

Supplementary table 5. Complete data of individual genes from six WG tissue samples

Adisplays the data summarized according to the predominant VH germline gene families found in the WG tissues.

patient #	VH germline gene	homology (% to germline)	CDR FR				R/H/ K	CDR3 length (amino acids)	annotation
			R	SR	S	E/D			
2	SA 6-71-2	94	4	17	2	2	0	9	
2	SC 6-21-2	88	6	111	1	1	1		not functional
6	Scy 133 1-2	95	3	05	4	1	0	21	
6	Scy14 7 1-2	93	3	09	1	1	0	11	
1	J2-13 3-7	96	3	21	3	1	0	11	
1	J3-22 3-7	94	5	07	2	1	0	11	
2	SF 8 3-7	91	9	15	7	0	1	10	
3	Wi- 9V 3-7	97	2	12	1	0	0	13	
5	Ko208 3-7	97	3	12	0	0	0	11	
5	Ko137 3-7	92	6	26	5	0	2	8	
1	J1-18 3-23	94	8	41	2	0	0	12	
1	J2-19 3-23	89	8	48	5	2	1	10	
1	J2-20 3-23	89	9	58	3	1	1	14	
1	J3-15 3-23	92	8	16	5	0	0	14	
2	SA4-4 3-23	93	6	16	0	1	1	11	
3	Wi- 13V 3-23	94	7	04	1	1	2	14	
4	Ro113 3-23	99	0	11	0	0	0	18	related to Ro112
4	Ro112 3-23	95	4	33	1	0	0	18	related to Ro113
4	Ro115 3-23	96	2	12	5	0	0	22	
4	Ro118 3-23	91	6	111	3	1	3	16	not functional
5	Ko205 3-23	93	4	17	2	1	0	10	
6	Scy07 3-23	92	5	36	5	1	2	14	related to Scy64
6	Scy54 3-23	95	6	02	3	0	0	6	
6	Scy49 3-23	96	1	35	1	0	0	12	
1	J2-4 3-30	99	2	00	0	0	2	14	
1	J2-6 3-30	90	8	210	3	0	1		not functional
1	J2-9 3-30	94	2	04	2	0	0	15	
1	J2-25 3-30	86	9	315	7	2	0	17	
1	J2-26 3-30	98	2	02	0	0	0		not functional
1	J3-12 3-30	97	2	13	1	0	0	13	
1	J3-20 3-30	87	5	311	6	0	0	18	
3	Wi-52 3-30	98	2	11	0	1	0	17	
3	Wi-1V 3-30	99	0	01	0	0	0	13	
4	Ro108 3-30					0	0		not functional

Adisplays the data summarized according to the predominant VH germline gene families found in the WG tissues.

patient	VH	homology	CDR FR				R/H/	CDR3 length	annotation
#	germline gene	(% to germline)	R	SR	S	E/D	K	(amino acids)	
4	Ro109 3-30	96	4	03	3	0	1	18	
4	Ro 39 3-30	90	4	211	5	1	0	13	
5	Ko01 3-30	89	8	08	4	0	1	14	
5	Ko135 3-30	91	3	27	5	0	0	13	
1	J2-2 4-34	94	4	07	2	2	0	12	
1	J2-21 4-34	86	6	215	102		1	12	
1	J2-23 4-34	93	2	29	2	0	0	17	
1	J3-19 4-34	88	7	19	101		3	19	
1	J3-21 4-34	97	1	04	1	0	0	16	
2	SE9-4 4-34	100	0	00	0	0	0		not functional
3	Wi-76 4-34	98	2	01	0	1	0	12	
3	Wi-77 4-34	99	1	01	0	1	0	12	
3	Wi-30V 4-34	99	1	01	0	1	0	12	
4	Ro 66 4-34	98	1	01	4	0	0	21	not functional
5	Ko150 4-34	93	4	17	1	0	0	17	
6	Scy 25 4-34	98	1	02	2	1	0	12	
6	Scy 75 4-34	91	3	110	4	1	0	19	
6	Scy 78 4-34	97	1	02	6	1	0	14	
6	Scy12 8 4-34	98	0	02	1	0	0	18	
1	J1-14 4-59	92	4	06	3	0	0	12	
1	J2-3 4-59	91	4	35	7	2	0	12	
1	J2-14 4-59	97	1	00	1	0	1	13	
1	J3-8 4-59	91	6	16	2	0	0	12	
3	Wi-62 4-59	95	1	15	3	0	0	19	
3	Wi-20V 4-59	95	1	14	3	0	0	19	
6	Scy 37 4-59	95	4	14	4	0	0	14	related to Scy66,83
6	Scy 66 4-59	97	2	06	0	0	0	14	related to Scy37,83
6	Scy 83 4-59	93	5	04	6	0	0	14	related to Scy37,66
6	Scy 74 4-59	97	3	03	1	1	0	18	
6	Scy 86 4-59	97	3	11	3	1	0	17	
6	Scy11 1 4-59	95	5	06	3	2	0	22	

