Supplemental Table 1: Prediction of nuclear localization signals, lipidation sites, and signal peptides in *A. thaliana* IQD proteins

						Nuclear Localization Signal	Palmitoylation (S-Acylation)		N-Myristoylation		Prenylation				Signal peptide	
						NLS (NLStradamus, 4 state HMM, static)	GPS-lipid, medium	CSS-Palm, Medium	GPS-lipid, medium	PlantsP	Farnesyl		Geranylgeranyl			
Gene Identifier	Protein	size [aa]	MW [kDa]	GFP-fusion MW [kDa]	Nucleus		Position (aa)	Position (aa)			GPS-lipid, medium	PrePS	GPS-lipid, medium	PrePS	Signal-Blast, SP1	SignalP 4.1, default
At3g09710	IQD1	454	50.5	79.2	yes	329 - NPRKKRPIPSSIKSKSS - 345, 417 - KAPAKKRLSTSASPAPKPRRSSAPPKVEK - 445	Cluster A	155	negative	negative	negative	negative	negative	negative	negative	negative
At5g03040	IQD2	461	50.5	79.1					non-consensus	negative	negative	negative	negative	negative	negative	negative
At3g52290	IQD3	430	48.1	76.8	yes	12 - ALSPEPKQKKEQKPHKSKKWFGKSKK - 37			non-consensus	negative	negative	negative	negative	negative	negative	negative
At2g26410	IQD4	527	58.3	85.3	yes	18 - KDKKNQKPEKPKRKWSFGKQKS - 39, 479 - KKKPP - 483, 488 - PKKR - 491	Cluster A, C	8,13	negative	negative	negative	negative	negative	negative	negative	negative
At3g22190	IQD5	400	44.5	75.5		355 - NPKERSR - 361			non-consensus	positive	negative	negative	negative	negative	negative	negative
At2g26180	IQD6	416	46.9	75.5	yes	24 - KGNGKNKKWK - 33			non-consensus	negative	negative	negative	negative	negative	negative	negative
At1g17480	IQD7	370	41	69.8			Cluster A	141	non-consensus	negative	negative	negative	negative	negative	negative	negative
At1g72670	IQD8	414	45.9	74.5			Cluster B	361	non-consensus	negative	negative	negative	negative	negative	negative	negative
At2g33990	IQD9	249	28.5	55.5	yes	12 - RLKKSKQGTEKKKTSAVKPKKGSKKKGT - 39, 58 - KAYKARKSLRRLKGIARA - 75	Cluster B	111	non-consensus	negative	negative	negative	negative	negative	negative	negative
At3g15050	IQD10	259	29.6	58.2	yes	229 - KK - 230	Cluster C	12	12	non-consensus	negative	negative	negative	negative	SP, cleavage site aa 12	negative
At5g13460	IQD11	443	50.8	77.8		22 - EKKEKRRKWTFWKLRIKKR - 40	Cluster A, B	158, 170, 370		negative	negative	negative	negative	negative	negative	negative
At5g03960	IQD12	403	46	73		20 - KARAEKPRRLRWVFKRLK - 37	Cluster C	17	17	negative	negative	non-consensus	negative	negative	not significant	SP, cleavage site aa 24	negative
At3g59690	IQD13	517	58.5	85.5		34 - KSENKEKKKKGFGKKLR - 50			MGXXXS/T	negative	negative	negative	negative	negative	negative	negative
At2g43680	IQD14	668	74.3	103.1		21 - EKLANQEPERKSGKEKKKKGFGKLR - 45		497	negative	negative	negative	negative	negative	negative	negative	negative
At3g49380	IQD15	352	40.8	67.8	yes	27 - RINRRQDNDLVEEVEDELHQRPKRRKRRWLFK - 58	Cluster B	302	non-consensus	negative	negative	negative	negative	negative	negative	negative
At4g10640	IQD16	423	48.7	77.4	yes	27 - KTHHHKETDIKRKEKKGWIF - 46, 363 - PRRRP - 367	Cluster B	390, 401	401	negative	negative	non-consensus	negative	negative	negative	negative
At4g00820	IQD17	534	60	87		42 - KKKEKRRWL - 50	Cluster A, B	510, 511	510	non-consensus	negative	negative	negative	negative	negative	negative
At1g01110	IQD18	527	59.2	86.2	yes	23 - KKDHSNDVEEDEEKKREKRRWFRKP - 47	Cluster B, C	377, 505	505	non-consensus	negative	negative	negative	negative	negative	negative
At4g14750	IQD19	387	43.9	70.9			Cluster A, B	28, 59		non-consensus	negative	negative	negative	negative	negative	negative
At3g51380	IQD20	103	11.8	40.5	yes				negative	negative	negative	negative	negative	negative	negative	negative
At3g49260	IQD21	471	52.1	79.1					MGXXXS/T	negative	negative	negative	negative	negative	negative	negative
At4g23060	IQD22	543	60.3	87.3			Cluster B	397	396, 397	non-consensus	negative	negative	negative	negative	negative	negative
At5g62070	IQD23	403	44.3	71.3	yes	11 - KKKSDKAASSRDKRR - 25			negative	negative	negative	negative	negative	negative	negative	negative
At5g07240	IQD24	401	45.3	72.3	yes	76 - QSSPRRRRKQK - 86			negative	negative	negative	negative	negative	negative	negative	negative
At4g29150	IQD25	383	41.4	68.4			Cluster B	305	305, 306	negative	negative	negative	negative	negative	negative	negative
At3g16490	IQD26	398	48.7	72			Cluster B	297		non-consensus	negative	negative	negative	negative	negative	negative
At1g51960	IQD27	351	39.3	68					346, 348	non-consensus	negative	non-consensus	p-value 0.278601	CC/CXC	p-value 0.198676	negative
At1g14380	IQD28	664	72.8	99.8	yes	260 - EAEKKRPKRSIKKPSGT - 276, 283 - SRFTAERNKPKRNVRKA - 299, 343 - KRSSLSNGSKKATLRSAEKKKK - 364	Cluster C	530	non-consensus	negative	negative	negative	negative	negative	negative	negative
At2g02790	IQD29	597	65.3	96.8	yes	17 - KKSSKSSLEKGGEKLRSA - 34, 272 - EAEKGKLKRGVRK - 284, 351 - KPRISHKKASLSNGIGKATRKSAEKKK - 377			MGXXXS/T	negative	negative	negative	negative	negative	negative	negative
At1g18840	IQD30	572	62.7	89.7		258 - KKASLRKSQKKFASNPQ - 274, 278 - AEFARPKKSVR - 288	Cluster B	155, 185	155, 156, 249	non-consensus	negative	negative	negative	negative	negative	negative
At1g74690	IQD31	587	65.2	92.9		278 - ESAKPKKSVRK - 288, 465 - SAGKENQKSRKKG - 477			253	non-consensus	negative	negative	negative	negative	negative	negative
At1g19870	IQD32	794	86.8	113.6	yes	656 - KARKGKSEKSGSSQKRKVSKK - 676	Cluster A, C	9, 15	9, 15	non-consensus	negative	negative	negative	negative	negative	negative
At5g35670	IQD33	442	49.5	78.2	yes	386 - RKSVPSYKSQRKHHKLQATKSDLQQQTKKAKKA - 418	Cluster B	425		non-consensus	negative	negative	negative	negative	negative	negative