Appendix

Fig. A1: Fresh weight of *C. cajan* and *Z. mays* plant roots considered for root exudate collection at 28 DAS. A total of 80 *C. cajan* and 60 *Z. mays* plants were taken for collection of root exudates in both monocropping and intercropping systems. DAS: Days after sowing.

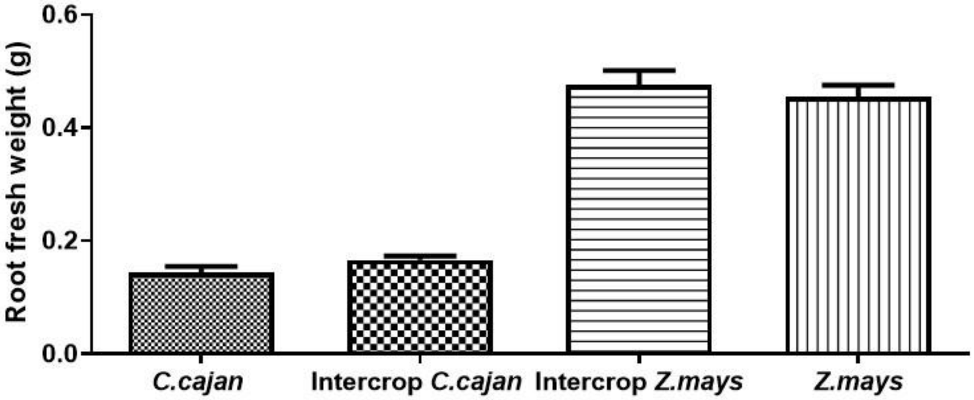

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Table A1. Metabolites detected in the root exudates of intercrop and monocrop plants cultivated *C. cajan* and *Z. mays*

Sr. No	Retention time	Identified Metabolites	*Cajanus cajan*		*Zea mays*	
			Monocrop	Intercrop	Monocrop	Intercrop
Amines						
1	8.34	Hydroxylamine, 3TMS	ND	0.53 ± 0.63	ND	2.23 ± 0.15 (p value = 0.028)
2	25.60	9H-Purin-6-amine	0.04 ± 0.03	1.97 ± 1.09	ND	ND
Amino acids						
3	6.46	N-Formylglycine	0.02 ± 0.03	0.24 ± 0.15	ND	ND
4	11.00	N-Acetyl-L-alanine	ND	0.98 ± 1.21	ND	ND
5	16.00	L-threonine, 3TMS	0.15 ± 0.02 (p value = 0.04)	1.24 ± 0.94	ND	ND
6	18.29	L-Proline, 2TMS ester	1.14 ± 0.95	8.43 ± 3.82**	ND	ND
7	19.78	L-Arginine	ND	ND	0.065 ± 0.004	0.58 ± 0.05**
8	27.76	L-Tyrosine, 3TMS ester	ND	0.5 ± 0.2	ND	ND

9	30.35	L-Histidine, N-à-(tert-Butoxycarbonyl)-	ND	ND	ND	13.83 ± 11.04
Aromatic compounds						
10	9.53	Benzaldehyde	ND	ND	0.5 ± 0.42	2.72 ± 0.1 (p value = 0.015)
11	10.42	Benzoic acid	0.14 ± 0.08	1.9 ± 1.66	0.6 ± 0.52	12.93 ± 11.33
12	16.90	Indole-7-carboxaldehyde	ND	0.2 ± 0.03 (p value=0.004)	0.06 ± 0.014 (p value=0.02)	ND
13	20.84	Benzene, 3TMS	ND	0.55 ± 0.27	ND	ND
14	20.86	1,2-Benzenedicarboxylic acid, 2TMS ester	0.31 ± 0.2	1.12 ± 0.06**	0.14 ± 0.08	ND
15	21.16	Benzene acetic acid	ND	ND	0.26 ± 0.06 (p value = 0.02)	ND
16	26.52	Trimethylsilyl 3,5-dimethoxy-4-(trimethylsilyloxy)benzoate	ND	ND	0.07 ± 0.03	ND
Fatty acids						
17	9.38	Pentanoic acid, 3TMS ester	ND	ND	0.55 ± 0.35	ND
18	12.78	2-(2-Butoxyethoxy)ethoxy-1TMS	ND	ND	2.31 ± 1.85	159.99 ± 111.51

19	14.06	Adipic acid	ND	0.05 ± 0.043	ND	0.5 ± 0.58
20	18.44	Pentanedioic acid	0.33 ± 0.25	ND	ND	ND
21	19.96	2-Isopropylmalic acid	ND	ND	ND	0.72 ± 0.58
22	22.64	Azelaic acid, 2TMS ester	0.39 ± 0.3	ND	ND	ND
23	29.05	Palmitelaidic acid, 1TMS ester	2.01 ± 1.42	9.78 ± 4.05	0.35 ± 0.24	ND
24	31.29	Heptadecanoic acid, 1TMS	0.21 ± 0.2	5.51 ± 1.78**	ND	0.69 ± 0.41
25	32.26	(Z,Z)-9,12-Octadecadienoic acid, TMS	0.45 ± 0.23	2.26 **±** 1.31	ND	ND
26	32.56	Trans-9-Octadecenoic acid, 1TMS ester	1.8 ± 1.03	10.79 **±** 7.87	ND	ND
27	32.56	Oleic acid, trimethylsilyl ester	0.93 ± 0.18	6.85 ± 2.44**	ND	ND
28	36.16	Eicosanoic acid, 1TMS ester	ND	2.05 ± 0.62 (p value = 0.03)	ND	ND
29	38.65	Hexadecanoic acid	1.21 ± 0.37	27.03 **±** 12.07**	3.89 ± 1.44	5 ± 1.41^{ns}
30	41.41	Octadecanoic acid, 2TMS oxy, propyl ester	2.83 ± 1.46	70.2 ± 36.5**	6.03 ± 0.99 (p value = 0.01)	ND

