

Figure S1. 2D gel replicates of *Lupinus albus* cultivars (Luxor, Multitalia and Modica Ecotype)

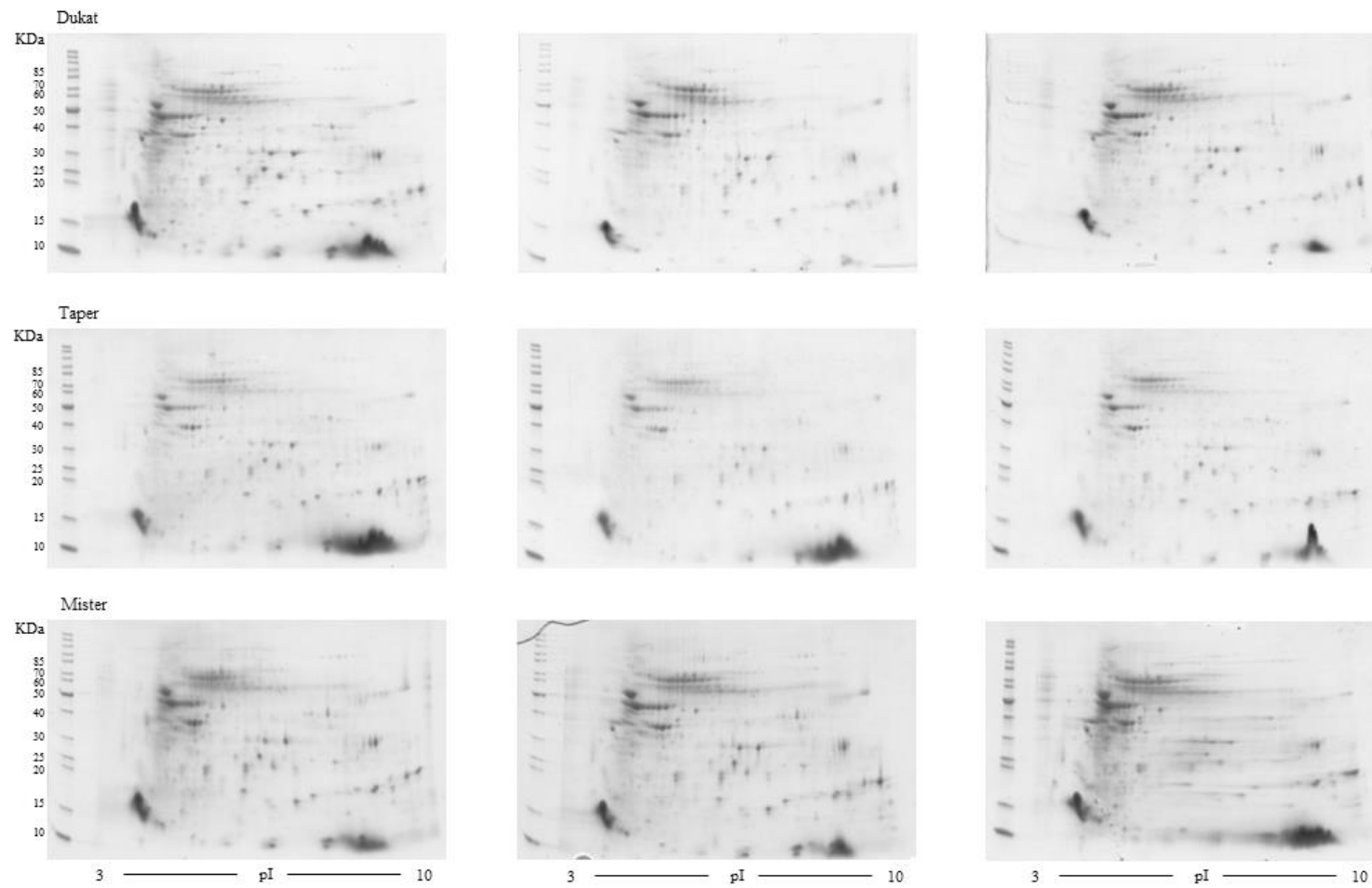
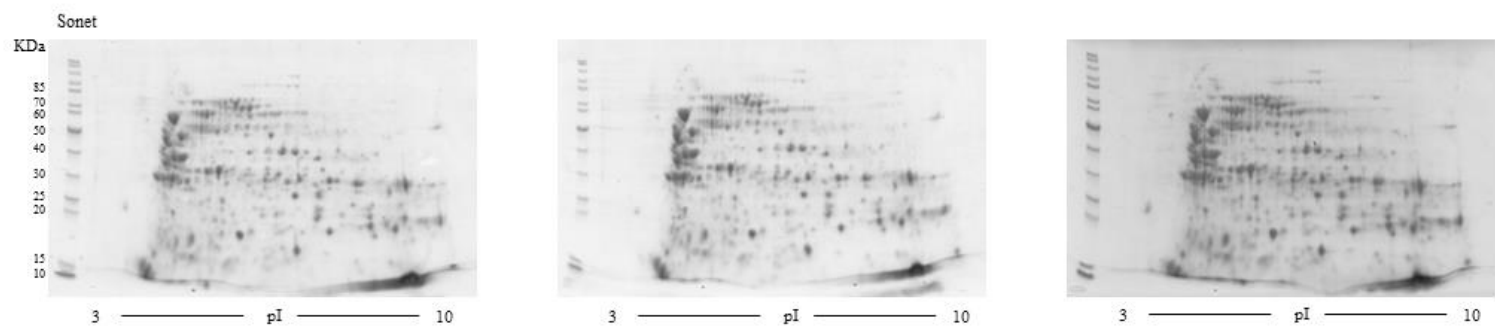


Figure S2. 2D gel replicates of *Lupinus luteus* cultivars (Dukat, Taper and Mister)

