06	1	NDISYPVK +
M2B7	gi|1351138	337	181.7	507.79	1013.57	1013.59	-0.02	0.00	51.45	0.03	1	NEIVALLSR +
M2B7	gi|74316933	337	51.45	507.79	1013.57	1013.56	0.01	1.00	51.45	0.03	2	NELVAKNAR +
M2B3	gi|1168190	188	55.85	454.26	906.51	906.52	0.00	0.00	40.93	0.14	1	NLISVAYK +
M2B4	gi|1168190	187	55.85	454.26	906.50	906.52	-0.02	0.00	16.56	55.28	2	NLISVAYK +
M2B3	gi|1168191	188	58.22	454.26	906.51	906.52	0.00	0.00	40.93	0.14	2	NLLSVAYK +
M2B3	gi|34452071	188	55.85	454.26	906.51	906.52	0.00	0.00	40.93	0.14	2	NLLSVAYK +
M2B3	gi|1168193	188	52.24	454.26	906.51	906.52	0.00	0.00	40.93	0.14	2	NLLSVAYK +
M2B3	gi|13928270	188	49.01	454.26	906.51	906.52	0.00	0.00	40.93	0.14	2	NLLSVAYK +
M2B3	gi|115476520	188	46.1	454.26	906.51	906.52	0.00	0.00	40.93	0.14	2	NLLSVAYK +
M2B3	gi|10719663	188	45.3	454.26	906.51	906.52	0.00	0.00	40.93	0.14	2	NLLSVAYK +
M2B1	gi|119912330	546	117.7	545.76	1089.50	1089.49	0.01	0.00	71.69	0.00	2	QAMQNLNDR + Deamidation (NQ)
M2B1	gi|6831664	305	47.56	499.79	997.56	997.56	0.00	0.00	47.56	0.03	1	QAVDISPLR +
M2B1	gi|116058572	305	47.56	499.79	997.56	997.56	0.00	0.00	47.56	0.03	2	QAVDLSPLR +
M2B7	gi|15228683	1368	191.3	811.38	1620.74	1620.76	-0.02	0.00	26.80	8.52	1	QAYYLSMEFLQGR + Oxidation (M)
M2B7	gi|629646	1368	190.1	811.38	1620.74	1620.76	-0.02	0.00	26.80	8.52	1	QAYYLSMEFLQGR + Oxidation (M)
M2B7	gi|13195430	1368	128.3	811.38	1620.74	1620.76	-0.02	0.00	26.80	8.52	1	QAYYLSMEFLQGR + Oxidation (M)
M2B7	gi|130172	1368	121.3	811.38	1620.74	1620.76	-0.02	0.00	26.80	8.52	1	QAYYLSMEFLQGR + Oxidation (M)
M2B7	gi|1730557	1368	118.3	811.38	1620.74	1620.76	-0.02	0.00	26.80	8.52	1	QAYYLSMEFLQGR + Oxidation (M)
M2B7	gi|40716501	676	47.1	574.76	1147.50	1147.52	-0.02	0.00	47.10	0.04	1	QDVFNSFYK + Deamidation (NQ)
M2B7	gi|109715750	1525	176.3	665.00	1991.99	1992.01	-0.02	1.00	35.10	1.74	2	QIVSSIDEDNKVIVFER + 2 Deamidation (NQ)
M2B7	gi|1771261	1525	564.8	665.00	1991.99	1992.02	-0.03	1.00	121.65	0.00	1	QIVSSTNEEDKVIVFER +
M2B2	gi|89074323	261	48.68	487.26	972.50	972.50	0.01	0.00	45.42	0.13	1	QNLSEINR +
M2B3	gi|89074323	260	48.68	487.26	972.50	972.50	0.00	0.00	48.68	0.06	1	QNLSEINR +
M2B7	gi|89074323	258	48.68	487.25	972.49	972.50	-0.01	0.00	30.25	3.80	1	QNLSEINR +
M2B4	gi|121892870	680	57.37	576.78	1151.55	1151.56	0.00	1.00	21.74	30.27	2	QNYDEIRSK +
M2B7	gi|57336886	1269	69.98	517.92	1550.73	1550.76	-0.02	1.00	34.74	1.70	1	QPIGTSAQTDKDYK +
M2B7	gi|13160142	370	191.4	514.27	1026.53	1026.55	-0.02	0.00	49.34	0.04	1	QQGLDITPR +
M2B7	gi|1351138	370	181.7	514.27	1026.53	1026.55	-0.02	0.00	49.34	0.04	1	QQGLDITPR +
M2B7	gi|80973758	370	177	514.27	1026.53	1026.55	-0.02	0.00	49.34	0.04	1	QQGLDITPR +
M2B7	gi|4733946	370	208.4	514.27	1026.53	1026.55	-0.02	0.00	49.34	0.04	2	QQGLNITPR + Deamidation (NQ)
M2B7	gi|22331535	370	182.9	514.27	1026.53	1026.55	-0.02	0.00	49.34	0.04	2	QQGLNITPR + Deamidation (NQ)
M2B1	gi|91092104	505	48.84	537.29	1072.57	1072.58	0.00	0.00	48.84	0.07	2	QTLDLEAGVK +
M2B1	gi|121582963	1336	53.39	793.89	1585.76	1585.79	-0.03	1.00	53.39	0.02	2	RAAIEEALQACPTGR + Deamidation (NQ)