Hydrocarbons						
31	9.31	Undecane	ND	ND	0.48 ± 0.1	ND
32	19.76	Hexadecane	0.11 ± 0.1	1.95 ± 1.67	0.25 ± 0.12	4.9 ± 3.7
33	24.88	Octadecane	0.27 ± 0.12	ND	ND	5.59 ± 4.4
34	17.06	3,6,9,12-Tetraoxa-2,13-disilatetradecane, 2,2,13,13-tetramethyl-	0.47 ± 0.2	ND	ND	ND
Organic acids						
35	14.00	Acetic acid, phenoxy-, TMS ester	0.09 ± 0.07	ND	ND	ND
36	15.15	Trans-Cinnamic acid	0.004 ± 0.002	0.17 ± 0.09	ND	1.82 ± 0.6
37	15.70	Phthalic anhydride	ND	ND	ND	3.15 ± 0.96
38	16.57	Butanedioic acid, [(trimethylsilyl)oxy]-, bis(trimethylsilyl) ester	0.08 ± 0.06	ND	ND	ND
39	22.41	(E)-1-Propene-1,2,3-tricarboxylic acid, 3TMS ester	ND	ND	0.55 ± 0.07 (p value=0.004)	ND

40	26.96	Sulfurous acid, 2-ethylhexyl isohexyl ester	ND	0.52 ± 0.27	ND	ND
41	27.37	Gluconic acid	ND	ND	ND	0.13 ± 0.007 (pvalue = 0.025)
Sugars						
42	27.80	D-Mannose, 5TMS, o-methyloxyme, (1Z)-	ND	2.6 ± 0.72 (p value=0.02)	1.26 ± 1.18	0.91 ± 0.5^{ns}
43	28.72	D-Mannitol, 6TMS	ND	ND	ND	0.31 ± 0.02 (p value = 0.043)
44	32.36	D-Galactose, 5TMS, o-methyloxyme, (1Z)-	ND	ND	0.16 ± 0.09	0.41 ± 0.09*
45	50.40	D-(+)-Turanose, 8TMS ether	0.08 ± 0.03	2.19 ± 0.63**	22.64 ± 5.64 (p value=0.02)	ND
46	50.58	3-à-Mannobiose, 8TMS ether (isomer 2)	ND	ND	ND	6.32 ± 4.48
Sugar Alcohols						
47	24.44	L-(-)-Arabitol, 5TMS ether	ND	ND	ND	3.47 ± 0.38
48	25.16	Ribonic acid, 5TMS ester	0.62 ± 0.31	ND	0.55 ± 0.2	0.82 ± 0.29**

49	31.44	Myo-Inositol, 6TMS	0.41 ± 0.11	2.19 ± 0.65**	5.12 ± 1.52**	0.67 ± 0.2
50	13.00	Glycerol, 3TMS ether	ND	ND	ND	2.05 ± 0.58 (p value =0.025)
51	11.64	Silanol, trimethyl-, phosphate (3:1)	0.39 ± 0.27	6.27 ± 3.72	1.28 ± 0.67	5.24 ± 0.68
Sugar Conjugates						
52	24.60	2-Desoxy-pentos-3-ulose, bis(methoxime),O,O'-2TMS	0.25 ± 0.17	ND	ND	ND
53	28.47	D-glucopyranoside, ethyl 4TMS-	ND	ND	0.16 ± 0.07	2.18 ± 0.005*
54	36.55	5-Methyluridine, 3TMS deriv.	ND	ND	ND	1.01 ± 0.24
Others						
55	5.33	Borate, 3TMS	0.05 ± 0.04	474.78 ± 259.97	ND	105.27 ± 29.87
56	8.57	Disiloxane, 1,3-bis(1,1-dimethylethyl)-1,1,3,3-tetramethyl-	0.07 ± 0.04	ND	ND	ND
57	10.18	Urea, 3TMS	ND	2.91 ± 1.9	ND	ND
58	16.26	Dimethyl phthalate	ND	ND	0.12 ± 0.15	ND

59	19.48	Silanamine	0.21 ± 0.14	ND	ND	ND
60	26.48	Melamine, 3TMS derivative	ND	0.44 ± 0.48	ND	0.51 ± 0.34
61	29.74	N-(Trifluoroacetyl)-3TMS normetanephrine	ND	ND	ND	0.46 ± 0.02 (pvalue = 0.015)
62	30.14	1,3-Dicyclohexylurea	0.6 ± 0.88	ND	ND	ND
63	16.71	Tris(hydroxymethyl) aminomethane, 3TMS ether	0.31 ± 0.21	1.89 ± 1.3	0.57 ± 0.45	0.53 ± 0.37

Values are expressed as a mean ± standard deviation. TMS, trimethylsilylation, ND means not detected in the sample

Table A2: Relative abundance of 161 proteins expressed differentially in NGR234 upon treatment with different root exudates

