

Table S2.

Mutations in E1							Allele frequency at given generation									
Chromosome	Position	Ref Allele	Alt Allele	Gene(s)	Effect	Amino Acid Change	Codon Change	Codon Position	7	70	133	196	266	322	385	448
chr01	39261G	A	GPB2	START_LOST	M/I	atG/ata		1	0	0.05243459	0.00385286	0.01013128	0	0	0	0
chr01	39425A	G	GPB2	NON_SYNONYMOUS_CODING	Y/C	tAt/gT		56	0.00286123	0.00088731	0.0019861	0	0	0	0.00313152	0.02065728
chr01	39834G	A	GPB2	STOP_GAINED	W/*	tgG/tgA		192	0	0.00215916	0.10195227	0.02235031	0	0	0	0
chr03	235882C	A	SED4	SYNONYMOUS_CODING	V/V	gtG/gT		147	0	0	0	0	0	0	0.0018315	0.03259827
chr04	111908T	C	SNF3	NON_SYNONYMOUS_CODING	L/S	tTa/tCa		110	0	0.02696178	0.15031983	0.03079397	0	0	0	0
chr04	112109G	C	SNF3	NON_SYNONYMOUS_CODING	S/T	gtG/tct		177	0.01041667	0.02896725	0.10597826	0.03001201	0	0	0	0
chr04	214167T	C	RG72	NON_SYNONYMOUS_CODING	Y/H	Tac/Tac		273	0	0.00787402	0.0270907	0.0020141	0	0	0	0
chr04	1014422C	G	MTH1	NON_SYNONYMOUS_CODING	W/C	tgC/tGc		427	0	0.01152074	0.0780379	0.00111982	0	0	0	0
chr04	1014457G	T	MTH1	NON_SYNONYMOUS_CODING	Q/K	Cag/Aag		416	0	0.00936768	0.0265252	0.0025428	0	0	0	0
chr04	1014707A	C	MTH1	STOP_GAINED	Y/*	tAt/tAg		332	0.0089172	0.0154355	0.07751092	0.06924644	0.00321888	0	0	
chr04	1014740G	C	MTH1	NON_SYNONYMOUS_CODING	C/W	tgG/tGc		106	0	0.0031679	0.02200995	0.2428727	0.98303287	0.99913345	0.99823789	
chr04	1014770G	T	MTH1	STOP_GAINED	Y/*	tac/taA		311	0	0.00703235	0.1376038	0.00134048	0.01568154	0	0	0
chr04	1014968A	T	MTH1	STOP_GAINED	Y/*	taT/taA		245	0.00158211	0.00254586	0.03146342	0.01408237	0	0	0	0
chr04	1014997G	A	MTH1	STOP_GAINED	Q/*	Cag/Tag		236	0	0.0042735	0.02406015	0.0262069	0	0	0.00088968	0
chr04	1015236A	C	MTH1	STOP_GAINED	L/*	tTa/tCa		156	0.01077326	0.02243313	0.01414877	0.01258851	0.0008881	0	0	0
chr04	1015286G	T	MTH1	STOP_GAINED	S/*	tCa/taA		106	0.00455581	0.03518124	0.02350176	0.01195219	0	0	0	0
chr09	400837T	TACTGGCATCCATTACTC	DAL81	CODON_DELETION	S/S	lccattactactactgagctata		357	0	0	0	0.035197	0.893491	0.986711	1	1
chrmt	28320T	C	ATP6	UPSTREAM				0.00536089	0.00116357	0.00217971	0.00320859	0.00163258	0.00757479	0.0006589	0.00031782	
chr06	70288A	T	RM15	STOP_GAINED	Y/*	taT/taA		1380	0	0.01666281	0.03787879	0.00121655	0	0	0	0
chr06	71396G	C	RM15	STOP_GAINED	Y/*	taC/tAg		1014	0	0	0	0	0	0.00066181	0.03151674	
chr10	438286A	C	CR1	NON_SYNONYMOUS_CODING	S/R	AgT/gct		1044	0.37113402	0	0.3466026	0.07276507	0.0022805	0	0	0
chr11	367181A	G	RG71	NON_SYNONYMOUS_CODING	Y/C	tAt/gT		526	0	0.00271003	0.01768708	0.04111246	0	0	0.0078927	0
