Online Supplementary Materials

“Genetic dissection of *HLA-DRB1*15:01* and XL9 region variants in Japanese patients with systemic lupus erythematosus: Primary role for *HLA-DRB1*15:01*” by Kawasaki A et al.

Contents

Supplementary Table S1 Primers and probes used in this study

	forward primer	reverse primer	VIC labeled probe	FAM labeled probe
rs9271375 rs9271378	TGGTCTCTCTGAATCTCAACWTTT*	AATCAGCATAGTGATTSCACAATA	NA	NA
rs2105898	GGCTCTTCCACACTCAYTCACAGT	CAGAGTTAGGGCCACTGTCTCAA	CCCTGGTTAATGTATTC	CCCTGGTTAATGTAGTC
rs9271593	GCATCATTTGTCTCTGGCAGACT	CTCCATCCAACTTCATGATTCATT	TGTTGAGTCTATGTATTTC	TGTTGAGTCTATATATTTC

NA, not applicable.

*Forward primer was used for amplification and cycle sequencing reaction.

Supplementary Table S2. Data on XL9 variants in GWAS of SLE in a Japanese population.

							effect allele frequency	
CHR	POS	SNV	effect allele	BETA	SE	P	SLE	controls
6	32587067	rs9271375	A	-0.320	0.084	1.4×10^{-4}	0.273	0.346
6	32587300	rs9271378	G	-0.393	0.115	6.1×10^{-4}	0.095	0.143
6	32590498	rs2105898	G*	-0.203	0.094	0.031	0.730	0.765
6	32591198	rs9271593	T*	-0.011	0.085	0.90	0.680	0.681

Based on GWAS reported by Sakaue et al. [19]

*The reported risk alleles of rs2105898 and rs9271593 are T and C, respectively.

Data was obtained from the NBDC Human Database (https://humandbs.biosciencedbc.jp/en/, Dataset ID: hum0197.v3.gwas.v1)

Supplementary Table S3. Association analysis of XL9 variants with subsets of SLE

	rs9271375A			rs9271378G			rs2105898T			rs9271593C		
	P	FDR Q*	OR (95% CI)	P	FDR Q*	OR (95% CI)	P	FDR Q*	OR (95% CI)	P	FDR Q*	OR (95% CI)
Age of onset												
< 20 years versus ≥ 20 years	0.75	0.87	0.94 (0.63-1.37)	0.59	0.79	1.15 (0.67-1.91)	0.29	0.63	1.21 (0.85-1.73)	0.22	0.63	1.24 (0.87-1.77)
Renal disorder												
Present versus Absent	0.29	0.63	0.84 (0.62-1.16)	0.36	0.63	1.23 (0.79-1.94)	0.51	0.74	0.90 (0.67-1.22)	0.42	0.68	0.89 (0.66-1.19)
Anti-dsDNA antibody												
Present versus Absent	0.87	0.87	0.97 (0.64-1.49)	0.33	0.63	0.76 (0.45-1.35)	0.82	0.87	1.05 (0.71-1.58)	0.85	0.87	0.96 (0.66-1.43)
Anti-Sm antibody												
Present versus Absent	0.12	0.48	0.72 (0.46-1.08)	0.054	0.44	0.51 (0.25-0.97)	0.11	0.48	0.72 (0.48-1.07)	0.011	0.18	0.60 (0.40-0.88)

FDR, false discovery rate; OR, odds ratio; CI, confidence interval.

* Significance level was set at FDR Q<0.05.

Supplementary Table S4. Comparisons of allele frequencies and linkage disequilibrium status of *HLA-DRB1*15* and XL9 variants among European, East Asian, and African populations

	CEU			JPT			CHB			YRI		
	Frequency	LD (r^2) with		Frequency	LD (r^2) with		Frequency	LD (r^2) with		Frequency	LD (r^2) with	
	(%)	rs2105898	rs9271593	(%)	rs2105898	rs9271593	(%)	rs2105898	rs9271593	(%)	rs2105898	rs9271593
XL9												
rs2105898T	19.2	NA	0.497	28.8	NA	0.725	21.4	NA	0428	19.9	NA	0.210
rs9271593C	32.3	0.497	NA	34.6	0.725	NA	38.8	0.428	NA	54.2	0.210	NA
HLA-DRB1												
**15:01*	16.2	0.782	0.389	8.1	0.220	0.168	9.3	0.396	0.169	0.5	0.019	0.005
**15:02*	0.5	0.021	0.011	12.9	0.352	0.270	3.7	0.130	0.055	0	NA	NA
**15:03*	0	NA	NA	0	NA	NA	0	NA	NA	15.3	0.674	0.142

CEU, Utah residents (CEPH) with Northern and Western European ancestry from the CEPH collection; JPT, Japanese in Tokyo, Japan; CHB, Han Chinese in Beijing, China; YRI, Yoruba in Ibadan, Nigeria; LD, linkage disequilibrium; NA, not applicable.