Figure S3. 2D gel replicates of *Lupinus angustifolius* cultivar (Sonet)



sp	F5B8W0	CONB2_LUPAN	MANMRVKFPTLVLLLGIVFLMAVSIGIAYGEKNAIKNHERPQEREQEERDPQQPRRHQ	60
sp	Q6EBC1	CONB2_LUPAL	MGKMRVRFPTLVVLGIVFLMAVSIGIAYGEKDLKSHERPEEREQ-----	46
sp	Q53HY0	CONB1_LUPAL	MGKMRVRFPTLVVLGIVFLMAVSIGIAYGEKDLKSHERPEEREQ-----	46
			*.:***:*****:*****:*****:*.:.***:***	
sp	F5B8W0	CONB2_LUPAN	EEQEREHGREERNREPSRGRSESEESREEEREQRREPSRGREQEQQPHGREEEEEEWQ	120
sp	Q6EBC1	CONB2_LUPAL	-----EEWQ	50
sp	Q53HY0	CONB1_LUPAL	-----EEWQ	50

sp	F5B8W0	CONB2_LUPAN	PRRQRPQSRREEREQ--EQGSSSSSGRQSGYERR-----EQREEREQQEQDSRSSESRR	172
sp	Q6EBC1	CONB2_LUPAL	PRRQRPQSRREEREQEQEQQSPSPYPRRQSGYERRQYHERSEQREEREQEQQGSPSYSRR	110
sp	Q53HY0	CONB1_LUPAL	PRRQRPQSRREEREQEQEQQSPSPYPRRQSGYERRQYHERSEQREEREQEQQGSPSYSRR	110
			*****:*.:.***:***	
sp	F5B8W0	CONB2_LUPAN	QRNPYYFSYERFQTLYKNRNGQIRVLERFDQRTNRLLENLQNYRIVEFQSKPNTLILPKHS	232
sp	Q6EBC1	CONB2_LUPAL	QRNPYHFSSQRFQTLYKNRNGKIRVLERFDQRTNRLLENLQNYRIVEFQSKPNTLILPKHS	170
sp	Q53HY0	CONB1_LUPAL	QRNPYHFNSQRFQTLYKNRNGKIRVLERFDQRTNRLLENLQNYRIVEFQSKPNTLILPKHS	170
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sp	F5B8W0	CONB2_LUPAN	DADYILVVLNGRATITIVNPDQRQAYNLEHGDALRLPAGTTSYILNPDDNQNLRVVKLAI	292
sp	Q6EBC1	CONB2_LUPAL	DADYVLVVLNGRATITIVNPDQRQAYNLEYGDALRIPAGSTSYILNPDDNQKL RVVKLAI	230
sp	Q53HY0	CONB1_LUPAL	DADYVLVVLNGRATITIVNPDQRQAYNLEYGDALRIPAGSTSYILNPDDNQKL RVVKLAI	230
			*****:*****:*****:*****:*****:*****:*****	
sp	F5B8W0	CONB2_LUPAN	PINNPGNFYDFYPSSTKDQQSYFNGFSRNTLEATFNTRYEEIQRILLGNEDGQEDEEQSR	352
sp	Q6EBC1	CONB2_LUPAL	PINNPGYFYDFYPSSTKDQQSYFSGFSRNTLEATFNTRYEEIQRILLGNEDQEYEEQRR	290
sp	Q53HY0	CONB1_LUPAL	PINNPGYFYDFYPSSTKDQQSYFSGFSRNTLEATFNTRYEEIQRILLGNEDQEYEEQRR	290
			*****:*****:*****:*****:*****:*****:*****	
sp	F5B8W0	CONB2_LUPAN	GQEQSHQDQGVIVRVSKEQIQELRKHAQSSSGKGKPSSESGPFNLRSDEPIYSNKGNFYE	412
sp	Q6EBC1	CONB2_LUPAL	GQEQSDQDEGVIIVSKKQIQKLTKHAQSSSGKDKPSDSGPFNLRSNEPIYSNKGNFYE	350
sp	Q53HY0	CONB1_LUPAL	GQEQSHQDEGVIIVRVSREQIQELTKYAQSSSGKDKPSQSGPFNLRSNEPIYSNKGNFYE	350
			*****:***:***:***:***:***:***:*****:*****:*****:*****	
sp	F5B8W0	CONB2_LUPAN	ITPDRNPQAQDLDISLTFIEINEGGLLLPHYNSKAIFV VVVDEGEGNYELVGIRDQERQQ	472
sp	Q6EBC1	CONB2_LUPAL	ITPDRNPQVQDLNISLTYIKINEGALLPHYNSKAIV VVVDEGEGNYELVGIRDQQRQQ	410
sp	Q53HY0	CONB1_LUPAL	ITPDRNPQVQDLDISLTFTEINEGALLPHYNSKAIFIVVVGEGNGKYELVGIRDQQRQQ	410
			*****:***:***:***:*****:*****:*****:*****:*****:*****	
sp	F5B8W0	CONB2_LUPAN	DEQE--QEEVRRYNAKLSEGDIFVIPAGHPISINASSNLRLLGFGINADENQRNFLAGSE	530
sp	Q6EBC1	CONB2_LUPAL	DEQEEKEEEVIRYSARLSEGDIFVIPAGYPISINASSNLRLLGFGINADENQRNFLAGSK	470
sp	Q53HY0	CONB1_LUPAL	DEQEEPEEEVRRYSARLSEGDIFVIPAGYPISVNASSNLRLLGFGINAYENQRNFLAGSE	470
			****:***:***:***:*****:*****:*****:*****:*****:*****	
sp	F5B8W0	CONB2_LUPAN	DNVIRQLDKEVKQLTFPGSVEDVERLIKNQQQSYFANAQPPQQQ--QREKEGRRGRRLS	588
sp	Q6EBC1	CONB2_LUPAL	DNVIRQLDRAVNELTFPGSAEDIERLIKNQQQSYFANGQPQQQQQQQSEKEGRRGRRGSS	530
sp	Q53HY0	CONB1_LUPAL	DNVIRQLDREVKELTFPGSAEDIERLIKNQQQSYFANALPQQQ--QQSEKEGRRGRRGPI	528
			*****:*.:.*****:*****:*****:*****:*****:*****	
sp	F5B8W0	CONB2_LUPAN	FPFRSLFTKLLSTIM	603
sp	Q6EBC1	CONB2_LUPAL	LPF-----	533
sp	Q53HY0	CONB1_LUPAL	SSI-----	531
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Figure S4. Sequence alignment of β -globulin/vicilin F5B8W0, Q6EBC1, and Q53HY0.