Table S4. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B7	gi|1688296	960	48.4	656.82	1311.63	1311.65	-0.02	0.00	48.40	0.06	1	SFGAAVIYNNEK +
M2B7	gi|15224999	960	48.4	656.82	1311.63	1311.65	-0.02	0.00	48.40	0.06	2	SFGAAVIYNNQK + Deamidation (NQ)
M2B7	gi|13516907	503	82.87	537.26	1072.50	1072.50	0.00	0.00	22.26	16.75	1	SFMVYAPSR + Oxidation (M)
M2B4	gi|92872649	969	71.82	658.35	1314.69	1314.71	-0.02	0.00	31.94	3.04	1	SIQVIVVTDGER +
M2B4	gi|57336886	400	69.98	517.30	1032.58	1032.60	-0.02	0.00	35.24	0.83	1	SLGAAIIFNK +
M2B4	gi|54873534	400	53.29	517.30	1032.58	1032.60	-0.02	0.00	35.24	0.83	1	SLGAAIIFNK +
M2B4	gi|91093032	1214	56.7	497.90	1490.69	1490.70	-0.01	0.00	21.60	30.10	1	SLSPNAVDPNSFSR + Deamidation (NQ)
M2B7	gi|3377802	1070	123.8	689.85	1377.68	1377.70	-0.02	0.00	62.09	0.00	1	SSSIGNGVQFLNR +
M2B7	gi|12082281	1070	123.8	689.85	1377.68	1377.70	-0.02	0.00	62.09	0.00	1	SSSIGNGVQFLNR +
M2B7	gi|29289943	1070	123.8	689.85	1377.68	1377.70	-0.02	0.00	62.09	0.00	1	SSSIGNGVQFLNR +
M2B7	gi|1771261	916	564.8	643.80	1285.59	1285.59	0.00	0.00	95.40	0.00	1	SVSEGGIGFDYR +
M2B7	gi|109715750	916	176.3	643.80	1285.59	1285.59	0.00	0.00	95.40	0.00	1	SVSEGGIGFDYR +
M2B2	gi|113476798	226	63.54	472.27	942.52	942.50	0.01	0.00	20.84	30.38	1	TASETPPLK +
M2B7	gi|1771261	245	564.8	480.73	959.45	959.45	-0.01	0.00	32.48	1.99	1	TCVVYYR + Carbamidomethyl (C)
M2B4	gi|92887207	975	160.3	659.81	1317.60	1317.62	-0.02	0.00	60.29	0.00	1	TIEVNNTDAEGR +
M2B7	gi|62122767	464	86.25	530.78	1059.54	1059.56	-0.02	0.00	49.15	0.08	2	TLLDLDNTR +
M2B7	gi|33326375	1031	157.3	676.35	1350.68	1350.71	-0.03	0.00	31.10	3.90	1	TLSIIDSGIGMTK + Oxidation (M)
M2B4	gi|62526587	1542	227.5	696.02	2085.05	2085.09	-0.04	1.00	64.12	0.00	1	TMGLTDKDIVVLSGGHTLGR + Oxidation (M)
M2B3	gi|62526587	686	227.5	577.76	1153.50	1153.52	-0.01	0.00	46.27	0.07	1	TNTGGPFGTMR + Oxidation (M)
M2B3	gi|62526587	689	227.5	577.77	1153.53	1153.52	0.01	0.00	17.10	78.01	2	TNTGGPFGTMR + Oxidation (M)
M2B4	gi|62526587	687	227.5	577.76	1153.51	1153.52	-0.01	0.00	50.56	0.03	1	TNTGGPFGTMR + Oxidation (M)
M2B3	gi|6984140	326	90.02	504.25	1006.49	1006.51	-0.02	0.00	32.79	2.62	1	TTIFSPEGR +
M2B4	gi|67043505	1210	174	744.34	1486.67	1486.69	-0.02	0.00	77.03	0.00	1	TTPSYVAFTDTER +
M2B4	gi|26892070	1210	174	744.34	1486.67	1486.69	-0.02	0.00	77.03	0.00	1	TTPSYVAFTDTER +
M2B4	gi|640325	1210	171.9	744.34	1486.67	1486.69	-0.02	0.00	77.03	0.00	1	TTPSYVAFTDTER +
M2B4	gi|8918240	1210	145.4	744.34	1486.67	1486.69	-0.02	0.00	77.03	0.00	1	TTPSYVAFTDTER +
M2B4	gi|47210309	1210	82.63	744.34	1486.67	1486.69	-0.02	0.00	77.03	0.00	1	TTPSYVAFTDTER +
M2B7	gi|6911553	1211	308.8	744.35	1486.68	1486.69	-0.01	0.00	73.56	0.00	1	TTPSYVAFTDTER +
M2B7	gi|26892070	1211	174	744.35	1486.68	1486.69	-0.01	0.00	73.56	0.00	1	TTPSYVAFTDTER +
M2B7	gi|67043505	1211	174	744.35	1486.68	1486.69	-0.01	0.00	73.56	0.00	1	TTPSYVAFTDTER +
M2B7	gi|640325	1211	171.9	744.35	1486.68	1486.69	-0.01	0.00	73.56	0.00	1	TTPSYVAFTDTER +
M2B7	gi|8918240	1211	145.4	744.35	1486.68	1486.69	-0.01	0.00	73.56	0.00	1	TTPSYVAFTDTER +
M2B7	gi|47210309	1211	82.63	744.35	1486.68	1486.69	-0.01	0.00	73.56	0.00	1	TTPSYVAFTDTER +
M2B7	gi|17647515	1211	109.5	744.35	1486.68	1486.69	-0.01	0.00	73.56	0.00	2	TTPSYVAFTESER +