chr11	367297G	C	RG71	NON_SYNONYMOUS_CODING	V/L	GtT/Ct		565	0	0.00242131	0.02706746	0.08089097	0.00131234	0	0	0
chr11	367328T	G	RG71	NON_SYNONYMOUS_CODING	L/W	tTg/tGg		575	0	0.002751323	0.11285267	0.00115741	0	0	0	0
chr12	54429T	C	VP53	NON_SYNONYMOUS_CODING	V/V	Att/GTt		3073	0.00114417	0.01816118	0.01256545	0	0	0	0	0
chr12	11312TAA	TCAAT	SSK1	FRAME_SHIFT				0	0	0	0.22638	0.986335	0.998209	0.998209	0.996253	
chr12	200286C	T	ADE12	NON_SYNONYMOUS_CODING	G/R	Ggg/Agg		344	0	0	0	0.2084474	0.9847631	0.99826087	1	
chr12	372230G	A	HOG1	NON_SYNONYMOUS_CODING	G/D	gGt/gAt		204	0	0.01220505	0.07127273	0	0	0	0	0
chr12	372319G	T	HOG1	STOP_GAINED	G/*	Gga/Tga		234	0	0.02328042	0.11365807	0.0010977	0	0	0	0
chr13	302056	TCACGACCAACATCGACAC GCAAGTTTGAAGATTG	ERG5	CODON_DELETION				143	0	0	0	0	0.00361011	0.42857143	0.71428571	1
chr14	440309C	A	RS2	NON_SYNONYMOUS_CODING	V/F	GtT/tTt		88	0	0	0	0.02726473	0	0	0	0
chr14	684890A	A	SSK2	STOP_GAINED	E/*	Gag/Tag		152	0	0.00324675	0.04701835	0.04468719	0.00109649	0	0	0
chr15	301909G	A	HRD1	NON_SYNONYMOUS_CODING	P/L	cCt/tCt		376	0	0	0.00214753	0.0268023	0.00223559	1.61E-05	0	0
chr15	3285T	A	CR5_YOR029W	UPSTREAM				0	0.00120919	0.03067485	0.00119561	0	0	0	0	0
chr15	438512A	C	YOR059C_Gene TKLUU10	DOWNSTREAM_UPSTREAM				0	0	0.0049505	0.35714286	0.85714286	1	1	1	
chr16	428459A	G	VP528	NON_SYNONYMOUS_CODING	H/R	cAt/cGt		178	0	0.00434153	0.05670103	0.00136054	0	0	0	0
chr16	522341T	G	SWI1	NON_SYNONYMOUS_CODING	L/R	cTt/cGt		443	0	0.00104275	0.02341137	0	0	0	0	0

Mutations in E2							Allele frequency at given generation									
Chromosome	Position	Ref Allele	Alt Allele	Gene(s)	Effect	Amino Acid Change	Codon Change	Codon Position	7	70	133	196	266	322	385	448
chr01	39261G	A	GPB2	START_LOST	M/I	atG/ata		1	0	0.00294772	0.04086741	0.16442322	0.012442	0.01722351	0.01787002	
chr03	184888C	A	BPH1	NON_SYNONYMOUS_CODING	S/Y	tCt/tAt		1790	0	0.00766284	0.02208202	0.02578797	0.04	0.04456311		
chr04	112987G	T	SNF3	NON_SYNONYMOUS_CODING	V/F	GtT/tTt		470	0.00719425	0.03861004	0	0	0	0	0	0
chr04	214167T	C	RG72	NON_SYNONYMOUS_CODING	Y/H	Tac/Tac		273	0	0.00403226	0.09507042	0.06944444	0	0	0	0
chr04	1014763T	G	MTH1	NON_SYNONYMOUS_CODING	N/H	AsT/cAt		314	0	0.01665667	0.19834711	0.03794038	0.03951368	0.0131579		
chr04	1014850T	A	MTH1	STOP_GAINED	R/*	Aga/Tga		285	0	0.00126597	0.042957695	0.6584417	0.67056437	0.79198941		
chr04	1014958G	A	MTH1	STOP_GAINED	E/*	Gag/Tag		249	0.00724638	0.03829787	0	0	0	0	0	
chr04	1015139A	T	MTH1	STOP_GAINED	C/*	tGt/tGg		188	0	0	0.03485255	0.00902935	0	0	0	0
chr04	1015401G	T	MTH1	STOP_GAINED	S/*	tCa/taA		101	0.01282051	0.04089249	0	0.00208817	0	0	0	0
