Additional file

Table S1 - Samples, theirs genbank/ Ensembl access numbers and phenotype

	ABO	
Accession number **NCBI/ Ensembl**	**Species**	**Phenotype**
	PRIMATE	
	CERCOPITHECIDAE	
AH008342	*Macaca fascicularis*	A
XM_005580531	*Macaca fascicularis*	B
AH0082202	*Macaca fascicularis*	O1
NW_001101647	*Macaca mulatta*	B
XM_003918629	*Papio anubis*	A
AH0066972	*Papio anubis*	B
	HOMINIDAE	
ENSGGOT00000032150	*Gorilla gorilla*	B
NM_020469.2	*Homo sapiens*	A1
JN791441.1	*Homo sapiens*	B
AF021846	*Pan troglodytes*	O
ENSPTRT00000039844	*Pan troglodytes*	
NM_001194925	*Pan troglodytes*	A
	PLATYRRHINI	
XM_003732072	*Callithrix jacchus*	
XM_003732072	*Callithrix jacchus*	
XM_003732072	*Aotus nancymaae*	
	STREPSIRRHINI (PROSIMIANS)	
NW_007079802	*Tarsius syrichta*	
ENSOGAT00000026266	*Otolemur_garnettii*	
	RODENTIA	
NM_0307184	*Mus musculus*	
AF469946	*Rattus norvegicus*	A
	LAGOMORPHA	
XM_ 002721538	*Oryctolagus cuniculus*	

	CARNIVORA	
XM_ 5483863	*Canis lupus familiaris*	ABO1

	CETARTIDACTYLA	
NM_001077926	*Bos taurus*	

GBGT1

Accession number	Species	Phenotype
NCBI/ Ensembl		

PRIMATE

	CERCOPITHECIDAE	
ENSCSAT00000013238	*Chlorocebus sabaeus*	
ENSMMUT00000021419	*Macaca mulatta*	
ENSPANG00000018174	*Papio anubis*	

	HOMINIDAE	
XM_004048799	*Gorilla gorilla*	Variant 1
ENSGGOT00000003467	*Gorilla gorilla*	
NM_021996	*Homo sapiens*	Variant 1
AY358175.1	*Homo sapiens*	
ENSPTRT00000039837	*Pan troglodytes*	
ENSPPYT00000023030	*Pongo abelii*	

	PLATYRRHINI	
XM_009004770.1	*Callithrix jacchus*	Variant X1
XM_010346403.1	*Saimiri boliviensis boliviensis*	Variant X1

	STREPSIRRHINI (PROSIMIANS)	
NW_007079802.1	*Tarsius syrichta*	

	RODENTIA	
NM 139197	*Mus musculus*	
ENSCPOT00000004927	*Cavia porcellus*	

	CARNIVORA	
XM_014116859.1	*Canis lupus familiaris*	

	CETARTIDACTYLA	
ENSOART00000005732	*Ovis aries*	

GGTA1

Accession number	Species	Phenotype

Accession number	Species	Phenotype
PRIMATE		
CERCOPITHECIDAE		
XM_011927427.1	*Colobus angolensis palliatus*	like
HOMINIDAE		
XM_003777440.2	*Pongo abelii*	like
PLATYRRHINI		
DQ985356.1	*Alouatta caraya*	
AF384428.1	*Callithrix jacchus*	
AY034181.1	*Sapajus apella*	
XM_010335883	*Saimiri boliviensis boliviensis*	Variant X1
STREPSIRRHINI (PROSIMIANS)		
AY126667	*Lemur catta*	
DQ985357	*Loris tardigradus*	
ENSOGAT00000001894	*Otolemur garnettii*	
ENSMICT00000016106	*Microcebus_murinus*	
XM_008049783	*Tarsius syrichta*	
RODENTIA		
ENSSTOT00000005449	*Ictidomys_tridecemlineatus*	
AF297615	*Mus musculus*	
AF488784	*Rattus norvegicus*	
CARNIVORA		
XM_014116859.1	*Canis lupus familiaris*	
NP_001009308.1	*Felis catus*	
LAGOMORPHA		
XM_002720464	*Oryctolagus cuniculus*	
CETARTIDACTYLA		
XM_010810167	*Bos taurus*	
AY447039	*Ovis aries*	
L36535	*Sus scrofa*	

iGb3S

Accession number	**Species**	**Phenotype**
NCBI/ Ensembl		

PRIMATE

CERCOPITHECIDAE

ENSCSAT00000017461	*Chlorocebus sabaeus*
XM_005544050	*Macaca fascicularis*
ENSMMUT00000004622	*Macaca mulatta*
XM_003891544	*Papio anubis*

HOMINIDAE

ENST00000442999	*Homo sapiens*
ENSGGOT00000003612	*Gorilla gorilla*
ENSPPYT00000001874	*Pongo abelii*

PLATYRRHINI

ENSCJAT00000002165	*Callithrix jacchus*
XM_003937545.1	*Saimiri boliviensis boliviensis*

RODENTIA

XM_003500624	*Cricetulus griseus*
ENSMUST00000030585	*Mus musculus*
ENSRNOT00000007851	*Rattus norvegicus*

CARNIVORA

XM_544424	*Canis lupus familiaris*

CETARTIDACTYLA

XM_005203048	*Bos taurus*

GT6m7

Accession number NCBI/ Ensembl	Species	Phenotype

PRIMATE

CERCOPITHECIDAE

Accession number	Species	Phenotype
NM_001283893	*Macaca fascicularis*	
ENSNLET00000011300	*Nomascus leucogenys*	
XM_008005684	*Chlorocebus sabaeus*	Variant_X1
XM_009187871	*Papio anubis*	
XM_010372750	*Rhinopithecus roxellana*	

