Supplementary Data S2: Somatic hypermutation analysis

IGH>2003/01

gaccgccgcggacacggctgtgtattactgtgcgagcctacattactctggttcggggag
tccctatcactttgactactggggccagggaaccctggtcaccgtctcctcag

Result summary: 2003/01-IGH_Amino acid translation: ASLHYSGSGSPYHFDY	Productive IGH rearranged sequence (no stop codon and in-frame junction)	
V-GENE and allele	Homsap IGHV4-34*01, or Homsap IGHV4-34*02 or Homsap IGHV4-34*04 or Homsap IGHV4-34*05	identity = 100.00% (31/31 nt)
J-GENE and allele	Homosap IGHJ4*02	identity = 95.83% (46/48 nt)
D-GENE and allele by IMGT/Junction analysis	Homosap IGHD3-10*01	

Nucleotide (nt) mutations

IMGT labels		V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
Nb of positions including IMGT gaps (nt)		317 (320)	78	36	51	30	117	5 (8)
Nb of nucleotides		36 (39)	0	0	0	0	31	5 (8)
Nb of identical nucleotides		36	0	0	0	0	31	5
Nb of mutations		0 (3)	0	0	0	0	0	0 (3)
Mutations	Silent	0 (2)	0	0	0	0	0	0 (2)
	Non Silent	0 (1)	0	0	0	0	0	0 (1)
Transitions	a>g	0	0	0	0	0	0	0
	g>a	0	0	0	0	0	0	0
	c>t	0	0	0	0	0	0	0
	t>c	0	0	0	0	0	0	0
Transversions	a>c	0 (1)	0	0	0	0	0	0 (1)
	c>a	0	0	0	0	0	0	0
	a>t	0	0	0	0	0	0	0
	t>a	0	0	0	0	0	0	0
	g>c	0 (1)	0	0	0	0	0	0 (1)
	c>g	0	0	0	0	0	0	0
	g>t	0 (1)	0	0	0	0	0	0 (1)
	t>g	0	0	0	0	0	0	0

IGH>2010/02

gaccgccgcggacacggctgtatattactgtgcgagcctacattacaatgcttcggggag
tcccaactattttgactactggggccagggaaccctggtcaccgtctcctcag

Result summary: 2010/02-IGH_ **Amino acid translation: ASLHYNASGSPNYFDY**	Productive IGH rearranged sequence (no stop codon and in-frame junction)	
V-GENE and allele	Homsap IGHV4-34*01, or Homsap IGHV4-34*02 or Homsap IGHV4-34*04 or Homsap IGHV4-34*05	identity = 96.77% (30/31 nt)
J-GENE and allele	Homosap IGHJ4*02	identity = 97.92% (47/48 nt)
D-GENE and allele by IMGT/Junction analysis	Homosap IGHD3-10*01	

Nucleotide (nt) mutations

IMGT labels		V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
Nb of positions including IMGT gaps (nt)		317 (320)	78	36	51	30	117	5 (8)
Nb of nucleotides		36 (39)	0	0	0	0	31	5 (8)
Nb of identical nucleotides		35	0	0	0	0	30	5
Nb of mutations		1 (4)	0	0	0	0	1	0 (3)
Mutations	Silent	1 (3)	0	0	0	0	1	0 (2)
	Non Silent	0 (1)	0	0	0	0	0	0 (1)
Transitions	a>g	0	0	0	0	0	0	0
	g>a	1	0	0	0	0	1	0
	c>t	0	0	0	0	0	0	0
	t>c	0	0	0	0	0	0	0
Transversions	a>c	0 (1)	0	0	0	0	0	0 (1)
	c>a	0	0	0	0	0	0	0
	a>t	0	0	0	0	0	0	0
	t>a	0	0	0	0	0	0	0
	g>c	0 (1)	0	0	0	0	0	0 (1)
	c>g	0	0	0	0	0	0	0
	g>t	0 (1)	0	0	0	0	0	0 (1)
	t>g	0	0	0	0	0	0	0

IGH>2017/02

gaccgccgcggacacggctatttattactgtgcgagcccacgttactatggttcggggag
tccctactactttgactactggggccagggaaccgtggtcaccgtctcctcag

Result summary: 2017/02-IGH_ Amino acid translation: ASPRYYGSGSPYYFDY	Productive IGH rearranged sequence (no stop codon and in-frame junction)	
V-GENE and allele	Homsap IGHV4-34*01, or Homsap IGHV4-34*02 or Homsap IGHV4-34*04 or Homsap IGHV4-34*05	identity = 93.55% (29/31 nt)
J-GENE and allele	Homosap IGHJ4*02	identity = 97.92% (47/48 nt)
D-GENE and allele by IMGT/Junction analysis	Homsap IGHD3-10*01	

