Supplementary Table 5 – GO enrichment on rapidly evolving genes. GO term and annotation of genes with more than 10 SNPs and dN/dS ratio (nonsynonymous-to-synonymous substitutions) higher than 1 in ‘Sultanina’ genome. Query Item refers to the number of genes classified in each GO term. Query Total refers to the number of rapidly evolving genes genes that presented a GO term associated. Although 520 genes were identified as rapidly evolving genes, only 410 presented a GO term associated.

GO Number	GO Description	Query Item	Query Total	p-value	FDR
GO:0006464	protein modification process	102	410	1.1e-14	3.9e-12
GO:0043412	macromolecule modification	106	410	1.4e-12	2.6e-10
GO:0051704	multi-organism process	64	410	5e-10	6.1e-08
GO:0022414	reproductive process	68	410	3.1e-08	1.9e-06
GO:0000003	reproduction	69	410	3.2e-08	1.9e-06
GO:0032501	multicellular organismal process	106	410	3e-08	1.9e-06
GO:0006950	response to stress	108	410	8e-08	4.1e-06
GO:0009607	response to biotic stimulus	55	410	2e-07	9.1e-06
GO:0007049	cell cycle	35	410	2.3e-07	9.4e-06
GO:0050896	response to stimulus	148	410	3.5e-07	1.3e-05

continued in next page

GO Number	GO Description	Query Item	Query Total	p-value	FDR
GO:0016265	death	24	410	6.2e-07	1.9e-05
GO:0008219	cell death	24	410	6.2e-07	1.9e-05
GO:0009791	post-embryonic development	63	410	7.5e-07	2.1e-05
GO:0003006	reproductive developmental process	59	410	1.4e-06	3.5e-05
GO:0048608	reproductive structure development	52	410	1.5e-06	3.6e-05
GO:0007275	multicellular organismal development	95	410	1.9e-06	4.3e-05
GO:0009790	embryonic development	26	410	3.5e-06	7e-05
GO:0019538	protein metabolic process	123	410	3.4e-06	7e-05
GO:0032502	developmental process	98	410	4e-06	7.6e-05
GO:0048856	anatomical structure development	84	410	5e-06	9.1e-05
GO:0044267	cellular protein metabolic process	113	410	6e-06	0.0001
GO:0040029	regulation of gene expression, epigenetic	22	410	7.5e-06	0.00012
GO:0065007	biological regulation	136	410	1.8e-05	0.00028
GO:0006259	DNA metabolic process	28	410	2.8e-05	0.00042
GO:0009875	pollen-pistil interaction	6	410	4.2e-05	0.00061
GO:0042592	homeostatic process	19	410	0.00011	0.0015

continued in next page

GO Number	**GO Description**	**Query Item**	**Query Total**	**p-value**	**FDR**
GO:0009605	response to external stimulus	33	410	0.00011	0.0015
GO:0051179	localization	86	410	0.00019	0.0024
GO:0009987	cellular process	275	410	0.0002	0.0025
GO:0065008	regulation of biological quality	43	410	0.00023	0.0028
GO:0007165	signal transduction	43	410	0.00042	0.0049
GO:0050794	regulation of cellular process	97	410	0.0005	0.0057
GO:0050789	regulation of biological process	108	410	0.00058	0.0064
GO:0016043	cellular component organization	70	410	0.00064	0.0068
GO:0006810	transport	78	410	0.00075	0.0078
GO:0051234	establishment of localization	79	410	0.00087	0.0085
GO:0043170	macromolecule metabolic process	178	410	0.00087	0.0085
GO:0009628	response to abiotic stimulus	59	410	0.00093	0.0088
GO:0044260	cellular macromolecule metabolic process	167	410	0.0011	0.0098
GO:0044238	primary metabolic process	216	410	0.0022	0.02
GO:0044237	cellular metabolic process	211	410	0.0029	0.026
GO:0000166	nucleotide binding	131	410	1.5e-18	1.4e-16

continued in next page

GO Number	GO Description	Query Item	Query Total	p-value	FDR
GO:0016772	transferase activity, transferring phosphorus-containing groups	67	410	3.6e-13	1.6e-11
GO:0016301	kinase activity	60	410	6.8e-13	2e-11
GO:0016817	hydrolase activity, acting on acid anhydrides	36	410	1.1e-07	2.5e-06
GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	35	410	2.1e-07	3.2e-06
GO:0017111	nucleoside-triphosphatase activity	34	410	2e-07	3.2e-06
GO:0004872	receptor activity	11	410	2.8e-07	3.7e-06
GO:0016740	transferase activity	82	410	4.7e-07	4.8e-06
GO:0016462	pyrophosphatase activity	34	410	4.3e-07	4.8e-06
GO:0003824	catalytic activity	192	410	1.8e-06	1.7e-05
GO:0005488	binding	238	410	2.1e-06	1.7e-05
GO:0060089	molecular transducer activity	16	410	7.3e-06	5.1e-05
GO:0004871	signal transducer activity	16	410	7.3e-06	5.1e-05
GO:0016787	hydrolase activity	69	410	0.00088	0.0057
GO:0030246	carbohydrate binding	9	410	0.0021	0.013
GO:0005515	protein binding	56	410	0.0049	0.028

continued in next page

GO Number	**GO Description**	**Query Item**	**Query Total**	**p-value**	**FDR**
GO:0005886	plasma membrane	111	410	1.5e-10	1.9e-08
GO:0016020	membrane	148	410	1.1e-07	7.1e-06