Table S4. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B4	gi|3114993	1210	174	744.34	1486.67	1486.69	-0.02	0.00	77.03	0.00	2	TTPSYVAFTNTER + Deamidation (NQ)
M2B4	gi|168324	1319	168.8	524.62	1570.84	1570.86	-0.02	0.00	24.01	16.68	1	TVPHLADAIHAAVTR +
M2B4	gi|115434198	1226	176.5	749.91	1497.81	1497.82	-0.01	0.00	42.36	0.17	1	TVVSIPCGPSALAVK + Carbamidomethyl (C)
M2B4	gi|77745483	1226	110.8	749.91	1497.81	1497.82	-0.01	0.00	42.36	0.17	1	TVVSIPCGPSALAVK + Carbamidomethyl (C)
M2B7	gi|1771261	1130	564.8	711.83	1421.65	1421.66	-0.01	0.00	71.00	0.00	1	VALDSDAWEFGGR +
M2B4	gi|531555	1047	102.4	680.37	1358.73	1358.75	-0.02	0.00	42.87	0.21	1	VATIQGLSGTGSLR +
M2B7	gi|136429	104	176.5	421.75	841.49	841.50	-0.02	0.00	51.65	0.02	1	VATVSLPR +
M2B7	gi|136429	106	176.5	421.75	841.49	841.50	-0.01	0.00	54.61	0.01	1	VATVSLPR +
M2B4	gi|21536853	1530	272.4	1008.47	2014.92	2014.94	-0.02	0.00	87.40	0.00	1	VDLNVPLDDNSNITDDTR +
M2B4	gi|114653460	435	48.13	524.24	1046.47	1046.49	-0.02	0.00	26.93	5.64	1	VELENAESR + Deamidation (NQ)
M2B4	gi|120666	64	263.1	407.75	813.48	813.50	-0.01	0.00	54.36	0.01	1	VIISAPSK +
M2B4	gi|462137	64	141	407.75	813.48	813.50	-0.01	0.00	54.36	0.01	1	VIISAPSK +
M2B4	gi|118351869	64	97.06	407.75	813.48	813.50	-0.01	0.00	54.36	0.01	2	VILSAPSK +
M2B1	gi|123534	182	155.3	451.25	900.49	900.50	-0.01	0.00	48.91	0.07	1	VLQISGER +
M2B1	gi|3582434	182	77.93	451.25	900.49	900.50	-0.01	0.00	48.91	0.07	1	VLQISGER +
M2B1	gi|2347090	182	48.91	451.25	900.49	900.50	-0.01	0.00	48.91	0.07	2	VLQISGQR + Deamidation (NQ)
M2B4	gi|17026394	961	69.6	656.87	1311.73	1311.75	-0.02	0.00	65.33	0.00	1	VLQLETAAGAAIR +
M2B7	gi|17026394	962	69.6	656.88	1311.75	1311.75	0.00	0.00	55.94	0.00	1	VLQLETAAGAAIR +
M2B1	gi|6012952	958	65.32	655.85	1309.68	1309.69	-0.01	0.00	65.32	0.00	1	VNQSYVIATSTK +
M2B7	gi|530207	1465	132.7	892.93	1783.85	1783.86	-0.01	0.00	45.28	0.16	1	VQLDSQPEEIDNLER +
M2B7	gi|537446	1465	92.13	892.93	1783.85	1783.86	-0.01	0.00	45.28	0.16	1	VQLDSQPEEIDNLER +
M2B4	gi|118390	857	59.37	619.32	1236.63	1236.62	0.01	0.00	59.37	0.01	1	VSAANSRPPNPQ +
M2B4	gi|47223978	584	113.1	553.76	1105.50	1105.52	-0.02	0.00	71.28	0.00	1	VTMQNLNDR + Oxidation (M)
M2B3	gi|12852628	586	117.6	553.76	1105.51	1105.52	-0.01	0.00	71.64	0.00	2	VTMQNLNNR + Deamidation (NQ); Oxidation (M)
M2B4	gi|12852628	584	117.6	553.76	1105.50	1105.52	-0.02	0.00	71.28	0.00	2	VTMQNLNNR + Deamidation (NQ); Oxidation (M)
M2B4	gi|76575132	1245	60.75	759.87	1517.73	1517.74	-0.01	0.00	60.75	0.00	1	VVGAFLEGGSPDENK +
M2B7	gi|13195430	403	128.3	518.75	1035.49	1035.51	-0.02	0.00	27.40	7.15	1	WSLDIMQK + Oxidation (M)
M2B7	gi|34305475	403	101.3	518.75	1035.49	1035.51	-0.02	0.00	27.40	7.15	1	WSLDIMQK + Oxidation (M)
M2B4	gi|2213867	1455	115.1	883.94	1765.86	1765.89	-0.03	0.00	82.41	0.00	1	YADELIANAAYIGTPGK +
M2B4	gi|92887207	1024	160.3	671.33	1340.65	1340.67	-0.02	0.00	71.94	0.00	1	YAGDVSSGIIFGR +
M2B7	gi|92887207	1023	160.3	671.33	1340.65	1340.67	-0.02	0.00	73.18	0.00	1	YAGDVSSGIIFGR +
M2B7	gi|1771261	708	564.8	579.77	1157.53	1157.52	0.01	0.00	20.97	24.04	1	YEGGLEEFSK +
M2B7	gi|4586236	708	66.73	579.77	1157.53	1157.52	0.01	0.00	20.97	24.04	1	YEGGLEEFSK +

Table S4. Contd…..