HOMINIDAE

NM_182974	*Homo sapiens*

XM_002820374	*Pongo abelii*	
ENSGGOT00000007894	*Gorilla gorilla*	
XM_008970052	*Pan paniscus*	
XM_528458	*Pan troglodytes*	

PLATYRRHINI		
XM_009005825	*Callithrix jacchus*	
XM_003941373	*Saimiri boliviensis boliviensis*	

STREPSIRRHINI (PROSIMIANS)		
XM_012782089.1	*Microcebus_murinus*	Variant X1
ENSOGAG00000030414	*Otolemur garnettii*	
XM_008070666.1	Tarsius syrichta	
XM_012654726.1	*Propithecus coquereli*	

RODENTIA		
NM_001039095	*Mus musculus*	
NM_001106559	*Rattus norvegicus*	

CARNIVORA		
XM_548383	*Canis lupus familiaris*	

CETARTIDACTYLA		
NM_001075928	*Bos taurus*	
ENSSSCG00000005758	*Sus scrofa*	

Table S2 - Tests of positive selection codons in the *ABO* protein by pairs M0-M1a, M1a-M2a, M7-M8 and M8-M8a (PAML).

Model	lnL[a]	df[b]	LRT[c]	Estimates of Parameters[d,e]	Selected Sites	ω and SE
M0	-4046.235	1	213.87**	$\kappa= 3.591$, $\omega= 0.101$	Not Allowed	
M1a	-3939.301			$\kappa= 4.030$, $p_0= 0.825$, $p_1= 0.174$, $\omega_0= 0.048$, $\omega_1= 1.000$	Not Allowed	
		2	1.67			
M2a	-3938.466			$\kappa= 4.027$, $p_0= 0.824$, $p_1= 0.170$, $p_2= 0.005$, $\omega_0= 0.048$, $\omega_1= 1.000$, $\omega_2= 4.053$	None	
M7	-3909.200			$\kappa= 3.821$, $p= 0.226$, $q= 1.409$	Not Allowed	
		2	11.97**			
M8	-3903.215			$\kappa= 3.828$, $p0= 0.971$, $(p1= 0.029)$, $p= 0.290$, $q= 2.531$, $\omega= 1.732$	266	1.717 +- 0.543
			3.61*			
M8a	-3905.020			$\kappa= 3.821$, $p0= 0.956$, $(p1= 0.044)$, $p= 0.296$, $q= 2.902$, $\omega= 1.000$	None	

[a] The likelihood indicates the fit of the data to the different models; [b] Degree of freedom for $\chi 2$ test; [c] Result of the Likelihood ratio test amont the pair models M1a-M2a, M7-M8 and M8-M8a. *Indicate statistically significant at 95% level and **indicate statistically significant at 99% level ; [d] Pi denotes the proportion of sites falling in sites class ω_1; [e] Parameters *p* and q are the shape parameters of the beta distribution which underlies M7, M8 and M8a models

Table S3 - Results obtained by PARRIS for *ABO* protein (LRT = 0.00015)

Null model (M1)			
Rate Class	1	2	Summary
ω	0.05	1.00	Mean : 0.237
Prob.	0.805	0.195	Std.Dev : 0.375

Alternative model (M2)				
Rate Class	1	2	3	Summary
ω	0.05	1.00	4.41	Mean : 0.238
Prob.	0.805	0.195	0.000	Std.Dev : 0.375

Table S4- Codons under positive selection obtained by Hyphy algorithms for *ABO* protein (values significant statistical are in highlighted in bold).

