

Human genes (HUM) and their mappings (UAMs) in Orangutans

IGHV(III)-82

GENE ALIGN SEQ

HUM:	A	A	G	T	C	C	T	-	G	T	T	G	A	A	G	C	T	T	A	C	T	G	A	T	G	G	A	G	T	C	A	G	A	G	G	G	G	A	A	A	C	A	T	T	G	T	A	C	A	
UAM:	A	A	G	T	-	C	T	T	G	T	C	G	A	A	G	C	T	T	A	C	T	G	A	T	G	G	A	G	T	C	A	G	A	G	G	G	G	G	A	A	C	A	T	T	G	T	T	C	A	
HUM:	G	C	C	C	A	G	C	G	G	T	T	C	T	C	A	C	A	G	A	C	T	C	T	C	C	T	G	C	A	A	A	G	C	C	T	C	T	G	A	T	T	T	C	A	C	T	T	G	T	A
UAM:	G	C	T	C	A	G	C	G	G	T	T	C	T	C	A	C	A	G	A	C	T	C	T	C	C	T	G	C	A	A	A	A	C	C	T	C	T	G	A	T	T	T	C	A	C	T	T	T	T	A
HUM:	C	T	G	G	C	T	A	C	A	G	C	A	T	G	A	G	C	T	T	G	G	T	C	C	A	G	C	A	G	G	C	T	T	C	A	T	G	A	C	A	G	G	A	T	T	T	G	T	G	
UAM:	C	T	G	G	C	T	A	C	A	G	C	A	T	G	A	G	C	T	T	G	G	T	C	C	A	G	C	A	A	G	C	T	T	C	A	T	G	A	C	A	G	G	A	T	T	G	T	G	T	G
HUM:	T	G	G	G	T	G	G	C	A	A	C	A	G	T	G	A	G	T	T	A	T	C	A	G	G	G	T	T	A	C	T	C	T	C	C	A	T	G	A	G	T	A	C	A	A	G	T	A	A	A
UAM:	T	G	G	G	T	G	G	C	A	A	C	A	C	T	G	A	G	T	T	C	T	C	A	G	G	G	T	T	A	C	T	C	T	C	C	A	T	G	A	C	T	A	C	A	A	G	A	A	A	A
HUM:	T	T	A	A	C	A	G	T	C	C	C	A	A	G	C	A	A	C	A	C	C	C	T	T	T	C	A	A	G	T	G	C	A	G	T	C	T	A	C	C	T	T	A	A	A	A	T	G	A	C
UAM:	T	T	A	A	C	A	G	T	C	C	C	A	A	G	C	A	A	C	A	C	C	C	T	T	T	C	T	A	G	T	G	C	A	G	T	C	T	A	C	C	T	T	A	A	A	A	T	G	A	C
HUM:	C	A	A	T	G	T	G	A	A	A	G	C	C	A	A	G	G	A	C	A	A	G	A	C	C	T	T	G	T	A	T	T	A	C	T	G	T	G	A	G	T	G	A							
UAM:	C	A	A	C	C	T	G	A	A	A	G	C	C	A	A	G	G	A	C	A	A	G	A	C	C	T	T	G	T	G	T	T	A	C	T	G	T	G	A	G	T	G	A							

D7

HUM:	C	A	T	A	G	G	A
UAM:	C	A	C	A	G	G	A

D9

HUM:	A	G	A	C	A	C	A	A	A	A	T
UAM:	A	G	A	C	A	C	A	A	A	A	T

Alignment stats: 'M': 275, 'I': 1, 'D': 1, 'X': 16

IGHV7-81

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	C	C	A	T	G	A	G	G	T	G	A	A	G	C	A	G	C	C	T	G	G	G	G	C	C	T	C
UAM:	C	A	G	G	T	G	C	A	G	T	T	G	G	T	G	C	A	G	T	C	T	G	G	T	C	A	T	G	A	G	G	T	G	A	A	G	C	A	G	C	C	T	G	G	G	G	C	C	T	C
HUM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	T	T	A	C	A	G	T	T	T	C	A	C	C	A	C	C	T	A	T	G	G	T	A
UAM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	A	T	T	C	T	G	G	T	T	A	C	A	G	T	T	T	C	A	C	C	A	C	C	T	A	T	G	G	T	A
HUM:	T	G	A	A	T	T	G	G	G	T	G	C	C	A	C	A	G	G	C	C	C	C	T	G	G	A	C	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	T	G	G
UAM:	T	G	A	A	T	T	G	G	G	T	G	C	A	A	C	A	G	G	C	C	C	C	T	G	A	A	C	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	T	G	G
HUM:	T	T	C	A	A	C	A	C	C	T	A	C	A	C	T	G	G	G	A	A	C	C	C	A	A	C	A	T	A	T	G	C	C	C	A	G	G	G	C	T	T	C	A	C	A	G	G	A	C	G
UAM:	T	T	C	A	A	C	A	C	C	T	A	C	A	C	T	G	G	G	A	A	C	C	C	A	A	C	A	T	A	T	G	C	C	C	A	G	G	G	C	T	T	C	A	C	A	G	G	A	T	G
HUM:	G	T	T	T	G	T	C	T	T	C	T	C	C	A	T	G	G	A	C	A	C	C	T	C	T	G	C	C	A	G	C	A	C	A	G	C	A	T	A	C	C	T	G	C	A	G	A	T	C	A
UAM:	G	T	T	T	G	T	C	T	T	C	T	C	C	A	T	G	G	A	C	A	C	C	T	C	T	G	T	C	A	G	C	A	C	A	G	C	A	T	A	C	C	T	G	C	A	G	A	T	C	A
HUM:	G	C	A	G	C	C	T	A	A	A	G	G	C	T	G	A	G	G	A	C	A	T	G	G	C	C	A	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	T	A				
UAM:	G	C	A	G	C	C	T	A	A	A	G	G	C	T	G	A	G	G	A	C	A	C	G	G	C	C	A	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	T	A				

D7

HUM:	C	A	C	C	A	T	G
UAM:	C	A	C	C	A	T	G

D9

HUM:	G	T	C	A	G	A	A	A	T	C	C
UAM:	G	T	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 287, 'I': 0, 'D': 0, 'X': 9

IGHV4-80

GENE ALIGN SEQ

HUM:	G	T	G	C	A	G	C	T	G	C	A	G	G	A	G	T	G	G	G	G	C	C	C	A	G	G	A	C	T	G	G	T	G	A	A	G	C	C	T	T	C	G	G	A	G	A	C	C	C	T
UAM:	G	T	G	C	A	G	C	T	G	C	A	G	G	A	G	T	G	G	G	G	C	C	C	A	G	G	A	C	T	G	G	T	G	A	A	G	C	C	T	T	C	G	G	A	G	A	C	C	C	T
HUM:	G	T	C	C	C	T	C	A	C	A	T	G	C	G	C	T	G	T	C	T	C	T	G	G	T	G	A	C	T	C	C	A	T	C	A	G	C	A	G	T	G	G	T	A	A	C	T	G	G	T
UAM:	G	T	C	C	C	T	C	A	C	C	T	G	C	G	C	T	G	T	C	T	C	T	G	A	T	G	A	C	T	C	C	A	T	C	A	G	C	A	G	T	G	G	A	A	A	C	T	G	G	T
HUM:	G	G	A	G	C	T	G	G	G	T	C	C	G	C	C	A	G	T	C	C	C	-	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	A	T	G	G	A	T	T	G	G	A	T	A
UAM:	G	G	A	T	C	T	G	A	G	T	C	C	G	C	C	A	G	-	C	C	C	T	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	A	T	G	C	A	T	T	G	G	T	A	
HUM:	C	A	T	C	T	A	T	T	A	T	A	G	T	G	G	G	A	G	G	A	G	C	T	A	C	T	A	C	A	C	C	C	C	G	T	C	C	C	T	C	A	G	G	A	G	T	T	G	A	G
UAM:	C	A	T	T	T	A	T	T	A	T	A	G	T	G	G	G	A	G	C	A	G	C	T	A	C	T	A	C	A	C	C	C	C	G	T	C	C	C	T	C	A	G	G	A	G	T	T	G	A	G
HUM:	T	C	A	C	C	A	T	G	T	C	A	A	T	A	G	A	A	A	C	G	T	C	C	A	A	G	A	A	C	C	A	G	T	T	T	T	C	C	C	T	G	A	A	G	C	T	G	A	G	C
UAM:	T	C	A	C	C	G	T	G	T	C	A	G	T	A	G	A	C	A	C	G	T	C	C	A	A	G	A	A	C	C	A	G	T	T	T	T	C	C	C	T	G	A	A	G	C	T	G	A	G	C
HUM:	T	C	T	G	T	G	A	C	C	G	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
UAM:	T	C	T	G	T	G	A	C	C	G	C	C	G	C	T	G	A	C	A	C	C	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	G	A	C	A	C	A	G	T
HUM:	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A		
UAM:	G	A	G	G	G	G	A	C	G	T	G	A	G	T	G	T	G	A	G	C	T	C	A	G	A	C	A	C	A	A	A	C	A	T	C	C	C	T	G	C	A	A	-	-	-	-	-	-		

D7

HUM:	G	G	G	A	G	G	C
UAM:	G	G	A	G	G	C	G

D9

HUM:	G	C	T	C	A	G	G	A	C	C	A
UAM:	C	T	C	A	G	G	A	C	C	A	G

Alignment stats: 'M': 247, 'I': 82, 'D': 2, 'X': 12

IGHV(II)-78-1

GENE ALIGN SEQ

HUM:	T	G	G	C	C	T	G	G	T	G	A	A	G	C	C	C	T	C	A	C	A	G	A	C	C	C	T	C	T	C	C	C	T	T	A	C	C	T	G	C	G	C	T	G	T	G	T	C	T	G
UAM:	T	G	G	C	C	T	G	G	T	G	A	A	G	C	C	C	T	C	A	C	A	G	A	C	C	C	T	C	T	C	C	C	T	C	A	C	C	T	G	T	G	C	T	G	T	G	T	C	T	G
HUM:	T	G	T	T	C	C	C	C	A	T	G	A	T	A	A	C	G	A	G	G	T	C	T	T	C	C	T	G	C	T	G	A	A	G	C	T	G	G	A	T	C	C	A	T	C	A	G	C	C	C
UAM:	T	G	T	T	C	C	C	C	A	T	-	-	-	A	A	T	G	A	G	G	T	C	T	T	C	C	T	G	C	T	G	A	A	G	C	T	G	G	A	T	A	C	A	T	C	A	G	C	C	C
HUM:	C	C	C	-	-	-	A	G	G	G	A	A	G	G	G	A	A	T	G	G	A	G	T	G	G	A	T	T	G	G	G	T	G	C	A	T	A	G	G	T	C	A	T	G	A	A	G	G	G	A
UAM:	C	C	C	T	C	T	-	G	G	G	-	A	G	G	G	A	A	T	G	G	A	G	T	G	G	A	T	C	G	G	G	T	G	C	A	T	A	G	G	T	C	A	T	G	A	A	G	G	G	A
HUM:	G	C	A	C	A	C	A	T	T	A	C	C	A	C	C	C	A	C	T	C	C	T	C	A	A	G	T	G	T	C	C	A	G	T	C	A	C	C	A	T	C	C	C	C	A	G	A	T	C	C
UAM:	G	C	A	C	A	C	G	T	T	A	C	C	A	C	C	C	G	C	T	T	C	T	C	A	A	G	A	G	T	C	C	A	G	T	C	A	C	C	A	T	C	C	C	C	A	G	A	T	C	C
HUM:	G	T	G	T	C	C	A	A	A	A	A	A	G	C	A	G	T	T	C	T	T	C	C	T	A	C	A	G	C	T	G	A	G	C	T	A	C	A	T	G	A	G	C	A	A	C	A	A	G	C
UAM:	A	T	G	T	C	C	A	A	A	A	A	A	C	A	G	T	T	C	T	T	C	C	T	A	C	A	G	C	T	G	A	G	C	T	G	C	G	T	G	A	G	C	A	A	C	A	A	G	C	
HUM:	A	C	A	T	A	G	C	C	A	T	G	T	A	T	T	T	T	A	A	G	C	C	A	A	A	G	A																							
UAM:	A	C	A	T	A	G	C	C	A	T	G	T	A	T	T	T	T	A	A	G	C	C	T	A	A	G	A																							

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	C	A	C	C	C	A	A	A	C	C	T
UAM:	C	A	C	C	C	A	A	A	C	C	T

Alignment stats: 'M': 256, 'I': 3, 'D': 5, 'X': 14

IGHV5-78

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	T	T	G	C	A	G	T	C	T	G	C	A	G	C	A	G	A	G	G	T	G	A	A	A	A	G	A	C	C	C	G	G	G	G	A	G	T	C
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	C	A	G	C	A	G	A	G	G	T	G	A	A	A	A	G	G	C	C	C	G	G	G	G	A	G	T	C
HUM:	T	C	T	G	A	G	G	A	T	C	T	C	C	T	G	T	A	A	G	A	C	T	T	C	T	G	G	A	T	A	C	A	G	C	T	T	T	A	C	C	A	G	C	T	A	C	T	G	G	A
UAM:	T	C	T	G	A	G	G	A	T	C	T	C	C	T	G	T	A	A	G	A	C	T	T	C	T	G	G	A	T	A	C	A	G	C	T	T	T	A	C	C	A	G	C	T	A	C	T	G	G	A
HUM:	T	C	C	A	C	T	G	G	G	T	G	C	G	C	C	A	G	A	T	G	C	C	C	G	G	G	A	A	A	G	A	A	C	T	G	G	A	G	T	G	G	A	T	-	G	G	G	G	A	G
UAM:	T	C	C	A	C	T	G	G	G	T	G	T	G	C	C	A	G	G	T	G	C	C	C	G	A	G	A	A	A	G	A	A	C	T	G	G	A	G	T	G	G	A	T	A	G	G	G	G	-	G
HUM:	C	A	T	C	T	A	T	C	C	T	G	G	G	A	A	C	T	C	T	G	A	T	A	C	C	A	G	A	T	A	C	A	G	C	C	C	A	T	C	C	T	T	C	C	A	A	G	G	C	C
UAM:	C	A	T	C	T	A	T	C	C	T	G	G	G	A	A	C	T	C	T	G	A	T	A	C	C	A	G	A	T	A	C	A	G	C	C	C	A	T	C	C	T	T	C	C	A	A	G	C	C	
HUM:	A	C	G	T	C	A	C	C	A	T	C	T	C	A	G	C	C	G	A	C	A	G	C	T	C	C	A	G	C	A	G	C	A	C	C	G	C	C	T	A	C	C	T	G	C	A	G	T	G	G
UAM:	A	T	G	T	C	A	C	C	A	T	C	T	C	A	G	C	C	G	A	C	A	G	C	T	C	T	A	T	C	A	G	C	A	C	C	A	C	C	T	A	C	C	T	G	C	A	G	T	G	G
HUM:	A	G	C	A	G	C	C	T	G	A	A	G	G	C	C	T	C	G	G	A	C	-	G	C	C	-	G	C	C	A	T	G	T	A	T	T	A	T	T	G	T	G	T	G	A	G	A			
UAM:	A	G	C	A	G	C	C	T	G	A	A	G	G	C	C	T	C	G	G	A	C	A	-	-	C	T	G	C	C	A	T	G	T	A	T	T	A	T	T	G	T	G	T	G	A	G	A			

D7

HUM:	G	G	G	A	C	C	A
UAM:	C	A	G	A	C	C	A

D9

HUM:	G	T	G	C	A	G	A	G	T	G	A
UAM:	G	T	G	C	A	G	A	G	T	G	A

Alignment stats: 'M': 281, 'I': 3, 'D': 3, 'X': 10

IGHV(III)-76-1

GENE ALIGN SEQ

HUM:	C	T	G	G	T	G	G	A	A	T	C	T	G	G	A	A	G	A	G	A	A	A	T	G	A	T	A	C	A	G	C	C	T	A	A	C	T	G	T	T	C	T	C	A	G	A	G	C	C	T	
UAM:	C	T	G	G	T	G	G	A	A	T	C	T	G	G	A	A	G	A	G	A	A	A	T	G	G	T	A	C	A	G	C	C	C	A	A	C	A	A	T	T	C	T	C	A	G	A	G	C	C	T	
HUM:	T	T	T	T	T	A	C	A	A	A	G	C	C	T	C	T	G	A	A	T	T	T	A	C	C	T	T	C	A	T	T	G	A	C	T	C	T	A	G	C	A	T	G	A	G	C	T	C	A	G	
UAM:	T	T	T	T	T	A	C	A	A	A	G	C	C	T	C	T	G	A	A	T	T	T	A	C	C	T	T	C	A	T	T	G	A	C	T	C	T	A	G	C	A	T	G	A	G	C	T	C	A	G	
HUM:	C	C	C	A	G	C	A	G	G	C	T	T	C	A	G	G	A	C	A	G	G	G	G	T	T	G	G	T	G	T	G	T	G	G	G	A	G	G	C	A	A	A	A	G	C	G	A	G	G	A	T
UAM:	C	C	C	A	G	C	A	G	G	C	T	T	C	A	G	G	A	C	A	G	G	G	G	T	T	G	T	T	G	T	G	G	G	A	G	G	C	A	A	C	A	G	C	A	A	G	T	G	A	T	
HUM:	T	C	A	A	G	T	G	G	A	A	T	T	T	G	T	T	A	G	T	G	G	T	A	C	C	C	T	C	C	A	T	C	A	A	T	A	C	A	A	A	G	A	A	A	A	T	C	A	T		
UAM:	T	C	A	A	G	T	G	G	A	A	T	T	T	G	T	T	A	G	T	G	G	T	A	C	C	C	T	C	C	A	T	C	A	A	T	A	C	A	A	A	G	A	A	A	A	T	C	A	T		
HUM:	A	A	T	C	C	T	C	A	G	G	G	A	C	A	C	C	C	T	T	G	T	C	A	G	C	A	C	A	G	T	C	T	C	C	C	T	C	A	A	A	A	T	G	A	C	C	A	A	C	C	
UAM:	A	A	T	C	T	T	C	A	G	G	G	A	C	A	C	C	C	T	T	G	T	C	A	G	C	A	C	A	G	T	C	T	C	C	C	T	C	A	A	A	A	T	G	A	C	C	A	A	C	C	
HUM:	T	G	A	G	A	G	C	C	G	A	G	G	A	G	A	A	G	G	C	C	A	T	G	T	A	T	T	A	C	T	G	T	G	A	G	A	G	A													
UAM:	T	G	A	G	A	G	C	C	G	A	G	C	A	G	A	A	G	G	C	C	A	T	G	T	A	T	T	A	C	-	-	T	G	A	G	A	G	A													

