Supplementary Table 8. The Occurrence of Junctional Modifications in IgM Repertoires

Junctional Modification [a]	Occurrence (%)									
	3VP	**5DP**	**3DP**	**5JP**	**N1**	**N2**	**3VT**	**5DT**	**3DT**	**5JT**
HH	20.92	6.40	6.21	7.26	90.17	88.21	60.62	85.65	84.44	83.16
IHB	20.67	5.88	6.40	6.80	89.71	87.95	61.02	86.11	84.54	83.72
CHB	19.40	5.44	6.18	6.38	89.10	87.80	61.85	86.32	84.70	83.84
p, [b]	0.001,	<2.2E−16,	6.0E-5,	<2.2E−16,	5.0E-15,	4.3E-5,	4.0E-5,	8.9E-12,	0.167,	1.0E-14,
OR(95%CI)	0.985	0.914	1.033	0.931	0.951	0.976	1.017	1.039	1.007	1.041
(HH *vs.* IHB)	(0.976,0.994)	(0.900,0.929)	(1.017,1.049)	(0.917,0.945)	(0.939,0.963)	(0.964,0.987)	(1.009,1.024)	(1.028,1.050)	(0.997,1.018)	(1.031,1.052)
p, [b]	<2.2E−16,	<2.2E−16,	0.645,	<2.2E−16,	<2.2E−16,	5.7E-10,	<2.2E−16,	<2.2E−16,	4.0E-4,	<2.2E−16,
OR(95%CI)	0.910	0.841	0.996	0.869	0.891	0.962	1.053	1.057	1.020	1.050
(HH *vs.* CHB)	(0.901,0.919)	(0.827,0.855)	(0.980,1.013)	(0.856,0.883)	(0.879,0.903)	(0.950,0.974)	(1.044,1.062)	(1.045,1.069)	(1.009,1.031)	(1.039,1.062)
p, [b]	<2.2E−16,	<2.2E−16,	1.2E-5,	<2.2E−16,	<2.2E−16,	0.021,	<2.2E−16,	<2.2E−16,	0.026,	0.117,
OR(95%CI)	0.924	0.920	0.965	0.934	0.937	0.986	1.036	1.017	1.012	1.009
(IHB *vs.* CHB)	(0.915,0.933)	(0.905,0.936)	(0.949,0.980)	(0.919,0.949)	(0.925,0.949)	(0.974,0.998)	(1.027,1.044)	(1.006,1.029)	(1.001,1.023)	(0.998,1.019)

a: Junctional modification: 3VP and 3VT: the palindromic nucleotides (P) additions and exonuclease trimmings observed at 3′-end of V regions, respectively; 5DP and 5DT: the P additions and exonuclease trimmings observed at 5′-end of D genes, respectively; 3DP and 3DT: the P additions and exonuclease trimmings observed at 3′-end of D genes, respectively; 5JP and 5JT: the P additions and exonuclease trimmings observed at 5′-end of J genes, respectively; N1: the non-template randomized nucleotides (N) additions happened at the region between the 3′-end of V gene and the 5′-end of D gene; N2: N additions happened at the region between the3′-end of D gene and the 5′-end of J gene.
b: Calculated by the logistic regression.