T: Protein IDs	Average Control	Average IM	Average M	(IM/ Control) p-value	(M/Control) p-value
C3KKF2_SINFN	1.9121	-0.344049267	-3.363525	0.023649	0.00559184
C3KLP6_SINFN	0.1315	-1.099723333	-0.0394229	0.0161754	0.773045
C3KLS9_SINFN	0.1084	-2.06129	-1.745463333	0.00371433	0.0186594
C3KLW3_SINFN	0.1397	-1.562614667	-1.248325	0.0394476	0.0709202
C3KLW5_SINFN	-0.0190	-1.800813333	-2.668296667	0.022745	0.00767827
C3KLW6_SINFN	0.1952	-1.827136667	-3.259763333	0.0888216	0.0205346
C3KLX6_SINFN	-0.8731	-1.121644	-1.483793333	0.303886	0.00575441
C3KM61_SINFN	-1.0031	-1.055663667	-0.529208	0.835805	0.173632
C3KM99_SINFN	-2.5058	-1.60762	-0.291592367	0.112667	0.00889974
C3KMA1_SINFN	-2.2972	-1.185750333	-0.003454257	0.0917302	0.019722
C3KMA2_SINFN	-2.2733	-1.546801333	0.322671333	0.549584	0.0757831
C3KMG0_SINFN	2.3802	3.859963333	3.602466667	0.0146333	0.00565581
C3KMG6_SINFN	-4.2276	2.117916667	1.763802333	0.00131673	0.0044745
C3KMU0_SINFN	0.9931	-1.383391667	-0.613821333	0.0313358	0.0710375
C3KN63_SINFN	0.3131	-0.653467667	-0.608361	0.0237158	0.363744
C3KNB2_SINFN	-0.7734	-2.344555	-1.574231	0.0157509	0.20113
C3KND2_SINFN	-0.1224	-1.082889	0.042786667	0.197771	0.745529
C3KNE5_SINFN	-1.0784	-1.55282	0.3146215	0.45331	0.0477433
C3KPY9_SINFN	2.2802	-0.482217667	-1.124201333	0.00159073	0.00319276
C3KQU9_SINFN	-1.0618	-2.582656667	-2.288551	0.0109489	0.153579
C3KR68_SINFN	1.3870	1.690436667	2.44332	0.17349	0.0016098
C3KR98_SINFN	0.3219	1.782276667	1.968073333	0.0115257	0.0500151
C3KRI5_SINFN	0.0004	0.233235667	1.38037	0.64328	0.0106187
C3KRR7_SINFN	0.1941	-0.855106	-1.069627667	0.0252498	0.0350733
C3M8G7_SINFN	0.5525	0.683755667	1.24007	0.725794	0.0398757
C3M8G9_SINFN	-0.5695	0.929693	0.724657767	0.0271653	0.0925105
C3M8Q0_SINFN	0.2508	-0.41519	-1.12428	0.013489	0.00855842
C3M8R5_SINFN	2.1299	3.226263333	2.511843333	0.0404633	0.606597

C3M8V5_SINFN	-0.1603	0.929795	0.139837667	0.00487792	0.655965
C3M8W4_SINFN	-0.1369	0.848219	-0.196253367	0.0478561	0.922431
C3M8Z0_SINFN	1.3020	1.78267	1.107848667	0.494565	0.775576
C3M920_SINFN	-0.3351	-0.783187	-0.57702135	0.043869	0.562311
C3M9A0_SINFN	1.3447	2.275383333	1.42548	0.050444	0.821568
C3M9D3_SINFN	-0.9033	0.4199061	0.573273667	0.0117602	0.0624897
C3M9D5_SINFN	-0.9616	-1.44146	0.1940815	0.345808	0.190225
C3M9F6_SINFN	-1.4364	0.098303333	0.729596	0.0599458	0.0384355
C3M9G1_SINFN	0.1787	-1.71862	-1.848293333	0.0479667	0.0434545
C3M9P2_SINFN	2.8609	2.602953333	1.212742	0.497173	0.0152221
C3M9P3_SINFN	1.1458	0.615384667	-0.129740967	0.390569	0.0733877
C3M9R2_SINFN	6.1880	5.123733333	2.101667333	0.19725	0.0096785
C3M9R3_SINFN	5.9535	4.36842	1.013727333	0.00390537	0.000117738
C3M9T3_SINFN	-1.9264	-2.149893333	-1.264485333	0.68915	0.292282
C3M9U4_SINFN	0.3127	1.058615	0.200915933	0.0802622	0.598423
C3M9X7_SINFN	-2.6654	-2.186575	-1.025473	0.715773	0.2781
C3MA02_SINFN	-3.0727	-2.66557	-0.2809155	0.334463	0.0322976
C3MA06_SINFN	-0.0062	0.790995	-0.779033667	0.539081	0.0146706
C3MA09_SINFN	0.5318	3.358723333	3.707856667	0.00847402	0.00235538
C3MA54_SINFN	-0.4621	0.414876667	0.136648667	0.0288096	0.626021
C3MA56_SINFN	-0.6117	0.660578733	-0.620062333	0.0398171	0.626021
C3MA57_SINFN	0.5777	2.382586667	1.505541	0.00965836	0.237116
C3MA58_SINFN	0.6236	1.193136	0.351157733	0.283508	0.596479
C3MA77_SINFN	0.3656	0.492611333	0.946583667	0.714395	0.000315758
C3MAB1_SINFN	-1.2645	0.515873	-0.498629667	0.195237	0.537021
C3MAC3_SINFN	0.0357	0.884189667	0.361602	0.0334123	0.262699
C3MAH0_SINFN	-0.2703	0.879237333	0.280262667	0.0345603	0.343693
C3MAK5_SINFN	1.8229	2.568403333	2.820086667	0.111915	0.0451224
C3MAL5_SINFN	-0.5653	0.274603133	-0.44458	0.138545	0.810722
C3MB12_SINFN	0.1762	0.735363	0.175642	0.03719	0.999064
C3MB21_SINFN	-0.6615	-0.95388	-1.117390333	0.110155	0.0378952

