

Intrathecally Expanding B Cell Clones in Herpes Simplex Encephalitis- A Case Report

Authors

Shila P. Coronel-Castello^{1*}, Gildas Lepennetier^{1*}, Jolien Diddens¹, Verena Friedrich¹,
Monika Pfaller¹, Bernhard Hemmer^{1,2}, Klaus Lehmann-Horn¹

¹Department of Neurology, School of Medicine, Technical University of Munich,
Munich, Germany

²Munich Cluster of Systems Neurology (SyNergy), Germany

*These authors contributed equally to this work

Corresponding author: Klaus Lehmann-Horn, MD, Department of Neurology, School
of Medicine, Technical University of Munich, Munich, Germany
klaus.lehmann-horn@tum.de

Full V(D)J sequence of expanded clones

clone	clonal group ID	ratio	time	origin tissue	celltype	frequency (cell count)	Isotype	V gene	D gene	J gene	C gene	total cells per time point	total cells per time point per clone	cell percent per time point
168_IGHV1-18_IGHJ4	168	11,8	t1	CSF	BCR	1	IGH;IGK	IGHV1-18;IGKV3-20	IGHD5-18	IGHJ4;IGKJ2	IGHG4;IGKC	1964	1	0,1
168_IGHV1-18_IGHJ4	168	11,8	t2	CSF	BCR	1	IGH;IGK	IGHV1-18;IGKV3-20	IGHD5-18	IGHJ4;IGKJ2	IGHG4;IGKC	333	2	0,6
168_IGHV1-18_IGHJ4	168	11,8	t2	CSF	BCR	1	IGH;IGK	IGHV1-18;IGKV3-20	IGHD5-18	IGHJ4;IGKJ2	IGHG4;IGKC	333	2	0,6
191_IGHV1-2_IGHJ2	191	11,8	t1	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV3-20	IGHD5-24	IGHJ2;IGKJ1	IGHG2;IGKC	1964	1	0,1
191_IGHV1-2_IGHJ2	191	11,8	t2	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV3-20	IGHD5-18	IGHJ2;IGKJ1	IGHG2;IGKC	333	2	0,6
191_IGHV1-2_IGHJ2	191	11,8	t2	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV3-20	IGHD5-18	IGHJ2;IGKJ1	IGHG2;IGKC	333	2	0,6
28_IGHV3-43_IGHJ3	28	11,8	t1	CSF	BCR	1	IGH;IGK	IGHV3-43;IGKV4-1	IGHD4-17	IGHJ3;IGKJ4	IGHG1;IGKC	1964	1	0,1
28_IGHV3-43_IGHJ3	28	11,8	t2	CSF	BCR	2	IGH;IGK	IGHV3-43;IGKV4-1	IGHD4-17	IGHJ3;IGKJ4	IGHG1;IGKC	333	2	0,6
4_IGHV4-59_IGHJ4	4	11,8	t1	CSF	BCR	2	IGH;IGK	IGHV4-59;IGKV2-28	IGHD4-23	IGHJ4;IGKJ3	IGHG1;IGKC	1964	2	0,1
4_IGHV4-59_IGHJ4	4	11,8	t2	CSF	BCR	3	IGH;IGK	IGHV4-59;IGKV2-28	IGHD4-23	IGHJ4;IGKJ3	IGHG1;IGKC	333	4	1,2
4_IGHV4-59_IGHJ4	4	11,8	t2	CSF	BCR	1	IGH;IGK	IGHV4-59;IGKV2-28	IGHD4-23	IGHJ4;IGKJ3	IGHG1;IGKC	333	4	1,2
46_IGHV1-69D_IGHJ6	46	11,8	t1	CSF	BCR	1	IGH;IGK	IGHV1-69D;IGKV1-5	IGHD6-6	IGHJ6;IGKJ2	IGHG1;IGKC	1964	1	0,1
46_IGHV1-69D_IGHJ6	46	11,8	t2	CSF	BCR	1	IGH;IGK	IGHV1-69D;IGKV1-5	IGHD6-6	IGHJ6;IGKJ2	IGHG1;IGKC	333	2	0,6
46_IGHV1-69D_IGHJ6	46	11,8	t2	CSF	BCR	1	IGH;IGK	IGHV1-69D;IGKV1-5	IGHD6-6	IGHJ6;IGKJ2	IGHG1;IGKC	333	2	0,6
51_IGHV1-2_IGHJ5	51	11,8	t1	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV3-15	IGHD3-10	IGHJ5;IGKJ1	IGHG1;IGKC	1964	1	0,1
51_IGHV1-2_IGHJ5	51	11,8	t2	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV3-15	IGHD3-10	IGHJ5;IGKJ1	IGHG1;IGKC	333	2	0,6
51_IGHV1-2_IGHJ5	51	11,8	t2	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV3-15	IGHD3-10	IGHJ5;IGKJ1	IGHG1;IGKC	333	2	0,6
14_IGHV4-39_IGHJ4	14	8,8	t1	CSF	BCR	2	IGH;IGK	IGHV4-39;IGKV4-1	IGHD2-15	IGHJ4;IGKJ4	IGHG1;IGKC	1964	2	0,1
14_IGHV4-39_IGHJ4	14	8,8	t2	CSF	BCR	2	IGH;IGK	IGHV4-39;IGKV4-1	IGHD2-15	IGHJ4;IGKJ4	IGHG1;IGKC	333	3	0,9
14_IGHV4-39_IGHJ4	14	8,8	t2	CSF	BCR	1	IGH;IGK	IGHV4-39;IGKV4-1	IGHD2-15	IGHJ4;IGKJ4	IGHG1;IGKC	333	3	0,9
6_IGHV1-18_IGHJ6	6	8,8	t1	CSF	BCR	1	IGH;IGL	IGHV1-18;IGLV2-8	IGHD5-12	IGHJ6;IGLJ2	IGHG1;IGLC2	1964	2	0,1
6_IGHV1-18_IGHJ6	6	8,8	t1	CSF	BCR	1	IGH;IGL	IGHV1-18;IGLV2-8	IGHD2-21	IGHJ6;IGLJ2	IGHG1;IGLC2	1964	2	0,1
6_IGHV1-18_IGHJ6	6	8,8	t2	CSF	BCR	3	IGH;IGL	IGHV1-18;IGLV2-8	IGHD1-1	IGHJ6;IGLJ2	IGHG1;IGLC2	333	3	0,9
8_IGHV5-51_IGHJ4	8	8,8	t1	CSF	BCR	1	IGH;IGL	IGHV5-51;IGLV3-25	IGHD3-10	IGHJ4;IGLJ1	IGHG1;IGLC1	1964	2	0,1
8_IGHV5-51_IGHJ4	8	8,8	t1	CSF	BCR	1	IGH;IGL	IGHV5-51;IGLV3-25	IGHD3-10	IGHJ4;IGLJ1	IGHG1;IGLC1	1964	2	0,1
8_IGHV5-51_IGHJ4	8	8,8	t2	CSF	BCR	3	IGH;IGL	IGHV5-51;IGLV3-25	IGHD3-10	IGHJ4;IGLJ1	IGHG1;IGLC1	333	3	0,9
109_IGHV2-5_IGHJ3	109	5,9	t1	CSF	BCR	1	IGH;IGL	IGHV2-5;IGLV2-23	IGHD3-22	IGHJ3;IGLJ1	IGHG1;IGLC1	1964	1	0,1
109_IGHV2-5_IGHJ3	109	5,9	t2	CSF	BCR	1	IGH;IGL	IGHV2-5;IGLV2-23	IGHD3-22	IGHJ3;IGLJ1	IGHG1;IGLC1	333	1	0,3
11_IGHV1-69D_IGHJ5	11	5,9	t1	CSF	BCR	2	IGH;IGK	IGHV1-69D;IGKV1D-39	IGHD6-19	IGHJ5;IGKJ2	IGHG1;IGKC	1964	2	0,1
11_IGHV1-69D_IGHJ5	11	5,9	t2	CSF	BCR	2	IGH;IGK	IGHV1-69D;IGKV1D-39	IGHD6-19	IGHJ5;IGKJ2	IGHG1;IGKC	333	2	0,6
112_IGHV1-69D_IGHJ4	112	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-69D;IGKV3-15	IGHD3-10	IGHJ4;IGKJ3	IGHG1;IGKC	1964	1	0,1
112_IGHV1-69D_IGHJ4	112	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-69D;IGKV3-15	IGHD2-21	IGHJ4;IGKJ3	IGHG1;IGKC	333	1	0,3
116_IGHV3-53_IGHJ3	116	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV3-53;IGKV3-11	IGHD3-10	IGHJ3;IGKJ2	IGHG1;IGKC	1964	1	0,1
116_IGHV3-53_IGHJ3	116	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-53;IGKV3-11	IGHD3-10	IGHJ3;IGKJ2	IGHG1;IGKC	333	1	0,3
117_IGHV4-61_IGHJ4	117	5,9	t1	CSF	BCR	1	IGH;IGL	IGHV4-61;IGLV2-23	IGHD6-19	IGHJ4;IGLJ2	IGHG1;IGLC2	1964	1	0,1
117_IGHV4-61_IGHJ4	117	5,9	t2	CSF	BCR	1	IGH;IGL	IGHV4-61;IGLV2-23	IGHD6-19	IGHJ4;IGLJ2	IGHG1;IGLC2	333	1	0,3
118_IGHV4-61_IGHJ4	118	5,9	t1	CSF	BCR	1	IGH;IGL	IGHV4-61;IGLV1-51	IGHD3-16	IGHJ4;IGLJ2	IGHG1;IGLC2	1964	1	0,1
118_IGHV4-61_IGHJ4	118	5,9	t2	CSF	BCR	1	IGH;IGL	IGHV4-61;IGLV1-51	IGHD3-16	IGHJ4;IGLJ2	IGHG1;IGLC2	333	1	0,3
135_IGHV4-61_IGHJ6	135	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV4-61;IGKV2D-28	IGHD6-25	IGHJ6;IGKJ2	IGHG1;IGKC	1964	1	0,1
135_IGHV4-61_IGHJ6	135	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV4-61;IGKV2-28	IGHD6-25	IGHJ6;IGKJ2	IGHG1;IGKC	333	1	0,3
136_IGHV3-21_IGHJ4	136	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV3-21;IGKV1-9	IGHD6-13	IGHJ4;IGKJ4	IGHG1;IGKC	1964	1	0,1
136_IGHV3-21_IGHJ4	136	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-21;IGKV1-9	IGHD6-13	IGHJ4;IGKJ4	IGHG1;IGKC	333	1	0,3
140_IGHV3-23_IGHJ4	140	5,9	t1	CSF	BCR	1	IGH;IGL	IGHV3-23;IGLV2-14	IGHD3-3	IGHJ4;IGLJ1	IGHG1;IGLC1	1964	1	0,1
140_IGHV3-23_IGHJ4	140	5,9	t2	CSF	BCR	1	IGH;IGL	IGHV3-23;IGLV2-14	IGHD3-3	IGHJ4;IGLJ1	IGHG1;IGLC1	333	1	0,3
142_IGHV4-30-2_IGHJ4	142	5,9	t1	CSF	BCR	1	IGH;IGL	IGHV4-30-2;IGLV1-51	IGHD3-9	IGHJ4;IGLJ2	IGHG1;IGLC2	1964	1	0,1
142_IGHV4-30-2_IGHJ4	142	5,9	t2	CSF	BCR	1	IGH;IGL	IGHV4-30-2;IGLV1-51	IGHD3-9	IGHJ4;IGLJ2	IGHG1;IGLC2	333	1	0,3
146_IGHV3-30_IGHJ2	146	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV3-30;IGKV3-11	IGHD3-16	IGHJ2;IGKJ5	IGHG1;IGKC	1964	1	0,1
146_IGHV3-30_IGHJ2	146	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-30;IGKV3-11	IGHD3-16	IGHJ2;IGKJ5	IGHG1;IGKC	333	1	0,3
149_IGHV3-11_IGHJ4	149	5,9	t1	CSF	BCR	1	IGH;IGL	IGHV3-11;IGLV1-40	IGHD3-22	IGHJ4;IGLJ1	IGHA1;IGLC1	1964	1	0,1
149_IGHV3-11_IGHJ4	149	5,9	t2	CSF	BCR	1	IGH;IGL	IGHV3-11;IGLV1-40	IGHD3-10	IGHJ4;IGLJ1	IGHA1;IGLC1	333	1	0,3
15_IGHV5-10-1_IGHJ4	15	5,9	t1	CSF	BCR	2	IGH;IGL	IGHV5-10-1;IGLV1-44	IGHD2-15	IGHJ4;IGLJ2	IGHG1;IGLC2	1964	2	0,1
15_IGHV5-10-1_IGHJ4	15	5,9	t2	CSF	BCR	2	IGH;IGL	IGHV5-10-1;IGLV1-44	IGHD2-15	IGHJ4;IGLJ2	IGHG1;IGLC2	333	2	0,6
158_IGHV1-18_IGHJ4	158	5,9	t1	CSF	BCR	1	IGH;IGL	IGHV1-18;IGLV2-23	IGHD3-3	IGHJ4;IGLJ2	IGHG1;IGLC2	1964	1	0,1
158_IGHV1-18_IGHJ4	158	5,9	t2	CSF	BCR	1	IGH;IGL	IGHV1-18;IGLV2-23	IGHD3-3	IGHJ4;IGLJ2	IGHG1;IGLC2	333	1	0,3
170_IGHV1-8_IGHJ5	170	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-8;IGKV1D-17	IGHD4-23	IGHJ5;IGKJ4	IGHG1;IGKC	1964	2	0,1
170_IGHV1-8_IGHJ5	170	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-8;IGKV1D-17	IGHD4-23	IGHJ5;IGKJ4	IGHG1;IGKC	333	2	0,6
170_IGHV1-8_IGHJ5	170	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-8;IGKV1D-17	IGHD4-23	IGHJ5;IGKJ4	IGHG1;IGKC	333	2	0,6

176_IGHV3-33_IGHJ5	176	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV3-33;IGKV1D-17	IGHD6-13	IGHJ5;IGKJ1	IGHG1;IGKC	1964	1	0,1
176_IGHV3-33_IGHJ5	176	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-33;IGKV1D-17	IGHD6-13	IGHJ5;IGKJ1	IGHG1;IGKC	333	1	0,3
18_IGHV1-8_IGHJ4	18	5,9	t1	CSF	BCR	2	IGH;IGK	IGHV1-8;IGKV3-15	IGHD3-10	IGHJ4;IGKJ1	IGHG1;IGKC	1964	2	0,1
18_IGHV1-8_IGHJ4	18	5,9	t2	CSF	BCR	2	IGH;IGK	IGHV1-8;IGKV3-15	IGHD3-10	IGHJ4;IGKJ1	IGHG1;IGKC	333	2	0,6
182_IGHV3-48_IGHJ4	182	5,9	t1	CSF	BCR	1	IGH;IGL	IGHV3-48;IGLV4-69	IGHD5-18	IGHJ4;IGLJ2	IGHM;IGLC2	1964	1	0,1
182_IGHV3-48_IGHJ4	182	5,9	t2	CSF	BCR	1	IGH;IGL	IGHV3-48;IGLV4-69	IGHD5-18	IGHJ4;IGLJ2	IGHG1;IGLC2	333	1	0,3
183_IGHV3-30_IGHJ4	183	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV3-30;IGKV1-9	IGHD3-10	IGHJ4;IGKJ3	IGHG1;IGKC	1964	1	0,1
183_IGHV3-30_IGHJ4	183	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-30;IGKV1-9	IGHD3-10	IGHJ4;IGKJ3	IGHG1;IGKC	333	1	0,3
195_IGHV3-23_IGHJ4	195	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV3-20	IGHD6-19	IGHJ4;IGKJ3	IGKC;None	1964	1	0,1
195_IGHV3-23_IGHJ4	195	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV3-20	IGHD6-19	IGHJ4;IGKJ3	IGHG2;IGKC	333	1	0,3
198_IGHV3-23_IGHJ4	198	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV4-1	IGHD3-3	IGHJ4;IGKJ2	IGHG1;IGKC	1964	2	0,1
198_IGHV3-23_IGHJ4	198	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV4-1	IGHD3-3	IGHJ4;IGKJ2	IGHG1;IGKC	1964	2	0,1
198_IGHV3-23_IGHJ4	198	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV4-1	IGHD3-3	IGHJ4;IGKJ2	IGHG1;IGKC	333	2	0,6
198_IGHV3-23_IGHJ4	198	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV4-1	IGHD3-3	IGHJ4;IGKJ2	IGHG1;IGKC	333	2	0,6
199_IGHV1-46_IGHJ5	199	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-46;IGKV3-15	IGHD2-21	IGHJ5;IGKJ2	IGHG1;IGKC	1964	1	0,1
199_IGHV1-46_IGHJ5	199	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-46;IGKV3-15	IGHD2-21	IGHJ5;IGKJ2	IGHG1;IGKC	333	1	0,3
201_IGHV4-59_IGHJ5	201	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV4-59;IGKV4-1	IGHD6-19	IGHJ5;IGKJ3	IGKC;None	1964	1	0,1
201_IGHV4-59_IGHJ5	201	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV4-59;IGKV4-1	IGHD6-19	IGHJ5;IGKJ3	IGHG1;IGKC	333	1	0,3
202_IGHV1-18_IGHJ4	202	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-18;IGKV1-16	IGHD3-10	IGHJ4;IGKJ2	IGHG1;IGKC	1964	1	0,1
202_IGHV1-18_IGHJ4	202	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-18;IGKV1-16	IGHD3-10	IGHJ4;IGKJ2	IGHG1;IGKC	333	1	0,3
210_IGHV1-46_IGHJ6	210	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-46;IGKV1-5	IGHD5-24	IGHJ6;IGKJ1	IGHG1;IGKC	1964	1	0,1
210_IGHV1-46_IGHJ6	210	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-46;IGKV1-5	IGHD5-24	IGHJ6;IGKJ1	IGHG1;IGKC	333	1	0,3
212_IGHV1-2_IGHJ4	212	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV3-15	IGHD3-10	IGHJ4;IGKJ1	IGHG1;IGKC	1964	1	0,1
212_IGHV1-2_IGHJ4	212	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV3-15	IGHD3-10	IGHJ4;IGKJ1	IGHG1;IGKC	333	1	0,3
212_IGHV1-8_IGHJ1	212	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-8;IGKV3-15	IGHD3-10	IGHJ1;IGKJ1	IGHG1;IGKC	1964	1	0,1
212_IGHV1-8_IGHJ1	212	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-8;IGKV3-15	IGHD1-1	IGHJ1;IGKJ1	IGHG1;IGKC	333	1	0,3
214_IGHV4-4_IGHJ1	214	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV4-4;IGKV3-15	IGHD4-11	IGHJ1;IGKJ1	IGHG1;IGKC	1964	1	0,1
214_IGHV4-4_IGHJ1	214	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV4-4;IGKV3-15	IGHD4-11	IGHJ1;IGKJ1	IGHG1;IGKC	333	1	0,3
218_IGHV4-39_IGHJ4	218	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV4-39;IGKV3-20	IGHD3-10	IGHJ4;IGKJ4	IGHA1;IGKC	1964	1	0,1
218_IGHV4-39_IGHJ4	218	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV4-39;IGKV3-20	IGHD3-10	IGHJ4;IGKJ4	IGHA1;IGKC	333	1	0,3
221_IGHV3-33_IGHJ4	221	5,9	t1	CSF	BCR	1	IGH;IGL	IGHV3-33;IGLV1-40	IGHD3-3	IGHJ4;IGLJ2	IGHG1;IGLC2	1964	1	0,1
221_IGHV3-33_IGHJ4	221	5,9	t2	CSF	BCR	1	IGH;IGL	IGHV3-33;IGLV1-40	IGHD3-3	IGHJ4;IGLJ2	IGHG1;IGLC2	333	1	0,3
240_IGHV4-39_IGHJ5	240	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV4-39;IGKV3-20	IGHD2-21	IGHJ5;IGKJ4	IGHG1;IGKC	1964	1	0,1
240_IGHV4-39_IGHJ5	240	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV4-39;IGKV3-20	IGHD2-21	IGHJ5;IGKJ4	IGHG1;IGKC	333	1	0,3
241_IGHV3-7_IGHJ4	241	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV3-7;IGKV4-1	IGHD6-6	IGHJ4;IGKJ2	IGHA1;None	1964	1	0,1
241_IGHV3-7_IGHJ4	241	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-7;IGKV4-1	IGHD6-13	IGHJ4;IGKJ2	IGHA1;IGKC	333	1	0,3
244_IGHV4-34_IGHJ6	244	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV4-34;IGKV2-28	IGHD6-13	IGHJ6;IGKJ2	IGHG1;IGKC	1964	1	0,1
244_IGHV4-34_IGHJ6	244	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV4-34;IGKV2-28	IGHD6-13	IGHJ6;IGKJ2	IGHG1;IGKC	333	1	0,3
59_IGHV1-46_IGHJ6	59	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-46;IGKV2-28	IGHD6-19	IGHJ6;IGKJ3	IGHG1;IGKC	1964	1	0,1
59_IGHV1-46_IGHJ6	59	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-46;IGKV2-28	IGHD6-19	IGHJ6;IGKJ3	IGHG1;IGKC	333	1	0,3
64_IGHV4-61_IGHJ3	64	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV4-61;IGKV3-20	IGHD6-19	IGHJ3;IGKJ3	IGHG1;IGKC	1964	1	0,1
64_IGHV4-61_IGHJ3	64	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV4-61;IGKV3-20	IGHD6-19	IGHJ3;IGKJ3	IGHG1;IGKC	333	1	0,3
66_IGHV4-59_IGHJ5	66	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV4-59;IGKV4-1	IGHD6-19	IGHJ5;IGKJ3	IGHA1;IGKC	1964	1	0,1
66_IGHV4-59_IGHJ5	66	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV4-59;IGKV4-1	IGHD6-19	IGHJ5;IGKJ3	IGHG1;IGKC	333	1	0,3
67_IGHV1-3_IGHJ3	67	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-3;IGKV1-39	IGHD2-15	IGHJ3;IGKJ4	IGHG1;IGKC	1964	1	0,1
67_IGHV1-3_IGHJ3	67	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-3;IGKV1-39	IGHD2-15	IGHJ3;IGKJ4	IGHG1;IGKC	333	1	0,3
69_IGHV5-10-1_IGHJ6	69	5,9	t1	CSF	BCR	1	IGH;IGK	IGHV5-10-1;IGKV1D-39	IGHD2-15	IGHJ6;IGKJ1	IGHG1;IGKC	1964	1	0,1
69_IGHV5-10-1_IGHJ6	69	5,9	t2	CSF	BCR	1	IGH;IGK	IGHV5-10-1;IGKV1D-39	IGHD2-15	IGHJ6;IGKJ1	IGHA1;IGKC	333	1	0,3
92_IGHV1-2_IGHJ4	92	5,9	t1	CSF	BCR	1	IGH;IGL	IGHV1-2;IGLV7-46	IGHD3-10	IGHJ4;IGLJ2	IGHG1;IGLC2	1964	2	0,1
92_IGHV1-2_IGHJ4	92	5,9	t1	CSF	BCR	1	IGH;IGL	IGHV1-2;IGLV7-46	IGHD3-10	IGHJ4;IGLJ2	IGHG1;IGLC2	1964	2	0,1
92_IGHV1-2_IGHJ4	92	5,9	t2	CSF	BCR	1	IGH;IGL	IGHV1-2;IGLV7-46	IGHD3-10	IGHJ4;IGLJ2	IGLC2;None	333	2	0,6
92_IGHV1-2_IGHJ4	92	5,9	t2	CSF	BCR	1	IGH;IGL	IGHV1-2;IGLV7-46	IGHD3-10	IGHJ4;IGLJ2	IGHG1;IGLC2	333	2	0,6
25_IGHV3-23_IGHJ4	25	4,6	t1	CSF	BCR	2	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGKJ1	IGHG1;IGKC	1964	9	0,5
25_IGHV3-23_IGHJ4	25	4,6	t1	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGKJ1	IGHG1;IGKC	1964	9	0,5
25_IGHV3-23_IGHJ4	25	4,6	t1	CSF	BCR	2	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGKJ1	IGHG1;IGKC	1964	9	0,5
25_IGHV3-23_IGHJ4	25	4,6	t1	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGKJ1	IGHG1;IGKC	1964	9	0,5
25_IGHV3-23_IGHJ4	25	4,6	t1	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGKJ1	IGHG1;IGKC	1964	9	0,5
25_IGHV3-23_IGHJ4	25	4,6	t1	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGKJ1	IGHG1;IGKC	1964	9	0,5
25_IGHV3-23_IGHJ4	25	4,6	t2	CSF	BCR	2	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGKJ1	IGHG1;IGKC	333	7	2,1

25_IGHV3-23_IGHJ4	25	4,6	t2	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGK1	IGHG1;IGKC	333	7	2,1
25_IGHV3-23_IGHJ4	25	4,6	t2	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGK1	IGHG1;IGKC	333	7	2,1
25_IGHV3-23_IGHJ4	25	4,6	t2	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGK1	IGHG1;IGKC	333	7	2,1
25_IGHV3-23_IGHJ4	25	4,6	t2	CSF	BCR	2	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGK1	IGHG1;IGKC	333	7	2,1
22_IGHV3-11_IGHJ4	22	4,4	t1	CSF	BCR	1	IGH;IGL	IGHV3-11;IGLV1-51	IGHD6-19	IGHJ4;IGLJ3	IGHA1;IGLC2	1964	4	0,2
22_IGHV3-11_IGHJ4	22	4,4	t1	CSF	BCR	1	IGH;IGL	IGHV3-11;IGLV1-51	IGHD6-19	IGHJ4;IGLJ3	IGHA1;IGLC2	1964	4	0,2
22_IGHV3-11_IGHJ4	22	4,4	t1	CSF	BCR	1	IGH;IGL	IGHV3-11;IGLV1-51	IGHD6-19	IGHJ4;IGLJ3	IGHA1;IGLC2	1964	4	0,2
22_IGHV3-11_IGHJ4	22	4,4	t1	CSF	BCR	1	IGH;IGL	IGHV3-11;IGLV1-51	IGHD6-19	IGHJ4;IGLJ3	IGHA1;IGLC2	1964	4	0,2
22_IGHV3-11_IGHJ4	22	4,4	t2	CSF	BCR	1	IGH;IGL	IGHV3-11;IGLV1-51	IGHD6-19	IGHJ4;IGLJ3	IGHA1;IGLC2	333	3	0,9
22_IGHV3-11_IGHJ4	22	4,4	t2	CSF	BCR	2	IGH;IGL	IGHV3-11;IGLV1-51	IGHD6-19	IGHJ4;IGLJ3	IGHA1;IGLC2	333	3	0,9
24_IGHV1-24_IGHJ2	24	4,4	t1	CSF	BCR	1	IGH;IGL	IGHV1-24;IGLV4-69	IGHD3-22	IGHJ2;IGLJ2	IGHG1;IGLC2	1964	4	0,2
24_IGHV1-24_IGHJ2	24	4,4	t1	CSF	BCR	2	IGH;IGL	IGHV1-24;IGLV4-69	IGHD3-22	IGHJ2;IGLJ2	IGHG1;IGLC2	1964	4	0,2
24_IGHV1-24_IGHJ2	24	4,4	t2	CSF	BCR	1	IGH;IGL	IGHV1-24;IGLV4-69	IGHD3-22	IGHJ2;IGLJ2	IGHG1;IGLC2	333	3	0,9
24_IGHV1-24_IGHJ2	24	4,4	t2	CSF	BCR	2	IGH;IGL	IGHV1-24;IGLV4-69	IGHD3-22	IGHJ2;IGLJ2	IGHG1;IGLC2	333	3	0,9
63_IGHV2-5_IGHJ5	63	3,9	t1	CSF	BCR	1	IGH;IGK	IGHV2-5;IGKV1-39	IGHD3-10	IGHJ5;IGK4	IGHG1;IGKC	1964	3	0,2
63_IGHV2-5_IGHJ5	63	3,9	t1	CSF	BCR	1	IGH;IGK	IGHV2-5;IGKV1-39	IGHD3-10	IGHJ5;IGK2	IGHG1;IGKC	1964	3	0,2
63_IGHV2-5_IGHJ5	63	3,9	t1	CSF	BCR	1	IGH;IGK	IGHV2-5;IGKV1-39	IGHD3-10	IGHJ5;IGK2	IGHG1;IGKC	1964	3	0,2
63_IGHV2-5_IGHJ5	63	3,9	t2	CSF	BCR	1	IGH;IGK	IGHV2-5;IGKV1-39	IGHD3-10	IGHJ5;IGK2	IGHG1;IGKC	333	2	0,6
63_IGHV2-5_IGHJ5	63	3,9	t2	CSF	BCR	1	IGH;IGK	IGHV2-5;IGKV1-39	IGHD3-10	IGHJ5;IGK2	IGHG1;IGKC	333	2	0,6
141_IGHV3-21_IGHJ3	141	3,5	t1	CSF	BCR	1	IGH;IGK	IGHV3-21;IGKV1D-39	IGHD2-2	IGHJ3;IGK1	IGHG1;IGKC	1964	5	0,3
141_IGHV3-21_IGHJ3	141	3,5	t1	CSF	BCR	2	IGH;IGK	IGHV3-21;IGKV1D-39	IGHD2-2	IGHJ3;IGK1	IGHG1;IGKC	1964	5	0,3
141_IGHV3-21_IGHJ3	141	3,5	t1	CSF	BCR	1	IGH;IGK	IGHV3-21;IGKV1D-39	IGHD2-2	IGHJ3;IGK1	IGHG1;IGKC	1964	5	0,3
141_IGHV3-21_IGHJ3	141	3,5	t1	CSF	BCR	1	IGH;IGK	IGHV3-21;IGKV1D-39	IGHD2-2	IGHJ3;IGK1	IGHG1;IGKC	1964	5	0,3
141_IGHV3-21_IGHJ3	141	3,5	t2	CSF	BCR	1	IGH;IGK	IGHV3-21;IGKV1D-39	IGHD2-2	IGHJ3;IGK1	IGHG1;IGKC	333	3	0,9
141_IGHV3-21_IGHJ3	141	3,5	t2	CSF	BCR	1	IGH;IGK	IGHV3-21;IGKV1D-39	IGHD2-2	IGHJ3;IGK1	IGHG1;IGKC	333	3	0,9
141_IGHV3-21_IGHJ3	141	3,5	t2	CSF	BCR	1	IGH;IGK	IGHV3-21;IGKV1D-39	IGHD2-2	IGHJ3;IGK1	IGHG1;IGKC	333	3	0,9
102_IGHV3-23_IGHJ4	102	2,9	t1	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD2-8	IGHJ4;IGK1	IGHG1;IGKC	1964	2	0,1
102_IGHV3-23_IGHJ4	102	2,9	t1	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGK1	IGHG1;IGKC	1964	2	0,1
102_IGHV3-23_IGHJ4	102	2,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD6-13	IGHJ4;IGK1	IGHG1;IGKC	333	1	0,3
108_IGHV1-8_IGHJ4	108	2,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-8;IGKV3-15	IGHD3-10	IGHJ4;IGK1	IGHG1;IGKC	1964	2	0,1
108_IGHV1-8_IGHJ4	108	2,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-8;IGKV3-15	IGHD3-10	IGHJ4;IGK1	IGHG1;IGKC	1964	2	0,1
108_IGHV1-8_IGHJ4	108	2,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-8;IGKV3-15	IGHD3-10	IGHJ4;IGK1	IGHG1;IGKC	333	1	0,3
150_IGHV1-69D_IGHJ3	150	2,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-69D;IGKV3-20	IGHD6-19	IGHJ3;IGK3	IGHG1;IGKC	1964	2	0,1
150_IGHV1-69D_IGHJ3	150	2,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-69D;IGKV3-20	IGHD6-19	IGHJ3;IGK3	IGHG1;IGKC	1964	2	0,1
150_IGHV1-69D_IGHJ3	150	2,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-69D;IGKV3-20	IGHD6-19	IGHJ3;IGK3	IGHG1;IGKC	333	1	0,3
175_IGHV3-30_IGHJ4	175	2,9	t1	CSF	BCR	2	IGH;IGK	IGHV3-30;IGKV6-21	IGHD3-10	IGHJ4;IGK4	IGHG4;IGKC	1964	2	0,1
175_IGHV3-30_IGHJ4	175	2,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-30;IGKV6-21	IGHD3-10	IGHJ4;IGK4	IGHG4;IGKC	333	1	0,3
188_IGHV1-69_IGHJ5	188	2,9	t1	CSF	BCR	1	IGH;IGL	IGHV1-69;IGLV2-11	IGHD6-6	IGHJ5;IGLJ2	IGHG1;IGLC2	1964	2	0,1
188_IGHV1-69_IGHJ5	188	2,9	t1	CSF	BCR	1	IGH;IGL	IGHV1-69;IGLV2-11	IGHD6-6	IGHJ5;IGLJ2	IGHG1;IGLC2	1964	2	0,1
188_IGHV1-69_IGHJ5	188	2,9	t2	CSF	BCR	1	IGH;IGL	IGHV1-69;IGLV2-11	IGHD6-6	IGHJ5;IGLJ2	IGHG1;IGLC2	333	1	0,3
228_IGHV3-21_IGHJ1	228	2,9	t1	CSF	BCR	1	IGH;IGL	IGHV3-21;IGLV6-57	IGHD6-13	IGHJ1;IGLJ2	IGHG1;IGLC2	1964	2	0,1
228_IGHV3-21_IGHJ1	228	2,9	t1	CSF	BCR	1	IGH;IGL	IGHV3-21;IGLV6-57	IGHD6-13	IGHJ1;IGLJ2	IGHG1;IGLC2	1964	2	0,1
228_IGHV3-21_IGHJ1	228	2,9	t2	CSF	BCR	1	IGH;IGL	IGHV3-21;IGLV6-57	IGHD6-13	IGHJ1;IGLJ2	IGHG1;IGLC2	333	1	0,3
233_IGHV3-74_IGHJ6	233	2,9	t1	CSF	BCR	2	IGH;IGL	IGHV3-74;IGLV3-25	IGHD2-2	IGHJ6;IGLJ3	IGHG1;IGLC2	1964	2	0,1
233_IGHV3-74_IGHJ6	233	2,9	t2	CSF	BCR	1	IGH;IGL	IGHV3-74;IGLV3-25	IGHD2-2	IGHJ6;IGLJ3	IGHG1;IGLC2	333	1	0,3
245_IGHV1-69D_IGHJ4	245	2,9	t1	CSF	BCR	2	IGH;IGK	IGHV1-69D;IGKV2-24	IGHD3-22	IGHJ4;IGK2	IGHA1;IGKC	1964	2	0,1
245_IGHV1-69D_IGHJ4	245	2,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-69D;IGKV2-24	IGHD3-22	IGHJ4;IGK2	IGHA1;IGKC	333	1	0,3
35_IGHV3-23_IGHJ4	35	2,9	t1	CSF	BCR	2	IGH;IGK	IGHV3-23;IGKV1-33	IGHD6-19	IGHJ4;IGK4	IGHG1;IGKC	1964	2	0,1
35_IGHV3-23_IGHJ4	35	2,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-33	IGHD4-23	IGHJ4;IGK4	IGHG1;IGKC	333	1	0,3
38_IGHV3-73_IGHJ4	38	2,9	t1	CSF	BCR	1	IGH;IGL	IGHV3-73;IGLV1-47	IGHD2-15	IGHJ4;IGLJ3	IGHG1;IGLC2	1964	2	0,1
38_IGHV3-73_IGHJ4	38	2,9	t1	CSF	BCR	1	IGH;IGL	IGHV3-73;IGLV1-47	IGHD2-15	IGHJ4;IGLJ3	IGHG1;IGLC2	1964	2	0,1
38_IGHV3-73_IGHJ4	38	2,9	t2	CSF	BCR	1	IGH;IGL	IGHV3-73;IGLV1-47	IGHD2-15	IGHJ4;IGLJ3	IGHG1;IGLC2	1964	1	0,3
53_IGHV4-39_IGHJ4	53	2,9	t1	CSF	BCR	2	IGH;IGL	IGHV4-39;IGLV3-10	IGHD6-19	IGHJ4;IGLJ2	IGHG3;IGLC2	333	6	0,3
53_IGHV4-39_IGHJ4	53	2,9	t1	CSF	BCR	1	IGH;IGL	IGHV4-39;IGLV3-10	IGHD6-19	IGHJ4;IGLJ2	IGHG4;IGLC2	1964	6	0,3
53_IGHV4-39_IGHJ4	53	2,9	t1	CSF	BCR	1	IGH;IGL	IGHV4-39;IGLV3-10	IGHD6-19	IGHJ4;IGLJ2	IGHG1;IGLC2	1964	6	0,3
53_IGHV4-39_IGHJ4	53	2,9	t1	CSF	BCR	1	IGH;IGL	IGHV4-39;IGLV3-10	IGHD6-19	IGHJ4;IGLJ2	IGHG3;IGLC2	1964	6	0,3
53_IGHV4-39_IGHJ4	53	2,9	t1	CSF	BCR	1	IGH;IGL	IGHV4-39;IGLV3-10	IGHD6-19	IGHJ4;IGLJ2	IGHG4;IGLC2	1964	6	0,3
53_IGHV4-39_IGHJ4	53	2,9	t2	CSF	BCR	1	IGH;IGL	IGHV4-39;IGLV3-10	IGHD6-19	IGHJ4;IGLJ2	IGHG3;IGLC2	333	3	0,9
53_IGHV4-39_IGHJ4	53	2,9	t2	CSF	BCR	1	IGH;IGL	IGHV4-39;IGLV3-10	IGHD6-19	IGHJ4;IGLJ2	IGHG3;IGLC2	333	3	0,9