tr Q53I54 Q53I54_LUPAL	MSNKLLALSFLPFLLLFFCGCFASFRQPQENECQFQRLNALEPDNTVQSEAGTIETW	60
tr Q53I55 Q53I55_LUPAL	-----	0
tr Q53I54 Q53I54_LUPAL	NPKNDELRCAGVALSRCTIQRNGLRRPFYTNAPQEIYIQQGRGIFGMIFPGCGETYEPEQ	120
tr Q53I55 Q53I55_LUPAL	-----	0
tr Q53I54 Q53I54_LUPAL	ESEKGQGPRPQDRHQKVEHFKEGDIIAVPTGIPFWMYNDGQTPVVAITLIDTTLNLDNQLD	180
tr Q53I55 Q53I55_LUPAL	-----	0
tr Q53I54 Q53I54_LUPAL	QIPRRFYLSGNQEQLQYQKEGGQGQQEGGNVLSGDFDEFLEEALSVNKEIVRNIGK	240
tr Q53I55 Q53I55_LUPAL	-----	0
tr Q53I54 Q53I54_LUPAL	KNDDREGGIVEVKGGLKVIIPPTMRPRHGREEEEEEEEDERRGDRRRRHPHHHHHEEEE	300
tr Q53I55 Q53I55_LUPAL	-----PVNRQLRSV-----FPGRPTRPGDRRRRHPHHHHHEEEE	34
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tr Q53I54 Q53I54_LUPAL	EEEEWSHQVRRVRRPHRHHHRKDRNGLEETLCTMKLRHNIGESTSPDAYNPQAGRFT	360
tr Q53I55 Q53I55_LUPAL	EEEEWSHQVRRVRRPHRHHHRKDRNGLEETLCTMKLRHNIGESTSPDAYNPQAGRFT	94

tr Q53I54 Q53I54_LUPAL	LTSIDFPILGWLGLAAEHGSIYKNALFVPYNNVANSILYVLNGSAWFQVDCSGNAVFN	420
tr Q53I55 Q53I55_LUPAL	LTSIDFPILGWLGLAAEHGSN-KNALFVPYNNVANSILYVLNGSAWFQVDCSGNAVFN	153

tr Q53I54 Q53I54_LUPAL	GELNEGQVLTIPQNYAAAIKSLSDNFRYVAFKTDIPQIATLAGANSEISALPLEVVAHA	480
tr Q53I55 Q53I55_LUPAL	GELNEGQVLTIPQNYAAAIKSLSDNFRYVAFKTDIPQIATLAGANSEISALPLEVVAHA	213

tr Q53I54 Q53I54_LUPAL	FNLNRDQARQLKNNNPYKFLVPPQSQLRAVA	512
tr Q53I55 Q53I55_LUPAL	FNLNRAQARQLKNTNPYKFLVPPQSQLRAVA	245
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Figure S5. Sequence alignment of legumin-like proteins Q53I54 and Q53I55.

sp F5B8V6 CONA1_LUPAN	MANK-LLALS--LFL-LFSGCFSTFRQQPQQNECQFQRLNALEPDNSVKSEAGTIETWN	56
sp F5B8V7 CONA2_LUPAN	MAKPCLFSLCLLLL-SSLCLAE---RPERYKECQLDRLNALEPDNRVESEGGVTETWN	56
sp F5B8V8 CONA3_LUPAN	MANPFLSLSLCLVLLYSACLGE--GLDRFNQCQLDRLNALEPDNRIESEGGVTETWN	57
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sp F5B8V6 CONA1_LUPAN	PNNDQLRCAGVALSRCTIQNRGLRRPFYTNAPQEIYIQQGRGIFGLIFPGCRETYEEPQE	116
sp F5B8V7 CONA2_LUPAN	SNRPELRCAGVAFEKHTIQPQGLHLPSTYNTYPQLIFIVEGEGALGISVPGCTETYEAAQQ	116
sp F5B8V8 CONA3_LUPAN	SNKPELRCAGVAFEKHTIEPKGLHLPSTYNTYPQIIMIVQGEALGISVPGCTETFEAAQQ	117
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sp F5B8V6 CONA1_LUPAN	QEQQGQP-----RPQDRHQKVEHFREGDIIAVPTGVPFWMYNNQTPVIAITL	164
sp F5B8V7 CONA2_LUPAN	SQSSQDPRRRSSRSQSQEQQQDSHQKIQYFREGDIIAIPPGIPYWTYNYGEQRLVAINL	176
sp F5B8V8 CONA3_LUPAN	SQSRQERRRG---QRSQSQEQQEDSHQKIRHFREGDILVIPPGTPYWTYNYGDEQLVAINL	174
	.. * . :* ****:*****:.* * * * * : :*** *	
sp F5B8V6 CONA1_LUPAN	IDTTNLDNQLDQIPRRFYLSGNQEQLFYQQKEGGQQQQ-----EGGNE	210
sp F5B8V7 CONA2_LUPAN	LDTTSLNQLDPSPRRFYIAGNPEEEHPETQEQQQQREQQQAGGRRRGKHQQEQEEEG	236
sp F5B8V8 CONA3_LUPAN	LDTTSLNQLDPNPRRFYLAGNPEEEYPETQQQR-QRQQHQRPQSGRRRHGQHQQEEEG	233
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sp F5B8V6 CONA1_LUPAN	GGNVLSGFNDFLEEAFFSVDREIVRNKGNDDREGSIVEVKEGLKVISPTLRPQGRE	270
sp F5B8V7 CONA2_LUPAN	KNNVLSGFDPQFLTQAFNVDEEIIINRLQNP-DELRKQIVRVKRGSLIISPKSQEEEE--	293
sp F5B8V8 CONA3_LUPAN	KNNILSGFDPQFLSQALNIDETVHKLQNP-NERIKQIRVEEGLGVISPKWQEQEEEE	292
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sp F5B8V6 CONA1_LUPAN	EE-----E-EEEEEEERRGDRR-----HR-----PHHH-EEE-	297
sp F5B8V7 CONA2_LUPAN	EEEEPRQGRQPERREERREEEEEEEEDEPRSRERYERQSRRRPGRQQGRQEEQEEES	353
sp F5B8V8 CONA3_LUPAN	EKEEPRQRRRRERREERREEEKEE---EDEPRESR-----HR-----GGHE-EEEV	335
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sp F5B8V6 CONA1_LUPAN	-----EEEEWSHQVRRV-----	310
sp F5B8V7 CONA2_LUPAN	ESEQEGRGQREWERTTRHRRRAQEEGEEEEETSTRVRRQQGRGRGQEQGQEQEQEQEQ	413
sp F5B8V8 CONA3_LUPAN	EEERGRGRGSEWKRTTRRRHTRGDEGQEEETTTTTEE-----	374
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sp F5B8V6 CONA1_LUPAN	-----RRPHHHREDRNGLEETLCTLKLHNIG	337
sp F5B8V7 CONA2_LUPAN	EEEQEGRRGRHGGRGRRSGQQREEEEEQQQQGRKRQESRNGLEETICTARLLENIA	473
sp F5B8V8 CONA3_LUPAN	-----RRRRRGGRSGRQEE-----E-----EEQSPPRSRNGLEETICTAILRENIA	415
	: ..*****:*** * .**.	
sp F5B8V6 CONA1_LUPAN	QSTSPDAYNPQAGRLKTLTSLDFPILRWLGAAEHGSIYKNAMFVPPYNNVANSILYVLN	397
sp F5B8V7 CONA2_LUPAN	KPSRADLYNPNAGRISVNSLTLPILRWFLSADYVNLRYNGIYAPHWNINANSVIFVTR	533
sp F5B8V8 CONA3_LUPAN	DPTRADLYNPAGRISTANSLTLPILGWFLSAEYVNLRYNGIYAPHWNINANSVIYVIR	475
	. : * *** ****:.. ** :*** * :*: :*: :*: :*: :*: :*	
sp F5B8V6 CONA1_LUPAN	GSAWFQVVDSCGNAVFNELNEGQVLTIPQNYAVAIKSLDDNFSYVAFKTNDIPQIAALA	457
sp F5B8V7 CONA2_LUPAN	GRGRVQVNCQGNVFNDDLRRGQLLVVPQNFVVAHQAGDEGFEFIAFKTNDLAATSP--	591
sp F5B8V8 CONA3_LUPAN	GRGRVQVNSQGNVFNDDLRRGQLLVVPQNFVVAHQAGDEGFEFIAFKTNDQATTSP--	533
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sp F5B8V6 CONA1_LUPAN	GLTSSIRALPLDVVAHAFNLDRDQARQLKNNNPYKFLVPPPQ--SQLRAV---A	506
sp F5B8V7 CONA2_LUPAN	-VKQVFRGIPAEVLANAFGLRLNQVSQLKYSNGQGPLVSPQSESEDHTLPKVA	643
sp F5B8V8 CONA3_LUPAN	-LKQVFRGIPAEVLANAFRLSLNQVSELKYNNGNHNPLVTPQSQSQDHNLVKVA	585
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Figure S6. Sequence alignment of α -globulin proteins F5B8V6, F5B8V7 and F5B8V8