Genotype data of *HLA-DRB1* alleles, rs2105898 and rs9271593 in the CEU, JPT, CHB, and YRI were obtained from the International Genome Sample Resource (2018 data, https://www.internationalgenome.org/category/hla/, accessed 28 Jun 2022) and the Ensembl database (Release 106, https://asia.ensembl.org/index.html, accessed 28 Jun 2022)[20].

r^2 values were calculated by the Haploview software.

Supplementary Table S5. Pair-wise linkage equilibrium values (r^2) between *HLA-DRB1* allele and XL9 region SNVs in the Japanese population.

HLA-DRB1	rs2105898	rs9271593	rs9271375	rs9271378
01:01	0.021	0.031	0.03	0.393
03:01	0	0.003	0.003	0.008
04:01	0.004	0.006	0.026	0.002
04:03	0.009	0.014	0.061	0.005
04:04	0.001	0.001	0.004	0
04:05	0.043	0.058	0.272	0.016
04:06	0.011	0.017	0.075	0.003
04:07	0.001	0	0.011	0.001
04:10	0.005	0.008	0.035	0.003
07:01	0	0	0.002	0.02
08:02	0.014	0.003	0.005	0.007
08:03	0.018	0.033	0.039	0.013
09:01	0.054	0.079	0.074	0.027
10:01	0	0	0.001	0
11:01	0.006	0.036	0.036	0.11
12:01	0.012	0.017	0.02	0.06
12:02	0.049	0.037	0.01	0.001
13:01	0.002	0	0.005	0
13:02	0.029	0.042	0.036	0.014
14:03	0.007	0.044	0.044	0.128
14:05	0.01	0.015	0.014	0.005
14:06	0.003	0.022	0.022	0.063
14:54	0.011	0.016	0.016	0.005
15:01	0.213	0.15	0.03	0.012
15:02	0.431	0.288	0.066	0.023
16:02	0.025	0.016	0.005	0.002

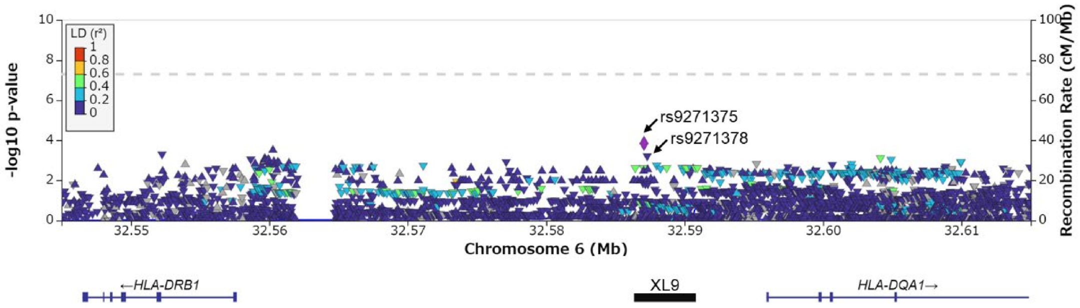
Linkage disequilibrium values (r^2) were calculated using Haploview software based on the genotypes of 779 healthy Japanese individuals. LD plot for *DRB1*15:0*1 and *DRB1*15:02* is shown in Supplementary Figure S2.

Supplementary Table S6. Association of XL9 variants with the expression of *HLA* genes in the GTEx Portal

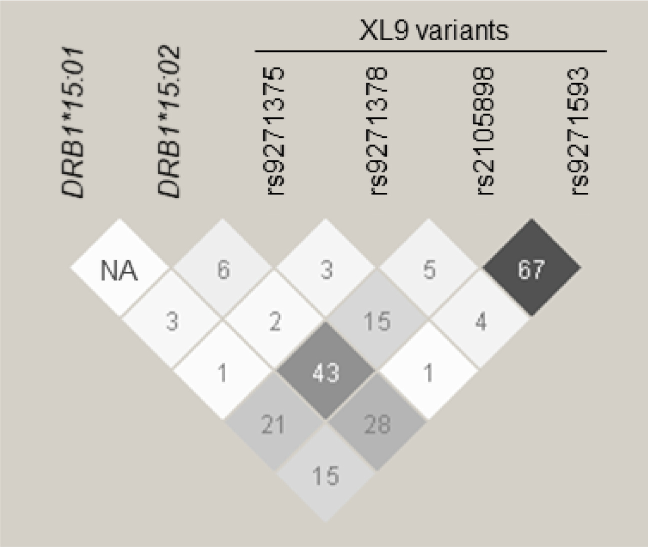
Gene	XL9 variant	P	Effect allele	NES	SLE risk allele	Effect of the risk allele	Tissue
HLA-DRB9	rs2105898	3.9×10^{-32}	G	0.60	T	down	Whole Blood
HLA-DRB5	rs2105898	3.1×10^{-94}	G	-0.78	T	up	Whole Blood
HLA-DRB6	rs2105898	2.3×10^{-59}	G	0.80	T	down	Whole Blood
HLA-DRB1	rs2105898	4.7×10^{-6}	G	-0.10	T	up	Whole Blood
HLA-DQA1	rs2105898	3.4×10^{-8}	G	-0.15	T	up	Whole Blood
HLA-DQB1	rs2105898	6.6×10^{-20}	G	-0.39	T	up	Whole Blood
HLA-DQA2	rs2105898	3.2×10^{-15}	G	0.49	T	down	Whole Blood
HLA-DQB2	rs2105898	2.1×10^{-12}	G	0.39	T	down	Whole Blood
HLA-DRB9	rs9271593	8.7×10^{-10}	T	0.25	C	down	Whole Blood
HLA-DRB5	rs9271593	3.9×10^{-13}	T	-0.24	C	up	Whole Blood
HLA-DRB6	rs9271593	4.1×10^{-46}	T	0.55	C	down	Whole Blood
HLA-DRB1	rs9271593	9.7×10^{-17}	T	-0.14	C	up	Whole Blood
HLA-DQA2	rs9271593	1.4×10^{-15}	T	0.38	C	down	Whole Blood