SDS_PAGE Zone Code	Accession	Query	Score	Observed	Mr (Expt)	Mr (Calc)	Delta	Miss	Score	Expect	Rank	Peptide Sequence
M2B7	gi|974782	1396	48.39	553.60	1657.79	1657.82	-0.03	0.00	48.39	0.07	1	YGAGIGPGVYDIHSPR +
M2B7	gi|15228683	1288	191.3	783.37	1564.73	1564.76	-0.02	0.00	90.34	0.00	1	YHAEFTPLFSPEK +
M2B7	gi|629646	1288	190.1	783.37	1564.73	1564.76	-0.02	0.00	90.34	0.00	1	YHAEFTPLFSPEK +
M2B7	gi|22331535	912	182.9	641.81	1281.61	1281.64	-0.03	0.00	73.10	0.00	1	YIGDGVEFLNR +
M2B3	gi|118099953	368	47.97	513.76	1025.50	1025.51	-0.02	1.00	47.97	0.05	2	YKSSISADR +
M2B4	gi|21536853	1223	272.4	499.93	1496.78	1496.81	-0.03	0.00	8.28	552.95	1	YLKPSVAGFLMQK + Oxidation (M)
M2B4	gi|21536853	500	272.4	536.82	1071.62	1071.64	-0.02	0.00	29.89	2.72	1	YSLKPLVPR +
M2B4	gi|115469436	500	191.5	536.82	1071.62	1071.64	-0.02	0.00	29.89	2.72	1	YSLKPLVPR +

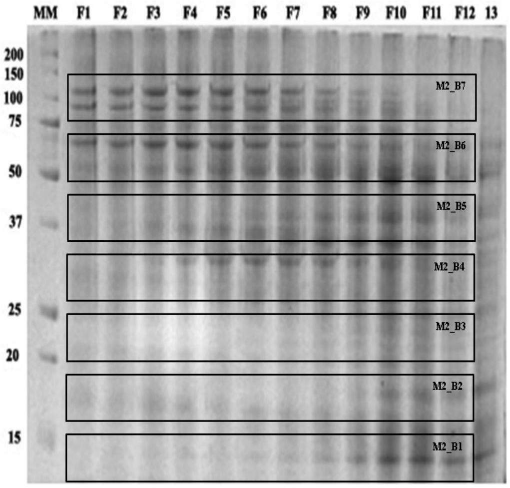

Image complement for Table S4: Proteins from Non-Carotenoid-Protein Complex (NCPC) separated in SDS_PAGE. Showing is the shaded area of fractions of the gel zone harvested for in gel tripityc digestion and MS/MS analysis. Label gel zone is coded as DCP1/DCP2/DCP3 in table discrimination.. Label gel zone is coded as M2_B1/ M2_B2/M2_B3/M2_B4/M2_B51/M2_B6/M2_B7 in table discrimination.

Table S5. Supplementary Data: Listing Identified Proteins in the Non Carotenoid-protein Complex (NCPC) Assined to Cassava EST Data Base (NCBI, ESTIMA, EMBRAPA, CIAT, and RIKEN) and Arabidopsis Loci Data Base

SDS_PAGE Zone Code	Peptide sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Proteins Abreviation
M2_B1	AAMENGILTVTVPKEEVK	scaff_8565_1	AT3G46230.1	142	1.0e-34	ATHSP17.4	HSP17.4
M2_B1	AAMENGILTVTVPKEEVK	scaff_8720_1	NP_194497	210	1.0e-54	HSP21	HSP21
M2_B1	AAMENGILTVTVPKEEVK	scaff_8870_1	AT5G59720.1	220	7.0e-58	HSP18.2	HSP18.2
M2_B5	AAQPSLIADDIATK +	CK644580	AT2G36390.1	40	4.0e-04	BE3, SBE2.1, F1O11.2, F1O11_2, BRANCHING ENZYME 3, STARCH BRANCHING ENZYME 2.1	BE3
M2_B6	AASFNIIPSSTGAAK	Cassava.415.C3.Contig531	At3g04120.1	582	2.3e-166	glyceraldehyde-3-phosphate dehydrogenase	GAPC

Table S5. Contd…..

SDS_PAGE Zone Code	Peptide sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Proteins Abreviation
M2_B5	AASFNIIPSSTGAAK +	Cassava.415.C3.Contig531	AT3G04120.1	582	2.3e-166	GAPC-1, GAPC | GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase	GAPC
M2_B1	ACMENGVLTVTVPK +	Cassava.2670.C1.Contig2792	AT3G46230.1	138	4.7e-033	ATHSP17.4 (Arabidopsis thaliana heat shock protein 17.4)	HSP17.4
M2_B1	ACMENGVLTVTVPKEEVK	scaff_8565_1	AT3G46230	142	1.0e-34	ATHSP17.4	HSP17.4
M2_B1	ACMENGVLTVTVPKEEVK	scaff_8870_1	AT5G59720	220	7.0e-58	HSP18.2	HSP18.2
M2_B4	AELKNGVLFISIPK	scaff_9466_1	AT4G25200	186	1.0e-47	ATHSP23.6	HSP23.6
M2_B4	AELKNGVLFISIPK	scaff_9466_1	AT4G25200	186	1.0e-47	ATHSP23.6	HSP23.6
M2_B1	AELKNGVLFISIPK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP21
M2_B3	AGIALDNNFVK +	BQ994705	AT3G04120.1	392	0.0e-109	GAPC, GAPC-1, GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT)	GAPC
M2_B3	AGIALNDNFIK +	BE363730	AT3G04120.1	282	2.0e-76	GAPC, GAPC1, GAPC-1, T6K12.26, T6K12_26, GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT	GAPC
M2_B3	AGIALNDNFLK	CD848129	AT3G04120.1	264	1.0e-83	GAPC, GAPC-1, GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT)	GAPC
M2_B6	AGIALNDNFVK +	CO497299	AT5G09810.1	369	0.0 e-102	actin 7	ACT7
M2_B5	AGIALNENFVK	scaff_9425_1	AT3G04120	140	4.0e-34	GAPC	GAPC
M2_B6	AGIALNENFVK +	CV194776	AT1G13440.1	463	0.0 e-130	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C2	GAPC-2
M2_B6	AGIALNENFVK +	CV194776	AT1G13440.1	463	0.0 e-130	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C2	GAPC-2
M2_B1	AMASTPADIKEYPNSYVFIIDMPGLK	CAS035_D18	AT3G46230	126	2.0e-47	ATHSP17.4	HSP17.4
M2_B1	AMASTPADIKEYPNSYVFIIDMPGLK	scaff_8870_1	AT5G59720	220	7.0e-58	HSP18.2	HSP18.2
M2_B3	AMASTPADIKEYPNSYVFIIDMPGLK	scaff_9075_1	AT4G10250.1	139	1.0e-33	ATHSP22.0	HSP22.0

Table S5. Contd…..

