

**Supplementary Table 1: The usage of IGKV genes in the HH and IHB library**

<b>HH-IgK</b>	<b>Frequency (%)</b>	<b>IHB-IgK</b>	<b>Frequency (%)</b>
IGKV4-1	12.94	IGKV4-1	13.40
IGKV3-20	11.80	IGKV3-20	10.95
IGKV2-30	10.08	IGKV2-30	10.10
IGKV3-11	8.03	IGKV3-11	8.17
IGKV1-39	7.10	IGKV1-39	6.87
IGKV2-28	6.04	IGKV1-5	6.07
IGKV1-5	5.85	IGKV2-28	6.02
IGKV1-33	4.94	IGKV1-33	5.66
IGKV3-15	3.61	IGKV3-15	3.23
IGKV1-12	3.01	IGKV1-9	3.07
IGKV1-16	2.90	IGKV1-17	2.96
IGKV1-9	2.61	IGKV1-16	2.37
IGKV2-24	2.46	IGKV1-12	2.36
IGKV2-29	2.11	IGKV2-29	2.09
IGKV1-17	2.09	IGKV1-27	2.00
IGKV1-27	1.97	IGKV2D-29	1.76
IGKV2D-29	1.41	IGKV2-24	1.73
IGKV1D-16	1.31	IGKV1-6	1.28
IGKV1-NL1	1.26	IGKV3D-15	1.20
IGKV1-6	0.95	IGKV1-8	1.14
IGKV1-8	0.94	IGKV1D-16	1.07
IGKV1D-12	0.93	IGKV1-NL1	0.95
IGKV6-21	0.86	IGKV3D-20	0.92
IGKV3D-15	0.86	IGKV1-13	0.74
IGKV3D-20	0.74	IGKV1D-12	0.69
IGKV2D-30	0.73	IGKV6-21	0.57
IGKV3D-11	0.51	IGKV2D-30	0.55
IGKV1-13	0.44	IGKV3D-11	0.53
IGKV6D-21	0.40	IGKV1D-13	0.33
IGKV2-40	0.27	IGKV2-40	0.27
IGKV1D-8	0.25	IGKV1D-8	0.26
IGKV1D-13	0.24	IGKV6D-21	0.23
IGKV3D-7	0.14	IGKV3D-7	0.19
IGKV1D-43	0.10	IGKV1D-43	0.18
IGKV5-2	0.07	IGKV5-2	0.05
IGKV2D-26	0.03	IGKV2D-26	0.04
IGKV1D-17	0.01	IGKV1D-17	0.00

**Supplementary Table 2: The usage of IGKJ genes in the HH and IHB library**

<b>HH-IgK</b>	<b>Frequency (%)</b>	<b>IHB-IgK</b>	<b>Frequency (%)</b>
<b>IGKJ4*01</b>	26.97	<b>IGKJ4*01</b>	28.00
<b>IGKJ5*01</b>	22.45	<b>IGKJ5*01</b>	22.15
<b>IGKJ1*01</b>	21.55	<b>IGKJ1*01</b>	20.70
<b>IGKJ2*01</b>	14.89	<b>IGKJ2*01</b>	15.75
<b>IGKJ3*01</b>	9.23	<b>IGKJ3*01</b>	8.74
<b>IGKJ2*02</b>	3.07	<b>IGKJ2*02</b>	3.15
<b>IGKJ4*02</b>	1.09	<b>IGKJ4*02</b>	1.08
<b>IGKJ2*03</b>	0.57	<b>IGKJ2*03</b>	0.38
<b>IGKJ2*04</b>	0.19	<b>IGKJ2*04</b>	0.05