NES, normalized effect size.

eQTL data of XL9 rs2105898 and rs9271593 in whole blood was obtained from the Genotype-Tissue Expression (GTEx) Portal V8 (https://gtexportal.org/home/, accessed 13 Mar 2023).



Supplementary Figure S1. Regional plot of XL9 variants in Genome-wide association study of Systemic lupus erythematosus in a Japanese population. GWAS data was obtained from the NBDC Human Database (Dataset ID: hum0197.v3.gwas.v1).[19] Regional plot of a region between *HLA-DRB1* and *DQA1* was drawn by LocusZoom (http://locuszoom.org/). Color of dots shows level of linkage disequilibrium between rs9271375 and each variant in the East Asian populations.



Supplementary Figure S2. Linkage disequilibrium among the XL9 region variants and *HLA-DRB1* alleles examined in this study.

Pair-wise linkage equilibrium values (r^2) were calculated using Haploview software based on the genotypes of 779 healthy individuals. Data for all alleles are is shown in Supplementary Table S5. NA: not applicable.

Supplementary Data   Genotyping data of sach subject

ID	DRB1*15:01 allele count	DRB1*15:02 allele count	rs9271375 genotype	rs9271375A allele count	rs9271378 genotype	rs9271378G allele count	rs2105898 genotype	rs2105898T allele count	rs9271593 genotype	rs9271593C allele count
SLE1	0	0	G/G	0	G/A	1	G/G		T/T	0
SLE2	0	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE3	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE4	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE5	0	2	G/G	0	A/A	0	T/T	2	C/C	2
SLE6	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE7	0	1	A/G	1	G/A	1	G/G	0	T/T	0
SLE8	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE9	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE10	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE11	1	0	A/G	1	G/A	1	T/G	1	C/C	2
SLE12	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE13	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE14	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE15	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE16	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE17	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE18	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE19	0	1	G/G	0	G/A	1	T/G	1	C/T	1
SLE20	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE21	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE22	2	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE23	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE24	2	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE25	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE26	2	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE27	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE28	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE29	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE30	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE31	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE32	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE33	2	0	G/G	0	G/A	1	T/G	1	C/T	1
SLE34	0	0	A/G	1	G/G	2	G/G	0	C/T	1
SLE35	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE36	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE37	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE38	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE39	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE40	0	1	G/G	0	G/A	1	T/G	1	C/T	1
SLE41	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE42	0	0	A/A	2	G/G	2	G/G	0	C/C	2
SLE43	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE44	1	0	G/G	0	A/A	0	T/G	1	C/T	1

SLE45	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE46	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE47	0	2	G/G	0	A/A	0	T/T	2	C/C	2
SLE48	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE49	0	0	A/A	2	G/G	2	G/G	0	C/C	2
SLE50	0	2	G/G	0	A/A	0	T/G	1	C/T	1
SLE51	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE52	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE53	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE54	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE55	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE56	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE57	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE58	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE59	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE60	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE61	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE62	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE63	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE64	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE65	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE66	0	0	A/G	1	G/A	1	G/G	0	T/T	0
SLE67	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE68	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE69	0	0	A/G	1	G/A	1	G/G	0	T/T	0
SLE70	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE71	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE72	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE73	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE74	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE75	2	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE76	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE77	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE78	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE79	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE80	0	0	A/G	1	G/A	1	T/G	1	C/C	2
SLE81	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE82	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE83	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE84	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE85	0	0	A/G	1	G/A	1	G/G	0	T/T	0
SLE86	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE87	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE88	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE89	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE90	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE91	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE92	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE93	0	1	G/G	0	A/A	0	T/G	1	C/T	1