Codon	SLAC dN-dS	SLAC p-value	FEL dN-dS	FEL p-value	MEME ω⁺	MEME p-value	FUBAR dN-dS	FUBAR Post. Pr.
130	-0.135	0.677	-0.276	0.723	>100	**0.008**	-0.102	0.312
268	0.738	0.571	-0.283	0.776	>100	**0.002**	-0.126	0.395
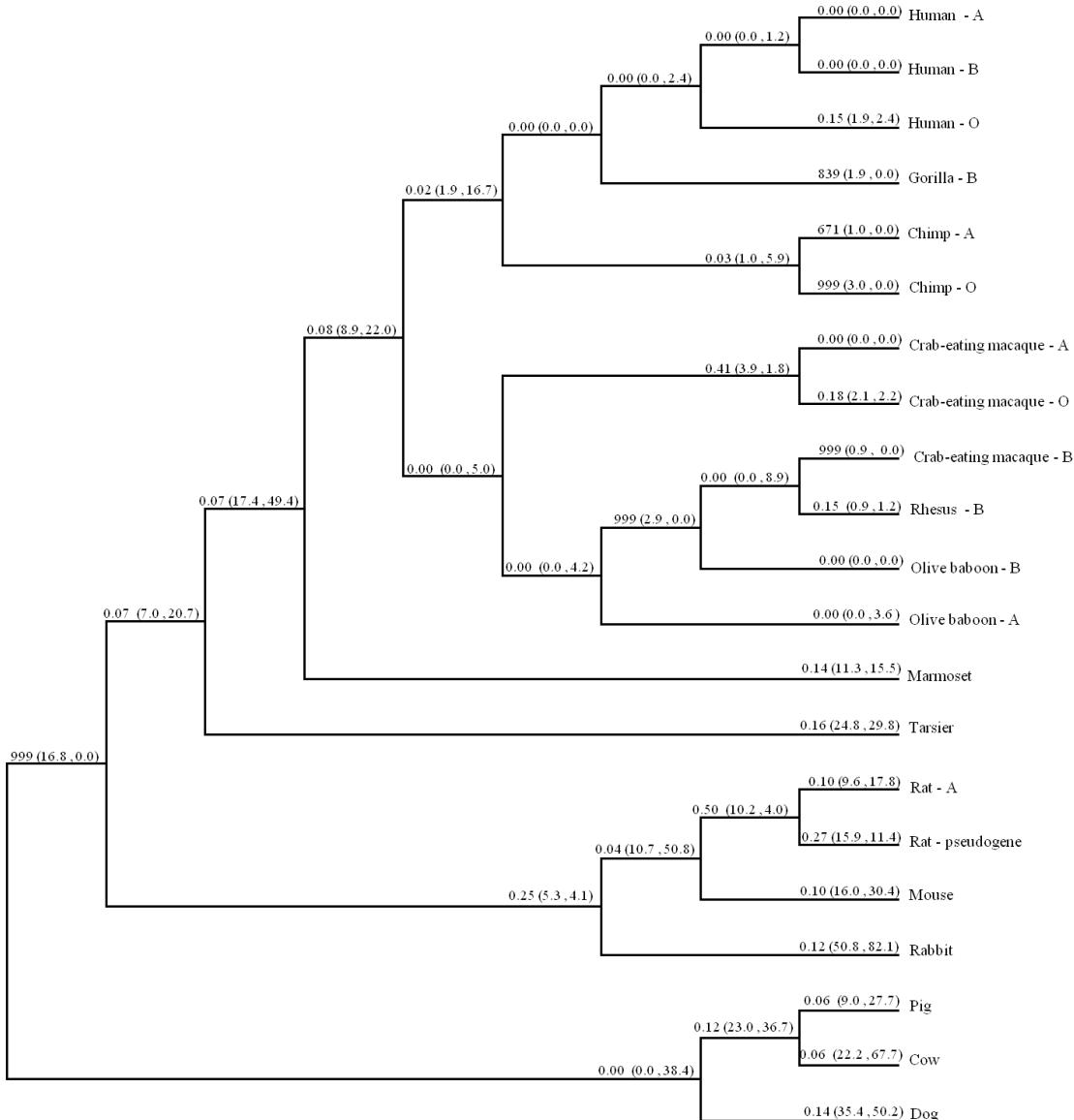
Figure S1 - Estimative of the Free-ratio model for the ABO protein. Samples with known phenotypes are indicated. The model estimated 594.1 and 116.9 nonsynonymous and synonymous sites, respectively. (M0 vs.Free-Ratio: *lnL*=- -4046.235288 and 4014.934, respectively; LRT = 62.6036; df= 39; 0.01< *p* < 0.05). The values on each branches corresponding to ω, nonsynonymous and synonymous sites, respectively. ω values < 0.5 indicate purifying selection, ω values > 0.5 is relaxed purifying selection and ω values > 1.0 is on positive selection.

Table S5- Tests of positive selection codons in the *Ggta1* protein by pairs M0-M1a, M1a-M2a, M7-M8 and M8-M8a (PAML).

Model	lnL[a]	df[b]	LRT[c]	Estimates of Parameters[d,e]	Selected Sites	ω and SE
M0	-5363.619	1	116.52**	κ= 4.182, ω= 0.264	Not Allowed	
M1a	-5305.348			κ= 4.417, p_0= 0.797, p_1= 0.202, ω_0= 0.132, ω_1= 1.000	Not Allowed	
		2	0			
M2a	-5305.348			κ= 4.417, p_0= 0.797, p_1= 0.171, p_2= 0.031, ω_0= 0.131, ω_1= 1.000, ω_2= 1.000	None	
M7	-5305.845			κ= 4.231, p= 0.458, q= 1.205	Not Allowed	
		2	6.37*			
M8	-5302.662			κ= 4.309, $p0$= 0.927, ($p1$= 0.073), p= 0.734, q= 2.727, ω= 1.260	109	1.492 +- 0.159
			0.308			
M8a	-5302.816			κ= 4.2934, $p0$= 0.864, ($p1$= 0.137), p= 0.989, q= 4.737, ω= 1.000	None	

[a] The likelihood indicates the fit of the data to the different models; [b] Degree of freedom for $\chi 2$ test; [c] Result of the Likelihood ratio test amont the pair models M1a-M2a, M7-M8 and M8-M8a. *Indicate statistically significant at 95% level and **indicate statistically significant at 99% level ;[d] Pi denotes the proportion of sites falling in sites class ω_1; [e] Parameters *p* and q are the shape parameters of the beta distribution which underlies M7, M8 and M8a models

Table S6- Results obtained by PARRIS for *Ggta1* gene (LRT = -2.61186e-05).

Null model (M1)				
Rate Class	1	2		
ω	0.12	1.00	Mean : 0.354	
Prob.	0.732	0.268	Std.Dev : 0.390	
Alternative model (M2)				
Rate Class	1	2	3	Summary
ω	0.12	1.00	4.57	Mean : 0.354
Prob.	0.732	0.268	0.000	Std.Dev : 0.390

Table S7- Codons under positive selection obtained by Hyphy algorithms for *Ggta1* gene (values significant statistical are in highlighted in bold).