SDS_PAGE Zone Code	Peptide sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Proteins Abreviation
M2_B1	AMASTPADIKEYPNSYVFIIDMPGLK +	Cassava.121.C1.Contig167	AT5G12020.1	161	4.9e-040	HSP17.6II (17.6 KDA CLASS II HEAT SHOCK PROTEIN)	HSP17.6II
M2_B1	APWDIKEDENEFK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP21
M2_B6	AQDLVSSNSVVVFSK +	Cassava.52.C1.Contig75	AT5G40370.1	157	5.6e-039	glutaredoxin, putative	glutaredoxin
M2_B2	ASMENGVLTGTIPR +	BE054707	AT2G29500.1	204	8.0e-53	HSP20-like chaperones superfamily	HSP20
M2_B2	ASMENGVLTVTVPK +	Cassava.388.C1.Contig493	AT5G59720.1	217	6.3e-057	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP18.2
M2_B1	ASMENGVLTVTVPKEEVQKPDVK	Cassava.859.C1.Contig1017	At2g29500.1	146	1.6e-035	17.6 kDa class I	HSP17.6I
M2_B1	ASMENGVLTVTVPKEEVQKPDVK	Cassava.859.C1.Contig1017	AT2G29500.1	146	1.6e-035	17.6 kDa class I small heat shock protein (HSP17.6B-CI)	HSP17.6I
M2_B4	ASMENGVLTVTVPNEEIKKPDVK	CAS011_L20	AT1G52560.2	141	6.0e-34	HSP20-like chaperones superfamily HSP26.5 kDa class I	HSP26.5I
M2_B1	ASMENGVLTVTVPREEAK	scaff_8565_1	AT3G46230.1	142	1.0e-34	ATHSP17.4	HSP17.4
M2_B1	ATMDNGVLTVTVPK	CAS037_L20	AT2G29500.1	162	2.0e-40	17.6 kDa class I	HSP17.6I
M2_B1	ATMDNGVLTVTVPK	scaff_8565_1	AT3G46230.1	142	1.0e-34	ATHSP17.4	HSP17.4
M2_B4	ATMDNGVLTVTVPK	scaff_9466_1	AT4G25200	186	1.0e-47	ATHSP23.6	HSP23.6
M2_B2	ATMDNGVLTVTVPK +	CV433420.	AT5G59720.1	181	1.0e-46	HSP18.2 | heat shock protein 18.2 |	HSP18.2
M2_B5	ATNLLLTENR +	Non Hit					
M2_B5	AVVTVPAYFNDSQR	scaff_9733_1	AT1G56410.1	355	5.0e-98	heat shock protein	ERD2, HSP70T-1
M2_B1	AVVTVPAYFNDSQR +	scaff_6393_1	AT5G02500.1	193	2.0e-58	HSC70-1	HSP70-1
M2_B1	AVVVHADPDDLGKGGHELSK	scaff_8667_1	AT1G08830.1	276	1.0e-74	CSD1	CSD1
M2_B3	AVVVHADPDDLGKGGHELSK +	Cassava.sd.2.C1.Contig3040	AT1G08830.1	243	7.7e-065	CSD1 (COPPER/ZINC SUPEROXIDE DISMUTASE 1); copper, zinc superoxide dismutase	CSD1
M2_B1	DIPFPSTALSAPR	scaff_8565_1	AT3G46230.1	142	1.0e-34	ATHSP17.4	HSP17.4
M2_B2	DIPFPSTALSAPR +	Cassava.388.C1.Contig493	AT5G59720.1	217	6.3e-057	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP18.2
M2_B5	EAEAVDQVSEEPVAPESDAPAEAVVETK +	Cassava.sd.1.C1.Contig3038	21585695	57	0.000002	allergenic-related protein Pt2L4 [Manihot esculenta]	Pt2L4
M2_B3	EEEKPQGEVIVTEFEEK	scaff_9841_1	AT1G20450.2	59	5.0e-09	LTI29, LTI45, ERD10 | Dehydrin family	ERD10
M2_B5	EEPAAETVVVEAPK +	Cassava.sd.1.C1.Contig3038	21585695	57	0.000002	allergenic-related protein Pt2L4 [Manihot esculenta]	Pt2L4
M2_B5	EGKLIPLLTEAGAVAK	scaff_10607_1	AT5G63030.1	81	3.0e-26	Thioredoxin superfamily protein	glutaredoxin

Table S5. Contd…..