SLE94	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE95	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE96	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE97	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE98	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE99	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE100	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE101	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE102	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE103	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE104	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE105	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE106	0	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE107	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE108	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE109	0	1	A/G	1	G/A	1	T/G	1	C/C	2
SLE110	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE111	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE112	0	1	A/G	1	G/A	1	T/G	1	C/C	2
SLE113	0	2	G/G	0	A/A	0	T/T	2	C/C	2
SLE114	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE115	2	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE116	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE117	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE118	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE119	1	0	A/G	1	G/A	1	T/G	1	C/C	2
SLE120	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE121	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE122	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE123	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE124	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE125	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE126	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE127	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE128	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE129	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE130	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE131	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE132	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE133	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE134	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE135	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE136	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE137	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE138	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE139	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE140	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE141	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE142	0	0	A/G	1	A/A	0	G/G	0	T/T	0

SLE143	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE144	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE145	0	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE146	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE147	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE148	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE149	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE150	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE151	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE152	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE153	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE154	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE155	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE156	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE157	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE158	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE159	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE160	1	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE161	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE162	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE163	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE164	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE165	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE166	0	0	A/G	1	G/G	2	G/G	0	C/T	1
SLE167	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE168	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE169	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE170	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE171	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE172	1	0	G/G	0	G/A	1	T/G	1	C/T	1
SLE173	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE174	0	1	A/G	1	G/A	1	T/G	1	C/C	2
SLE175	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE176	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE177	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE178	0	0	A/G	1	G/A	1	G/G	0	T/T	0
SLE179	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE180	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE181	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE182	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE183	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE184	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE185	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE186	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE187	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE188	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE189	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE190	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE191	0	0	G/G	0	A/A	0	T/T	2	C/C	2

SLE192	2	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE193	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE194	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE195	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE196	0	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE197	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE198	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE199	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE200	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE201	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE202	1	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE203	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE204	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE205	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE206	0	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE207	0	0	G/G	0	G/A	1	T/G	1	C/T	1
SLE208	0	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE209	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE210	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE211	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE212	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE213	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE214	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE215	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE216	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE217	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE218	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE219	0	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE220	1	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE221	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE222	1	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE223	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE224	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE225	0	0	A/G	1	G/A	1	T/G	1	C/C	2
SLE226	0	0	A/G	1	G/A	1	G/G	0	T/T	0
SLE227	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE228	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE229	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE230	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE231	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE232	0	0	A/G	1	G/A	1	G/G	0	T/T	0
SLE233	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE234	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE235	0	0	A/G	1	G/A	1	G/G	0	T/T	0
SLE236	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE237	0	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE238	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE239	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE240	0	0	A/G	1	G/A	1	G/G	0	C/T	1

SLE241	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE242	0	0	A/A	2	G/G	2	G/G	0	C/C	2
SLE243	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE244	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE245	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE246	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE247	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE248	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE249	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE250	0	0	A/G	1	G/A	1	G/G	0	T/T	0
SLE251	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE252	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE253	2	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE254	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE255	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE256	0	1	G/G	0	G/A	1	T/G	1	C/T	1
SLE257	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE258	0	0	A/G	1	G/A	1	T/G	1	C/C	2
SLE259	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE260	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE261	0	0	G/G	0	G/A	1	T/G	1	C/T	1
SLE262	2	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE263	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE264	1	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE265	0	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE266	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE267	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE268	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE269	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE270	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE271	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE272	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE273	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE274	1	0	A/G	1	G/A	1	T/G	1	C/C	2
SLE275	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE276	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE277	0	2	G/G	0	A/A	0	T/T	2	C/C	2
SLE278	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE279	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE280	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE281	0	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE282	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE283	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE284	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE285	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE286	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE287	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE288	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE289	0	1	G/G	0	A/A	0	T/T	2	C/C	2

SLE290	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE291	0	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE292	0	0	A/G	1	G/A	1	T/G	1	C/C	2
SLE293	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE294	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE295	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE296	0	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE297	0	2	G/G	0	A/A	0	T/T	2	C/C	2
SLE298	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE299	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE300	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE301	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE302	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE303	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE304	0	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE305	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE306	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE307	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE308	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE309	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE310	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE311	1	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE312	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE313	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE314	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE315	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE316	0	2	G/G	0	A/A	0	T/T	2	C/C	2
SLE317	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE318	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE319	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE320	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE321	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE322	1	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE323	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE324	1	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE325	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE326	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE327	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE328	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE329	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE330	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE331	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE332	2	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE333	0	0	G/G	0	G/G	2	G/G	0	T/T	0
SLE334	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE335	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE336	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE337	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE338	0	0	A/G	1	A/A	0	G/G	0	T/T	0