| Codon	SLAC dN-dS	SLAC p-value	FEL dN-dS	FEL p-value	MEME ω^+	MEME p-value	FUBAR dN-dS	FUBAR Post. Pr.
82	2.012	0.249	3.036	0.072	**>100**	**0.012**	0.639	0.925
92	1.349	0.389	1.786	0.378	**57.251**	**0.035**	0.617	0.850
193	0.536	0.984	0.455	0.832	**>100**	**0.030**	-0.483	0.322
240	1.605	0.966	1.393	0.825	**>100**	**0.014**	-0.605	0.521
279	1.935	0.153	1.812	0.031	**>100**	**0.047**	0.253	0.874
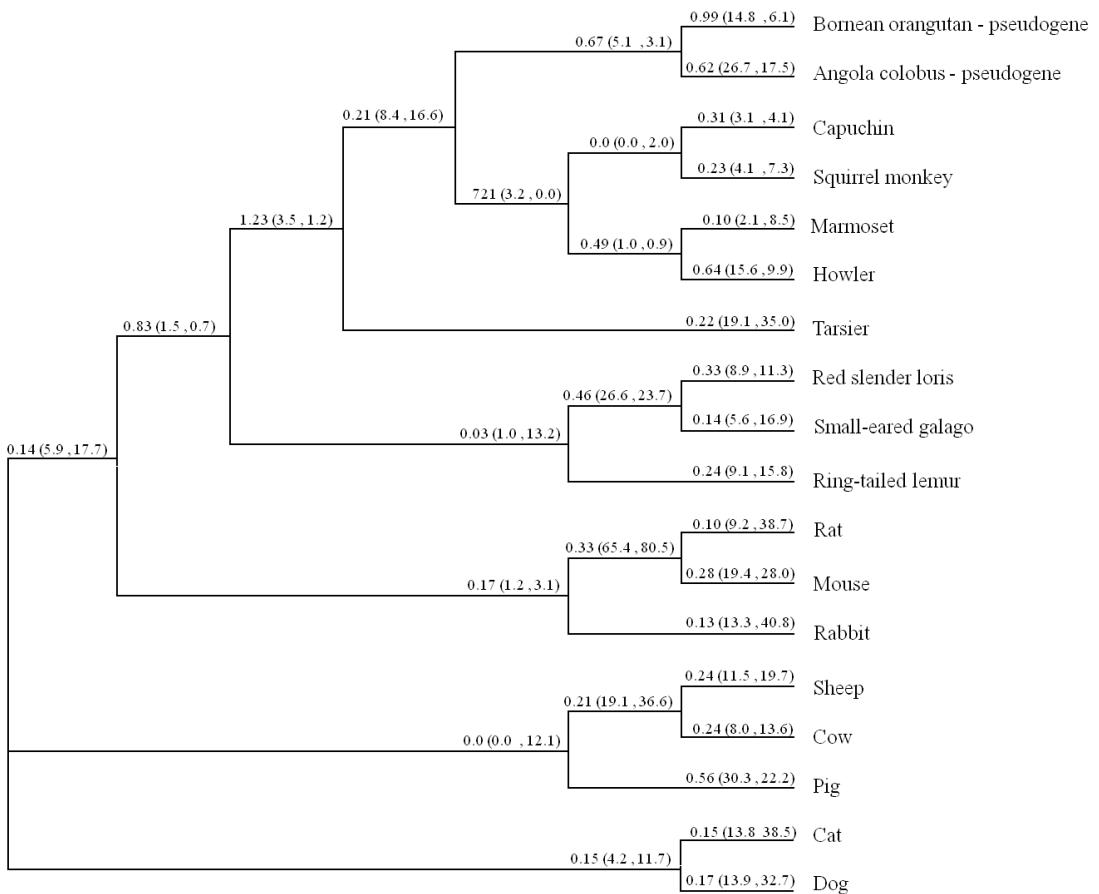
Figure S2 - Estimative of the Free-ratio model for the *Ggta1* gene. Samples with known phenotypes are indicated. The model estimated 697.3 and 286.7 nonsynonymous and synonymous sites, respectively. (M0 vs.Free-Ratio: *lnL*=- - 5363.619 and - 5332.404, respectively; LRT = 62.433; df= 33; 0.01< P< 0.05). The values on each branches corresponding to ω, nonsynonymous and synonymous sites, respectively. ω value < 0.5 indicate purifying selection, ω value > 0.5 is relaxed purifying selection and ω value > 1.0 is positive selection.

Table S8- Tests of positive selection codons in the *iGb3S* gene by pairs M0-M1a, M1a-M2a, M7-M8 and M8-M8a (PAML).

Model	lnL[a]	df[b]	LRT[c]	Estimates of Parameters[d,e]	Selected Sites	ω and SE
M0	-4244.063	1	94.85**	κ= 2.612, ω= 0.241	Not Allowed	
M1a	-4196.640			κ= 2.721, p_0= 0.728, p_1 0.272, ω_0= 0.105, ω_1= 1.000	Not Allowed	
		2	0			
M2a	-4196.640			κ= 2.721, p_0= 0.728, p_1= 0.187, p_2= 0.085, ω_0= 0.105, ω_1= 1.000, ω_2= 1.000	None	
M7	-4188.957			κ= 2.690, p= 0.364, q= 0.914	Not Allowed	
		2	5.69			
M8	-4186.112			κ= 2.688, $p0$= 0.985, ($p1$= 0.015), p= 0.427, q= 1.180, ω= 3.433	None	
			5.59**			
M8a	-4188.905			κ= 2.688, $p0$= 0.942, ($p1$= 0.058), p= 0.414, q= 1.291, ω= 1.000	Not Allowed	

[a] The likelihood indicates the fit of the data to the different models; [b] Degree of freedom for χ2 test; [c] Result of the Likelihood ratio test amont the pair models M1a-M2a, M7-M8 and M8-M8a. *Indicate statistically significant at 95% level and **indicate statistically significant at 99% level ;[d] Pi denotes the proportion of sites falling in sites class ω_1; [e] Parameters p and q are the shape parameters of the beta distribution which underlies M7, M8 and M8a models

Table S9- Results obtained by PARRIS for *iGb3S* gene (LRT = -0.00025)

	Null model (M1)		
Rate Class	1	2	Summary
ω	0.13	1.00	Mean 0.372
Prob.	0.718	0.282	Std.Dev: 0.394

	Alternative model (M2)			
Rate Class	1	2	3	Summary
ω	0.13	1.00	4.54	Mean 0.371
Prob.	0.719	0.281	0.000	Std.Dev 0.393

Table S10- Codons under positive selection obtained by Hyphy algorithms for *iGb3S* gene (values significant statistical are in highlighted in bold).