SDS_PAGE Zone Code	Peptide sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Proteins Abreviation
M2_B6	EGKLIPLLTEAGAVAK +	Cassava.52.C1.Contig75	AT5G40370.1	157	5.6e-039	glutaredoxin, putative	glutaredoxin
M2_B1	EKPSIGTIIAVGPGPIDEEGNRKPLSVSPGNTVLYSK +	Cassava.882.C1.Contig1045	AT5G20720.1	354	4.9e-098	CPN10, CHCPN10, ATCPN21, CPN21, CPN20 | CPN20 (CHAPERONIN 20); calmodulin binding	CPN20
M2_B1	ETLDAHIFKADLPGLK	scaff_7155_1	AT2G29500	175	2.0e-44	17.6 kDa class I	HSP17.6I
M2_B1	ETPEAHVFEADLPGLK +	Cassava.859.C1.Contig1017	AT2G29500.1	146	1.6e-035	17.6 kDa class I small heat shock protein (HSP17.6B-CI)	HSP17.6I
M2_B2	ETPESHVFKADLPGLK +	Cassava.388.C1.Contig493	AT5G59720.1	217	6.3e-057	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP18.2
M2_B3	ETSAFINAR +	Cassava.388.C1.Contig493	AT5G59720.1	217	6.3e-057	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP18.2
M2_B5	ETTEAATEAEAPAPESAPASAPETPAEEEVPKEEEGDEK +	Cassava.sd.1.C1.Contig3038	21585695	57	0.000002	allergenic-related protein Pt2L4 [Manihot esculenta]	Pt2L4
M2_B7	FALLVDDLK +	scaff_7000_1	AT1G65980.1	272	1.0e-73	thioredoxin-dependent peroxidase 1	TPX1
M2_B1	FALLVDDLKVK +	scaff_7000_1	AT1G65980.1	272	1.0e-73	TPX1 | thioredoxin-dependent peroxid	TPX1
M2_B4	FDMPGLSKDEVK +	scaff_8720_1	AT4G27670.1	210	1.0e-54	heat shock protein 21	HSP21
M2_B1	FDMPGLSKEDVK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP21
M2_B3	FHTVFDYGNLR	Cassava.sd.3.C1.Contig3041	AT1G11910.1	407	0.0e-114	APA1, ATAPA1 | aspartic proteinase A1	aspartyl protease
M2_B2	FHTVFDYGNLR	CAS022_P15.r	AT1G62290.1	200	3.0e-52	pepsin A [EC:3.4.23.40]	pepsin A
M2_B3	FRLPENAEVDQVK	scaff_9075_1	AT4G10250.1	139	1.0e-33	ATHSP22.0	HSP22.0
M2_B1	FRLPENAEVDQVK +	scaff_8565_1	AT3G46230.1	142	1.0e-34	ATHSP17.4	HSP17.4
M2_B1	FRLPENANLDQVK	scaff_6764_1	AT2G29500.1	211	3.0e-55	17.6 kDa class I	HSP17.6I
M2_B3	FRLPENANMDQIR	Cassava.503.C1.Contig639	AT5G59720.1 189 3e-48	189	3.0e-48	HSP18.2 | heat shock protein 18.2 |	HSP18.1I
M2_B6	FRLPENANMDQIR +	Cassava.503.C1.Contig639	AT5G59720.1	189	2.3e-048	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP18.2
M2_B5	FRLPENAQVDQVK +	Non hit					
M2_B5	GGDDAPAEVAVETK +	Cassava.sd.1.C1.Contig3038	21585695	57	0.000002	allergenic-related protein Pt2L4 [Manihot esculenta]	Pt2L4
M2_B4	GLEIDPNNEALKSGLADAQAAASR +	CV03037A2D05.f1	AT1G62740.1	269	1,00E-72	stress-inducible protein	stress-inducible
M2_B4	GLEIDPNNEALKSGLADAQAGATR	CAS051_I09.f	AT1G12270	205	1.0e-53	stress-inducible protein	stress-inducible

Table S5. Contd…..

SDS_PAGE Zone Code	Peptide sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Proteins Abreviation
M2_B3	GLFDFMGKK +	Cassava.550.C1.Contig687	AT1G20450.1	62	4.6e-010	LTI45, ERD10, LTI29 | ERD10/LTI45 (EARLY RESPONSIVE TO DEHYDRATION 10)	ERD10
M2_B3	GQDGNEVFFR +	scaff_9886_1	AT5G55160	104	1.0e-23	SUM2	SUM2
M2_B3	GRVFDVTTGK +	scaff_6529_1	AT2G24940	170	5.0e-43	ATMAPR2	ATMAPR2
M2_B1	GTMENGVLTVTVPK +	Non Hit					
M2_B1	HAAEQGHAANNGLDIAVR +	Cassava.394.C2.Contig501	AT3G09640.1	376	1.3e-104	APX1B | APX2 (ASCORBATE PEROXIDASE 2); L-ascorbate peroxidase	APX2
M2_B1	HAGDLGNVTAGDDGTASFTIVDKDIPLSGPHSIVGR +	Cassava.sd.2.C1.Contig3040	AT1G08830.1	243	7.7e-065	CSD1 (COPPER/ZINC SUPEROXIDE DISMUTASE 1); copper, zinc superoxide dismutase	CSD1
M2_B1	IAGLEVLR +	Non Hit					
M2_B1	IDWKETPDAHIFK	CAS037_L03.f	AT3G46230.1	192	1.0e-49	ATHSP17.4	HSP17.4
M2_B1	IDWKETPDAHIFK	scaff_7380_1	AT5G59720.1	194	7.0e-50	HSP18.2	HSP18.2
M2_B1	IDWKETPEAHVFQADLPGLR	scaff_7357_1	AT2G29500.1	197	5.0e-51	17.6 kDa class I	HSP17.6I
M2_B1	IDWKETPEAHVFQADLPGLR +	Cassava.1764.C1.Contig1943	AT2G29500.1	146	1.6e-035	17.6 kDa class I small heat shock protein (HSP17.6B-CI)	HSP17.6I
M2_B5	IDWKETPESHVFK +	Cassava.388.C1.Contig493	AT5G59720.1	217	6.3e-057	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP18.2
M2_B3	IEVEDGRVLQISGER	scaff_6708_1	AT4G10250.1	125	1.0e-28	ATHSP22.0 | HSP20-like chaperones	HSP22.0
M2_B1	IEVEDGRVLQISGER +	scaff_8565_1	AT3G46230.1	142	1.0e-34	ATHSP17.4	HSP17.4
M2_B1	IFFQDSDVSAPLVQR +	Cassava.2234.C1.Contig2395	AT5G16550.1	134	1.3e-031	similar to unknown [Gossypium hirsutum] (GB:ABO31374.1)	Unkown
M2_B1	IINEPTAASLAYGFEK +	Non Hit					
M2_B5	IPAVQELVK +	Non Hit					
M2_B5	IPFPSTSPPASR +	Non Hit					
M2_B5	IRFDMPGLSK +	scaff_8720_1	AT4G27670.1 1	210	1.0e-54	heat shock protein 2	HSP21
M2_B5	ISADFDNFR +	Non Hit					
M2_B4	IYDVTAGKSFYGPGGAYSMFAGK +	Cassava.1143.C1.Contig1309	AT2G24940.1	175	2.2e-044	ATMAPR2 | ATMAPR2 (ARABIDOPSIS THALIANA MEMBRANE-ASSOCIATED PROGESTERONE BINDING PROTEIN 2); heme binding / transition metal ion binding	ATMAPR2
M2_B4	KEEEKPQGEVIVTEFEEK +	Cassava.550.C1.Contig687	AT1G20450.1	62	4.6e-010	LTI45, ERD10, LTI29 | ERD10/LTI45 (EARLY RESPONSIVE TO DEHYDRATION 10)	ERD10