SLE339	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE340	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE341	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE342	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE343	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE344	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE345	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE346	1	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE347	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE348	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE349	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE350	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE351	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE352	2	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE353	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE354	0	0	G/G	0	G/G	2	G/G	0	T/T	0
SLE355	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE356	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE357	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE358	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE359	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE360	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE361	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE362	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE363	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE364	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE365	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE366	1	0	A/G	1	G/A	1	T/G	1	C/C	2
SLE367	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE368	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE369	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE370	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE371	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE372	0	1	A/G	1	A/A	0	T/G	1	C/T	1
SLE373	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE374	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE375	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE376	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE377	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE378	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE379	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE380	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE381	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE382	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE383	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE384	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE385	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE386	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE387	0	0	A/G	1	G/A	1	G/G	0	C/T	1

SLE388	1	0	A/G	1	G/A	1	T/G	1	C/C	2
SLE389	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE390	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE391	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE392	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE393	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE394	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE395	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE396	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE397	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE398	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE399	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE400	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE401	1	0	G/G	0	G/A	1	T/G	1	C/T	1
SLE402	0	0	A/A	2	G/A	1	G/G	0	C/T	1
SLE403	2	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE404	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE405	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE406	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE407	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE408	0	2	G/G	0	A/A	0	T/T	2	C/C	2
SLE409	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE410	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE411	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE412	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE413	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE414	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE415	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE416	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE417	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE418	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE419	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE420	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE421	1	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE422	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE423	0	1	G/G	0	A/A	0	T/T	2	C/C	2
SLE424	1	0	G/G	0	A/A	0	T/T	2	C/C	2
SLE425	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE426	0	0	A/G	1	A/A	0	G/G	0	T/T	0
SLE427	0	1	G/G	0	A/A	0	T/G	1	C/T	1
SLE428	0	0	A/A	2	A/A	0	G/G	0	T/T	0
SLE429	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE430	0	0	G/G	0	G/A	1	G/G	0	T/T	0
SLE431	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE432	0	0	G/G	0	A/A	0	T/G	1	C/T	1
SLE433	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE434	0	1	G/G	0	G/A	1	T/G	1	C/T	1
SLE435	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE436	1	0	G/G	0	G/A	1	T/G	1	C/T	1

SLE437	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE438	1	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE439	0	0	A/G	1	A/A	0	T/G	1	C/T	1
SLE440	0	0	G/G	0	A/A	0	G/G	0	T/T	0
SLE441	0	0	A/G	1	G/A	1	G/G	0	C/T	1
SLE442	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC1	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC2	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC3	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC4	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC5	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC6	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC7	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC8	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC9	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC10	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC11	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC12	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC13	1	0	G/G	0	G/A	1	T/G	1	C/T	1
HC14	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC15	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC16	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC17	2	0	G/G	0	A/A	0	T/T	2	C/C	2
HC18	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC19	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC20	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC21	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC22	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC23	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC24	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC25	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC26	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC27	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC28	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC29	2	0	G/G	0	A/A	0	T/T	2	C/C	2
HC30	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC31	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC32	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC33	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC34	0	0	G/G	0	G/A	1	T/G	1	C/T	1
HC35	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC36	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC37	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC38	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC39	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC40	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC41	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC42	0	0	G/G	0	G/A	1	T/G	1	C/T	1
HC43	0	0	A/A	2	A/A	0	G/G	0	T/T	0

HC44	1	0	G/G	0	G/A	1	T/G	1	C/T	1
HC45	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC46	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC47	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC48	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC49	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC50	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC51	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC52	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC53	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC54	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC55	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC56	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC57	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC58	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC59	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC60	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC61	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC62	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC63	0	0	G/G	0	G/G	2	G/G	0	T/T	0
HC64	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC65	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC66	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC67	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC68	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC69	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC70	0	2	G/G	0	A/A	0	T/T	2	C/C	2
HC71	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC72	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC73	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC74	0	0	G/G	0	A/A	0	G/G	0	C/T	1
HC75	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC76	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC77	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC78	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC79	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC80	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC81	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC82	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC83	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC84	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC85	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC86	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC87	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC88	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC89	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC90	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC91	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC92	1	0	G/G	0	A/A	0	T/G	1	C/T	1

HC93	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC94	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC95	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC96	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC97	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC98	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC99	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC100	1	0	A/G	1	G/A	1	T/G	1	C/C	2
HC101	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC102	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC103	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC104	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC105	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC106	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC107	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC108	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC109	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC110	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC111	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC112	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC113	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC114	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC115	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC116	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC117	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC118	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC119	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC120	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC121	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC122	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC123	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC124	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC125	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC126	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC127	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC128	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC129	0	1	G/G	0	A/A	0	T/T	2	C/C	2
HC130	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC131	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC132	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC133	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC134	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC135	0	0	G/G	0	G/A	1	T/G	1	C/T	1
HC136	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC137	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC138	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC139	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC140	1	1	G/G	0	A/A	0	T/T	2	C/C	2
HC141	0	1	G/G	0	A/A	0	T/T	2	C/C	2