tr B0YJF8 B0YJF8_LUPAN	MAKMRVRLPMLILLGVVFLLAASIGIAYGEKDFTKNP---PKEREEEEHEPRQOPRPRQ	58
sp F5B8V9 CONB1_LUPAN	MAKMRVRLPMLILLGVVFLLAASIGIAYGEKDFTKNP---PKEREEEEHEPRQOPRPRQ	58
tr B8Q5G0 B8Q5G0_LUPAN	MAKMRVRLPMLILLGVVFLLAASIGIAYGEKDFTKNP---PKEREEEEHEPRQOPRPRQ	58
sp F5B8W3 CONB5_LUPAN	MAKMRVRFPMILLGVVFLLAASIGIAYGEKDVTKNPERPEERQEEDRPQPPRSRQ	60
tr B0YJF7 B0YJF7_LUPAN	-----	0
sp F5B8W0 CONB2_LUPAN	MANMRVKFPTLVLLLGIVFLMAVSIGIAYGEKNAIKNHERPQEREQEEDRPQOPRPRHQ	60
sp F5B8W1 CONB3_LUPAN	MAKMRVRFPTLVLLLGIVFLMAVSIGIAYGEKNVKNHERPQEREQEEDRPQOPRPHHQ	60
sp F5B8W2 CONB4_LUPAN	MIKMRVRFPTLVLLLGIVFLMAVSIGIAYGEKNVKNHERPQEREQEEDRPQOPRPHHQ	60
tr B0YJF8 B0YJF8_LUPAN	EEQEREHRREEKHGDEPSRGRSQSEESQEEEHERRREHHREREQEOPRPRQROEEE----	115
sp F5B8V9 CONB1_LUPAN	EEQEREHRREEKHGDEPSRGRSQSEESQEEEHERRREHHREREQEOPRPRQROEEE----	115
tr B8Q5G0 B8Q5G0_LUPAN	EEQEREHRREEKHGDEPSRGRSQSEESQEEEHERRREHHREREQEOPRPRQROEEE----	115
sp F5B8W3 CONB5_LUPAN	EEQEREHRREEKRDREPSRGRSESKQSEEEERRRKHDREREQEOPYGRHHEEEKG	120
tr B0YJF7 B0YJF7_LUPAN	-----EERQEEERERRRPRCREREQEOPQHGRREE----	33
sp F5B8W0 CONB2_LUPAN	EEQEREHGREERNRPSRGRSEESREEREORRPSRGREREQEOPQHGRREE----	115
sp F5B8W1 CONB3_LUPAN	EEQEREHRRES-----EESQEEEREORRPRREREQEOPQHGRREE----	102
sp F5B8W2 CONB4_LUPAN	EEQEREHRREEEDRPSRGRSEESREEREORRPRREREQEOPQHGRREE----	115
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tr B0YJF8 B0YJF8_LUPAN	EEEEEWOPRRORPQSRREEREEREQEGSSSGSRGSGDERRH-----	159
sp F5B8V9 CONB1_LUPAN	EEEEEWOPRRORPQSRREEREEREQEGSSSGSRGSGDERRH-----	159
tr B8Q5G0 B8Q5G0_LUPAN	EEEEEWOPRRORPQSRREEREEREQEGSSSGSRGSGDERRH-----	159
sp F5B8W3 CONB5_LUPAN	EEEEEGQARRORPQRRREE---REQEQSSSESRRQSGDERRHREKREOREEREQEGS	177
tr B0YJF7 B0YJF7_LUPAN	-----EEEEWOPRLLRPQSRKEE---REQEQSSSSSRKQSGYERRQY-----	73
sp F5B8W0 CONB2_LUPAN	-----EEEWOPRRORPQSRREE---REQEQSSSSSGRQSGYERRQ-----	154
sp F5B8W1 CONB3_LUPAN	-----EEEEWOPRRORPQSRREE---REQEQSSSSSRQSGYERRQ-----	141
sp F5B8W2 CONB4_LUPAN	-----EEEWOPRRORPQSRREE---REQEQSSSSSRQSGYERR-----	153
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tr B0YJF8 B0YJF8_LUPAN	-----RERRVHREEREQEODSRSDSRQRNPYHFSNRFQTYNRRNGQIRV	206
sp F5B8V9 CONB1_LUPAN	-----RERRVHREEREQEODSRSDSRQRNPYHFSNRFQTYNRRNGQIRV	206
tr B8Q5G0 B8Q5G0_LUPAN	-----RERRVHREEREQEODSRSDSRQRNPYHFSNRFQTYNRRNGQIRV	206
sp F5B8W3 CONB5_LUPAN	SSGRQSDYGRQRHGREOREEREQEQSSSESHRLNPNYFSSERFQTRYNNKNGQIRV	237
tr B0YJF7 B0YJF7_LUPAN	-----HERREORDEKEQEODSRSDSRQRNPYHFSNRFQTRYNNKNGQIRV	120
sp F5B8W0 CONB2_LUPAN	-----REEREQ---QOEQDSRSSESRQRNPYFYSERFQTRYNNKNGQIRV	197
sp F5B8W1 CONB3_LUPAN	-----REEREQ---EQEGSRSDSRQRNPYFYSERFQTRYNNKNGQIRV	184