C3MB52_SINFN	0.4520	1.735186667	1.408946333	0.0425997	0.165724
C3MB53_SINFN	0.7383	1.531086667	0.807139	0.0205354	0.936483
C3MBD1_SINFN	-0.1192	0.493443233	-0.1730259	0.344592	0.925355
C3MBG5_SINFN	-0.4522	-0.961208333	-1.687842667	0.029238	0.0543331
C3MBP2_SINFN	2.4228	3.749333333	5.82274	0.016183	0.0850317
C3MBT5_SINFN	0.7004	1.34836	0.700247	0.00152874	0.999522
C3MBU7_SINFN	-0.2241	0.499975667	-0.220349396	0.20353	0.994266
C3MC00_SINFN	1.0121	1.980473333	2.01243	0.00889922	0.0296504
C3MC21_SINFN	1.4164	2.457926667	2.58207	0.0507839	0.0400365
C3MC24_SINFN	0.4380	-1.55711	-1.66785	0.0138718	0.0106486
C3MC48_SINFN	-0.1818	1.536053333	1.087444633	0.0277626	0.147113
C3MC50_SINFN	0.0582	0.560674	-0.0540903	0.169458	0.733464
C3MC56_SINFN	0.2116	0.356894	-0.038357823	0.773364	0.621567
C3MC68_SINFN	0.9152	1.892896667	1.185099333	0.0212955	0.622937
C3MC72_SINFN	1.7929	2.895693333	1.947466667	0.00272225	0.0584953
C3MC91_SINFN	0.4878	0.557772333	-1.2475326	0.786028	0.0584953
C3MCE4_SINFN	-1.7322	-2.950113333	-2.398293333	0.0325748	0.168482
C3MCE9_SINFN	-0.4273	-1.40104	-1.503746667	0.0443288	0.0537462
C3MCM3_SINFN	0.7823	1.686723333	1.251930333	0.0436	0.631197
C3MCM9_SINFN	-1.2381	-0.450958	-2.874386667	0.376111	0.00173382
C3MCR8_SINFN	-0.0094	0.318860667	1.347525	0.559054	0.0114707
C3MCU7_SINFN	-0.3116	0.62735	1.160035	0.0548172	0.0213465
C3MCZ3_SINFN	0.9030	0.807701667	0.261526333	0.817856	0.145887
C3MCZ6_SINFN	1.7936	1.71598	1.111956333	0.862677	0.183149
C3MD23_SINFN	-0.7598	-1.305223333	-1.66471	0.0711468	0.0261492
C3MD32_SINFN	-0.8832	0.394749333	-0.71291	0.0525316	0.712216
C3MD75_SINFN	1.5198	2.881716667	3.438583333	0.042	0.043
C3MDD9_SINFN	-0.3439	-0.316020633	-0.706398333	0.877531	0.0438807
C3MDL0_SINFN	0.1618	-0.438156	-0.424033667	0.0696395	0.0482095
C3MDR3_SINFN	0.2845	-0.600247667	-0.296238267	0.023153	0.131258
C3MDT3_SINFN	0.0895	2.48058	2.081704333	0.00136533	0.110971

C3ME53_SINFN	-0.5502	-2.173823333	-1.3380535	0.00098942	0.12279
C3ME93_SINFN	-0.6207	-2.110323333	-2.292415	0.00980392	0.0759587
C3MEC4_SINFN	-4.0347	-3.973976667	-2.052165	0.902784	0.0633916
C3MEJ6_SINFN	-1.0767	-0.329725333	2.11673	0.316112	0.0353315
C3MEK2_SINFN	0.1456	-1.755690667	-2.24859	0.165249	0.0207115
C3MEQ2_SINFN	0.4778	1.915696667	1.078281333	0.019844	0.529825
C3MEQ9_SINFN	1.7949	2.811793333	3.071796667	0.026205	0.0603334
C3MER7_SINFN	-2.0418	-3.860613333	-4.326035	0.0852061	0.0383445
C3MET9_SINFN	-1.4794	2.280086667	1.8738	0.00891278	0.00627486
C3MF24_SINFN	-3.1302	-0.915106	-0.1451415	0.00296723	0.000982035
C3MF93_SINFN	-0.3929	0.268908033	-0.175834733	0.0412166	0.509244
C3MF99_SINFN	0.5412	-0.244651667	-0.177544067	0.0100672	0.0308988
C3MFB3_SINFN	-0.4198	1.081162667	1.31861	0.0261144	0.0543531
C3MFB4_SINFN	-0.7290	0.374060667	-0.052462667	0.0293534	0.276224
C3MFI3_SINFN	0.8741	2.429906667	3.39149	0.156346	0.0201733
C3MFI5_SINFN	-0.6240	1.090384	1.387549333	0.0103466	0.042
C3MFJ9_SINFN	1.3781	2.452843333	1.75167	0.018904	0.212628
C3MFM9_SINFN	1.3911	2.640183333	1.879453333	0.00283501	0.0813075
C3MFX5_SINFN	1.0722	2.323046667	2.961475	0.0423226	0.00164596
C3MG56_SINFN	0.5278	1.62297	0.059513333	0.114457	0.523119
C3MG69_SINFN	1.3247	2.405586667	2.079886	0.0239181	0.386751
C3MGE2_SINFN	1.9601	2.81375	2.87604	0.098841	0.012362
C3MGG7_SINFN	-0.3173	-1.676816667	-0.443624	0.0420315	0.906726
C3MGH4_SINFN	0.0390	0.806098667	0.049277667	0.00280276	0.981206
C3MGJ7_SINFN	0.6939	0.846681667	0.446177	0.533062	0.342069
C3MGK1_SINFN	1.0562	1.879836667	2.088616667	0.021292	0.090872
C3MGK3_SINFN	-0.7018	-2.25248	-2.41681	0.0641534	0.0123567
C3MGL9_SINFN	-1.2563	0.849483	1.417336667	0.0190078	0.336245
C3MGT2_SINFN	1.1427	1.701496667	1.058054333	0.0848408	0.735343
C3MGU1_SINFN	-2.5125	4.683286667	3.375343333	0.000949352	0.000675115
C3MGY3_SINFN	0.0920	-3.560293333	-2.69326	0.00151228	0.0212864

