List of genes studied

Red: genes discarded because of insufficient taxonomic sample
Orange: tRNA synthetases and genes discarded because of too many paralogs, retained for fusion P4
Green: genes retained for fusion P1

Genes	number of species	number of positions	
efg	43	631	not retained in fusion P2
efp	44	177	too many paralogs
efts	45	234	too many paralogs
eftu	43	371	
fmt	45	213	not retained in fusion P2
glna	37	327	insufficient taxonomic sample
glnb	37	403	insufficient taxonomic sample
glnc	33	67	insufficient taxonomic sample
hpt	45	137	not retained in fusion P2
if-1	44	68	
if-2	45	488	not retained in fusion P2
if-3	45	140	
ipp	40	180	insufficient taxonomic sample
ksga	45	151	not retained in fusion P2
npt	42	534	
pdf	45	119	too many paralogs
rba	54	81	
rf1	42	243	
rf2	42	298	
rfr	43	164	
rpl1	44	219	
rpl2	44	264	
rpl3	43	181	
rpl4	44	136	
rpl5	45	176	not retained in fusion P2
rpl6	45	139	
rpl7	45	107	not retained in fusion P2
rpl9	45	76	not retained in fusion P2
rpl10	43	102	
rpl11	43	137	
rpl13	42	136	
rpl14	43	121	
rpl15	45	59	not retained in fusion P2
rpl16	45	133	
rpl17	45	96	
rpl18	45	98	not retained in fusion P2
rpl19	44	109	
rpl20	43	111	
rpl21	43	79	
rpl22	44	93	
rpl23	43	72	
rpl24	45	79	not retained in fusion P2
rpl27	44	77	
rpl28	44	70	too many paralogs
rpl29	45	57	not retained in fusion P2
rpl30	36	55	insufficient taxonomic sample
rpl31	45	63	too many paralogs
rpl32	40	42	insufficient taxonomic sample

Genes	number of species	number of positions	
rpl33	43	47	too many paralogs
rpl34	42	43	
rpl35	39	56	insufficient taxonomic sample
rpl36	43	37	too many paralogs
rps2	44	210	
rps3	45	201	
rps4	44	165	
rps5	45	150	not retained in fusion P2
rps6	45	71	
rps7	44	147	
rps8	45	112	
rps9	44	119	
rps10	38	100	insufficient taxonomic sample
rps11	45	117	
rps12	43	135	
rps13	45	115	
rps14	45	106	too many paralogs
rps15	44	69	
rps16	41	63	insufficient taxonomic sample
rps17	43	70	
rps18	43	62	
rps19	42	82	
rps20	42	71	
rps21	32	80	insufficient taxonomic sample
sp2	44	199	
trmd	44	180	
trua	44	164	
trub	40	164	insufficient taxonomic sample

tRNA synthetase

	number of species	number of positions	
ala	44	548	
arg	44	367	
asn	-	-	insufficient taxonomic sample
asp	44	485	
cys	44	316	
gln	-	-	insufficient taxonomic sample
glu	44	308	
gly	-	-	2 classes of sequences
his	43	278	
iso	45	668	
leu	44	667	
lys	-	-	2 classes of sequences
met	44	406	
phe	45	-	forgotten by mistake for the fusion P4
pro	45	344	
ser	44	401	
thr	44	530	
trp	43	307	
tyr	42	357	
val	44	675	