Codon	SLAC dN-dS	SLAC p-value	FEL dN-dS	FEL p-value	MEME ω⁺	MEME p-value	FUBAR dN-dS	FUBAR Post. Pr.
96	3.644	0.190	**2.434**	**0.032**	**>100**	**0.009**	0.218	0.878
135	1.044	0.544	1.635	0.542	**>100**	**0.035**	-0.071	0.501
228	1.654	0.383	1.112	0.220	**>100**	**0.001**	0.048	0.620
233	2.664	0.281	4.846	0.112	**>100**	**0.024**	0.567	0.853

Table S11- Tests of positive selection codons in the *GBGT1* gene by pairs M0-M1a, M1a-M2a, M7-M8 and M8-M8a (PAML).

Model	lnL[a]	df[b]	LRT[c]	Estimates of Parameters[d,e]	Selected Sites	ω and SE
M0	-4055.301	1	89.85**	κ= 4.829, ω=0.149	Not Allowed	
M1a	-4010.374			κ= 5.478, p_0= 0.839, p_1 0.161, ω_0= 0.082, ω_1= 1.000	Not Allowed	
		2	0			
M2a	-4010.374			κ= 5.478, p_0= 0.839, p_1= 0.116; p_2= 0.045, ω_0= 0.082, ω_1= 1.000, ω_2= 1.000	None	
M7	-3998.633			κ= 5.223, p= 0.344, q= 1.581	Not Allowed	
		2	0.15			
M8	-3998.558			κ= 2.688, $p0$= 0.978, ($p1$= 0.021), p= 0.374, q= 1.926, ω= 3.433	None	
			0.006			
M8a	-3998.561			κ= 5.223, $p0$= 0.975, ($p1$= 0.025), p= 0.375, q= 1.956, ω= 1.000	Not Allowed	

[a] The likelihood indicates the fit of the data to the different models; [b] Degree of freedom for χ2 test; [c] Result of the Likelihood ratio test amont the pair models M1a-M2a, M7-M8 and M8-M8a. *Indicate statistically significant at 95% level and **indicate statistically significant at 99% level ; [d] Pi denotes the proportion of sites falling in sites class ω_1; [e] Parameters *p* and q are the shape parameters of the beta distribution which underlies M7, M8 and M8a models

Table S12- Results obtained by PARRIS for *GBGT1* gene (LRT = 0.0001)

	Null model (M1)			
Rate Class	1	2	Mean	
ω	0.11	1.00	0.270	
Prob.	0.821	0.179	Std.Dev: 0.341	
	Alternative model (M2)			
Rate Class	1	2	3	Summary
ω	0.11	1.00	1.00	Mean 0.271
Prob.	0.821	0.179	0.000	Std.Dev 0.341

Table S13- Codons under positive selection obtained by Hyphy algorithms for *GBGT1* gene (values significant statistical are in highlighted in bold).

Codon	SLAC dN-dS	SLAC p-value	FEL dN-dS	FEL p-value	MEME ω^+	MEME p-value	FUBAR dN-dS	FUBAR Post. Pr.
18	-0.672	0.893	-0.198	0.771	**>100**	**0.016**	-0.077	0.262
21	2.061	0.599	1.241	0.405	**>100**	**0.018**	-0.010	0.552
237	-1.925	0.902	-0.885	0.565	**13.072**	**0.046**	-0.226	0.213
266	-2.625	0.958	-1.361	0.272	**29.819**	**0.025**	-0.247	0.139

Table S14- Tests of positive selection codons in the *GT6m7* pseudogene by pairs by pair M0-M1a, M1a-M2a, M7-M8 and M8-M8a (PAML).

Model	lnL[a]	df[b]	LRT[c]	Estimates of Parameters[d,e]	Selected Sites	ω and SE
M0	-4347.778	1	105.09**	$\kappa= 3.096$, $\omega= 0.239$	Not Allowed	
M1a	-4295.233			$\kappa= 3.647$, $p_0= 0.637$, p_1 0.363, $\omega_0= 0.139$, $\omega_1= 1.000$	Not Allowed	
		2	0			
M2a	-4295.233			$\kappa= 3.647$, $p_0= 0.637$, $p_1= 0.309$, $p_2= 0.053$, $\omega_0= 0.139$, $\omega_1= 1.000$, $\omega_2= 1.000$	None	
M7	-4262.267			$\kappa= 3.298$, $p= 0.612$, q= 1.560	Not Allowed	
		2	0.002			
M8	-4262.268			$\kappa= 3.298$, $p0= 0.999$, ($p1= 0.00001$), $p= 0.612$, $q= 1.560$, $\omega= 1.000$	None	
			0.18			
M8a	-4262.178			$\kappa= 3.296$, $p0= 0.999$, ($p1= 0.00001$), $p= 0.609$, $q= 1.558$, $\omega= 1.000$	Not Allowed	

[a] The likelihood indicates the fit of the data to the different models; [b] Degree of freedom for $\chi2$ test; [c] Result of the Likelihood ratio test among the pair models M1a-M2a, M7-M8 and M8-M8a. *Indicate statistically significant at 95% level and **indicate statistically significant at 99% level ; [d] Pi denotes the proportion of sites falling in sites class ω_1; [e] Parameters *p* and q are the shape parameters of the beta distribution which underlies M7, M8 and M8a models
.