HC142	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC143	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC144	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC145	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC146	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC147	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC148	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC149	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC150	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC151	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC152	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC153	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC154	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC155	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC156	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC157	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC158	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC159	0	0	G/G	0	G/A	1	T/G	1	C/T	1
HC160	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC161	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC162	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC163	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC164	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC165	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC166	0	0	G/G	0	G/A	1	T/G	1	C/T	1
HC167	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC168	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC169	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC170	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC171	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC172	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC173	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC174	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC175	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC176	0	0	A/A	2	G/G	2	G/G	0	C/C	2
HC177	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC178	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC179	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC180	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC181	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC182	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC183	0	2	G/G	0	A/A	0	T/T	2	C/C	2
HC184	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC185	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC186	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC187	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC188	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC189	0	0	A/A	2	G/G	2	G/G	0	C/C	2
HC190	0	0	A/G	1	A/A	0	G/G	0	T/T	0

HC191	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC192	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC193	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC194	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC195	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC196	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC197	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC198	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC199	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC200	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC201	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC202	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC203	0	0	G/G	0	A/A	0	T/T	2	C/C	2
HC204	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC205	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC206	0	0	G/G	0	G/A	1	T/G	1	C/T	1
HC207	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC208	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC209	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC210	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC211	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC212	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC213	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC214	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC215	2	0	G/G	0	A/A	0	T/T	2	C/C	2
HC216	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC217	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC218	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC219	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC220	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC221	1	1	G/G	0	A/A	0	T/T	2	C/C	2
HC222	2	0	G/G	0	A/A	0	T/T	2	C/C	2
HC223	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC224	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC225	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC226	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC227	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC228	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC229	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC230	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC231	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC232	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC233	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC234	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC235	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC236	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC237	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC238	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC239	0	0	A/G	1	A/A	0	G/G	0	T/T	0

HC240	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC241	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC242	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC243	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC244	0	0	A/G	1	G/A	1	T/G	1	C/C	2
HC245	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC246	1	0	G/G	0	G/A	1	T/G	1	C/T	1
HC247	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC248	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC249	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC250	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC251	0	1	G/G	0	A/A	0	T/T	2	C/C	2
HC252	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC253	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC254	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC255	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC256	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC257	1	1	G/G	0	A/A	0	T/T	2	C/C	2
HC258	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC259	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC260	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC261	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC262	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC263	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC264	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC265	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC266	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC267	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC268	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC269	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC270	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC271	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC272	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC273	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC274	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC275	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC276	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC277	1	0	G/G	0	G/A	1	T/G	1	C/T	1
HC278	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC279	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC280	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC281	0	1	G/G	0	G/A	1	T/G	1	C/T	1
HC282	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC283	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC284	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC285	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC286	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC287	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC288	0	1	G/G	0	G/A	1	T/G	1	C/T	1

HC289	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC290	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC291	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC292	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC293	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC294	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC295	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC296	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC297	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC298	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC299	0	0	A/G	1	G/A	1	T/G	1	C/C	2
HC300	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC301	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC302	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC303	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC304	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC305	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC306	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC307	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC308	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC309	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC310	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC311	2	0	G/G	0	A/A	0	T/T	2	C/C	2
HC312	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC313	1	0	A/A	2	G/A	1	G/G	0	C/T	1
HC314	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC315	0	0	A/G	1	G/G	2	G/G	0	C/T	1
HC316	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC317	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC318	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC319	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC320	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC321	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC322	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC323	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC324	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC325	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC326	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC327	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC328	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC329	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC330	1	0	A/G	1	G/A	1	T/G	1	C/C	2
HC331	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC332	0	2	G/G	0	A/A	0	T/T	2	C/C	2
HC333	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC334	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC335	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC336	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC337	0	0	G/G	0	A/A	0	G/G	0	T/T	0

HC338	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC339	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC340	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC341	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC342	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC343	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC344	1	1	G/G	0	A/A	0	T/T	2	C/C	2
HC345	0	0	A/G	1	G/G	2	G/G	0	C/T	1
HC346	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC347	0	1	G/G	0	G/A	1	T/G	1	C/T	1
HC348	1	0	A/G	1	A/A	0	T/G	1	C/C	2
HC349	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC350	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC351	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC352	0	1	G/G	0	A/A	0	T/T	2	C/C	2
HC353	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC354	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC355	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC356	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC357	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC358	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC359	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC360	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC361	1	0	G/G	0	A/A	0	T/T	2	C/C	2
HC362	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC363	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC364	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC365	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC366	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC367	0	2	G/G	0	A/A	0	T/T	2	C/C	2
HC368	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC369	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC370	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC371	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC372	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC373	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC374	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC375	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC376	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC377	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC378	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC379	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC380	0	1	G/G	0	A/A	0	T/T	2	C/C	2
HC381	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC382	1	0	G/G	0	G/A	1	T/G	1	C/T	1
HC383	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC384	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC385	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC386	0	0	G/G	0	A/A	0	G/G	0	T/T	0