D7

HUM:	C	A	C	A	G	G	A
UAM:	C	A	C	A	G	G	A

D9

HUM:	A	C	A	G	G	G	G	A	C	A	C
UAM:	A	C	A	G	G	A	G	A	C	A	C

Alignment stats: 'M': 276, 'I': 0, 'D': 2, 'X': 10

IGHV3-76

GENE ALIGN SEQ

HUM:	G	A	A	G	T	G	T	A	G	C	T	G	G	T	A	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	T	T	G	G	G	G	G	T	C		
UAM:	G	A	A	G	T	G	T	A	G	C	T	G	T	T	A	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	A	A	G	C	C	T	G	G	G	G	G	T	C		
HUM:	C	A	T	G	T	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	A	C	A	C	T	T	T	C	A	G	T	A	A	C	T	A	T	G	G	C	A
UAM:	C	A	T	G	T	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	A	C	A	C	C	T	T	C	A	G	T	A	G	C	T	A	T	G	G	C	A
HUM:	T	G	C	A	C	T	A	G	G	T	G	G	A	C	C	A	A	G	C	T	C	C	A	G	G	G	A	A	G	G	G	A	C	T	G	G	A	G	T	G	G	G	T	C	T	T	A	C	A	T
UAM:	T	G	C	A	C	T	A	G	G	T	G	G	A	C	C	A	A	A	C	T	C	C	A	A	G	G	A	A	G	G	G	A	C	T	G	G	A	G	T	G	G	G	T	C	T	T	A	C	A	T
HUM:	T	A	A	T	G	C	T	A	G	T	G	G	T	G	G	A	G	G	C	A	T	A	T	A	C	T	A	C	T	C	A	G	A	C	T	C	T	G	T	G	A	A	G	G	G	C	C	G	G	T
UAM:	T	A	A	T	G	C	T	A	G	T	G	G	T	G	G	A	A	G	C	A	C	A	T	A	C	T	A	C	T	C	A	G	A	C	T	C	T	T	T	G	A	A	G	G	G	C	C	G	A	T
HUM:	T	G	A	C	C	A	T	C	T	C	C	A	G	A	G	A	A	A	A	C	A	C	C	A	A	G	A	A	C	T	C	A	C	T	G	T	A	T	C	T	G	C	A	A	A	T	A	A	A	C
UAM:	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	A	A	A	C	A	C	C	A	A	G	A	A	C	T	C	A	C	T	G	T	A	T	C	T	G	C	A	A	A	T	A	A	A	C
HUM:	A	G	T	T	T	C	A	T	T	G	C	T	G	A	C	A	C	C	A	T	G	G	C	C	G	T	C	T	A	T	T	A	C	T	G	T	A	A	G	A	G	A								
UAM:	A	G	T	T	T	G	A	T	T	G	C	T	G	A	C	A	C	C	A	T	G	G	C	T	G	T	C	T	A	T	T	A	C	T	G	T	A	A	G	A	G	A								

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	C	A	A	A	C	C	T
UAM:	G	T	A	A	C	A	A	A	C	C	T

Alignment stats: 'M': 278, 'I': 0, 'D': 0, 'X': 14

IGHV3-74

GENE ALIGN SEQ

HUM: G A G G T G C A G C T G G T G G A G T C C G G G G G A G G C T T A G T T C A G C C T G G G G G T C
UAM: G A G G T G C A G C T G T T G G A G T C A G G G G A G G C T T G G T A C A G C C T G A G G G T C

HUM: C C T G A G A C T C T C C T G T G C A G C C T C T G G A T T C A C C T T C A G T A G C T A C T - - -
UAM: C C T G A G A C T C T C C T G T G C A G C C T C T G G A T T C A C C T T C A G T A A C T A C T A C A

HUM: - G G A T G C A C T G G G T C C G C C A A G C T C - C A G G - G A A G G G G C T G G T G T G G G T C
UAM: T - G A - - - A C T G G G T C T G C C A G G C T C T - - G G A G A A G G G G T T G G A G T G G T T C

HUM: T C A C G T A T T A A T A G T G A T G G G A G T A G C A C A A G C T A C G C G G A C T C C G T G A A
UAM: T C A C C T A T T A A T A G A G A T G G G A G T A G C A T A A G C T A T G C A G A C T C C A T G A A

HUM: G G G C C G A T T C A C C A T C T C C A G A G A C A A C G C C A A G A A C A C G C T G T A T C T G C
UAM: G G G C C A A T T T A C C A T C T C C A G A G A C A A C G C C A A G A A C A C G C T A T A T C T G C

HUM: A A A T G A A C A G T C T G A G A G C C G A G G A C A C G G C T G T G T A T T A C T G T G C A - - A
UAM: G A A T G A A C A G T C T G A G A G C C G A G A A C A C G A C T G T G T A T T A C T G T - - A C T A

HUM: G A G A
UAM: G A G A

D7
HUM: C A C A G T G
UAM: C G C A G T G

D9
HUM: G A C A C A A A C C T
UAM: G A C A C A A A C C T

Alignment stats: 'M': 265, 'I': 8, 'D': 8, 'X': 23

IGHV3-73

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	C	G	G	G	G	A	G	G	C	T	T	G	G	T	C	C	A	G	C	C	T	G	G	G	G	T	C				
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	A	G	T	C	C	A	G	C	C	T	G	G	C	G	G	G	T	C		
HUM:	C	C	T	G	A	A	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	G	T	T	C	A	C	C	T	T	C	A	G	T	G	-	G	C	T	C	T	G	C	T	
UAM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	T	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	C	C	A	G	T	G	A	-	-	-	-	-	-	C	T	
HUM:	A	-	-	-	-	-	T	G	C	A	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	T	C	C	G	G	G	A	A	A	G	G	G	C	T	G	G	A	G	T	G	G	G	T	T	
UAM:	A	C	C	A	G	A	T	G	T	A	C	T	G	G	G	T	G	C	G	C	C	A	G	G	C	T	T	C	T	G	G	G	A	A	A	G	G	A	C	C	G	G	A	G	T	G	G	G	T	T	
HUM:	G	G	C	C	G	T	A	T	T	A	G	A	A	G	C	A	A	A	G	C	T	A	A	C	A	G	T	T	A	C	G	C	G	A	C	A	G	C	A	T	A	T	G	C	T	G	C	G	T	C	
UAM:	G	G	C	T	A	T	A	T	T	G	G	A	A	G	C	A	A	A	T	C	T	A	A	C	A	G	T	T	A	T	G	C	G	A	C	A	G	C	A	T	A	C	G	C	T	G	C	G	T	C	
HUM:	G	G	T	G	A	A	A	G	G	C	A	G	G	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	T	G	A	T	T	C	A	A	A	G	A	A	C	A	C	G	G	C	G	T	
UAM:	T	G	T	G	A	A	A	G	G	C	A	G	G	T	T	C	A	C	C	A	T	C	T	C	A	A	G	A	G	A	T	G	A	T	T	C	A	A	A	G	A	A	C	A	C	A	C	G	T		
HUM:	A	T	C	T	G	C	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	A	A	A	C	C	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	
UAM:	A	T	C	T	G	C	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	A	A	A	C	C	G	A	G	G	A	C	A	C	G	G	C	C	C	T	G	T	A	T	T	A	C	T	G	T	
HUM:	A	C	T	A	G	A	C	A																																											
UAM:	G	C	T	A	G	A	T	A																																											
D7																																																			
HUM:	C	A	C	A	G	T	G																																												
UAM:	C	A	C	A	G	T	G																																												
D9																																																			
HUM:	G	A	C	A	C	A	A	A	C	C	T																																								
UAM:	G	A	T	A	C	A	A	A	C	C	T																																								

Alignment stats: 'M': 271, 'I': 6, 'D': 6, 'X': 25

IGHV3-72

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	C	T	T	G	G	T	C	C	A	G	C	C	T	G	G	A	G	G	T	C			
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	T	A	G	G	C	T	T	G	G	T	C	C	A	G	C	C	T	G	G	G	G	G	T	C	
HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	G	A	C	C	A	C	T	A	C	A
UAM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	G	A	C	C	A	C	T	A	C	A
HUM:	T	G	G	A	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	T	G	G	C	C	G	T
UAM:	T	G	G	A	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	T	G	C	C	C	G	T
HUM:	A	C	T	A	G	A	A	A	C	A	A	A	G	C	T	A	A	C	A	G	T	T	A	C	A	C	C	A	C	A	G	A	A	T	A	C	G	C	C	G	C	G	T	C	T	G	T	G	A	A
UAM:	A	T	T	A	G	A	A	A	C	A	A	A	G	C	T	A	A	C	A	G	T	T	A	C	A	C	C	A	C	A	G	A	A	T	A	C	G	C	C	G	C	G	T	C	T	G	T	G	A	A
HUM:	A	G	G	C	A	G	A	T	T	C	A	C	C	A	T	C	T	C	A	A	G	A	G	A	T	G	A	T	T	C	A	A	A	G	A	A	C	T	C	A	C	T	G	T	A	T	C	T	G	C
UAM:	A	G	G	A	A	G	A	T	T	T	A	C	C	A	T	C	T	C	A	A	G	A	G	A	T	G	A	T	T	C	A	A	A	G	A	A	C	A	C	A	C	T	G	T	A	T	C	T	G	C
HUM:	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	A	A	A	C	C	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	T	A	G	A
UAM:	A	A	A	T	G	A	G	C	A	G	C	C	T	G	A	A	A	A	C	C	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	T	A	G	A
HUM:	G	A																																																
UAM:	G	A																																																
D7																																																		
HUM:	C	A	C	A	G	C	G																																											
UAM:	C	A	C	A	G	T	G																																											
D9																																																		
HUM:	G	A	C	A	C	A	A	A	C	C	T																																							
UAM:	G	A	C	A	C	A	A	A	C	C	T																																							

Alignment stats: 'M': 294, 'I': 0, 'D': 0, 'X': 8

IGHV2-70

GENE ALIGN SEQ

HUM: C A G G T C A C C T T G A G G G A G T C T G G T C C T G C G C T G G T G A A A C C C A C A C A G A C
UAM: C A G G T C A C C T T G A A G G A G T C T G G T C C T G C G T T G G T G A A A C C C A C A C A G A C

HUM: C C T C A C A C T G A C C T G C A C C T T C T C T G G G T T C T C A C T C A G C A C T A G T G G A A
UAM: C C T C A C G C T G A C C T G C A C C T T C T C T G G G T T C T C A C T C A G C A C T A G T G G A -

HUM: T G T - - G T G T G A G C T G G A T C C G T C A G C C C C C A G G G A A G G C C C T G G A G T G G C
UAM: - G T G G G T G T G G G C T G G A T C C G T C A G C C C C C A G G G A A G G C C C T G G A G T G G C

HUM: T T G C A C T C A T T G A T T G G G A T G A T G A T A A A T A C T A C A G C A C A T C T C T G A A G
UAM: T T G C A A G A A T T G A T T G G G A T G A T G A T A A A T A C T A C A G C C C A T C T C T G A A G

HUM: A C C A G G C T C A C C A T C T C C A A G G A C A C C T C C A A A A A C C A G G T G G T C C T T A C
UAM: A G C A G G C T C A C C A T C T C C A A G G A C A C C T C C A A A A A C C A G G T G G T C G T T A C

HUM: A A T G A C C A A C A T G G A C C C T G T G G A C A C A G C C A C G T A T T A C T G T G C A C G G A
UAM: A A T G A C C A A C A T G G A C C C T G T G G A C A C A G C C A C A T A T T A C T G T G C A C G G A

HUM: T A C
UAM: T A C

D7
HUM: C A C A G A G
UAM: C A C A G A G

D9
HUM: T A C A A G A A C C C
UAM: T A C A A G A A C C C

Alignment stats: 'M': 288, 'I': 2, 'D': 2, 'X': 11

IGHV1-69D

GENE ALIGN SEQ

HUM: C A G G T G C A G C T G G T G C A G T C T G G G G C T G A G G T G A A G A A G C C T G G G T C C T C
UAM: C A G G T C C A G C T G G T G C A G T C T G G G G C T G A G G T G A A G A A G C C T G G G T C C T C

HUM: G G T G A A G G T C T C C T G C A A G G C T T C T G G A G G C A C C T T C A G C A G C T A T G C T A
UAM: A G T G A A G A T C T C C T G C A A G G T T T C T G A A G A C A C C T T C A G C A G C T A T G C T A

HUM: T C A G C T G G G T G C G A C A G G C C C C T G G A C A A G G G C T T G A G T G G A T G G G A G G G
UAM: T C A G C T G G G T G C G A C A G G C C C C T G G A C A A G G G C T T G A G T G G A T G G G A G T G

HUM: A T C A - T C C C T A T C T T - - T G G T A C A G C A A A C T A C G C A C A G A A G T T C C A G G G
UAM: A T C A T T C C - - - T G T T G C T G G T A T A A C A A A C T A C G C A C A G A A G T T T C A G G G

HUM: C A G A G T C A C G A T T A C C G C G G A C G A - A T C C A C G A G C A C A G C C T A C A T G G A G
UAM: C A G A G T C A C G A T T A C T G C G G A C - A C A T C C A C G A G C A C A G C C C A C A T G G A G

HUM: C T G A G C A G C C T G A G A T C T G A G G A C A C G G C C G T G T A T T A C T G T G C G A - - G A
UAM: C T G A G C A G C C T G A G A T C T G A G G A C A C G G C C G T G T A T T A C T G T G C - A A C - A

HUM: G A
UAM: G A

D7
HUM: C A C A G T G
UAM: C A C A G T G

D9
HUM: G T C A G A A A C C C
UAM: G T C A G A A A C C C

Alignment stats: 'M': 277, 'I': 6, 'D': 6, 'X': 13

IGHV2-70D

GENE ALIGN SEQ

HUM: C A G G T C A C C T T G A A G G A G T C T G G T C C T G C G C T G G T G A A A C C C A C A C A G A C
UAM: C A G A C C A C C T T G A A G G A G T C T G G T C C T G C G C T G G T G A A A T C C A C A C A G A C

HUM: C C T C A C A C T G A C C T G C A C C T T C T C T G G G T T C T C A C T C A G C A C T A G T G G A A
UAM: C C T C A C G C T G A C C T G C A C C T T C T C T G G G T T C T C A C T C A G C A C T A G T G G A G

HUM: T G C G T G T G A G C T G G A T C C G T C A G C C C C C A G G G A A G G C C C T G G A G T G G C T T
UAM: T G G G T G T G G G C T G G A T C C G T C A G C C C C C A G G G A A G G C C C T G G A G T G G C T T

HUM: G C A C G C A T T G A T T G G G A T G A T G A T A A A T T C T A C A G C A C A T C T C T G A A G A C
UAM: G C A A G C A T T G A T T G G G A T G A T G A T A A A T A C T A C A G C C C A T C T C T G A A G A G

HUM: C A G G C T C A C C A T C T C C A A G G A C A C C T C C A A A A A C C A G G T G G T C C T T A C A A
UAM: C A G G C T C A C C A T C T C C A A G G A C A C C T C C A A A A A C C A G G T G G T C G T T A C A A

HUM: T G A C C A A C A T G G A C C C T G T G G A C A C A G C C A C G T A T T A C T G T G C A C G G A T A
UAM: T G A C C A A C A T G G A C C C T G T G G A C A C A G C C A C A T A T T A C T G T G C A C G G A G A

HUM: C
UAM: C

D7

HUM: C A C A G A G
UAM: C A C A G A G

D9

HUM: T A C A A G A A C C C
UAM: T A C A A G A A C T C

Alignment stats: 'M': 287, 'I': 0, 'D': 0, 'X': 14

IGHV1-69

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	T	C	C	T	C
UAM:	C	A	G	G	T	C	C	A	G	C	T	G	G	T	G	C	A	G	T	C	G	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	T	C	C	T	C
HUM:	G	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	A	G	G	C	A	C	C	T	T	C	A	G	C	A	G	C	T	A	T	G	C	T	A
UAM:	A	G	T	G	A	A	G	A	T	C	T	C	C	T	G	C	A	A	G	G	T	T	T	C	T	G	A	A	G	A	C	A	C	C	T	T	C	A	G	C	A	G	C	T	A	T	G	C	T	A
HUM:	T	C	A	G	C	T	G	G	G	T	G	C	G	A	C	A	G	G	C	C	C	C	T	G	G	A	C	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	G	G	G
UAM:	T	C	A	G	C	T	G	G	G	T	G	C	G	A	C	A	G	G	C	C	C	C	T	G	G	A	C	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	G	G	G
HUM:	A	T	C	A	T	C	C	C	T	A	T	-	C	T	T	T	G	G	T	A	C	A	G	C	A	A	A	C	T	A	C	G	C	A	C	A	G	A	A	G	T	T	C	C	A	G	G	G	C	A
UAM:	A	T	C	A	T	C	C	C	T	G	T	G	C	-	T	T	G	G	T	A	C	A	G	C	A	G	A	C	T	A	T	G	C	A	C	A	G	A	A	G	T	T	C	C	A	G	G	G	C	A
HUM:	G	A	G	T	C	A	C	G	A	T	T	A	C	C	G	C	G	G	A	C	A	A	A	T	C	C	A	C	G	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G	G	A	G	C	T	G
UAM:	G	A	G	T	C	A	C	G	A	T	T	A	C	C	G	C	G	G	A	C	A	C	A	T	C	A	A	C	G	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G	G	A	G	C	T	G
HUM:	A	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	-	-	G	A	G	A	
UAM:	A	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	-	A	A	C	-	A	G	A	