Table S15- Results obtained by PARRIS for *GT6m7* pseudogene (LRT = -0.0021)

Null model (M1)			
Rate Class	1	2	Summary
ω	0.13	1.00	Mean 0.475
Prob.	0.603	0.397	Std.Dev 0.427

Alternative model (M2)				
Rate Class	1	2	3	Summary
ω	0.13	1.00	4.42	Mean 0.475
Prob.	0.602	0.398	0.000	Std.Dev 0.427

Table S16- Codons under positive selection obtained by Hyphy algorithms for *GT6m7* pseudogene (values significant statistical are in highlighted in bold).

Codon	SLAC dN-dS	SLAC p-value	FEL dN-dS	FEL p-value	MEME ω^+	MEME p-value	FUBAR dN-dS	FUBAR Post. Pr.
5	-0.191	0.845	-0.093	0.736	**>100**	**0.002**	-0.054	0.304
6	0.494	0.345	0.516	0.254	**>100**	**0.001**	-0.022	0.623
12	0.648	0.208	**0.492**	**0.052**	**>100**	**0.071**	0.135	0.842
42	-0.018	0.698	-0.057	0.916	**>100**	**0.009**	-0.066	0.334
88	0.799	0.125	0.639	0.039	**>100**	**0.046**	0.155	0.857
96	**1.277**	**0.048**	**1.149**	**0.017**	**>100**	**0.021**	0.495	**0.960**
105	-0.374	0.900	-0.310	0.350	**>100**	**0.002**	-0.121	0.179
107	0.066	0.610	-0.047	0.941	**>100**	**0.034**	-0.025	0.468

Figure S3- Alignment obtained by BLASTN Ensembl of intron 2 of the GT6M7 (query sequence) against Human GRCh38. Are shown the four best hits. (A) Intron2 against ADGRL3-AS1; (B)Intron2 against RUNX1 (C) Intron2 against SRBD1; (D) Intron2 against CTNND2 and (E) Intron2 against FEZ2. The exon is highlighted in red FEZ2.

A)

```
BLAST/BLAT type: BLASTN

Query location:1 768 to 1117 (+)

Database locatin: 4 62101554 to 62101904 (+)

Genomic location: 4 62101554 to 62101904 (+)

Alignment score: 490

E-value: 1e-133

Alignment length: 351

Percentage identity: 92.88


Query    Query_1:     768 TATGGTTTGGCTCTTTCCCCACCCAAATCTCAACTTGAATTGTATCTCCCAGAATTCCCA Query_1:    827
                         ||||||||||| | |||||||||||||||||||| ||||||||||||||||
Subject      4:62101554 TATGGTTTGGCTGTGTCCCCACCCAAATCTCAACTTGAACTGTATCTCCCAGAATTCCCA 4:62101613


Query    Query_1:     828 CGTGTTGTGGGAGGGACCC-GGGGGAGGTAATTGAATCATGGGGGCTGGTCTTTCCCATG Query_1:    887
                          |||||||||||||||||| |||||||||||||||||||||| |||||||||||||
Subject      4:62101614 TGTGTTGTGGGAGGGACCCAGGGGGAGGTAATTGAATCATGGGGACTGGTCTTTCCCATG 4:62101673


Query    Query_1:     888 CTATTCTCATGATAGTGAATACGTCTCATGAGATCTGATGGGTTTATCAGGGGTTTCCAC Query_1:    947
                          ||||||||||||||||||| |||||||||||||||||||||||||||| |||||||| |
Subject      4:62101674 CTATTCTCATGATAGTGAATAAGTCTCATGAGATCTGATGGGTTTATCAGAGGTTTCCGC 4:62101733


Query    Query_1:     948 TTTTCCGTCTTTCTCATTTTCTCTTGCCGCTGCCATGGAAGACATGCCTTTTGCCTCCTG Query_1:   1007
                          |||| | |||| |||||||||||||| ||||| |||| |||||||| |||||||
Subject      4:62101734 TTTTGCTTCTTCCTCATTTTCTCTTGCCGCCACCATGTAAGAAGTGCCTTTTACCTCCTG  4:62101793


Query    Query_1:    1008 CCATGATTCTGAGGCCTCCCCAGCCATGTGGAACTGTAAGTCCAATTAAACCTCTTTTTC Query_1:   1067
                          |||||||| |||| |||||||||||||||||||||||||||||||||||   |||||||
Subject      4:62101794 CCATGATTTTGAGACCTCCCCAGCCATGTGGAACTGTAAGTCCAATTAAAAAACTTTTTC  4:62101853


Query    Query_1:    1068 TTCCCAGTCTTGGGTATGTCTTTATCAGCAGCGTGAAAACAGACTAATACA  Query_1:   1118
                          |||||||||| |||||||||||||||||||||| |||||||||||||||||
Subject      4:62101854 TTCCCAGTCTCGGGTATGTCTTTATCAGCAGCATGAAAACAGACTAATACA  4:62101905
```

B)

BLAST/BLAT type: BLASTN

Query location: 1 768 to 1117 (+)

Database location: 21 35804644 to 35804995 (-)

Genomic location: 21 35804644 to 35804995 (-)