sp F5B8W2 CONB4_LUPAN	-----EREQ---EQEGSRSDSRQRNPYFYSERFQTRYNNKNGQIRV	194
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tr B0YJF8 B0YJF8_LUPAN	LERFNQRTNRLLENLQNYRIIEFQSKPNTLILPKHSDADFILVVLNGRATITIVNPKRQV	266
sp F5B8V9 CONB1_LUPAN	LERFNQRTNRLLENLQNYRIIEFQSKPNTLILPKHSDADFILVVLNGRATITIVNPKRQV	266
tr B8Q5G0 B8Q5G0_LUPAN	LERFNQRTNRLLENLQNYRIIEFQSKPNTLILPKHSDADFILVVLNGRATITIVNPKRQV	266
sp F5B8W3 CONB5_LUPAN	LERFDQRTNRLLENLQNYRIVEFQSRPNTLILPKHSDADYILVVLNGRATITIVNPKRQA	297
tr B0YJF7 B0YJF7_LUPAN	LERFDQRTNRLLENLQNYRIVEFQSNPNTLILPKHSDADYILVVLNGRATITIVNPKRQA	180
sp F5B8W0 CONB2_LUPAN	LERFDQRTNRLLENLQNYRIVEFQSKPNTLILPKHSDADYILVVLNGRATITIVNPKRQA	257
sp F5B8W1 CONB3_LUPAN	LERFDQRTNRLLENLQNYRIVEFQSKPNTLILPKHSDADYILVVLNGSATITIVNPKRQS	244
sp F5B8W2 CONB4_LUPAN	LERFDQRTNRLLENLQNYRIVEFQSKPNTLILPKHSDADYILVVLNGSATITIVNPKRQS	254
	::*****:***:*****:*****:*****:*****:*****:*****	
tr B0YJF8 B0YJF8_LUPAN	YNLEQGDALRLPAGTTSYILNPDNDQNLRAKLAIPINNPGKLYDFPSTTKDQSQSYFSG	326
sp F5B8V9 CONB1_LUPAN	YNLEQGDALRLPAGTTSYILNPDNDQNLRAKLAIPINNPGKLYDFPSTTKDQSQSYFSG	326
tr B8Q5G0 B8Q5G0_LUPAN	YNLEQGDALRLPAGTTSYILNPDNDQNLRAKLAIPINNPGKLYDFPSTTKDQSQSYFSG	326
sp F5B8W3 CONB5_LUPAN	YNLEYGDALRLPAGTTSYILNPDNDQNLRAKLAIPINNPGKLYDFPSTTKDQSQSYFSG	357
tr B0YJF7 B0YJF7_LUPAN	YNLEYGDALRLPAGTTSYILNPDNDQNLRAKLAIPINNPGKLYDFPSTTKDQSQSYFSG	240
sp F5B8W0 CONB2_LUPAN	YNLEHGDALRLPAGTTSYILNPDNDQNLRAKLAIPINNPGKLYDFPSTTKDQSQSYFSG	317
sp F5B8W1 CONB3_LUPAN	YNLENGDALRLPAGTTSYILNPDNDQNLRAKLAIPINNPGKLYDFPSSSKDQSQSYFSG	304
sp F5B8W2 CONB4_LUPAN	YNLENGDALRLPAGTTSYILNPDNDQNLRAKLAIPINNPGKLYDFPSSSKDQSQSYFSG	314
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tr B0YJF8 B0YJF8_LUPAN	FSKNTLEATNTRYEEIERVLGDDDELQENKQRRGEQSHODEGVIVRVSKKQIQELRK	386
sp F5B8V9 CONB1_LUPAN	FSKNTLEATNTRYEEIERVLGDDDELQENKQRRGEQSHODEGVIVRVSKKQIQELRK	386
tr B8Q5G0 B8Q5G0_LUPAN	FSKNTLEATNTRYEEIERVLGDDDELQENKQRRGEQSHODEGVIVRVSKKQIQELRK	386
sp F5B8W3 CONB5_LUPAN	FSKNTLEATNTRYEEIQRIILGDEDEQEEORRGEQSHODEGVIVRVSKQIQELRK	417
tr B0YJF7 B0YJF7_LUPAN	FSKNTLEATNTRYEEIQRIILGDEDEQEEORRGEQSHODEGVIVRVSKQIQELRK	300
sp F5B8W0 CONB2_LUPAN	FSRNTLEATNTRYEEIQRIILGDEDEQEEORRGEQSHODEGVIVRVSKQIQELRK	377
sp F5B8W1 CONB3_LUPAN	FSKNTLEATNTRYEEIQRIILGDEDEQEEORRGEQSHODEGVIVRVSKQIQELRK	364
sp F5B8W2 CONB4_LUPAN	FSRNTLEATNTRYEEIQRIILGDEDEQEEORRGEQSHODEGVIVRVSKQIQELRK	374
	**:*	
tr B0YJF8 B0YJF8_LUPAN	HAQSSSGEGKPSSEGPFLRSNKPITYSNKFGNFYEITPDINPQFQDLNISLTFTEINELW	446
sp F5B8V9 CONB1_LUPAN	HAQSSSGEGKPSSEGPFLRSNKPITYSNKFGNFYEITPDINPQFQDLNISLTFTEINELW	446