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	G	A	A	A	C	C	C
UAM:	G	T	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 281, 'I': 3, 'D': 3, 'X': 12

IGHV1-68

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	G	G	G	C	A	G	T	C	T	G	A	G	G	C	T	G	A	G	G	T	A	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C
UAM:	C	A	G	G	T	G	C	A	G	C	T	G	G	G	G	C	A	G	T	C	T	G	A	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C
HUM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	C	T	T	C	C	G	G	A	T	A	C	A	C	C	T	T	C	A	C	T	T	G	C	T	G	C	T	C	C	T
UAM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	C	T	T	C	C	G	G	A	T	A	C	A	C	C	T	T	C	A	C	C	T	A	C	T	G	C	T	A	C	T
HUM:	T	G	C	A	C	T	G	G	T	T	G	C	A	A	C	A	G	G	C	C	C	C	T	G	G	A	C	A	A	G	G	G	C	T	T	G	A	A	A	G	G	A	T	G	A	G	A	T	G	G
UAM:	T	G	C	A	C	T	G	G	T	T	G	T	G	A	C	A	G	G	C	C	C	C	T	G	G	A	C	A	A	G	G	G	C	T	T	G	A	A	T	G	G	A	T	G	A	G	A	T	G	G
HUM:	A	T	C	A	C	A	C	T	T	T	A	C	A	A	T	G	G	T	A	A	C	A	C	C	A	A	C	T	A	T	G	C	A	A	A	G	A	A	G	T	T	C	C	A	G	G	G	C	A	G
UAM:	A	T	C	A	C	A	C	T	T	T	G	C	A	A	T	G	G	T	A	A	C	G	C	C	A	A	C	T	G	C	G	C	A	C	A	G	A	A	G	T	T	C	C	A	G	G	G	C	A	G
HUM:	A	G	T	C	A	C	C	A	T	T	A	C	C	A	G	G	G	A	C	A	T	G	T	C	C	C	T	G	A	G	G	A	C	A	G	C	C	T	A	C	A	T	A	G	A	G	C	T	G	A
UAM:	A	G	T	C	A	C	C	A	T	T	A	C	C	A	G	G	G	A	C	A	T	G	T	C	C	C	T	G	A	G	G	A	C	A	G	C	C	T	A	C	A	T	G	G	A	G	C	T	G	A
HUM:	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	G	G	A	C	T	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	G	G	C	A	A	G	A	T	A				
UAM:	G	T	A	G	C	C	T	G	A	G	A	T	C	T	G	A	G	G	A	C	T	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	G	G	C	A	A	G	A	T	A				

D7

HUM:	C	A	C	G	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	G	G	A	A	C	C	C
UAM:	G	T	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 281, 'I': 0, 'D': 0, 'X': 15

IGHV(III)-67-4

GENE ALIGN SEQ

HUM:	A	A	G	T	T	C	A	G	T	G	G	T	G	G	A	G	T	C	A	G	A	G	G	G	G	T	A	A	A	C	G	T	A	G	T	A	C	A	G	C	C	C	A	G	T	G	G	T	T	C
UAM:	A	A	G	T	T	C	A	G	T	G	G	T	G	G	A	G	T	C	A	G	A	G	G	G	G	T	A	A	A	C	G	T	T	G	T	A	C	A	G	C	C	C	A	G	T	G	G	T	T	C
HUM:	A	C	T	G	A	G	A	C	T	T	T	C	T	T	G	C	A	A	A	G	C	G	T	C	T	G	G	A	T	T	C	A	C	C	T	T	T	T	C	T	G	G	C	A	A	C	A	G	C	C
UAM:	A	C	T	G	A	G	A	C	T	T	T	C	T	T	G	C	A	A	A	G	C	G	T	C	T	G	G	A	T	T	C	A	C	C	T	T	T	G	C	T	G	G	C	A	A	C	A	G	C	C
HUM:	T	G	A	G	G	T	T	G	G	T	C	C	A	G	C	A	G	G	C	T	T	C	A	C	A	A	C	A	G	G	G	A	T	T	G	T	G	G	T	G	G	C	T	G	G	C	A	A	C	A
UAM:	T	G	A	G	G	T	T	G	G	T	C	C	A	G	C	A	G	G	C	T	T	C	A	C	A	A	C	A	G	G	G	A	C	T	G	T	T	G	T	G	G	C	T	G	G	C	A	A	T	A
HUM:	G	T	G	A	G	T	C	A	A	C	A	A	G	T	G	G	G	A	G	T	G	C	T	C	A	G	G	T	T	T	A	C	T	C	T	T	C	A	T	G	A	G	T	A	C	A	A	A	T	A
UAM:	G	T	G	A	G	T	C	A	T	C	A	A	G	T	G	G	G	A	G	T	G	C	T	C	A	G	G	T	T	A	C	T	C	T	T	C	A	T	G	A	G	T	A	C	A	A	A	T	A	
HUM:	A	A	T	T	A	A	C	T	G	G	T	C	C	A	G	C	G	A	C	A	C	C	C	T	T	T	C	A	C	G	T	G	C	A	C	T	C	T	A	C	C	T	T	A	C	A	A	T	G	A
UAM:	A	A	T	T	A	A	C	T	G	G	T	C	C	A	G	T	G	A	C	A	C	C	C	T	T	T	C	A	C	G	T	G	C	A	G	T	C	T	A	C	C	T	T	A	C	A	A	T	G	A
HUM:	C	T	A	A	C	C	T	G	A	A	A	G	C	C	A	A	G	G	A	C	A	A	G	G	T	T	G	T	G	T	A	A	T	A	C	T	G	T	G	A	G	C	T	T						
UAM:	C	T	A	A	C	C	T	G	A	A	A	G	C	C	A	A	G	G	A	C	A	A	G	G	T	T	G	T	G	T	A	A	T	A	C	T	G	T	G	G	G	G	T	T						

D7

HUM:	C	A	C	A	G	G	A
UAM:	C	A	C	A	G	G	A

D9

HUM:	A	G	A	C	A	C	A	A	A	A	A
UAM:	A	G	A	C	A	C	A	A	A	A	A

Alignment stats: 'M': 283, 'I': 0, 'D': 0, 'X': 11

IGHV(III)-67-3

GENE ALIGN SEQ

HUM: C A G C C T G G C T G T T C T C T T A G C C T C T T T T G C A A A G C A T C A A G A T T C A C C T T
UAM: C A G C C T G G C T G T T C T C T T A G C C T C T T C T G C A A A G C A T C A A G A T T C G C C T T

HUM: C A C T G A C T A C A G C A T A - A A T T G A G C C C A G A T G G C T G G G G G A C A G A G G C T G
UAM: C A C T G A C T A C A G C A - A G A A T T G A G C C C A G A T G G C T G G A G G A G A G A G G C T G

HUM: G A G T G G G T G G T A A C A G T G A T T G A T T C A A G T G G A A G T T C T C A G T G A T A T T C
UAM: G A G T G G G T G G T A A C A G T G A T T G A T T C A A G T G T A A G T T C T C A G T G A T A C T C

HUM: T G C A T C A G C A T A A T G A A G A T T C A C A A T T C C C A G G G A C A C C A A T T A C C A G C
UAM: T G C A T C A G C A C A A T G A A G A T T C A C A A T T C C C A G G G A C A C C A A T T A C C A G C

HUM: A C A G T C T C C C T T A A A A T A A T C T A C - T T G G A A G C T G A G G G G G C T C T C A C A G
UAM: A C A G T C T C C C T T A A A A T A A T C T - C T T T G C A A G C T G A G G G G G C T C T C A C A G

HUM: G G G T A G G C A G T G T A T T A C T G T G A G A G A
UAM: A G G T A G G C A G T G T A T T A C T - - - G A G A

D7

HUM: C A C A G C G
UAM: C A C A G C G

D9

HUM: A C A G A A A C C T C
UAM: A C A G A A A C C T T

Alignment stats: 'M': 260, 'I': 2, 'D': 6, 'X': 9

IGHV(III)-67-2

GENE ALIGN SEQ

HUM: G A T T T A T T G T C T C C A G A G A C A A T G T C A A G A A T A T G C T A T A T C T G C A A A T G
UAM: G A T T T A T C A T C T C C A G A G A C A A T G T C A A G A A T A T G C T G T A T C T G C A A A T G

HUM: G G C G A T C T G T A A A C C A A G A A C A C A T C A G T A T A T C A C T G T G C A A G A G G A G
UAM: G G C A A T C T G T A A A C C A A G A A C A C A T C A G T A T A T C A C T G T G C A A G A G G A G

D7
HUM: C A C A T G A
UAM: C A C A T G A

D9
HUM: A C A T A A A C C T C
UAM: A C A T C A A C C T C

Alignment stats: 'M': 95, 'I': 0, 'D': 0, 'X': 4

IGHV(II)-67-1

GENE ALIGN SEQ

HUM:	A	G	G	A	G	C	A	G	C	T	A	C	A	G	C	A	G	T	C	A	T	G	C	C	T	A	G	G	T	G	T	G	A	A	G	A	T	C	A	C	A	C	A	C	T	G	A	C	C	T
UAM:	A	G	G	A	G	C	A	G	C	T	A	C	A	G	C	A	G	T	C	A	T	G	C	C	T	A	G	A	T	G	T	G	A	A	G	A	T	C	A	C	A	C	A	C	T	G	A	C	C	T

HUM:	C	A	C	C	C	A	T	G	C	T	G	T	C	T	C	T	G	G	C	C	A	C	T	T	C	A	T	C	A	C	A	A	C	C	A	A	T	G	C	T	T	A	A	T	A	T	T	G	G	A
UAM:	C	A	C	C	C	A	T	G	C	T	G	T	C	T	C	T	G	G	C	C	A	C	T	T	C	A	T	C	A	C	A	A	C	C	A	A	T	G	C	T	T	A	A	T	A	C	T	G	G	A

HUM:	C	G	T	G	G	A	T	C	T	G	C	C	A	G	T	C	C	C	C	G	G	G	G	A	A	T	G	G	G	T	T	G	A	A	T	G	G	A	T
UAM:	C	G	T	G	G	A	T	C	T	G	C	C	A	G	T	C	C	C	C	A	G	G	G	A	A	T	G	G	G	T	T	G	A	A	T	G	G	A	T

D7

HUM:	A	A	A	A	T	G	C
UAM:	A	A	A	A	T	G	C

D9

HUM:	C	A	T	T	C	C	T	A	C	T	G
UAM:	C	A	G	T	C	C	T	A	C	T	G

Alignment stats: 'M': 136, 'I': 0, 'D': 0, 'X': 3

IGHV1-67

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	A	-	-	-	T	G	A	G	A	T	G	A	A	G	A	A	G	G	C	T	G	G	G	G	C	
UAM:	C	A	G	G	T	A	C	A	G	C	C	G	G	T	G	A	A	G	T	C	T	G	-	-	-	A	G	G	C	T	G	A	G	A	T	G	A	A	G	A	A	G	G	C	T	G	G	G	G	C
HUM:	A	T	C	A	G	T	G	A	A	A	G	T	C	T	C	C	T	G	C	A	A	G	A	C	T	T	G	T	G	G	A	T	A	C	A	C	C	T	A	C	C	T	T	C	A	C	C	A	G	T
UAM:	A	T	C	A	G	T	G	A	A	A	G	T	C	T	C	C	T	G	C	A	A	G	A	C	T	T	G	T	G	G	A	T	A	C	A	C	C	T	-	-	-	-	T	C	A	C	C	A	G	T
HUM:	T	A	C	T	C	T	A	T	G	C	A	C	T	A	G	G	T	G	C	G	C	C	A	G	G	C	C	C	A	T	G	C	A	C	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T
UAM:	T	A	C	T	G	T	A	T	G	C	A	C	T	G	G	G	T	G	C	G	C	C	A	G	G	C	C	C	A	T	G	C	A	C	A	A	C	G	G	C	T	T	G	A	G	T	G	G	A	T
HUM:	G	G	G	A	A	G	G	A	T	G	T	G	C	C	C	T	A	G	T	G	A	T	G	G	C	A	G	C	A	T	A	A	G	C	T	A	C	G	C	A	G	A	G	A	A	G	T	T	C	C
UAM:	G	G	G	A	A	G	G	A	T	G	T	G	C	C	C	T	A	G	T	G	A	T	G	G	C	A	G	C	A	C	A	A	G	C	T	A	C	G	C	A	G	A	G	A	A	G	T	T	C	C
HUM:	A	G	G	G	C	A	G	A	G	T	C	A	C	C	A	T	G	A	C	C	A	G	G	A	C	A	C	A	T	C	C	A	C	G	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G	
UAM:	A	G	G	G	C	A	G	A	G	T	C	A	C	C	A	T	T	A	C	C	A	G	G	A	A	C	A	C	A	T	C	C	A	C	A	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G
HUM:	G	A	G	C	T	G	A	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	A	G	A	C	A	C	G	G	C	C	A	T	G	T	A	T	T	-	-	A	C	T	G	T	G	G	G
UAM:	G	A	G	C	T	G	A	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	A	G	A	C	A	C	G	G	C	C	A	C	G	T	A	T	T	T	A	A	C	T	G	T	G	G	G
HUM:	A	G	A	G	A																																													
UAM:	A	G	A	G	A																																													

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	G	T	A	A	C	C	C
UAM:	G	T	C	A	G	T	A	A	C	C	C

Alignment stats: 'M': 282, 'I': 5, 'D': 7, 'X': 11

IGHV3-66

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	A	G	G	C	T	T	G	A	T	C	C	A	G	C	C	T	G	G	G	G	G	T	C				
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	T	C			
HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	G	T	T	C	A	C	C	G	T	C	A	G	T	A	G	C	A	A	C	T	-	A	C
UAM:	C	C	T	C	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	G	T	C	A	G	T	A	G	C	A	A	-	T	G	A	G
HUM:	A	T	G	A	G	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	G	C	T	G	G	A	G	T	G	G	G	T	C	T	C	A	G	T		
UAM:	A	T	G	A	G	C	T	G	G	A	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	G	C	T	G	G	A	G	T	G	G	G	T	C	T	C	A	A	C		
HUM:	T	A	T	T	-	-	T	A	T	A	G	C	T	G	T	G	G	T	A	G	C	A	C	A	T	A	C	T	A	C	G	C	A	G	A	C	T	C	C	G	T	G	A	A	G	G	G	C	C	G
UAM:	C	A	T	T	A	G	T	A	T	A	G	-	-	G	T	G	G	T	A	G	C	A	C	A	T	A	C	T	A	C	A	C	A	G	A	C	T	C	C	G	T	G	A	A	G	G	G	C	A	G
HUM:	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	A	G	A	A	C	A	C	G	C	T	G	T	A	T	C	T	T	C	A	A	A	T	G	A
UAM:	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	A	G	A	A	C	A	C	G	C	T	G	T	A	T	C	T	T	C	A	A	A	T	G	A
HUM:	A	C	A	G	C	C	T	G	A	G	A	G	C	T	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	G	A				
UAM:	A	C	A	G	C	C	T	G	A	G	G	G	C	T	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	A	A	G	A				

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 276, 'I': 3, 'D': 3, 'X': 14

IGHV(II)-65-1

GENE ALIGN SEQ

HUM:	C	A	A	C	A	A	C	T	G	T	G	T	T	T	C	T	C	C	T	G	C	A	C	T	C	T	T	G	G	G	C	T	A	G	T	G	A	A	G	C	T	C	T	C	A	C	A	G	A	C
UAM:	C	A	A	C	A	A	C	T	G	T	G	T	T	T	C	T	T	C	T	G	C	A	C	T	C	T	T	G	G	G	C	T	A	G	T	G	A	A	G	C	T	C	T	C	A	C	C	G	A	C
HUM:	C	C	T	C	T	C	T	C	T	C	A	C	C	T	G	T	G	C	T	G	T	C	T	C	T	G	C	A	T	T	C	T	C	C	A	T	C	A	C	A	A	C	C	A	G	T	G	C	T	T
UAM:	C	C	T	C	T	C	T	C	T	C	A	C	C	T	G	T	G	C	T	G	T	C	T	C	T	G	C	A	T	T	C	T	C	C	A	T	C	A	C	A	A	C	C	A	G	T	G	-	T	T
HUM:	C	C	T	G	C	T	G	G	A	G	C	T	G	C	A	T	C	C	A	T	C	A	-	C	C	C	C	C	G	C	A	A	G	G	A	A	G	G	G	A	C	T	G	G	A	G	C	G	A	
UAM:	C	C	T	G	C	T	G	G	A	A	C	T	G	C	A	T	C	C	A	T	C	A	G	C	C	C	C	C	-	C	A	A	G	G	A	A	G	G	G	A	C	T	G	G	A	G	T	G	A	
HUM:	A	T	C	A	G	G	T	G	C	A	C	A	G	G	T	C	A	T	G	A	G	G	G	A	G	T	G	C	A	C	A	T	T	C	C	A	A	C	C	C	A	C	T	C	C	T	C	A	A	G
UAM:	A	T	C	A	G	G	T	G	C	A	C	A	G	G	T	C	A	T	G	A	G	G	G	A	G	T	G	C	A	C	A	A	T	C	C	A	A	C	C	C	A	C	T	C	C	T	C	A	A	G
HUM:	A	G	T	C	C	A	G	T	C	A	C	T	A	T	C	T	C	C	A	G	A	T	C	C	A	C	A	T	C	C	A	A	A	A	A	A	C	A	G	T	G	T	T	T	C	C	T	G	T	A
UAM:	A	G	T	C	C	A	G	T	C	A	C	C	A	T	C	T	C	C	A	G	A	T	C	C	A	C	A	T	C	C	A	A	A	A	A	A	C	A	G	T	G	T	T	T	C	C	T	A	C	A
HUM:	G	C	T	G	A	G	C	T	A	C	C	T	G	A	G	C	A	A	C	A	-	-	-	A	G	T	A	C	A	C	A	A	C	C	A	T	G	A	-	-	A	T	T	T	T	A	A	T	A	C
UAM:	G	C	T	G	A	G	C	T	A	C	C	T	G	-	-	-	A	A	C	A	A	C	G	A	G	T	A	C	A	C	A	A	C	C	A	T	G	A	G	T	-	T	T	T	T	A	-	T	A	C
HUM:	A	A	A	A	G	A																																												
UAM:	A	A	A	A	G	A																																												