53_IGHV4-39_IGHJ4	53	2,9	t2	CSF	BCR	1	IGH;IGL	IGHV4-39;IGLV3-10	IGHD6-19	IGHJ4;IGLJ2	IGHG3;IGLC2	333	3	0,9
54_IGHV4-61_IGHJ4	54	2,9	t1	CSF	BCR	1	IGH;IGK	IGHV4-61;IGKV1D-17	IGHD5-18	IGHJ4;IGKJ1	IGHG1;IGKC	1964	2	0,1
54_IGHV4-61_IGHJ4	54	2,9	t1	CSF	BCR	1	IGH;IGK	IGHV4-61;IGKV1D-17	IGHD5-18	IGHJ4;IGKJ2	IGHG1;IGKC	1964	2	0,1
54_IGHV4-61_IGHJ4	54	2,9	t2	CSF	BCR	1	IGH;IGK	IGHV4-61;IGKV1D-17	IGHD5-18	IGHJ4;IGKJ1	IGHG1;IGKC	333	1	0,3
74_IGHV3-15_IGHJ3	74	2,9	t1	CSF	BCR	2	IGH;IGK	IGHV3-15;IGKV4-1	IGHD5-12	IGHJ3;IGKJ2	IGHG1;IGKC	1964	2	0,1
74_IGHV3-15_IGHJ3	74	2,9	t2	CSF	BCR	1	IGH;IGK	IGHV3-15;IGKV4-1	IGHD1-26	IGHJ3;IGKJ2	IGHG1;IGKC	333	1	0,3
80_IGHV1-2_IGHJ3	80	2,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV1D-39	IGHD1-20	IGHJ3;IGKJ2	IGHA1;IGKC	1964	2	0,1
80_IGHV1-2_IGHJ3	80	2,9	t1	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV1D-39	IGHD1-20	IGHJ3;IGKJ2	IGHG1;IGKC	1964	2	0,1
80_IGHV1-2_IGHJ3	80	2,9	t2	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV1D-39	IGHD1-20	IGHJ3;IGKJ2	IGHA1;IGKC	333	1	0,3
20_IGHV4-30-2_IGHJ5	20	2,4	t1	CSF	BCR	5	IGH;IGK	IGHV4-30-2;IGKV3-11	IGHD3-9	IGHJ5;IGKJ2	IGHG1;IGKC	1964	5	0,3
20_IGHV4-30-2_IGHJ5	20	2,4	t2	CSF	BCR	2	IGH;IGK	IGHV4-30-2;IGKV3-11	IGHD3-9	IGHJ5;IGKJ2	IGHG1;IGKC	333	2	0,6
94_IGHV3-23_IGHJ4	94	2,4	t1	CSF	BCR	3	IGH;IGK	IGHV3-23;IGKV1-5	IGHD1-16	IGHJ4;IGKJ1	IGHG1;IGKC	1964	5	0,3
94_IGHV3-23_IGHJ4	94	2,4	t1	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD1-26	IGHJ4;IGKJ1	IGHG1;IGKC	1964	5	0,3
94_IGHV3-23_IGHJ4	94	2,4	t1	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD1-26	IGHJ4;IGKJ1	IGKC;None	1964	5	0,3
94_IGHV3-23_IGHJ4	94	2,4	t2	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD3-16	IGHJ4;IGKJ1	IGHG1;IGKC	333	2	0,6
94_IGHV3-23_IGHJ4	94	2,4	t2	CSF	BCR	1	IGH;IGK	IGHV3-23;IGKV1-5	IGHD1-26	IGHJ4;IGKJ1	IGHG1;IGKC	333	2	0,6
119_IGHV3-21_IGHJ4	119	2,0	t1	CSF	BCR	2	IGH;IGK	IGHV3-21;IGKV1D-17	IGHD3-22	IGHJ4;IGKJ3	IGHG4;IGKC	1964	3	0,2
119_IGHV3-21_IGHJ4	119	2,0	t1	CSF	BCR	1	IGH;IGK	IGHV3-21;IGKV1D-17	IGHD3-22	IGHJ4;IGKJ3	IGHG1;IGKC	1964	3	0,2
119_IGHV3-21_IGHJ4	119	2,0	t2	CSF	BCR	1	IGH;IGK	IGHV3-21;IGKV1D-17	IGHD3-22	IGHJ4;IGKJ3	IGHG4;IGKC	333	1	0,3
120_IGHV5-51_IGHJ4	120	2,0	t1	CSF	BCR	1	IGH;IGL	IGHV5-51;IGLV3-25	IGHD6-13	IGHJ4;IGLJ2	IGHG1;IGLC2	1964	3	0,2
120_IGHV5-51_IGHJ4	120	2,0	t1	CSF	BCR	1	IGH;IGL	IGHV5-51;IGLV3-25	IGHD6-13	IGHJ4;IGLJ2	IGHA1;IGLC2	1964	3	0,2
120_IGHV5-51_IGHJ4	120	2,0	t2	CSF	BCR	1	IGH;IGL	IGHV5-51;IGLV3-25	IGHD6-13	IGHJ4;IGLJ2	IGHG1;IGLC2	1964	3	0,2
120_IGHV5-51_IGHJ4	120	2,0	t2	CSF	BCR	1	IGH;IGL	IGHV5-51;IGLV3-25	IGHD6-13	IGHJ4;IGLJ2	IGHG1;IGLC2	333	1	0,3
164_IGHV3-74_IGHJ4	164	2,0	t1	CSF	BCR	2	IGH;IGK	IGHV3-74;IGKV2-30	IGHD3-10	IGHJ4;IGKJ4	IGHA1;IGKC	1964	3	0,2
164_IGHV3-74_IGHJ4	164	2,0	t1	CSF	BCR	1	IGH;IGK	IGHV3-74;IGKV2-30	IGHD5-12	IGHJ4;IGKJ4	IGHG1;IGKC	1964	3	0,2
164_IGHV3-74_IGHJ4	164	2,0	t2	CSF	BCR	1	IGH;IGK	IGHV3-74;IGKV2-30	IGHD3-10	IGHJ4;IGKJ4	IGHG1;IGKC	333	1	0,3
167_IGHV1-69_IGHJ4	167	2,0	t1	CSF	BCR	2	IGH;IGK	IGHV1-69;IGKV2-30	IGHD1-26	IGHJ4;IGKJ1	IGHG1;IGKC	1964	3	0,2
167_IGHV1-69_IGHJ4	167	2,0	t1	CSF	BCR	1	IGH;IGK	IGHV1-69;IGKV2-30	IGHD1-26	IGHJ4;IGKJ1	IGHG1;IGKC	1964	3	0,2
167_IGHV1-69_IGHJ4	167	2,0	t2	CSF	BCR	1	IGH;IGK	IGHV1-69;IGKV2-30	IGHD1-26	IGHJ4;IGKJ1	IGHG1;IGKC	333	1	0,3
60_IGHV4-59_IGHJ3	60	2,0	t1	CSF	BCR	1	IGH;IGK	IGHV4-59;IGKV2D-28	IGHD5-18	IGHJ3;IGKJ1	IGHG1;IGKC	1964	3	0,2
60_IGHV4-59_IGHJ3	60	2,0	t1	CSF	BCR	2	IGH;IGK	IGHV4-59;IGKV2-28	IGHD5-18	IGHJ3;IGKJ1	IGHG1;IGKC	1964	3	0,2
60_IGHV4-59_IGHJ3	60	2,0	t2	CSF	BCR	1	IGH;IGK	IGHV4-59;IGKV2-28	IGHD1-26	IGHJ3;IGKJ1	IGHG1;IGKC	333	1	0,3
61_IGHV1-24_IGHJ4	61	2,0	t1	CSF	BCR	2	IGH;IGK	IGHV1-24;IGKV2-30	IGHD3-9	IGHJ4;IGKJ4	IGHG1;IGKC	1964	3	0,2
61_IGHV1-24_IGHJ4	61	2,0	t1	CSF	BCR	1	IGH;IGK	IGHV1-24;IGKV2-30	IGHD3-9	IGHJ4;IGKJ4	IGHG1;IGKC	1964	3	0,2
61_IGHV1-24_IGHJ4	61	2,0	t2	CSF	BCR	1	IGH;IGK	IGHV1-24;IGKV2-30	IGHD3-9	IGHJ4;IGKJ4	IGHG1;IGKC	333	1	0,3
97_IGHV3-48_IGHJ4	97	2,0	t1	CSF	BCR	1	IGH;IGK	IGHV3-48;IGKV2-24	IGHD3-10	IGHJ4;IGKJ5	IGHG1;IGKC	1964	3	0,2
97_IGHV3-48_IGHJ4	97	2,0	t1	CSF	BCR	1	IGH;IGK	IGHV3-48;IGKV2-24	IGHD2-15	IGHJ4;IGKJ5	IGHG1;IGKC	1964	3	0,2
97_IGHV3-48_IGHJ4	97	2,0	t1	CSF	BCR	1	IGH;IGK	IGHV3-48;IGKV1-9	IGHD3-10	IGHJ4;IGKJ2	IGHG1;IGKC	1964	3	0,2
97_IGHV3-48_IGHJ4	97	2,0	t2	CSF	BCR	1	IGH;IGK	IGHV3-48;IGKV2-24	IGHD3-3	IGHJ4;IGKJ5	IGHG1;IGKC	333	1	0,3
107_IGHV4-61_IGHJ4	107	1,5	t1	CSF	BCR	1	IGH;IGK	IGHV4-61;IGKV3-15	IGHD5-24	IGHJ4;IGKJ2	IGHG1;IGKC	1964	4	0,2
107_IGHV4-61_IGHJ4	107	1,5	t1	CSF	BCR	2	IGH;IGK	IGHV4-61;IGKV3-15	IGHD5-24	IGHJ4;IGKJ2	IGHG1;IGKC	1964	4	0,2
107_IGHV4-61_IGHJ4	107	1,5	t1	CSF	BCR	1	IGH;IGK	IGHV4-61;IGKV3-15	IGHD5-24	IGHJ4;IGKJ2	IGKC;None	1964	4	0,2
107_IGHV4-61_IGHJ4	107	1,5	t2	CSF	BCR	1	IGH;IGK	IGHV4-61;IGKV3D-15	IGHD5-24	IGHJ4;IGKJ2	IGHG1;IGKC	333	1	0,3
123_IGHV3-33_IGHJ5	123	1,5	t1	CSF	BCR	4	IGH;IGL	IGHV3-33;IGLV1-40	IGHD4-23	IGHJ5;IGLJ3	IGHA1;IGLC2	1964	4	0,2
123_IGHV3-33_IGHJ5	123	1,5	t2	CSF	BCR	1	IGH;IGL	IGHV3-33;IGLV1-40	IGHD4-23	IGHJ5;IGLJ3	IGHA1;IGLC2	333	1	0,3
126_IGHV3-30_IGHJ4	126	1,5	t1	CSF	BCR	1	IGH;IGK	IGHV3-30;IGKV1-9	IGHD3-10	IGHJ4;IGKJ3	IGHM;IGKC	1964	4	0,2
126_IGHV3-30_IGHJ4	126	1,5	t1	CSF	BCR	1	IGH;IGK	IGHV3-30;IGKV1-9	IGHD3-10	IGHJ4;IGKJ3	IGHG1;IGKC	1964	4	0,2
126_IGHV3-30_IGHJ4	126	1,5	t1	CSF	BCR	2	IGH;IGK	IGHV3-30;IGKV1-9	IGHD3-10	IGHJ4;IGKJ3	IGHG1;IGKC	1964	4	0,2
126_IGHV3-30_IGHJ4	126	1,5	t2	CSF	BCR	1	IGH;IGK	IGHV3-30;IGKV1-9	IGHD3-10	IGHJ4;IGKJ3	IGHG1;IGKC	333	1	0,3
217_IGHV1-2_IGHJ6	217	1,5	t1	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV1D-39	IGHD3-10	IGHJ6;IGKJ1	IGHM;IGKC	1964	4	0,2
217_IGHV1-2_IGHJ6	217	1,5	t1	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV1D-39	IGHD3-10	IGHJ6;IGKJ1	IGHM;IGKC	1964	4	0,2
217_IGHV1-2_IGHJ6	217	1,5	t1	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV1D-39	IGHD3-10	IGHJ6;IGKJ1	IGHG1;IGKC	1964	4	0,2
217_IGHV1-2_IGHJ6	217	1,5	t1	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV1D-39	IGHD3-10	IGHJ6;IGKJ1	IGHM;IGKC	1964	4	0,2
217_IGHV1-2_IGHJ6	217	1,5	t2	CSF	BCR	1	IGH;IGK	IGHV1-2;IGKV1D-39	IGHD3-10	IGHJ6;IGKJ1	IGHG3;IGKC	333	1	0,3
125_IGHV4-34_IGHJ4	125	1,2	t1	CSF	BCR	1	IGH;IGK	IGHV4-34;IGKV4-1	IGHD3-10	IGHJ4;IGKJ5	IGHA1;IGKC	1964	5	0,3
125_IGHV4-34_IGHJ4	125	1,2	t1	CSF	BCR	1	IGH;IGK	IGHV4-34;IGKV4-1	IGHD3-10	IGHJ4;IGKJ5	IGHG1;IGKC	1964	5	0,3
125_IGHV4-34_IGHJ4	125	1,2	t1	CSF	BCR	1	IGH;IGK	IGHV4-34;IGKV4-1	IGHD3-10	IGHJ4;IGKJ5	IGHG1;IGKC	1964	5	0,3
125_IGHV4-34_IGHJ4	125	1,2	t1	CSF	BCR	1	IGH;IGK	IGHV4-34;IGKV4-1	IGHD3-10	IGHJ4;IGKJ5	IGHG1;IGKC	1964	5	0,3
125_IGHV4-34_IGHJ4	125	1,2	t2	CSF	BCR	1	IGH;IGK	IGHV4-34;IGKV4-1	IGHD3-10	IGHJ4;IGKJ5	IGHG1;IGKC	333	1	0,3

Full V(D)J sequence of expanded clones

clone	nucleotide sequence
168_I_GHV1-18_I_GHJ4	ATCACATAAACACACATCCCTCCTCTAAAGAAGCCCCGGGAGCACAGCTCATACCATTGACTGGACCTGGAGGATCCTCTTTGGTGGCAGCAGCTACAGGTGTCAGTCCCAGGTGCAGCTGGTGAGTCTGGGGCTGAGTCAAGAAGCCTGGGTCTTCGGTGAAAG GTCTCCTGCACGGCTTCTGGAGGCACTTTCAGCAGTAATGCTTTCACCTGGGTGGCAGCGACCCCTGGCAGGGCTTGGAGTGGCTGGGAGGCTTATCCCTATTTTGGGACATCAAACACAGCACAGAAGTTCAGGGGAGAAATCACGATTAAACGGACGAGTCCACGA GTACAGTCTACATGAACTGAGTAGCTGAGAACTGACGACACGGCCGTGTACTTCTGTGGCAGCGTGATAAAGAAAAGTTCCCTCTATGCTTACTATGTACTCCTGGGGCCAGGGAACCTGGTACCCTCTCGTACGTTCCACCAAGGGCCCATCCGTCTTCCCTCT GGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCTGGCTGGTCTGCTCAAGGACTACTTCCCCAACCCTGGACGGTGTCTGTGGAAGTCAAGCGCCCTGACACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCCAGGA
168_I_GHV1-18_I_GHJ4	ATCACATAAACACACATCCCTCCTCTAAAGAAGCCCCGGGAGCACAGCTCATACCATTGACTGGACCTGGAGGATCCTCTTTGGTGGCAGCAGCTACAGGTGTCAGTCCCAGGTGCAGCTGGTGAGTCTGGGGCTGAGTCAAGAAGCCTGGGTCTTCGGTGAAAG GTCTCCTGCACGGCTTCTGGAGGCACTTTCAGCAGTAATGCTTTCACCTGGGTGGCAGCGACCCCTGGCAGGGCTTGGAGTGGCTGGGAGGCTTATCCCTATTTTGGGACTTCAAACACAGCACAGAAGTTCAGGGGAGAAATCACGATTAAACGGACGAGTCCACGC GTACAGTCTACATGAACTGAGTAGCTGAGAACTGACGACACGGCCGTGTACTTCTGTGGCAGCGTGATAAAGAAAAGTTCCCTCTATGCTTACTATGTACTCCTGGGGCCAGGGAACCTGGTACCCTCTCGTACGTTCCACCAAGGGCCCATCCGTCTTCCCTCT GGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCTGGCTGGTCTGCTCAAGGACTACTTCCCCAACCCTGGACGGTGTCTGTGGAAGTCAAGCGCCCTGACACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCCAGGA
168_I_GHV1-18_I_GHJ4	ATCACATAAACACACATCCCTCCTCTAAAGAAGCCCCGGGAGCACAGCTCATACCATTGACTGGACCTGGAGGATCCTCTTTGGTGGTGGCAGCAGCTACAGGTGTCAGTCCCAGGTGCAGCTGGTGAGTCTGGGGCTGAGTCAAGAAGCCTGGGTCTTCGGTGAAAG GTCTCCTGCACGGCTTCTGGAGGCACTTTCAGCAGTAATGCTTTCACCTGGGTGGCAGCGACCCCTGGCAGGGCTTGGAGTGGCTGGGAGGCTTATCCCTATTTTGGGACATCAAACACAGCACAGAAGTTCAGGGGAGAAATCACGATTAAACGGACGAGTCCACGA GTACAGTCTACATGAACTGAGTAGCTGAGAACTGACGACACGGCCGTGTACTTCTGTGGCAGCGTGATAAAGAAAAGTTCCCTCTATGCTTACTATGTACTCCTGGGGCCAGGGAACCTGGTACCCTCTCGTACGTTCCACCAAGGGCCCATCCGTCTTCCCTCT GGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCTGGCTGGTCTGCTCAAGGACTACTTCCCCAACCCTGGACGGTGTCTGTGGAAGTCAAGCGCCCTGACACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCCAGGA
191_I_GHV1-2_I_GHJ2	GAGCATCACCCAGCAACACATCTGTCTCTAGAGAATCCCCTGAGAGCTCCGTTCTCACCATTGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCCACAGGAGCCCACTCCAGGTGCAGCTGGTGACAGTCTGGGCTGAGGTGGGAAGCCTGGGGCTCAATG AAGGTCTCCTGCAAGGCTTCTGGAACCACTTCCGCCCTACTATATCAACTGGATTGCACAGGCCCTGGACAAGGGCTTGGAGTGGATGGATGATCAATGCTGTCTCTGGCAGACAACTATGCCAGAAATTCAGGGCCGGTACCATGACCAGGGACACGTCCCTC AAAACAGCCGACATGAGCTGAGTAGCTGAAATATGACGACACGGCCGTGTATTATTGTGCGAAGACGGGGATCCCGCTCAAGACTGGTACTTGGATCTTGGGGCCCTGGCAGCCTGGTCACTGTCTCCTCAGCTCCACCAAGGGCCCATCCGTCTTCCCTCTGGCGCC TGCTCCAGGAGCACCTCCGAGAGCACAGCGCCCTGGCTGGTCTGCTCAAGGACTACTTCCCCAACCCTGGACGGTGTCTGTGGAAGTCAAGCGCCCTGACACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCCAGGA
191_I_GHV1-2_I_GHJ2	GGGAGCATCACCCAGCAACACATCTGTCTCTAGAGAATCCCCTGAGAGCTCCGTTCTCACCATTGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCCACAGGAGCCCACTCCAGGTGCAGCTGGTGACAGTCTGGGCTGAGGTGGGAAGCCTGGGGCTCA GGGAAGGTCTCCTGCAAGGCTTCTGGAGGCACTCCGGCGCCTATTATATCAACTGGGTTGCGACAGGCCCTGGACAAGGGCTTGGAGTGGATGGATGGATCAATGCTGTCTCTGGCAGACAACTATGCCAGAAATTCAGGGCCGGTACCATGACCAGGGGACGTCCCTC CCCGCAACACAGCCGACATGAGCTGAGTAGCTGAAATCTGACGACACGGCCGTGTATTATTGTGCGAAGACGGGGATCCCGCTCAAGACTGGTACTTGGATCTTGGGGCCCTGGCAGCCTGGTCACTGTCTCCTCAGCTCCACCAAGGGCCCATCCGTCTTCCCTCTGGCGCC CGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGCCCTGGCTGGTCTGCTCAAGGACTACTTCCCCAACCCTGGACGGTGTCTGTGGAAGTCAAGCGCCCTGACACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCCAGGA
191_I_GHV1-2_I_GHJ2	GGGAGCATCACCCAGCAACACATCTGTCTCTAGAGAATCCCCTGAGAGCTCCGTTCTCACCATTGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCCACAGGAGCCCACTCCAGGTGCAGCTGGTGACAGTCTGGGCTGAGGTGGGAAGCCTGGGGCTCAG TGAAGGTCTCCTGCAAGGCTTCTGGAAGCACCTTCAGCGCTACTATATCAACTGGGTTGCGACAGGCCCTGGACAAGGGCTTGGAGTGGATGGATGGATCAACCTGTACTGTGACACAACTATGCCAGAAATTCAGGGCCGGTACCATGACCAGGGGACGTCC CTCAACACAGCCGACATGAGCTGAGTAGCTGAAATCTGACGACATGCGCGTGTATTATTGTGCGAAGACGGGGATCCCGCTCAAGACTGGTACTTGGATCTTGGGGCCCTGGCAGCCTGGTCACTGTCTCCTCAGCTCCACCAAGGGCCCATCCGTCTTCCCTCTGGCGCC CCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGCCCTGGCTGGTCTGCTCAAGGACTACTTCCCCAACCCTGGACGGTGTCTGTGGAAGTCAAGCGCCCTGACACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCCAGGA
28_I_GHV3-43_I_GHJ3	GAAGTGTAATCACTCTGGGACACAGCCCACTCAGAGGCGTCCCTCCAGAACCCCTATATAGTAGGAGACATGAAATAGGGCCCTCCTCTGTGATGAAAACAGCCCACTCCAGGTGCAGCTGGGAGAGGAGCCCAAGCCCTGAGATTCCAGGTGTTCCATTCA GTGATCAGCACTGAAACACAGAGGACTCACCATTGGAGTTGGGACTGAGCTGGATTTTCCCTTTTAAAGGTGTCCAGTGTGAAGTGCAGCTGGTGGAGTCTGGAGTCTGGGGAGGCTTGGAGTCTGGGGAGGCTTGGAGTCTGGGGAGGCTTGGAGTCTGGGGAGGCTTGG TTGATGATTATGCCATGCACTGGGTCCGGCAAGCTCCAGGATGGCCCTGGAGTGGGTCTCAAGTATAAATGGTGAATGATAGATAGATGCGACTCTGTGAAGGGCCGATTCAACATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCAGATGAACAGTCTG AGACCTGAGGACACGGCCTGTATTACTGTGCAAGGAAAGGACCGAGAATACTACTTACTTGTCTGTATGCTGTGGGCAAGGGACAATGGTACCCTGTCTTCCAGCTCCACCAAGGGCCCATCCGTCTTCCCTCTGGCGCCCTCCTCAAGAGCACCTCTGGGGCACAGCG GCCCTGGGCTGCTGTCAAGGACTACTTCCCCAACCCTGGACGGTGTCTGTGGAAGTCAAGCGCCCTGACACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCCAGGA
28_I_GHV3-43_I_GHJ3	TGGGGGGGAGAGGAGCCCAAGCCCTGAGATTCCAGGTGTTCCATTCACTGATCAGCACTGAACACAGAGGACTCACCATTGGAGTTGGGACTGAGCTGGATTTCCCTTTTGGGCTTAAAGGTGTCCAGTGTGAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTGG GTACAGCTTGGCAGTCCCTGAGACTCTCCTGTGCAGCTCTGATTCACTTGTGATGATTATGCCATGCACTGGTCCGGCAAGCTCCAGGATGGGCTGGAGTGGTCTCAAGTATAAATGGTGAATGATAGACTATGCGACTCTGTGAAGGGCCGATTCA CCATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCAGATGAACAGTCTGAGACCTGAGGACACGGCCTTGTATTACTGTGCAAGGAAAGACCGAGAATACTACTTACTTGTCTGTATGCTGTGGGGCAAAGGGACAATGGTACCCTGTCTTCCAGCTCCACCAAGGGCCCA TGGTCTTCCCTCTGGCAGCTCCTCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGGTCTGCTCAAGGACTACTTCCCCAACCCTGGACGGTGTCTGTGGAAGTCAAGCGCCCTGACACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCCAGGA
4_I_GHV4-59_I_GHJ4	TGGGAATGCTTCTGAGAGTCTGGACCTCCTGTGAAAGAATATGAACATCTGTGTTTCTTCTTCTCCTGGTGGCAGCTCCAGATGTGCTGTCCAGGTGGCCCTGAGGAGTCCGGCCCAAGCTGGTGAAGCCTTCGAGACCTGTCCCTCACTTGCAGTGTCT TGGTACTCAATGAATACCTATTATTGGTACTGATCCGGCAGCCCCAGGGAAAGGGCTGGAGTGGATTGGGTATATCTATTACAGTGGAGCACCAACTACAACCCCTCCCTCAAGAGTCTGAGTCCATATCAGTAGACCTGTCCAAGAGCCACTCTCCCTGAACCTGACCT CTGTACCCTGCGGACACGGCCGTTTATTATTGTGCGAGAGACTGTGGTACGTCCCTGACCCTGGGGCCAGGGAACCTGGTACCCTGTCTCAGCTCCACCAAGGGCCCATCCGTCTTCCCTCTGGCAGCTCCTCAAGAGCACCTCTGGGGCACAGCGCCCTG GGCTGCTGTCAAGGACTACTTCCCCAACCCTGGACGGTGTCTGTGGAAGTCAAGCGCCCTGACACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCCAGGA

4_I_GHV4-59_I_GHJ4	AGGTTCCAGCTCACATGGGAATGCTTCTGAGAGTCTCTGACCTCTGTGAAAGAAATATGAACATCTGTGGTTCTTCTTCTCTCTGGTGGCAGCTCCAGATGTCTCTGCCAGGTGCGCCTGCGAGTGGGCCAGGACTGGTGAAGCCTTCGAGACCTGTCC TCACTGCACTGTCTCTGGTACTCAATGAATACCTATTGTTGACTGGGACTCGGCGAGCCCGGGAAGGGGCTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCACTACAACCCCTCCCTCAAGAGTCAGTCTCATATCAGTAGACCTGTCCAAGAGCCACTTC TCCCTGAACCTGACCTGTCTACCCGCTGCGGACACGGCCGTTTATTATTGTGCGAGAGGACTGTGTGACCTCCCTGACCACTGGGGCCAGGAAACCTGTCCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTGTGG GGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGTGAACTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCAGGA
4_I_GHV4-59_I_GHJ4	CTTCTGAGAGTCTCTGACCTCTGTGCAAGAAATATGAACATCTGTGGTTCTTCTTCTCTCTGGTGGCAGCTCCAGATGGTCTCTGCCAGGTGCGCCTGCGAGTGGGCCAGGACTGGTGAAGCCTTCGAGACCTGTCCCTCACTTGCAGTGTCTCTGGTACT CATGAATACCTATTATTGGTATTGGATTGCGGAGCCCCAGGGAAAGGACTGGAGTGGATTGGGTATATCTATTACAGTGGGACCACTACAACCCCTCCCTCAAGAGTCAGTCTCATATCAATAGACCTGTCCAAGAGCCACTTCTCCCTGAACCTGACCTGTACCCG TGCAGACACGGCCGTTTATTATTGTGCGAGAGGACTGTGTGACCTCCCTGACCACTGGGGCCCGGAAACCTGTCCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTGTGGGGGCACAGCGCCCTGGCTGCTGG TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCAGGA
46_I_GHV1-69D_I_GHJ6	ATCACATAACAACCACATCTCTCTTAAGAAAGCCCTGGGAGCACAGCTCATCACCATGGACTGGACTGGAGGTTCTCTTTTGGTGGCAGCAGCTACAGGTGTCCAGTCCCAGGTGCACCTGGTGCAGTCTGGGGCTGAGGTGAAGAAAGCTGGGTCTCGGTGAAG GTCTCTTGAAGGCTTCTGGTGGCACCTTCAAGCACTATGCCATCAGCTGGGTGCGACAGGCCGCTGGACAAGGCTTGGAGTGGATGGGAGGATCATCCCTATGTTTGAACAGCAAGGTATCACAGAAAGTCCAGGGCAGAAATCACGATTGACACGGACGCTCAAGCA ACACAGGTTACATGAGATGAGGAGCCTGAAATATGAGGACACGGCCATATATTACTGTGTGAGAGTGGCCAGGGCAGTCCCTCGAGGCGCTATGACGCTGTGGGGCCAGGGACCAAGGTCCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTGTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCAGGA
46_I_GHV1-69D_I_GHJ6	ATCACATAACAACCACATCTCTCTTAAGAAAGCCCTGGGAGCACAGCTCATCACCATGGACTGGACTGGAGGTTCTCTTTTGGTGGCAGCAGCTACAGGTGTCCAGTCCCAGGTGCACCTGGTGCAGTCTGGGGCTGAGGTGAAGAAAGCTGGGTCTCGGTGAAG GTCTCTTGAAGGCTTCTGGTGGCACCTTCAAGCACTATGCCATCAGCTGGGTGCGACAGGCCGCTGGACAAGGCTTGGAGTGGATGGGAGGATCATCCCTATGTTTGAACAGCAAGGTATCACAGAAAGTCCAGGGCAGAAATCACGATTGACACGGACGCTCAAGCA ACACAGGTTACATGAGATGAGGAGCCTGAAATATGAGGACACGGCCATATATTACTGTGTGAGAGTGGCCAGGGCAGTCCCTCGAGGCGCTATGACGCTGTGGGGCCAGGGACCAAGGTCCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTGTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCAGGA
46_I_GHV1-69D_I_GHJ6	ATCACATAACAACCACATCTCTCTTAAGAAAGCCCTGGGAGCACAGCTCATCACCATGGACTGGACTGGAGGTTCTCTTTTGGTGGCAGCAGCTACAGGTGTCCAGTCCCAGGTGCACCTGGTGCAGTCTGGGGCTGAGGTGAAGAAAGCTGGGTCTCGGTGAAG GTCTCTTGAAGGCTTCTGGTGGCACCTTCAAGCACTATGCCATCAGCTGGGTGCGACAGGCCGCTGGACAAGGCTTGGAGTGGATGGGAGGATCATCCCTATGTTTGAACAGCAAGGTATCACAGAAAGTCCAGGGCAGAAATCACGATTGACACGGACGCTCAAGCA ACACAGGTTACATGAGATGAGGAGCCTGAAATATGAGGACACGGCCATATATTACTGTGTGAGAGTGGCCAGGGCAGTCCCTCGAGGCGCTATGACGCTGTGGGGCCAGGGACCAAGGTCCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTGTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCAGGA
51_I_GHV1-2_I_GHJ5	GAGCATCACCCAGCAACACATCTGTCTCTAGAGAAATCCCCTGAGAGTCCGTTCTCACCATGGACTGGACTGGAGGATCTCTTCTTGGTGGCAGCAGCCAGAGCCAGTCCCAGGTGCAGTGGTGCAGTCTGGGGCTGAGGTGAAGAAAGCTGGGGCTCAGTA AAGGTCTCTGCAAGGCTCTGATACACCTTCAAGTGGCCAGTATATGACTGGTGGCAGAGTCCCTGGACAAGGCTTGGAGTGGATGGGGTGGATCAACCCCAAGAGTGGCGGCACACTCTTGCAGCAAGTTCAGGGCAGGCTCATCATGACCAGGGACACCTCCA TCACACCGCTCATGAGCTGCAAGTCTGAGATCTGACGACACGGCCGTTTACTGTGCGAGAGATCTAGGATCAATATGGTTCGGGAGAGTGTGGTCTTGGACCCCTGGGGCCAGGAAACCTGTCCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGT CTTCCCCCTGGCACCTCTCCAAGAGCACCTGTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCAGGA
51_I_GHV1-2_I_GHJ5	GGGAGCATCACCCAGCAACACATCTGTCTCTAGAGAAATCCCCTGAGAGTCCGTTCTCACCATGGACTGGACTGGAGGATCTCTTCTTGGTGGCAGCAGCCAGAGCCACTCCCAGGTGCAGTGGTGCAGTCTGGGGCTGAGGTGAAGAAAGCTGGGGCTCAGTA TGAAGGTCTCTGCAAGGCTCTGTGATACAGCTTCAAGGCTACTATATACACTGTTGCGACAGGCCCTGGACAAGGACTTCAAGTGGATGGGGTGGATCAACCCCAAGAGTGGCGGCACACTCTATGCAAAAGAACTTTCAGGGCAGGCTCATCATGACCAGGGACACCTCCA ATCAGCACAGTCTACATGATCTGAGCAGGCTGAGATCCGACGACACGGCCGTTTATTCTGTGCGAGAGATCTAGGATTAATTGGTTTGGGGAGAGAGTGTGGTCTTGGACCCCTGGGGCCAGGAAACCTGTCCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGG TCTTCCCCCTGGCACCTCTCCAAGAGCACCTGTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCAGGA
51_I_GHV1-2_I_GHJ5	GGGAGCATCACCCAGCAACACATCTGTCTCTAGAGAAATCCCCTGAGAGTCCGTTCTCACCATGGACTGGACTGGAGGATCTCTTCTTGGTGGCAGCAGCCAGAGCCACTCCCAGGTGCAGTGGTGCAGTCTGGGGCTGAGGTGAAGAAAGCTGGGGCTCA GTAAGGTCTCTGCAAGGCTCTGTGATACAGCTTCAAGGCTACTATATACACTGTTGCGACAGGCCCTGGACAAGGACTTCAAGTGGATGGGGTGGATCAACCCCAAGAGTGGCGGCACACTCTTGCAGCAAGTTCAGGGCAGGCTCATCATGACCAGGGACACCTCCA CCATCACACCGCTCATGAGCTGAGAGCCTGAGATCTGGCGACACGGCCGTTTATTCTGTGCGAGAGATCTAGGATTAATTGGTTTGGGGAGAGAGTGTGGTCTTGGACCCCTGGGGCCAGGAAACCTGTCCACCGTCTCTCAGCCTCCACCAAGGGCCCATC GGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTGTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCAGGA
14_I_GHV4-39_I_GHJ4	AACACGTTCAAGTGGACACCTGGATGCTTCTGAGAGTCAATGATCTCATGTGCAAGAAATGAAGCACCTGTGGTTATTCTCTCTGCTGGTGGCCTCCAGATGGTCTGCCAGCTGCAGTGGGAGTGGGCCAGGACTGGTGAAGCCTTCGAGACCTGTCC CTCTATGCACTGTCTCTGGTCCGTCAGCAGTAACTGTTTCTATTGGGGCTGGATCCGCGAGCCCCAGGGAAAGGAGTTCGAGTGGATTGGGAGTATATACTATACTGGAGGACTACTACAACCCCTCCCTCAGAGTGGAGTCCACATATCCGTTGACACCTCAAG AACAGTTCCTCAAGTTGAACCTGTGACCGCGCAGACACGGCTGTCTATTACTGTGTACACAAGTCTTGTACTGTTGATAGTTGCGGTCCACTGGGGCCAGGAAACCTGTCCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCC TCCAAGAGCACCTGTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCAGGA
14_I_GHV4-39_I_GHJ4	GGGATGCTTCTGAGAGTCAATGATCTCATGTGCAAGAAATGAAGCACCTGTGGTTATTCTCTCTGCTGGTGGCCTCCAGATGGTCTGTGCCAGCTGCAGTGGGAGTGGGCCAGGACTGGTGAAGCCTTCGAGACCTGTCCCTCTATGACTGTCT GGTGGCTCCGTCAGCAGTAACTGTTTCTATTGGGGCTGGATCCGCGAGCCCCAGGGAAAGGAGTTCGAGTGGATTGGGAGTATATACTATACTGGAGGACTACTACAACCCCTCCCTCAGAGTGGAGTCCACATATCCGTTGACACCTCAAG TTGAACCTGTGTACCGCGCAGACAGGCTGTCTATTACTGTGTACACAAGTCTTGTACTGTTGATAGTTGCGGTCCACTGGGGCCAGGAAACCTGTCCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTGTG GGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCAGGA

14_I_GHV4-39_I_GHJ4	TTTCTTATATGGGGATGCTTCTGAGAGTCTATGATCTCATGTGCAAGAAAAGAACTGCTGTTATTCTCTCTGCTGGTGGCGCTCCAGATGGTCTGCCCCAGCTGAGCTGAGTGGGGCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCCTCTATG CAGTGTCTGTGGTGGCTCCGTGAGCAGTAACTGTTCTATTGGGGTGGATCCGCGACCCAGGAAAGGAGTTGGAGTGGAGTATATCTATAGTGGAGGACCTACTACAACCCGTCCTCAGAGTGGAGTACCATATCCCTTGACACGTCCAAGAACGATT CTCCCTCAAGTTGAACTGTGTACCGCCGACACAGCGTGTCTTACTGTGTACACAGGCTCTTTGACTGTTGATAGTTGCCGTGCCACTGGGCCAGGAAACCTGTCTCAGCTCTCCTCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCACCTCTCAAGA GCACCTCTGGGGCACAGCGCCCTGGCTGCTGTCAAGACTACTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
6_I_GHV1-18_I_GHJ6	ACCCAAAAACACACCCCTCCTTGGGAGAAATCCCTAGATCACAGCTCCTCACCATGGAAGCTGGAGCATCTTTCTTGGTGGCAGCAGCAACAGGTGCCACTCCCAGGTTTCCAGTCTGGAGTGGAGTGAAGAACCTGGGGCTCAGTGAAGTCTCC TGCAAGGCTCTGGTTACACCTTTACAGTCAAGTATCAGCTGGGTGCGACAGGCCCTGGACAAGGACTTGAAGTGGATGGATCCGCACTTCCAATGGTGACACAATTTGACAGAAAGTTCAGAACAGTCTCCATGACACAGACACATCCAGAGCGCAGCTT TACATGAGCTGAGGAGCTGAGATCTGACGACAGCGCCGTATTACTGTGCGAGAGGGAAATAGATTACCTGGGAGATTACTACGGTATGACGTCTGGGCCAAGGACACAGGTCTGCTCTCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCAC CTCCTCAAGAGCACTCTGGGGCACAGCGCCCTGGGTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
6_I_GHV1-18_I_GHJ6	ACCCAAAAACACACCCCTCCTTGGGAGAAATCCCTAGATCACAGCTCCTCACCATGGAAGCTGGAGCATCTTTCTTGGTGGCAGCAGCAACAGGTGCCACTCCCAGGTTCAACTGGTGCAGTCTGGAGTGGAGTGAAGAACCTGGGGCTCAGTGAAGTCTCC GTACGGCTCTGGTTACACCTTTACCAGCCAGGTATTAGCTGGGTGCGACAGGCCCTGGACAAGGACTTGAAGTGGATGGATCCGCACTTCCAATGGTGACACAATTTGACAGAAAGTTCAGAACAGTCTCCATGACACAGACACATCCAGAGCGCAGCTT CATGGAGCTGAGGAGCTGAGATCTGACGACAGCGCCGTATTACTGTGCGAGAGAGGGAAATAGATTACCTGGGAGATTACTACGGTATGACGTCTGGGCCAAGGACACAGGTCTCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCACCC TCTCCAAGAGCACTCTGGGGCACAGCGCCCTGGGTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
6_I_GHV1-18_I_GHJ6	ACCCAAAAACACACCCCTCCTTGGGAGAAATCCCTAGATCACAGCTCCTCACCATGGAAGCTGGAGCATCTTTCTTGGTGGCAGCAGCAACAGGTGCCACTCCCAGGTTCAACTGGTGCAGTCTGGAGTGGAGTGAAGAACCTGGGGCTCAGTGAAGTCTCC GTACGGCTCTGGTTACACCTTTACCAGCCAGGTATTAGCTGGGTGCGACAGGCCCTGGACAAGGACTTGAAGTGGATGGATCCGCACTTCCAATGGTGACACAATTTGACAGAAAGTTCAGAACAGTCTCCATGACACAGACACATCCAGAGCGCAGCTT CATGGAGCTGAGGAGCTGAGATCTGACGACAGCGCCGTATTACTGTGCGAGAGAGGGAAATAGATTACCTGGGAGATTACTACGGTATGACGTCTGGGCCAAGGACACAGGTCTCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCACCC TCTCCAAGAGCACTCTGGGGCACAGCGCCCTGGGTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
8_I_GHV5-51_I_GHJ4	GCCAGCTGGGATCTCAGGCTTCAATTTCTGTCGCGACCATCATGGGTCAACCCCATCTCCCTCTCTGGTCTTCCAAGAGTCTGTGCGAGGTGCAGTGGTGCAGTCTGGAGCAGAGTGAAGAACCCGGGAGTCTGAAAGCTCTCTGTCAAGG TTCTGGATAACAATTTACCCTTACTGATCGGCTGGTGGCCAGATGCCGGGAAAGGCTGAGTGGTGGGATCATCTATCTGGTACTCTGATACCAGATTAGCCCGTCTTCCGAGGCCAGTCTCAGCATCTCAGCCGACAACCTCATCAGACCCCTACTGCA CTGGACCAGCTGAAGGCTCGACACCCCATGATTAAGTGTGCGATCTTTATTGGCGAGGGGCACTACTTGGCCAGGAAACCTGTGCACCGTCTCTCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCACCTCTCCAAGAGCACTCTGGGGCACAGC GGCCCTGGGCTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
8_I_GHV5-51_I_GHJ4	GCCAGCTGGGATCTCAGGCTTCAATTTCTGTCGCGACCATCATGGGTCAACCCCATCTCCCTCTCTGGTCTTCCAAGAGTCTGTGCGAGGTGCAGTGGTGCAGTCTGGAGCAGAGTGAAGAACCCGGGAGTCTGAAAGCTCTCTGTCAAGG TTCTGGATAACAATTTACCCTTACTGATCGGCTGGTGGCCAGATGCCGGGAAAGGCTGAGTGGTGGGATCATCTATCTGGTACTCTGATACCAGATTAGCCCGTCTTCCGAGGCCAGTCTCAGCATCTCAGCCGACAACCTCATCAGACCCCTACTGCA TGACCAGCTGAAGGCTCGACACCCCATGATTAAGTGTGCGATCTTTATTGGCGAGGGGCACTACTTGGCCAGGAAACCTGTGCACCGTCTCTCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCACCTCTCCAAGAGCACTCTGGGGCACAGCG GCCCTGGGCTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
8_I_GHV5-51_I_GHJ4	GCCAGCTGGGATCTCAGGCTTCAATTTCTGTCGCGACCATCATGGGTCAACCCCATCTCCCTCTCTGGTCTTCCAAGAGTCTGTGCGAGGTGCAGTGGTGCAGTCTGGAGCAGAGTGAAGAACCCGGGAGTCTGAAAGCTCTCTGTCAAGG TTCTGGATAACAATTTACCCTTACTGATCGGCTGGTGGCCAGATGCCGGGAAAGGCTGAGTGGTGGGATCATCTATCTGGTACTCTGATACCAGATTAGCCCGTCTTCCGAGGCCAGTCTCAGCATCTCAGCCGACAACCTCATCAGACCCCTACTGCA TGACCAGCTGAAGGCTCGACACCCCATGATTAAGTGTGCGATCTTTATTGGCGAGGGGCACTACTTGGCCAGGAAACCTGTGCACCGTCTCTCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCACCTCTCCAAGAGCACTCTGGGGCACAGCG GCCCTGGGCTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
109_I_GHV2-5_I_GHJ3	AGTACTCTGTGCCACCATGGACACTTTGCTCCAGCTCTGCTGCTGACCATCCCTCATGGGTCTGTGCCAGATCACCTTGAAGGAGTCTGTCTACGCTGTGAAACCCACACAGACCTCAGCTGACCTGACCTTCTGGGTTCTCACTCACCCTACCGAGT GGGTGGGCTGGATCCGTGAGCCCCAGGAAAGGCCCTGGAGTGGCTTCTTACTATTGGGGTATGATAAGCGCTACAGCCCATCTGGAAGAGCAGGCTCACCATCACAAGGACACTCCAACCAAGGTTGGCCCTTACTATGACCAACATGACCCCTGTGACAC AGCCACATATTTCTGTGCACACAACCTACTAATAGTCTGAGGGTCTTTGATATCTGGGCCAAGGACAATGGTCAACCGTCTCTCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCACCTCTCCAAGAGCACTCTGGGGCACAGCGCCCTGGGTGCTG GTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
109_I_GHV2-5_I_GHJ3	GGAATCTGTGCCACCATGGACACTTTGCTCCAGCTCTGCTGCTGACCATCCCTCATGGGTCTGTGCCAGATCACCTTGAAGGAGTCTGTCTACGCTGTGAAACCCACACAGACCTCAGCTGACCTGACCTTCTGGGTTCTCACTCAGCACTAGCGAGT GGTGGGCTGGATCCGTGAGCCCCAGGAAAGGCCCTGGAGTGGCTTGCATACATTTATTGGGGTATGATAAGCGCTACAGCCCATCTGGAAGAGCAGGCTCACCATCACAAGGACACTCCAACCAAGGTTGGCCCTTACAATGACCAACATGACCCCTGTGACACA GCCACATATTTCTGTGCACACAACCTACTAATAGTCTGAGGGTCTTTGATATCTGGGCCAAGGACAATGGTCAACCGTCTCTCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCACCTCTCCAAGAGCACTCTGGGGCACAGCGCCCTGGGTGCTGCTG TCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
11_I_GHV1-69D_I_GHJ5	ATCAGTAAACAACCAATCTCTCTAAAGAACCCCTGGGAGCACAGCTCATCACCATGGAAGCTGGAGTGGTCTCTTTGGTGGTGGCAGCAGTGCAGGTGTCAGTCCCAGGTGCAGTGGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGTCTCGTGAAG GTCTCTGCAAGGCTCTGGAGGACCTTCAACCTATATATCAACTGGGTGCGACAGGCCCCAGGAAAGGGCTGTAGTGGATGGAGGAGCATCCCTATCTTGGTACAGCAAACCTACGACAGAAAGTTCAGGGCAGAGTACGATTACCGCGACGAATCGACGA GCACAGTCTACATGGAGTTGAGTACCTGAGATCTGAGGACAGCGCCGTATTACTGTACAAGAGCAGTGGTGTAAACAGGGTGGTTCGACCCCTGGGGCCAGGAAACCTGTGCACCGTCTCTCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCACCTCT TCCAAGAGCACTCTGGGGCACAGCGCCCTGGGTGCTGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA

11_I_GHV1-69D_I_GHJ5	ATCACATAAACACCCATTCTCTCTAAAGAACCCCTGGGAGCACAGCTCATACCATGGACTGGACCTGGAGGTTCTCTTTGTGGTGCGCAGCTGACAGTGTCCAGTCCCAGGTGCAGCTGGTGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGCTCGTGGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTACACCTATATATCACTGGGTGGACAGGCCCAGGAAAGGCTTGTAGTGGATGGAGGGAGCATCCCTATCTTTGGTACAGCAAACCTACGACAGAAAGTTCAGGTGAGAGTACAGATTACCGCGACGAAATCGACAGACACAGCTACATGAGTTGAGTAGCCTGAGATCTGAGACACGGCCGTATTACTGTACAAGACAGTGGCTGTAACCAAGGGTGGTTGACCCCTGGGGCCAGGAAACCTGTCCACCTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCC
112_I_GHV1-69D_I_GHJ4	ATCACATAAACAGCCATTCTCTCTACAGAACCCCTGGGAGCACCGCTCATACCATGGACTGGACCTGGAGGTTCTCTTTGTGGTGCGGCGCAGCTACAGTGTCCAGTCCCAGGTGCAGCTGGTACAATCTGGGGCTGAAGTGAAGAAGCCTGGGCTCGTGGAAGGTCTCTGCAAGGCTTCTGGAGGCTCTTACCACCTGATGCTCACTTGGTTCGCGCAGGCCCTGGACAAGGGCTTGTAGTGGATGGAGGGCTCACCCCTGTCTTGGTTCAGCCAACCTACGACAGAAAGTTGTCGCGCAGAGTACCATTACCGCGACGAAATCGACGACACAGGGTACATGAGATGTTAGCCTGACATCCGAAGACACGGCCGTTTATTACTGTGCGAGACATGTGGACGTGTTGAGAACCTAGGCTACTTGCAGTCTGGGGCCAGGAAACCTAATAACCGTCTCTCCGCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCTCAAGAGCACCTTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
112_I_GHV1-69D_I_GHJ4	CCACATTCCTCTACAGAACCCCTGGGAGCACAGCTCATACCATGGACTGGACCTGGAGGTTCTCTTTGTGGTGCGCAGCTACAGTGTCCAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGGCTCGGTGAAGGTCTCTGCAAGGTCTCTGGAGGCTCTTACCACCTGATGCTCACTTGGTTCGCGCAGGCCCTGGACAAGGGCTGACTGATCGGGGACTCACCCCTGTCTTGGTTCAGCCAACCTACGACAGAAAGTTGTCGCGCAGAGTACCATTACCGCGACGAGTGCACGACACACTACATGGAGATTAGTGGACTGACATCTGAAGACACGGCCGTTTATTACTGTGCGAGACATGTGGACGTGTTGAGAATTTAGGGTACTTCCACCACTGGGGCCAGGAAACCTGGTACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGA
116_I_GHV3-53_I_GHJ3	GGGAGAGGAGCCGCACTGGGATCCGAGGTGTTCCATTGCGTGATCAGCACTGAACACAGAGGACTCACCATGAGTTTTGGCTGAGTGGTTTTCTTGTCTATTCAAAGGTGTCCAGTGTGAGGTGCAGCTGGTGGAGACTGGAGAGGCTTGTATCCAGCTGGGGGCTCCCTGAGACTCTCTGTGCAAGCCTCTGGGTTCAACGTCACTAGCACTACATGAGCTGGTCCGCGAGCTCCAGGGAAAGGGCTGAGTGGTCTCACTATTATATCGTGGTACCACATACGCAAGTCCGGAAGGGCCGATTACCATCTCCAGACAAATCCAAAGAACCCCTGATCTTCAAATGAACAGCCTGAGAGCCGAGACACGGCCGTATTACTGTGCGAGAGATCCCTCTTACCGATTCCGGAGTATTACGGGGAGGGATGTTTTGATATCTGGGCAAGGACAATGTCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAAGGA
116_I_GHV3-53_I_GHJ3	GGGAGAGGAGCCGCACTGGGATCCGAGGTGTTCCATTGCGTGATCAGCACTGAACACAGAGGACTCACCATGAGTTTTGGCTGAGTGGTTTTCTTGTCTATTCAAAGGTGTCCAGTGTGACGTGCAGCTGGTGGAGACTGGAGAGGCTTGTATCCAGCTGGGGGCTCCCTGAGACTCTCTGTGCAAGCCTCTGGGTTCAACGTCACTAGCACTACATGAGCTGGTCCGCGAGCTCCAGGGAAAGGGCTGAGTGGTCTCACTATTATACCGTGGTACCACATACGCAAGTCCGGAAGGGCCGATTACCATCTCCAGACAAATCCAAAGAACCCCTGATCTTCAAATGAACAGCCTGAGAGCCGAGACACGGCCGTATTACTGTGCGAGAGATCCCTCTTACCGATTCCGGAGTATTACGGGGAGGGATGTTTTGATATCTGGGCAAGGACAATGTCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAAGGA
117_I_GHV4-61_I_GHJ4	ACTTCTGAGAGTCTGCACTCTGTGCAAGAACATGAACACCTGTGGTTCTCTCTCTGTTGCGCAGCTCCAGATGGTCTGTCACAGTGCAGTGCAGAGTGGGGCCAGACTGGTGAAGCCTCGGAGACCTGTCCCTCACCTGCTGTCTGTCTGTGGCTCCATCAGCGGTAGTAATTAATCTCTGAGAGTGGATCCGCGAGCCCCAGGAAAGGGACTGGAGTGGATTGGCTATATCTATCAAAATGGGAGAACCACTACAACCCCTCCCTCAAGAGTGCAGTACCATATCAGTACACAGTCCAAAGAACAGTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTTTATTACTGTGCGAGATGAACAGTGGCTGGTACCAGTGGTCTACTGGGGCCAGGAAACCTGTCCACCGTCTCCTCAGCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
117_I_GHV4-61_I_GHJ4	ATTTCTTAAATCAGTTCCAGTCCATGACATGGAAATCTTCTGAGAGTCTGACCTCTGTGCAAGAACATGAACACCTGTGGTTCTCTCTCTGTTGCGCAGCTCCAGATGGTCTGTCACAGTGGGCTGTCCAGTGCAGCTGCAGAGTGGGGCCAGACTGGTGAAGCCTCGGAGACCTGTCCCTCACCTGCTGTCTGTCTGTGGCTCCATCAGCCTGCTGTCTGTCTGTGGTCCATCAGTGGTAGTAATTAATCTCTGAGAGTGGATCCGCGAGCCCCGGGAAAGGGACTGGAGTGGATTGGATATATTAATATAATGAGGAGAACGACTACAGCCCCCTCCGAGAGTGCAGTCCCATATCAGTACACAGTCCAAAGAACAGTCTCCCTGAAGCTGAGCTGGACACGTTCCAAGAACAGTCTCCCTGAACCTGACCTCTGTGACCGCAGCGGACACGGCCGTACTACTCTGTGCGAGATGAACAGTGGCTGGTACCGGTTGGTACTGGGGCCAGGAAACCTGGTACCCTGTCTCAGCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
118_I_GHV4-61_I_GHJ4	GGGAAATGCTTTCTGAGAGTCTGATCTCATGTGCAAGAAATGATCCACCTGTGGTTCTCTCTGTTGCGGCTCCAGATGGTCTGTCACAGTGGTGTGAGTGGGGCCAGACTGGTGAATCCTCGGAGACCTGTCCCTCGCTGCAAGTCTTGGCGCTCCATCACCCTAGTAATTAATCTGGGGCTGGATCCGCGAGCCCCAGGAAAGGGCTGGAATGATTGCCAATATTAATATCGTGGAAATCTACCACAGCCCCTCCAGAGTGCAGTACCATATCCATTGACGCGTCAAGAAATCAGTTGCTCCGTAAGTTGAAGTCTGTGACCGCCGAGATACGCTGTACTACTGTGCGAGAGTGGGGATCCCTGGGGCTATCGTTTTGAATATTTGACCAGTGGGGCCAGGGAGCCCTGTTACCGTCTCCTCAGCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
118_I_GHV4-61_I_GHJ4	GAGGTCCACCTCATAAGGAGATGCTTCTGAGAGTCGATCTCATGTGCAAGAAATGATCCACCTGTGGTTCTCTCTGTTGCGGCTCCAGATGGTCTGTCACAGTGGTGTCCAGTGGTGTGAGTGGGGCCAGACTGGTGAATCCTCGGAGACCTGTCCCTCGCTGCAAGTCTTGGCGCTCCATCACCCTAGTAATTAATCTGGGGCTGGATCCGCGAGCCCCAGGAAAGGGCTGGAATGATTGCCAATATTAATATCGTGGAAATCTACCACAGCCCCTCCAGAGTGCAGTACCATATCCATTGACGCGTCAAGAAATCAGTTGCTCCGTAAGTTGAAGTCTGTGACCGCCGAGATACGCTGTACTACTGTGCGAGAGTGGGGATCCCTGGGGCTATCGTTTTGAATATTTGACCAGTGGGGCCAGGGAGCCCTGTTACCGTCTCCTCAGCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
135_I_GHV4-61_I_GHJ6	ATACTTCTGAGAGTCTGCACTCTGTGCAAGAACATGAACACCTGTGGTTCTCTCTCTGTTGCGCAGCTCCAGATGGTCTGTCACAGTGCAGTGCAGAGTGGGGCCAGACTGGTGAAGCCTCGGAGACCTGTCCCTCACCTGCACTGTCTGTGGTCTCCGTCAGCACTAGTACTCTGACCTGGATCCGCGAGCCCCGGGAAAGACTGGAATGATTGCGTATATGATTATAGTGGAGCACCACTCTAACCCCTCTCTGAAGAGTGCAGTCACTCATACATCAGTTGACAGTCCAAAGAACCAATCTCGCTGAAGCTGACGTCTGTGACCGCTGCGGACACGGCTGATTATTGTGCGAGACAGCGAAAGTATTAACACGGTATGAGCTGTGGGCAAGGACCAAGGCTATTGTTTCTCAGCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA

149_I_GHV3-11_I_GHJ4	GCTCTGGGAGAAAGCCCCAGCCCCAAGTCCCAGGAGTTCCATTCCGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTTGGGCTGAGCTGGTTTTCTTGTGCTATTAAAAAGGTGCCAGGGTCAGGTGAGCTGGTGGGAGGCTGGTCAGCCCTGGAGGGTCCCTGAGACTCTCTGTGCAGCTCTGGATTCACTTCCAGTCACTGACTCTACATGACTCCAGTGGATCCGCGAGGCTCCAGGGAAAGGGCTGGAGTGGATGGGAGGATTGATCCTAGTACTCAACACCAACTACAGCCCGTCTTCCAAGGCCAGTCACTTCTCAGTTGACAAGTCCACCGGTAGTGTCTCCAGGGACAACGCCAGGAACCTCAGTGTCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGATTACTGTGCAGAGCCATCGTTCGGGGACTCAGATCGTCTACTTGTACTGCTGGGCCAGGGAGCCCTGTCACCGTGTCTCAGCATCCCCAGCACCCCAAGGCTTCCCGCTGAGCCTCTGCAGCACCCAGCCAGATGGAACTGGTTCATCGCTCTGGTCCAGGCTTCTCCCCAGGAGCCACTCAGTGTACCTGGAGCGAAAGCGACAGGGCGTGACCCGACAACTCCC
15_I_GHV5-10-1_I_GHJ4	AGTCTCCTCACCACCAGCTGGGATCTCAGGGCTTCTTTCTGTCTCTCCAGGATGGGGTCAACCCCATCTCGCCCTCCTCTGGCTTCTCCAAGGAATCTGTGCCGAAGTGCAGCTGGTGCAGTCCGGAGCAGAGGTAACAAAGCCCCGAGAGTCTCTGAGGATCTCTGTAAGACTTCTGGATAACAACCTTCCAGCTACTGGATCAACTGGGTGCGCCAGATGCCGGAAAGGCCCTGGAGTGGATGGGAGGATTGATCCTAGTACTCAACACCAACTACAGCCCGTCTTCCAAGGCCAGTCACTTCTCAGTTGACAAGTCCACCGGTAGTGTCTACTACAGTGGAGCAGCCTGAAGGCCCTCGACACCCCGGTATTACTGTGCGAGACAGGTCTCGCTATCGAGACAGGTGGTGGGGGGTGGACTTGGGGCCAGGGAACTTGTACCCGCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCACGGCGGTGCACACCTTCCCGCTGTCTCAGTCTCTCAGGA
15_I_GHV5-10-1_I_GHJ4	AGTCTCCTCACCACCAGCTGGGATCTCAGGGCTTCTTTCTGTCTCTCCAGGATGGGGTCAACCCCATCTCGCCCTCCTCTGGCTTCTCCAAGGAATCTGTGCCGAAGTGCAGCTGGTGCAGTCCGGAGCAGAGGTAACAAAGCCCCGAGAGTCTCTGAGGATCTCTGTAAGACTTCTGGATAACAACCTTCCAGCTACTGGATCAACTGGGTGCGCCAGATGCCGGAAAGGCCCTGGAGTGGATGGGAGGATTGATCCTAGTACTCAACACCAACTACAGCCCGTCTTCCAAGGCCAGTCACTTCTCAGTTGACAAGTCCACCGGTAGTGTCTACTACAGTGGAGCAGCCTGAAGGCCCTCGACACCCCGGTATTACTGTGCGAGACAGGTCTCGCTATCGAGACAGGTGGTGGGGGGTGGACTTGGGGCCAGGGAACTTGTACCCGCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCACGGCGGTGCACACCTTCCCGCTGTCTCAGTCTCTCAGGA
158_I_GHV1-18_I_GHJ4	ACCCAAAAACACACCCCTCTTGGGAGAAATCCCTAGATCACAGCTCCTCACCATGGACTGGACCTGGAGCATCTTTTCTTGGTGGCAGCAGCAACAGGTGCCACTCCCAGTTCAGCTGGTGCAGTCTGGAGCTGAGTGAAGCCTGGGCTCAGTGAAGTCTCCGCAAGACTTCTGGTACAGCTTTAACACTTATGGAATTACCTGGGTGCGACAGGCCCTGACAAGGGCTTGAATGGATGGATGGATCAGCGTCTACAATGGCAACACAACTATGCACAGAAAGTACCAGGGCAGAGTCAACATGACCACAGACACATCCACGAAACAGGCCCTACATGGAAGTCAAGGCTCAGATCTGACGACACGGCCATATATTACTGTGCGAGACAGTTTTTGGAGCGATTTCCCCAACTGGTCTTTGACTTGTGGGCCAGGGAACTTGTACCCGCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCTCTCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCACGGCGGTGCACACCTTCCCGCTGTCTCAGTCTCTCAGGA
158_I_GHV1-18_I_GHJ4	TGGGACCCAAAAACACACCCCTCTTGGGAGAAATCCCTAGATCACAGCTCCTCACCATGGACTGGACCTGGAGCATCTTTTCTTGGTGGCAGCAGCAACAGGTGCCACTCCCAGTTCAGCTGGTGCAGTCTGGAGCTGAGTGAAGCCTGGGCTCAGTGAAGTCTCTGCAAGACTTCTGGTACAGCTTTAACACTTATGGAATTACCTGGGTGCGACAGGCCCTGACAAGGGCTTGAATGGATGGATGGATCAGCGTCTACAATGGCAACACAACTATGCACAGAAAGTACCAGGGCAGAGTCAACATGACCACAGACACATCCACGAAACACCGCTACATGGAAGTCAAGGCTCAGATCTGACGACACGGCCATATATTACTGTGCGAGACAGTTTTTGGAGCGATTTCCCCAACTGGTCTTTGACTTGTGGGCCAGGGAACTTGTACCCGCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCACGGCGGTGCACACCTTCCCGCTGTCTCAGTCTCTCAGGA
170_I_GHV1-8_I_GHJ5	GCATCACTCAACAACACATCTGCTCTAGAGAAAAGCCTGTGAGCACAGCTCCTCACCATGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAAGTCCCAGTCCAGTGCAGCTGGTGCAGTCTGGGGCTGAGTGAAGAAAGCCTGGGCTCAGTGAAGGCTCTGATACATCTTCAACAATATGACATCAACTGGGTGCGACAGGCCCTGGACAAGGGCTTGAAGTGGATGGGTTGATGAACCTAGTGTGACACAGCTTTCGCGAGAATCTCTGGGAGTCACTTACCAGGAACACCCCATAGGCACAGCCTACATGAGCAGCCTAACATCTGACGACACGGCCGTCTATTCTGTGCGAGAGGCTCTACGGTGTAGTCCGGCTCCTGGGGCCAGGGAACTTGTACCCGCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGCGCGTGCAC
170_I_GHV1-8_I_GHJ5	GGATAGTATATTGGTGCCTGAGAGCATCACTCAACAACACATCTGCTCTAGAGAAAAGCCTGTGAGCACAGCTCCTCACCATGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAAGTCCCAGTCCAGTGCAGCTGGTGCAGTCTGGGGCTGAGTGAAGAAAGCCTGGGCTCAGTGAAGGCTCTGCAAGGCTTCTGATACATCTTCAACAATATGACATCAACTGGGTGCGACAGGCCCTGGACAAGGGCTTGAAGTGGATGGGTTGATGAACCTAGTGTGACACAGCTTTCGCGAGAATCTCTGGGAGTCACTTACCAGGAACACCCCATAGTACAGCCTACATGAGCTGAGCAGCCTAACATCTGACGACACGGCCGTATTCTGTGCGAGAGGCTCTACGGTGTAGTCCGGCTCCTGGGGCCAGGGAACTTGTACCCGCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTCAGTCTCTCAGGA
170_I_GHV1-8_I_GHJ5	GTTTTATATGGGATCACTCAACAACACATCTGCTCTAGAGAAAAGCCTGTGAGCACAGCTCCTCACCATGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAAGTCCCAGTCCAGTGCAGCTGGTGCAGTCTGGGGCTGAGTGAAGAAAGCCTGGGCTCAGTGAAGGCTCTGCAAGGCTTCTGATACATCTTCAACAATATGACATCAACTGGGTGCGACAGGCCCTGGACAAGGGCTTGAAGTGGATGGGTTGATGAACCTAGTGTGACACAGCTTTCGCGAGAATCTCTGGGAGTCACTTACCAGGAACACCCCATAGTACAGCCTACATGAGCTGAGCAGCCTAACATCTGACGACACGGCCGTATTCTGTGCGAGAGGCTCTACGGTGTAGTCCGGCTCCTGGGGCCAGGGAACTTGTACCCGCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTCAGTCTCTCAGGA
170_I_GHV1-8_I_GHJ5	ACCGATTTCTATATGGGATCACTCAACAACACATCTGCTCTAGAGAAAAGCCTGTGAGCACAGCTCCTCACCATGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAAGTCCCAGTCCAGTGCAGCTGGTGCAGTCTGGGGCTGAGTGAAGAAAGCCTGGGCTCAGTGAAGGCTCTGCAAGGCTTCTGATACATCTTCAACAATATGACATCAACTGGGTGCGACAGGCCCTGGACAAGGGCTTGAAGTGGATGGGTTGATGAACCTAGTGTGACACAGCTTTCGCGAGAATCTCTGGGAGTCACTTACCAGGAACACCCCATAGTACAGCCTACATGAGCTGAGCAGCCTAACATCTGACGACACGGCCGTATTCTGTGCGAGAGGCTCTACGGTGTAGTCCGGCTCCTGGGGCCAGGGAACTTGTACCCGCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTCAGTCTCTCAGGA
176_I_GHV3-33_I_GHJ5	GCTCCTCTACTGATGAAACCCAGCCCAGCCCTGACCCTGCAGCTGGGAGACGAGCCGACTGGAAGTGCAGGTTTCCATTCCGGTGATCATCACTGAACACAGAGGACTCACCATGGAGTTTGGGCTGAGCTGGTTTTCTTCTGTTTCTTTAAGAGGTGCCAGTGCAGCTGGTGGAGTCTGGGGAGGGTGGTCCAGCCTGGGAGGCCACAGACTCTCTGTGCAGCTCTGATTCACTTCACTTCACTTCACTGGGCTCCGCGAGCTCCAGGCAAGGGCCTGGAATGGTGGCATTATATACATGATGGAAGTAATAGTATTACGAGACTCCGTGAAGGGCCGATTATCATCTCCAGAGACAATCCAAAGAAACAGTTTATCTGCAAAATGACAGCCTGAGAAGTGAAGACAGGCTGTATATTACTGTGCGAGAATCCACAGCGACAGGGGGTAGGAGACCCGGTAGCTCCGGTGGCGAACACTGGTTGACCCCTGGGCCAGGGAGTCTGTCAACGCTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTCAGTCTCTCAGGA

176_I_GHV3-33_I_GHJ5	CCCTCTACTGATGAAAACCAGCCCAGCCCTGACCCTGACGCTCTGGGAGACGAGCCCAGCACTGGAAGTCGCCGTGTTCCATTCCGCTGATCATCACTGAAACACAGAGGACTCACCATTGGAGTTTGGCTGAGCTGGTTTTCTCGTAGTCTTTAAGAGGTGTCCAATG CAGGTGACGCTGGTGGAGTCTGGGGAGGGGTGGTCCAGCTGGAGGTCACACAGACTCTCTGTGACGCTCTGATTACCTCAGTAGTTATGCTTCCACTGGGCCAGGCTCCAGGCAAGGGCTGGAATGGTGGCATTATATCATATATGGAAGTAAT AAGTACTTCGCAGACTCCGTGAAGGGCCGATTCCACATCTCCAGAGACAATCCAAGAATACAGTTTATCTGCAAAATGAACAGCCTGAGAAGTGAAGACACGCTGTCTATTACTGTGCGAGAAATACCCACGACGCGGAGGGGTAGGAGACCCGGTAGCTCCCGGTCCGC GAACAACCTGTTGACCCCTGGGGCAGGAGCCCTGCTCACCCTCTCCTCAGCTCCACCAAGGGCCCATCGTCTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGCTGCTGCTCAAGGACTACTTCCCCAACCCGGTACGCGTGTGCT GGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGCTCTACAGTCTCAGGA
18_I_GHV1-8_I_GHJ4	CTGAGAGCATCACTCAACAACACATCTGTCTCTAGAGAAAACCTGTGAGCACAGCTCCTCACCATTGGACTGGACCTGGAGATTCTCTTCTGGTGGCAGCAGCTACAAGTCCCACGCCAGGTGCAACTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCTGGGGCTCA GTGAAGGTCTCTGCGAGGCTTCTGGATACACCTTCACTCATTACGATGCAACTGGTGGCAGACGCGCTGGACAAGGGCTTGAAGTGGTGGCCTGGATGAACCTAATAGTGGCAATACCCCTATGACACAGAACTCCAGGGCAGAGTTACCTTGACCCGGAAACCTCC CCTAAGCACAGCCTACATGAGCTCAACACCTGAGGTCTGAGGACACGCGCGTATTACTGCGCGAGCCACCTCGTTCATTCTCTGTTGGGGACTTTTTCAACCCTTTCTACTGGGTGAGGGACCCCTGGTACCCGTCTCCTCAGCTCCACCAAGGGCCCAT CGGCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTTCCCCAACCCGGTACGCGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGCTCTACAGTCTCAGGA
18_I_GHV1-8_I_GHJ4	GGGGATCACTCAACAACACATCTGTCTCTAGAGAAAACCTGTGAGCACAGCTCCTCACCATTGGACTGGACCTGGAGATTCTCTTCTGGTGGCAGCAGCAACAAGTCCCACGCCAGGTGCAACTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCTGGGGCTCAGT GAAGGTCTCTGCAAGGCTTCTGGATACACCTTCACTCATTATGATATCAACTGGTGGCAGACGCGCTGGACAAGGGCTTGAAGTGGTGGCCTGGATGAACCTAATAGTGGCAATACCCCTATGACACAGAACTCCAGGGCAGAGTTACCTTGACCCGGAAACCTCC TAAGCACAGCCTACATGAGCTCAACACCTGAGGTCTGAGGACACGCGCGTATTACTGCGCGAGCCACCTCGTTCATTCTCTGTTGGGGACTTTTTCAACCCTTTCTACTGGGTGAGGGACCCCTGGTACCCGTCTCCTCAGCTCCACCAAGGGCCCATCG GTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTTCCCCAACCCGGTACGCGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGCTCTACAGTCTCAGGA
182_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGTGCTTAGCCCTGATTCCAAGCAITTCACCTGTGTATCAGCACTGAACACAGAGGACTCACCATTGGAGTTGGGCTGTCTGGTTTTCTTGTGTTCTTTTGAAGATGTCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGAGGCTTGTG ACAGCTGGAGGCTCCCTGAGACTCTCTGTGACAGCTCTGATTCACTTTCAGTAGTTTTAAATGAACCTGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGATTTCATACATTAGTAGTAGTGTAGTACCATATACTACGACACTCTGTGAAGGGCCGATTACCA TCTCCAGAGACAACGCAAAGAACTCACTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGCTATTTTACTGTGCGAGAGATGTATCGAACCGGATACAACCTATGAGTTTCCCCACTACTTACCAGTGGCCAGGAAACCTGGTACCCGTCTCCAGGGAG TGCATCCGCCAACCTTTTCCCCCTGCTCCTGTGAGAAATCCCCGTCGATACGAGCAGCGT
182_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGTGCTTAGCCCTGATTCCAAGCAITTCACCTGTGTATCAGCACTGAACACAGAGGACTCACCATTGGAGTTGGGCTGTCTGGTTTTCTTGTGTTCTTTTGAAGATGTCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGAACTTGTG ACAGCTGGAGGCTCCCTGAGACTCTCTGTACAGCTCTGATTCACTTTCAGTAGTTTTAAATGAACCTGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGATTTCATACATTAGTAGTAGTGTAGTACCATATACTACGACACTCTGTGAAGGGCCGATTACCA TCTCCAGAGACAACGCAAAGAACTCACTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGCTATTTTACTGTGCGAGAGATGTATCGAACCGGATACAACCTATGAGTTTCCCCACTACTTACCAGTGGCCAGGAAACCTGGTACCCGTCTCCAGGGAG CACCAGGGCCCATCGTCTTCCCCCTGACCCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTTCCCCAACCCGGTACGCGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGCTCTACAGTCTCAGGA
183_I_GHV3-30_I_GHJ4	GAGCTCTGGGAGAGAGCCAGCACTAGAAAGTCGGCGGTGTTCCATTCCGCTGATCAGCACTGAACACAGAGGACTCACCATTGGAGTTTGGGCTGAGCTGGTTTTCTCGTCTCTTTAAGAGGTGTCCAGTGTGAGTGTGAGTCTGGGGAGGCGT GGTCCAGCTGGGAAGTCCCTGAGACTCTCTGTGACGCTCTCGATTCACTTTCAGTAGTATGATCATGACTGGTCCGCGAGGCTCCAGGCAAGGGCTGGAGTGGTGGCGATTATTTAGATGATGGAATAAAAAATATATGAGGACTCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAATCCAGGAACAGCTGTATTGCAATTGAACAGCCTGAGAAATGAGGACACGCGTGTATTATTGTGCGAAAGGGCCGCTCCACTACTATGTTGCGGGGACTAATGATTGGGCCAGGGAACCCCTAGTACCCTCTCCTCAGCTCCACCAAGG GCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTTCCCCAACCCGGTACGCGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGCTCTACAGTCTCAGGA
183_I_GHV3-30_I_GHJ4	GGGAGAGAGCCAGCACTAGAAAGTCGGCGGTGTTCCATTCCGCGATCAGCACTGAACACAGAGGACTCACCATTGGAGTTTGGGCTGAGCTGGTTTTCTCGTCTCTTTAAGAGGTGTCCAGTGTGAGTGTGAGTCTGGGGAGGCGTGTCCAG CCTGGGAAGTCCCTGAACTCTCATGTGACGCTCTCGATTCAATTTCACTTCTATGCCATGCACTGGTCCGCGAGGCTCCAGGCAAGGGCTGGAGTGGTGCACAATATTTCAAATGATGGAACGAAAAATTTATGAGGACTCCGTGAAGGGCCGATTACCATCTCCA GAGACAATCCAGGAACACCCTGTATCTGCAATTGAACAGCCTGAGGGTTGAGGACACGCGTGTCTATTACTGTGCGAAAGAGGGCCCTCCACTACTATGTTGCGGGGACTAATGATTGGGCCAGGGAACCCCTGTCACCGTCTCCTCAGCTCCACCAAGGGCCCATCG GTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTTCCCCAACCCGGTACGCGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGCTCTACAGTCTCAGGA
195_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCAGCCCTGGGATTTTTCAGGTGTTTTCACTTGGTGTATCAGCACTGAACACAGAGAACTCACCATTGGAGTTTGGGCTGAGCTGGCTTTCTTGTGGCTATTTAAGAGGTGTCCAGTGTGAGTGTGAGTCTGGGGAGGCTTGG TACAGCCGGGGGCTCCCTGAGAGTTTCTGTGTTGCTCTGATTGACCTTTAACCACTATGCTTGAATGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGTCTCCGCTATTAGTGTAGTGTACTATGACGACTACGCACTCCGTGAAGGGCCGTTCA CCGTCTCCAGAGACAACCTAAGAAACACATTATATCTGCAACTGAACAGCCTGCGAGTGAAGGACACGCGCTTTTACTGTGCGAAAGGGGGCAGCAGTGTGCTGCCACTACTTTGAATCTGGGCCAGGGAACCCCTGGTACCCGTCTCCTCAGCTCCACCAAGGGCCCATCG
195_I_GHV3-23_I_GHJ4	GAGAGAGAGCCAGCCCTGGGATTTTTCAGGTGTTTTCACTTGGTGTATCAGCACTGAACACAGAGAACTCACCATTGGAGTTTGGGCTGAGCTGGCTTTCTTGTGGCTATTTAAGAGGTGTCCAGTGTGAGTGTGAGTCTGGGGAGGCTTGGTACAGC CGGGGGGCTCCTGAGAGTTTCTGTGACGCTCTGATTGACCTTTAACCACTATGCTTGAATGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGTCTCAGCCATTAGTGTAGTGTCTATGACATACTACGCACTCCGTGAAGGGCCGTTACCCGTCT CCAGAGACAACCTCCAAGAACACCTGTATCTGCAACTGAACAGCCTGCGAGCAGGAGGACACGCGCAATTTACTGTACGAAAGGGGGCAGCAGTGTGTTCCACTACTTTGAATCTGGGGCCAGGGAACCCCTGGTACCCGTCTCCTCAGCTCCACCAAGGGCCCATCG CTTCCCCCTGGCCCTGCTCCAGAGCACCTCCGAGACACAGCGCCCTGGCTGCTGTTCAAGGACTACTTCCCCAACCCGGTACGCGTGTGCTGGAACCTCAGCGCTCTGACCAGCGCGTGCACACCTTCCAGCTGCTCTACAGTCTCAGGA
198_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCAGCCCTGGGATTTTTCAGGTGTTTTCACTTGGTGTATCAGCACTGAACACAGAGAACTCACCATTGGAGTTTGGGCTGAACTGGCTTTTCTTGTGGCTATTTAAGAGGTGTCCAGTGTGAGTGTGAGTCTGGGGAGTCTTGG TACAGCCTGGGGTCCCTGAGACTCTCTGTGACGCTCTGATTCACTTTAGCAGTATGCCATGAGTTGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGTCTCAACTATTAGTGTAGTGTGGTGTAGCACATACTACGCACTCCGTGAAGGGCCGTTCA CCGTCTCCAGAGACAGTTCCAAGAACACGCTGTATCTGCAAAATCAATAGCCTGAGAGTGAAGGACACGCGCTATATTACTGTGCGAAAGCCCCCGACACTCTGGTCTATTTGATTATTGGGCCAGGGAACCCCTGGTACCCGTCTCCTCAGCTCCACCAAGGGCCCATC GGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTTCCCCAACCCGGTACGCGTGTGCTGGAACCTCAGCGCTCTGACCAGCGCGTGCACACCTTCCCGCTGCTCTACAGTCTCAGGA

198_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCAGCCCTGGGATTTTCAGGTGTTTTATTGGTGATCAGGACTGAACAGAGAGAAGTACCATTGAGTTGGGCTGAGCTGGCTTTTTCTGTGACTATTTAAAGGTGCCAGTGTGGGGTGACGCTGGTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGCTCCTGAGACTCTCTGTGCAGCCTCTGGATTGATTGATCTTTAGCGACCATGCCCTGACCTGGTCCGCGAGGCTCCAGGGAAGGGAAGTGGGCTGAGTGGGCTCAACTATTAGTGGTAGTGGTAGCACATATTATGCAAACTCCGTGAGGGCCGGTTCCACGTTTCCAGAGACAGGTCCAAGAACACGCTGTATCTGCAGATGAATAGCCTGAGAGTCGAGGACACGCGCCGTATATTACTGTGCGAAAGCCCCCGGACCTCTGGTCTTATTTGATTATTGGGGCCAGGGAACCTGGTATCTGCTCCCTCAGCCTCCACCAAGGCCCATCGTCTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTG
198_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCAGCCCTGGGATTTTCAGGTGTTTTATTGGTGATCAGGACTGAACAGAGAGAAGTACCATTGAGTTGGGCTGAGCTGGCTTTTTCTGTGACTATTTAAAGGTGCCAGTGTGGGGTGACGCTGGTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGCTCCTGAGACTCTCTGTGCAGCCTCTGGATTGATTGATCTTTAGCGACCATGCCCTGACCTGGTCCGCGAGGCTCCAGGGAAGGGAAGTGGGCTGAGTGGGCTCAACTATTAGTGGTAGTGGTAGCACATATTATGCAAACTCCGTGAGGGCCGGTTCCACGTTCCAGTACAGAGCCTCCAAGAACACGCTGTATCTGCAAAATGAATAGCCTGAGAGTCGAGGACACGCGCCGTATATTACTGTGCGAAAGCCCCCGGACCTCTGGTCTTATTTGATTATTGGGGCCAGGGAACCTGGTATCTGCTCCCTCAGCCTCCACCAAGGCCCATCGTCTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTACCAGCGCGTGACACCTTCCCGCTGTCTACAGTCTCAGGA
198_I_GHV3-23_I_GHJ4	CTCTGAGAGAGAGCCAGCCCTGGGATTTTCAGGTGTTTTATTGGTGATCAGGACTGAACAGAGAGAAGTACCATTGAGTTGGGCTGAACTGGCTTTTTCTGTGCTATTTAAAGGTGCCAGTGTGAGGTGCAACTGGTGGAGTCTGGGGAGTCTTGGTACAGCCTGGGGGCTCCTGAGACTCTCCTGTGCAGCCTCTGGATTGATTGATCTTTAGCGACCATGCCCTGACCTGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGCTCAACTATTAGTGGTAGTGGTAGCACATATTATGCAAACTCCGTGAGGGCCGGTTCCACGTTCCAGAGACAGTCCAAGAACACGCTGTATCTGCAAAATGAATAGCCTGAGAGTCGAGGACACGCGCCGTATATTACTGTGCGAAAGCCCCCGGACCTCTGGTCTTATTTGATTATTGGGGCCAGGGAACCTGGTACCTCTCCACCAAGGCCCATCGTCTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTACCAGCGCGTGACACCTTCCCGCTGTCTACAGTCTCAGGA
199_I_GHV1-46_I_GHJ5	CCCTGAAAGCATCATCCAACAACACATCCCTTCTCCACAGAAAGCCTCTGAGAGAAAGTCTTACCATTGACTGACCTGGAGGCTTCTGCTTCTGCTGTAGCTTCCAGGCTCCTACTGCCAGTGTGAGTGTGAGTGTGAGGCTGGGCTGAGGTGAAGAACCTGGGGCTTCAGTGAAGATTTCTGCGAGCTTCTGATTACGTTACCCAGGTTCTATATGCACTGGCTGCGACAGGCCCTGGACAAGGGCTGAGTGGATGGGAATAATCAACCTAGTGGAGTAGAACAACTACGCACAGAGTTCCAGGGCAGAGTCCAGGGCAGAGTCCATGACCAGGACTGTCCGCGACTGTCCGCGAGCACAGTTTTCATGGAGTTGAGCAGCCTGACATCTGAAGACACGCGCGTATTTTTGTCGGGAGCCGCTGTCGGGGCTGTAGTGTGCGGATTGACCCCTGGGGCCAGGGAACCTGGTATCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTACCAGCGCGTGACACCTTCCCGCTGTCTACAGTCTCAGGA
199_I_GHV1-46_I_GHJ5	ATCATCCAACAACACATCCCTTCTCCACAGAAAGCCTCTGAGAGAAAGTCTTACCATTGACTGACCTGGAGGCTTCTGCTTCTGCTGTAGCTTCCAGGCTCCTACTGCCAGTGTGAGTGTGAGTGTGAGGCTGGGCTGAGGTGAAGAACCTGGGGCTCAGTGAAGATTTCTGCGAGCTTCTGATTACGTTACCCAGGTTCTATATGCACTGGCTGCGACAGGCCCTGGACAAGGGCTGAGTGGATGGGAATAATCAACCTAGTGGAGTAGAACAACTACGCACAGAGTTCCAGGGCAGAGTCCATGACCAGGACTGTCCGCGAGCACAGTTTTCATGGAGTTGAGCAGCCTGACATCTGAAGACACGCGCGTATTTTTGTCGGGAGCCGCTGTCGGGGCTGTAGTGTGCGGATTGACCCCTGGGGCCAGGGAACCTGGTATCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTACCAGCGCGTGACACCTTCCCGCTGTCTACAGTCTCAGGA
201_I_GHV4-59_I_GHJ5	ATACTTCTGAGAGTCTGACTCCTGTGCAAGAACATGAACATCTGTGGTTCTTCTTCTCCTGTGGCAGCTCCAGATGGTCTGTCACAGTGTGAGTGTGAGGAGTGGGGCCCGGACTGGTGAAGCCTTCCAGAGACCTGTCCCTCACCTGACTGTCTGTGGTCTCCATGACTAATTACTACTGAGCTGGATCCGCGAGCCCCAGGGAAGGGACTGGAGTGGATTGGGAATATCTTACAGTGGGAGTACCAGCTACAACCCCTCCCTCCAGAGTCCAGTACCATATCGTAGACACGTCCAAGAACAGTTCCCTGAACCTGACTGTCTGCTGCTGACCGCTGCGACACGCGCGTATATTACTGTGCGAGATTGACACGCGCGAGTGGCTGTGGGCGCGGAGTCTGTGGGGTGGTTCGACCCCTGGGGCCAGGGAATCCTGTCTCCACAGCCTCCACCAAGGCCCATCGTCTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTACCAGCGCGTGACACCTTCCCGCTGTCTACAGTCTCAGGA
201_I_GHV4-59_I_GHJ5	ATACTTCTGAGAGTCTGACTCCTGTGCAAGAACATGAACATCTGTGGTTCTTCTTCTCCTGTGGCAGCTCCAGATGGTCTGTCACAGTGTGAGTGTGAGGAGTGGGGCCCGGACTGGTGAAGCCTTCCAGAGACCTGTCCCTCACCTGACTGTCTGTGGTCTCCATGACTAATTACTACTGAGCTGGATCCGCGAGCCCCAGGGAAGGGACTGGAGTGGATTGGGAATATCTTACAGTGGGAGTACCAGCTACAACCCCTCCCTCCAGAGTCCAGTACCATATCGTAGACACGTCCAAGAACAGTTCCCTGAACCTGACTGTCTGCTGCTGACCGCTGCGACACGCGCGTATATTACTGTGCGAGATTGACACGCGCGAGTGGCTGTGGGCGCGGAGTCTGTGGGGTGGTTCGACCCCTGGGGCCAGGGAATCCTGTCTCCACAGCCTCCACCAAGGCCCATCGTCTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTACCAGCGCGTGACACCTTCCCGCTGTCTACAGTCTCAGGA
202_I_GHV1-18_I_GHJ4	ACCCAAAACACACCCCTCCTTGGGAGAAATCCCTAGATCACAGCTCCTCACATGACTGACCTGGAGCATCCTTTTTCTTGGTGGCAGCAACAGAGTGTCACTCCAGGTTCAACTGGTGCAGTCTGGAGGTGAGGTGAAGAACCTGGGGCTCAGTAAAGTCTCTGCAAGGCTGCTGTACACCTTCAACAATATGGGATCAGCTGGTGCAGGCCCCCTGACAAGGACTCGAATGGATGGATGATCAGTGGTACAATGTTACACACTATATGCTCAGAAATCCAGGGCAGAGTACCATGACCAGACACATCCACGAACACAGCCTACATGGAAGTAAAGGACGTCAAATCTGACGACACGCGCGTCTATTACTGCGCGAGATTGGGGAGATACTACGAACCTGACTATTGGGGCCAGGGAACCTGGTCAACCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTACCAGCGCGTGACACCTTCCCGCTGTCTACAGTCTCAGGA
202_I_GHV1-18_I_GHJ4	TGGGACCCAAAGAACACACCCCTCCTTGGGAGAAATCCCTAGATCACAGCTCCTCACCATTGACTGACCTGGAGCATCCTTTTTCTTGGTGGCAGCAACAGAGTGTCACTCCAGGTTCAACTGGCAGTCTGGAGGTGAGGTGAAGAACCTGGGGCTCAGTAAAGTCTCTGCTCCTGCAAGGCTGCTGTTACACCTTCAACAATACCGTGTGCTGAGTGGTGCAGGCCCCCTGACAAGGACTCGAATGGATGGATGATCAGTGGTACAATGTTACACACTATATGCTCAGAAATCCAGGGCAGAGTACCATGACCAGACACATCCACGAATACAGCCTACATGGAATGAAGGAGCGTCAAATCTGACGACACGCGCGTCTATTACTGCGCGAGATTGGGGAGATACTACGAACCTGACTATTGGGGCCAGGGAACCTGGTCAACCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTACCAGCGCGTGACACCTTCCCGCTGTCTACAGTCTCAGGA
210_I_GHV1-46_I_GHJ6	GGGCCCTGAAAGCATCATCCAACAACACATCCCTTCTCACAGAAAGCCTCTGAGAGAAAGTCTTACCATTGACTGACCTGGAGGCTTCTGCTTCTGCTGTAGTCCAGTGTCTACTCCAGTGTGAGTGGGCTGAGGTGAAGAACCTGGGGCTCAGTGAAGGTTCTCCTGCAAGCATCTGGTACACCTTCAACGACTTCTATTTCCACTGGTGCAGACAGGCCCTGGACAAGGCTTGTAGTGTGATGGGAATGATCAACCTAGTGTACCACAAATACGCACAGAGTTCCAGGGCAGAGTACCATGACCAGGACACGACGCTCAACGAGCCTGCTACATGAGCTGAGCAGCCTGAGATCTGAGGACACGCGCATGATTTTTGTGCGAGATAAAGGCCAGCTCTCTTCTACGTTTTGACGCTCTGGGGCCAGGGAACCTGGTCAACCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTACCAGCGCGTGACACCTTCCCGCTGTCTACAGTCTCAGGA

210_I_GHV1-46_I_GHJ6	ATCATCCAACAACCACATCCCTTCTACAGAACCTCTGAGAGAAAGTTCTCACCATTGACTGGACCTGGAGGGTCTTCTGCTTGGCTGTAGCTCCAGGTGCTCACTCCCAGGTGCAGCTGGTGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCTCAGTGAAGTTTCTCTGCAAGGCTGAATACACCTTACCACCTTCTAATTCACCTGGGTGCGACAGGCCCTGGACAGGGCTTGGAGTGGGAATGATCAACCTAGTAGTGACCACAAATACGCACAGCTCCAGGGCAGAGTACCATTGACCAGGACACGTCCACGACCAGTGCTACATGGAGCTGAGCAGCTGAGATCTGAGGACACGGCCATGTATTACTGTGCGAGATAAGGCCACGTCTTCTACGGTTTGGACGTCTGGGCCAAGGACCACGTCCACCTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
212_I_GHV1-2_I_GHJ4	CAACCACATCTGTCTCTAGAGAAAACCTGTGAGCACAGCTCCTCACCATTGACTGGACCTGGAGGATTCTTCTTGGTGGCAGCAGCCCAAGTGCACGCCCAGTGCAGCTGGTGAGTGAAGAAGCCTGGGGCTCAGTGAAGGTCTCGTCAAGGCTTCTGGATACACCTTCACTCATTACGATATCAACTGGGTGCGACAGGCCGTGGACGAGACTTGGAGTGGTGGCTGGTTGAACCTTAACAGTGGCAGAACCCCTATGCACAGAACTCCAGGGCAGAGTTACCTTGACCCGGAAACCTCCATAAGCTGAGTTCAACACCTGACGTCTGACGACACGGCCGTCTACTACTGCGCGAGCCACTTGGTCTACTCCGCTGGTTCGGGGACTTTTTCTAATCACTTCTAATCTGGGTGAGGGACCTGGTACCCTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCACTCTCTCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
212_I_GHV1-2_I_GHJ4	GGGACTCAACAACCACATCTGTCTCTAGAGAAAACCTGTGAGCACAGCTCCTCACCATTGACTGGACCTGGAGGATTCTTCTTGGTGGCAGCAGTACAAGTGCACGCCCAGTCCAGCTGGTGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCTCAGTGAAGGTCTCTGCAAGGCTTCTGGATACACCTTCACTCATTACGATATCAACTGGGTGCGACAGGCCGTGGACGAGACTTGGAGTGGTGGCTGGTTGAACCTTAACAGTGGCAGAACCCCTATGCACAGAACTCCAGGGCAGAGTTACCTTGACCCGGAAACCTCCATAAGCTGCTGCTACATGGAGTTCAACACCTGAAGTCTGACGACACGGCCGTCTACTACTGCGCGAGCCACTTGGTCTACTCCGCTGGTTCGGGGACTTTTTCTAATCACTTCTAATCTGGGTGAGGGACCTGGTACCCTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCTCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
212_I_GHV1-8_I_GHJ1	GAGCATCACTCAACAACCACATCTGTCTCTAGAGAAAACCTGTGAGCACAGCTCCTCACCATTGACTGGACCTGGAGGATTCTTCTTGGTGGCAGCAGTACAAGTGCACGCCCAGTCCAGCTGGTGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCTCACTGAAGGTCTCTGCAAGGCTTCTGGATACACCTTCACTCATTACGATATCAACTGGGTGCGACAGGCCGTGGACGAGGCTTGGAGTGGTGGCTGGTTGAACCTTAACAGTGGCAGAACCCCTATGCACAGAACTCCAGGGCAGAGTTACCTTGACCCGGAAACCTCCATAAGCTGCTGCTACATGGAGTTCAACACCTGAAGTCTGAGGACACGGCCGTCTACTACTGCGCGAGGCCACTTGGTCCATTCCGCTGGTTCGGGGACTTTTTCTAACCCTTCTACTACTGGGTGAGGGACCTGGTACCCTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCTCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
212_I_GHV1-8_I_GHJ1	CGGCGGATTTCTATATGGGACTCAACAACCACATCTGTCTCTAGAGAAAACCTGTGAGCACAGCTCCTCACCATTGACTGGACCTGGAGGATTCTTCTTGGTGGCAGCAGTACAAGTGCACGCCCAGTCCAGCTGGTGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCTCAGTGAAGGTCTCTGCAAGACTTCTGGATACACCTTCACTCATTACGATATCAACTGGGTGCGACAGGCCGTGGACGAGGCTTGGAGTGGTGGCTGGTTGAACCTTAACAGTGGCAGAACCCCTATGCACAGAACTTCCAGGGCAGAGTTTCTTGACCCGGAAACCTCCATAAGCTGAGTTCAACACCTGACGTCTGACGACACGGCCGTCTACTACTGCGCGAGGCCACTTGGTCCATTCCGCTGGTTCGGGGACTTTTTCTAACCCTTCTACTACTGGGTGAGGGACCTGGTACCCTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCTCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
214_I_GHV4-4_I_GHJ1	GGGTCAGCTCACATGGAAACTTTCTGAGACTCATGGCCCTCTGACAAGAATCAAAACCTGTGGTTCTTCTCTCTGGTGGCAGCTCCAGATGGTCTCTCAGTGCAACTGCAGAGTGGGTCCCGACTGGTGAAGCCCTGGGGACCTGTCTCACCTGCGCTGTCTGGTGGCCCCATCAACAATAGTAATTTGGTGGGGTGGTCCGCCAGTCCCAGGGAAAGGACTGGAATGGCTTGGAGAAATCAATCACAGGGGAAGTACCAATACAAGTCTCCCTCAGAAACCGAGTACCATTCTTTGGACAAGTCCAGGAACCAATCTCCCTGACTGTGACTCTGTGACCGCCGCGACACCGCATATATTACTGTGTGAGAGAGACTACTGACTACTGTATTCTTTGACCCCTGGAGCCCGGGTCCCTGATCACCCTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
214_I_GHV4-4_I_GHJ1	ATACTTCTGAGACTCATGGCCCTCTGACAAGAATCAAAACCTGTGGTTCTTCTCTCTGGTGGCAGCTCCAGATGGTCTCTCAGTGCAACTGCAGAGTGGGTCCCGACTGGTGAAGCCCTCGGGACCTGTCTCTCACCTGCGCTGTGTGTTGGCCCCATCAACAATAGTAATTTGGTGGGGTCCGCCAGTCCCAGGGAAAGGACTGGAATGGCTTGGAGAAATCAATCACAGGGGAAGTACCAATACAAGTCTCCCTCAGAAACCGAGTACCATTCTTTGGACAAGTCCAGGAACCAATCTCCCTGACTGTGACTCTGTGACCGCCGCGACACCGCATATATTACTGTGTGAGAGAGACTACTGACTACTGTATTCTTTGACCCCTGGAGCCCGGGTCCCTGATCACCCTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
218_I_GHV4-39_I_GHJ4	ATTTCTTCAATCAGTCCAACCTATAAGGGAAATGCTTTCTGAGAGTCAATGATCATGTGCAAGAAAATGAAGCACCTGGTCTTCTCTCTGGTGGCAGCTCCAGATGGTCTCTCAGTGCAACTGCAGAGTGGGTCCCGACTGGTGAAGCCCTCGGGACCTGTCTCTCACCTGCGCTGTGTGTTGGCCCCATCAACAATAGTAATTTGGTGGGGTCCGCCAGTCCCAGGGAAAGGACTGGAATGGCTTGGAGAAATCAATCACAGGGGAAGTACCAATACAAGTCTCCCTCAGAAACCGAGTACCATTCTTTGGACAAGTCCAGGAACCAATCTCCCTGACTGTGACTCTGTGACCGCCGCGACACCGCATATATTACTGTGTGAGAGAGACTACTGACTACTGTATTCTTTGACCCCTGGAGCCCGGGTCCCTGATCACCCTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
218_I_GHV4-39_I_GHJ4	ATTTCTTCAATCAGTCCAACCTATAAGGGAAATGCTTTCTGAGAGTCAATGATCATGTGCAAGAAAATGAAGCACCTGGTCTTCTCTCTGGTGGCAGCTCCAGATGGTCTCTCAGTGCAACTGCAGAGTGGGTCCCGACTGGTGAAGCCCTCGGGACCTGTCTCTCACCTGCGCTGTGTGTTGGCCCCATCAACAATAGTAATTTGGTGGGGTCCGCCAGTCCCAGGGAAAGGACTGGAATGGCTTGGAGAAATCAATCACAGGGGAAGTACCAATACAAGTCTCCCTCAGAAACCGAGTACCATTCTTTGGACAAGTCCAGGAACCAATCTCCCTGACTGTGACTCTGTGACCGCCGCGACACCGCATATATTACTGTGTGAGAGAGACTACTGACTACTGTATTCTTTGACCCCTGGAGCCCGGGTCCCTGATCACCCTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
218_I_GHV4-39_I_GHJ4	ACGCGCTATGTTTCTATAGGGATGCTTCTGAGAGTCAATGATCATGTGCAAGAAAATGAAGCACCTGGTCTTCTCTCTGGTGGCAGCTCCAGATGGTCTCTCAGTGCAACTGCAGAGTGGGTCCCGACTGGTGAAGCCCTCGGGACCTGTCTCTCACCTGCGCTGTGTGTTGGCCCCATCAACAATAGTAATTTGGTGGGGTCCGCCAGTCCCAGGGAAAGGACTGGAATGGCTTGGAGAAATCAATCACAGGGGAAGTACCAATACAAGTCTCCCTCAGAAACCGAGTACCATTCTTTGGACAAGTCCAGGAACCAATCTCCCTGACTGTGACTCTGTGACCGCCGCGACACCGCATATATTACTGTGTGAGAGAGACTACTGACTACTGTATTCTTTGACCCCTGGAGCCCGGGTCCCTGATCACCCTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
221_I_GHV3-33_I_GHJ4	GAGCTCTGGGAGAGGAGCCAGCACTAGAAGTGGCGGTGTTCCAATCGGTATCAGCACTGAACACAGAGGACTCACCATTGAGTTTGGCTGAGTGGTTTTCTCTGTTGCTTTTTAAGAGTGTCCAGTGTCCAGTGTGAGTGTGGGGAGGTGGTCCAACTGGGAGTCCCTGAGACTCTCTGTACAGCGTCTGATTCGACTCAAACCTATGGCATGCACTGGTCCGCGAGCTCCAGGCAAGGGCTGGAGTGGTGGCAGTATTGGCATGATGGAGAGATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCATTCTCCAGAGACAATCCAAGAACACTGTATCTCCAATGAACAGTCTGCGAGCCAGGACACCGCTGTATTACTGTGCGAGACAGCGGGCATATCTGTTGCGGGAGATGGGGGGCTTGACTACTGGGGCAGGGACCCCTGGTACCCTCTCTCAGCATCCCCACAGCCCCAAGGTTCCCAGTGTGAGTCCAGTCCAGTGGAAAGTGGTATCGCTGCTGGTCCAGGGCTTCTTCCCAGGAGCACTAGTGTGACTGGAGCGAAAGCGACAGGGCTGACCCGCAAGAACTCCCAGGA