Alignment score: 468

E-value: 4e-127

Alignment length: 352

Percentage identity: 92.33

```
Query    Query_1:      768 TATGGTTTGGCTCTTTCCCCACCCAAATCTCAACTTGAATTGTATCTCCCAGAATTCCCA Query_1:  827
                             ||||||||||| | |||||||||||||||||||||||||| ||||||||||||||| |
Subject       21:35804995 TATGGTTTGGCTGTGTCCCCACCCAAATCTCAACTTGAATTATATCTCCCAGAATTCTCT  21:35804936


Query    Query_1:      828 CGTGTTGTGGGAGGGACCC-GGGGGAGGTAATTGAATCATGGGGGCTGGTCTTTCCCATG Query_1:  887
                             | |||||||||||||||||| |||||||||||||||||||||||||||||||||||  ||
Subject       21:35804935 CATGTTGTGGGAGGGACCCAGGGGGGAGGTAATTGAATCATGGGGGCTGGTCTTTCCTGTG  21:35804876


Query    Query_1:      888 CTATTCTCATGATAGTGAATACGTCTCATGAGATCTGATGGGTTTATCAGGGGTTTCCAC Query_1:  947
                             ||||||| ||||||||||| |||||| |||||||||||||||||||||||||||||||| |
Subject       21:35804875 CTATTCTTGTGATAGTGAATAAGTCTCAAGAGATCTGATGGGTTTATCAGGGGTTTCCGC  21:35804816


Query    Query_1:      948 TTTTCCGTCTTTCTCATTTTCTCTTGCCGCTGCCATGG-AAGACATGCCTTTTGCCTCCT Query_1: 1007
                             |||| | |||| |||||||||||||| |||||||||| ||||  |||||||||||||||||
Subject       21:35804815 TTTTGCTTCTTCCTCATTTTCTCTTGCTGCTGCCATGGTAAGAACTGCCTTTTGCCTCCT  21:35804756


Query    Query_1:     1008 GCCATGATTCTGAGGCCTCCCCAGCCATGTGGAACTGTAAGTCCAATTAAACCTCTTTTT Query_1: 1067
                              ||||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||
Subject       21:35804755 ACCATGATTCTGAGGGCTCTCCAGCCATGTGGAACTGTAAGTCCAATTAAACCTCTTTTT  21:35804696


Query    Query_1:     1068 CTTCCCAGTCTTGGGTATGTCTTTATCAGCAGCGTGAAAACAGACTAATACA  Query_1: 1119
                              |||||||||| |||||||||||||||||| ||||||||||||||||||||||
Subject       21:35804695 CTTCCCAGTCTCAGGTATGTCTTTATCAGCAGTGTGAAAACAGACTAATACA  21:35804642
```

C)

BLAST/BLAT type: BLASTN

Query location: 1 768 to 1117 (+)

Database location: 2 45591918 to 45592268 (+)

Genomic location: 2 45591918 to 45592268 (+)

Alignment score: 466

E-value: 1e-126

Alignment length: 351

Percentage identity: 92.02

```
Query    Query_1:    768 TATGGTTTGGCTCTTTCCCCACCCAAATCTCAACTTGAATTGTATCTCCCAGAATTCCCA Query_1:  827
                         ||||||||||| | | ||||||||||||||||||||||||||||||||||||||||||||
Subject      2:45591918 TATGGTTTGGCTATGTGCCCACCCAAATCTCAACTTGAATTGTATCTCCCAGAATTCCCA  2:45591977


Query    Query_1:    828 CGTGTTGTGGGAGGGACCC-GGGGGGAGGTAATTGAATCATGGGGGCTGGTCTTTCCCATG Query_1: 887
                         |||||||| |||||||||| ||||||||||||||||||||||||| |||| ||| ||
Subject      2:45591978 CGTGTTGTAGGAGGGACCCAGGGGGGAGGTAATTGAATCATGGGGGCCAGTCTCTCCTGTG  2:45592037


Query    Query_1:    888 CTATTCTCATGATAGTGAATACGTCTCATGAGATCTGATGGGTTTATCAGGGGTTTCCAC Query_1: 947
                         |||||||    ||||||||||| |||||| ||||||||||||||||||||||||||||||
Subject      2:45592038 CTATTCTTGCGATAGTGAATAAGTCTCACCAGATCTGATGGGTTTATCAGGGGTTTCCAC  2:45592097


Query    Query_1:    948 TTTTCCGTCTTTCTCATTTTCTCTTGCCGCTGCCATGGAAGACATGCCTTTTGCCTCCTG Query_1:  1007
                         |||| | |||| |||||||||||||| ||||||||| ||||  |||||||||||||
Subject      2:45592098 TTTTGCTTCTTCCTCATTTTCTCTTGCTGCTGCCATGTAAGAAGTGCCTTTTGCCTCCCA  2:45592157


Query    Query_1:   1008 CCATGATTCTGAGGCCTCCCCAGCCATGTGGAACTGTAAGTCCAATTAAACCTCTTTTTC Query_1: 1067
                         |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Subject      2:45592158 CCATGATTCTGAGGCCTCCCCAGCCATGTGGAACTGTAAGTCCAATTAAACCACTTTTTC  2:45592217


Query    Query_1:   1068 TTCCCAGTCTTGGGTATGTCTTTATCAGCAGCGTGAAAACAGACTAATACA  Query_1: 1118
                         |||||||||||||||||||||| |||||||| ||||||||||||||||||
Subject      2:45592218 TTCCCAGTCTTGGGTATGTCTTTGTCAGCAGCATGAAAACAGACTAATACA   2:45592269
```

D)

BLAST/BLAT type: BLASTN

Query location: 1 768 to 1117 (+)

Database location: 5 11312296 to 11312643 (-)