D7

HUM:	C	A	C	A	A	C	G
UAM:	T	A	C	A	G	C	G

D9

HUM:	G	A	T	A	C	A	A	A	C	C	T
UAM:	G	A	T	A	C	A	A	A	C	C	T

Alignment stats: 'M': 285, 'I': 6, 'D': 7, 'X': 8

IGHV3-64

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	A	G	G	C	T	T	G	G	T	C	C	A	G	C	C	T	G	G	G	G	G	T	C	
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	A	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	G	T	C		
HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	C	T	A	T	G	C	T	A
UAM:	C	C	T	A	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	C	T	A	T	G	C	T	A
HUM:	T	G	C	A	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	A	C	T	G	G	A	-	A	T	A	T	G	-	-	T	T	-	T	C
UAM:	T	G	C	A	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	A	C	C	A	G	G	G	A	A	G	G	G	T	C	T	G	G	A	G	-	-	-	T	G	G	G	-	T	C	T	C
HUM:	A	G	C	T	A	T	T	-	A	G	T	A	G	T	A	A	T	G	G	G	G	T	A	G	C	A	C	A	T	A	T	T	A	T	G	C	A	G	A	C	T	C	T	G	T	G	A	A	G	
UAM:	A	G	T	T	A	T	T	T	A	-	T	A	G	T	G	G	T	G	G	A	G	T	A	G	C	A	C	A	T	A	C	T	A	T	G	C	A	G	A	C	T	C	T	G	T	G	A	A	G	
HUM:	G	G	C	A	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	A	G	A	A	C	A	C	G	C	T	G	T	A	T	C	T	T	C	A
UAM:	G	G	C	A	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	G	C	C	A	A	G	A	A	C	A	C	A	C	T	G	T	A	T	C	T	T	C	A
HUM:	A	A	T	G	G	G	C	A	G	C	C	T	G	A	G	A	G	C	T	G	A	G	G	A	C	A	T	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	C	-	-	-	G	A
UAM:	A	A	T	G	A	A	C	A	G	T	C	T	G	A	G	A	G	C	T	G	A	G	G	A	C	A	C	G	G	C	T	G	T	C	T	A	T	T	A	C	T	G	T	G	C	A	A	A	-	A
HUM:	G	A	G	A																																														
UAM:	G	A	C	A																																														

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	T	G	C	A	G	A	A	A	C	C	T
UAM:	T	A	C	A	G	A	A	A	C	C	T

Alignment stats: 'M': 271, 'I': 8, 'D': 6, 'X': 19

IGHV3-63

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	G	A	G	C	T	G	A	T	A	G	A	G	T	C	C	A	T	A	G	A	G	G	G	C	C	T	G	A	G	A	C	A	A	C	T	T	G	G	G	A	A	G	T	T
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	A	T	A	G	A	G	T	C	C	A	T	A	G	A	G	G	A	C	C	T	G	A	G	A	C	A	A	C	C	T	G	G	G	A	A	G	T	T
HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	T	A	G	C	C	T	-	C	-	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	C	T	A	C	T	G
UAM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	T	A	G	C	C	T	A	C	A	-	-	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	A	C	T	A	C	T	G
HUM:	A	A	T	G	A	G	C	T	G	G	G	T	C	A	A	T	G	A	G	A	C	T	C	T	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	G	G	A	G	T	A	A	T	A	G
UAM:	A	A	T	G	A	G	C	T	G	G	A	T	C	A	A	T	G	A	G	A	C	T	C	T	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	G	G	A	G	T	A	A	T	A	G
HUM:	A	T	G	T	A	A	A	A	T	A	T	G	A	T	G	G	A	A	G	T	C	A	G	A	T	A	T	A	C	C	A	T	G	C	A	G	A	C	T	C	T	G	T	G	A	A	G	G	G	C
UAM:	A	T	G	T	A	A	A	A	T	A	C	G	A	T	G	G	A	A	G	T	C	A	G	A	T	A	T	A	C	C	A	T	G	C	A	G	A	C	T	C	T	G	T	G	A	A	G	G	G	C
HUM:	A	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	A	A	G	A	C	A	A	T	G	C	T	A	A	G	A	A	C	T	C	A	C	C	G	T	A	T	C	T	G	C	A	A	A	C
UAM:	A	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	A	A	G	A	A	A	A	T	G	C	T	A	A	G	A	A	C	T	C	G	C	C	G	T	A	A	C	T	G	C	A	A	A	C
HUM:	G	A	A	C	A	G	T	C	T	G	A	G	A	G	C	T	G	A	G	G	A	C	A	T	G	A	C	C	A	T	G	C	A	T	G	G	C	T	G	T	A	C	A	T	A	A	G	G	T	T
UAM:	G	A	A	C	A	G	T	C	T	G	A	G	A	G	C	T	G	A	G	G	A	C	A	T	G	G	C	C	A	T	G	C	A	C	G	G	C	T	G	T	A	C	A	T	A	A	G	G	T	T

D7

HUM:	C	C	A	A	G	T	G
UAM:	C	C	A	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	T	T
UAM:	G	A	C	A	C	A	A	A	T	T

Alignment stats: 'M': 285, 'I': 2, 'D': 2, 'X': 11

IGHV(II)-62-1

GENE ALIGN SEQ

HUM: G G C C T G G T G A A G C C C T C A C A G A C C C T C T C C C T C A T G T G T G T C A T C T C T G C
UAM: G G C C T G G T G A A G C C C T C A C A G A C C C T C T C C C T C C T G T G T G C C A T C T C T G C

HUM: A T T C T C C A T C A C A A C C A G T G C T T C C T C C T G G A G C T G C A T C C A T C A G C C C C
UAM: A T T C T C C A T C A C A A C C A G T G T T T C C T C C T G G A G C T G C A T C C C T C A G C C C -

HUM: T C T C - - T G G G A G G G A A T G G A G T G G A T T G G G T G C A T A G G T C A T G A A G G G A G
UAM: - - T C A C - G G G A G G G A A T G G A G T G G A T C G G G T G C A T A G G T C A C G G A G G G A G

HUM: C A C A C A T T A C T C C C C T T T C C T C A A G A G T C C A G T C A C C A T C C C C A G A T C C A
UAM: C A C A C A T T A C T C C C C T C T C C T C A A G A G T C C A G T C A C C A T C C C C T G A T C C A

HUM: T G T C C A A A A C A G T T C T T C C T A C A G C T G A G C T A C A T G A G C A A C A A T C A C A
UAM: T G T C C A A A A C A G T T C T T C C T A C A G C T G A G C T A C A T G A G C A A T A A T C A C A

HUM: T A G C C A T A T A T T T T T A A G C A A A A G A
UAM: T A G C C A C G T A T T T T T A A G C A A A A G A

D7

HUM: C A C A G T G
UAM: C A C A G T G

D9

HUM: C A C C A A A A C C T
UAM: C A C C A A A A C C T

Alignment stats: 'M': 257, 'I': 2, 'D': 4, 'X': 12

IGHV4-61

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	C	A	G	G	A	G	T	C	G	G	G	C	C	C	A	G	G	A	C	T	G	G	T	G	A	A	G	C	C	T	T	C	G	G	A	G	A	C			
UAM:	-	-	-	-	-	-	C	A	G	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
HUM:	C	C	T	G	T	C	C	C	T	C	A	C	C	T	G	C	A	C	T	G	T	C	T	-	-	-	-	C	T	G	G	T	G	G	C	T	C	C	G	T	C	A	G	C	A	G	T	G	G	T			
UAM:	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	A	C	T	G	T	C	T	G	G	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
HUM:	A	G	T	T	A	C	T	A	C	T	G	G	A	G	C	T	-	-	-	-	-	-	-	-	G	G	-	-	-	A	T	C	-	-	-	C	G	G	C	A	G	C	C	-	C	-	C	C	A	G			
UAM:	-	-	-	-	-	-	-	-	-	-	-	G	G	A	G	C	T	C	C	C	A	G	C	A	T	G	G	G	T	G	-	T	C	T	T	T	-	G	G	C	A	-	-	C	A	C	A	C	C	A	G		
HUM:	G	-	G	A	A	G	G	G	A	C	-	-	-	T	G	-	-	-	G	A	G	T	G	G	A	T	T	G	G	G	T	A	T	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
UAM:	G	T	-	-	-	-	-	G	A	C	G	G	G	T	G	T	T	A	G	A	G	T	G	C	A	-	-	-	-	G	T	A	C	A	G	C	A	G	C	T	G	G	C	G	T	C	T	G	G				
HUM:	T	C	T	A	T	T	A	C	A	G	T	G	G	G	A	G	C	A	C	C	A	A	C	T	A	C	A	A	C	C	C	T	C	C	C	T	C	A	A	G	A	G	T	C	G	A	G	T	C				
UAM:	T	C	T	A	T	T	-	-	-	-	-	G	G	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
HUM:	A	C	C	A	T	A	T	C	A	G	T	A	G	A	C	A	C	G	T	C	C	A	A	G	A	A	C	C	A	G	T	T	C	T	C	C	C	T	G	A	A	G	C	T	G	-	-	-	-	-			
UAM:	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	T	C	C	C	T	G	A	T	G	C	T	G	G	A	G	G	G	
HUM:	-	-	-	-	-	-	-	-	A	G	C	-	-	-	T	C	T	G	T	G	A	C	C	G	C	T	G	C	G	G	A	C	A	C	G	G	C	C	-	G	T	G	T	A	-	T	T	A	C	T			
UAM:	A	T	A	A	G	A	G	G	T	-	G	C	A	T	T	C	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	A	G	G	G	C	C	A	-	-	G	C	A	C	-	-	A	C	T
HUM:	G	T	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	G				
UAM:	G	T	T	T	A	T	G	G	A	T	T	T	T	T	A	T	A	T	A	A	A	A	A	C	T	A	T	-	G	A	T	T	T	T	A	C	T	T	C	A	T	T	T	T	C	T	C	A	G				
HUM:	A	-	-	G	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					
UAM:	A	T	A	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	A	A	T	T	G	T	G	A	T	G	T

Alignment stats: 'M': 93, 'I': 106, 'D': 201, 'X': 5

IGHV(II)-60-1

GENE ALIGN SEQ

HUM: G G C C T G G T G G A G C C C T C G C A G A C C C T C T C C C T C A C C T G T G C T G T C T C T G G
UAM: G G C C C G G T G G A G C C C T A G C A G A C C C T C T C C C T C A C C T G T G C T G T C T C T G G

HUM: A T T T T C C A T C A C A A C C A G T G T T T C C T G C T G G A G C T G G A T C C A C G A G T C C A
UAM: A T T T T C C A T C A C A A C C A G T G C T T C C T G C T G G A G C T G G A T C C A C G A G T C C A

HUM: C A T G G G A A G G A C T G G A G T G G A C C A G G C G C A C A C G T C A T G A A G G G A G C A A A
UAM: C A T G G G A A G G A C T G G G G T G G A C C A G G T G C A C A C G T C A T G A A G G G A G C A A A

HUM: A A T T C C C A C C C A C T C C T T A T G A A T C C A G T C A C C A T C T C C A A A T T C G G G T C
UAM: A A T T C C C A C C C A C T C C T T A T G A A T C C A G T C A C C A T C T C C A A A T T C G G G T C

HUM: C A A A A A A C A C T T G T T T T T A C A G T G G A G C T A T G T G A G C A A C A A G C T C A C A G
UAM: C A A A A A - C A C T T G T T T T T A C A G T G G A G C T A T G T G A G C A A C A A A C A C A C A G

HUM: C C A T G - - - T T T T A A A G A A G A G A
UAM: C C C T G T A T T T T T A A A G A A G A G A

D7
HUM: C A G A G T G
UAM: C A G A G T G

D9
HUM: C A C C C A A A C C T
UAM: C A C C C A A A C C T

Alignment stats: 'M': 260, 'I': 3, 'D': 1, 'X': 8

IGHV3-60

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	A	G	T	A	A	A	G	A	C	T	-	-	-	-	-	-	G			
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	A	G	G	G	G	A	G	G	C	T	T	A	G	T	A	A	A	G	A	C	T	T	G	G	G	G	C	-		
HUM:	G	A	G	G	G	G	T	C	T	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	
UAM:	-	-	G	G	G	G	T	C	T	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	
HUM:	C	T	C	T	G	C	T	A	T	G	C	A	C	T	G	G	G	T	C	C	A	C	C	A	G	G	C	T	C	C	A	G	G	A	A	A	G	G	G	T	T	T	G	G	A	G	T	G	G	G	
UAM:	C	T	A	T	G	C	T	A	T	G	A	A	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	A	G	G	G	T	T	T	C	G	A	G	T	G	G	G	
HUM:	T	C	T	C	A	G	T	T	A	T	T	A	G	T	A	C	A	A	G	T	G	G	T	G	A	T	A	C	C	G	T	A	C	T	C	T	A	C	A	C	A	G	A	C	T	C	T	G	T	G	
UAM:	T	C	T	C	A	G	T	T	A	T	T	A	G	T	A	C	A	A	G	T	G	G	T	G	G	T	A	C	C	A	A	A	C	T	C	T	A	C	A	C	A	G	A	C	T	C	T	G	T	G	
HUM:	A	A	G	G	G	C	T	G	A	T	T	C	A	C	C	A	T	C	T	C	T	A	G	A	G	A	C	A	A	T	G	C	C	C	A	G	A	A	T	T	C	A	C	T	G	T	C	T	C	T	
UAM:	A	A	G	G	G	C	C	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	G	T	C	C	A	G	A	A	C	T	C	A	C	T	G	T	A	T	C	T	
HUM:	G	C	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	G	A	G	C	C	G	A	G	G	G	C	A	C	A	-	G	-	-	T	T	G	T	G	T	A	C	T	A	C	T	G	T	G	
UAM:	G	C	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	G	A	G	C	C	G	A	G	G	-	-	A	C	A	C	G	G	C	-	T	T	G	T	G	T	A	T	T	A	C	T	G	T	G
HUM:	-	T	G	A	A	A	G	A																																											
UAM:	C	-	-	-	A	A	G	A																																											
D7																																																			
HUM:	C	G	C	A	G	T	G																																												
UAM:	G	A	G	G	C	A	G																																												
D9																																																			
HUM:	A	C	A	A	A	C	C	T	C	C	T																																								
UAM:	A	C	A	C	A	A	A	C	C	T	C																																								

Alignment stats: 'M': 274, 'I': 11, 'D': 9, 'X': 14

IGHV4-59

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	C	A	G	G	A	G	T	C	G	G	G	C	C	C	A	G	G	A	C	T	G	G	T	G	A	A	G	C	C	T	T	C	G	G	A	G	A	C
UAM:	C	A	G	G	T	G	C	A	G	C	T	G	C	A	G	G	A	G	T	C	G	G	G	C	C	C	A	G	G	A	C	T	G	G	T	G	A	A	G	C	C	T	T	C	G	G	A	G	A	C
HUM:	C	C	T	G	T	C	C	C	T	C	A	C	C	T	G	C	A	C	T	G	T	C	T	C	T	G	G	T	G	G	C	T	C	C	A	T	C	A	G	T	A	G	T	T	A	C	T	A	C	T
UAM:	C	C	T	G	T	C	C	C	T	C	A	C	C	T	G	C	G	C	T	G	T	C	T	C	T	G	G	T	G	G	C	T	C	C	A	T	C	A	G	T	A	G	T	A	A	C	T	A	C	T
HUM:	G	G	A	G	C	T	G	G	A	T	C	C	G	G	C	A	G	C	C	C	C	C	A	G	G	G	A	A	G	G	G	A	C	T	G	G	A	G	T	G	G	A	T	T	G	G	G	T	A	-
UAM:	G	G	A	G	C	T	G	G	A	T	C	C	G	G	C	A	G	C	C	A	C	C	A	G	G	G	A	A	G	A	G	A	C	T	G	G	A	G	T	G	G	A	T	T	G	G	G	-	A	G
HUM:	T	A	T	C	T	A	T	T	A	C	A	G	T	G	G	G	A	G	C	A	C	C	A	A	C	T	A	C	A	A	C	C	C	C	T	C	C	C	T	C	A	A	G	A	G	T	C	G	A	G
UAM:	T	A	T	C	T	A	T	T	C	C	A	G	T	G	G	G	A	G	C	A	C	C	T	A	C	T	A	C	A	A	C	C	C	G	T	C	C	C	T	C	A	A	G	A	G	T	C	G	A	G
HUM:	T	C	A	C	C	A	T	A	T	C	A	G	T	A	G	A	C	A	C	G	T	C	C	A	A	G	A	A	C	C	A	G	T	T	C	T	C	C	C	T	G	A	A	G	C	T	G	A	G	C
UAM:	T	C	A	C	C	A	T	A	T	C	A	A	T	A	G	A	C	T	C	G	T	C	C	A	A	G	A	A	C	C	A	G	T	T	C	T	C	C	C	T	G	A	A	G	C	T	G	A	G	C
HUM:	T	C	T	G	T	G	A	C	C	G	C	-	T	G	C	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	G	A					
UAM:	T	C	T	G	T	G	A	C	C	G	C	T	-	C	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	G	A						