tr B8Q5G0 B8Q5G0_LUPAN	HAQSSSGEGKPSSEGPFLRSNKPITYSNKFGNFYEITPDINPQFQDLNISLTFTEINELW	446
sp F5B8W3 CONB5_LUPAN	HAQSSSRKGPSESGPFLRSNKPITYSNKFGNFYEITPDINPQFQDLNISLTFTEINELW	477
tr B0YJF7 B0YJF7_LUPAN	HAQSSSRKGPSESGPFLRSNKPITYSNKFGNFYEITPDINPQFQDLNISLTFTEINELW	360
sp F5B8W0 CONB2_LUPAN	HAQSSSGKGPSESGPFLRSNKPITYSNKFGNFYEITPDINPQFQDLNISLTFTEINELW	437
sp F5B8W1 CONB3_LUPAN	YAQSSSRKGPSESGPFLRSNKPITYSNKFGNFYEITPDINPQFQDLNISLTFTEINELW	424
sp F5B8W2 CONB4_LUPAN	YAQSSSRKGPSESGPFLRSNKPITYSNKFGNFYEITPDINPQFQDLNISLTFTEINELW	434
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tr B0YJF8 B0YJF8_LUPAN	LTKEKE---IMN-----	455
sp F5B8V9 CONB1_LUPAN	LLLPHYNSKAIPIVVVDEGEQNYELVGIRDQRRQDEQEEEYEQGEVEVRRYSKLSKGD	506
tr B8Q5G0 B8Q5G0_LUPAN	LLLPHYNSKAIPIVVVDEGEQNYELVGIRDQRRQDEQEEEYEQGEVEVRRYSKLSKGD	506
sp F5B8W3 CONB5_LUPAN	LLLPHYNSKAIPIVVVDEGEQNYELVGIRNQRRQDEQE-----VEEVRRYSARLSEGD	531
tr B0YJF7 B0YJF7_LUPAN	LLLPHYNSKAIPIVVVDEGEQNYELVGIRDQRRQDEQE-----VEEVRRYSARLSEGD	416
sp F5B8W0 CONB2_LUPAN	LLLPHYNSKAIPIVVVDEGEQNYELVGIRDQRRQDEQE-----QEEVRRYSARLSEGD	491
sp F5B8W1 CONB3_LUPAN	LLLPHYNSKAIPIVVVDEGEQNYELVGIRDQRRQDEQE-----EVRRYSARLSEGD	475
sp F5B8W2 CONB4_LUPAN	LLLPHYNSKAIPIVVVDEGEQNYELVGIRDQRRQDEQE-----EVRRYSARLSEGD	485
	* : *	
tr B0YJF8 B0YJF8_LUPAN	VFIIIPAGHPLSINASSNRLLLGFGINANENQORNFLAGSEDNVIKQLDREVKELTFPGSIE	455
sp F5B8V9 CONB1_LUPAN	VFIIIPAGHPLSINASSNRLLLGFGINANENQORNFLAGSEDNVIKQLDREVKELTFPGSIE	566
tr B8Q5G0 B8Q5G0_LUPAN	VFIIIPAGHPLSINASSNRLLLGFGINANENQORNFLAGSEDNVIKQLDREVKELTFPGSIE	566
sp F5B8W3 CONB5_LUPAN	ILVIPAGHPLSINASSNRLLLGFGINADENQORNFLAGSEDNVIRQLDREVKELTFPGSAE	591
tr B0YJF7 B0YJF7_LUPAN	IFVIPAGHPLSINASSNRLLLGFGINANENQORNFLAGSEDNVISQLDREVKELTFPGSAE	476
sp F5B8W0 CONB2_LUPAN	IFVIPAGHPLSINASSNRLLLGFGINADENQORNFLAGSEDNVIRQLDREVKELTFPGSAE	551
sp F5B8W1 CONB3_LUPAN	IFVIPAGHPLSINASSNRLLLGFGINADENQORNFLAGSEDNVIRQLDREVKELTFPGSAE	535
sp F5B8W2 CONB4_LUPAN	IFVIPAGHPLSINASSNRLLLGFGINADENQORNFLAGSEDNVIRQLDREVKELTFPGSTE	545
tr B0YJF8 B0YJF8_LUPAN	-----	455
sp F5B8V9 CONB1_LUPAN	DVERLIKNOQSSYFANAQPQ00-QOREKEGRRGRGPISILLNALLY-----	611
tr B8Q5G0 B8Q5G0_LUPAN	DVERLIKNOQSSYFANAQPQ00-QOREKEGRRGRGPISILLNALLY-----	611
sp F5B8W3 CONB5_LUPAN	DVERLIRNOQSSYFANAQPQ00QOREKEGRRGRGPISILLNALLY-----	637
tr B0YJF7 B0YJF7_LUPAN	DVERLIKNOQSSYFANAQPQ0K-QOREKEGRRGRRLSILLSTLY-----Y	521
sp F5B8W0 CONB2_LUPAN	DVERLIKNOQSSYFANAQPQ00-QOREKEGRRGRRLSPFRSLFTKLLSTIM	603
sp F5B8W1 CONB3_LUPAN	DVERLIKNOQSSYFANAQPQ00-QOREKEGRRGRRLSILLSTLY-----	580
sp F5B8W2 CONB4_LUPAN	DVERLIKNOQSSYFANAQPQ00-QOREKEGRRGRRLSILLSTLY-----	590