C3MHE2_SINFN	0.2682	0.685959333	0.629174	0.0700276	0.0258743
C3MHG3_SINFN	-0.8384	-0.614055	-1.860836667	0.561856	0.0479306
C3MHH6_SINFN	1.4568	2.169416667	1.876583333	0.016095	0.195365
C3MHL4_SINFN	0.9969	2.111353333	2.18425	0.00130052	0.0209594
C3MHN7_SINFN	-0.7449	-0.776888333	0.612309	0.944696	0.0488926
C3MHQ3_SINFN	1.1473	2.001176667	1.72807	0.00145768	0.0496317
C3MHV6_SINFN	-2.3747	-3.357586667	-3.81963	0.326079	0.0172039
C3MI04_SINFN	1.1446	1.84745	1.670858333	0.012494	0.538909
C3MI07_SINFN	0.9477	1.67955	1.938766333	0.0338667	0.260752
C3MIG7_SINFN	-0.3465	-2.185383333	-0.7296875	0.0321994	0.422272
C3MII7_SINFN	-2.5029	-1.76918	-0.159859	0.206438	0.0340971
C3MIK8_SINFN	-0.3528	1.079476	1.179364667	0.0274366	0.101942
C3MIN5_SINFN	2.0270	-1.084014333	-0.44450537	0.00470201	0.0088061
C3MIQ1_SINFN	-0.4926	0.742146	-0.094745767	0.0533907	0.409242
C3MIU7_SINFN	-0.4436	-0.021372133	1.249998667	0.348251	0.019935
CH602_SINFN	1.3868	2.14168	0.84675	0.0259696	0.619315
DEOB_SINFN	-0.4441	-0.352263933	-0.828324333	0.793435	0.0222111
DNAJ_SINFN	0.7694	1.877803333	1.138516	0.0198005	0.263838
GCSH_SINFN	-0.7003	0.813921	-0.3195686	0.0341056	0.706002
HSLU_SINFN	2.0027	2.941153333	2.31101	0.0177694	0.136423
HSLV_SINFN	0.4379	0.330408267	-1.05966	0.757111	0.00336484
ILVD_SINFN	0.4639	1.88991	1.026434333	0.00914967	0.111503
LEUC_SINFN	0.9919	2.232963333	1.27439	0.0295857	0.290041
LEUD_SINFN	-0.4724	1.308398333	0.393815	0.031475	0.344347
LNT_SINFN	-0.3298	-1.154632333	-1.81205	0.161121	0.0217885
LPXD_SINFN	1.5349	1.981643333	1.32326	0.195299	0.501034
MOAC_SINFN	-2.2211	-1.001165	-0.8880015	0.333716	0.263345
NUSB_SINFN	-0.4364	1.416923333	2.222235	0.00831603	0.0113717
PLSX_SINFN	1.0637	1.256486667	0.817084	0.322359	0.134068
Q6W164_SINFN	0.4234	2.808846667	2.786185	0.0246825	0.0111777
Q6W1E2_SINFN	1.0904	-0.549916	0.374611	0.00295803	0.25909

Q6W1U0_SINFN	-0.6203	-0.51985	2.23867	0.927856	0.0118364
Q6W1U2_SINFN	-0.8915	-0.864427333	1.359255	0.975351	0.00765976
RL23_SINFN	1.5161	2.443413333	0.98314	0.0101824	0.780383
RS20_SINFN	0.8534	1.176873333	-0.143301767	0.641358	0.267452
SYFA_SINFN	0.8947	1.129865	0.590212667	0.480339	0.370885
UREE_SINFN	0.0983	0.337005333	1.32248	0.547938	0.0249111
Y2839_SINFN	-1.6195	1.52	1.3377415	0.0018766	0.0367384
Y4KP_SINFN	0.1342	0.271568533	0.5314705	0.342661	0.0107722
Y4LR_SINFN	0.1371	-1.030746667	-1.452891	0.00931319	0.153378

The table lists the 161 proteins represented in heat map and can be correlated with the IDs provided in **Fig. 4.9**. Control, IM and M represent untreated, and treated with Intercrop Z. mays and with Monocrop Z. mays RE samples. Three biological replicates for each samples were considered. p-value was calculated by t-test (unpaired) of fold change considering 3 biological replicates.