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	A	A	A	C	C	T
UAM:	G	A	C	A	A	A	A	C	C	T

Alignment stats: 'M': 282, 'I': 2, 'D': 2, 'X': 9

IGHV1-58

GENE ALIGN SEQ

HUM:	C	A	A	A	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	C	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	A	C	C	T	C
UAM:	C	A	A	A	T	G	C	A	G	C	T	T	G	T	G	C	A	A	T	C	T	G	G	G	C	C	T	G	A	G	G	T	T	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C
HUM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	A	T	T	C	A	C	C	T	T	T	A	C	T	A	G	C	T	C	T	G	C	T	G
UAM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	A	T	A	C	A	C	C	T	T	T	A	C	T	A	G	C	T	C	T	G	C	T	A
HUM:	T	G	C	A	G	T	G	G	G	T	G	C	G	A	C	A	G	G	C	T	C	G	T	G	G	A	C	A	A	C	G	C	C	T	T	G	A	G	T	G	G	A	T	A	G	G	A	T	G	G
UAM:	T	G	C	A	G	T	G	G	G	T	G	T	G	A	C	A	G	G	C	T	C	C	T	G	G	A	C	A	A	G	G	C	C	T	T	G	A	G	T	G	G	A	T	A	G	A	A	T	G	G
HUM:	A	T	C	G	T	C	G	T	T	G	G	C	A	G	T	G	G	T	A	A	C	A	C	A	A	A	C	T	A	C	G	C	A	C	A	G	A	A	G	T	T	C	C	A	G	G	A	A	A	G
UAM:	A	T	C	A	T	C	G	T	T	G	G	C	A	G	T	G	G	T	A	A	C	G	C	A	A	A	C	T	A	C	G	C	A	C	A	G	A	A	G	T	T	C	C	A	G	G	-	-	-	G
HUM:	-	A	G	T	C	A	C	C	A	T	T	A	C	C	A	G	G	G	A	C	A	T	G	T	C	C	A	C	A	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G	G	A	G	C	T	G
UAM:	C	A	G	T	C	A	C	C	A	A	T	A	C	C	A	G	G	G	A	C	A	C	G	T	C	C	A	C	G	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G	G	A	G	C	T	G
HUM:	A	G	C	A	G	C	C	T	G	A	G	A	T	C	C	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	G	C	A	G	A			
UAM:	A	G	C	A	G	C	C	T	G	A	G	A	T	C	C	A	A	G	G	A	C	A	T	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	G	C	A	G	A			

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	G	A	A	A	C	G	C
UAM:	G	T	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 276, 'I': 1, 'D': 3, 'X': 17

IGHV3-57

GENE ALIGN SEQ

HUM:	G	A	A	G	T	T	T	A	T	T	G	A	T	G	G	A	G	T	C	A	G	A	G	G	C	A	G	A	A	A	T	T	G	T	A	C	A	G	C	C	C	A	G	T	-	-	-	-	-	
UAM:	G	A	A	G	T	T	T	A	T	T	G	A	T	G	G	A	G	T	C	A	G	A	G	G	G	G	A	A	A	A	T	T	G	T	A	C	A	G	-	-	-	-	-	T	G	C	A	G	G	
HUM:	G	G	T	T	C	A	C	T	G	A	G	A	C	T	C	T	C	C	T	G	C	A	A	A	G	C	C	T	C	T	G	A	T	T	T	C	A	C	C	T	T	T	A	C	T	G	G	C	T	A
UAM:	G	G	T	T	C	A	C	T	G	A	G	A	C	T	C	T	C	C	T	G	C	A	A	A	G	C	C	T	C	T	G	A	T	G	T	C	A	C	C	T	T	C	A	C	T	G	G	C	T	A
HUM:	C	A	G	C	A	T	G	A	G	C	T	T	G	G	T	C	C	A	G	C	A	G	G	C	T	T	C	A	T	G	A	C	A	G	G	A	T	T	G	G	T	G	T	G	G	G	T	G	G	
UAM:	C	A	G	C	A	T	G	A	C	C	T	T	G	G	T	C	C	A	T	C	A	G	G	C	T	T	C	A	T	G	A	C	A	G	A	A	T	T	G	G	T	G	T	G	G	G	T	G	G	
HUM:	A	A	A	C	A	G	T	G	A	G	T	G	A	T	C	A	A	G	T	-	-	G	G	G	A	G	T	T	C	T	C	A	G	A	G	T	T	A	C	T	C	T	C	C	A	T	G	A	G	T
UAM:	A	A	A	C	A	G	T	G	A	G	T	G	A	T	C	A	-	-	T	G	C	G	G	G	A	G	T	T	C	T	C	A	G	A	G	T	T	A	C	T	C	T	C	C	T	T	G	A	G	T
HUM:	A	C	A	A	A	T	A	A	A	T	T	A	A	C	A	G	T	C	C	C	A	A	G	C	G	A	C	A	C	C	T	T	T	T	C	A	T	G	T	G	C	A	G	T	C	T	A	C	C	T
UAM:	A	C	A	A	A	T	A	A	A	T	T	A	A	C	A	G	T	T	C	C	A	A	G	C	G	A	C	G	C	C	T	T	T	T	C	A	T	G	T	G	C	A	G	T	C	T	A	C	C	T
HUM:	T	A	C	A	A	T	G	A	C	C	A	A	C	C	T	G	A	A	A	G	C	C	A	A	G	G	A	C	A	A	G	G	C	-	-	T	G	T	G	T	A	-	T	T	A	C	T	G	T	G
UAM:	T	A	C	A	A	T	G	A	C	C	A	A	C	C	T	G	A	A	A	G	T	C	A	A	G	G	C	A	A	G	G	C	C	T	T	G	T	-	T	A	G	-	-	A	C	T	G	T	G	
HUM:	A	G	G	G	A																																													
UAM:	A	G	G	G	A																																													
D7																																																		
HUM:	C	A	C	A	G	G	A																																											
UAM:	C	A	C	A	G	G	A																																											
D9																																																		
HUM:	A	G	A	C	A	C	A	A	A	A	A																																							
UAM:	A	G	A	C	A	G	A	A	A	A	A																																							

Alignment stats: 'M': 273, 'I': 10, 'D': 10, 'X': 12

IGHV7-56

GENE ALIGN SEQ

HUM: C G A G T G C A G C T G G T G C A G T C T G G G C C T G A G G T G A A G C A G C C T G G G G C C T C
UAM: C G A G T G C A G C T G G T G C A G T C T G G G C C T G A G G T G A A G C A G C C T G G G G A C - C

HUM: G G C G A A G G T C T C C T G C A A G G - T G T C T G G T T A A A C T G T C A T C A C C T A T G G T
UAM: G G T G A A G T T C T C C T G C A A G G C T - T C T G G T T A A A C T G T C A T C A C C T A T G G T

HUM: A T G A A T T G G A T A C G A C A G A C C C C A G G A C A G G G G C T T G A G T G G A T G G G A T G
UAM: A T G A A T T G G A T A T G A C A G A C C C C A G G A C A G G G G C T T G A G T G G A T G G A A T G

HUM: G A T C A T C C T A C C C T G G T G A A C C C A A T G T A T G C C C A C A G A T T C A C A C A C G G
UAM: G A T C A T C C T A C C C T G G T G A A C C C A A C G T A T G C C C A C A G C T T C A C A C A C G G

HUM: T T T G T C T T C T C C A T G G A C A C C T C T G T C A G C A C G G C G G A T C T G C A G A C T A G
UAM: T T T G T C T T C T C C A T G G A C A C A T C T G T C A G C A T G G C A G A T C T G C A G A C T A G

HUM: C T G C C T A A A G A C T G A G G A T G C A G C C A T T T A T T A C T G T G T G A G G T A
UAM: C T G C C T G A A G A C T G A G G A T G C A G C C A T T T A T T A C T G T G T G A G G T A

D7

HUM: C A C C G T G
UAM: C A C C G T G

D9

HUM: T T T A G A A A C C C
UAM: T T T A G A A A C C C

Alignment stats: 'M': 281, 'I': 1, 'D': 2, 'X': 11

IGHV4-55

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	C	A	G	G	A	G	T	C	G	G	G	C	C	C	A	G	G	A	C	T	G	G	T	G	A	A	G	C	C	T	T	C	G	G	A	G	A	C
UAM:	C	A	G	G	T	G	C	A	G	T	T	G	C	A	G	G	A	G	T	C	G	G	G	C	C	C	A	G	G	A	C	T	G	G	T	G	A	A	G	C	C	T	T	C	G	G	A	G	A	C
HUM:	C	C	T	G	T	C	C	C	T	C	A	T	C	T	G	C	G	C	T	G	T	C	T	C	T	G	G	T	G	A	C	T	C	C	A	T	C	A	G	C	A	G	T	G	G	T	A	-	-	A
UAM:	C	C	T	G	T	C	C	C	T	C	A	C	C	T	G	C	G	C	T	G	T	C	T	C	T	G	G	T	G	G	C	T	C	C	A	T	C	A	G	T	A	G	T	-	-	T	A	C	T	A
HUM:	C	T	G	G	T	G	A	-	-	-	-	-	A	T	C	T	G	G	G	T	C	C	G	C	C	A	G	C	C	C	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	
UAM:	C	T	G	G	-	-	A	G	C	T	G	G	A	T	-	-	-	-	-	-	C	C	G	G	C	A	G	C	C	A	C	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G
HUM:	G	A	T	T	G	G	G	G	-	-	A	A	-	-	-	A	-	T	C	C	A	T	C	A	T	A	G	T	G	G	G	A	G	C	A	C	C	T	A	C	T	A	C	A	A	C	C	C	G	T
UAM:	G	A	T	T	G	G	G	G	T	-	A	T	C	T	A	T	T	C	C	-	-	-	-	-	A	G	T	G	G	G	A	G	C	A	C	C	T	A	C	T	A	C	A	A	C	C	C	G	T	
HUM:	C	C	C	T	C	A	A	G	A	G	T	C	G	A	A	T	C	A	C	C	A	T	G	T	C	C	G	T	A	G	A	C	A	C	G	T	C	C	A	A	G	A	A	C	C	A	G	T	T	C
UAM:	C	C	C	T	C	A	A	G	A	G	T	C	G	A	G	T	C	A	C	C	A	T	A	T	C	A	G	T	A	G	A	C	A	C	G	T	C	C	A	A	G	A	A	C	C	A	G	T	T	C
HUM:	T	A	C	C	T	G	A	A	G	C	T	G	A	G	C	T	C	T	G	T	G	A	C	C	G	C	C	G	C	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G		
UAM:	T	C	C	C	T	G	A	A	G	C	T	G	A	G	C	T	C	T	G	T	G	A	C	C	G	C	C	G	C	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G		
HUM:	T	G	C	G	A	G	A	T	A																																									
UAM:	T	G	C	G	A	G	A	G	A																																									

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	A	A	A	A	C	C	T

Alignment stats: 'M': 269, 'I': 13, 'D': 16, 'X': 11

IGHV3-54

GENE ALIGN SEQ

HUM: G G - - A T C C C T G A G A C T C T C C T G T G C A G A C T C T G G A T T A A C C T T C A G T A G C
UAM: G G G G - T C G C T G A G A C T C T C C T G T G C A G C C T C T G G A T T A A C C T T C A G T A G C

HUM: T A C T G A A T G A G C T C A G - - A T T C C C A G G C T C C A G G G A A G G G G C T G G A G T G A
UAM: T A C T G A A T G A G C T C - G G T - T T C C C A G G C T C C A G G G A A G G G G C T G G A G T G A

HUM: G T A G T A G A T A T A T A G T A C G A T A G A A G T C A G A T A T G T T A T G C A C A A T C T G T
UAM: G T A G T A G A T A A A T A G T A C G A T A G A A G T C A G A T A T G T T A T G C A C A A T C T G T

HUM: G A A G A G C A G A T T C A C C A T C T C C A A A G A A A A T G C C A A G A A C T C A C T C T G - -
UAM: G A A G A G C A G A T T C A C C A T C T C C A A A G A A A A T G C C A A G A A C T C A C T - - G T A

HUM: T T T G C A A A T G A A C A G T C T G A G A G C A G A G G G C A C A G C T G T G T G T T A C T G T A
UAM: T T T G C A A A T G A A C A G T C T G A G A G C A G A G G G C A C C G C C G T G T A T T A C T G T A

HUM: T G T G A G
UAM: T G T G A G

D7
HUM: G C A C C A G
UAM: G C A C C A G

D9
HUM: A C A G A C A C A G A
UAM: A C A G G T A C A G A

Alignment stats: 'M': 239, 'I': 6, 'D': 5, 'X': 6

IGHV(II)-53-1

GENE ALIGN SEQ

HUM: G G C C T G G T G A A G C C C T C A C A G A C C C T C T C C C T C A C C T G T G C T G T C T C T G G
UAM: G G C C T G G T G A A G C C C T C A C A G A C C C T C T C C A T T A C C T G T G C C G T C T C T G G

HUM: A T T C C C C A T C A C A A C C A G T G C T T C C T G C T G T A G C T G C A T T C A T A A A C C C C
UAM: A T T C C C C A T C A C A A C C A G T G T T T C C T G C T G G A G C T G C A - T C A T A A A T C C C

HUM: C C A G G A A G G G A C T G G A G T G A A T C C G G T G C A C A G G T C A T G A G G G A G T G C A C
UAM: C C A G G A A G G G A C T G G A G T G A A T C C A C T G C A C A G G T C A T G A G G G A G T G C A C

HUM: A T T C C A A C C C A C T C C T C A A G A G T C C A G T C A C C A T C T C C A G A T C C A T G T C C
UAM: A T T C C A A C C T A C T C C T C A A G A G T C C A G T C A C C A T C T C C A G A T C C A T G T C C

HUM: A A A A A G C A G T T C T T C C T A C A G C C G A G C T A A G T G A G C C G C A A G C A C A C A G C
UAM: A A A A A G C A G T T C T T C C T A C A G C T G A G C T A A G T G A G T C G C A A G C A C A T A G C

HUM: C A T G T A T T T T T A A C A A A A G A
UAM: C A T G T A T T T T T A A C A A A A G A

D7

HUM: C A C A G T A
UAM: C A C A G T G

D9

HUM: C A C C C A A A C C T
UAM: C A T C C A A A C C T

Alignment stats: 'M': 257, 'I': 0, 'D': 1, 'X': 12

IGHV3-53

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	A	C	T	G	G	A	G	A	G	G	C	T	T	G	A	T	C	C	A	G	C	C	T	G	G	G	G	G	T	C
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	A	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	T	C

HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	G	T	T	C	A	C	C	G	T	C	A	G	T	A	G	C	-	A	A	C	T	A	-
UAM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	G	T	C	A	G	T	A	G	C	T	-	-	C	T	A	G

HUM:	C	A	T	G	A	G	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	G	C	T	G	G	A	G	T	G	G	G	T	C	T	C	A	G
UAM:	C	A	T	G	A	T	C	T	G	G	G	T	C	T	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	G	C	T	G	G	A	G	T	G	G	G	T	C	T	C	A	-

HUM:	T	T	-	-	A	T	T	T	A	-	T	A	G	-	C	G	G	-	T	G	G	T	A	G	C	A	C	A	T	A	C	T	A	C	G	C	A	G	A	C	T	C	C	G	T	G	A	A	G	G
UAM:	-	T	A	C	A	T	T	-	A	G	T	A	G	T	-	-	G	A	T	G	G	T	A	G	C	G	C	A	T	A	C	T	A	C	G	C	A	G	A	C	T	C	C	G	T	G	A	A	G	G

HUM:	G	C	C	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	A	G	A	A	C	A	C	G	C	T	G	T	A	T	C	T	T	C	A	A
UAM:	G	T	A	G	A	T	T	C	A	C	C	G	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	A	G	A	A	C	A	C	G	C	T	G	T	A	T	C	T	T	C	A	A

HUM:	A	T	G	A	A	C	A	G	C	C	T	G	A	G	A	G	C	C	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	G	A
UAM:	A	T	G	A	A	C	A	G	C	C	T	G	A	G	A	G	C	T	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	-	T	A	C	T	G	T	G	C	G	A	A	A	G	A

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	G	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 272, 'I': 7, 'D': 8, 'X': 13

IGHV3-52

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	T	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	A	G	G	G	T	C
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	T	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	A	G	G	G	T	C
HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	C	T	C	C	T	G	G	A
UAM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	T	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	C	T	C	C	T	G	G	A
HUM:	T	G	C	A	C	T	G	G	G	T	C	T	G	C	C	A	G	G	C	T	C	C	G	G	A	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	G	G	C	C	G	A	C
UAM:	T	G	C	A	C	T	G	G	G	T	C	T	G	C	C	A	G	G	C	T	C	C	A	G	A	G	A	A	G	G	G	G	C	T	G	G	A	G	A	G	G	G	T	G	G	C	C	A	A	C
HUM:	A	T	A	A	A	G	T	G	T	G	A	C	G	G	A	A	G	T	G	A	G	A	A	A	T	A	C	T	A	T	G	T	A	G	A	C	T	C	T	G	T	G	A	A	G	G	G	C	C	G
UAM:	A	T	A	A	A	G	T	G	T	G	A	T	G	G	A	A	G	T	G	A	G	A	A	A	T	A	C	T	A	T	G	C	A	G	A	C	T	C	T	G	T	G	A	A	G	G	G	C	C	G
HUM:	A	T	T	G	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	G	C	C	A	A	G	A	A	C	T	C	C	C	T	C	T	A	T	C	T	G	C	A	A	G	T	G	A
UAM:	A	T	T	G	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	G	C	C	A	A	G	A	A	C	T	C	T	C	T	C	T	A	T	C	T	G	C	A	A	A	T	G	A
HUM:	A	C	A	G	C	C	T	G	A	G	A	G	C	T	G	A	G	G	A	C	A	T	G	A	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	T	G	A	G	A	G	G				
UAM:	A	C	A	G	C	C	T	G	A	G	A	G	C	T	G	A	G	G	A	C	A	T	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	T	G	A	G	A	G	A				