64_I_GHV4-61_I_GHJ3	CCGCAATTACTTCTTATATGGGGAGGGTCTGCTCACATGGAAGACTTCTGAGAGTCTGACCTCTGTGCAAGAACATGAACACCTGTGGTTCTTCTCTGCTGGTGGCAGCTCCCAGATGGTCTGCCAGGTGCAGCTGCAGGAGTCGGGCCAAGACTGTGAAGCCTTCACAGACCCCTGTCTCTCACCTGCACCTGTCTGTGGTGGTCCATCAGCACTGGAAATCACTACTGAGCTGGATCCGACAGCACCCCGGGAAGGGCCTGAGTGTGATCGGGTTCACTATTACAGTGGAAACCACTACTAACCCTGCTCACAGTTCGAGTTA GTATGTAGTGGACCCCTCTAAGAACCACTTCTCCCTGAAGTTAGAGCTGTGACTGCCGCGACACGCGCCGTATATTACTGTGCGAAAGGGCAGTGGCTGATACGGGGTCTTTTGATATCTGGGGCCAAGGGACAGTGTACCCTCTCTCAGCTCCACCAAGGGCC ATCGTCTTCCCCCTGACCCTCTCCAAGAGCACCTGTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTCCCCAACCGGTGACGGTGTGTTGAACTCAGCGCCCTGACCAGCGGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
66_I_GHV4-59_I_GHJ5	TCCTTAAATTCAGGTTCCAGCTCACATGGAAACTTCTGAGAGTCTGGACCTCTGTGCAAGAACATGAACATCTGTGGTTCTTCTCTCTGCTGGCAGCTCCCAGATGGTCTGCCAGGTGCATCTGCAGGAGTCGGGCCCGGACTGTGAAGCCTTCGGAG ACCTGTCCCTCAACTGTACTGTCTGTTGGTCCGTTCAGTGGTTACTACTGAGACTGTGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGAACATCTATTACAGTGGAGCACCACTACAACCCCTCCCTCCAGAGTCAGTCCACATACAGTAGACAGTCC AAGAACCAGCTCTCCCTGAACCTGAACCTGTGACCCGCTGCGACACGCGCGTATTACTGTGCGAGAGTGAACCGGGCAGTGGCTGTGACGTGCGGAGTGTGGGGTGGTTCGACCCCTGGGCCAGGGAATCTGGTGTCTCTCAGCATCCCCGACCAG CCCAAGTCTTCCCGCTGAGCCTCTGCAGCACCCAGCCAGATGGAACGTGTCTATCGCTGCTGCTGACAGGCTTCTCCCCAGAGCCACTCAGTGTGACTGTGAGCGAAAGCGACAGGCGGTGACCGCCAGAACTCCC
66_I_GHV4-59_I_GHJ5	ATACTTCTGAGAGTCTGGACCTCTGTGCAAGAACATGAACATCTGTGGTTCTTCTCTCTGCTGGCAGCTCCCAGATGGCCCTGTCCAAGTGCAGCTGCAAGAGTCGGGCCCGGACTGTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGCACTGTGTGGTGG CTCCCTCACTTTTACTACTGGAGCTGATCCGGCAGCCCCCGGGAAGGGACCGGAGTGGATTGGGAATGTATTTCAATGGCAGCACCACTACAACCCCTCCACCAAGTGCAGTGCATATCAGTGGACAGTCCAAGAACCAGTTCTCCCTGAACCTGAGTCTGCG ACCGACGCGACACGCGGTATTACTGTGCGAGAGTGAACCGGGCAGTGGCTGTGACGTGCGGAGTGTGGGGTGGTTCGACCCCTGGGCCAGGGAATCTGGTGTCTCTCAGCATCCCCGACCAG AGCACCTGTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTGTTGAACTCAGCGCCCTGACCAGCGGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
67_I_GHV1-3_I_GHJ3	AGCACATAACAACCACATTCTCTCTTAAAGAGCCCTGGGACACAGCTCATCACCATGACTGGACCTGGAGTTCCTCTTGGTGGCAGCAGTACAGGTGTCCAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCGGAGGTGAAGAAGCCTGGTCTCGTGAAG GTCTCTGCAAGGCTCTGGTCTCCTCAGCAGTTCGGCTTCACTGCTGGTGGCGACTGGCCCTGGACAGGACTGAGTGCATGGGAGGAATCATCCCTATGTATGGCACAGCAGACTACGCACAGAGTTCCAGGACAGACTCACTATTGTGCGACGAACTCACAGC CACAGTCCCATGGAAGTGCAGGCTGACATCTGAAGACACGCGCATGTATTTCTGCGCGAGACGAAAGCTGTATAGTGGTGGCCCGCCCGCGAGCTTTTGATATCTGGGCCAAGGACAATGATCATGTCTCTCAGCTCCACCAAGGGCCCATGGTCTTCCC CTGTGGCACCTCTCCAAGAGCACCTGTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTGTTGAACTCAGCGCCCTGACCAGCGGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
67_I_GHV1-3_I_GHJ3	GGCAGCACATAACAACCACATTCTCTCTTAAAGAGCCCTGGGACACAGCTCATCACCATGACTGGACCTGGAGTTCCTCTTGGTGGCAGCAGTACAGGTGTCCAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGTCTCGTGAAG AAGTCTCCTGCAAGGCTCTGGTACTCCTCAGCAGTTTTGGCTTCACTGCTGGTGGCGACAGGCCCTGGACAAGGACTTGAAGTGCATGGGAGGAATCATCCCTATGTACGGAAGCGCAGACTACGCACAGAGTTCCAGGGCAGACTCAGATTGTGCGACGAACTCA CAGCCACAGTCCCATGGAAGTGCAGGCTGACATCTGAAGACACGCGCGTTATTTCTGCGCGAGACGAAAGCTGTATAGTGGTGGCCCGCCCGCGAGCTTTTGATATCTGGGCCAAGGACAATGATCATGTCTCTCAGCTCCACCAAGGGCCCATGGTCTTCCC TTCCCCCTGACCCTCTCCAAGAGCACCTGTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTGTTGAACTCAGCGCCCTGACCAGCGGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
69_I_GHV5-10-1_I_GHJ6	AGTCTCCTTACCACCCAGCTGGGATCTCAGGGCTTCTTTCTGTCTCTCCAGGATGGGGTCAACCCCATCTCGCCCTCCTGCTGTTCTCCAAGGAGTCTGTGCGGAAGTGCAGCTGGTGCAGTCCGGAGCAGAGGTGAAGAAGCCCGGGAGTCTGTAGGAT CTCTGTAAAGGTTCTGGATACAGCTTACCAGCTACTGGATCAGCTGGGTGCGCCAGATGCCCGGGAAGGCTGGAGTGGATGGGGAAGATTGATCTACTACTCTTATACCACCTACAGCCCGTCTTCCAAGGCCAGTCCACATCTCAGTGCACAAGTCCATCAGCACT GCCTACCTGCAGTGGAGCAGCCTGAAGGCTCGACACCCGATATATTACTGTGCGAGCCGGTGGCCGCGACGACCCTACTACGGTTTTGACGTGTGGGCCAAGGACCAGGTACCCTGTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCCTC CTTCCAAGAGCACCTGTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTGTTGAACTCAGCGCCCTGACCAGCGGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
69_I_GHV5-10-1_I_GHJ6	AGTCTCCTTACCACCCAGCTGGGATCTCAGGGCTTCTTTCTGTCTCTCCAGGATGGGGTCAACCCCATCTCGCCCTCCTGCTGTTCTCCAAGGAGTCTGTGCGGAAGTGCAGTGGTGCAGTCCGGAGCAGAGGTGAAGAAGCCCGGGAGTCTGTAGGAT CTCTGTGAGGTTCTGGATACACTTTAACAGCTACTGGATCAGCTGGGTGCGCCAGATGCCCGGGAAGGCTGGAGTGGATGGGGAAGATTGATCTACTACTCTTATACCACCTACAGCCCGTCTTCCAAGGCCAGTCCAGTCTCAGTGCACAAGTCCATCAGCACT GCCTACCTGCAGTGGAGCAGCCTAAGGACTCGACACCCGCTATATTACTGTGCGAGCCGGTGGCCGCGACGACCCTACTCGTTTTGACGTGTGGGCCAAGGACCAGGTACCCTGTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCCTC CAGCACCCAGCAGATGGGAACGTGTCTATCGCTGCTGGTCCAGGACTACTTCCCCAACCGGTGACGGTGTGTTGAACTCAGCGCCCTGACCAGCGGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
92_I_GHV1-2_I_GHJ4	GAGCATACCCAGCAACCACATCTGTCTCTAGAGAAATCCCCTGAGAGTCCGTTCTCACCATGACTGGACCTGGAGATCCTCTTCTGGTGGCAGCAGCCACAGGAGCCCACTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGGGCTCAGTG AGGGTCTCCTGCAAGACTTCTGATACACTTACCAGCTACTGATCAGCTGGGTGCGCCAGATGCCCGGGAAGGCTGGAGTGGATGGGGAAGATTGATCTACTACTCTTATACCACCTACAGCCCGTCTTCCAAGGCCAGTCCAGTCTCAGTGCACAAGTCCATCAGCACT GCCTACCTGCAGTGGAGCAGCCTAAGGACTCGACACCCGCTATATTACTGTGCGAGCCGGTGGCCGCGACGACCCTACTCGTTTTGACGTGTGGGCCAAGGACCAGGTACCCTGTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCCTCTCCA AAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGTTGAACTCAGCGCCCTGACCAGCGGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
92_I_GHV1-2_I_GHJ4	GAGCATACCCAGCAACCACATCTGTCTCTAGAGAAATCCCCTGAGAGTCCGTTCTCACCATGACTGGACCTGGAGATCCTCTTCTGGTGGCAGCAGCCACAGGAGCCCACTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGGGCTCAGTG AAGGTCTCCTGCAAGCTTCTGATACACTTACCAGCTACTGATCAGCTGGGTGCGCCAGATGCCCGGGAAGGCTGGAGTGGATGGGGAAGATTGATCTACTACTCTTATACCACCTACAGCCCGTCTTCCAAGGCCAGTCCAGTCTCAGTGCACAAGTCCATCAGCACT GCCTACCTGCAGTGGAGCAGCCTAAGGACTCGACACCCGCTATATTACTGTGCGAGCCGGTGGCCGCGACGACCCTACTCGTTTTGACGTGTGGGCCAAGGACCAGGTACCCTGTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCCTCTCCA AAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGTTGAACTCAGCGCCCTGACCAGCGGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
92_I_GHV1-2_I_GHJ4	GAGCATACCCAGCAACCACATCTGTCTCTAGAGAAATCCCCTGAGAGTCCGTTCTCACCATGACTGGACCTGGAGATCCTCTTCTGGTGGCAGCAGCCACAGGAGCCCACTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGGGCTCAGTG AAGGTCTCCTGCAAGCTTCTGATACACTTACCAGCTACTGATCAGCTGGGTGCGCCAGATGCCCGGGAAGGCTGGAGTGGATGGGGAAGATTGATCTACTACTCTTATACCACCTACAGCCCGTCTTCCAAGGCCAGTCCAGTCTCAGTGCACAAGTCCATCAGCACT GCCTACCTGCAGTGGAGCAGCCTAAGGACTCGACACCCGCTATATTACTGTGCGAGCCGGTGGCCGCGACGACCCTACTCGTTTTGACGTGTGGGCCAAGGACCAGGTACCCTGTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCCCTCTCCA AAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTTCCCCAACCGGTGACGGTGTGTTGAACTCAGCGCCCTGACCAGCGGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA

24_I_GHV1-24_I_GHJ2	ACCATCACAAACAGCCACATCCCTCCCCTACAGAAGCCCCAGAGCGCAGCACCTCACCATGGACTGCACTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAGGCACGCACGCCCAGTCCAGTTGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAAAGTTTCCGGAGACAGCCTCACTGAATATCCATGCACTGGGTGCGACAGACTCCTGAAAAGGGCTTGAAGTGGTGGAGCAATGATCCTGAGGAAGATGAAATAGTCTACGCACAGAAGTTCCAGGGCAGAGTACCATGACCGAGACACATCAACAGACACAGTCTACCTGGAGCTGAGCAGCCTGAGATCTGAGACACGGCCGTATTACTGTGCAACAGATTACTATGATAAATAGTGGTACTATCCAACTGGTACTTCGATCTCTGGGGCCGTGGCACCTGGTCAATTGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGGCGCCCTGACCAAGCGCGTGCACACCTCCCGGCTGTCTACAGTCTCAGGA
24_I_GHV1-24_I_GHJ2	ACCATCACAAACAGCCACATCCCTCCCCTACAGAAGCCCCAGAGCGCAGCACCTCACCATGGACTGCACTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAGGCACCCACGCCCAGTCCAGTTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAAAGTTTCCGGAGAAAGGCTCACTGAATATCCATGCACTGGGTGCGACAGACTCCTGAAAAGGACTTGAAGTGGATGGAGGTTCTGATCCTGAGGAAGATGAAATAGTCTACGCACAGAAGTTCCAGGGCAGAGTACCATGACCGAGACACATCAACAGACACAGTCTACCTGGAGCTGAGCAGCCTGAGATCTGACGACACGGCCGTATTACTGTGCAACAGATTACTTGTAAACAGTGGTATTACCCAACTGGTACTTCGATCTCTGGGGCCGTGGCACCTGGTCAATTGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGGCGCCCTGACCAAGCGCGTGCACACCTCCCGGCTGTCTCT
24_I_GHV1-24_I_GHJ2	ACCATCACAAACAGCCACATCCCTCCCCTACAGAAGCCCCAGAGCGCAGCACCTCACCATGGACTGCACTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAGGCACCCACGCCCAGTCCAGTTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAAAGTTTCCGGAGAAAGGCTCACTGAATATCCATGCACTGGGTGCGACAGACTCCTGAAAAGGACTTGAAGTGGATGGAGGTTCTGATCCTGAGGAAGATGAAATAGTCTACGCACAGAAGTTCCAGGGCAGAGTACCATGACCGAGACACATCAACAGACACAGTCTACCTGGAGCTGAGCAGCCTGAGATCTGACGACACGGCCGTATTACTGTGCAACAGATTACTTGTAAACAGTGGTATTACCCAACTGGTACTTCGATCTCTGGGGCCGTGGCACCTGGTCAATTGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGGCGCCCTGACCAAGCGCGTGCACACCTCCCGGCTGTCTCTACAGTCTCAGGA
24_I_GHV1-24_I_GHJ2	ACCATCACAAACAGCCACATCCCTCCCCTACAGAAGCCCCAGAGCGCAGCACCTCACCATGGACTGCACTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAGGCACGCACGCCCAGTCCAGTTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAAAGTTTCCGGAGAAAGGCTCACTGAATATCCATGCACTGGGTGCGACAGACTCCTGAAAAGGACTTGAAGTGGATGGAGGTTCTGATCCTGAGGAAGATGAAATAGTCTACGCACAGAAGTTCCAGGGCAGAGTACCATGACCGAGACACATCAACAGACACAGTCTACCTGGAGCTGAGCAGCCTGAGATCTGACGACACGGCCGTATTACTGTGCAACAGATTACTTGTAAACAGTGGTATTACCCAACTGGTACTTCGATCTCTGGGGCCGTGGCACCTGGTCAATTGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGGCGCCCTGACCAAGCGCGTGCACACCTCCCGGCTGTCTCTACAGTCTCAGGA
63_I_GHV2-5_I_GHJ5	AGTGACTCCTGCCCCACATGGACACACTTTGCTCCAGCTCCTGCTGCTGACCTCCCTCATGGTCTTGTCCAGATCACCTTGACGGAGTCTGGTCTACGCTGGTGAACCACACAGACCTCAGCTGACCTGCAATTTCTGGAATCTCACTCATCACTAGTGAAGTGGTGGTGGTGGTTCAGCCCCAGAAAGGCCCTGAGTCCCTGCACTCATTCTTGGATGGAGATAAGCGCTACAGCCCATCTCTGAACCGCAGGCTCACCATCAACAAGACACCTCCAAAAACAGGTGTCCTTACAATGACCAACATGGACCTGTGGACACAGCCACATATTACTGTGACACCTCGCTATGTTCCGGGAATTTGTTCCACCTGGGGCCAGGAATCTGTCACCTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGGCGCCCTGACCAAGCGCGTGCACACCTCCCGGCTGTCTCTACAGTCTCAGGA
63_I_GHV2-5_I_GHJ5	GGGTTTTCTTATATGGGAGTGAAGTCTGCTGCCCCACATGGACACACTTTGCTCCAGCTCCTGCTGCTGACCTCCCTCATGGTCTTGTCCAGATCACCTTGACGGAGTCTGGTCCAAGCTGGTGAACCACACAGACCTCAGCTGACGTGCAACTTCTCTGATTCTCACTCATCACCAGTGAATGGGTGGTGGTCCGTGAGTGGTCCGTGAGTGGTCCGTGCACTCATTCTTGGATGGAGATAAGCGCTACAGCCATCTCTGAACCGCAGGCTCACCATCAACAAGACACCTCCAAAAACAGGTGTCCTGACAATGACCAACATGGACCTGTGGACACAGCCACATATTACTGTGACACCTCGCTATGTTCCGTGGGAATTTGTTCCACCTGGGGCCAGGAATCTGTCACCGTCTCCTCGGCTCCACCAAGGGCCCATCGTCTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGGCGCCCTGACCAAGCGCGTGCACACCTCCCGGCTGTCTCTACAGTCTCAGGA
63_I_GHV2-5_I_GHJ5	GCACATCCTTCTTATATGGGAGTGAAGTCTGCTGCCCCACATGGACACACTTTGCTCCAGCTCCTGCTGCTGACCTCCCTCATGGTCTTGTCCAGATCACCTTGACGGAGTCTGGTCCAAGCTGGTGAACCACACAGACCTCAGCTGACCTGCAACTTCTCTGATTCTCACTCATCACTAGTGAATGGGTGGTGGTCCGTGAGTGGTCCGTGAGTGGTCCGTGCACTCATTCTTGGATGGAGATAAGCGCTACAGCCATCTCTGAACCGCAGGCTCACCATCAACAAGACACCTCCAAAAACAGGTGTCCTTACAATGACCAACATGGACCTGTGGACACAGCCACATATTACTGTGACACCTCGCTATGTTCCGTGGGAATTTGTTCCACCTGGGGCCAGGAATCTGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGGCGCCCTGACCAAGCGCGTGCACACCTCCCGGCTGTCTCTACAGTCTCAGGA
63_I_GHV2-5_I_GHJ5	CAAGTTTTCTTATATGGGAGTGAAGTCTGCTGCCCCACATGGACACACTTTGCTCCAGCTCCTGCTGCTGACCTCCCTCATGGTCTTGTCCAGATCACCTTGACGGAGTCTGGTCCAAGCTGGTGAACCACACAGACCTCAGCTGACCTGCAACTTCTCTGATTCTCACTCATCACTAGTGAATGGGTGGTGGTCCGTGAGTGGTCCGTGAGTGGTCCGTGCACTCATTCTTGGATGGAGATAAGCGCTACAGCCATCTCTGAACCGCAGGCTCACCATCAACAAGACACCTCCAAAAACAGGTGTCCTGACAATGACCAACATGGACCTGTGGACACAGCCACATATTACTGTGACACCTCGCTATGTTCCGTGGGAATTTGTTCCACCTGGGGCCAGGAATCTGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGGCGCCCTGACCAAGCGCGTGCACACCTCCCGGCTGTCTCTACAGTCTCAGGA
63_I_GHV2-5_I_GHJ5	AAATGGTTTTCTTATATGGGAGTGAAGTCTGCTGCCCCACATGGACACACTTTGCTCCAGCTCCTGCTGCTGACCTCCCTCATGGTCTTGTCCAGATCACCTTGACGGAGTCTGGTCCAAGCTGGTGAACCACACAGACCTCAGCTGACCTGCAACTTCTCTGATTCTCACTCATCACTAGTGAATGGGTGGTGGTCCGTGAGTGGTCCGTGAGTGGTCCGTGCACTCATTCTTGGATGGAGATAAGCGCTACAGCCATCTCTGAATGGAGGCTCACCATCAACAAGACACCTCCAAAAACAGGTGTCCTGACAATGACCAACATGGACCTGTGGACACAGCCACATATTACTGTGACACCTCGCTATGTTCCGTGGGAATTTGTTCCACCTGGGGCCAGGAATCTGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGGCGCCCTGACCAAGCGCGTGCACACCTCCCGGCTGTCTCTACAGTCTCAGGA
141_I_GHV3-21_I_GHJ3	AGCTCTGAGAGAGGACCTTGGCCCTGATTCCAAGGCTATCCACTTGGTATCAGCAGTACGACCCAGGATTACCATGAACTGGGGCTCCGTGATTTCTAGTTGCTATTTAGAAAGTTTTCCAGTGTAGGTGAGTGGTGGGAGGCTGGTCAAGCCTGGGGTCCCTGAGACTCTCCTGTGCACTCCTGATTCAGTTCAGTAAATGATGATGAAGTGGTCCGCGAGTGGTCCGCGAGTGGTCTCCTCATTAGTGGTCCAGTAGTTTCAATACTACGCAGACTCAATGAAGGGCCGATTACCACTCCAGAGACAACGCTAGAACTCACTATATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTCCAGAGATACCCGCTAGCCCGGATACTTTGATTCTGGGGCCAAGGGACAATGTGACCGTTTTCTCAGCCTCCACCAAGGGCCCATCGTCTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGGCGCCCTGACCAAGCGCGTGCACACCTCCCGGCTGTCTCTACAGTCTCAGGA

108_I_GHV1-8_I_GHJ4	GGAGAGCATCACTCAACAACCACATCTGTCTCTAGAGAAAACCTGTGAGCAGCGTCTCACCATGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAAGTCCCACGCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGGCCTCA GTGAGAATCTCTGCAAGCTTCTGAATACACCTTACCACCTATGATATCAACTGGGTGCGACAGGCGCTGGACAAGGCTTGAAGTGGGTGGCTGGATGAACCTAATACTGGCGACACCGCCTATGGCGAAGTCCAGGGCAGAGTACCCTGACCCGGAACACCTCC ATAGCCACAGCCTACATGAGCTGAGCAGCCTGCGATCTGAGACACGCGGTATTATTGTGCGAGAGCCACCTTCTGACTTCTATGTTTGGGGACTTATTCAACCACTTATATACTGGGTGAGGAAACCTGCTCACCGTCTCCTCAGCCTCCACCAAGGGCCCAT GGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
108_I_GHV1-8_I_GHJ4	ATCACTCAACAACCACATCTGTCTCTAGAGAAAACCTGTGAGCAGCTCCTCACCATGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAAGTCCCACGCCAGGTGCAGCTGGTGCAGTCTGGGACTGAAGTGAAGAACCTGGGGCCTCAGTGAAGGT TTCTGTAAAGCTTCTGATACACCTTACCATTATGATATCAACTGGGTGCGACAGGCTGCTGGACAAGGCTTGAAGTGGATGGGATGAACCTCAAAGTGGCAAACCGCCTATGACAGAAAGTCCAGGGCAGACTTATCATGACCCGGAACACCTCCATGAAGCACA GCCTACATGAGCTGAAGCAGCTGAGATCTGACGACACGCGCTTACTACTGCGAGAGCCAGTTCGTACTTCTATGATTGGGGACTTATTCAACCACTTATATACTGGGTGAGGAAACCTGCTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTTCCC CCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
150_I_GHV1-69D_I_GHJ3	ATCACATAACAACCACATCTCTCTAAGAACCCCTGGGAGCAGCTCATCACCATGACTGGACCTGGAGGTTCTCTTTGGTGGCAGCAGCTACAGGTGTCCAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGTCTCGGTGAAG GTCTCTGCAAGGCTTCTGAGGACCTTCAAGCAATATGCTATCACCTGGGTGCGACAGGCCCTGGACAAGGCTTGAAGTGGATGGAGGATCATCCCTATCTTTGATACAGCAGACTACACAGCAGTCCAGGGCAGAGTACCATACCCTGACGAAATCCACGAA CACAGCCTACATGAGGTGAGCAGCTCAGATCTGAGGACACGCGGTATTATTGTGCGAGAGGATGGAGGCTCGGCATGGCAGTCTGATGCTTTGATATCTGGGGCAAGGGACAATGTCTGTCTTCCAGCCTCCACCAAGGGCCCATCGTCTTCCC CCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
150_I_GHV1-69D_I_GHJ3	ATCACATCAACAACCACATCTCTCTAAGAACCCCTGGGAGCAGCTCATCACCATGACTGGACCTGGAGGTTCTCTTTGGTGGCAGCGCCACAGGTGTCCAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGTCTCGGTGAAG GTCTCTGCAAGGCTTCTGAGGACCTTCAAGCAATATGCTATCACCTGGGTGCGACAGGCCCTGGACAAGGCTTGAAGTGGATGGAGGATCATCCCTATCTTTGATACAGCAGACTACACAGCAGTCCAGGGCAGAGTACCATACCCTGACGAAATCCACGAA CACAGCCTACATGAGGTGAGCAGCTCAGATCTGAGGACACGCGGTATTATTGTGCGAGAGGATGGAGGCTCGGCATGGCAGTCTGATGCTTTGATATCTGGGGCAAGGGACAATGTCTGTCTTCCAGCCTCCACCAAGGGCCCATCGTCTTCCC CCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
150_I_GHV1-69D_I_GHJ3	AACCACATCTCTCTAAGAACCCCTGGGAGCAGCTCATCACCATGACTGGACCTGGAGGTTCTCTTTGGTGGCAGCAGCTACAGGTGTCCAGTCCCAGGTGCAGTGGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGTCTCGGTGAAG GGGCTTCTGAGGACCTTCAAGCAATATGCTATCACCTGGGTGCGACAGGCCCTGGACAAGGCTTGAAGTGGATGGAGGATCATCCCTATCTTTGATACACCAACTACGACAGAAAGTCCAGGGAAAGTACAGGTTAGTGTGACGAGAGCCAGAACACAGCCTA CATGGAGCTGACTACTGACATCTGAAGACACGCGGTATTACTGTGCGAGGATGGAGGCTCGGCATGGCAGTCTGATGCTTTGATATCTGGGGCAAGGGACAATGTCTCACCGTCTTCCAGCCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCAC CTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
175_I_GHV3-30_I_GHJ4	GAGCTCTGGAGAGAGCCAGCACTAGAAGTGGCGGTGTTCCATTGCTGATCAGCACTGAACACAGAGGACTCACCATGAGTTTGGGTGAGCTGGTCTCTCTGTTGCTTTAAGAGTGTCCAGTGTGATGAGTGTGAGTCTGGGGAGGCGT GGTCCAGCCTGGAGGTTCTGAGACTCTCTGTGAGCCTCTGGATTGAGTTCAAGATGAGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGCTGAGTGGTGGCAGCCATGCTAATGATGAGTAAAAAATACTATGAGACTCCGTGAAGGGCGGATT CACCATCTCCAGACAATCCAAGAACCACTGATCTGAAATGAACAGCCTGAGAACTGAGACACGGCTATGATTACTGTGCGAAAGATGGGACATATGTTTGGGGAGTTATCAGAGTTGACTACTGGGCCAGGGAACCCGGTCCAGCTCTCCTCAGCTTCCAC CAAGGGCCATCGTCTCCCCCTGGCCCTGCTCCAGGAGCACCTCCGAGACACG
175_I_GHV3-30_I_GHJ4	GGGAGAGAGCCAGCACTAGAAGTGGCGGTGTTCCATTGCTGATCAGCACTGAACACAGAGGACTCACCATGAGTTTGGGTGAGCTGGTCTCTCTGTTGCTTTAAGAGTGTCCAGTGTGATGAGTGTGAGTCTGGGGAGGCGTGGTCCAG CTGGGGGCTCCTGAGACTCTCTGTGAGCCTCTGATTGAGTCTGAGGCTATGAGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGACTGAGTGGTGGTGGTCCATATCTAATGATGAAGTAAACAAATACTATGAAGACTCCGTGAAGGGCGGATTACCATCTCC AGAGACAATCCAAGAACAGCTGTTCTGCAATGAACAGCCTGAGACCTGAGACACGCTATGATTACTGTGCGAAAGATGGGACATATGTTTGGGGAGTTATCAGAACTGGACTGTGGGGCCAGGGAACCTGTTACCCTCTCCTCAGCTTCCACCAAGGGCCC ATCCGTCTCCCCCTGGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
188_I_GHV1-69_I_GHJ5	AGCATCACATAACAACCACATCTCTCTGAAGAACCCCTGGGAGCAGCTCATCACCATGACTGGACCTGGAGGTTCTCTGTGTGGTGGCAGCAGCTACAGGTGTCCAGTCCCAGGTGCATCTGGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGTCTCGGTG AAGGTCTCCTGCAAGGCTTCTGAGGACCTTCTATGCTATCAGCTGGGTGCGACAGGCCCTGGACAAGGACTTGAAGTGGTGGAGGCTCGTCCGATGTTGATACACCAAGCTATGACAGAAAGTCAAGGGCAGAGTACCATACCCTGACAAATCCACGAGCAC AGCCTACATGAGCTGTACAGCCTGACATCTGAGGACACGCGCTTATTACTGTGCGAGAGGCTTATAGCAGTCTTCTGTGTTGACCCCTGGGGCCAGGGAACCTGTCTCATCTCTCAACCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGA GCACCTCTGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
188_I_GHV1-69_I_GHJ5	ATCACATAACAACCACATCTCTCTGAAGAACCCCTGGGAGCAGCTCATCACCATGACTGGACCTGGAGGTTCTCTTTGGTGGCAGCAGCTACAGGTGTCCAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGTCTCGGTGAAG GTCTCTGCAAGGCTTCTGAGGACCTTCAAGCAATATGCTATCACCTGGGTGCGACAGGCCCTGGACAAGGACTTGAAGTGGTGGAGGCTCGTCCGATGTTGATACACCAAGCTATGACAGAAAGTCAAGGGCAGAGTACCATACCCTGACAAATCCACGAGCAC ATGCTACTACTTGGAGCTGAGCAGCCTGACATCTGACGACACAGCCCTTATTACTGTGCGAGCGACCTATAGCAGTCTTCTGTGTTGACCCCTGGGGCCAGGGAACCTGTCTCATCTCTCAACCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCC AAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
188_I_GHV1-69_I_GHJ5	GGGATCACATAACAACCACATCTCTCTGAAGAACCCCTGGGAGCAGCTCATCACCATGACTGGACCTGGAGGTTCTCTTTGGTGGCGCAGCTACAGGTGTCCAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGTCTCGGTGAG GAAGTCTCCTGCAAGGCTTCTGAGGACCTTCAACAGCTATGCTATCAGCTGGGTGCGACAGGCCCTGGACAAGGCTTGAAGTGGTGGAGGATCGTCCCTATCTTTGAGACACCAAGTACGACAGAAAGTCCAGGGCAGAGTACCATACCCTGACAAATCCACGAGCAC GAGCACAGCCTACATGAGCTGACAGCCTGAGATCTGAGGACACGCGCTTATTACTGTGCGAGCGACCTATAGCAGTCTTCTGTGTTGACCCCTGGGGCCAGGGAACCTGTCTCATCTCTCAACCTCCACCAAGGGCCCATCGTCTTCCCCCTGGCACCTCTCC TCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA

228_I_GHV3-21_I_GHJ1	AGCTCTGAGAGAGGAGCCTTAGCCCTGGATTCCAAGGCCATCCACTTGGTGATCAGCACTGAGCACCGAGGATTACCATTGGAAGTGGGGCTCCGCTGGGCTTCTCTTGTGCTATTTAGAAGGTGTCCAGTGTGAGGTGCAGCTGGTGGAGTCGGGGGAGGCGCTGTCAGCCGGGGGCTCCCTGAGAGTTTCTGTGAGAGTTCCTGTGAGCCTCTGATTCACTTCACTTCTCTACAGCATGAGCTGGTCCGCGAGGCTCCAGGGAAGGGCTGAAGTGGGTCTCATCTATTAGCAGTAGTGGAAATTACATATACTACGCAGACTCAGTGAAGGGCCGATTACCGTGTCCAGAGACAACCTCAAGAACTCAATATATCTGAGATGAACAGCCTGAGAGCCGAGGACACGGTGTGATTACTGTGCGAGAGATAGTGTGCGCAGCACCTGGTATTGGATGGCTAACACTTCCAACACTGGGGCCCCGGCACCTGTCCAGCTCTCCTCAGCCTCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
228_I_GHV3-21_I_GHJ1	AGCTCTGAGAGAGGAGCCTTAGCCCTGGATTCCAAGGCCATCCACTTGGTGATCAGCACTGAGCACCGAGGATTACCATTGGAAGTGGGGCTCCGCTGGGTTTTCTTGTGGTATTTAGAAGGTGTCCAGTGTGAGGTGCAGTGGTGGAGACTGGGGAGGCGCTGTCAGCCGGGGGCTCCCTGAGACTCTCCTGTGAGCCTCTGATTCACTTCACTAGTAGTACAGCATGAGCTGGTCCGCGAGGCTCCAGGGAAGGGCTGAAGTGGGTCTCTCTATCAGTAGTAGTGGTAGTTACATGACTATGAGACTCCGTGAAGGGCCGATTACCATTTCCAGAGACAACGCCAGAACTCACTGTTTCTGCAAGTGAACAGCCTGAGAGCCGAGACACGGTGTATTACTGTGCGAGAGATAGTGTGCGCAGTACCTGGTACTGGATGGCTAACACTTCCAGCGCTGGGGCCCCGGCACCGTGGTACCCTGTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
228_I_GHV3-21_I_GHJ1	ATGGGGGAGAGAGGAGCCTTAGCCCTGGATTCCAAGGCCATCCACTTGGTGATCAGCACTGAGCACCGAGGATTACCATTGGAAGTGGGGCTCCGCTGGGTTTTCTTGTGGTATTTAGAAGGTGTCCAGTGTGAGGTGCAGTGGTGGAGACTGGGGAGGCGCTGTCAGCCGGGGGCTCCCTGAGACTCTCCTGTGAGCCTCTGATTCACTTCACTAGTAGTACAGCATGAGCTGGTCCGCGAGGCTCCAGGGAAGGGCTGAAGTGGGTCTCTCTATCAGTAGTAGTGGTAGTTACATGACTATGAGACTCCGTGAAGGGCCGATTACCATTTCCAGAGACAACGCCAGAACTCACTGTTTCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGTGTATTACTGTGCGAGAGATAGTGTGCGCAGTACCTGGTACTGGATGGCTAACACTTCCAGCGCTGGGGCCCCGGCACCGTGGTACCCTGTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
233_I_GHV3-74_I_GHJ6	CACCTCTGTGAAGAAAACCCAGCCCTGCAGCTCTGGAGAGAGCCCCAGCCCTGGGATTCCCAGCTGTTCTGTCTGATCAGCACTGACACAGAGAAGTACCATTGGGCTGACCTGGTTTTCTTGTGCTATTTAAAGGTGTCCAGTGTGAGGGCAGCTGGTGGAGTCCGGGGGAGCCTTAGTTCACTCTGGGGGCTCCCTGAGACTCTCTGTGAGCCTCTGATTCACTTCACTTCACTACTGATGACTGGATGACTGGTCCGCGAAGCTCCAGGGAAAGGGCTGAAGTGGGTCTCATCTAGTATTAAAGGTGACGGGAGTAGCACAACTACGCGGACTCCGTGAAGGCCGATTACCATTCCAGAGACAACGCCAAGAACACACTGTTTTGCAAAATAACTCTGAGAGCCGACGACACGGCTGTATTACTGTGCAAAAGCGGGCGGATATTGCACTAGTACCACCTGCCATATCCTAGTATGAGCTGTGGGCCAAGAACACGTCACCGTCTCCTCAGCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
233_I_GHV3-74_I_GHJ6	GGAGCCCCAGCCCTGGATTCCCAGCTGTTCTGCTTGTGATCAGCACTGACACAGAGAAGTACCATTGGGCTGACCTGGTTTTCTTGTGCTATTTAAAGGTGTCCAGTGTGAGGGCAGCTGGTGGAGTCCGGGGAGGCTTAGTTAGTCCAGCTGGGGTCTCTGTGAGCTCTCCTGTGAGCCTCTGATTCACTTCACTTCACTACTGATGACTGGTCCGCGAAGCTCCAGGGAAGGGCTGGTGGGTCTCAGTATTAAAGGTGATGGAGTGGCACAACTACGCGACTCCGTGAAGGGCCGATTACCATTCTCCAGAGACAAGCCAAAGAACACTGTTTCTGAGATGAACACTCTGAGAGCCGAGACACGGCTGTATTACTGTGCAAAAGCGGGCGGATTTGCACTAGTACCACCTGCCATATCCTAGTATGAGCTGTGGGCCAAGGACTACGGTACCCTGTCTCAGCTCCACCAAGGGCCCATCGT
245_I_GHV1-69D_I_GHJ4	ATCACGTAACAACCACATCTCCTCTATAGAAGCCCTGGGAGCACAGCTCTGACCATGACTGACCTGGAGTTCCTCTTGTGTGGCAGCAGTACAGGTGTCGGTCCCAGTGCAGTGTGTCAGTCTGGGGCTGAGGTAAAGGAGCCTGGGTCTCGGTGAAAGTCTCCTGCAAGGCTTCTGAGGACACTTCCAGCAGTATGCTTTCACTGGGTGCGACAGGCCCTGGACAAGGGCTTGAAGTGGATGGGAGGAATCATGCTCTATTGTTGGAACAAGAACTACGCACAGAAAGTTCAGGGTAGAGTACGATTACCGCGACGAATCCACGAGCAGCTTACATGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTATTATTGTGCGAGAACTTTATTATGATAACAGTGGCTATTATTGGGCCAGGAACTCCTGTCCAGTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCTGAGCACACCAGCCAGATGGGAACGTGTCATCGCCTGCTGTCAGGCGCTTCCCCCAGGAGCCACTCAGTGTGACTGGAGCGAAAGCGACAGGGCGTGACCCAGAACTCCC
245_I_GHV1-69D_I_GHJ4	ATCACATACAACCACATCTCCTCTAAAGAAGCCCTGGGAGCACAGCTCATCACCATGACTGACCTGGAGTTCCTCTTGTGTGGCAGCAGTACAGGTGTCAGTCCCAGTGCAGCTGGTGCAGTCTGGGGCTGAAGTGAAGAGCCTGGGTCTCGGTGAAGTCTCCTGCAAGGCTTCTGAGGACACTTCCAGCAGTACGTTACGTTTTCAGCTGGTGGCGACAGGCCCTGGACAAGGGCTTGAAGTGGATGGGAGGAATCATGCTCTATTGTTGACAGTAAATACGCACAGAGTTCAGGGCAGAGTACGATTCCGCGCCGAATCCACGAGCACAGCTTACATGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCATGATTACTGTGTGAGAACTTTACTATGATAAAGTGGTATTACTGGGGCCAGGAACTCCGGTACCCTGTCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCTGAGCACCAGCCAGATGGGAACGTGTCATCGCCTGCTGTCAGGCGCTTCCCCCAGGAGCCACTCAGTGTGACTGGAGCGAAAGCGACAGGGCGTGACCCAGAACTCCC
35_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGGAGCCAGCCCTGGGATGTTCAAGTGTGTTTCACTTGGTGATCAGCACTGAAACAGAGAACTACCATTGAGTTTGGGCTGAGTGGTTTTCTTGTGCTATTTAAAGGTGTCCAGTGTGAGGTGCAGCTGGTGGACTCTGGGGAGGCTTGTACACGCGGGGTGTCCTGAGACTCTCCTGTGAGCCTCTGATTCACTTTCAGCTATGCCATGAGTTGGTCCGTCAGGCTCCAGGGAAGGGCTGGAGTGGTCTCAGTATAAGTGGTAGTGGTGGCACTTACTACGCAGACTCCGTGAGGGCCGGTTCACCATCTCCAGAGACAATCCAAGCAAATCTGTCTCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCCGTTTACTGTGCGAGAGGTGGCAGGGCTGGTAAATACGGCGGAAATGTGACTACTGGGCCAGGAACTCCGTGGTACCCTGTCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
35_I_GHV3-23_I_GHJ4	GAGAGAGGAGCCAGCCCTGGGATGTTCAAGTGTGTTTCACTTGGTGATCAGCACTGAAACAGAGAACTACCATTGAGTTTGGGCTGAGTGGTTTTCTTGTGCTATTTAAAGGTGTCAAGACTGAGGTGCAACTGGTGGACTCTGGGGAGGCTTGTACAGCGGGGCTGCTGAGACTCTCCTGTGAGCCTCTGATTCACTTTCAGCTATGCCATGAGTTGGTCCGTCAGGCTCCAGGGAAGGGCTGGAGTGGTCTCAGTATAAGCGTAGTGGTGGCACTTACTACGCAGACTCCGTGAGGGCCGGTCCACCATCTCCAGAGACAATCCAAGCAAATCTGTCTCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCCGTTTACTGTGCGAGAGCGGAGGGCTGGTGAATACGGCGGAAATGTGACTACTGGGCCAGGAACTCCGTGGTACCCTGTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
38_I_GHV3-73_I_GHJ4	AGGTCGTGGAGAGGAGCTCCAGCCTTGGATTCCCAGCTGTCGCACTCGGTGTCGCACTGAAACAGAGACTACCATTGAGTTTGGGCTGAGTGGTTTTCTTGTGCTATTTAAAGGTGTCCAGTGTGAGGTGCAGCTGGTGGAGTCCGGGGAGGCTTGGTCCAGCCTGGGGCTCCGAACTCTCCTGTGAGCCTCTGGGTTCAAGTTCAGTGGCTCTGTATGACTGGTCCGCGAGCTCCGCGAAAGGGCTGGAGTGGTGGCCGATTAGAAGCAACGCTAACAACTACGCGACAGCATATGGTGGTGGTGAAGGACAGGTTACCATTCCAGAGATGATTCAAAGAACACGGCGTATCTGCAATGAACAGCCTGAAATCGAGGACACGGCCGTTTACTGTGCGAGAGCGGAGGGCTGGTGAATACGGCGGAAATGTGACTACTGGGCCAGGAACTCCGTGGTACCCTGTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA

54_I_GHV4-61_I_GHJ4	GCGAGTGTTCCTATATGAGGGAGGGTCTGCTCACATGGAATACTTTCTGAGAGTCTGGACCTCTGTGCAAGAACATGAAACACCTGTGTTCTTCTCTGCTGGTGGCAGCTCCCAGATGGTCTCTGCCAGATGAGCTGAGAGTCCGGGCCAGGACTGGTGAAGCCTTCAGAGACCCCTGCCCTCACCTGACTGTCTGGTGGCTCCATCACCACTGATGATTACTCTGGAGCTGGATCCGCCAGCACCCAGGAGGGCTGGAAATGGATCGGGTACACTATAAACATGGAAATCACCAACTTCAACCCGTCCCTCAGGATCGACTAGCATGTGACAGCTTAAAGAACCTTCTCCCTGAAGCTGAGCTGTGACTGCCGGACACGCCATTTATTTCTGTGCGAGAGAGGATACTGTAATGAAGAACCTGCTTCTGGCTTTTACTCTGCTGGGGCCAGGGAGCCCTGTTATTGTCTCTCAGCTCCACCAAGGCCATCGTCTCCCCCTGCACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTCCCCAACCCGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
54_I_GHV4-61_I_GHJ4	ACCTGTCATACAGAGGCCACCACCCACATGCAAACTCACTTAGGCCACCCACAGAAAACCCACACATTTCTTAAATCAGGGTCTGCTCACATGGAATACTTTCTGAGAGTCTGGACCTCTGTGCAAGAACATGAAACACCTGTGTTCTTCTCTGCTGGTGGCAGCTCCAGATGGTCTCTGCCAGATGAGCTGCGAGAGTCCGGCCAGACTGGTGAAGCCTTCAGAGACCCCTGCTCCCTCACCTGACTGTCTAGTGGCTCCATGACCAGTGTATTACTACTGAGCTGGATCCGCCAGCACCCAGGAGGGCTGGAAATGGATCGGGTACATATAAACATGGAAATCACCAACTTCAACCCGTCCCTCAGGAGTGCAGTGTAGCATGTGACTGCCGGACACGCCATTTATTTCTGTGCGAGAGAGGATACTGTAATGAAGAACCTGCTTCTGGCTTTTACTCTGCTGGGGCCAGGGAGCCCTGTTATTGTCTCTCAGCTCCACCAAGGCCATCGTCTCCCCCTGCACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTCCCCAACCCGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
54_I_GHV4-61_I_GHJ4	CTTTCTATATGAGGGAGGGTCTGCTCACATGGAATACTTTCTGAGAGTCTGGACCTCTGTGCAAGAACATGAAACACCTGTGTTCTTCTCTGCTGGTGGCAGCTCCCAGATGGTCTTCCAGATGAGCTGAGAGTCCGGGCCAGGACTGGTGAAGCCTTCAGAGACCCCTGCCCTCACCTGACTGTCTGTGGTGGCTCCATCAGCAGTGTATTACTACTGAGCTGGATCCGCCAGCACCCAGGAGGGCTGGAAATGGATCGGGTACATATAAACATGGAAATCACCAACTTCAACCCGTCCCTCAGGAGTGCAGTGTAGCATGTGACTGCCGGACACGCCATTTATTTCTGTGCGAGAGAGGATACTGTAATGAAGAACCTGCTTCTGGCTTTTACTCTGCTGGGGCCAGGGAGCCCTGTTATTGTCTCTCAGCTCCACCAAGGCCATCGTCTCCCCCTGCACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTCCCCAACCCGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
74_I_GHV3-15_I_GHJ3	CTCCCTCTCTGATGAAAACCCAGCCCAGTCTGACCCCTGAGCTGTGGAGAGAGAGCCCCAGCCTTGGATTCCCAAGTGTCTTTCATTGATGATCAGGACTGAACACAGAGGACTCACCATGGAGTTTGGCTGAACCTGATTTTCTTGTGCTATTTAAAGTGTCCAGTGTGAGGTGAGCTGGTGGCTCTGGGGAGGCTGGTAAACCCGGGGGCTCTTACACTCTCTGTGAAGCCTCTGGATTCAATTTAGTAACTCTGATGAGTTGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGTTGGCCGTGTTAAAGCAAACCTGATGGTGGACACCCAGACTCGCTGACCCCGTAAAGGAGCAGTGTCAAGAGTATTCAAAAACACATTTCTCTGCAATGAACAGCCTGAAAACCGAGACACAGCCGTGATTATTGTTAAAGTCGATAGAGGAGGGCTTTGATATCTGGGCCAAGGGACATTGGTCAACCGTCTCTCAGCCTCCACCAAGGCCATCGTCTCCCCCTGCACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTCCCCAACCCGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
74_I_GHV3-15_I_GHJ3	ATGGGGGGAGAGGAGCCAGCCTTGGATTCCCAAGTGTCTTTCATTGATGATCAGGACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGAACCTGATTTTCTGCTGCTATTTAAAGTGTCCAGTGTGAGGTGAGCTGGTGGCTGGGGAGGCTGGTAAACCCGGGGGCTCTTACACTCTCTGTGAAGCCTCTGGATTCAATTTAGTAACTCTGATGAGTTGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGTTGGCCGTGTTAAAGTAATCTGATGTTGGCTCACAGACTACCGTGCACCCGTGAAGGAGATTGAGCTCAAGAGTATTCAAAAACACATTTCTCTGACATGAACAGCCTGAAAACCGAGACACAGCCATGATTACTGTGTTAAAGTCGATAGAAGGAGGCTTTTATCTGCTGGGCCAAGGGACGATGTCACCGTCTCTCAGCCTCCACCAAGGCCATCGTCTCCCCCTGCACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTCCCCAACCCGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
80_I_GHV1-2_I_GHJ3	GAGAGCATCACCCAGCAACACATCTGTCTCTAGAGAAATCCCTGAGAGTCCGTTCTCACCATGAGACTGGACCTGGAGGATCCTCTTCTGGTGGCAGCAGCCACAGAGCCCACTCCCAGGTGAGATGGTGCAGTCTGGGGCTGAGGTGAAGAGCCTGGGCCTCATGTAAGGTCTCCTGCAAGGCTTCTGATACACTTACCCTGACTATTTGCACTGGGTGCGACAGGCCCTGGACAAGGGCTTGGAGTGGATGGCATGATGACACCTAACCCGTGGTGGCACAACATGACAAAAGTTTTCAGGGCAGGGTACCTTGACCAGGGACACGTCATCACACAGCCTACATGGAACCTGAGCAGGCTGAGATCTGACGACACGGCCGTGTAATCTGCGAGAGATATCGTAACCTGGAACACCAAAATGATGCTTTTATCTGCTGGGGCCAGGGACAATGTCACCGTCTCTCAGCATCCCCAGCCCAAGGCTCTCCGCTGAGCCTCTGAGCACCAGCCAGATGGAAACGTGGTATCGCTGCTGGTCCAGGGCTTCTCCCCAGGAGCCACTCAGTGTGACCTGGAGCGAAAGCGGACAGGGCTGACCCCAGAAACTTCCC
80_I_GHV1-2_I_GHJ3	GAGAGCATCACCCAGCAACACATCTGTCTCTAGAGAAATCCCTGAGAGTCCGTTCTCACCATGAGACTGGACCTGGAGGATCCTCTTCTGGTGGCAGCAGCCACAGAGCCCACTCCCAGGTGAGATGGTGCAGTCTGGGGCTGAGGTGAAGAGCCTGGGCCTCATGTAAGGTCTCCTGCAAGGCTTCTGATACACTTACCCTGACTATTTGCACTGGGTGCGACAGGCCCTGGACAAGGGCTTGGAGTGGATGGCATGATGACACCTAACCCGTGGTGGCACAACATTTGACAAAAGTTTTCAGGGCAGGGTACCTTGACCAGGGACACGTCATCACACAGCCTACATGGAACCTGAGCAGGCTGAGATCTGACGACACGGCCGTGTAATCTGCGAGAGATATCGTAACCTGGAACACCAAAATGATGCTTTTATCTGCTGGGGCCAGGGACAATGTCACCGTCTCTCAGCCTCCACCAAGGGCCATCGTCTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTCCCCAACCCGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
80_I_GHV1-2_I_GHJ3	GGGAGCATCACCCAGCAACACATCTGTCTCTAGAGAAATCCCTGAGAGTCCGTTCTCACCATGAGACTGGACCTGGAGGATCCTCTTCTGGTGGCAGCAGCCACAGAGCCCACTCCCAGGTGAGATGGTGCAGTCTGGGGCTGAGGTGAAGAGCCTGGGCCTCATGTAAGGTCTCCTGCAAGGCTTCTGATACACTTACCCTGACTATTTGCACTGGGTGCGACAGGCCCTGGACAAGGGCTTGGAGTGGATGGCATGATGACACCTAACCCGTGGTGGCACAACATTTGACAAAAGTTTTCAGGGCAGGGTACCTTGACCAGGGACACGTCATCACACAGCCTACATGGAACCTGAGCAGGCTGAGATCTGACGACACGGCCGTGTAATCTGCGAGAGATATCGTAACCTGGAACACCAAAATGATGCTTTTATCTGCTGGGGCCAGGGACAATGTCACCGTCTCTCAGCCTCCACCAAGGGCCATCGTCTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTCCCCAACCCGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
20_I_GHV4-30-2_I_GHJ5	GGGGAGGTCTGCTCACATGGAATACTTTCTGAGAGTCTGGACCTCTGTGCAAGAACATGAAACACCTGTGTTCTTCTCTGCTGGTGGCCAGTCCCAGATGGTCTGCCCAGGTGAGCTGCGAGAGTCCGGGCCAGGACTGGTGAAGCCTTACAGACCCCTGCTCCCTCAGTGTCTGTGGCTCCATCAACAGTGGTATTACTACTGAGTTGGATCCGCCAGCCCCAGGAGGGCTGGAGTGGATTGGTACATGTAATCCAGTGGGATCAACTACCACAACCCGTCCCTCAAGAGTGCAGTACCATATCAGAGACAGTCAAGAACCTGATCCCTGAACCTGAACTCTGTGACTGCCGACACAGCCGTGTAATCTGCGAGAGATATCGTAACCTGGAACACCAAAATGATGCTTTTATCTGCTGGGGCCAGGGACAATGTCACCGTCTCTCAGCCTCCACCAAGGGCCATCGTCTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTCCCCAACCCGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
20_I_GHV4-30-2_I_GHJ5	GGTAGATGATTTCTATATGAGGGAGGGTCTGCTCACATGGAATACTTTCTGAGAGTCTGGACCTCTGTGCAAGAACATGAAACACCTGTGTTCTTCTCTGCTGGTGGCCAGTCCCAGATGGTCTGCCCAGGTGAGCTGCGAGAGTCCGGGCCAGGACTGGTGAAGCCTTACAGACCCCTGCTCCCTCAGTGTCTGTGGCTCCATCAACAGTGGTATTACTACTGAGTTGGATCCGCCAGCCCCAGGAGGGCTGGAGTGGATTGGTACATGTAATCCAGTGGGATCAACTACCACAACCCGTCCCTCAAGAGTGCAGTACCATATCAGAGACAGTCAAGAACCTGATCCCTGAACCTGAACTCTGTGACTGCCGACACAGCCGTGTAATCTGCGAGAGATATCGTAACCTGGAACACCAAAATGATGCTTTTATCTGCTGGGGCCAGGGACAATGTCACCGTCTCTCAGCCTCCACCAAGGGCCATCGTCTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTCCCCAACCCGTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA

94_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCCAGCCCTGGGATTTTCAGCGCTTTTCATTGGTGATCAGGACTGAACAGAGAGAAGCTCACCATTGGAGTTGGGCTGAGCTGGCTTTTCTTGTTGCTATTTTAAAAGGTGCCAGTGTGAGGTGCAGTTGGTGGAGTCTGGGGAGGCGTGTACAGCCTGGGGGTCCTGAGACTCTCCTGTGCAGCCTCTGATTACCTTTAGAAATATGCCATGAGCTGGTCCGCGAGGCTCCAGGAAAGGGCCGAGTGGGTCTCAGAAATTAGTGTAGTGGGATGACATACTACGACACTCCGAGAAAGGCCGGTTCACCATCTCCAGAGACAACCTCAAAGAGCACGGTGTCTGCAAATGAGCAGCCTGAGAGCCGAGGACACGGCCATATATTACTGTGCGAAAGCTACTATAGCGGGAGGTAGTGGGGCTCCTATGACTACTGGGGCCAGGAAACCTGTTCCGTCTCCTCAGCTCCACCAAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCCTGTCTACAGTCTCAGGA
94_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCCAGCCCTGGGATTTTCAGCGCTTTTCATTGGTGATCAGGACTGAACAGAGAGAAGCTCACCATTGGAGTTGGGCTGAGCTGGCTTTTCTTGTTGCTATTTTAAAAGGTGCCAGTGTGAGGTGCAGTTGGTGGAGTCTGGGGAGGCGTGTACAGCCTGGGGGTCCTGAGACTCTCCTGTGCAGCCTCTGATTACCTTTAGAAATATGCCATGAGCTGGTCCGCGAGGCTCCAGGAAAGGGCCGAGTGGGTCTCAGAAATTAGTGTAGTGGGATGACATACTACGACACTCCGAGAAAGGCCGGTTCACCATCTCCAGAGACAACCTCAAAGAGCACGGTGTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCATATATTACTGTGCGAAAGCTACTATAGCGGGAGGTAGTGGGGCTCCTATGACTACTGGGGCCAGGAAACCTGTTCCACCGTCTCCTCAGCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCCTGTCTACAGTCTCAGGA
94_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCCAGCCCTGGGATTTTCAGCGCTTTTCATTGGTGATCAGGACTGAACAGAGAGAAGCTCACCATTGGAGTTGGGCTGAGCTGGCTTTTCTTGTTGCTATTTTAAAAGGTGCCAGTGTGAGGTGCAGTTGGTGGAGTCTGGGGAGGCGTGCACAGCCTGGGGGTCCTGAGACTCTCCTGTGCAGCCTCTGATTACCTTTAGAAATATGCCATGAGCTGGTCCGCGAGGCTCCAGGAAAGGGCCGAGTGGGTCTCAGAAATTAGTGTAGTGGGATGACATACTACGACACTCCGAGAAAGGCCGGTTCACCATCTCCAGAGACAACCTCAAAGAGCACGGTGTCTGCAAATGAGCAGCCTGAGAGCCGAGGACACGGCCATATATTACTGTGCGAAAGCTACTATAGCGGGAGGTAGTGGGGCTCCTATGACTACTGGGGCCAGGAAACCTGTTCCCGTCTCCTCAGCTCCAC
94_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCCAGCCCTGGGATTTTCAGCGCTTTTCATTGGTGATCAGGACTGAACAGAGAGAAGCTCACCATTGGAGTTGGGCTGAGCTGGCTTTTCTTGTTGCTATTTTAAAAGGTGCCAGTGTGAGGTGCAGTTGGTGGAGTCTGGGGAGGCGTGTACAGCCTGGGGGTCCTGAGACTCTCCTGTGCAGCCTCTGATTACCTTTAGAAATATGCCATGAGCTGGTCCGCGAGGCTCCAGGAAAGGGCCGAGTGGGTCTCAGAAATTAGTGTAGTGGGATGACATACTACGACACTCCGAGAAAGGCCGGTTCACCATCTCCAGAGACAACCTCAAAGAGCACGGTGTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCATATATTACTGTGCGAAAGCTACTATTGCGGGAGGTAGTGGGGCTCCTATGACTACTGGGGCCAGGAAACCTGTTCCACCGTCTCCTCAGCTCCACCAAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCCTGTCTACAGTCTCAGGA
94_I_GHV3-23_I_GHJ4	ATGGGGAGAGAGAGCCCAGCCCTGGGATTTTCAGGTGTTTCATTGGTGATCAGGACTGAACAGAGAGAAGCTCACCATTGGAGTTGGGCTGAGCTGGCTTTTCTTGTTGCTATTTTAAAAGGTGCCAGTGTGAGGTGCAGTTGGTGGAGTCTGGGGAGGCGTGTACAGCCTGGGGGTCCTGAGACTCTCCTGTGCAGCCTCTGATTACCTTTAGAAATATGCCATGAGCTGGTCCGCGAGGCTCCAGGAAAGGGCCGAGTGGGTCTCAGAAATTAGTGTAGTGGGATGACATACTACGACACTCCGAGAAAGGCCGGTTCACCATCTCCAGAGACAACCTCAAAGAGCACGGTGTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAGCTACTATAGCGGGAGGTAGTGGGGCTCCTATGACTACTGGGGCCAGGAAACCTGTTCCACCGTCTCCTCAGCTCCACCAAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCCTGTCTACAGTCTCAGGA
119_I_GHV3-21_I_GHJ4	AGCTCTGAGAGAGAGCCTTAGCCCTGATTCCAAGGCCTATCCACTTGGTGATCAGCACTGAGCACCGAGGATTACCATGGAAGTGGGCTCCGCTGGGTTTTCTTGTGCAATTTAGAAAGGTGCCAGTGTGACGTACAGCTGGTGAATCTGGGGAGGCGTGGTGCAGCCGGGGGTCCTGAGACTCTCCTGTGCAGCCTCTGATTACCTTCAATTTATACCATCAACTGGGTCGCGAGGCGCCAGGAAAGGGACTGGAGTGGTCTCAGCCATCACCAGTAGTAATAATCTATTACGACAGACTCAGTGGGGCCGATTACCATCTCAGAGACAACGTCAAAGAACTCAATGTATCTCCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGCGGAGACTGGGCATTTTTTTGATAGTAGTGTGATTGCGTTATTGGGGCCCGGAAACCCAGTCCAGGTTCTCCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCCTGTCTACAGTCTCAGGA
119_I_GHV3-21_I_GHJ4	AGCTCTGAGAGAGAGCCTTAGCCCTGATTCCAAGGCCTATCCACTTGGTGATCAGCACTGAGCACCGAGGATTACCATGGAAGTGGGCTCCGCTGGGTTTTCTTGTGCAATTTAGAAAGGTGCCAGTGTGACGTACAGCTGGTGAATCTGGGGAGGCGTGGTGCAGCCGGGGGTCGCTGAGACTCTCCTGTGCAGCCTCTGATTACCTTCAATTTATACCATCAACTGGGTCGCGAGGCGCCAGGAAAGGGACTGGAGTGGTCTCAGCCATCACCAGTAGTAATAATTTATATTACGACAGACTCAGTGGGGCCGATTACCATCTCCAGAGACAACGTCAAAGAACTCATGTATCTCCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGCGGAGACTGGGCATTTTTTTGATAGTAGTGTGATTGCGTTATTGGGGCCCGGAAACCCAGTCCAGGTTCTCCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCCTGTCTACAGTCTCAGGA
119_I_GHV3-21_I_GHJ4	AGCTCTGAGAGAGAGCCTTAGCCCTGATTCCAAGGCCTATCCACTTGGTGATCAGCACTGAGCACCGAGGATTACCATGGAAGTGGGCTCCGCTGGGTTTTCTTGTGCAATTTAGAAAGGTGCCAGTGTGACGTACAGCTGGTGAATCTGGGGAGGCGTGGTGCAGCCGGGGGTCGCTGAGACTCTCCTGTGCAGCCTCTGATTACCTTCAATTTATACCATCAACTGGGTCGCGAGGCGCCAGGAAAGGGACTGGAGTGGTCTCAGCCATCACCAGTAGTAATAATTTATATTACGACAGACTCAGTGGGGCCGATTACCATCTCCAGAGACAACGTCAAAGAACTCATGTATCTCCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGCGGAGACTGGGCATTTTTTTGATAGTAGTGTGATTGCGTTATTGGGGCCCGGAAACCCAGTCCAGGTTCTCCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCCTGTCTACAGTCTCAGGA
120_I_GHV5-1_I_GHJ4	GGAGTCTCCCTCACTGCCAGCTGGATCTCAGGCTTTCATTCTCTCCACCAGCATGGGTTCAACCCCATCTCCCTCTCCTGGTGTCTCCAAGAGTCTGTCCGAGGTGCAGTGTGTGAGTCTGGAGCAGAGGTGAAAAAGCCCGGGAGTCTCTGAAGATCTCCTGTAAAGGTTCTGGATACAGATTTACCAACTACTGATCGGCTGGTGGCGCAGATGCCGGGAAAGGCTGGAGTGGATGATCTCTGACTCTGATACCAGATACAGCCCGTCTCCAAGTGCAGTCCACATCTCAGCCGACAAGTCCATCAGCACCGCTCACTGAGCAGCTGAAGGCTCGGACACCGCCACGTATTACTGTGCGAAAGGAGGATGGCAGCAGCTGGGGGCTCTACTTGACTACTGGGGCCAGGAAACCTGGTCCAGTCTCCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCCTGTCTACAGTCTCAGGA
120_I_GHV5-51_I_GHJ4	GGAGTCTCCCTCACTGCCAGCTGGATCTCAGGCTTTCATTCTCTCCACCATCATGGGTTCAACCCCATCTCCCTCTCCTGGTGTCTCCAAGAGTCTGTCCGAGGTGCAGTGTGTCAATCTGGAGCAGAGGTGAAAAAGCCCGGGAGTCTCTGAAGATCTCCTGTAAAGGTTCTGGATACAGATTTACCAACTACTGATCGGCTGGTGGCGCAGATGCCGGGAAAGGCTGGAGTGGATGATCTCTGACTCTGATACCAGATACAGCCCGTCTCCAAGTGCAGTCCACATCTCAGCCGACAAGTCCATCAGCACCGCTCACTGAGCAGCTGAAGGCTCGGACACCGCCACGTATTACTGTGCGAAAGGAGGATGGCAGCAGCTGGGGGCTCTACTTGACTACTGGGGCCAGGAAACCTGGTCCAGTCTCCTCAGCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCCTGTCTACAGTCTCAGGA

60_I_GHV4-59_I_GHJ3	ACTTTCTGAGAGTCTGTGACCTCCTGTGCAAGAACATGAAACATCTGTGGTTCTTCTCTCTCTGTTGGCAGTCCCAGATGGTCTGTCCCGGGTGCGACTGCGAGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCCTCACCTGCGCTGTCTGTGGTGGTCCGTGAGTAGTTCATTGACTTGGATCCGGCAGTCCCAGGAAGGGACTGGAAATGGCTATATCTATTCAGTGGGACCAACATTAACAACCCCTCCCTGAGAGTCCACATATCAATGACACGTCGAAACAACAGTTCCCTGAACTGAGCTGTGACCGCTGCGACACGGCCGTCTTACTGTGCGAGAGATCGACAATGATGCTTAGTGGAAAGCTTGTATGTCTGGGCCAGGGACAGTGGTACCCTCTCTCAACCTCCACCAAGGCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGCTGCAAGGACTACTCCCGAACCGGTGACGGTGTGCGAACTCAGCGCCCTGACCAGCGCGTGCACACCTCCCGCTGTCTACAGTCTCAGGA
61_I_GHV1-24_I_GHJ4	ACCATCACAAACAGCCACATCCCTCCCCTACAGAAGCCCCAGAGCGCAGCACCTCACCATGGACTGCACCTGGAGGATCCTCTTCTGTGGTGCATCAGCTACAGGCACCCAGGTGAGTCCAGTGTACAATCTGGGGCTCAGGTGAAGAAGCCTGGGACCTCTGTGAGGGTCTCTGCAAGGTTTCCGGATACACCGTCAGTGAATATCCATGCACTGGTGGACAGGCTCCTGGAAAAGGGCTTGTAGTGGATGGGAGGATTTGATCCTGAAGATGGTGAACAATCTACGACCAGAAATTAAGGGCAGAGTACCATGACCGAGACACATCTACTGACACAGCCTACATGGAGCTTACCAGCCTGAGACCTGAGGACACGGCCCTCTTACTGTGCAACAGACCTAATCTTTTGTACTGGCTACTACATTAGAGACTACTGGGCCAGGAAACCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
61_I_GHV1-24_I_GHJ4	ACCATCACAAACAGCCACATCCCTCCCCTACAGAAGCCCCAGAGCGCAGCACCTCACCATGGACTGCACCTGGAGGATCCTCTTCTGTGGTGCATCAGCTACAGGCACCCAGGTGAGTCCAGTGTACAATCTGGGGCTCAGGTGAAGAAGCCTGGGACCTCTGTGAGGGTCTCTGCAAGGTTTCCGGATACACCGTCAGTGAATATCCATGCACTGGTGGACAGGCTCCTGGAAAAGGGCTTGTAGTGGATGGGAGGATTTGATCCTGAAGATGGTGAACAATCTACGACCAGAAATTAAGGGCAGAGTACCATGACCGAGACACATCTACTGACACAGCCTACATGGAGCTTACCAGCCTGAGACCTGAGGACACGGCCCTCTTACTGTGCAACAGACCTAATCTTTTGTACTGGCTACTACATTAGAGACTACTGGGCCAGGAAACCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
61_I_GHV1-24_I_GHJ4	GGGATCACAAACAGCCACATCCCTCCCCTACAGAAGCCCCAGAGCGCAGCACCTCACCATGGACTGCACCTGGAGGATCCTCTTCTGTGGTGCATCAGCTACAGGCACCCAGGTGAGTCCAGTGTACAATCTGGGGCTCAGGTGAAGAAGCCTGGGACCTCTGTGAGGGTCTCTGCAAGGTTTCCGGATACAAAGTCACTGAATATCCATGCACTGGTGGACAGGCTCCTGGAAAAGGGCTTGTAGTGGATGGGAGGATTTGATCCTGAGATGGTGAACAATCTACGACCAGAAATTAAGGGCAGAGTACCATGACCGAGACACATCTACTGACACGGCCTACATGGAGCTTACCAACCTGACACCTGAAGACACGGCCCTGTATTACTGTGCAACAGACCTATTCTTTTGTACTGGCTACTATATTAGAGACTACTGGGCCAGGAAACCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
97_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGTGCTTAGCCCTGATTCCAAGGCATTTCACTTGTGTATCAGCACTGAACACAGAGACTCACCATGGAGTTGGGGCTGTCTGGTCTTCTTCTTGTCTATTAGAAAGTGTCCAGAGTGAAGTGCAGTGGTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGAACTCTCCTGCGCGCCTCTGATTCACTTCACTGCTATGCGAATGAAGTGGTCCCGCAGGCTCCAGGAAAGGGCTAGAGTGGTTCATATATTAGTAGTGTAGTAGTGGCATACTACTCAGACTCTGTGAAGGCCGATTACCATCTCCAGAGACAATGCCAAGAAAGTCTTCTGATCTGCAAAATGAACAGCCTGAGAGACGAGACAGGCTATTTTACTGTGCGAGAGTTGGGAAAGTATTATTGGGCCAGGAAACCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
97_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGTGCTTAGCCCTGATTCCAAGGCATTTCACTTGTGTATCAGCACTGAACACAGAGACTCACCATGGAGTTGGGGCTGTCTGGTGTCTTCTTGTCTATTAGAAAGTGTCCAGAGTGAAGTGCAGTGGTGGAGTCTGGGGAGGCTTGGTACAGCCGGGGGTCCTGAGACTCTCTGCGCAGCCTCGGATTCACTTCACTTCACTGCTATGCGAATGAAGCCTGAGAGACGAGACAGGCTTTTACTACTGTGCGAGAGTTGGGGTAGTATTGGGCCAGGAAACCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
97_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGTGCTTAGCCCTGATTCCAAGGCATTTCACTTGTGTATCAGCACTGAACACAGAGACTCACCATGGAGTTGGGGCTGTCTGGTGTCTTCTTGTCTATTAGAAAGTGTCCAGAGTGAAGTGCAGTGGTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGAGTCCCTGAACTCTCCTGCGCGCCTGATTCACTTCACTTCACTGCTATGCGAATGAAGCCTGAGAGACGAGACAGGCTTTTACTACTGTGCGAGAGTTGGGGTAGTATTGGGCCAGGAAACCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
97_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGTGCTTAGCCCTGATTCCAAGGCATTTCACTTGTGTATCAGCACTGAACACAGAGACTCACCATGGAGTTGGGGCTGTCTGGTGTCTTCTTGTCTATTAGAAAGTGTCCAGAGTGAAGTGCAGTGGTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGAGTCCCTGAACTCTCCTGCGCGCCTGATTCACTTCACTTCACTGCTATGCGAATGAAGCCTGAGAGACGAGACAGGCTTTTACTACTGTGCGAGAGTTGGGGTAGTATTGGGCCAGGAAACCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
107_I_GHV4-61_I_GHJ4	TTCTTAAATTCAGGTCACAGTCCACATGGAATACTTTCTGAGAGTCTGTGACCTCCTGTGCAAGAACATGAAACACCTGTGGTCTTCTCCTCCTGTTGGCAGTCCCAGATGGTCTGTCCCAGGTGCGAGTCCGGGCCAGGACTGGTGAAGCCTTGGAGACCTGTCCCTCACCTGCTCTGTGGTACTCCGTGACCTAGTAGTCACTACTGAGCTGTGATCCGGCAGTCCCAGGAAAGGGACTGGAATGATTGGTACATTTATACAGTGGGAACAACCACTACAACCCCTCCCTCAAGAGTCACTCACCATATCAGTGGACAGTCCAAGAACATTTCCCTGAAGCTGACTCTGTGACCGCTGACAGACGGCCGTATATTCTGCGAGAGTGGGATGATGAGATGGCCACAAGTTATGGGGAGGGCCCTTGAACACTGGGGCCAGGATCCCTGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
107_I_GHV4-61_I_GHJ4	ACATTTCTTAAATTCAGGTCACAGTCCACATGGAATACTTTCTGAGAGTCTGTGACCTCCTGTGCAAGAACATGAAACACCTGTGGTCTTCTCCTCCTGTTGGCAGTCCCAGATGGTCTGTCCCAGGTGCGAGTCCGGGCCAGGACTGGTGAAGCCTTGGAGACCTGTCCCTCACCTGCTCTGTGTACTCCGTGACCTAGTGTAGTCACTACTGAGCTGGATCCGGCAGCCCCAGGAAAGGGACTGGAGTGGATTGATATATTAACAATGCGAAACAACCACTACAACCCCTCCCTCAGAGTCACTCACCATATCAGTGGAGACAGTCCAAGAACCATTTCCCTGAAGCTGACTCTGTGACCGCTGACAGACGGCCGTATATTCTGCGAGAGTGGGATGATGAGATGGCCACAAGTTATGGGGAGGGCCCTTGAACACTGGGGCCAGGATCCCTGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA

107_I_GHV4-61_I_GHJ4	TTTTCTTAAATTCAGGGTCCAGCTCACATGGAAATACTTTCTGAGAGTCTGGACCTCTGTGCAAGAACATGAAACACCTGTGGTTCTCTCTCTCTGGTGGCAGCTCCAGATGGGTCTGTCCAGGTGCAGCTGCAGAGTGGGGCCAGGACTGGTGAAGCCCTCGGAGACCTGTCCCTCACCTGCAGCTGTCTGTGGTACTCCGTGACAGTGGTAGTCACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGACTGGAGTGGATTGGGTATATGTATTACAGTGGCAACCACTACAACCCCTCCCTCAAGAGTCGACTCACATATCAGGAGACACGTCGAAGAACAGTTCTCCCTGAAACTGAGTTCTGTGACCGCTGCGGACTCGGCCGTTTATTACTGCGCAGAGTAGGGATAGGGTTGGAGATGGCCACAAGTTACGGGGAGGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCTCAG
107_I_GHV4-61_I_GHJ4	ACATTTCTTAAATTCAGGGTCCAGCTCACATGGAAATACTTTCTGAGAGTCTGGACCTCTGTGCAAGAACATGAAACACCTGTGGTTCTCTCTCTCTGGTGGCAGCTCCAGATGGGTCTGTCCAGGTGCAGCTGCAGAGTGGGGCCAGGACTGGTGAAGCCCTCGGAGACCTGTCCCTCACCTGCAGCTGTCTGTGGTACTCCGTGACAGTGGTAGTCACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGACTGGAAATGGATTGGGTACATTTATTACAGTGGCAACCACTACAACCCCTCCCTCAAGAGTCGACTCACATATCAGTGGACACGTCCAAGAACATTTCTCCCTGAAGCTGACTCTGTGACCGCTGCGACAGCGCCGTATATTTCTGCGCAGAGTTCGGATAGGGTTGGAGATGGCCACAAGTTACGGGGAGGGCCCTTTGACCACTGGGGCCAGGATCCCTGTCACCGTCTCTCAGCTCCCAAGGGCCATCGGTCTTCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCAGCGGCCCTGGGCTGCTGTGAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAAGGA
123_I_GHV3-33_I_GHJ5	CGAGCCCAGCACTGGGAGTCCGGGTGTTCCATTGCGGTGATCATCACTGAACACAGAGGACTCACCATGGAGTCTGGGCTGAGCTGGGTTTCTCGTTGCTCTTTAAGAGGTGTCAGTGTGAGTGTGAGTGGAGTGGAGTGGGGAGCGGTGTCACCGCTGGGAGTCCCTGAGACTCTCTGTGCAAGCTCTGGATTCAAGTTTCACTCTATGCTCCACTGGGTCCGGCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCATTGTGTATGATGAACTGAAAAATACTACGCGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAGCACTCTATCTATGAAATGAACAGCCTGAGAGTTGAAGACACGGCTATGATTACTGTGCGAGAGATTGGCCGGCCGACGTTGGTTGATGTACAAGTGTTCGACCCCTGGGGCCAGGGAACCTGTCACCGTCTCTCAGCATCCCGACAGCCCCAAGGTCTTCCCGCTGAGCCTCTGCAACCCAGCCAGATGGGAACGTGTCATCGCCTGCTGTCAGGCTTCTTCCCGCAGGACCACTCAGTGTGACCTGGAGCGAAGCGACAGGGCGTGAACCGCAAGAACTTCCC
123_I_GHV3-33_I_GHJ5	CGAGCCCAGCACTGGGAGTCCGGGTGTTCCATTGCGGTGATCATCACTGAACACAGAGGACTCACCATGGAGTCTGGGCTGAGCTGGGTTTCTCGTTGCTCTTTAAGAGGTGTCAGTGTGAGTGTGAGTGGAGTGGGGAGCGGTGTCACCGCTGGGAGTCCCTGAGACTCTCTGTGCAAGCTCTGGATTCAAGTTTCACTCTATGCTCCACTGGGTCCGGCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCATTGTGTATGATGAACTGAAAAATACTACGCGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAGCACTCTATCTATGAAATGAACAGCCTGAGAGTTGAAGACACGGCTATGATTACTGTGCGAGAGATTGGCCGGCCGACGTTGGTTGATGTACAAGTGTTCGACCCCTGGGGCCAGGGAACCTGTCACCGTCTCTCAGCATCCCGACAGCCCCAAGTCTTCCCGCTGAGCCTCTGCAACCCAGCCAGATGGGAACGTGTCATCGCCTGCTGTCAGGCTTCTTCCCGCAGGACCACTCAGTGTGACCTGGAGCGAAGCGACAGGGCGTGAACCGCAAGAACTTCCC
126_I_GHV3-30_I_GHJ4	GCTCTGGGAGAGGAGCCAGCACTAGAAGTCCGGGTGTTCCATTGCGGTGATCCGCACTGAACACAGAGGACTCACCATGGAGTTGGGCTGAGCTGGGTTTCTCGTCTCTTTAAGAGGTGTCAGTGTGAGTGTGAGTCTGGGGAGCGGTGTCACCGCTGGGAGTCCCTGAGACTCTCTGTGCAAGCTCTCGATTCACTTCACTCTATGCTCCACTGGGTCCGGCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCATTGTGTATGATGAACTGAAAAATACTATGAGACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATTCCAGGAACAGCCTGATTTGCAACTGACAGTCTGAGAGTGGAGGACACGGCTGTTTATTACTGTGCGAAGAGGGCCCTCCACATTAATGTTCCGGGACTACTGATTGGGGCCAGGGAACCTGGTCACCGTCTCTCAGCATCCCGACAGCCCCAAGCAACCTTTTCCCGTCTCTGTGAGAATTTCCCGTCGGATACGAGCAGCGT
126_I_GHV3-30_I_GHJ4	GAGCTCTGGGAGAGGAGCCAGCACTAGAAGTCCGGGTGTTCCATTGCGGTGATCCGCACTGAACACAGAGGACTCACCATGGAGTTGGGCTGAGCTGGGTTTCTCGTCTCTTTAAGAGGTGTCAGTGTGAGTGTGAGTGTGAGTCTGGGGAGCGGTGGTCCAGCCTGGGAAGTCCCTGAGACTCTCTGTGCAAGCTCTCGATTCACTTCACTAGCTATGCCATGCACTGGGTCGGCCAGGTTCCAGGCAAGGGCTGGAGTGGGTGGCAATTTTCACTAATGAACTAAAAATACTATGAACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATTCCAGGAACAGCCTGATTTGCAATTGAACAGCCTGAGAGTTGAGGACACGGCTGTTTATTACTGTGCGAAGAGGGCCCTCCAACTAATGTTCCGGGACTACTGATTGGGGCCAGGGAACCTGGTCACCGTCTCTCCGCTCCACCAAGGGCCCATCGGTCTTCCCGTGGCACCTCTCCAAGAGCACCTCTGGGGCAGAGCGCCCTGGGCTGCTGTGAAGGACTACTTCCCGAACCGGTGACGGTGTGTTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
126_I_GHV3-30_I_GHJ4	GAGCTCTGGGAGAGGAGCCAGCACTAGAAGTCCGGGTGTTCCATTGCGGGATCAGCTGAACACAGAGGACTCACCATGGACTTTGGGCTGAGCTGGGTTTCTCGTTGCTCTTTAAGAGGTGTCAGTGTGAGTGTGAGTGTGAGTCTGGGGAGCGGTGGTCCAGCCTGGGAAGTCCCTGAGACTCTCTGTGCAAGCTCTCGATTCACTTCACTAATATGCCATGCACTGGGTCGGCCAGGTTCCAGGCAAGGGCTGGAGTGGGTGGCAATTTTCACTAATGAACTAAAAATACTATGAACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATTCCAGGAACAGCCTTATCTGCAATTGAACAGCCTGAGAGTTGAGGACACGGCTGTTTATTACTGTGCGAAGAGGGCCCTCCAACTAATGTTCCGGGACTACTGATTGGGGCCCGGGAACCTGGTCACCGTCTCTCAGCCTCCACCAAGGGCCATCGGTCTTCCCGTGGCACCTCTCCAAGAGCACCTCTGGGGCAGAGCGCCCTGGGCTGCTGTGAAGGACTACTTCCCGAACCGGTGACGGTGTGTTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
126_I_GHV3-30_I_GHJ4	GGGAGAGGAGCCAGCACTAGAAGTCCGGGTGTTCCATTGCGGGATCAGCTGAACACAGAGGACTCACCATGGAGTTGGGCTGAGCTGGGTTTCTCGTTGCTCTTTAAGAGGTGTCAGTGTGAGTGTGAGTGTGAGTCTGGGGAGCGGTGGTCCAGCCTGGGAAGTCCCTGAGACTCTCTGTGCAAGCTCTCGATTCACTTCACTAGCTATGCCATGCACTGGGTCGGCCAGGTTCCAGGCAAGGGCTGGAGTGGGTGGCAATTTTCACAAAATGAACTAAAAATACTATGAACTCCGTGAAGGGCCGATTCAACATCTCCAAGACAATTCCAGGAACAGCCTTATCTGCAATTGAACAGCCTGAGAGTTGAGGACACGGCTGTTTATTACTGTGCGAAGAGGGCCCTCCAACTAATGTTCCGGGACTACTGATTGGGGCCCGGGAACCTGGTCACCGTCTCTCAGCCTCCACCAAGGGCCATCGGTCTTCCCGTGGCACCTCTCCAAGAGCACCTCTGGGGCAGAGCGCCCTGGGCTGCTGTGAAGGACTACTTCCCGAACCGGTGACGGTGTGTTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCAGGA
217_I_GHV1-2_I_GHJ6	GAGAGCATCACCCAGCAACACATCTGCTCTAGAGAATCCCTGAGAGTCCGTTCTCACCATGGACTGGACCTGGAGATCCTCTTCTGGTGGCAGCAGCCAGAGTCCACTCCCAGGTGCAGCTGTGAGTGTGGGCTGAGTGAAGAACCTGGGCTCAGTGAAGGTCTCTGCAAGGCTTGTGATACACCTCACCGCTACTATACACTGGTGCAGACAGCCCCCTGGACAGGGCTTGGAGTGGTGGATCAACCTAACAGAGTGGCACAACTATGAGAGCAGTTTTCAGGGCAGGGTCCATGACCAGCGACAGTCCATCACCAAGCCTACATGGAGCTGAGCAGGCTGACTTCTGACGACACGGCCGTATTACTGTGCGAAGAGCGGTTCCGGGACTTTTATCTCGGCCATGGACGCTGTGGGGCCAAGGACCAGTCCCGTCTCTCAGGGAGTCACTCCGCCCAACCTTTTCCCGTCTCTGTGAGAATTTCCCGTCGGATACGAGCAGCGT
217_I_GHV1-2_I_GHJ6	GGGAGCATCACCCAGCAACACATCTGCTCTAGAGAATCCCTGAGAGTCCGTTCTCACCATGGACTGGACCTGGAGATCCTCTTCTGGTGGCAGCAGCCAGAGTCCACTCCCAGGTGCAGCTGTGAGTGTGGGCTGAGTGAAGAACCTGGGCTCAGTGAAGGTCTCTGCAAGGCTTGTGATACACCTCACCGCTACTATACACTGGTGCAGACAGCCCCCTGGACAGGGCTTGGAGTGGTGGATCAACCTAACAGAGTGGCACAACTATGAGAGCAGTTTTCAGGGCAGGGTCCATGACCAGCGACAGTCCATCACCAAGCCTACATGGAACTGAGCAGGCTGAGTTCTGACGACACGGCCGTATTACTGTGCGAAGAGCGGTTCCGGGAAATTTTGTCTCGGCCATGGACGCTGTGGGGCCAAGGACCAGTCCCGTCTCTCAGGGAGTCACTCCGCCCAACCTTTTCCCGTCTCTGTGAGAATTTCCCGTCGGATACGAGCAGCGT

217_I_GHV1-2_I_GHJ6	GAGAGCATCACCCAGCGACCACATCTGTCTCTAGAGAATCCCCTGAGAGCTCCGTTCTCACCATTGGACTGGACCTGGAGGATCCTCTTGGTGGCAGCAGCCACAGGAGCCCCTCCAGGTGAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA GTGAAGGTCTCCTGCAAGGCTCTGGATACACCTTCACCGCTATTATATGCACTGGTGGCAGACGCCCCGGGACAGGCGTTGAGTGGATGGATGATCAACCCTAACAGAGGTGGCAGAGATTATGACAGAAAGTTTCGGGGCAGGTCACCATGACCAGGGACACAT CCATCAGCAGCTACTATGACTGAGCAGCCTGAGATCTGACGACACGCGCTATATTACTGTGCGAGAAGCGGTTTCGGGGATTCTTATCTCGGGCCATGAGCCTGTGGGCCAAGGACCACGCTCACCGTCTCCTCAGCCTCCACCAAGGGCCCCATCGGTCTCCCC TGGCACCCCTCTCAAGAGCACCTGTGGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCACGCGGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
217_I_GHV1-2_I_GHJ6	GAGAGCATCACCCAGCAACCACATCTGTCTCTGAGAATCCCCTGAGAGCTCCGTTCTCACCATTGGACTGGACCTGGAGGATCCTCTTCTTGGCGGAGCAGCCACAGAGTCCACTCCCAGGTGAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGACTCAG TGAAGGTCTCCTGCAAGGCTCTGGATACACCTTCACCGCTACTATATACACTGGTGGCAGACGCCCCGGGACAGGCGTTGAGTGGATGGATGATCAACCCTAACAGAGGTGGCACAACCTATGGAGAGAAGTTTCAGGGCAGGTCGCCATGACCAGGGACACGTC CATCAGCACAGCTACATGAGCTGAGCAGGCTGAGTTCTGACGACACGCGCTGATTACTGTGCGAGAAGCGGTTTCGGGGATTCTTATCTCGGGCCATGAGCCTGTGGGCCAAGGACCACGCTCACCGTCTCCTCAGGGAGTGCATCGCCCCAACCTTTTCCCC CTCGTCTCCTGTGAGAATCCCCCTCGGATACGAGCAGCGTG
217_I_GHV1-2_I_GHJ6	GGGAGCATCACCCAGCAACCACATCTGTCTCTAGAGAATCCCCTGAGAGCTCCGTTCTCACCATTGGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCCACAGAGTCCACTCCCAGGTGAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA GTGAAGGTCTCCTGCAAGGCTCTGGATACACCTTCACCGCTACTATATACACTGGTGGCAGACGCCCCGGGACAGGCGTTGAGTGGATGGATGATCAACCCTAACAGAGGTGGCACAACCTATGGAGAGAAGTTTCAGGGCAGGTCGCCATGACCAGGGACACG TCCATCAGCACAGCTACATGAACTGAGCAGGCTGAGTTCTGACGACACGCGCTGATTACTGTGCGAGAAGCGGTTTCGGGGAAATTTTGTCTCGGGCCATGAGCCTGTGGGCCAAGGACCACGCTCACCGTCTCCTCAGCTCCACCAAGGGCCCCATCGGTCTCCC CCTGGCGCCCTGTCCAGGAGCACCTGTGGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
125_I_GHV4-3_I_GHJ4	GTGCTTCTGAGAGTCTGACCTCCTGCACAAGAACATGAACACCTGTGGTTCTCTCCTCCTGTTGGCAGCTCCAGATGGTCTGTCCAGGTGAGCTACAGCAATGGGGCGCAGACTTTTGAAGCCCTGGAGACCTGTCCCTCACCTGCGTGTCTGTGGTG GTCCCTCAGTGATTACTTCTGGAAGTGGATCCGCAAGTCCCGAGGGAAGGGCTGGAGTGGATTGGCAGATCAATCTTAGTGGAAACCACCACTACAACCCGTCCTCAAGAGTGCAGTCCCGTATCAATAGACACGTCACAAACCCAGTTCTCCCTAAAAGTACCTCTGTA CCGCCGCGACACGGCTGTGATTACTGTGCGAGAGCGCGTTTCGGGGAGCCTATGTTGGAGTTCCCTTGGTTTTTGCAGTACTGGGCCAGGAAACCTGTGTAACCTGTCTCAGCATCCCCACCAGCCCCAAGGCTTCCCGCTGAGCCTCTGAGCACCCAGCCA GATGGGAACGTGGTATCGCTGCTGCTCCAGGCTTCTCCCCAGGAGCACTCAGTGTGACTGGAGCGAAAGCGGACAGGGCGTACCGCCAGAACTTCCC
125_I_GHV4-34_I_GHJ4	AGTGCTTCTGAGAGTCTGACCTCCTGCACAAGAACATGAACACCTGTGGTTCTCTCCTCCTGTTGGCAGCTCCAGATGGTCTGTCCAGGTGAGCTACAGCAGTGGGGCGCAGACTATTGAAGCCTTGGAGACCTGTCCCTGACCTGCGTGTCTGTGGT GGGTGGTTCAGTGATTACTTCTGGAAGTGGATCCGCAAGTCCCGAGGGAAGGGCTGGAGTGGATTGGAAATCAATTTTGTGGATCCACCACTACAACCCGTCCTCAAGAGTGCAGTCCCATTTAGTAGACAGTCCAAGAACCAAGTTCTCCCTGAAGTAACTCTG TGACCGCCGCGACACGGCTGTCTTACTGTGCGAGAGCGCGGTTTCGGGGAGCCTATCGTGGAGTCCCTTGGTTTTTGCAGTACTGGGCCAGGAAACCTGTGTAACCTGTCTCAGCTCCACCAAGGGCCCCATCGTCTCCCCCTGGCACCCCTCTCAAGAGC ACCTCTGGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
125_I_GHV4-34_I_GHJ4	GGGTCCAGCTCATGGAAGTCTTCTGAGAGTCTGACCTCCTGCACAAGAACATGAACACCTGTGGTTCTCTCCTCCTGTTGGCAGCTCCAGATGGTCTGTCCAGGTGAGCTACAGCAGTGGGGCGCAGACTTTTGAAGCCCTCGGAGACCTGTCCCTCACCTGCGTGTCTGTGGT ACCTGCGGTGTCTGTGGTGGTCTTTAGTATTACTTCTGTACTGATTCCGCAAGTCCCGAGGGAAGGGCTGGAAATGGAATGGCCAGATCAATTTTGGTGAAGTACGAACTACAACCCGTCCTCCAGAGTGCAGTCCATTTAGTAGACAGTCCAAGAACCAAGTT TCCCTGAGGCTGACCTCTGTACCAGCGGACACGGCAGTCTATTACTGTGCGAGAGCGCGGTTTCGGGGAGCCTATGTTGGAGTCCCTTGGTTTTTGCAGTACTGGGCCAGGAAACCTGTGTAACCTGTCTCAGCTCCACCAAGGGCCCCATCGTCTCCCCCT GGCACCCCTCTCAAGAGCACCTGTGGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
125_I_GHV4-34_I_GHJ4	AGTGCTTCTGAGAGTCTGACCTCCTGCACAAGAACATGAACACCTGTGGTTCTCTCCTCCTGTTGGCAGCTCCAGATGGTCTGTCCAGGTGAGCTACAGCAATGGGGCGCAGACTTTTGAAGCCCTGGAGACCTGTCCCTCACCTGCGTGTCTGTGGT GGTCCCCAGTATTACTTCTGGAAGTGGATCCGCAAGTCCCGAGGGAAGGGCTGGAGTGGATTGGCAGATCAATCTTGGTGGATCCACCACTACAACCCGTCCTCAAGAGTGCAGTCCCATTTAGTAGACAGTCCAAGAACCAAGTTCTCCCTGAAGTAACTCTGT GACCGCCGCGACACGGCTGTTTACTGTGCGAGAGCGCGGTTTCGGGGAGCCTATGTTGGAGTCCCTTGGTTTTTGCAGTACTGGGCCAGGAAACCTGTGTAACCTGTCTCAGCTCCACCAAGGGCCCCATCGTCTCCCCCTGGCACCCCTCTCAAGAGCA CCTCTGGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
125_I_GHV4-34_I_GHJ4	AGTGCTTCTGAGAGTCTGACCTCCTGCACAAGAACATGAACACCTGTGGTTCTCTCCTCCTGTTGGCAGCTCCAGATGGTCTGTCCAGGTGAGCTACAGCAGTGGGGCGCAGACTATTGAAGCCTTGGAGACCTGTCCCTCACCTGCGTGTCTGTGGT GGTCTTTCAGGATTACTTCTGGAAGTGGATCCGCAAGTCCCGAGGGAAGGGCTGGAGTGGATTGGCAGATCAATCTTGGTGGATCCACCACTACAACCCGTCCTCAAGAGTGCAGTCCCATTTAGTAGACAGTCCAAGAACCAATTTCTCCCTGAAGTAACTCTGT TGACCGCCGCGACACGGCTGTATTCTGTGCGAGAGCGCGGTTTCGGGGAGCCTATGTTGGAGTCCCTTGGTTTTTGCAGTACTGGGCCAGGAAACCTGTGTAACCTGTCTCAGCTCCACCAAGGGCCCCATCGTCTCCCCCTGGCACCCCTCTCAAGAGCA CCTCTGGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
125_I_GHV4-34_I_GHJ4	TTTCTTATATGGGAGTCTTCTGAGAGTCTGACCTCCTGCACAAGAACATGAACACCTGTGGTTCTCTCCTCCTGTTGGCAGCTCCAGATGGTCTGTCCAGGTGAGCTACAGCAGTGGGGCGCAGACTTTTGAAGCCCTCGGAGACCTGTCCCTCACCT CGGTGTCTGTGGTGGTCCCTCAGTATTACTTCTGGAAGTGGATCCGCAAGTCCCGAGGGAAGGGCTGGAGTGGATTGGCAGATCAATCTTGGTGGAGCCACCACTACAACCCGTCCTCAAGAGTGCAGTCCCGTATCAATAGACAGTCCAAGAACCAAGTTGCCC TGAAGCTGACCTCTGTACCAGCGGACACGGCTGTGATTCTGTGCGAGAGCGCGGTTTCGGGGAGCCTATGTTGGAGTCCCTTGGTTTTTGCAGTACTGGGCCAGGAAACCTGTGTAACCTGTCTCAGCTCCACCAAGGGCCCCATCGTCTCCCCCTGGCACCCCTCTCAAGAGCA ACCCTCTCAAGAGCACCTGTGGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
156_I_GHV1-46_I_GHJ4	GGCCCTGAAAGCATCTCAACAACCAACCTCTCTACAGAAGCCTCTGAGAGGAAGTTCTCACCATTGGACTGGACCTGGAGGTTCTTCTGTTGCTGGTGTAGCTCCAGTGTCTCACTCCCAGGTGAGTGGTGGTGCAGTCTGGGGCTGAGGTGAGGAAGCCTGGG GCCTCAGTGAAGGTTTCTGCAAGCATCTGATACAGCTTACCAGCTTCTATATCTACTGGTGGAAAGCCCCCTGGACAAGGCTTGTAGTGGATGGAGTAACTGACCTAGTGGTGTAGTACCAGTACGACAGAGGTTCCAGGGCAGAGTACCATGACCCGGG ACACTCCAGAGCGAGTCTACATGGAGCTGAGCAGCTGAGATTTGAGGACACGCGCGTATTACTGTGCGGAATCGTGGGAGTACTAGTACTACTGGGCCAGGAAACCTGTGTAACCTGTCTCAGCTCCACCAAGGGCCCCATCGTCTCCCCCTGGCACCC TCTCCAGAGCACCTGTGGGGGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA

156_I_GHV1-46_I_GHJ4	CCCTGAAAGCATCATCCAACAACCACATCCCTTCTTACAGAAGCCTCTGAGAGAAAGTTCTTACCATGACTGGACCTGGAGGGTCTTCTGCTTCTGCTGTAGTCCAGTGGTCACTCCCAGGTGCAACTGGTGCAGTCTGGGGCTGAGGTGAGGAAGCCTGGGGCTTCAGTGAAGGTTTCTGCAAGGCATCTGGATAGGTTTACCAGTTTCTATATTCACTGGGTGCGAAAGGCCCCAGGACAAAGGCTTGAATGGATGGGGTTAATCGACCTAGTGGTGGTACCGCATTGACGACAGAAATCCAGGACAGTACCATGACCGGGACA CGTCCACGAGCGAAGTCTACTTGGAGTTGAGCAGCCTGAGATCTGAAGACACGCCATGTATTACTGTGGAGAATCGTGGAGGACTAGTACTACTGGGGCCAGGAAACCTGTGTCCAGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCC TCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCGCGTGCACACTTCCCCTGCTCTACAGTCTCAGGA
156_I_GHV1-46_I_GHJ4	GAAAGCATCATCCAACAACCACATCCCTTCTTACAGAAGCCTCTGAGAGAAAGTTCTTACCATGACTGGACCTGGAGGGTCTTCTGCTTCTGCTGTAGTCCAGTGGTGCAGTCCAGGTGCACTGGTGCAGTCTGGGGCTGAGGTGAGGAAGCCTGGGGCTCCCTCA GTGAAAATTTCTGCAAGGCATCTGGATACAGTTTACCAGTTTCTATATTCACTGGGTGCGAAAGGCCCTGGACAAGGGCTTGAATGGATGGGGTTAATCGACCTAGTGGTGGTACCGCATTGACGACAGAGTTCCAGGACAGACTCACATGACCAAGTCCACGTTCC ACGAGCGAAGTCTACATGATGATCTGAGAAGGCTGACATTTAGGACACGGCCATATATTACTGTGGAGAATCGTGGAGGCACTAGTACTACTGGGGCCAGGAAACCTGATCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAG AGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCGCGTGCACACTTCCCCTGCTCTACAGTCTCAGGA
156_I_GHV1-46_I_GHJ4	AAAGCATCATCCAACAACCACATCCCTTCTTACAGAAGCCTCTGAGAGAAAGTTCTTACCATGACTGGACCTGGAGGGTCTTCTGCTTCTGCTGTAGTCCAGTGGTGCAGTCCAGGTGCACTGGTGCAGTCTGGGGCTGAGGTGAGGAAGCCTGGGGCTCAGT GAAGGTTTCTGCAAGGCATCTGGATACAGTTTACCAGTTTCTATATTCACTGGGTGCGAAAGGCCCTGGACAAGGGCTTGAATGGATGGGGTTAATCGACCTAGTGGTGGTACCGCATTGACGACAGAGTTCCAGAACAGAGTCCCATGACCAAGTCCACGTTCC GAGAAAAGTCTACATGAGTTGAGTCCAGTCTGAGAGACACGGCCGTATATTGTTGGAGAATCGTGGAGGACTAGTACTACTGGGGCCAGGAAACCTGTGTCCAGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGA GCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCGCGTGCACACTTCCCCTGCTCTACAGTCTCAGGA
156_I_GHV1-46_I_GHJ4	ATCATCCAACAACCACATCCCTTCTTACAGAAGCCTCTCAGAGAAAGTTCTTACCATGACTGGACCTGGAGGGTCTTCTGCTTCTGCTGCTGTAGTCCAGTGGTGCAGTCCAGGTGCACTGGTGCAGTCTGGGGCTGAGGTGAGGAAGCCTGGGGCTCAGTGAAG TTTCTGCAAGGCATCTGGATAGGTTTACCAGTTTCTATATTCACTGGGTGCGAAAGGCCCCAGGACAAGGGCTTGAATGGATGGGGTTAATCGACCTAGTGGTGGTACCGCATTGACGACAGAGTTCCAGAACAGAGTCCCATGACCAAGTCCACGTTCC GAAGTCTACATGAGTTGAGCAGCCTGAGATCTGAGGACACGGCCATGTATTACTGTGGAGAATCGTGGAGGACTAGTACTACTGGGGCCAGGAAACCTGTGTCCAGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCAC CTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCGCGTGCACACTTCCCCTGCTCTACAGTCTCAGGA
67_I_GHV1-69D_I_GHJ3	AGCACATAACAACCACATCTCCTCTTAAAGAACCCCTGGGAGCAGAGCTCATCACCATGACTGGACCTGGAGGTTCTCTTTGGTGGGAGCAGTACAGGTGTCAGTCCCAGGTGCGAGTGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGCTCGTGAA GTCTCTGCAAGGCCTCTGGTGGCTCCTCAGCAGCTTGGCTTCTCAGTGGTGGCGACAGGCCCTGGACAAGGACTTGAATGATGGGGTTAATCGACCTAGTGGTGGTACCGCATTGTCGGAAACCGCAGACTACGACAGAAAGTTCCAGAACAGACTCAGATTGTCGGGACGAA CACAGTCCCATGGAAGTGAAGGCTGACATCTGAAGACACGGCCGTATTTCTGCGGAGACGAAAGGCTGTGATAGTGGTCCCCCCCCGGCGAGGCTTTTGATATCTGGGGCCAAGGACAATGATCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCC CCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCGCGTGCACACTTCCCCTGCTCTACAGTCTCAGGA
67_I_GHV1-69D_I_GHJ3	AGCACATAACAACCACATCTCCTCTTAAAGAACCCCTGGGAGCAGAGCTCATCACCATGACTGGACCTGGAGGTTCTCTTTGGTGGGAGCAGTACAGGTGTCAGTCCCAGGTGCGAGTGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGCTCGTGAA GTCTCTGCAAGGCCTCTGGTGGCTCCTCAGCAGCTTGGCTTCTCAGTGGTGGCGACAGGCCCTGGACAAGGACTTGAATGATGGGGAAATCATCCCTTTGTCAGGAAACCGTACTACGACAGAAAGTTCCAGAACAGACTCAGATTGTCGGGACGAAAGTACAGC CACAGTCCCATGGAAGTGAAGGCTGACATCTGAAGACACGGCCGTATTTCTGCGGAGACGAAAGGCTGTGATAGTGGTCCCCCCCCGGCGAGGCTTTTGATATCTGGGGCCAAGGACAATGATCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCC CCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCGCGTGCACACTTCCCCTGCTCTACAGTCTCAGGA
67_I_GHV1-69D_I_GHJ3	AGCACATAACAACCACATCTCCTCTTAAAGAACCCCTGGGAGCAGAGCTCATCACCATGACTGGACCTGGAGGTTCTCTTTGGTGGGAGCAGTACAGGTGTCAGTCCCAGGTGCGAGTGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGCTCGTGAA GTTTCTGCAAGGCTTCTGAGGCGCCTTCAAGGCTTGGCTTCTCAGTGGTGGCGACAGGCCCTGGACAAGGACTTGAATGATGGGGAAATCATCCCTATTTGGAGCAGCAGACTACGACAGAAAGTTCCAGAACAGACTCAGATTGTCGGGACGAAAGTACAGC GACAGTCCCATGGAAGTGAAGGCTGACATCTGAAGACACGGCCGTATTTCTGCGGAGACGAAAGGCTGTGATAGTGGTCCCCCCCCGGCGAGGCTTTTGATATCTGGGGCCAAGGACAATGATCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCC CCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCGCGTGCACACTTCCCCTGCTCTACAGTCTCAGGA
67_I_GHV1-69D_I_GHJ3	AGCACATAACAACCACATCTCCTCTTAAAGAACCCCTGGGAGCAGAGCTCATCACCATGACTGGACCTGGAGGTTCTCTTTGGTGGGAGCAGTACAGGTGTCAGTCCCAGGTGCGAGTGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGCTCGTGAA GTCTCTGCAAGGCTTCTGAGGCGCCTTCAAGGCTTGGCTTCTCAGTGGTGGCGACAGGCCCTGGACAAGGACTTGAATGATGGGGAAATCATCCCTATTTGGAGCAGCAGACTACGACAGAAAGTTCCAGAACAGACTCAGATTGTCGGGACGAAAGTACAGC GTACAATATACATGGAATGAGAGGCTGACATCTGAAGACACGGCCGTATTTCTGCGGAGACGAAAGGCTGTGATAGTGGTCCCCCCCCGGCGAGGCTTTTGATATTTGGGGCCAAGGACAATGATCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCC CCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCGCGTGCACACTTCCCCTGCTCTACAGTCTCAGGA
67_I_GHV1-69D_I_GHJ3	AGCACATAACAACCACATCTCCTCTTAAAGAACCCCTGGGAGCAGAGCTCATCACCATGACTGGACCTGGAGGTTCTCTTTGGTGGGAGCAGTACAGGTGTCAGTCCCAGGTGCGAGTGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGCTCGTGAA GTCTCTGTAAGGCTTCTGAGGCGCCTTCAAGGCTTGGCTTCTCAGTGGTGGCGACAGGCCCTGGACAAGGACTTGAATGATGGGGAAATCATCCCTAGTTTGGGAGCAGCAGACTACGACAGAAAGTTCCAGAACAGACTCAGATTGTCGGGACGAAAGTACG AGCACGTTTATATGACTGAGAGGCTGACATCTGAAGACACGGCCGTATTTCTGCGGAGACGAAAGGCTGTGATAGTGGTCCCCCCCCGGCGAGGCTTTTGATATTTGGGGCCAAGGACAATGATCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCC CCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCGCGTGCACACTTCCCCTGCTCTACAGTCTCAGGA
67_I_GHV1-69D_I_GHJ3	AGCACATAACAACCACATCTCCTCTTAAAGAACCCCTGGGAGCAGAGCTCATCACCATGACTGGACCTGGAGGTTCTCTTTGGTGGGAGCAGTACAGGTGTCAGTCCCAGGTGCGAGTGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGCTCGTGAA GTCTCTGTAAGGCTTCTGAGGCGCCTTCAAGGCTTGGCTTCTCAGTGGTGGCGACAGGCCCTGGACAAGGACTTGAATGATGGGGAAATCATCCCTAGTTTGGGAGCAGCAGACTACGACAGAAAGTTCCAGAACAGACTCAGATTGTCGGGACGAAAGTACG AGCACGTTTATATGACTGAGAGGCTGACATCTGAAGACACGGCCGTATTTCTGCGGAGACGAAAGGCTGTGATAGTGGTCCCCCCCCGGCGAGGCTTTTGATATTTGGGGCCAAGGACAATGATCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGTCTTCC CCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCGCGTGCACACTTCCCCTGCTCTACAGTCTCAGGA

84_I_GHV1-2_I_GHJ4	GAGAGCATCACCCAGCAACCACATCTGTCTCTAGAGAATCCCCTGAGAGCTCCGTTCTCACCATGGACTGGACCTGGAGGATCCTCTTCTTGGTGCGAGCAGCCACAGAGCCCCTCCAGGGCCAGCTGGTGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAT TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTACCCTGCTACTATGTGATTGGGTGCGACAGGCCCTGGACAAGGCTTGAGTGGATGGCATGGATGAACCTAACACTAGTCCGCTCTTTGCACAGAAATTTAGGGCAGGATCGCCGTGACCACGGACACGTCCA TCAGCACAGCCTACATGGAGCTGAGCCGGCTCACATCTGACGACACGGCCGTCTATTCTGTGCGCGCGTATACCATCGACTGTTACTTTACCTCTGGGGCCAGGAAACCTGGTCATGGTCTCCTCAGGGAGTGCATCCGCCCAACCTTTTCCCCTCGTCTCCTGTGA GAATTCGCCGTCGGATACGAGCAGCGTG
84_I_GHV1-2_I_GHJ4	GGGAGCATCACCCAGCAACCACATCTGTCTCTAGAGAATCCCCTGAGAGCTCCGTTCTCACCATGGACTGGACCTGGAGGATCCTCTTCTTGGTGCGAGCAGCCACAGAGCCCCTCCAGGGCCAGCTGGTGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAT TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTACCCTGCTACTATGTGATTGGGTGCGACAGGCCCTGGACAAGGCTTGAGTGGATGGCATGGATGAACCTAACACTAGTCCGCTCTTTGCACAGAAATTTAGGGCAGGATCGCCGTGACCACGGACACGTCCA TCAGTACAGCCTACATGGAGCTGAGCCGGCTCACATCTGACGACACGGCCGTCTATTACTGTGCGCGCGTATACCATCAACGGGTTACTTTACCTCTGGGGCCAGGAAACCTGGTCACCGTCTCCTCAGGGAGTGCATCCGCCCAACCTTTTCCCCTCGTCTCCTGTGA GAATTCGCCGTCGGATACGAGCAGCGTG
84_I_GHV1-2_I_GHJ4	GAGAGCATCACCCAGCAACCACATCTGTCTCTAGAGAATCCCCTGAGAGCTCCGTTCTCACCATGGACTGGACCTGGAGGATCCTCTTCTTGGTGCGAGCAGCCACAGAGCCCCTCCAGGGCCAAGTGGTGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAT TAAAGGTCTCCTGCAAGGCTTCTGGATACACCTTACCCTGCTACTATGTGATTGGGTGCGACAGGCCCTGGACAAGGCTTGAGTGGATGGCATGGATGAACCTAACACTAGTCCGCTCTTTGCACAGAAATTTAGGGCAGGATCGCCGTGACCACGGACACGTCCA GACGACAGCCTCCATGGAGCTGAGCAGGCTGACATCTGACGACACGGCCGTCTATTACTGTGCGCGCGTATACCATCAACGGGTTACTTTACCTCTGGGGCCAGGAAACCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCCTC CAAGAGCACCTCTGGGGCCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCACGGCGTGCACACCTTCCCGCTGTCTCAGTCTCCTCAGGA
84_I_GHV1-2_I_GHJ4	GGGAGCATCACCCAGCAACCACATCTGTCTCTAGAGAATCCCCTGAGAGCTCCGTTCTCACCATGGACTGGACCTGGAGGATCCTCTTCTTGGTGCGAGCAGCCACAGAGCCCCTCCAGGGCCAGCTGGTGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAT TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTACCCTGCTACTATGTGATTGGGTGCGACAGGCCCTGGACAAGGCTTGAGTGGATGGCATGGATGAACCTAACACTAGTCCGCTCTTTGCACAGAAATTTAGGGCAGGATCGCCGTGACCACGGACACGTCCA ATCAGCACAGCCTACATGGAGCTGAGCCGGCTCACATCTGACGACACGGCCGTCTATTACTGTGCGCGCGTATACCATCAACGGGTTACTTTACCTCTGGGGCCAGGAAACCTGGTCACCGTCTCCTCAGGGAGTGCATCCGCCCAACCTTTTCCCCTCGTCTCCTGTGA GAATTCGCCGTCGGATACGAGCAGCGTG
84_I_GHV1-2_I_GHJ4	GAGAGCATCACCCAGCAACCACATCTGTCTCTAGAGAATCCCCTGAGAGCTCCGTTCTCACCATGGACTGGACCTGGAGGATCCTCTTCTTGGTGCGAGCAGCCACAGAGCCCCTCCAGGGCCAGCTGGTGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAT TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTACCCTGCTACTATGTGATTGGGTGCGACAGGCCCTGGACAAGGCTTGAGTGGATGGCATGGATGAACCTAACACTAGTCCGCTCTTTGCACAGAAATTTAGGGCAGGATCGCCGTGACCACGGACACGTCCA ATCAGCACAGCCTACATGGAGCTGAGCAGGCTGACATCTGACGACACGGCCGTCTATTACTGTGCGCGCGTATACCCTCAACTGTTACTTTACCTCTGGGGCCAGGAAACCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCCTC CCAAGAGCACCTCTGGGGCCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCACGGCGTGCACACCTTCCCGCTGTCTCAGTCTCCTCAGG
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGACTCACCATGGAGTTGGGGCTGTGCTGGTTTTCTTGTGCTATTTAGAAGGTGCCAGTGTGAGGTGCAGTGGTGAGTCTGGGGAGGCTTGG TACAGCCGGGGGCTCCTGAGCCTCTTGTGTGAAGCCTCTGGATTCAACTCAGTAGATATAGCATGAACCTGGGTCGCCAGGCTCCAGGAAAGGGCTGGAGTGGTCTCATACTTATAGCAGAAGTAGTTGAAAGACTATGCACTCTCTGTGAAGGGCCGATTCA CCATCTCCAGAGACAATGCCAAGAGTCAAGTATCTGCAATGAACAGCCTGAGCGACGAGAACAGCGCTGTTTATTACTGTGCCAGAGGTACTTACTACTGGGGCCAGGAAATGTTGTCCAGCTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCT CTCCTCCAAGAGCACCTCTGGGGCCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCACGGCGTGCACACCTTCCCGCTGTCTCAGTCTCCTCAGGA
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGACTCACCATGGAGTTGGGGCTGTGCTGGTTTTCTTGTGCTATTTAGAAGGTGCCAGTGTGCGGTACAGCTGGTGAGTCTGGGGAGGCTTGTGATA CAGCCTGGGGGCTCCTCAGACTCTCCTGTGAGCCTCTGATTCAACTCAGTAGATATAGCATGAACCTGGGTCGCCAGGCTCCAGGAAAGGGCTGGAGTGGTTTTATACATTATAGTAGAAGTACCACAGAGACTACGACGCTCTGTGAGGGCCGATTACCAT CTCCAGAGACAATGCCAAGAGTCAAGTATCTGACATGAACAGCCTGAGCGACGAGACACGGCTGTGTTACTGTGCGAGAGAGTCTCGACTACTGGGGCCAGGAAAGTGTGTTCCAGCTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCT CCTCCAAGAGCACCTCTGGGGCCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCACGGCGTGCACACCTTCCCGCTGTCTCAGTCTCCTCAGG
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGACTCACCATGGAGTTGGGGCTGTGCTGGTTTTCTTGTGCTATTTAGAAGGTGCCAGTGTGCGGTACAGCTGGTGAGTCTGGGGAGGCTTGTGATA ACAGCCTGGGGGCTCCTGAGACTCTCCTGTGAACCTCTGATTCAATTTCAATAATATAGTATGAACCTGGGTCGCCAGGCTCCCGGAAAGGGCCGCAATGATATCATATGTTAGCAGTATAGTGTACCAACGATACGACACTCTGTGAGGGCCGATTACCACCA TCTCCAGAGACAATGCCAAGAGTCTCTATATCTGGAATGAACAGCCTGACTGACGAGGACACGGCTGTGTTACTGTGCGAGAGAGTCTCGACTACTGGGGCCAGGAAAGTGTGTTCCAGCTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCT GCAGCACCCAGCCAGATGGAAAGTGTCTCATGCTGCTGCTGCTCCAGGGCTTCTTCCCCAGGAGCCACTCAGTGTGACCTGGAGCGAAAGCGACAGGGCGTGACCCCGAAGAACTCCC
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGACTCACCATGGAGTTGGGGCTGTGCTGGTTTTCTTGTGCTATTTAGAAGGTGCCAGTGTGCGGTACAGCTGGTGAGTCTGGGGAGGCTTGTGATA ACAGCCTGGGGGCTCCTGAGACTCTCCTGTGAACCTCTGATTCAATTTCAATAATATAGTATGAACCTGGGTCGCCAGGCTCCCGGAAAGGGCCGCAATGATATCATATGTTAGCAGTATAGTGTACCAACGATACGACACTCTGTGAGGGCCGATTACCACCA ATCTCCAGAGACAATGCCAAGAGTCTCTATATCTGGAATGAACAGCCTGACTGACGAGGACACGGCTGTGTTACTGTGCGAGAGAGTCTCGACTACTGGGGCCAGGAAAGTGTGTTCCAGCTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCT GCAGCACCCAGCCAGATGGAAAGTGTCTCATGCTGCTGCTGCTCCAGGGCTTCTTCCCCAGGAGCCACTCAGTGTGACCTGGAGCGAAAGCGACAGGGCGTGACCCCGAAGAACTCCC
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGACTCACCATGGAGTTGGGGCTGTGCTGGTTTTCTTGTGCTATTTAGAAGGTGCCAGTGTGCGGTACAGCTGGTGAGTCTGGGGAGGCTTGTGATA ACAGCCTGGGGGCTCCTGAGACTCTCCTGTATAGTCTCTGATTCAACTCAGTAGATATAGTATGAACCTGGGTCGCCAGGCTCCAGGAAAGGGCTGGAGTGGTTTTATACATTATCAGTAGTATAGTGTACCAACGATACGACACTCTGTGAGGGCCGATTACCACCA ATCTCCAGAGACAATGCCAAGAGTCTCTCTGCAATGAACACCTGAGAGACGGGGACACGGCCCTGTATTTACTGTGCGAGAGAGTCTTACTACTGGGGCCAGGAAAGTGTGTTCCAGCTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCT GCAGCACCCAGCCAGATGGAAAGTGTCTCATGCTGCTGCTGCTCCAGGGCTTCTTCCCCAGGAGCCACTCAGTGTGACCTGGAGCGAAAGCGACAGGGCGTGACCCCGAAGAACTCCC