Table A3: List of upregulated and downregulated proteins found upon treated and untreated samples of NGR234

Untreated NGR234 cells

Up-regulated proteins

Sr.No.	Protein IDs	Protein Names	Average
1.	C3M9R2	Putative iron transport protein, periplasmic-binding protein	6.19
2.	C3M9R3	Putative iron transport protein, ATP-binding component	5.95
3.	C3M9P2	Arginase	2.86
4.	C3MBP2	Phasin 2 domain-containing protein	2.42
5.	C3KMG0	Glycotrans 4-likeN domain-containing protein	2.38
6.	C3KPY9	L-allo-threonine aldolase	2.28
7.	C3M8R5	4-hydroxy-tetrahydrodipicolinate synthase (HTPA synthase)	2.13
8.	C3MIN5	Arginine deiminase (ADI)	2.03
9.	HSLU	Hemin-degrading family protein	2.00
10.	C3MGE2	Putative metal cation transporter	1.96
11.	C3KKF2	Putative transcriptional regulator, CarD family	1.91
12.	C3MAK5	Uncharacterized protein	1.82
13.	C3MEQ9	Glycine dehydrogenase (decarboxylating)	1.79
14.	C3MCZ6	Methyltransferase small	1.79
15.	C3MC72	Glutaredoxin	1.79
16.	LPXD	Putative iron transport protein, periplasmic-binding protein	1.53
17.	C3MD75	Putative iron transport protein, ATP-binding component	1.52
18.	RL23	Arginase (EC 3.5.3.1)	1.52

Downregulated Proteins

Sr.No.	Protein IDs	Protein Names	Average
1.	C3KMG6	Possible nucleoside-diphosphate-sugar epimerase	-4.23
2.	C3MEC4	Putative glutathione S-transferase protein	-4.03
3.	C3MF24	Peptide deformylase (PDF)	-3.13
4.	C3MA02	tRNA_edit domain-containing protein	-3.07
5.	C3M9X7	Acetyltransferase	-2.67
6.	C3KM99	Propionyl-CoA carboxylase beta subunit	-2.51
7.	C3MGU1	Rhodanese domain protein	-2.51
8.	C3MII7	Uncharacterized protein	-2.50
9.	C3MHV6	Putative methyltransferase	-2.37
10.	C3KMA1	Propionyl-CoA carboxylase	-2.30
11.	C3KMA2	Methylmalonyl-CoA mutase	-2.27
12.	MOAC	Amino acid/metabolite permease	-2.22
13.	C3MER7	Putative oxidoreductase (YgfF)	-2.04
14.	C3M9T3	Probable sugar ABC transporter, ATP-binding protein	-1.93
15.	C3MCE4	Putative ABC transporter periplasmic binding protein	-1.73

16.	Y2839	Phosphoribosylglycinamide formyltransferase	-1.62
17.	C3MET9	Phasin_2 domain-containing protein	-1.48
18.	C3M9F6	Putative NADH-ubiquinone oxidoreductase subunit	-1.44
19.	C3MGL9	Cysteine desulfurase (Nitrogenase metalloclusters biosynthesis protein NifS)	-1.26
20.	C3MAB1	Predicted phosphotransferase system	-1.26
21.	C3MCM9	Putative substrate-binding component of ABC transporter	-1.24
22.	C3MEJ6	Transcriptional regulator, XRE family	-1.08
23.	C3KNE5	Possible nucleoside-diphosphate-sugar epimerase	-1.08
24.	C3KQU9	Putative glutathione S-transferase protein	-1.06

Intercrop *Z. mays* REs treated NGR234 cells

Up-regulated Proteins

Sr. No.	Protein IDs	Protein Names	Average
1.	C3M9R2	Putative iron transport protein, periplasmic-binding protein	5.12
2.	C3MGU1	Rhodanese domain protein	4.68
3.	C3M9R3	Putative iron transport protein, ATP-binding component	4.37
4.	C3KMG0	Glyco_trans_4-like_N domain-containing protein	3.86
5.	C3MBP2	Phasin_2 domain-containing protein	3.75
6.	C3MA09	Pseudoazurin	3.36
7.	C3M8R5	4-hydroxy-tetrahydrodipicolinate synthase	3.23
8.	C3MBC8	ATP-dependent protease ATPase subunit HslU	2.94
9.	C3MC72	Methyltransferase small	2.90
10.	C3MD75	Glutaredoxin	2.88
11.	C3MGE2	Hemin-degrading family protein	2.81
12.	C3MEQ9	Uncharacterized protein	2.81
13.	Q6W164	10 kDa chaperonin (GroES protein) (Protein Cpn10)	2.81
14.	C3MFM9	Ribosome-binding ATPase YchF	2.64
15.	C3M9P2	Arginase	2.60
16.	C3MAK5	Putative transcriptional regulator, CarD family	2.57
17.	C3MDT3	Corrinoid methyltransferase protein	2.48
18.	C3MC21	Putative efflux transporter, RND family, MFP subunit	2.46
19.	C3MFJ9	Ribose-phosphate pyrophosphokinase (RPPK)	2.45
20.	C3MAY2	50S ribosomal protein L23	2.44
21.	C3MFI3	Putative cold shock protein	2.43
22.	C3MG69	Activator of Hsp90 ATPase 1 family protein	2.41
23.	C3MA57	NADH-quinone oxidoreductase subunit C	2.38
24.	C3MFX5	Translation initiation factor IF-1	2.32
25.	C3MET9	Putative ABC transporter periplasmic binding protein	2.28
26.	C3M9A0	Amidophosphoribosyltransferase (ATase)	2.28