Genomic location: 5 11312296 to 11312643 (-)

Alignment score: 462

E-value: 2e-125

Alignment length: 351

Percentage identity: 92.02

```
Query    Query_1:     768 TATGGTTTGGCTCTTTCCCCACCCAAATCTCAACTTGAATTGTATCTCCCAGAATTCCCA Query_1: 827
                         |||||||||||| | |||||||||||||||||| ||||||||||||||||||||||||||
Subject      5:11312643 TATGGTTTGGCTGTGTCCCCACCCAAATCTCAGCTTGAATTGTATCTCCCAGAATTCCCA  5:11312584


Query    Query_1:     828 CGTGTTGTGGGAGGGACCC-GGGGGAGGTAATTGAATCATGGGGGCTGGTCTTTCCCATG Query_1:  887
                         | ||||||| ||||||||| |||| |||||||||||||||||||| |||||||||||
Subject      5:11312583 CATGTTGTGAGAGGGACCCAGGGGGAAGGTAATTGAATCATGGGGGCCGGTCTTTCCCATC  5:11312524


Query    Query_1:     888 CTATTCTCATGATAGTGAATACGTCTCATGAGATCTGATGGGTTTATCAGGGGTTTCCAC Query_1:  947
                         |||||||| ||||||||||| |||||||||||| ||||| |||||||||||||  |
Subject      5:11312523 CTATTCTCGTGATAGTGAATAAGTCTCATGAGATCTAATGGGCTTATCAGGGGTTTCTGC  5:11312464


Query    Query_1:     948 TTTTCCGTCTTTCTCATTTTCTCTTGCCGCTGCCATGGAAGACATGCCTTTTGCCTCCTG Query_1: 1007
                         |||| | |||   |||||||||||||||||||||||||| ||||  ||||||| |||||| |
Subject      5:11312463 TTTTGCTTCT---TCATTTTCTCTTGCCGCTGCCATGTAAGAACTGCCTTTCGCCTCCCG  5:11312404


Query    Query_1:    1008 CCATGATTCTGAGGCCTCCCCAGCCATGTGGAACTGTAAGTCCAATTAAACCTCTTTTTC Query_1: 1067
                         |||||||||||||||||||||||||||||||||||||||||||| |||||||| |||||||
Subject      5:11312403 CCATGATTCTGAGGCCTCCCCAGCCATGTGGAACTGTAAGTCCGATTAAACCCCTTTTTC  5:11312344


Query    Query_1:    1068 TTCCCAGTCTTGGGTATGTCTTTATCAGCAGCGTGAAAACAGACTAATACA         Query_1: 1118
                         ||||||||||||||||||||||||||||||| |||||||||||||||||||
Subject      5:11312343 TTCCCAGTCTTGGGTATGTCTTTATCAGCAGCATGAAAACAGACTAATACA  5:11312295
```

E)

```
BLAST/BLAT type: BLASTN

Query location: 1 4 to 338 (+)

Database location: 2 36594350 to 36594685 (-)

Genomic location: 2 36594350 to 36594685 (-)

Alignment score: 460

E-value: 1e-125

Alignment length: 336

Percentage identity:


Query   Query_1:       4 GGTTTGGCTCTTTCCCCACCCAAATCTCAACTTGAATTGTATCTCCCAGAATTCCCACGT Query_1:  63
                         ||||||||| | |||||||||||||||||||||||||||||||||||||||||||||||||
Subject     2:36594685 GGTTTGGCTGTGTCCCCACCCAAATCTCAACTTGAATTGTATCTCCCAGAATTCCCACGT  2:36594626


Query   Query_1:      64 GTTGTGGGAGGGA-CCCGGGGGAGGTAATTGAATCATGGGGGCTGGTCTTTCCCATGCTA Query_1: 123
                         |||||||||||||| || |||||||||||||||||||||||||||||||||||| ||||||
Subject     2:36594625 GTTGTGGGAGGGATCCAGGGGGAGGTAATTGAATCATGGGGGCTGGTCTTTCCTATGCTA  2:36594566


Query   Query_1:     124 TTCTCATGATAGTGAATACGTCTCATGAGATCTGATGGGTTTATCAGGGGTTTCCACTTT Query_1: 183
                         ||||||||||||||||| |||| |  |||||||||| ||||||||||| ||||
Subject     2:36594565 TTCTCATGATAGTGAATAAGTCTTACAAGATCTGATGGGCTTATCAGGGGTTTCCGCTTT  2:36594506


Query   Query_1:     184 TCCGTCTTTCTCATTTTCTCTTGCCGCTGCCATGGAAGACATGCCTTTTGCCTCCTGCCA Query_1: 243
                         | |   ||| ||||||||| ||||| || |||||| ||||  ||||||||||||||||||
Subject     2:36594505 TGCTCCTTCCTCATTTTCCCTTGCTGCCGCCATGTAAGAAGTGCCTTTTGCCTCCTGCCA  2:36594446


Query   Query_1:     244 TGATTCTGAGGCCTCCCCAGCCATGTGGAACTGTAAGTCCAATTAAACCTCTTTTTCTTC Query_1: 303
                         ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Subject     2:36594445 TGATTCTGAGGCCTCCCCAGCCATGTGGAACTGTAAGTCCAATTAAACCTCGTTTTCTTC  2:36594386


Query   Query_1:     304 CCAGTCTTGGGTATGTCTTTATCAGCAGCGTGAAAA  Query_1: 339
                         ||||||| |||||||||||||||||| || ||||||
Subject     2:36594385 CCAGTCTCGGGTATGTCTTTATCAGCTGCATGAAAA  2:36594349
```