2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGGTTTTCTTGTGCTATTTAGAAAGGTGTCCACTGTGAGTGCCTGGTGAATCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCTCTGGCTTCAACTTATAGTAGATATAGTAGTAAGTAACTGGTCCGCGAGGTTCCGGGGAGGGGCTGGAATGGATTCATATATCGATAGTGTAGTACTTCGAAAATACGCGAGGCTCTGTGAAGGGCCGATTCACTATCTCCAGAGACAATGCCAAGAGGTCACTGTATCTGCACATGAACAGCCTGAGTACCGAAGACACGGCTATATATTACTGTGCAAGAGAGTCTTACTATTGGGCCAGGGATCCCTGTCCAGCTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGGTTTTCTTGTGCTATTTAGAAAGGTGTCCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGAGGCAATGGTGCAGCCGGGGTCCCTGAGACTCTCCTGTGAGCCTCTGATTCAATTTCACTAGATATAGTAGTAAGTAACTGGTCCGCGAGGCTCCAGGGAAGGGCCGGAGTGATTTATACATAGCAGTATCAAACTACGCTGACTCTGTGAGGGCCGATTCACTATCCAGAGACAACGCCAGAACTCACTGTGGCTGCAAAAGAACAGCCTGAGAGACGAGACACGGCTTTTATTACTGTGCGAGAGAGTACTCGACTATTGGGCCAGGGAACCTGTCCAGCTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	TCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCCTTGGCGATCAGCACTGAGCACAGCGGACTCACCATGGAGTTGGGGCTGTCTGGTTTTCTTGTGCTATTTAGAAAGGTGTCCAGTGTGAAAGTGCAGTGTGAGTCTGGGGAGGCTTGTACAGACCGGGGGTCCCTGAGACTCTCCTGTGAGCCTCTGATTCACTTCAATAAATATCCATGAACCTGGTCCGCGAGGCTCCAGGGAAGGGCCGGAGTGATTTATACATAGTACAGTATTAACACTACGCTGACTCTGTGAGGGCCGATTCACTATCCAGAGACAACGCCAGAACTCACTGTCTTCAAAATGGACAACCTGAGAGACGACACGGCTATCTATTACTGTGCGAGAGAGTCTTACTATTGGGCCAGGGAAGTCTGTCAGCGTCTCCGCGCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGAAATCCAAGGCATATCCACTTGGTGACCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGTTTTCTTGTGCTATTTAGAAAGGTGTCCCTTGTGAGTGCAACTGGTGGAGTCTGGGGAGGCTTGTACAGCCGGGGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGATTCACTTCACTAGATATAGTAGTAAGTAACTGGTCCGCGAGGCTCCAGGGAAGGGCCGGAGTGATTTATACATAGTACAGTATTAACACTACGCTGACTCTGTGAGGGCCGATTCACTATCCAGAGACAACGCCAAGTGTGATCTGCAGATGAACAGCCTGAGCGACGAGACACGGCTTTTATTATTGTCGAGAGGTGCTTACTATTGGGCCAGGGAATGTTGTCAGTCTCCTCAGCCTCCACCAAGGGCCCATCGTCTTCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGATTGGTTTTCTTGTGCTTTTTTTGGAGTGTCCACTGTGAGTGCAACTGGTGGAGTCTGGGGAGGCTTGTCCAGTCGGGGGGTCCCTGAGACTCTCCTGCACAGCCTCTGATTCACTTAAATATAGTAGTAAGTAACTGGTCCGCGAGGCTCCAGGGAAGGGCCGGAGTGTGATCGCATACTAGCAGTACAGTACAAACAATATGAGACTCTGTGAGGGCCGATTCACTATCCAGAGACAATGACAAGAACTCAATGTTTTCTGAAATGAGCAGCCTGACAGACGCGGACACGGCTGTATATTACTGTGCGAGAGAGTCTTACTACTGGGCCAGGGAAGCCCTGTGACCGTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCTGCAACCCAGCCAGATGGGAACGTGGTATCGCCTGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTACTGGTTTTCTTGTGCTATTTAGAAAGGTGTCCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGAAAATGATACAGTCCCGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGATTCACTTCACTAAATATGCCATGAACCTGGTCCGCGAGGCTCCAGTGTGAGGGCTGGAGTGGATTGCATACATCAATAAAGACAGTGAAGCCATGATCTACTCAGACTTTGTGAAGGGCCGATTCACTATCCAGAGACAATGACAAGAACTCAATGATCTAGAAATGAATAGCCTGAGAGACGAGACACGGCTGTGATTACTGTGCGAGAGAGTCTTACTACTGGGCCAGGGAAGCCCTGTGACCGTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	ACCTCTCAGAGAGGTGCCTTAGCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGTTTTCTTGTGCTATTTAGCAGTGTCCAGTGTGAGTGCATTAAGTGTGAGTCTGGGGAGGCTTGTACAGCCGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGATTCACTTCACTAGATACAGCATGAACCTGGTCCGCGAGGCTCCAGGGAAGGGCCGGAGTGTGATTTATACATGACAGTACTAGTGTATCCCCAAAATACGCGACTCTGTGAAGGGCCGATTCACTATCTCCAGAGACAATGCCAAGAGGGCGCTGTCTGCAGCTGACCAGCCTGAGAGACGAGACACGGCTGTCTATTATTGTGCGAGAGGGGCTTACTACTGGGCCAGGGAAGCCCTGTGACCGTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCTGCAGCACCAGCCAGATGGGAACGTGGTATCGCCTGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGTTTTCTTGTGCTATTTAGAAAGGTGTCCAGTGTGCGTACAGCTGATGAGTCTGGGGAGGCTTGTACAGCCGGGGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGATTCACTTCAATAAATATAGTAGTAAGTAACTGGTCCGCGAGGCTCCCGGGAAGGGCTGGAATGATATATAGTGTAGCAGTATAGTGTACCAACAGTACGCGACTCTGTGAGGGCCGATTCACTATCTCCAGAGACAATGACAAGAACTCACTATATCTGAAATGAACAGCCTGACTGACGGGGACACGGCTATCTATTACTGTGCGAGAGAGTACTTACTACTGGGCCAGGGAAGTGTGTCACCGTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCTGCAGCACCAGCCAGATGGGAACGTGGTATCGCCTGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGTTTTCTTGTGCTATTTAGAAAGGTGTCCAGTGTGCGTACAGCTGATGAGTCTGGGGAGGCTTGTACAGCCGGGGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGATTCACTTCAATAAATATAGTAGTAAGTAACTGGTCCGCGAGGCTCCCGGGAAGGGCTGGAATGATATATAGTGTAGCAGTATAGTGTACCAACAGTACGCGACTCTGTGAGGGCCGATTCACTATCTCCAGAGACAATGACAAGAACTCACTATATCTGAAATGAACAGCCTGACTGACGGGGACACGGCTATCTATTACTGTGCGAGAGAGTACTTACTACTGGGCCAGGGAAGTGTGTCACCGTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCTGCAGCACCAGCCAGATGGGAACGTGGTATCGCCTGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGTTTTCTTGTGCTATTTAGAAAGGTGTCCAGTGTGAGTGCAGTGTGAGTCTGGGGAGGCTTGTACAGCCGGGGGGTCCCTCAGACTTTCATGTACAGCCTCTGTTTTCACTTCACTAAATACAGCATGAACCTGGTCCGCGAGGCTCCAGGGAAGGGCCGGAGTGTGATTTATACATGATTTAGCAGTATAGTGTACCAACAGTACGCGACTCTGTGAGGGCCGATTCACTATCTCCAGAGACAATGACAAGAACTCACTATATCTGAAATGAACAGCCTGACTGACGGGGACACGGCTATCTATTACTGTGCGAGAGAGTACTTACTACTGGGCCAGGGAAGTGTGTCACCGTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCTGCAGCACCAGCCAGATGGGAACGTGGTATCGCCTGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGTCTTAGCCCTGATTCCAAGGCATTTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAAATGGGGCTGTGCTGGTTTTCTTGTGCTATTTAGAAAGGTGTCCAGTGTGAGTGCAGTGTGAGTCTGGGGAGGCTTGTACAGCCGGGGGGTCCCTGAGACTCTCTGTGCAGCCTCTGATTAAATTCAGTAGATATAGTAGTAAGTAACTGGTCCGCGAGGCTCCAGGGAAGGGCCGGAGTGTGATTTATACATGATTTAGCAGTATAGTGTACCAACAGTACGCGACTCTGTGAGGGCCGATTCACTATCTCCAGAGACAATGACAAGAACTCACTGACTTGAATGAACAGCCTGAGAGACGAGACACGGCTGTCTATTATTGTGCGAGAGAGTCTTACTACTGGGCCAGGGAAGCCCTGTGACCGTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCCTGAGCCTCTGCAGCACCAGCCAGATGGGAACGTGGTATCGCCTGCTGCTGCTCAAGGACTACTTCCCCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGTGCACACTTCCCGCTGTCTACAGTCTCAGGA

2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCTTCCCTGATCCCAAGGCATTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGGTTTTCTTGTGCTATTTAGCAGGTGTCAGTGTGAGGTGCACTAGTGCAGTCTGGGGAGGCTCGTACAGCCGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTCAAGTATGAACTGGTCCGCGAGCTCCAGGGGAAGGGCCGGAGTGGATCTCGTACATTGATAGTAGTGAAGCAGAAGATATGCAGACTCTGTGAAGGGCCGATTTCATCGTTTTCCAGAGACAATGCCAAGAGGGCACTGTCTGTCAACTAATAGCCTGAGAGACGAGACACGGCTGTCTACTGTGCGAGAGAGTGTCTTACTACTGGGGCCAGGGAGCCCTGTCCACCTCTCGTCCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCGCCTGTCCAGAGCACCTCCGAGAGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACACTCAGCGCTCTGACCAGCGCGTGCACACCTCCAGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCTTCCCTGATCCCAAGGCATTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGGTTTTCTTGTACTATTTAGAAAGGTGTCGGGTGTCGGTGCAGTTGGTGAAGTTCGGGGAGGCTTGGTAATGCCCGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAAATTTGCAATGAACGGTCCGCGAGCTCCAGGGGAAGGGCCGGAGTGGATTCATATATTAGCAGTAAAGTGAAGGCATATCGTACGCAGACTCCGTGAAGGGCCGATTACCCGTCTCCAGAGACAATGACAAGAAATCAATTTATCTCAAATGAACAGCCTGAGAGACGAGGACACGGCTGTCTACTACTGTGCGAGAGAGTGTCTTACTACTGGGGCCAGGGAGCCCTGTCCACCTCTCCTCAGCATCCCCACCAGCCCCAAGTCTTCCCGTGTGAGCTCTGCGAGCACCAGCCAGATGGGAACGTGTATCGCTGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACACTCAGCGCTCTGACCAGCGCGTGCACACCTCCAGCTGTCTACAGTCTCAGGA
2_I_GHV3-48_I_GHJ4	AGCTCTCAGAGAGGTGCTTCCCTGATCCCAAGGCATTCCACTTGGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGGTTTTCTTGTGCTATTTAGCAGGTGTCAGTGTGAGGTGCAGTGTGGAGTCTGGGGAGGCTTGGTACAGCCGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAGATATAGTATGAACTGGTCCGCGAGCTCCAGGGGAAGGGCCGGAGTGGATTCATACATTGACAGTAGTGTGAACCAGAAGATACGCAGACTCTGTGAAGGGCCGATTACCATCTCCAGAGACAATGCCAAGAGGGCACTGTCTGTGCAGCTGAACAGCCTGAGAGACGAGACACGGCTGTCTACTACTGTGCGAGAGAGTGTCTTACTACTGGGGCCAGGGAGCCCTGTCCACCTCTCCTCAGCTCCACCAAGGGCCCATCGTCTCCCTGGCGCCTGTCCAGAGACGACTCCGAGAGCACAGCGCCCTGGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACACTCAGCGCTCTGACCAGCGCGTGCACACCTCCAGCTGTCTACAGTCTCAGGA
131_I_GHV3-23_I_GHJ6	AGCTCTGAGAGAGGAGCCAGCCCTGGGATTTTCAGGTGTTTTCATCTGGTGATCAGCACTGAACACAGAGAACTCACCATGGAGTTGGGGCTGAGTGGCTTTTTCTTGTGCTATTTAAAGGTGTCAAGTGTGAGGTGAAGTTGGTGAAGTCTGGGGAGGCTTGGTACAGCCTGGGGAGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAAATTTGCAATGAACGGTCCGCGAGCTCCAGGGGAAGGGCCGGAGTGGATTCATACATTGACAGTAGTGTGAACCAGAAGATACGCAGACTCCGTGAAGGGCCGATTACCTCTCCAGAGACAATCCAGAACACCTGTATCTCAAATGAACAGCCTGAGCGCGATGACACGGCCATATATTACTGTGCGAAGACTGTGGCCCTTGTGCGAGTGTGCTCCACGACGCGCGCCGGAACCTTTGGAGTCTGGGGCCAAGGACCACGGTCCACCGTCTCAGCCTCCACCAAGGGCCATCGTCTTCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACACTCAGCGCCCTGACCAGCGCGTGCACACCTCCCGCTGTCTACAGTCTCAGGA
131_I_GHV3-23_I_GHJ6	AGCTCTGAGAGAGGAGCCAGCCCTGGGATTTTCAGGTGTTTTCAITTTGGTGATCAGCACTGAACACAGAGAGGACTCACCATGGAGTTGGGGCTGAGTGGCTTTTTCTTGTGCTATTTAAAGGTGTCCAGTGTGAGGTGAAGCTGGTGAAGTCTGGGGAGGCTTGGTACAGCCGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAAATTTGCAATGAACGGTCCGCGAGCTCCAGGGGAAGGGCCGGAGTGGATTCAGGATTTAGTTTGGGGGATAAACACATTTACACAGACTCCGTGAAGGGCCGTTTCCATCTCCAGAGACAATCCAAAGAACACCTGTATCTGCAATGAACAGCCTGAGCCGAGACACGGCCGTATATTACTGTGCGAAGACTGTGGCCCTTGTGCGAGTGTGCTCCACGACGCGCGCCGGAGCTTTGGAGTCTGGGGCCAAGGACCACGGTCCACCGTCTCCACAGCCTCCACCAAGGGCCATCGTCTTCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACACTCAGCGCCCTGACCAGCGCGTGCACACCTCCCGCTGTCTACAGTCTCAGGA
131_I_GHV3-23_I_GHJ6	AGCTCTGAGAGAGGAGCCAGCCCTGGGATTTTCAGGTGTTTTCAITTTGGTGATCAGCACTGAACACAGAGAGGACTCACCATGGAGTTGGGGCTGAGTGGCTTTTTCTTGTGCTATTTAAAGGTGTCCAGTGTGAGGTGAAGCTGGTGAAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAAATTTGCAATGAACGGTCCGCGAGCTCCAGGGGAAGGGCCGGAGTGGATTCAGGATTTAGTTTGGGGGATAAACACATTTACACAGACTCCGTGAAGGGCCGTTTCCATCTCCAGAGACAATCCAAAGAACACCTGTATCTGCAATGAACAGCCTGAGCCGAGACACGGCCATATATTACTGTGCGAAGACTGTGGCCCTTGTGCGAGTGTGCTCCACGACGCGCGCCGGAGCTTTGGAGTCTGGGGCCAAGGACCACGGTCCACCGTCTCCACAGCCTCCACCAAGGGCCATCGTCTTCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACACTCAGCGCCCTGACCAGCGCGTGCACACCTCCCGCTGTCTACAGTCTCAGGA
131_I_GHV3-23_I_GHJ6	AGCTCTGAGAGAGGAGCCAGCCCTGGGATTTTCAGGTGTTTTCAITTTGGTGATCAGCACTGAACACAGAGAACTCACCATGGAGTTGGGGCTGAGTGGCTTTTTCTTGTGCTATTTAAAGGTGTCCAGTGTGAGGTGAAGCTGGTGAAGTCTGGGGAGGCTTGGTACAGCCGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAAATTTGCAATGAACGGTCCGCGAGCTCCAGGGGAAGGGCCGGAGTGGATTCAGGATTTAGTTTGGGGGATAAACACATTTACACAGACTCCGTGAAGGGCCGTTTCCATCTCCAGAGACAATCCAAAGAACACCTGTATCTGCAATGAACAGCCTGAGCCGAGACACGGCCATATATTACTGTGCGAAGACTGTGGCCCTTGTGCGAGTGTGCTCCACGACGCGCGCCGGAGCTTTGGAGTCTGGGGCCAAGGACCACGGTCCACCGTCTCCTCAGCCTCCACCAAGGGCCATCGTCTTCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACACTCAGCGCCCTGACCAGCGCGTGCACACCTCCCGCTGTCTACAGTCTCAGGA
131_I_GHV3-23_I_GHJ6	AGCTCTGAGAGAGGAGCCAGCCCTGGGATTTTCAGGTGTTTTCAITTTGGTGATCAGCACTGAACACAGAGAACTCACCATGGAGTTGGGGCTGAGTGGCTTTTTCTTGTGCTATTTAAAGGTGTCCAGTGTGAGGTGAAGCTGGTGAAGTCTGGGGAGGCTTGGTACAGCCGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAAATTTGCAATGAACGGTCCGCGAGCTCCAGGGGAAGGGCCGGAGTGGATTCAGGATTTAGTTTGGGGGATAAACACATTTACACAGACTCCGTGAAGGGCCGTTTCCATCTCCAGAGACAATCCAAAGAACACCTGTATCTGCAATGAACAGCCTGAGCCGAGACACGGCCATATATTACTGTGCGAAGACTGTGGCCCTTGTGCGAGTGTGCTCCACGACGCGCGCCGGAGCTTTGGAGTCTGGGGCCAAGGACCACGGTCCACCGTCTCCTCAGCCTCCACCAAGGGCCATCGTCTTCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACACTCAGCGCCCTGACCAGCGCGTGCACACCTCCCGCTGTCTACAGTCTCAGGA
131_I_GHV3-23_I_GHJ6	AGCTCTGAGAGAGGAGCCAGCCCTGGGATTTTCAGGTGTTTTCAITTTGGTGATCAGCACTGAACACAGAGAACTCACCATGGAGTTGGGGCTGAGTGGCTTTTTCTTGTGCTATTTAAAGGTGTCCAGTGTGAGGTGAAGCTGGTGAAGTCTGGGGAGGCTTGGTACAGCCGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAAATTTGCAATGAACGGTCCGCGAGCTCCAGGGGAAGGGCCGGAGTGGATTCAGGATTTAGTTTGGGGGATAAACACATTTACACAGACTCCGTGAAGGGCCGTTTCCATCTCCAGAGACAATCCAAAGAACACCTGTATCTGCAATGAACAGCCTGAGCCGAGACACGGCCATATATTACTGTGCGAAGACTGTGGCCCTTGTGCGAGTGTGCTCCACGACGCGCGCCGGAGCTTTGGAGTCTGGGGCCAAGGACCACGGTCCACCGTCTCCTCAGCCTCCACCAAGGGCCATCGTCTTCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACACTCAGCGCCCTGACCAGCGCGTGCACACCTCCCGCTGTCTACAGTCTCAGGA
131_I_GHV3-23_I_GHJ6	GAGAGAGGAGCCAGCCCTGGGATTTTCAGGTGTTTTCAITTTGGTGATCAGCACTGAACACAGAGAACTCACCATGGAGTTGGGGCTGAGTGGCTTTTTCTTGTGCTATTTAAAGGTGTCCAGTGTGAGGTGAAGCTGGTGAAGTCTGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAAATTTGCAATGAACGGTCCGCGAGCTCCAGGGGAAGGGCCGGAGTGGATTCAGGATTTAGTTTGGGGGATAAACACATTTACACAGACTCCGTGAAGGGCCGTTTCCATCTCCAGAGACAATCCAAAGAACACCTGTATCTGCAATGAACAGCCTGAGCCGAGACACGGCCATATATTACTGTGCGAAGACTGTGGCCCTTGTGCGAGTGTGCTCCACGACGCGCGCCGGAGCTTTGGAGTCTGGGGCCAAGGACCACGGTCCACCGTCTCCTCAGCCTCCACCAAGGGCCATCGTCTTCCCTGGCACCTCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGCTGCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACACTCAGCGCCCTGACCAGCGCGTGCACACCTCCCGCTGTCTACAGTCTCAGGA

181_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCAGCCCTGGGATTTTCAGTGTTTTCTTTGGTGATCAGGACTGAACAGAGAGAAGCTCACCATGGAGTTTGGGCTGAGCTGGCTTTTCTTGTTGGCCATTGTAAGAGTTGCCAGTGTGATGTGCAGCTGGTGGAGTCCGGGGGAGGCTTCA AAAAGCCGGGGGGTCCCTGACACTCTCCTGTGCAGCCTCTGATTACCTTTAGAGACTATGCCATGACCTGGTCCGCGAGTCCAGGGAGGGGGCTGGAGAGCGTCTCAGTTATTAGCGGTAGTGAAGAGGCACATTCTACTCCGACTCCGTGAAGGGCCGCTTCA CATCTCCAGAGACAATTCAGGAACACACTGTCTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCATATTTACTGTGCGAAAGGAAGAGGGCAGCAGTTGATCTACCGACTGGGGCCGGGAATCCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGT CTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
181_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCAGCCCTGGGATTTTCAGTGTTTTCTTTGGTGATCAGGACTGAACAGAGAGAAGCTCACCATGGAGTTTGGGCTGAGCTGGCTTTTCTTGTTGGCTATTGTAAGAGTTGCCAGTGTGATGTGCAGCTGGTGGAGTCCGGGGGAGGCTTCA AAAAGCCGGGGGGTCCCTGACACTCTCCTGTGCAGCCTCTGATTACCTTTAGAGACTATGCCATGACCTGGTCCGCGAGTCCAGGGAGGGGGCTGGAGAGCGTCTCAGTTATTAGCGGTAGTGAAGAGGCACATTCTACTCCGACTCCGTGAAGGGCCGCTTCA CATCTCCAGAGACAATTCAGGAACACACTGTCTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCATATTTACTGTGCGAAAGGAAGAGGGCAGCAGTTGATCTACCGACTGGGGCCGGGAACCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGTCT TTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
181_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCAGCCCTGGGATTTTCAGTGTTTTCACTTGGTGGTGCAGGACTGAACAGAGAGAAGCTCACCATGGAGTTTGGGCTGAGCTGGCTTTTCTTGTTGGCTATTGTAAGAGTTGCCAGTGTGATGTGCAGCTGGTGGAGTCTGGGGCGGCTTG GTACAGCCTGGGGGGTCCCTGACACTCTCCTGTGCAGCCTCTGATTACCTTTAGAGACTATGCCATGACTTGGTCCGCGAGTCCAGGGAGGGGGCTGGAGAGCGTCTCAGTTATTAGCGGTAGTGAAGAGGCACATTCTACTCCGACTCCGTGAAGGGCCGCTTCA ACCATCTCCAGAGACAATTCAGGAACACACTGTCTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCATATTTACTGTGCGAAAGGAAGAGGGCAGCAGTTGATCTACCGACTGGGGCCAGGAACCCCGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGT GTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
181_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCAGCCCTGGGATTTTCAGTGTTTTCTTTGGTGATCAGGACTGAACAGAGAGAAGCTCACCATGGAGTTTGGGCTGAGCTGGCTTTTCTTGTTGGCTATTGTAAGAGTTGCCAGTGTGATGTGCAGCTGGTGGAGTCCGGGGGAGGCTTCA AAAAGCCGGGGGGTCCCTGACACTCTCCTGTGCAGCCTCTGATTACCTTTAGAGACTATGCCATGACTTGGTCCGCGAGTCCAGGGAGGGGGCTGGAGAGCGTCTCAGTTATTAGCGGTAGTGAAGAGGCACATTCTACTCCGACTCCGTGAAGGGCCGCTTCA CATCTCCAGAGACAATTCAGGAACACACTGTCTCTGCTAATGAACAGCCTGAGAGCCGAGGACACGGCCATATTTACTGTGCGAAAGGAAGAGGCACAGTTGATCTACCGACTGGGGCCGGGAACCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGTCT TTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
181_I_GHV3-23_I_GHJ4	AGCTCTGAGAGAGAGCCAGCCCTGGGATTTTCAGTGTTTTCTTTGGTGATCAGGACTGAACAGAGAGAAGCTCACCATGGAGTTTGGGCTGAGCTGGCTTTTCTTGTTGGCTATTGTAAGAGTTGCCAGTGTGATGTGCAGCTGGTGGAGTCCGGGGCGGCTTG TACAGCCTGGGGGGTCCCTGAGACTCTCCTGTAGCCTCTGATTACCTTTAGAGACTATGCCATGAGTTGGTGGCGCAGGCTCCAGGGAGGGGGCTGGAGTGGTCTCAGTTATTAGTGTAGTGGTGGTGGCACATTCTACACAGACTCCGTGAAGGGCCGCTTCA CCATCTCCAGAGACAATTCAGGAACACACTGTCTCTGCTAATGAACAGCCTGAGAGCCGAGGACACGGCCATATTTACTGTGCGAAAGGAAGAGGGCAGCAGTTGATCTACCGACTGGGGCCAGGAACCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGT CTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
181_I_GHV3-23_I_GHJ4	ATGGGGGAGAGAGAGCCAGCCCTGGGATTTTCAGTGTTTTCTTTGGTGATCAGGACTGAACAGAGAGAAGCTCACCATGGAGTTTGGGCTGAGCTGGCTTTTCTTGTTGGCTATTGTAAGAGTTGCCAGTGTGATGTGCAGCTGGTGGAGTCCGGGGGAGGCTTCA AAAAGCCGGGGGGTCCCTGACACTCTCCTGTGCAGCCTCTGATTACCTTTAGAGACTATGCCATGACTTGGTCCGCGAGTCCAGGGAGGGGGCTGGAGAGCGTCTCAGTTATTAGCGGTAGTGAAGAGGCACATTCTACTCCGACTCCGTGAAGGGCCGCTTCA CCATCTCCAGAGACAATTCAGGAACACACTGTCTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCATATTTACTGTGCGAAAGGAAGAGGGCAGCAGTTGATCTACCGACTGGGGCCAGGAACCTGGTACCCTCTCCTCAGCCTCCACCAAGGCCCATCGG TCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTACAGTCTCAGGA
232_I_GHV3-73_I_GHJ5	AGGTCGTGGAGAGAGCTCCAGCCTTGGGATTTCCAGCTGTCTCACTCGGTGATCGGCACTGAATACAGAGACTCACCATGGAGCTTGGGCTGAGCTGGGTTTCTTGTGCTATTGTAAGAGTTGCCAGTGTGAGTGTGAGTGTGAGTCCGGGGGGGGCTT GGTCCAGCCGGGGGGTCCCTGAACTCTCCTGTGCAGCCTCTGGTTTTCAGCTTCACTGGCTCTGCTATGCACTGGTCCGCGAGTCCGGGAAAGGCTGGAGTGGTGGCCGTATAAAAAACAAGCCAACAGTTACGCGACAGCATATGCTGCGTGGTGAAGG CAGGTTACCATCTCCAGAGATGATTCAAAGGACACGGCGTATCTGAAATGAACAGCCTGAAAAGCGAGGACACGGCCGTATTACTGCACCAGACATCGATTCTGATGCGCAGCCTGGGGAGAAAATTGTTGACTCTGGGGCCAGGAAACCTGTACCCTCTC CTCAGCCTCCACCAAGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTA CAGTCTCAGGA
232_I_GHV3-73_I_GHJ5	AGGTCGTGGAGAGAGCTCCAGCCTTGGGATTTCCAGCTGTCTCACTCGGTGATCGGCACTGAATACAGAGACTCACCATGGAGCTTGGGCTGAGCTGGGTTTCTTGTGCTATTGTAAGAGTTGCCAGTGTGAGTGTGAGTGTGAGTCCGGGGGGGGCTTG GTCCAGCCGGGGGGTCCCTGAACTCTCCTGTGCAGCCTCTGGTTTTCAGCTTCACTGGCTCCGCTATTCACTGGTCCGCGAGTCCGGGAAAGGCTGGAGTGGTGGCCGTATAAGAAACAAGCCAACAGTTACGCGACAGCATATGCTGCGTGGTGAAGGCA GGTTACCATCTCCAGAGATGATTCAAAGGACACGGCGTATCTGAAATGAACAGCCTGAAAGCGAGGACACGGCCGTATTACTGCACCAGACATCGATTCTGATGCGCCAGCCTGGGGAGAAAATTGTTGACTCATGGGGCCAGGAAACCTGTACCCTCTCCT TCAGCCTCCACCAAGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTA CAGTCTCAGGA
232_I_GHV3-73_I_GHJ5	AGGTCGTGGAGAGAGCTCCAGCCTTGGGATTTCCAGCTGTCTCACTCGGTGATCGGCACTGAATACAGAGACTCACCATGGAGCTTGGGCTGAGCTGGGTTTCTTGTGCTATTGTAAGAGTTGCCAGTGTGAGTGTGAGTGTGAGTCCGGGGGGAGGCTTG GTCCAGCCTGGGGGGTCCCTGAACTCTCCTGTGCAGCCTCTGGTTTTCAGCTTCACTGGCTCCGCTATTCACTGGTCCGCGAGTCCGGGAAAGGCTGGAGTGGTGGCCGTATAAGAAACAAGCCAACAGTTACGCGACAGCATATGCTGCGTGGTGAAGGCA GGTTACCATCTCCAGAGATGATTCAAAGGACACGGCGTATCTGAAATGAACAGCCTGAAAGCGAGGACACGGCCGTATTACTGCACCAGACATCGATTCTGATGCGCCAGCCTGGGGAGAAAATTGTTGACTCATGGGGCCAGGAAACCTGTACCCTCTCCT AGCCTCCACCAAGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTA CAGTCTCAGGA
232_I_GHV3-73_I_GHJ5	AGCTCTGGAGAGAGCTCCAGCCTTGGGATTTCCAGCTGTCTCACTCGGTGATCGGCACTGAATACAGAGACTCACCATGGAGTTTGGGCTGAGCTGGGTTTCTTGTGCTATTGTAAGAGTTGCCAGTGTGAGTGTGAGTGTGAGTCCGGGGGAGGCTTG GTCCAGCCGGGGGGTCCCTGAACTCTCCTGTGCAGCCTCTGGTTTTCAGCTTCACTGGCTCCGCTATTCACTGGTCCGCGAGTCCGGGAAAGGCTGGAGTGGTGGCCGTATAAGAAACAAGCCAACAGTTACGCGACAGCATATGCTGCGTGGTGAAGGCA AGGTTACCATCTCCAGAGATGATTCAAAGGACACGGCGTATCTGAAATGAACAGCCTGAAAGCGAGGACACGGCCGTATTACTGCACCAGACATCGATTCTGATGCGCCAGCCTGGGGAGAAAATTGTTGACTCATGGGGCCAGGAAACCTGTACCCTCTCCT CAGCCTCCACCAAGGCCCATCGTCTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGTTCAAGGACTACTCCCCAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCTA CAGTCTCAGGA

232_IHV3-73_IHJ5

AGGTCTGGGAGAGGAGCTCCAGCCTTGGGATTCCAGCTGTCTCCACTCGGTGATCGGCACTGAATACAGGAGACTCACCATGGAGCTTGGGCTGAGCTGGGTTCCTTGTTGCTATTTAAAGGTGTCCAGTGTGAGGTGCAACTGGTGAGTCCGGGGGGGCTTG
GTCCAGCCGGGGGGTCCCTGAAAGTCTCTGTGCAGCCTCTGGTTTCACTGCTCCGCTATTCACTGGGTCGCGCAGGCTTCCGGGAAAGCCCTGGAGTGGGTTGGCCGTATAAGAAACAAGCCAACAGTTACGCGACAGCATATGTCGTCGGTGAAGGC
AGGTTCCACATCTCCAGAGATGATTCAAAGGACACGGCGTATCTGGAATGAACAGCCTGAAAAGCGAGGACACGGCCGTATTACTGCACCAGACATCGGATTCGTATGGCCGACCTTGGGGAGAAAAGTTGTTGACTCCTGGGGCCAGGGAACCTGGTCACCGTCTCC
TCAGCCTCCACCAAGGGCCCATCGGTCTCCCTGCGACCCCTCTCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCTGTTCAAGGACTACTCCCGAACCGGTGACGGTGTGTTGAACTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCGGCTGTCTTA
CAGTCTCAGGA