HC387	1	1	G/G	0	A/A	0	T/T	2	C/C	2
HC388	1	0	A/G	1	G/A	1	T/G	1	C/C	2
HC389	0	0	A/G	1	G/G	2	G/G	0	C/T	1
HC390	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC391	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC392	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC393	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC394	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC395	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC396	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC397	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC398	0	0	G/G	0	G/G	2	G/G	0	T/T	0
HC399	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC400	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC401	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC402	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC403	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC404	0	2	G/G	0	A/A	0	T/T	2	C/C	2
HC405	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC406	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC407	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC408	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC409	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC410	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC411	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC412	1	0	G/G	0	G/A	1	T/G	1	C/T	1
HC413	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC414	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC415	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC416	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC417	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC418	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC419	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC420	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC421	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC422	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC423	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC424	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC425	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC426	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC427	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC428	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC429	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC430	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC431	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC432	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC433	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC434	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC435	0	0	A/G	1	A/A	0	G/G	0	T/T	0

HC436	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC437	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC438	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC439	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC440	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC441	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC442	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC443	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC444	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC445	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC446	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC447	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC448	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC449	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC450	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC451	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC452	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC453	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC454	0	1	G/G	0	G/A	1	T/G	1	T/T	0
HC455	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC456	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC457	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC458	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC459	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC460	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC461	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC462	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC463	0	2	G/G	0	A/A	0	T/T	2	C/C	2
HC464	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC465	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC466	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC467	0	0	A/G	1	G/G	2	G/G	0	C/T	1
HC468	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC469	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC470	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC471	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC472	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC473	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC474	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC475	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC476	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC477	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC478	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC479	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC480	0	0	G/G	0	A/A	0	T/T	2	C/C	2
HC481	0	1	G/G	0	G/A	1	T/G	1	C/T	1
HC482	2	0	G/G	0	A/A	0	T/T	2	C/C	2
HC483	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC484	0	0	A/G	1	A/A	0	G/G	0	T/T	0

HC485	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC486	1	1	G/G	0	A/A	0	T/T	2	C/C	2
HC487	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC488	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC489	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC490	0	0	A/G	1	G/G	2	G/G	0	C/T	1
HC491	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC492	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC493	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC494	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC495	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC496	1	1	G/G	0	A/A	0	T/T	2	C/C	2
HC497	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC498	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC499	0	1	G/G	0	G/A	1	T/G	1	C/T	1
HC500	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC501	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC502	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC503	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC504	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC505	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC506	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC507	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC508	0	0	A/G	1	G/G	2	G/G	0	C/T	1
HC509	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC510	0	0	A/A	2	G/G	2	G/G	0	C/C	2
HC511	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC512	0	0	A/G	1	G/G	2	G/G	0	C/T	1
HC513	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC514	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC515	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC516	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC517	1	1	G/G	0	A/A	0	T/T	2	C/C	2
HC518	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC519	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC520	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC521	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC522	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC523	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC524	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC525	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC526	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC527	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC528	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC529	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC530	0	2	G/G	0	A/A	0	T/T	2	C/C	2
HC531	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC532	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC533	0	0	G/G	0	A/A	0	G/G	0	T/T	0

HC534	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC535	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC536	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC537	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC538	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC539	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC540	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC541	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC542	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC543	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC544	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC545	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC546	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC547	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC548	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC549	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC550	0	1	G/G	0	A/A	0	T/T	2	C/C	2
HC551	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC552	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC553	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC554	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC555	0	1	G/G	0	A/A	0	T/T	2	C/C	2
HC556	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC557	0	2	G/G	0	A/A	0	T/T	2	C/C	2
HC558	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC559	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC560	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC561	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC562	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC563	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC564	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC565	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC566	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC567	0	0	G/G	0	G/A	1	T/G	1	C/T	1
HC568	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC569	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC570	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC571	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC572	2	0	G/G	0	A/A	0	T/T	2	C/C	2
HC573	1	0	A/G	1	G/A	1	T/G	1	C/C	2
HC574	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC575	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC576	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC577	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC578	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC579	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC580	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC581	0	1	G/G	0	G/A	1	T/G	1	C/T	1
HC582	0	2	G/G	0	A/A	0	T/T	2	C/C	2