Table S5. Contd…..

SDS_PAGE Zone Code	Peptide sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Proteins Abreviation
M2_B4	KVIDVEIQ +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP21
M2_B4	LGDFEGINETSPADAVAKQEDLK +	CK644580	AT2G36390.1	40	4.0e-04	starch branching enzyme	SBE2.1, BE3
M2_B2	LGDYLIDQGI +	Non Hit					
M2_B1	LPENANMDQIR +	Cassava.503.C1.Contig639	AT5G59720.1	189	2.3e-048	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP18.2
M2_B3	LRFDMPGLSK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP21
M2_B4	LTPEQVEQISKQPGVLQVVPSR +	Cassava.801.C2.Contig961	AT1G71950.1	139	2.1e-033	identical protein binding / subtilase	HSP21
M2_B1	LTPQQVEEISKQPGVLQVVPSR	scaff_10041_1	AT1G71950.1	139	2.0e-33	identical protein binding / subtilase	subtilase
M2_B7	NGVLFISIPK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP21
M2_B7	NSSSVEKSYELPDGQVITIGAER +	Cassava.146.C2.Contig201	AT5G09810.1	316	1.3e-086	ACT2/7, ACT7 | ACT7 (actin 7)	ACT7
M2_B7	NYELPDGQVITIGAER +	CV01007B1B03.f1	AT1G49240.1	451	2.8e-127	ACT8 | ACT8 (ACTIN 8); structural constituent of cytoskeleton	ACT8
M2_B7	QLAVDVSPFGLLDPLSPMR +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP21
M2_B3	QLEDAATLSXYNIQKESTLHLVLR	scaff_10081_1	AT5G03240	355	1.0e-98	UBQ3	UBQ3
M2_B2	QLEDAATLSXYNIQKESTLHLVLR	CAS030_P11.f	AT2G47110	249	9.0e-67	UBQ6	UBQ6
M2_B7	QLEDAATLSXYNIQKESTLHLVLR +	Cassava.2493.C1.Contig2630	AT2G36170.1	245	1.5e-065	ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A)	UBQ2
M2_B3	QLEDGRPLADXXIQKESTLHLVLR	Cassava.2493.C1.Contig2630	AT3G52590.1	245	2.0e-65	ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A)	UBQ2
M2_B4	QLEDGRPLADXXIQKESTLHLVLR	scaff_7980_1	AT4G05320.4	313	0.0e-158	polyubiquitin 10	UBQ10
M2_B7	QMMDTMDRIFEDAMTLPGSR +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP21
M2_B5	SAEEVKVSEIVTEEAAPAVEPVAEEPK +	Cassava.sd.1.C1.Contig3038	21585695	57	0.000002	allergenic-related protein Pt2L4 [Manihot esculenta]	Pt2L4
M2_B7	SEFANETSAFANTR +	Cassava.388.C1.Contig493	AT5G59720.1	217	6.3e-057	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP18.2
M2_B3	SELANETSAFANTR +	DR085468	AT1G07400.1	53	4.0e-08	HSP20-like chaperones superfamily	HSP20

Table S5. Contd…..