Figure S7. Sequence alignment of β -globulin proteins B0YJF7, B0YJF8, F5B8W0, F5B8W1, F5B8W2, F5B8W3, F5B8V9 and B8Q5G0.

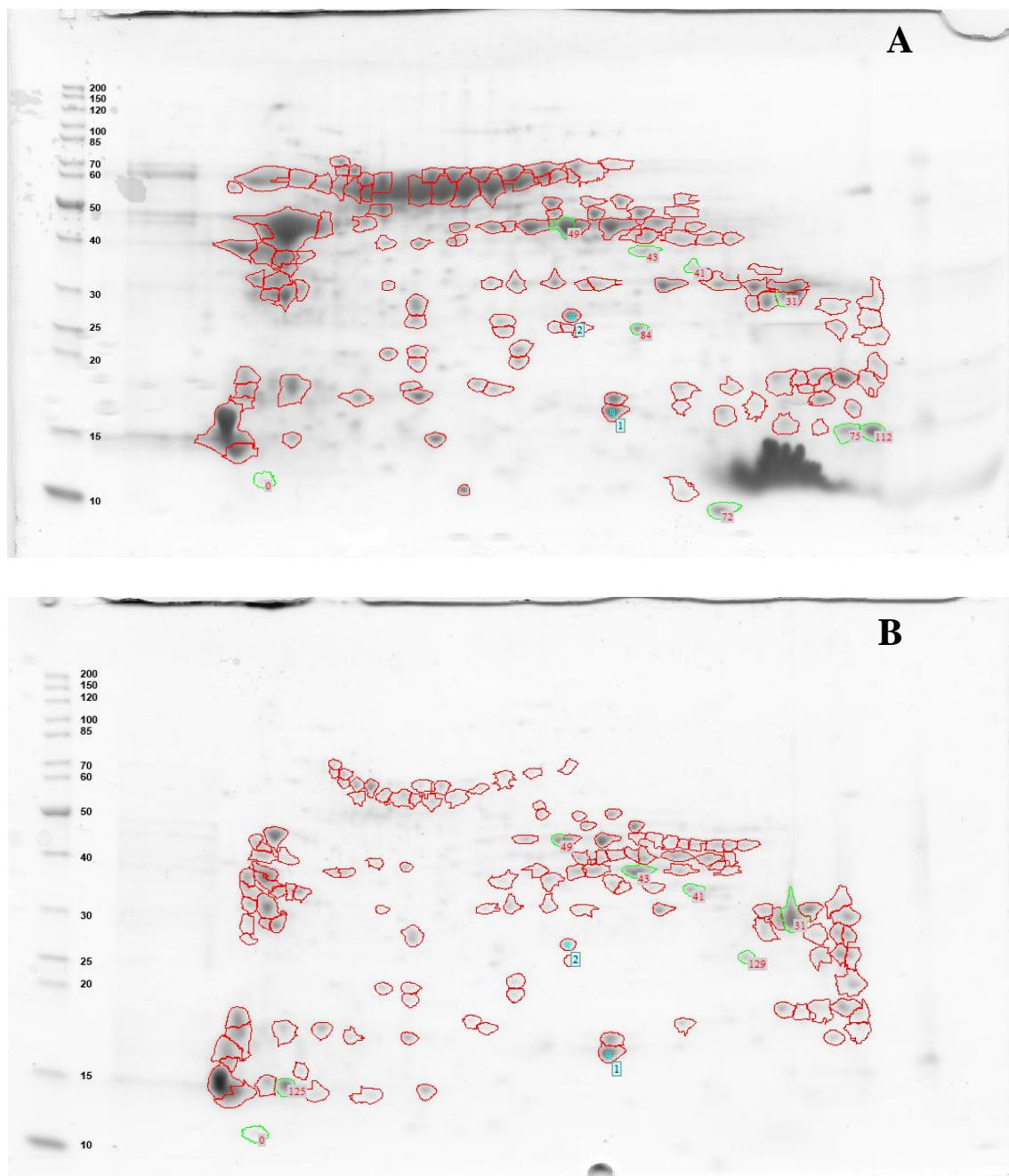


Figure S8. 2D gel map comparison of Modica Ecotype (A) and Luxor cultivar (B). Excised spots are highlighted in green. The corresponding identifications are reported in **Tables S2 – 4**, where spot ID are reported with an asterisk (*).