27.	C3M9V0 (LEUC)	3-isopropylmalate dehydratase large subunit	2.23
28.	C3MHH6	Zn-dependent protease protein	2.17
29.	Q6W1D5	60 kDa chaperonin 2 (GroEL protein 2) (Protein Cpn60 2)	2.14
30.	C3KMG6	Possible nucleoside-diphosphate-sugar epimerase	2.12
31.	C3MHL4	Uncharacterized protein	2.11
32.	C3MHQ3	DUF4167 domain-containing protein	2.00
33.	C3MBR0	UDP-3-O-acylglucosamine N-acyltransferase	1.98
34.	C3MC00	Uncharacterized protein	1.98
35.	C3MEQ2	Methylenetetrahydrofolate reductase	1.92
36.	C3MC68	tRNA pseudouridine synthase B	1.89
37.	C3MIR3	Dihydroxy-acid dehydratase (DAD)	1.89
38.	C3MGK1	6-phosphogluconolactonase (6PGL)	1.88
39.	C3MC05	Chaperone protein DnaJ	1.88
40.	C3MI04	Two-component response regulator	1.85
41.	C3M8Z0	Glutamate--tRNA ligase	1.78
42.	C3KR98	Autoinducer 2-binding protein LsrB	1.78
43.	C3MB52	Putative NAD(P)H nitroreductase	1.74
44.	C3MCZ6	Glycine dehydrogenase (decarboxylating)	1.72
45.	C3MGT2	Histidine--tRNA ligase	1.70
46.	C3KR68	Putative iron transport ATP-binding component of ABC transporter protein	1.69
47.	C3MCM3	Thioredoxin peroxidase	1.69
48.	C3MI07	Uncharacterized protein	1.68
49.	C3MG56	Omega-amino acid--pyruvate aminotransferase	1.62
50.	C3MC48	Cytochrome c, class I	1.54
51.	C3MB53	Flavin_Reduct domain-containing protein	1.53
52.	Y2839	Putative iron transport protein, periplasmic-binding protein	1.52

Downregulated Proteins

Sr.No.	Protein IDs	Protein Names	Average
1.	C3MEC4	Putative glutathione S-transferase protein	-3.97
2.	C3MER7	Amino acid/metabolite permease	-3.86
3.	C3MGY3	ATP-dependent dethiobiotin synthetase BioD	-3.56
4.	C3MHV6	Putative methyltransferase	-3.36
5.	C3MCE4	Probable sugar ABC transporter, ATP-binding protein	-2.95
6.	C3MA02	tRNA_edit domain-containing protein	-2.67
7.	C3KQU9	Transcriptional regulator, XRE family	-2.58
8.	C3KNB2	Type III secretion system translocation protein, RhcQ	-2.34
9.	C3MGK3	Probable oxidoreductase OrdL	-2.25
10.	C3MIG7	Tol-Pal system protein TolQ	-2.19

11.	C3M9X7	Acetyltransferase	-2.19
12.	C3ME53	Efflux transporter, RND family, MFP subunit	-2.17
13.	C3M9T3	Putative oxidoreductase (YgfF)	-2.15
14.	C3ME93	Uncharacterized protein	-2.11
15.	C3KLS9	NH(3)-dependent NAD(+) synthetase	-2.06
16.	C3KLW6	Serine--glyoxylate aminotransferase	-1.83
17.	C3KLW5	Serine racemase	-1.80
18.	C3MII7	Uncharacterized protein	-1.77
19.	C3MEK2	Signal peptide peptidase S49, SppA	-1.76
20.	C3M9G1	Exopolyphosphatase	-1.72
21.	C3MGG7	Putative transcriptional regulator, TetR family	-1.68
22.	C3KM99	Propionyl-CoA carboxylase beta subunit	-1.61
23.	C3MC24	Putative sugar ABC transporter, ATP-binding protein	-1.56
24.	C3KLW3	Ornithine cyclodeaminase 2	-1.56
25.	C3KMA2	Methylmalonyl-CoA mutase	-1.55
26.	C3KNE5	Putative substrate-binding component of ABC transporter	-1.55
27.	C3M9D5	Uncharacterized protein	-1.44
28.	C3MCE9	Uncharacterized protein	-1.40
29.	C3KMU0	Putative membrane protein	-1.38
30.	C3MD23	Predicted zinc protease protein	-1.31
31.	C3KMA1	Propionyl-CoA carboxylase	-1.19
32.	C3MF13	Apolipoprotein N-acyltransferase	-1.15
33.	C3KLX6	Putative transcriptional regulatory protein, LacI family	-1.12
34.	C3KLP6	Uncharacterized protein	-1.10
35.	C3KND2	Uncharacterized protein	-1.08
36.	C3MIN5	Arginine deiminase (ADI)	-1.08
37.	C3KM61	Putative hydrolase protein	-1.06
38.	P55558	Uncharacterized protein y4lR	-1.03