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 286, 'I': 0, 'D': 0, 'X': 10

IGHV(II)-51-2

GENE ALIGN SEQ

HUM: G G C C T G G T G A G G C C C T C A C - A G A C C C C C T C C C T C A C C T G T G C T G T C T C T G
UAM: G G C C T G G T G A G G C C C T C - C G A G A C C C C C T C C C T C A C C T G T G C T G T C T C T G

HUM: G A T T C T C C A T C A C A A C T A G T G C T T C C T G C T G G A G C T G G A T C C G C C A G T C C
UAM: G A T T C T C C A T C A C A A C C A G C G C T T C C T G C T G G A G C T G G A T C C G C C A G T C C

HUM: T C A G T C A A G G G A G T G G A T C A G G G C A T A G G T C A C G A G G G A G C A C A A A T T C T
UAM: T C A G T C A A G G A A G T G G A T C A G G G C A T A G G T A A C G A G G G A G C A C A A A T T C T

HUM: A A C C C A C T C C T C A T G A G C T C A G T C A C C A T C T C C A G A T C C A C G T C C A A G A A
UAM: A A C C C A C T C C T C A T G A G C T C A G T C A C C A T C T C C A G A T C C A A G A A

HUM: C C A A A T T T T C T T T T A G C T G A G T T C T G T G A C C A A C A A T G C C A C A A C C T T G T
UAM: C C A A A T T T T C T T T T A G C T G A G T T C T G T G A C C A A C A A C G C C A C A A C C T T G T

HUM: A T T A C T G T G A G A G G
UAM: A T T A C T G T G A G A G G

D7
HUM: A A C A G A A
UAM: A A C A G A G

D9
HUM: C A C A A A C T T C C
UAM: C A C A A A C T T C C

Alignment stats: 'M': 256, 'I': 1, 'D': 1, 'X': 6

IGHV5-51

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	A	G	C	A	G	A	G	G	T	G	A	A	A	A	A	G	C	C	C	G	G	G	G	A	G	T	C
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	A	G	C	A	G	A	G	G	T	G	A	A	A	A	G	G	C	C	C	G	G	G	G	A	G	T	C
HUM:	T	C	T	G	A	A	G	A	T	C	T	C	C	T	G	T	A	A	G	G	G	T	T	C	T	G	G	A	T	A	C	A	G	C	T	T	T	A	C	C	A	G	C	T	A	C	T	G	G	A
UAM:	T	C	T	G	A	G	G	A	T	C	T	C	C	T	G	T	A	A	G	A	C	T	T	C	T	G	G	A	T	A	C	A	G	C	T	T	T	A	C	C	A	G	C	T	A	C	T	G	G	A
HUM:	T	C	G	G	C	T	G	G	G	T	G	C	G	C	C	A	G	A	T	G	C	C	C	G	G	G	A	A	A	G	G	C	C	T	G	G	A	G	T	G	G	A	T	G	G	G	G	A	T	C
UAM:	T	C	A	G	C	T	G	G	G	T	G	C	G	C	C	A	G	A	T	G	C	C	C	G	G	G	A	A	A	G	G	C	C	T	G	G	A	G	T	G	G	A	T	G	G	G	A	G	C	
HUM:	A	T	C	T	A	T	C	C	T	G	G	T	G	A	C	T	C	T	G	A	T	A	C	C	A	G	A	T	A	C	A	G	C	C	C	G	T	C	C	T	T	C	C	A	A	G	G	C	C	A
UAM:	A	T	C	T	A	T	C	C	T	G	G	T	G	A	C	T	C	T	G	A	T	A	C	C	A	G	A	T	A	C	A	G	C	C	C	A	T	C	C	T	T	C	C	A	A	G	G	C	C	A
HUM:	G	G	T	C	A	C	C	A	T	C	T	C	A	G	C	C	G	A	C	A	A	G	T	C	C	A	T	C	A	G	C	A	C	C	G	C	C	T	A	C	C	T	G	C	A	G	T	G	G	A
UAM:	C	G	T	C	A	C	C	A	T	C	T	C	A	G	C	C	G	A	C	A	A	G	T	C	C	A	T	C	A	G	C	A	C	C	A	C	C	T	A	C	C	T	G	C	A	G	T	G	G	A
HUM:	G	C	A	G	C	C	T	G	A	A	G	G	C	C	T	C	G	G	A	C	A	C	C	G	C	C	A	T	G	T	A	T	T	A	C	T	G	T	G	C	-	-	-	G	A	G	A	C	A	
UAM:	G	C	A	G	C	C	T	G	A	A	G	G	C	C	T	C	G	G	A	C	A	C	C	G	C	C	A	T	G	T	A	T	T	A	C	T	G	T	G	C	A	A	A	-	A	G	-	-	A	

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	T	C	T	A	A	A	A	C	C	C	T
UAM:	T	C	T	A	A	A	A	C	C	C	T

Alignment stats: 'M': 284, 'I': 3, 'D': 3, 'X': 9

IGHV3-50

GENE ALIGN SEQ

HUM:	G	G	G	G	T	G	C	A	G	A	T	G	G	T	G	G	A	G	T	C	T	T	G	G	G	A	G	A	G	T	T	G	G	C	A	C	A	A	G	C	T	G	A	A	T	G	T	G	C	
UAM:	G	A	G	G	T	G	C	A	G	G	T	G	G	T	G	G	A	G	T	C	T	T	G	G	G	A	G	A	G	T	T	G	G	C	A	C	A	A	G	C	T	G	G	A	T	G	T	G	C	
HUM:	C	T	G	A	G	A	C	T	C	T	G	C	C	G	T	G	C	A	T	C	C	T	C	T	G	A	A	T	C	C	A	C	C	T	T	C	T	G	T	A	G	C	T	A	C	T	A	G	A	T
UAM:	C	T	G	A	G	A	C	T	C	T	G	C	T	G	T	G	C	A	G	C	C	T	C	T	G	A	A	T	C	C	A	C	C	T	T	C	C	G	T	A	G	C	T	A	C	T	A	G	A	T
HUM:	C	A	G	C	T	G	A	A	T	C	T	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	A	G	G	G	G	C	T	G	C	A	G	T	G	A	G	T	A	G	T	A	G	A	T	A
UAM:	C	A	G	C	T	G	A	A	C	C	T	G	C	C	A	G	G	C	T	T	C	A	G	G	A	A	A	G	G	G	G	C	T	G	C	A	G	T	G	A	A	T	A	G	T	A	G	A	T	A
HUM:	T	A	A	T	G	T	A	C	G	A	T	G	G	A	A	G	T	C	A	G	A	C	A	T	A	A	T	A	T	G	C	A	G	A	C	T	C	T	G	T	G	A	A	G	G	T	C	A	G	A
UAM:	T	A	A	T	G	T	A	C	G	G	T	G	G	A	A	G	T	C	A	G	A	C	A	A	A	A	T	A	T	G	C	A	G	A	C	T	C	T	G	T	G	A	A	G	G	T	C	A	G	A
HUM:	T	T	C	A	C	C	A	T	C	T	C	C	A	A	A	G	A	C	A	A	T	G	C	C	A	A	G	C	A	C	A	G	G	T	T	G	T	A	T	C	T	G	C	A	A	A	T	G	A	A
UAM:	T	T	C	A	C	C	A	T	C	T	C	C	A	A	A	G	A	C	A	A	T	G	C	C	A	A	G	C	A	C	A	C	G	T	T	G	T	A	T	C	T	G	C	A	A	A	T	G	A	A
HUM:	C	A	G	T	C	T	G	A	G	A	G	C	T	G	A	G	A	A	T	A	T	G	G	C	T	C	T	G	T	A	T	T	A	T	T	G	A	G	T	C	A	A	A	G	G	T	A			
UAM:	C	A	G	T	C	T	G	A	G	A	G	C	T	G	A	G	A	A	T	A	T	G	G	C	T	C	T	G	T	A	T	T	A	T	T	G	A	G	A	C	A	A	A	G	G	T	A			

D7

HUM:	C	C	A	A	A	T	G
UAM:	C	C	A	A	A	T	G

D9

HUM:	G	A	C	A	C	A	A	A	T	T
UAM:	G	A	C	A	C	A	A	A	T	T

Alignment stats: 'M': 283, 'I': 0, 'D': 0, 'X': 14

IGHV(II)-49-1

GENE ALIGN SEQ

GENE: **ATG16L1** (100%)
 HUM: C G A C A T C T G T A T T T C T C G T G C G T T C T T G G C C T G G C G A A G C C C T C A C A G A C
 UAM: C G A C A T C T G T G T T T C T C G T G C A T T C T T G G C C T G G C G A A G C C C T C A C A G A C

HUM: C C T C T C C C T C A T C T G T G C T G T C T C T G C - T T C T C C A T C A C A A C C A G T G C T T

UAM: C C T C T C C C C C A T C T G T G C T G T C T C T G C A T T C A A A C A G T G C T T

HUM:	C	C	T	G	C	T	G	G	A	G	C	T	G	G	A	T	C	C	C	T	C	A	G	C	T	C	C	C	C	A	G	G	G	A	A	G	G	G	A	C	T	G	G	A	G	T	G	A	A	T
UAM:	C	C	T	G	C	T	G	G	A	G	C	T	G	G	A	T	C	C	A	T	C	A	G	C	T	C	C	C	C	A	G	G	G	A	A	G	G	G	A	C	T	G	G	A	G	C	G	A	A	T

HUM:	C	A	G	G	T	G	C	A	C	A	G	G	T	C	A	T	G	A	G	G	G	A	G	A	A	C	A	C	A	A	C	G	C	A	A	C	C	C	A	C	G	C	C	T	C	A	A	G	A	G
UAM:	C	A	G	G	T	G	C	A	C	A	G	G	T	C	A	T	G	A	G	G	G	A	G	A	G	C	A	C	A	A	C	G	C	A	A	C	C	C	A	C	T	C	C	T	C	A	A	G	A	G

HUM: T C C A G T C A C C A T C T C C A G A T C C A C A T C C A A A A C A C A G - - T T T C - T T C T A C

UAM: T C C A G T C A C C A T C T C C A G A T C C A C A C C C A A A A A A C T G T T T T T C G - - - T A C

HUM:	A	G	C	T	G	A	G	C	T	A	C	C	T	G	A	G	C	A	A	C	G	A	G	T	A	C	A	C	A	A	C	C	A	T	G	A	A	T	T	T	T	T	A	C	A	C	A	A	A	A
UAM:	A	G	C	T	G	A	G	C	T	A	C	C	T	G	A	G	C	A	A	C	G	A	G	T	A	C	A	C	A	A	C	C	A	T	G	A	A	T	T	T	T	T	A	C	A	C	A	A	A	A

HUM:

G	A
G	A

D7

HUM:	T	A	C	A	G	C	A
UAM:	T	A	C	A	G	C	G

D9

HUM:	G	A	A	A	C	A	A	A	C	C	T
UAM:	G	A	A	A	C	A	A	A	T	C	C

Alignment stats: 'M': 282, 'I': 4, 'D': 3, 'X': 13

IGHV3-49

GENE ALIGN SEQ

HUM: G A G G T G C A G C T G G T G G A G T C T G G G G G A G G C T T G G T - - A C A G C C A G G G C G G
UAM: G A G G T G C A G C T G G T G G A G T C T G G G G G A G G C T T G G T C C A C - - C C A G G G G G G

HUM: T C C C T G A G A C T C T C C T G T A C A G C T T C T G G A T T C A C C T T T G G T G A T T A T G C
UAM: T C C C T G A G A C T C T C C T G T A C A G C T T C T G G A T T C A C C T T T G G T G A T T A T G C

HUM: T A T G A G C T G G G T C C G C C A G G C T C C A G G G A A G G G G C T G G A G T G G G T A G G T T
UAM: C A T G A G G T G G G T C C G C C A G G C T C C A G G G A A G G G G C T G G A G T G G G T A G G T T

HUM: T C A T T A G A A G C A A A G C T T A T G G T G G G A C A A C A G A A T A C G C C G C G T C T G T G
UAM: T C A T T A G A A G C A A A G C T T A T G G T G G G A C A A C A G A A T A C G C T G C G T C T G T G

HUM: A A A G G C A G A T T C A C C A T C T C A A G A G A T G A T T C C A A A A G C A T C G C C T A T C T
UAM: A A A G G C A G A T T C A C C A T C T C A A G A G A T G A T T C C A A A A G C A T C G C C T A T C T

HUM: G C A A A T G A A C A G C C T G A A A A C C G A G G A C A C A G C C G T G T A T T A C T G T A C T A
UAM: G C A A A T G A A C A G C C T G A A A A C C G A G G A C A C G G C C G T G T A T T A C T G T G C T A

HUM: G A G A
UAM: G A G A

D7

HUM: C A C A G T G
UAM: C A C A G T G

D9

HUM: G A C A C A A A C C T
UAM: G A C A C A A A C C T

Alignment stats: 'M': 294, 'I': 2, 'D': 2, 'X': 6

IGHV3-48

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	A	G	G	T	C		
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	A	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	T	C		
HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	T	T	A	T	G	A	A	A
UAM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	A	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	T	-	-	-	-	A	A	
HUM:	T	G	A	-	-	-	-	-	-	A	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	T
UAM:	T	G	A	C	A	T	G	A	G	-	C	T	G	G	G	T	C	C	A	C	C	A	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	A	C	T	G	G	A	G	T	G	G	G	T	C
HUM:	T	C	A	T	A	C	A	T	T	A	G	T	A	G	T	A	G	T	G	G	T	A	G	T	A	C	C	A	T	A	T	A	C	T	A	C	G	C	A	G	A	C	T	C	T	G	T	G	A	A
UAM:	T	C	A	T	A	C	A	T	T	A	G	T	A	A	C	A	G	T	G	G	T	A	G	A	A	C	C	A	C	A	T	A	C	T	A	T	G	C	A	G	A	C	T	C	C	G	T	G	A	A
HUM:	G	G	G	C	C	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	C	G	C	C	A	A	G	A	A	C	T	C	A	C	T	G	T	A	T	C	T	G	C
UAM:	G	G	G	C	C	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	C	G	C	C	A	A	G	A	A	C	T	C	A	C	T	G	T	A	T	C	T	G	C
HUM:	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	G	A	G	C	C	G	A	G	G	A	C	A	C	G	G	C	T	G	T	T	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A
UAM:	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	G	A	G	C	C	G	A	G	G	A	C	A	C	A	G	C	T	G	T	T	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A
HUM:	G	A																																																
UAM:	G	A																																																
D7																																																		
HUM:	C	A	C	A	G	T	G																																											
UAM:	C	A	C	A	G	T	G																																											
D9																																																		
HUM:	G	A	C	A	C	A	A	A	C	C	T																																							
UAM:	G	A	C	A	C	A	A	A	C	C	T																																							

Alignment stats: 'M': 277, 'I': 6, 'D': 6, 'X': 13

IGHV(III)-47-1

GENE ALIGN SEQ

HUM:	G	A	A	G	T	T	A	A	T	T	A	C	T	G	G	A	G	T	C	T	C	T	C	A	G	A	G	A	A	A	T	A	C	T	A	C	A	G	A	C	C	A	A	G	A	A	T	T	C	T
UAM:	G	A	A	G	T	T	A	A	T	T	A	G	T	G	G	A	G	T	C	T	C	T	C	A	G	A	G	A	A	A	T	A	C	T	A	C	A	G	A	C	C	A	A	G	A	A	T	T	C	T
HUM:	C	A	G	A	C	T	T	T	T	C	T	G	G	A	A	A	C	C	C	T	G	T	G	G	A	T	T	C	A	C	T	T	T	C	A	C	T	G	A	A	A	A	C	A	G	C	A	T	A	A
UAM:	C	A	G	A	C	T	T	T	T	C	T	G	G	A	A	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	T	T	T	C	A	C	T	G	A	A	A	A	C	A	G	C	A	T	A	A
HUM:	G	C	T	T	G	G	T	C	C	A	G	C	A	G	G	C	T	T	C	A	T	G	A	C	A	G	G	G	G	T	G	G	G	T	G	T	A	G	G	T	G	A	T	A	A	C	A	T	C	A
UAM:	G	C	T	T	C	G	T	C	C	A	G	C	A	G	G	C	T	T	C	A	T	G	A	C	A	G	G	G	G	T	T	G	G	T	G	T	G	G	G	T	G	A	T	A	A	C	A	T	C	A
HUM:	G	T	A	A	T	T	C	A	A	G	T	G	G	A	A	G	T	T	C	T	C	A	G	T	G	G	G	A	C	T	C	T	C	C	T	T	G	A	G	T	A	C	A	A	A	G	A	A	G	A
UAM:	G	T	A	A	T	T	C	A	A	G	T	G	G	A	A	G	T	T	C	T	C	A	G	T	G	G	G	A	C	T	C	T	C	C	T	T	G	A	C	T	A	C	A	A	A	G	A	A	G	A
HUM:	T	T	A	A	C	A	G	T	C	C	T	C	A	G	A	G	A	C	A	C	G	C	T	T	T	T	C	A	G	A	T	G	A	T	T	C	T	C	T	C	T	T	A	A	G	A	T	G	A	T
UAM:	T	T	A	A	C	A	G	T	C	C	T	C	A	G	A	G	A	C	A	C	T	C	T	T	T	T	C	A	G	A	T	G	A	T	T	C	T	C	T	T	T	T	A	A	G	A	T	G	A	T
HUM:	T	A	A	C	C	T	G	A	G	A	G	C	T	C	A	G	G	A	A	A	A	T	T	C	C	G	T	T	T	A	T	T	A	C	T	G	T	G	A	G	G	G	A							
UAM:	T	A	A	C	C	T	G	A	G	A	G	C	T	C	A	G	G	A	A	A	A	T	T	C	C	G	T	T	T	A	T	T	A	C	T	G	T	G	A	G	G	G	A							