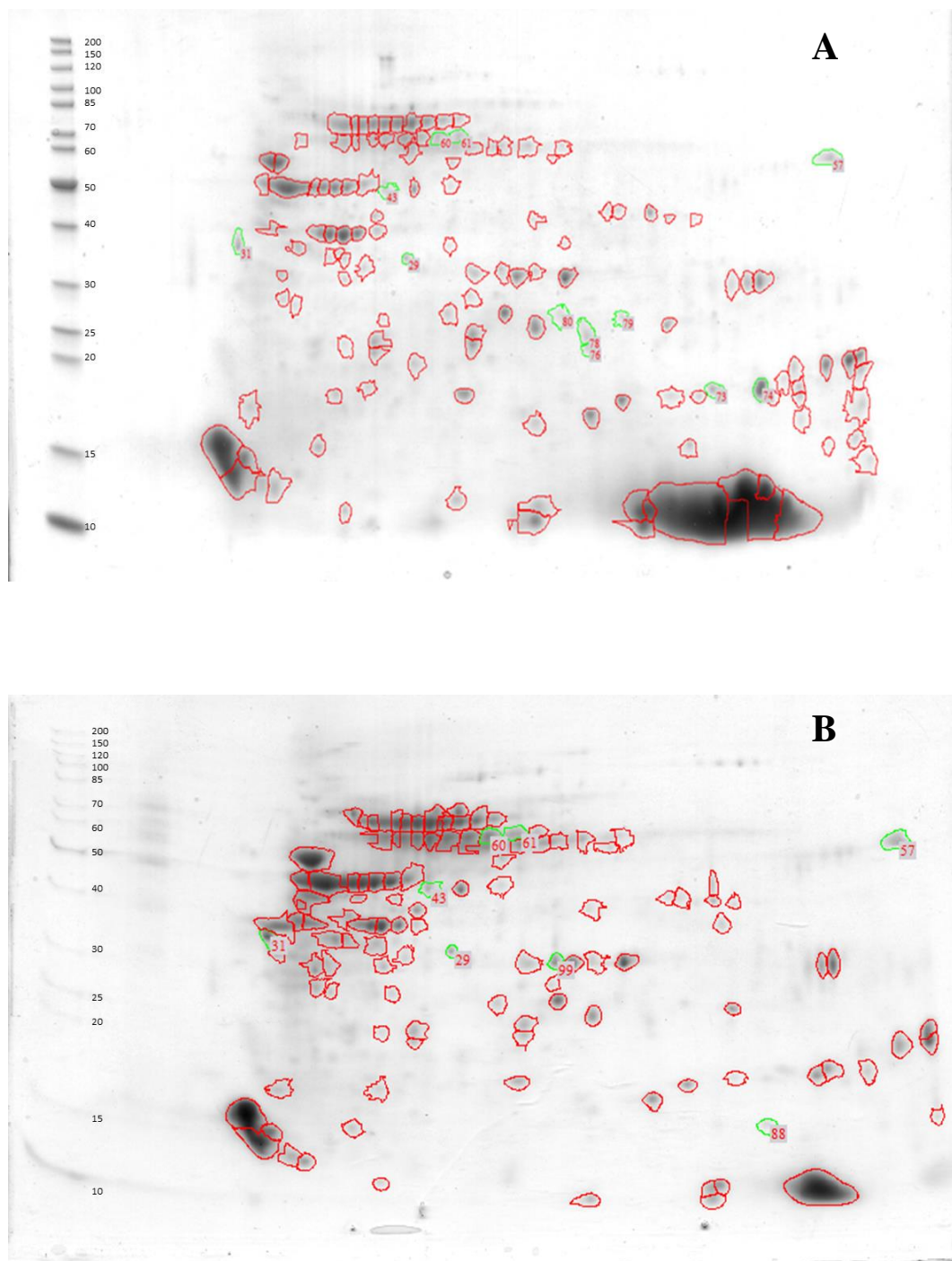


Figure S9. 2D gel map comparison of Taper (A) and Dukat cultivar (B). Excised spots are highlighted in green. The corresponding identifications are reported in **Tables S5 – 6**, where spot ID are reported with an asterisk (*).

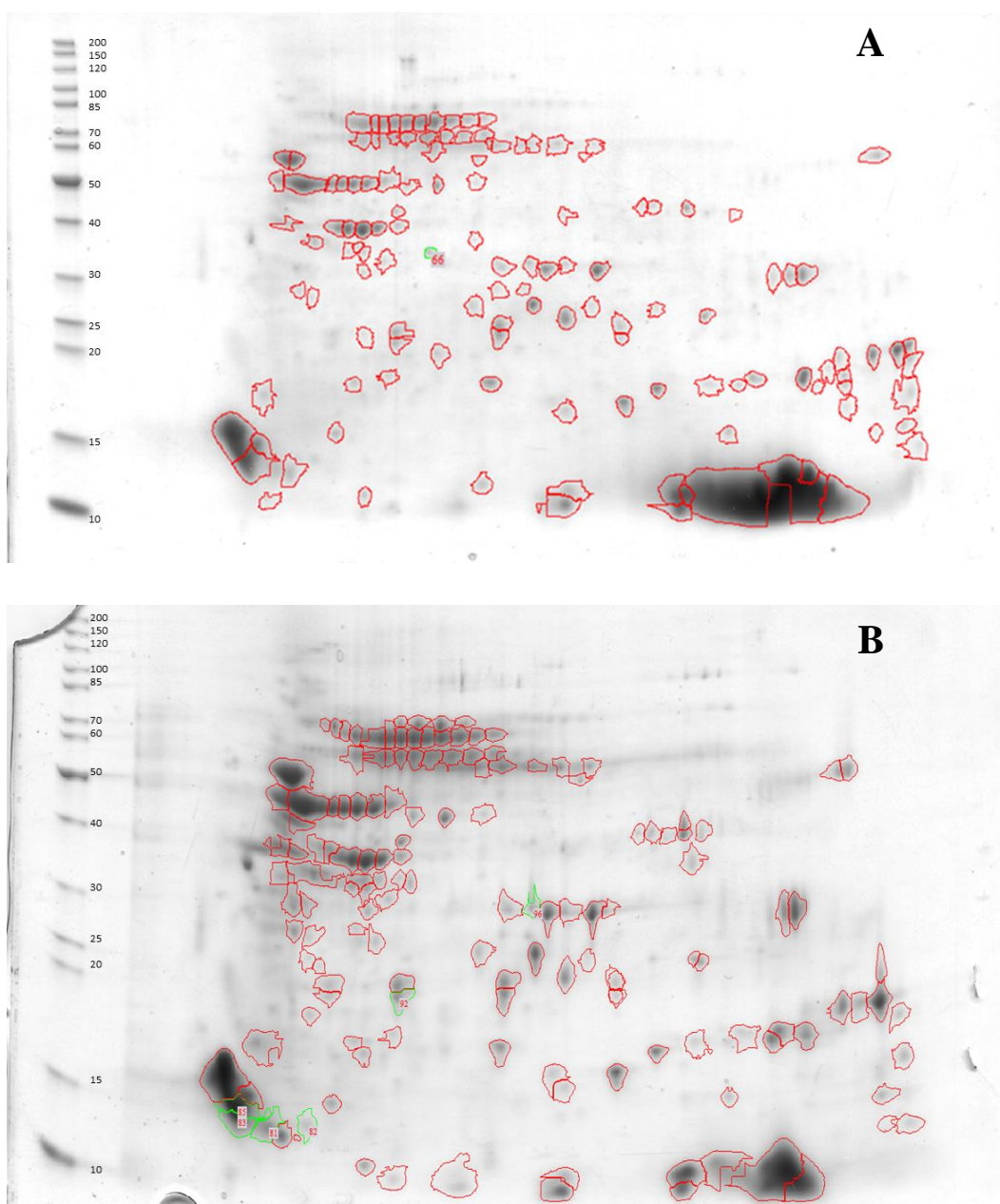


Figure S10. 2D gel map comparison of cv Taper (A) cv Mister (B). Excised spots are highlighted in green. The corresponding identifications are reported in **Tables S7 - 8**, where spot ID are reported with an asterisk (*).