SDS_PAGE Zone Code	Peptide sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Proteins Abreviation
M2_B4	SFYGPGGSFCMFAGK +	Cassava.1143.C1.Contig1309	AT2G24940.1	175	2.2e-044	ATMAPR2 | ATMAPR2 (ARABIDOPSIS THALIANA MEMBRANE-ASSOCIATED PROGESTERONE BINDING PROTEIN 2); heme binding / transition metal ion binding	ATMAPR2
M2_B3	SFYGSGGDYSIFAGK +	BP582014.	AT2G24940.1	91	3.0e-19	AtMAPR2, MAPR2 | membrane-associated	
M2_B5	SLATIDGSAFLR +	Cassava.1296.C1.Contig1469	AT3G18570.1	148	2.7e-036	glycine-rich protein / oleosin	glycine-rich protein
M2_B5	TAEEETPEEETSQEEPAPETVVEEAPK +	Cassava.sd.1.C1.Contig3038	21585695	57	0.000002	allergenic-related protein Pt2L4 [Manihot esculenta]	Pt2L4
M2_B6	TAGGLLLTEAAK +	Cassava.882.C1.Contig1045	AT5G20720.1	354	4.9e-098	CPN10, CHCPN10, ATCPN21, CPN21, CPN20 | CPN20 (CHAPERONIN 20); calmodulin binding	CPN20
M2_B5	TEEEEETPKEETPEPVVVK +	Cassava.sd.1.C1.Contig3038	21585695	57	0.000002	allergenic-related protein Pt2L4 [Manihot esculenta]	Pt2L4
M2_B5	TFPQQAGTIR +	Non Hit					
M2_B1	TFSGLLQSSGVIK +	CK643021	AT2G45470.1	254	2.0e-68	FASCICLIN-like ARABINOGALACTAN PROTEIN 8	FLA8, AGP8
M2_B1	TVPNVFIGGK +	Cassava.52.C1.Contig75	AT5G40370.1	157	5.6e-039	glutaredoxin, putative	glutaredoxin
M2_B2	VAEEKTDGGILLPTSAQNKPQGGEVVAVGEGK +	Cassava.882.C1.Contig1045	AT5G20720.1	354	4.9e-098	CPN10, CHCPN10, ATCPN21, CPN21, CPN20 | CPN20 (CHAPERONIN 20); calmodulin binding	CPN20
M2_B1	VALDSDAWEFGGRGR +	CK644580	AT2G36390.1	40	4.0e-04	starch branching enzyme (EC.2.4.1.18)	SBE2.1, BE3
M2_B2	VEEGRVLQISGER	CAS010_O01.f	AT5G59720	171	3.0e-43	HSP18.2	HSP18.2
M2_B1	VEEGRVLQISGER	scaff_8565_1	AT3G46230.1	142	1.0e-34	ATHSP17.4	HSP17.4
M2_B3	VEEGRVLQISGER	scaff_9075_1	AT4G10250	139	1.0e-33	ATHSP22.0	HSP22.0
M2_B1	VEEGRVLQISGER +	scaff_7357_1	AT2G29500.1	197	5.0e-51	17.6 kDa class I	HSP17.6I
M2_B1	VEIEDDRVLQISGER +	Cassava.1764.C1.Contig1943	AT2G29500.1	146	1.6e-035	17.6 kDa class I small heat shock protein (HSP17.6B-CI)	HSP17.6I
M2_B2	VELEDGRVLQISGER +	Cassava.388.C1.Contig493	AT5G59720.1	217	6.3e-057	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	HSP18.2
M2_B7	VEVEDDRLLQISGER +	CV03027A2C01.f1					
M2_B3	VEVEEDRVLQISGER +	scaff_6708_1	AT4G10250.1	125	1.0e-28	ATHSP22.0 | HSP20-like chaperones	HSP22.0
M2_B3	VEVEEGRILQVSGER	Non Hit					

Table S5. Contd…..

SDS_PAGE Zone Code	Peptide sequence (MASCOT Server)	Cassava EST Database	Arabidopsis Locus	Total Score	E_Value	Protein Name	Proteins Abreviation
M2_B4	VEVEEGRVLNITGER	Non Hit					
M2_B4	VEVEEGRVLQISGER	scaff_8870_1	AT5G59720	220	7.0e-58	HSP18.2	HSP18.2
M2_B1	VEWKETPEAHVFK +	Cassava.1764.C1.Contig1943	AT2G29500.1	146	1.6e-035	17.6 kDa class I small heat shock protein (HSP17.6B-CI)	HSP17.6I
M2_B5	VFDLSPEQYVLK +						
M2_B1	VFDVTTGKSFYGPGGSYAMFAGK +	Cassava.1143.C1.Contig1309	AT2G24940.1	175	2.2e-044	ATMAPR2 | ATMAPR2 (ARABIDOPSIS THALIANA MEMBRANE-ASSOCIATED PROGESTERONE BINDING PROTEIN 2); heme binding / transition metal ion binding	ATMAPR2
M2_B1	VFFDMAIGGQPAGR +	Cassava.267.C1.Contig351	AT4G38740.1	280	9.2e-076	ROC1 | ROC1 (rotamase CyP 1); peptidyl-prolyl cis-trans isomerase	ROC1
M2_B3	VFVEEDVLVIK +	Cassava.1282.C1.Contig1455	AT4G27670.1	213	1.2e-055	HSP21 (HEAT SHOCK PROTEIN 21)	HSP21
M2_B3	VGHDVDHFTSPEGIPGVPETNFNNRPNSFK +	CK644580	AT2G36390.1	40	4.0e-04	starch branching enzyme	SBE2.1, BE3
M2_B5	VQIVGDDLLVTNPK +	Non Hit					
M2_B4	VQVEDDNVLLISGER +	Cassava.121.C1.Contig167	AT5G12020.1	161	4.9e-040	HSP17.6II (17.6 KDA CLASS II HEAT SHOCK PROTEIN)	HSP17.6II
M2_B5	VSEIVTEEAAPAVEPVAEEPKEAEPVAVSEEPK +	Cassava.sd.1.C1.Contig3038	21585695	57	0.000002	allergenic-related protein Pt2L4 [Manihot esculenta]	Pt2L4
M2_B3	YAADEEAFFADYAESHMK +	Cassava.394.C2.Contig501	AT3G09640.1	376	1.3e-104	APX1B | APX2 (ASCORBATE PEROXIDASE 2); L-ascorbate peroxidase	APX2
M2_B5	YAGNDFKGNDGSIYIALR +	Cassava.882.C1.Contig1045	AT5G20720.1	354	4.9e-098	CPN10, CHCPN10, ATCPN21, CPN21, CPN20 | CPN20 (CHAPERONIN 20); calmodulin binding	CPN20
M2_B4	YMDIQGEPGAVIR +	Non Hit					
M2_B3	YMVIQGEPGAVIR +	Non Hit					