Monocrop *Z. mays* REs treated NGR234 cells

Up-regulated Proteins

Sr.No.	Protein IDs	Protein Names	Average
1.	C3MBP2	Phasin_2 domain-containing protein	5.82
2.	C3MA09	Pseudoazurin	3.71
3.	C3KMG0	Glyco_trans_4-like_N domain-containing protein	3.60
4.	C3MD75	Glutaredoxin	3.44
5.	C3MFI3	Putative cold shock protein	3.39
6.	C3MGU1	Rhodanese domain protein	3.38
7.	C3MEQ9	Uncharacterized protein	3.07
8.	C3MFX5	Translation initiation factor IF-1	2.96

9.	C3MGE2	Hemin-degrading family protein	2.88
10.	C3MAK5	Putative transcriptional regulator, CarD family	2.82
11.	Q6W164	10 kDa chaperonin (GroES protein) (Protein Cpn10)	2.79
12.	C3MC21	Putative efflux transporter, RND family, MFP subunit	2.58
13.	C3M8R5	4-hydroxy-tetrahydrodipicolinate synthase (HTPA synthase)	2.51
14.	C3KR68	Putative iron transport ATP-binding component of ABC transporter protein	2.44
15.	C3MC72	Methyltransferase small	2.31
16.	Q6W1U0	Y4yB	2.24
17.	C3M9I9	Transcription antitermination protein NusB (Antitermination factor NusB)	2.22
18.	C3MHL4	Uncharacterized protein	2.18
19.	C3MEJ6	Predicted phosphotransferase system, phosphoenolpyruvate-dependent sugar EIIA 2	2.12
20.	C3M9R2	Putative iron transport protein, periplasmic-binding protein	2.10
21.	C3MGK1	6-phosphogluconolactonase (6PGL)	2.09
22.	C3MDT3	Corrinoid methyltransferase protein	2.08
23.	C3MG69	Activator of Hsp90 ATPase 1 family protein	2.08
24.	C3MC00	Uncharacterized protein	2.01
25.	C3KR98	Autoinducer 2-binding protein LsrB	1.97
26.	C3MC72	Uncharacterized protein	1.95
27.	C3MI07	Ribosome-binding ATPase YchF	1.94
28.	C3MFM9	Zn-dependent protease protein	1.88
29.	C3MHH6	Putative ABC transporter periplasmic binding protein	1.88
30.	C3MET9	Possible nucleoside-diphosphate-sugar epimerase	1.87
31.	C3KMG6	Ribose-phosphate pyrophosphokinase (RPPK)	1.76
32.	C3MFJ9	DUF4167 domain-containing protein	1.75
33.	C3MHQ3	Two-component response regulator	1.73
34.	C3MI04	NADH-quinone oxidoreductase subunit C	1.67
35.	C3MA57	Phasin_2 domain-containing protein	1.51

Downregulated Proteins

Sr.No.	Protein IDs	Protein Names	Average
1.	C3MER7	Amino acid/metabolite permease	-4.33
2.	C3MHV6	Putative methyltransferase	-3.82
3.	C3KKF2	Putative metal cation transporter	-3.36
4.	C3KLW6	Serine--glyoxylate aminotransferase	-3.26
5.	C3MCM9	Cysteine desulfurase	-2.87
6.	C3MGY3	ATP-dependent dethiobiotin synthetase BioD	-2.69
7.	C3KLW5	Serine racemase	-2.67

8.	C3MGK3	Probable oxidoreductase OrdL	-2.42
9.	C3MCE4	Probable sugar ABC transporter, ATP-binding protein	-2.40
10.	C3KQU9	Transcriptional regulator, XRE family	-2.29
11.	C3ME93	Uncharacterized protein	-2.29
12.	C3MEK2	Signal peptide peptidase S49, SppA	-2.25
13.	C3MEC4	Putative glutathione S-transferase protein	-2.05
14.	C3MHG3	1-deoxy-D-xylulose-5-phosphate synthase	-1.86
15.	C3M9G1	Exopolyphosphatase	-1.85
16.	C3MF13	Apolipoprotein N-acyltransferase	-1.81
17.	C3KLS9	NH(3)-dependent NAD(+) synthetase	-1.75
18.	C3MBG5	Putative sugar ABC transporter, ATP-binding protein	-1.69
19.	C3MC24	Putative sugar ABC transporter, ATP-binding protein	-1.67
20.	C3MD23	Predicted zinc protease protein	-1.66
21.	C3KNB2	Type III secretion system translocation protein, RhcQ	-1.57
22.	C3MCE9	Uncharacterized protein	-1.50
23.	C3KLX6	Putative transcriptional regulatory protein, LacI family	-1.48
24.	P55558	Uncharacterized protein y4lR	-1.45
25.	C3ME53	Efflux transporter, RND family, MFP subunit	-1.34
26.	C3M9T3	Putative oxidoreductase (YgfF)	-1.26
27.	C3MC91	3'-5' exonuclease	-1.25
28.	C3KLW3	Ornithine cyclodeaminase 2	-1.25
29.	C3MB21	Octanoyltransferase	-1.12
30.	C3KPY9	L-allo-threonine aldolase	-1.12
31.	C3M8Q0	AMP nucleosidase	-1.12
32.	C3KRR7	Urocanate hydratase (Urocanase)	-1.07
33.	C3MBC6	ATP-dependent protease subunit HslV	-1.06
34.	C3M9X7	Acetyltransferase	-1.03

Here, up-regulated protein expression represents Log_2 fold increase >1.5 while down-regulated proteins represents Log_2 fold decrease >1.0