

Supplemental Table 1. Average normalized DIGE intensity values and protein identification data for maternally-inherited co-dominantly expressed spots containing aphid proteins

Spot #	Anova (p)	Fold	Average Normalised Volumes ^a											Protein Identification Information			
			Vector			RT-1		RT-2	RT-3			RT-ND	Name	Accession	pI ^c	Protein Score ^f	
			Sg-F	A3	CC6	CC1	C2	BB1	Sg-SC	K2	MM1	K3					
13	0	7	0.238	0.776	1.103	0.883	0.851	1.198	1.675	0.771	1.147	1.483	dihydropteridine reductase ^c	gij193627466	5.69	168	
22	0	6.5	0.243	0.709	0.851	1.402	1.451	0.847	1.576	1.36	1.255	0.93	coA ligase ^b	gij193598809	5.85	198	
27	0	4.9	0.387	1.284	1.532	1.559	1.892	0.649	1.083	1.221	1.534	0.387	troponin-T ^c	gij187179335	5.1	242	
52	0	4	0.569	0.532	1.094	1.437	2.123	1.182	1.406	1.135	0.939	0.577	cuticle protein ^b	gij193706873	6.4	314	
345 ^d	0.1	1.6	0.892	0.902	0.93	0.688	1.055 ^{^F}	1.069 ^{^F}	1.09 ^{^F}	0.97 ^{^F}	0.96 ^{^F}	1.088 ^{^F}	ATP synthase D ^b	gij187109136	5	205	
42	2.22E-16	3.1	0.692	0.688	0.654	1.269	1.433	1.517	1.512	0.536	0.513	0.483	GAPDH ^c	gij193688110	6.2	93	
493	0	2.7	0.498	0.828	1.227	1.258	1.236	1.009	1.354	0.894	0.981	1.236	replication protein 70A ^c	gij193667016	6	541	
269 ^d	1.57E-08	1.6	0.855	0.734	1.118	1.135	0.923 ^{^SC}	1.087	1.126	1.178	1.082	1.047 ^{^F}	electron-transferring dehydrogenase ^c	gij193620163	5.9	188	

a: Mean separations of log normalized volume shown via gray scale, darker shades is higher expression level on a spot by spot basis, ANOVA, p-value <0.05

b: Method of protein identification MALDI MS-MS/MS

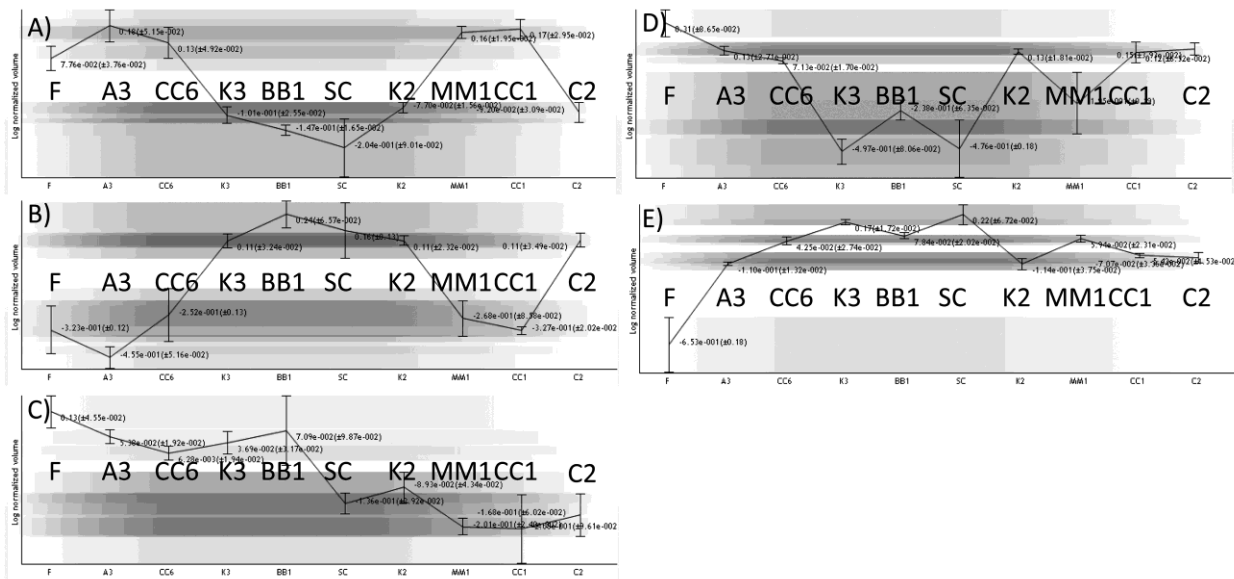
c: Method of protein identification ESI MS-MS/MS on SYNAPT HDMS

d: There are multiple proteins in this spot and this accounts for higher spot volume in Sg-F, see Figure 4E, maternal isoform is red spot behind yellow spot