chr04	1015447T	A	MTH1	STOP_GAINED	K/*	Aaa/taA		86	0	0.00355872	0.0292526	0.04892966	0.07166124	0.02320186		
chr04	1393816C	A	RM72	SYNONYMOUS_CODING	G/G	ggG/gGt		253	0	0.0070922	0.01683393	0.05275705	0.08459215	0.0950324		
chrmt	5237AG	A		DELETION				0.080673	0.058112	0.52224	0.814544	0.892617	0.865747	0.903259		
chrmt	48457T	C	Gene ISUGAQZ_VARI	DOWNSTREAM_UPSTREAM				0.00034389	0.01013765	0.1205405	0.00651069	0.0040732	0	0		
chr06	71813A	C	RM15	NON_SYNONYMOUS_CODING	M/R	tTg/tGg		872	0	0.14089347	0.07231657	0.33797909	0.10479042	0	0	0
chr07	31970G	A	RM1	NON_SYNONYMOUS_CODING	E/K	Gag/Aag		21	0.0027027	0.01829268	0.00808525	0.03217822	0.01474202	0.02956989	0.0227172	
chr07	146779T	C	CDC55	NON_SYNONYMOUS_CODING	D/G	gAc/gGc		204	0.00343643	0.09703504	0.03801117	0.53881662	0.19518101	0.97186701	0.99420849	
chr08	368657A	C	ECM14	NON_SYNONYMOUS_CODING	V/D	Tac/Gac		380	0	0	0.004	0.00835655	0.00537634	0.04692082	0.07940447	
chr10	117822G	A	P82	NON_SYNONYMOUS_CODING	P/S	CtT/tCt		528	0	0.00322581	0.00952381	0.03646037	0.01160093	0.04057279	0.0186957	
chr10	619248A	T	VP52	STOP_GAINED	C/*	Ggg/Tga		344	0	0	0.00325733	0	0.015628	0.0466975	0.0454546	
chr10	619248A	T	VP52	NON_SYNONYMOUS_CODING	L/P	tCt/cCt		173	0	0.04545455	0.00302135	0.02941177	0.00715991	0.02898551	0.0510215	
chr11	367541G	T	RG71	NON_SYNONYMOUS_CODING	C/F	tGt/tTt		646	0.00245098	0.00278552	0.01975309	0.0286346	0	0	0	0
chr11	368053G	A	RG71	NON_SYNONYMOUS_CODING	E/K	Gaa/taA		817	0	0.04271357	0.02702703	0.03151261	0.01818182	0.01570681		
chr12	162282G	A	SSK1	STOP_GAINED	E/*	Gaa/taA		538	0	0	0	0	0	0.03188406	0.03929273	
chr12	162807T	A	SSK1	STOP_GAINED	S/*	taT/taA		307	0	0	0	0	0	0.02272727	0.0925408	
chr12	162807T	A	SSK1	STOP_GAINED	Q/*	CaA/taA		363	0	0	0.01044386	0.01358966	0.0204897	0.00809717		
chr12	162975G	A	SSK1	STOP_GAINED	Q/*	Cag/Tag		307	0	0	0.00208768	0.03207547	0.03981265	0.03448276		
chr12	909689C	T	COX8_C59	DOWNSTREAM_DOWNSTREAM				0	0.00444444	0.0035461	0.03021148	0.01602564	0.00571429			
chr13	302398C	T	CGCTAC_ERG5	CODON_INSERTION				30	0	0	0	0	0.00307692	0.11439114		
chr14	68202C	T	SSK2	STOP_GAINED	W/*	tGg/tAg		1509	0	0	0.00592338	0.02608066	0.02479339	0.01601831		
chr14	681026T	G	SSK2	NON_SYNONYMOUS_CODING	T/P	Act/CtT		1470	0	0	0.02475248	0.14761905	0.12142857	0.02819557		
chr14	684767G	A	SSK2	STOP_GAINED	Q/*	Cag/Tag		223	0	0	0.00232558	0.01455302	0.01110818	0.00606061		
chr15	412148G	T	WH12	STOP_GAINED	E/*	Gaa/taA		427	0	0	0.0240816	0.07692308	0.0361446	0.04789272		
chr15	412274C	T	WH12	STOP_GAINED	R/*	Cga/Tga		469	0	0.00310						