

Table S10:**apomictic initial cell**

ID	Significant	Expected	p value	description
PF00324	5	0.629483	0.00100098	Amino acid permease
PF01490	9	1.6366558	0.00011589	Transmembrane amino acid transporter protein
PF02309	7	1.84648347	0.00427111	Aux/IAA family
PF03088	4	0.58751747	0.00515508	Strictosidine synthase
PF03110	4	0.58751747	0.00515508	SBP domain
PF04674	3	0.33572427	0.00849502	Phosphate-induced protein 1 conserved region
PF06507	6	0.79734513	0.0003965	Auxin response factor

egg cell

ID	Significant	Expected	p value	description
PF00010	42	24.88	0.00476216	Helix-loop-helix DNA-binding domain
PF00069	183	131.90	0.00016034	Protein kinase domain
PF00560	131	73.15	6.30E-08	Leucine rich repeat HhH-GPD superfamily base excision DNA repair protein
PF00730	9	2.25	0.00288164	P21-Rho binding domain
PF00786	10	2.99	0.004385	NB-ARC domain
PF00931	68	31.43	5.85E-07	Pentacortico repeat
PF01535	197	82.32	3.67E-21	Toll Interleukin receptor
PF01582	42	24.88	0.00476216	Kelch motif
PF07646	12	3.74	0.00238746	Protein tyrosine kinase
PF07714	100	63.80	0.00017157	Leucine rich repeat, LRR_3
PF07725	34	15.34	0.00027842	Leucine rich repeat N-terminal domain
PF08263	75	39.10	5.75E-06	

central cell

ID	Significant	Expected	p value	description
PF00010	48	26.1526398	0.00058139	Helix-loop-helix DNA-binding domain
PF00069	222	138.628655	7.03E-09	protein kinase domain
PF00076	23	48.1759154	0.00025011	RNA recognition motif
PF00225	26	11.9948198	0.00198709	Kinesin motor domain
PF00560	137	76.8848283	4.57E-08	Leucine rich repeat
PF00612	24	11.0116378	0.00227686	IQ calmodolin binding domain
PF00931	64	33.0349134	2.48E-05	NB-ARC domain
PF01486	19	8.06209197	0.00435678	K-box domain
PF01535	191	86.5200114	1.47E-17	Pentacorticopeptide repeat
PF01582	44	26.1526398	0.00422265	Toll-interleukin receptor
PF02183	12	4.12936418	0.00722254	Homeobox associated leucine zipper
PF02362	33	18.2871842	0.00530936	B3 domain
PF02458	24	12.3880925	0.00850195	Transferase family
PF03000	16	6.48900085	0.00559973	NPH3-family
PF03514	17	6.48900085	0.00323279	GRAS domain family
PF04570	11	3.14618223	0.00233681	DUF581
PF04770	13	3.34281862	0.00047255	ZF-HD protein dimerisation region
PF04784	10	3.14618223	0.0059545	DUF547
PF07714	115	67.0530088	2.29E-06	Tyrosine kinase
PF07725	36	16.1241839	0.00015028	Leucine rich repeat, LRR3
PF08263	84	41.0970054	2.01E-07	Leucine rich repeat N-terminal domain
PF11721	16	6.29236446	0.005044	Di-glucose binding with endoplasmatic reticulum