D7

HUM:	C	A	C	G	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 284, 'I': 0, 'D': 0, 'X': 9

IGHV3-47

GENE ALIGN SEQ

HUM:	G	A	G	G	A	T	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	G	T	C	
UAM:	G	A	G	G	A	T	C	A	G	C	T	G	G	T	G	G	T	G	T	C	T	G	C	G	G	A	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	G	T	C

HUM:	C	C	T	G	C	G	A	C	C	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	G	C	C	T	T	C	A	G	T	A	G	C	T	A	T	G	C	T	C
UAM:	C	C	T	G	A	G	A	C	C	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	G	C	C	T	T	C	A	G	T	A	G	C	T	A	T	G	T	T	C

HUM:	T	G	C	A	C	T	G	G	G	T	T	C	G	C	C	G	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	T	C	T	G	G	A	G	T	G	G	G	T	A	T	C	A	G	C	T
UAM:	T	G	C	A	C	T	G	G	G	T	T	C	G	C	C	G	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	T	C	T	G	G	A	G	T	G	G	G	T	A	T	C	A	G	C	T

HUM:	A	T	T	G	G	T	A	C	T	G	G	T	G	G	T	G	A	T	A	C	A	T	A	C	T	A	T	G	C	A	G	A	C	T	C	C	G	T	G	A	T	G	G	G	C	C	G	A	T	T
UAM:	A	T	T	G	G	T	A	C	T	G	G	T	G	G	T	G	A	T	A	C	A	T	A	C	T	A	T	G	C	A	G	A	C	T	C	C	G	T	G	A	T	G	G	G	C	C	G	A	T	T

HUM:	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	C	G	C	C	A	A	G	A	A	G	T	C	C	T	T	G	T	A	T	C	T	T	C	A	T	A	T	G	A	A	C	A
UAM:	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	G	C	C	A	A	G	A	A	G	T	C	C	T	T	G	T	A	T	C	T	T	C	A	A	A	T	G	A	A	C	A

HUM:	G	C	C	T	G	A	T	A	G	C	T	G	A	G	G	A	C	A	T	G	G	C	T	G	T	G	T	A	T	T	A	T	T	G	T	G	C	A	A	G	A	G	A					
UAM:	G	C	C	T	G	A	T	A	T	C	T	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	C	A	A	G	A	G	A					

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	T	A	C	A	A	A	C	T	T
UAM:	G	A	T	A	C	A	A	A	C	T	T

Alignment stats: 'M': 284, 'I': 0, 'D': 0, 'X': 9

IGHV(II)-46-1

GENE ALIGN SEQ

HUM: C A G G A G C A G C T G C A G G A G T C A G C C C T G G A C C T G A A T A G C A C A C A C T T A C C
UAM: C A G G A G C A G C T G C A G G A G T C A G C C C T G G A C C T G A A T A G C A C A C A C T T A C C

HUM: C T C T G C C T C A C C T A C A C T G T T A C T G G C C A C T C C G T C A C A A C C A G T C C T T A
UAM: C T C T G C C T C A C C T A C A C C G T T T C T G G C C A C T C C A T C A C A A C C A G T C C T T A

HUM: C T A G T G G A C C T G G A T C T G C C G G C T C T C A G G G A G G G G C T G C A A T G G A T
UAM: C T A G T G G A C C T G G A T C T G C C A G C T C T C A G A G A G G G G C T G A A A T G G A T

D7

HUM: A A A A T C C
UAM: A A A A T G C

D9

HUM: C A T T T G T C T T G
UAM: C A C T G G T C T T G

Alignment stats: 'M': 141, 'I': 0, 'D': 0, 'X': 6

IGHV1-46

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C
UAM:	C	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C
HUM:	A	G	T	G	A	A	G	G	T	T	T	C	C	T	G	C	A	A	G	G	C	A	T	C	T	G	G	A	T	A	C	A	C	C	T	T	C	A	C	C	A	G	C	T	A	C	T	A	T	A
UAM:	A	G	T	G	A	A	G	G	T	T	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	T	T	A	C	A	C	C	T	T	C	A	C	C	A	G	C	T	G	C	T	A	T	A
HUM:	T	G	C	A	C	T	G	G	G	T	G	C	G	A	C	A	G	G	C	C	C	C	T	G	G	A	C	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	A	T	A
UAM:	T	G	T	A	C	T	G	G	G	T	G	C	A	A	C	A	G	G	C	C	C	C	T	G	G	A	C	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	G	T	A
HUM:	A	T	C	A	A	C	C	C	T	A	G	T	G	G	T	G	G	T	A	G	C	A	C	A	A	G	C	T	A	C	G	C	A	C	A	G	A	A	G	T	T	C	C	A	G	G	G	C	A	G
UAM:	A	T	C	A	A	C	C	C	T	A	G	T	G	A	T	G	G	T	A	G	C	A	C	A	A	G	C	T	A	C	G	C	A	C	A	G	A	A	G	T	T	C	C	A	G	G	G	C	A	G
HUM:	A	G	T	C	A	C	C	A	T	G	A	C	C	A	G	G	G	A	C	A	C	G	T	C	C	A	C	G	A	G	C	A	C	A	G	T	C	T	A	C	A	T	G	G	A	G	C	T	G	A
UAM:	A	G	T	C	A	C	C	A	T	G	A	C	C	A	G	G	G	A	C	A	C	A	T	C	C	A	C	A	A	G	C	A	C	A	G	T	C	T	A	C	A	T	G	G	A	G	C	T	G	A
HUM:	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	G	A				
UAM:	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	A	T	G	C	A	A	G	A	G	A				

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	G	A	A	A	C	C	C
UAM:	G	T	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 285, 'I': 0, 'D': 0, 'X': 11

IGHV1-45

GENE ALIGN SEQ

HUM:	C	A	G	A	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	T	G	A	A	G	A	A	G	A	C	T	G	G	G	T	C	C	T	C	
UAM:	C	A	G	A	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	A	T	G	A	A	G	A	A	G	C	C	T	G	G	G	T	C	C	T	C
HUM:	A	G	T	G	A	A	G	G	T	T	T	C	C	T	G	C	A	A	G	G	C	T	T	C	C	G	G	A	T	A	C	A	C	C	T	T	C	A	C	C	T	A	C	C	G	C	T	A	C	C
UAM:	A	G	T	G	A	A	G	G	T	T	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	A	T	A	C	A	C	C	T	T	C	A	C	C	G	A	C	C	G	C	T	A	C	C
HUM:	T	G	C	A	C	T	G	G	G	T	G	C	G	A	C	A	G	G	C	C	-	C	C	C	G	G	A	C	A	A	G	C	G	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	T	G
UAM:	T	G	C	A	C	T	G	G	G	T	G	C	G	A	C	A	G	G	C	C	T	-	-	-	G	G	A	C	A	A	G	A	G	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	T	G
HUM:	G	A	T	C	A	C	A	C	C	T	T	T	C	A	A	T	G	G	T	A	A	C	A	C	C	A	A	C	T	A	C	G	C	A	C	A	G	A	A	A	T	T	C	C	A	G	G	A	C	A
UAM:	G	A	T	C	A	C	A	C	C	T	T	A	C	A	A	T	G	G	T	A	A	C	A	C	C	A	A	C	T	A	T	G	C	A	C	A	G	A	A	G	T	T	C	T	A	G	G	A	C	A
HUM:	G	A	G	T	C	A	C	C	A	T	T	A	C	C	A	G	G	G	A	C	A	A	G	T	C	T	A	T	G	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G	G	A	G	C	T	G
UAM:	G	A	G	T	C	A	C	C	A	T	T	A	C	C	A	G	G	G	A	C	A	A	G	T	C	T	A	T	G	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G	G	A	G	C	T	G
HUM:	A	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	G	G	A	C	A	C	A	G	C	C	A	T	G	T	A	T	T	A	C	T	G	T	G	C	A	A	G	A	T	A			
UAM:	A	G	C	A	G	C	C	T	G	A	G	A	C	C	T	G	A	G	G	A	C	A	C	A	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	A	A	G	A	T	A			

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	G	A	A	A	C	C	C
UAM:	G	T	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 282, 'I': 1, 'D': 3, 'X': 11

IGHV(II)-44-2

GENE ALIGN SEQ

HUM:	C	T	C	T	T	C	C	T	C	A	C	A	T	G	C	C	C	C	A	T	T	T	C	T	G	G	G	T	T	G	T	C	C	A	T	C	C	C	A	A	C	C	A	A	C	A	G	T	T	A
UAM:	C	T	G	T	T	C	C	T	C	A	C	A	T	G	C	C	C	C	A	T	T	T	C	T	G	G	G	T	T	G	T	C	C	A	T	C	C	C	A	A	C	C	A	A	C	A	G	T	T	A
HUM:	C	T	G	C	T	G	G	A	G	C	T	G	A	A	T	C	C	A	C	T	A	G	C	C	C	G	C	T	T	C	C	A	T	G	G	G	C	T	G	T	C	A	G	G	A	A	C	A	C	A
UAM:	C	T	G	C	T	G	G	A	G	C	T	G	C	A	T	C	C	A	C	T	A	G	C	C	C	G	C	T	T	C	C	A	T	G	G	G	C	T	G	T	C	A	G	G	A	A	C	A	C	A
HUM:	T	T	G	C	A	A	G	G	G	T	G	A	C	A	C	A	C	A	C	G	A	T	G	A	T	C	C	A	T	C	T	C	T	G	C	A	G	A	G	C	C	A	A	C	T	C	T	C	C	T
UAM:	T	T	G	C	A	A	G	G	G	T	G	A	C	A	C	A	C	G	C	G	A	T	G	A	T	C	C	A	T	C	T	C	T	G	C	A	G	A	G	C	C	A	A	C	T	C	T	C	C	T
HUM:	T	C	T	C	C	A	G	A	G	A	T	T	C	A	T	C	C	A	A	G	A	A	C	A	A	T	T	T	T	G	A	C	T	A	T	A	C	C	T	G	A	G	C	T	C	T	G	T	G	
UAM:	T	C	T	C	C	A	G	A	G	A	T	T	C	A	T	C	C	A	A	G	A	A	C	A	A	T	T	T	T	G	A	C	T	A	T	A	C	C	T	G	A	G	C	T	C	T	G	T	G	
HUM:	A	C	A	T	C	T	G	A	G	G	A	C	A	T	G	G	T	T	T	G	T	A	T	T	A	C	T	G	T	G	C	A	A	G	A	C	A													
UAM:	A	C	A	T	C	T	G	A	G	G	A	C	A	T	G	G	T	T	T	G	T	A	T	T	A	C	T	G	T	G	C	A	A	G	A	T	A													

D7

HUM:	A	A	C	A	G	T	G
UAM:	A	A	C	A	G	T	G

D9

HUM:	G	A	C	A	T	A	A	A	C	C	T
UAM:	G	A	C	A	T	A	A	A	C	C	T

Alignment stats: 'M': 233, 'I': 0, 'D': 0, 'X': 4

IGHV(IV)-44-1

GENE ALIGN SEQ

HUM:	G	A	G	G	A	C	C	A	C	C	T	T	G	T	G	C	A	A	T	G	G	G	A	G	G	A	A	G	A	A	G	T	A	G	T	G	G	T	C	C	C	C	T	T	G	G	T	C	A	T
UAM:	G	A	G	G	A	C	C	A	C	C	T	T	G	T	G	C	A	A	T	G	G	G	A	G	G	A	A	G	A	A	G	T	A	G	T	G	G	T	C	C	C	C	T	T	G	G	T	C	A	T

HUM:	G	C	T	C	A	G	C	C	T	C	A	C	C	T	A	-	T	G	C	C	G	C	C	T	A	T	G	C	A	C	A	T	T	C	A	A	T	T	T	C	T	G	A	A	C	A	T	T	C	T
UAM:	G	C	T	C	A	G	C	C	T	C	A	C	C	-	A	G	T	G	C	C	G	C	C	T	A	C	G	C	A	C	A	T	T	C	A	A	T	T	T	C	T	G	A	A	C	A	T	-	-	T

HUM:	G	T	T	T	C	C	T	G	G	A	T	C	C	A	C	C	A	T	C	T	C	C	C	A	T	C	A	A	A	A	G	G	T	C	T	T	C	A	G	T	G	T	G	T	T	G	G	T	G	T
UAM:	G	T	T	T	C	C	T	G	G	A	T	C	C	A	C	C	A	T	C	T	C	C	C	A	T	C	A	A	A	A	G	G	T	C	T	T	G	A	G	T	G	T	G	T	T	G	G	T	G	T

HUM:	G	A	T	A	T	G	G	G	T	T	A	A	G	G	G	A	A	A	C	A	C	T	A	-	-	-	-	A	G	C	C	C	C	A	A	C	C	T	T	C	A	G	G	G	C	A	G	A	G	
UAM:	G	A	T	A	T	G	G	G	T	T	A	A	G	G	G	A	A	A	C	A	C	T	A	A	C	T	G	C	A	G	C	C	C	C	A	A	C	C	T	T	C	A	G	G	G	C	A	G	A	G

HUM:	C	T	A	G	C	A	T	C	T	C	C	A	G	A	A	A	C	A	C	A	T	A	G	T	A	A	A	A	A	C	A	A	G	A	A	A	A	C	T	T	A	C	A	G	C	T	G	A	G	
UAM:	C	T	A	G	C	A	T	C	T	C	C	A	G	A	A	A	C	A	C	A	T	A	G	T	G	A	A	A	A	A	C	A	A	G	A	A	A	A	C	T	T	A	C	A	G	C	T	G	A	G

HUM:	A	A	G	T	G	T	G	A	T	G	G	C	T	G	G	G	A	G	-	-	-	G	C	A	G	G	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	T	C	A	A	G	G	
UAM:	A	A	G	T	G	T	G	A	T	G	G	C	T	G	-	-	-	A	G	G	A	T	G	C	A	G	G	C	G	T	G	T	A	T	T	A	C	T	T	T	G	C	T	C	A	A	G	G

D7

HUM:	C	A	C	T	G	T	G
UAM:	C	A	C	T	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 279, 'I': 9, 'D': 6, 'X': 4

IGHV(II)-43-1

GENE ALIGN SEQ

HUM: T C T G G A T T C C C C A A C A G A A C C A G T G C T T C C T G C T G G A G C T G G A T C C A T C A

UAM: G C T G G A T T C C C C A A C A A A A C C A G T G C T T C C T G C T G G A G C T G G A T C C A T C A

HUM: G C C C C C A G G G A A G G G A C T G G A G T G G G T C A G G T G C A C A G G T C A T G A A G G G A
UAM: G C C C C C A G G G A A G G G A T T G G A G T G G G T C G G G T G C A C A G G T C A T G A A A G G A

HUM: G C A C A A A T T C T A A C C C A C T C C T C A A G A G T C C A G T C A C C A C C T C C A G A T C T
UAM: G C A C A A A T T C C A A C C C A C T C C T C A A G A G T C C A G T C A C C A C C T C C A G A T C T

HUM: A T G T C C A A A A A - - C A G C T C T T C G T A T G G C T G A G T G A C A T - T - A G C A A C A A
UAM: A T G T C C A A A A A A T - A G C T C T T C C T A T G G C T G A G T G A - - T G T G A G C A A C A A

HUM: G C A C A C A G C C A T G - - - - - T
UAM: G C A C A C A A C C A T G T T T A T T T T

D7

HUM:	T	T	G	T	T	T	T
UAM:	T	T	G	T	T	T	T

D9

HUM: G T G T G T G T T T T
UAM: T T T T G A T A G A G

Alignment stats: 'M': 199, 'I': 11, 'D': 3, 'X': 8

IGHV3-43

GENE ALIGN SEQ

HUM:	G	A	A	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	T	C	G	-	-	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	G	G	
UAM:	G	A	A	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	A	G	G	A	G	-	-	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	T		
HUM:	T	C	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	T	G	A	T	G	A	T	T	A	T	A	C
UAM:	T	C	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	T	G	A	T	G	A	T	T	A	T	G	C
HUM:	C	A	T	G	C	A	C	T	G	G	G	T	C	C	G	T	C	A	A	G	C	T	C	C	G	G	G	A	A	G	G	G	T	C	T	G	G	A	G	T	G	G	G	T	-	C	T	C	T	
UAM:	C	A	T	G	C	A	C	T	G	G	G	T	C	C	G	T	C	A	A	G	C	T	C	C	A	G	G	A	A	G	G	G	T	C	T	G	A	A	G	T	G	G	G	T	T	-	-	-	T	
HUM:	C	T	-	-	T	A	T	T	A	G	T	T	G	G	G	A	T	G	G	T	G	G	T	A	G	C	A	C	A	T	A	C	T	A	T	G	C	A	G	A	C	T	C	T	G	T	G	A	A	G
UAM:	C	T	G	G	T	A	T	T	A	A	T	T	G	G	A	A	T	G	G	T	G	G	T	A	G	C	A	C	A	T	A	C	T	A	T	G	C	A	G	A	T	T	C	T	G	T	G	A	A	G
HUM:	G	G	C	C	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	C	A	G	C	A	A	A	A	A	C	T	C	C	C	T	G	T	A	T	C	T	G	C	A
UAM:	G	G	C	C	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	C	A	G	C	A	A	A	A	A	C	T	C	C	C	T	G	T	A	T	C	T	G	C	A
HUM:	A	A	T	G	A	A	C	A	G	T	C	T	G	A	G	A	A	C	T	G	A	G	A	C	A	C	C	G	C	C	T	T	G	T	A	T	T	A	C	T	G	T	G	C	A	A	A	A	G	
UAM:	A	A	T	G	A	A	C	A	G	T	C	T	G	A	G	A	G	C	T	G	A	G	A	C	A	C	G	G	C	C	T	T	G	T	A	T	T	A	C	T	G	T	G	C	A	A	A	A	G	
HUM:	A	T	A																																															
UAM:	A	C	A																																															