B shows the remaining data grouped by their patient's origin

patient	VH	homology	CDR FR				R/H/	CDR3 length	annotation
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		germline	(% to	R	SR	S	E/D	R/H/K	(amino	
		gene	germline)						acids)	
1	J3-17	3-48	98	1	04	1	0	0	13	
1	J3-13	3-64	94	4	17	3	1	0	12	
1	J3-7	3-73	94	4	0		0	0		frameshift
1	J2-5	3-9	92	6	2		1	0		frameshift
1	J2-12	4-30	93	7	05	4	1	0	9	related to J2-8
1	J2-8	4-30	92	4	05	4	1	0	9	
1	J3-10	4-31	87	8	28	7	1	0	13	
1	J3-18	4-4	95	3	03	5	0	0	15	
1	J2-7	4-61	90	8	36	9	0	1	13	
1	J2-10	4-61	88	8	111	7	1	0	19	
1	J2-15	4-61	86	6	39	12	1	0	13	
1	J3-3	4-61	87	11	111	8	1	2	11	
1	J3-9	4-61	90	9	110	3	2	1	10	
2	SA6-4	1-18	92	6	35	3	2	1	18	
2	SA6-2	1-3	96	3	07	1	1	1		not functional
2	SE7-4	1-3	92	4	17	1	1	2		not functional
2	SF7	1-58	95	3	16	0	0	2	14	
2	SC6-4	1-69	91	5	05	5	0	1	14	
2	SD7-1	1-69	91	5	110	4	0	1	12	
2	SA5-2	2-5	97	2	0		0	0		not functional
2	SA5-6	2-5	85	5	08	4	1	0	11	
2	SC5-4	2-5	93	4	06	8	0	0	14	
2	SD2-3	2-5	97	1	01	2	0	0	10	
2	SF2	2-5	94	5	06	4	1	0	21	
2	SC6-1	2-70	96	2	03	0	0	0		not functional
2	SF6	3-13	97	5	03	1	0	1	15	
2	SA4-1	3-43	92	6	04	3	1	0	20	
2	SF4	3-48	91	5	14	2	2	1	14	
2	SE3-5	3-53	95	2	36	2	0	1	11	
2	SB3-1	3-74	91	7	05	5	0	1	9	
2	SF1	4-30	95	8	14	2	0	0	9	
2	SF5	4-31	98	0	11	1	0	0	15	
2	SF12	4-31	83	5	19	6	0	1	11	
2	SA3-5	4-4	94	6	02	2	1	1	13	
2	SD4-2	4-61	94	4	05	4	1	0	16	
2	SA2-4	5-51	90	2	16	2	1	0	16	
2	SA6-1	7-81	99	0	01	1	0	0		not functional
2	SB7-4	7-81	86	5	24	2	1	1		not functional
3	Wi-22	1-18	93	4	14	4	0	2	16	
3	Wi-27	1-18	91	4	35	6	0	1	16	related to Wi-22
3	Wi-16	1-3	95	3	04	4	0	0	12	
3	Wi-6V	3-15	98	0	01	2	0	0	13	
3	Wi-54	3-48	91	7	013	2	0	0	16	
3	Wi-48	3-53	95	4	13	0	0	0	13	

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patient	VH germline gene	homology (% to germline)	CDR FR				CDR3 length (amino acids)	annotation	
			R	SR	S	E/D			
3	Wi-50 3-53	91	4	17	5	0	0	12	
3	Wi-11V 3-53	96	4	14	1	0	0	13	
3	Wi-9V 3-7	97	2	12	1	0	0	13	
3	Wi-49 3-9	100	0	00	0	0	0	16	
3	Wi-31V 4-30	91	7	25	3	1	1	14	
3	Wi-34V 4-30	100	0	00	0	0	0	12	
3	Wi-61 4-31	90	6	113	6	0	1	12	
3	Wi-63 4-39	96	3	14	1	1	0	12	
3	Wi-64 4-4	96	1	14	1	0	0	15	
3	Wi-16V 4-4	100	0	00	0	0	0	17	
4	Ro85 1-46	94	4	15	4	0	3	16	related to Ro89
4	Ro89 1-46	92	6	26	5	1	3	16	related to Ro85
4	Ro99 1-69	88	3	215	0	2	0	20	not functional
4	Ro101 1-8	91	5	110	4	1	2	26	related to Ro151
4	Ro151 1-8	89	7	013	7	1	2	26	related to Ro101
4	Ro92 2-5	95	5	02	4	0	0	15	
4	Ro119 2-5	90	3	010	9	0	0	19	
4	Ro22 3-9	93	2	211	2	0	0	13	
4	Ro45 3-53	100	0	00	0	0	0	10	
4	Ro34 3-53	91	3	26	6	0	0	20	
4	Ro38 3-21	93	5	25	4	0	1	13	
4	Ro24 3-48	88	6	312	2	1	3	13	
4	Ro47 3-9	88	2	416	7	0	0	13	
4	Ro114 3-11	93	3	13	9	0	2	13	
4	Ro179 3-33	95	2	23	5	0	0	18	
4	Ro75 4-4	96	1	04	4	0	0	12	
4	Ro132 4-39	100	0	01	0	0	0	13	related to Ro131
4	Ro131 4-39	97	2	13	1	0	0	13	related to Ro132
4	Ro133 4-39	89	5	212	7	0	0	18	
4	Ro230 4-61	93	5	16	5	1	0	15	
4	Ro13 5-a03	96	2	14	2	0	0	19	
5	Ko76 1-8	93	3	19	4	0	1	12	related to Ko81