**Supplementary Table 3: The usage of IGLV genes in the HH and IHB library**

<b>HH-IgL</b>	<b>Frequency (%)</b>	<b>IHB-IgL</b>	<b>Frequency (%)</b>
<b>IGLV3-1</b>	17.66	<b>IGLV3-1</b>	22.66
<b>IGLV3-21</b>	15.01	<b>IGLV9-49</b>	15.70
<b>IGLV10-54</b>	11.02	<b>IGLV3-21</b>	14.91
<b>IGLV9-49</b>	9.54	<b>IGLV3-27</b>	8.08
<b>IGLV3-27</b>	6.46	<b>IGLV3-19</b>	5.95
<b>IGLV6-57</b>	5.05	<b>IGLV10-54</b>	5.18
<b>IGLV3-19</b>	4.57	<b>IGLV6-57</b>	4.57
<b>IGLV2-8</b>	4.08	<b>IGLV2-8</b>	2.99
<b>IGLV5-52</b>	3.60	<b>IGLV5-37</b>	2.60
<b>IGLV1-44</b>	2.82	<b>IGLV5-52</b>	2.39
<b>IGLV1-40</b>	2.72	<b>IGLV1-40</b>	2.12
<b>IGLV5-37</b>	2.46	<b>IGLV2-14</b>	1.97
<b>IGLV2-14</b>	2.28	<b>IGLV1-51</b>	1.52
<b>IGLV1-51</b>	2.00	<b>IGLV3-9</b>	1.36
<b>IGLV2-11</b>	1.73	<b>IGLV1-44</b>	1.20
<b>IGLV3-9</b>	1.57	<b>IGLV3-25</b>	1.15
<b>IGLV1-47</b>	1.51	<b>IGLV1-47</b>	1.13
<b>IGLV3-25</b>	1.41	<b>IGLV4-3</b>	0.86
<b>IGLV2-23</b>	0.75	<b>IGLV2-11</b>	0.79
<b>IGLV5-45</b>	0.66	<b>IGLV5-45</b>	0.64
<b>IGLV3-10</b>	0.66	<b>IGLV2-18</b>	0.57
<b>IGLV2-18</b>	0.65	<b>IGLV2-23</b>	0.52
<b>IGLV4-3</b>	0.57	<b>IGLV3-10</b>	0.38
<b>IGLV5-39</b>	0.49	<b>IGLV8-61</b>	0.31
<b>IGLV8-61</b>	0.24	<b>IGLV4-60</b>	0.15
<b>IGLV4-69</b>	0.22	<b>IGLV4-69</b>	0.05
<b>IGLV1-36</b>	0.11	<b>IGLV1-36</b>	0.05
<b>IGLV3-16</b>	0.07	<b>IGLV3-12</b>	0.05
<b>IGLV7-46</b>	0.03	<b>IGLV3-16</b>	0.05
<b>IGLV7-43</b>	0.03	<b>IGLV5-39</b>	0.05
<b>IGLV3-12</b>	0.02	<b>IGLV7-43</b>	0.02
<b>IGLV4-60</b>	0.00	<b>IGLV7-46</b>	0.02
<b>IGLV3-22</b>	0.00	<b>IGLV3-22</b>	0.00

**Supplementary Table 4: The usage of IGLJ genes in the HH and IHB library**

HH-IgL	Frequency (%)	IHB-IgL	Frequency (%)
IGLJ2*01	41.24	IGLJ3*02	37.38
IGLJ3*02	33.74	IGLJ2*01	37.33
IGLJ1*01	19.33	IGLJ1*01	18.97
IGLJ7*01	5.24	IGLJ7*01	5.43
IGLJ6*01	0.18	IGLJ6*01	0.35
IGLJ5*01	0.15	IGLJ5*01	0.32
IGLJ4*01	0.06	IGLJ4*01	0.20
IGLJ5*02	0.04	IGLJ5*02	0.03
IGLJ7*02	0.02	IGLJ7*02	0.01

**Supplementary Table 5: The comparisons of the somatic hypermutation levels between the HH and IHB library**

	Library		<i>p</i> , <i>OR(95%CI)</i> <sup>a</sup>
	HH (%)	IHB (%)	IHB vs. HH
<b>IgK repertoire</b>			
<b>P (V<sub>Identity</sub>≥90%)<sup>b</sup></b>	87.59	86.92	<2.2E-16, 1.062(1.047,1.077)
<b>P(mut in CDR1)<sup>c</sup></b>	65.47	64.01	<2.2E-16, 1.066(1.056,1.076)
<b>P(mut in CDR2)<sup>d</sup></b>	29.77	29.32	<2.2E-16, 1.021(1.011,1.032)
<b>IgL repertoire</b>			
<b>P (V<sub>Identity</sub>≥90%)</b>	69.15	74.62	<2.2E-16, 0.762(0.750,0.775)
<b>P(mut in CDR1)</b>	65.52	56.00	<2.2E-16, 1.493(1.472,1.515)
<b>P(mut in CDR2)</b>	56.79	52.63	<2.2E-16, 1.183(1.166,1.20)

a: Calculated by the logistic regression.

b: Frequency of the sequences with ≥90% V gene identity as the germline genes.

c: Frequency of the sequences with amino acid mutations in CDR1 regions.

d: Frequency of the sequences with amino acid mutations in CDR2 regions.

**Supplementary Table 6: The comparisons of the occurrence of junctional modifications in IgK and IgL repertoires**

Junctional modifications	Occurrence (%)				
	3VP	3VT	5JP	5JT	N
<b>IgK repertoire</b>					
<b>HH</b>	4.50	85.02	9.39	72.83	68.11
<b>IHB</b>	4.51	86.65	9.54	73.08	69.21
<i>p</i> ,	0.776,	<2.2E-16,	0.033,	0.017,	<2.2E-16,
<b>OR(95%CI)<sup>a</sup></b>	1.003	1.143	1.017	1.013	1.053
<b>(HH vs. IHB)</b>	(0.981,1.026)	(1.128,1.159)	(1.001,1.033)	(1.002,1.023)	(1.042,1.063)
<b>IgL repertoire</b>					
<b>HH</b>	2.53	89.40	10.41	67.90	71.07
<b>IHB</b>	3.04	88.36	10.37	69.03	70.73
<i>p</i> ,	<2.2E-16,	<2.2E-16,	0.719,	2.3E-11,	0.034,
<b>OR(95%CI)<sup>a</sup></b>	1.208	0.900	0.996	1.054	0.983
<b>(HH vs. IHB)</b>	(1.157,1.261)	(0.880,0.920)	(0.973,1.019)	(1.038,1.070)	(0.968,0.999)

a: Calculated by the logistic regression.