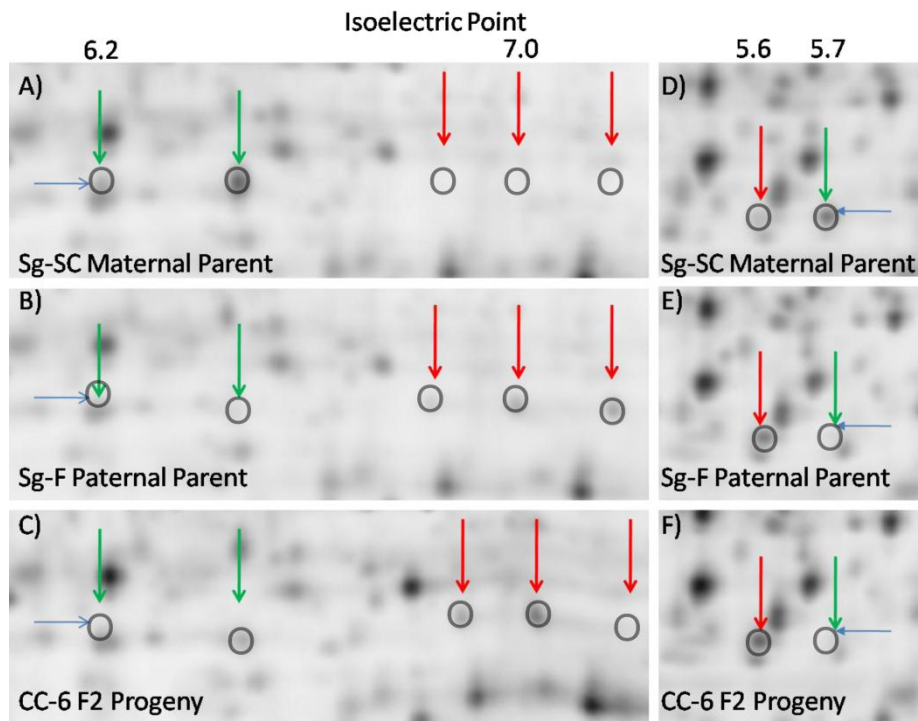
e: pI is the observed pI of the maternal isoform on the 2D gel

f: The protein score reported by MASOT is the sum of the ion scores which equal $-10 * (\text{Log})P$, where P is the probability that the observed match is a random event. For the search of the NCBI nr database, a score of 48 or greater represents significant homo

^: Mean is higher but p-value >0.05 in mean separation 1-way ANOVA with Sg-F or Sg-SC as noted.



Supplemental Figure 1: Graphs from the Nonlinear Samespots workflow showing examples of the expression profiles of individual spots selected for involvement in virus transmission, log-normalized spot volume is plotted on the Y-axis. Profiles of 2-D DIGE spots selected for analysis include those (A) up-regulated in the competent genotypes (Sg-F, A3, CC6) and down-regulated in the refractive parent genotype, Sg-SC, (B) up-regulated in the refractive parental genotype, Sg-SC, and down-regulated in the competent genotypes, (C) up-regulated in competent and RT-2 genotype (BB1) and down-regulated in RT-1 (C2, CC1) and RT-3 (Sg-SC, K2, MM1), and (D) up-regulated in competent genotypes aphids and RT-1 genotypes, which likely contain the full complement of vectoring genes at the ASG (10), (E) up-regulated in the maternal genotype Sg-SC and all F2 progeny genotypes but not the transmission competent parent genotype Sg-F. Panels D (spot 14) and E (spot 13) display an isoform pair of the same protein, dihydropteridine reductase.



Supplemental Figure 2: The *pI* of numerous *Buchnera* proteins in transmission competent F2 genotypes matched the competent male parental Sg-F, not the refractive maternal parent Sg-SC, even though *Buchnera* are inherited transovarially through the maternal line. For outer membrane protein F precursor, gi|21672662, there are a total of five isoforms found in the population. (A) Two of the isoforms (1 and 2) are visible in the refractive parent Sg-SC, isoform 1 is specific to SC and isoform 2 is also found in the competent parent Sg-F. (B) Four isoforms (isoforms 2-5) are visible in the competent paternal Sg-F genotype, three specific, more basic isoforms and the one isoform also found in Sg-SC. (C) Three isoforms are found in the vector F2 progeny, two of the basic isoforms (3 and 4) and the shared isoform, 2. The F2 genotype CC6, a strong CYDV-RPV transmitter, is shown here. A similar pattern of isoform inheritance is observed for *Buchnera* protein EF-Tu, the refractive parent Sg-SC (D) and competent parent Sg-F (E) have two different isoforms that differ slightly in *pI*. The EF-Tu protein expression in the competent F2 progeny CC6 (F) unexpectedly matches the paternal isoform. The gel was visualized using the Typhoon Variable Mode Imager (GE Healthcare) according to the manufacturer's instructions on imaging cyanine dyes.