Nucleotide (nt) mutations

IMGT labels		V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
Nb of positions including IMGT gaps (nt)		317 (320)	78	36	51	30	117	5 (8)
Nb of nucleotides		36 (39)	0	0	0	0	31	5 (8)
Nb of identical nucleotides		34	0	0	0	0	29	5
Nb of mutations		2 (5)	0	0	0	0	2	0 (3)
Mutations	Silent	0 (2)	0	0	0	0	0	0 (2)
	Non Silent	2 (3)	0	0	0	0	2	0 (1)
Transitions	a>g	0	0	0	0	0	0	0
	g>a	1	0	0	0	0	1	0
	c>t	0	0	0	0	0	0	0
	t>c	0	0	0	0	0	0	0
Transversions	a>c	0 (1)	0	0	0	0	0	0 (1)
	c>a	0	0	0	0	0	0	0
	a>t	0	0	0	0	0	0	0
	t>a	0	0	0	0	0	0	0
	g>c	0 (2)	0	0	0	0	0	0 (2)
	c>g	0	0	0	0	0	0	0
	g>t	1	0	0	0	0	1	0
	t>g	0	0	0	0	0	0	0

IGH>2003/01

gaacagcctgggagtcgacgacacggctgtttattactgtgcgaaacctactacgtagac
cgttgtgggcagctgctgtcggggcgcgccagggaatcctggtcaccgtctcctca

Result summary: 2003/01-IGH_Amino acid translation: AKPTT*TVVGSCCRG	Unproductive IGH rearranged sequence (stop codons, out-of-frame junction)	
V-GENE and allele	Homsap IGHV3-48*03, or Homsap IGHV3-69-1*02	identity = 92.50% (37/40 nt)
J-GENE and allele	Homsap IGHJ4*02	identity = 68.09% (32/47 nt)
D-GENE and allele by IMGT/Junction analysis	Homsap IGHD2-15*01	

Nucleotide (nt) mutations

IMGT labels		V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
Nb of positions including IMGT gaps (nt)		316 (320)	78	36	51	30	117	4 (8)
Nb of nucleotides		44 (48)	0	0	0	0	40	4 (8)
Nb of identical nucleotides		41 (42)	0	0	0	0	37	4 (5)
Nb of mutations		3 (6)	0	0	0	0	3	0 (3)
Mutations	Silent	0 (2)	0	0	0	0	0	0 (2)
	Non Silent	3 (4)	0	0	0	0	3	0 (1)
Transitions	a>g	1	0	0	0	0	1	0
	g>a	0 (1)	0	0	0	0	0	0 (1)
	c>t	1	0	0	0	0	1	0
	t>c	0	0	0	0	0	0	0
Transversions	a>c	0 (1)	0	0	0	0	0	0 (1)
	c>a	0	0	0	0	0	0	0
	a>t	0	0	0	0	0	0	0
	t>a	0	0	0	0	0	0	0
	g>c	1 (2)	0	0	0	0	1	0 (1)
	c>g	0	0	0	0	0	0	0
	g>t	0	0	0	0	0	0	0
	t>g	0	0	0	0	0	0	0

IGH>2010/02 and IGH>2017/01

gagagccgaggacacggctatggattagtgtgcgagagttgtcacgtaaaccgatgtggg
cagctaatatcggggcgcgccagggaatcctggtcaccgtctcctca

Result summary: 2003/01-IGH_ Amino acid translation: ARVVT*TDVGS*YRG	Unproductive IGH rearranged sequence (stop codons, out-of-frame junction	
V-GENE and allele	Homsap IGHV3-11*04, or Homsap IGHV3-11*06 or Homsap IGHV3-21*01 or Homsap IGHV3-21*02 or Homsap IGHV3-21*05	identity = 90.32% (28/31 nt)
J-GENE and allele	Homsap IGHJ4*02	identity = 65.96% (31/47 nt)
D-GENE and allele by IMGT/Junction analysis	Homsap IGHD3-10*01	

Nucleotide (nt) mutations

IMGT labels		V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
Nb of positions including IMGT gaps (nt)		319 (320)	78	36	51	30	117	7 (8)
Nb of nucleotides		38 (39)	0	0	0	0	31	7 (8)
Nb of identical nucleotides		35	0	0	0	0	28	7
Nb of mutations		3 (4)	0	0	0	0	3	0 (1)
Mutations	Silent	0 (1)	0	0	0	0	0	0 (1)
	Non Silent	3	0	0	0	0	3	0
Transitions	a>g	0	0	0	0	0	0	0
	g>a	1	0	0	0	0	1	0
	c>t	0	0	0	0	0	0	0
	t>c	0	0	0	0	0	0	0
Transversions	a>c	0	0	0	0	0	0	0
	c>a	0	0	0	0	0	0	0
	a>t	0 (1)	0	0	0	0	0	0 (1)
	t>a	0	0	0	0	0	0	0
	g>c	0	0	0	0	0	0	0
	c>g	1	0	0	0	0	1	0
	g>t	0	0	0	0	0	0	0
	t>g	1	0	0	0	0	1	0