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patient	VH germline gene	homology (% to germline)	CDR FR				CDR3 length (amino acids)	annotation		
			R	SR	S	E/D				
5	Ko81	1-8	89	7	211	5	0	1	12	related to Ko76
5	Ko77	1-69	93	4	26	6	0	0	16	
5	Ko158	1-8	98	2	00	4	0	1	18	related to Ko198
5	Ko198	1-8	97	3	01	3	0	1	18	related to Ko158
5	Ko166	1-69	95	6	04	3	2	0	15	
5	Ko169	1-18	93	5	37	2	2	0	19	
5	Ko197	1-8	97	2	02	4	0	1	10	
5	Ko1162	5	97	2	13	3	1	0	13	
5	Ko1182	70						-		not functional
5	Ko170	2-5	95	3	16	3	0	0	13	
5	Ko10	3-21	93	5	36	2	1	1	18	
5	Ko22	3-9	96	0	04	4	0	0	10	
5	Ko202	3-11	94	5	23	3	1	2	19	
5	Ko203	3-21	90	6	110	5	1	1	14	
5	Ko204	3-21	94	6	15	1	1	1	14	
5	Ko207	3-49	99	0	02	0	0	0	23	
5	Ko47	4-61	93	5	07	5	0	1	22	
5	Ko152	4-30	96	1	14	3	0	0	12	related to Ko155
5	Ko155	4-30	95	2	16	3	0	0	12	related to Ko152
5	Ko123	5-51	100	0	01	0	0	0	9	
5	Ko176	5-51	95	2	36	2	0	0	18	
6	Scy13	9								
6	9	1-69	95	3	05	5	1	0	17	
6	Scy14	1								
6	1	1-3	96	5	03	1	0	0	20	
6	Scy14	2								
6	2	1-46						-	-	frameshift
6	Scy13	2								
6	2	1-3	93	4	18	5	1	1	11	
6	Scy16	3								
6	3	2-70	100	0	00	0	0	0	19	
6	Scy60	3-48	95	4	06	1	1	0	20	
6	Scy03	3-74	92	6	23	4	0	1	10	
6	Scy53	3-11	94	3	15	6	1	0	11	
6	Scy01	3-11	100	0	00	1	0	0	12	
6	Scy08	3-11	98	0	02	3	0	0	13	
6	Scy17	3-43	91	4	29	4	2	0	11	
6	Scy50	3-33	98	1	12	1	1	0	11	not functional

B shows the remaining data grouped by their patient's origin

patient	VH germline gene	homology (% to germline)	CDR FR				CDR3 length (amino acids)	annotation		
			R	SR	S	E/D				
6	Scy61	3-33	96	5	03	3	0	1	16	
6	Scy12	3-49	97	0	26	0	0	0	20	not functional
6	Scy59	3-49	93	5	03	6	1	0	14	
6	Scy64	3-23	90	3	08	9	1	1	14	related to Scy07
6	Scy65	3-64	98	1	04	1	0	0	8	
6	Scy69	4-39	95	5	06	2	0	0	21	
6	Scy73	4-39	99	1	01	0	0	0	17	
6	Scy10	4-39	96	4	04	1	1	0	12	
6	Scy12	4-4	95	2	16	2	0	0	11	not functional
6	Scy16	6-1	99	1	00	1	0	0	25	
6	Scy17	6-1	95	4	16	2	1	1	12	

Germline gene and homology indicate the percentage of identical nucleic acids compared to the respective germline gene. The total number of replacement (R) and silent (S) mutations within the complementarity determining region (CDR) and the framework region (FR) as well as the number of replacement mutations leading to aspartate (D) or glutamate (E) as well as to arginin (R), histidine (H) or lysin (K) are listed. The CDR3 length is given in amino acid numbers. In the annotation non-functional genes (*i.e.* genes with a non-translatable reading frame) are indicated.