HC583	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC584	0	0	A/G	1	G/A	1	T/G	1	C/C	2
HC585	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC586	0	0	A/A	2	G/G	2	G/G	0	C/C	2
HC587	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC588	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC589	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC590	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC591	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC592	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC593	0	1	G/G	0	G/A	1	T/G	1	C/T	1
HC594	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC595	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC596	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC597	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC598	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC599	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC600	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC601	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC602	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC603	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC604	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC605	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC606	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC607	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC608	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC609	0	2	G/G	0	A/A	0	T/T	2	C/C	2
HC610	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC611	1	0	G/G	0	A/A	0	T/T	2	C/C	2
HC612	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC613	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC614	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC615	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC616	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC617	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC618	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC619	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC620	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC621	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC622	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC623	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC624	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC625	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC626	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC627	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC628	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC629	0	1	G/G	0	A/A	0	T/T	2	C/C	2
HC630	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC631	0	0	A/G	1	A/A	0	G/G	0	T/T	0

HC632	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC633	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC634	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC635	0	0	A/A	2	G/G	2	G/G	0	C/C	2
HC636	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC637	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC638	0	0	G/G	0	G/A	1	T/G	1	C/T	1
HC639	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC640	0	0	A/G	1	G/G	2	G/G	0	C/T	1
HC641	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC642	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC643	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC644	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC645	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC646	1	0	G/G	0	A/A	0	T/T	2	C/C	2
HC647	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC648	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC649	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC650	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC651	0	0	G/G	0	G/A	1	T/G	1	C/T	1
HC652	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC653	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC654	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC655	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC656	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC657	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC658	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC659	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC660	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC661	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC662	0	1	G/G	0	G/A	1	T/G	1	C/T	1
HC663	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC664	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC665	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC666	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC667	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC668	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC669	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC670	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC671	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC672	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC673	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC674	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC675	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC676	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC677	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC678	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC679	1	0	G/G	0	G/A	1	T/G	1	C/T	1
HC680	0	1	G/G	0	A/A	0	T/G	1	C/T	1

HC681	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC682	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC683	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC684	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC685	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC686	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC687	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC688	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC689	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC690	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC691	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC692	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC693	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC694	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC695	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC696	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC697	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC698	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC699	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC700	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC701	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC702	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC703	1	0	G/G	0	A/A	0	T/T	2	C/C	2
HC704	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC705	0	1	G/G	0	G/A	1	T/G	1	C/T	1
HC706	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC707	0	2	G/G	0	A/A	0	T/T	2	C/C	2
HC708	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC709	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC710	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC711	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC712	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC713	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC714	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC715	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC716	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC717	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC718	1	0	G/G	0	G/A	1	T/G	1	C/T	1
HC719	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC720	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC721	0	0	A/A	2	G/A	1	G/G	0	C/T	1
HC722	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC723	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC724	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC725	0	1	A/G	1	G/A	1	T/G	1	C/C	2
HC726	0	1	G/G	0	A/A	0	T/T	2	C/C	2
HC727	0	0	G/G	0	G/A	1	T/G	1	C/T	1
HC728	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC729	0	1	G/G	0	A/A	0	T/G	1	C/T	1

HC730	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC731	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC732	0	1	G/G	0	A/A	0	T/T	2	C/C	2
HC733	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC734	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC735	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC736	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC737	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC738	0	0	G/G	0	A/A	0	T/G	1	C/T	1
HC739	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC740	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC741	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC742	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC743	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC744	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC745	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC746	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC747	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC748	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC749	0	0	G/G	0	A/A	0	G/G	0	T/T	0
HC750	1	1	G/G	0	A/A	0	T/T	2	C/C	2
HC751	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC752	0	0	A/G	1	A/A	0	T/G	1	C/T	1
HC753	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC754	0	0	A/A	2	G/G	2	G/G	0	C/C	2
HC755	0	1	G/G	0	A/A	0	T/G	1	C/T	1
HC756	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC757	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC758	0	1	G/G	0	A/A	0	T/T	2	C/C	2
HC759	0	1	A/G	1	A/A	0	T/G	1	C/T	1
HC760	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC761	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC762	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC763	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC764	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC765	1	0	A/G	1	A/A	0	T/G	1	C/T	1
HC766	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC767	0	1	G/G	0	G/A	1	T/G	1	C/T	1
HC768	1	0	G/G	0	A/A	0	T/T	2	C/C	2
HC769	0	0	A/G	1	G/A	1	G/G	0	C/T	1
HC770	0	1	G/G	0	A/A	0	T/T	2	C/C	2
HC771	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC772	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC773	1	0	G/G	0	A/A	0	T/G	1	C/T	1
HC774	0	0	A/A	2	A/A	0	G/G	0	T/T	0
HC775	0	0	G/G	0	G/A	1	G/G	0	T/T	0
HC776	0	0	A/G	1	A/A	0	G/G	0	T/T	0
HC777	0	0	A/G	1	G/A	1	G/G	0	T/T	0
HC778	0	0	A/G	1	A/A	0	G/G	0	T/T	0

HC779	0	0	A/G	1	G/A	1	G/G	0	C/T	1