IGL>2003/01

actgcggaacatgggatagcagcctgagtgctgtgatattcggcggagggaccaagctga
ccgtcctag

Result summary: 2003/01-IGL_ Amino acid translation: GTWDSSLSAVI	Productive IGL rearranged sequence (no stop codon and in-frame junction)	
V-GENE and allele	Homsap IGLV1-51*01, or Homsap IGLV1-51*02	identity = 100.00% (23/23 nt)
J-GENE and allele	Homsap IGLJ2*01, or Homsap IGLJ3*01	identity = 97.22% (35/36 nt)

Nucleotide (nt) mutations

IMGT labels		V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
Nb of positions including IMGT gaps (nt)		340 (341)	78	36	51	30	117	28 (29)
Nb of nucleotides		33 (34)	0	0	0	0	5	28 (29)
Nb of identical nucleotides		33	0	0	0	0	5	28
Nb of mutations		0 (1)	0	0	0	0	0	0 (1)
Mutations	Silent	0 (1)	0	0	0	0	0	0 (1)
	Non Silent	0	0	0	0	0	0	0
Transitions	a>g	0	0	0	0	0	0	0
	g>a	0	0	0	0	0	0	0
	c>t	0	0	0	0	0	0	0
	t>c	0	0	0	0	0	0	0
Transversions	a>c	0	0	0	0	0	0	0
	c>a	0	0	0	0	0	0	0
	a>t	0	0	0	0	0	0	0
	t>a	0	0	0	0	0	0	0
	g>c	0	0	0	0	0	0	0
	c>g	0	0	0	0	0	0	0
	g>t	0 (1)	0	0	0	0	0	0 (1)
	t>g	0	0	0	0	0	0	0

IGL>2010/02

actgcggaacatgggataccagcctgagtgctgtggtattcggcggagggaccaagctga
ccgtcctag

Result summary: 2010/02-IGL_Amino acid translation: GTWDTSLSAVV	Productive IGL rearranged sequence (no stop codon and in-frame junction)	
V-GENE and allele	Homsap IGLV1-51*01, or Homsap IGLV1-51*02	identity = 95.65% (22/23 nt)
J-GENE and allele	Homsap IGLJ2*01, or Homsap IGLJ3*01	identity = 100.00% (36/36 nt)

Nucleotide (nt) mutations

IMGT labels		V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
Nb of positions including IMGT gaps (nt)		340 (341)	78	36	51	30	117	28 (29)
Nb of nucleotides		33 (34)	0	0	0	0	5	28 (29)
Nb of identical nucleotides		32	0	0	0	0	5	27
Nb of mutations		1 (2)	0	0	0	0	0	1 (2)
Mutations	Silent	0 (1)	0	0	0	0	0	0 (1)
	Non Silent	1	0	0	0	0	0	1
Transitions	a>g	0	0	0	0	0	0	0
	g>a	0	0	0	0	0	0	0
	c>t	0	0	0	0	0	0	0
	t>c	0	0	0	0	0	0	0
Transversions	a>c	0	0	0	0	0	0	0
	c>a	0	0	0	0	0	0	0
	a>t	0	0	0	0	0	0	0
	t>a	0	0	0	0	0	0	0
	g>c	1	0	0	0	0	0	1
	c>g	0	0	0	0	0	0	0
	g>t	0 (1)	0	0	0	0	0	0 (1)
	t>g	0	0	0	0	0	0	0

IGL>2017/02

actgcggaacatgggatagcaccctgagtgctgtggtattcggcggagggaccaagctga
ccgtcctag

Result summary: 2017/02-IGL_Amino acid translation: GTWDSTLSAVV	Productive IGL rearranged sequence (no stop codon and in-frame junction)	
V-GENE and allele	Homsap IGLV1-51*01, or Homsap IGLV1-51*02	identity = 95.65% (22/23 nt)
J-GENE and allele	Homsap IGLJ2*01, or Homsap IGLJ3*01	identity = 100.00% (36/36 nt)

Nucleotide (nt) mutations

IMGT labels		V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT
Nb of positions including IMGT gaps (nt)		340 (341)	78	36	51	30	117	28 (29)
Nb of nucleotides		33 (34)	0	0	0	0	5	28 (29)
Nb of identical nucleotides		32	0	0	0	0	5	27
Nb of mutations		1 (2)	0	0	0	0	0	1 (2)
Mutations	Silent	0 (1)	0	0	0	0	0	0 (1)
	Non Silent	1	0	0	0	0	0	1
Transitions	a>g	0	0	0	0	0	0	0
	g>a	0	0	0	0	0	0	0
	c>t	0	0	0	0	0	0	0
	t>c	0	0	0	0	0	0	0
Transversions	a>c	0	0	0	0	0	0	0
	c>a	0	0	0	0	0	0	0
	a>t	0	0	0	0	0	0	0
	t>a	0	0	0	0	0	0	0
	g>c	1	0	0	0	0	0	1
	c>g	0	0	0	0	0	0	0
	g>t	0 (1)	0	0	0	0	0	0 (1)
	t>g	0	0	0	0	0	0	0