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	A	A	A	A	C	C	T
UAM:	G	A	C	A	A	A	A	A	C	C	T

Alignment stats: 'M': 282, 'I': 5, 'D': 5, 'X': 11

IGHV3-42

GENE ALIGN SEQ

HUM:	G	A	G	G	C	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	-	-	T	A	C	A	G	C	C	T	G	G	G	T	G	G	
UAM:	G	A	G	G	C	A	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	T	A	C	A	G	C	C	T	G	G	G	T	G	G	
HUM:	G	T	C	C	C	C	G	A	G	A	C	T	C	T	C	A	T	T	T	G	C	A	G	C	T	T	C	T	A	G	A	T	T	C	A	C	C	T	T	C	A	G	T	G	A	C	T	T	C	T
UAM:	G	T	C	C	C	T	G	A	G	A	C	T	C	T	C	A	T	T	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	G	A	C	T	T	C	T
HUM:	G	A	A	T	G	C	A	C	T	G	G	A	T	C	C	G	C	C	A	G	G	C	T	T	C	T	G	G	A	A	A	G	G	G	C	T	G	G	A	G	T	G	G	G	T	T	G	G	C	
UAM:	G	G	A	T	G	C	A	C	T	G	G	A	T	C	C	G	C	C	A	G	G	C	T	T	C	T	G	G	C	A	A	A	G	G	G	C	T	G	G	A	G	T	G	G	G	T	T	G	G	C
HUM:	C	G	T	A	T	T	A	G	A	A	C	C	A	A	A	C	G	T	A	A	C	A	G	T	T	A	C	A	C	G	A	C	A	G	A	A	T	G	C	G	C	T	G	C	A	T	C	T	G	T
UAM:	C	G	T	A	T	T	A	G	A	A	C	C	A	A	A	C	G	T	A	A	C	A	G	T	T	A	C	G	T	G	A	C	A	G	A	A	T	G	C	G	C	T	G	C	A	T	C	T	G	T
HUM:	G	A	A	A	G	G	C	A	G	G	T	T	C	A	C	C	A	T	C	T	C	A	A	G	A	G	A	T	G	A	T	T	C	A	A	A	G	A	A	C	A	C	A	C	T	G	T	A	T	C
UAM:	G	A	A	A	G	G	C	A	G	G	T	T	C	A	C	C	A	T	C	T	C	A	A	G	A	G	A	T	G	A	T	T	C	A	A	A	G	A	A	C	A	C	A	C	T	G	T	A	T	A
HUM:	T	G	C	A	A	G	T	G	A	A	T	A	C	C	C	T	G	A	A	A	A	C	C	G	A	G	T	-	-	-	-	A	C	A	C	G	G	C	C	A	T	C	T	A	T	T	A	C	T	G
UAM:	T	G	C	A	A	A	T	G	A	A	T	A	C	C	C	T	G	A	A	A	A	C	-	-	-	-	T	G	A	G	G	A	C	A	C	G	G	C	C	A	T	C	T	A	T	T	A	C	T	G
HUM:	T	A	C	T	A	G	A	G	A																																									
UAM:	T	A	C	T	A	G	A	G	A																																									

D7

HUM:	C	A	G	T	G	A	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	A	C	A	C	A	A	A	T	C	T	C
UAM:	T	A	C	A	C	A	A	A	T	C	T

Alignment stats: 'M': 289, 'I': 6, 'D': 4, 'X': 10

IGHV3-41

GENE ALIGN SEQ

HUM: G A G G T G C A G C T G G T G G A G T C T G G G G G A G G C T T G G T C C A G C C T G G G G G T C
UAM: G A G G T G C A G C T G A T G G A A T C T G G G G G A G G T T T G G T A C A G C C T G G G G G T C

HUM: C C T G - - - A G A C T C T C C T G T G C A G C C T C A G G A T T C T C C T T T A G T A G C T A T
UAM: - - T G T A A A - - A C T C T C T T G T G C A G C C T C A G G A T T C A C C T T T A G T A G C T A T

HUM: G G C A T G A G - C T G G G T C C G C C A G G C T C C A G G G A A G G G G C T G G A C T G A G T G G
UAM: G G C A T G - G A C T G G G T C T G C C A G G C T C C A G G C A A G G G G C T G G A - - - G T G G

HUM: - - - - C A C A T A T C T G G A A T G A T G G A A G T C A G A A A T A C T A T G C A G A C T C T G
UAM: G T G G T - A C A T A T A T G G A A T G A T G G A A G T C A G A A A T A C T A T G C A G A C T C T G

HUM: T G A A G G G C C G A T T C A C A A T C T C C A G A G A C A A T T C T A A G A G C A T G C T C T A T
UAM: T G A A G G G C C A A T T C A C G A T C T C C A G A G A C A A T T C T A A G A G C A T G C T C T A T

HUM: C T G C A A A T G G A C A G T C T G A A A G C T A A G G A C A C G G C C A T G T A T T A C T G T A C
UAM: C T G C A A A T G G A C A G T C T G A A A G C T G A G G A C A C G G C C A T G T A T T A C T G T A C

HUM: C A G A
UAM: C A G A

D7
HUM: C A C A G T G
UAM: C A G A G T G

D9
HUM: G A C A C A A A C C T
UAM: G A C A C A A A C T T

Alignment stats: 'M': 272, 'I': 10, 'D': 10, 'X': 12

IGHV(II)-40-1

GENE ALIGN SEQ

HUM:	A	G	C	C	T	G	G	T	G	A	A	G	C	C	C	T	T	G	C	A	A	A	C	C	C	C	T	C	A	C	T	C	A	C	C	T	G	T	G	C	T	G	C	C	T	C	T	G	G
UAM:	A	G	C	C	T	A	G	T	G	A	A	G	C	C	C	T	T	G	C	A	A	A	C	C	C	C	T	C	A	C	T	C	A	C	C	T	G	T	G	C	T	G	C	C	T	G	T	G	G

HUM:	A	T	T	C	T	C	T	G	T	C	A	C	A	A	T	C	A	G	T	G	C	T	T	C	C	T	G
UAM:	A	T	T	C	T	C	C	A	T	C	A	C	A	A	T	C	A	G	T	G	C	T	T	C	C	T	G

D7

HUM:	T	A	G	G	C	A	C
UAM:	T	A	G	G	C	A	C

D9

HUM:	G	T	C	A	G	G	T	G	C	A	T
UAM:	G	T	C	A	G	G	T	G	C	A	T

Alignment stats: 'M': 73, 'I': 0, 'D': 0, 'X': 4

IGHV7-40

GENE ALIGN SEQ

HUM:	T	A	T	G	G	T	A	T	G	A	A	T	T	C	A	G	T	G	T	G	A	C	C	A	G	C	C	C	C	T	G	G	A	C	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T
UAM:	T	A	T	G	G	T	A	T	G	A	A	T	T	C	G	G	T	G	T	G	A	C	C	G	G	C	C	C	C	T	G	G	A	C	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T

HUM:	G	G	G	A	T	G	G	A	T	C	A	T	C	A	C	C	T	A	C	A	C	T	G	G	G	A	A	C	C	C	A	A	C	A	T	A	T	A	C	C	A	A	C	-	-	G	G	C	T	T
UAM:	G	G	G	A	T	G	G	A	T	C	A	T	C	A	C	C	T	A	C	A	C	T	G	G	G	A	A	C	C	C	A	A	G	G	T	A	T	A	C	C	-	-	C	A	T	G	G	C	T	T

HUM:	C	A	C	A	G	G	A	C	G	G	T	T	T	C	T	A	T	T	C	T	C	C	A	T	G	G	A	C	A	C	C	T	C	T	G	T	C	A	G	C	A	T	G	G	C	G	T	A	T	C
UAM:	C	C	C	A	G	G	A	C	G	G	T	T	T	G	T	C	T	T	C	T	C	C	A	T	G	G	A	G	A	C	C	T	C	T	G	T	C	A	G	C	A	T	G	G	C	A	T	A	T	C

HUM:	T	G	C	A	G	A	T	C	A	G	C	A	G	C	C	T	A	A	A	G	G	C	T	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	G	A	C	T	G	T	A	T	G
UAM:	T	G	C	A	G	A	T	C	A	G	C	A	G	C	C	T	A	A	A	G	G	C	T	G	A	G	G	A	C	A	T	G	G	C	C	A	T	G	T	A	T	G	A	C	T	G	T	A	T	G

HUM:	A	G	A	G	A
UAM:	A	G	A	G	A

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	G	A	A	A	C	C	C
UAM:	G	T	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 190, 'I': 2, 'D': 2, 'X': 11

IGHV4-39

GENE ALIGN SEQ

HUM: C A G C T G C A G C T G C A G G A G T C G G G C C C A G G A C T G G T G A A G C C T T C G G A G A C
UAM: C A G G T G C A G C T G C A G G A G T C G G G C C C A G G A C T G G T G A A G C C T T C G G A G A C

HUM: C C T G T C C C T C A C C T G C A C T G T C T C T G G T G G C T C C A T C A G C A G T A G T A G T T
UAM: C C T G T C C C T C A C C T G C G C T G T C T C T G G T G G C T C C A T C A G - - - T A G T A - - -

HUM: A C T A C T G G G G C T G G A T C C G - - - C C A G C C C C A G G G A A G G G G C T G G A G T G
UAM: A C T A C T G G A G C T G G A T C C G G C A A C C A - - - C C A G G G A A G G G G C T G G A G T G

HUM: G A T T G G G - A G T A T C T A T T A T A G T G G G A G C A C C T A C - T A C A A C C C G T C C C T
UAM: G A T T G G G C A - T A T C C A T T A T G G T G G T A G C A A C T A C C T - C A A C C C G T C C C T

HUM: C A A G A G T C G A G T C A C C A T A T C C G T A G A C A C G T C C A A G A A C C A G T T C T C C C
UAM: C A A G A G T C G A G T C A C C A T A T C A G T A G A C A C G T C C A A G A A C C A G T T C T C C C

HUM: T G A A G C T G A G C T C T G T G A C C G C C G C A G A C A C G G C T G T G T A T T A C T G T G C G
UAM: T G A A G C T G A G C T C T G T G A C C G C C G C A G A C A C A G C C G T G T A T T A C T G T G C G

HUM: A G A C A
UAM: A G A G A

D7

HUM: C A C A G T G
UAM: C A C A G T G

D9

HUM: G A C A A A A A C C T
UAM: G A C A C A A A C T T

Alignment stats: 'M': 276, 'I': 6, 'D': 12, 'X': 11

IGHV(III)-38-1

GENE ALIGN SEQ

HUM:	G	A	A	G	T	T	A	A	C	T	A	G	T	G	G	A	G	T	C	A	G	A	C	A	G	G	-	-	A	A	A	A	T	A	C	T	A	C	A	G	A	C	C	A	A	G	A	A	T	T	
UAM:	G	A	A	G	T	T	A	A	C	T	A	G	T	G	G	A	G	T	C	A	G	A	C	A	G	G	C	-	-	-	-	-	-	-	C	T	A	C	A	G	A	C	G	A	A	G	A	A	T	T	
HUM:	C	T	C	A	G	A	C	T	G	T	T	C	T	G	C	A	A	A	G	C	C	C	C	T	G	G	A	T	T	C	A	C	T	G	A	A	A	A	A	G	A	A	C	A	A	G	T	T	T		
UAM:	C	T	C	A	G	A	C	T	G	T	T	C	T	G	C	A	A	A	G	C	C	C	C	T	A	G	A	T	T	C	A	C	T	G	A	A	A	A	C	A	G	A	A	C	A	A	G	T	T	T	
HUM:	G	G	T	C	C	A	G	C	A	G	G	A	T	T	C	A	T	G	G	C	A	A	G	T	G	T	T	G	G	T	G	A	G	G	A	G	A	T	A	A	C	A	G	T	A	A	T	T	C		
UAM:	G	G	T	C	C	A	G	C	A	G	G	A	T	T	C	A	T	G	A	C	A	A	G	G	T	T	G	G	T	G	T	G	G	A	G	A	T	A	A	C	A	G	T	A	A	T	T	C			
HUM:	A	A	G	T	G	G	A	A	G	T	T	C	T	C	A	A	T	G	G	G	A	C	T	C	G	C	C	T	T	C	A	G	T	A	C	A	A	A	G	A	A	G	A	T	T	A	A	C	A	G	
UAM:	A	A	G	T	G	G	A	A	G	T	T	C	T	C	A	A	T	G	G	G	A	C	T	C	T	C	C	C	T	T	C	A	G	T	A	C	A	A	A	G	A	A	G	A	T	T	A	A	C	A	G
HUM:	T	C	C	T	C	A	G	A	G	A	C	A	C	T	G	T	T	C	A	G	A	A	G	A	T	T	C	T	C	T	T	T	T	A	A	G	A	T	A	A	T	A	A	A	A	C	T	G	A	G	
UAM:	T	C	C	T	C	A	G	A	G	A	C	A	C	T	G	T	T	C	A	G	A	A	G	A	T	T	C	T	C	T	T	T	T	A	A	G	A	T	A	A	T	A	A	A	A	C	T	G	A	G	
HUM:	A	G	C	C	C	A	A	G	A	C	A	A	G	T	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	A	G	G	G	A																	
UAM:	A	G	C	C	C	A	A	G	A	C	A	A	G	T	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	A	G	G	G	A																	

D7

HUM:	C	A	C	A	G	T	G
UAM:	G	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	A	G	T
UAM:	G	A	C	A	C	A	A	A	A	C	T

Alignment stats: 'M': 266, 'I': 2, 'D': 6, 'X': 10

IGHV3-38

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	A	G	G	G	G	T	C		
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	T	C			
HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	G	T	C	A	G	T	A	G	C	A	A	T	G	A	G	A
UAM:	C	C	T	C	A	G	A	C	T	C	T	C	C	T	A	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	T	G	T	C	A	G	T	A	G	C	A	A	T	G	A	G	A
HUM:	T	G	A	G	C	T	G	G	A	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	C	T	C	A	T	C	C	
UAM:	T	G	A	G	C	T	G	G	A	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	C	T	C	A	A	C	C	
HUM:	A	T	T	A	G	T	-	-	-	G	G	T	G	G	T	A	G	C	A	C	A	T	A	C	T	A	C	G	C	A	G	A	C	T	C	C	A	G	-	G	A	A	G	G	G	C	A	G	A	T
UAM:	A	T	T	A	G	T	A	G	A	G	G	T	G	G	T	A	G	C	A	C	A	T	A	C	T	A	C	A	C	A	G	A	C	T	C	C	-	G	T	G	A	A	G	G	G	C	A	G	A	T
HUM:	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	A	G	A	A	C	A	C	G	C	T	G	T	A	T	C	T	T	C	A	A	A	T	G	A	A	C
UAM:	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	A	G	A	A	C	A	C	G	C	T	G	T	A	T	C	T	T	C	A	A	A	T	G	A	A	C
HUM:	A	A	C	C	T	G	A	G	A	G	C	T	-	G	A	G	G	G	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	C	A	G	A	-	T	A	T	A		
UAM:	A	G	C	C	T	G	A	G	A	G	-	T	G	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	G	-	-	-	A		

D7

HUM:	C	A	C	A	G	A	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	C	A	C	A	A	A	C	C	T	C	C
UAM:	A	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 277, 'I': 6, 'D': 5, 'X': 10

IGHV3-37

GENE ALIGN SEQ

HUM: G A G G T G C A G C T G G T A G A G T C T G G G G G A G A C T T G G T A C A G C T G T G G T G G G G
UAM: G A G G T G C A G C T G G T A G A G T C T G G G G G A G A C T T G G T A C A G C T G T G G C G G G G

HUM: T T G G G G G T G T C C T G A G A C T C T C A T G T G C A G C C T G C G G A T T C A T C T T G A G A
UAM: T T G G G G G T G T C C T G A G A C T T T C C T G T G C A G C C T G T G G A T T C A C C T T G A G A

HUM: A G C A A T G A C A T G A A C T G G G C C C A C C G G G C T T C A A G A A A G G G C T G G A A T G
UAM: A G C A A T G A C A T G A A C T G G G T C C A C C G G G C T T C A A G A A A G G G C T G G A G T G

HUM: G G T C T C A T A C A T T A G T G C T A G T G G T G G T A G C C T A T A C T A T G C A G A C A C T G
UAM: A G T C T C A T A C A T T A G T G C T A G T G G T G G T A G C C T A T A C T A T G C A G A C A C T G

HUM: A A G G G T A G A T T C A C C A T C T C T A G A G A C A A T G G C A A G A A C A T G C T G T A C T T
UAM: A A G G G T A G A T T C G C C A T C T G T A G A G A C A A T G G C A A G A G C A T G C T G T A C T T

HUM: G C A A A T G A A C A G T C T G A G A G A T G A G G A C T C G G C T G T G T G A G A G A
UAM: G C A A A T G C A C A G T C T G A G A G A T G A G G A C T C G G C C G T G T G A G A G A

D7
HUM: C A T G G T G
UAM: C A T G G T G

D9
HUM: G C C A G A A A C C T
UAM: G C C A G A A A C C T

Alignment stats: 'M': 281, 'I': 0, 'D': 0, 'X': 13

IGHV3-36

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	T	T	G	G	G	A	G	G	C	T	T	G	T	T	A	T	A	G	C	C	T	G	G	G	G	T	C	C			
UAM:	G	A	G	G	T	G	C	T	T	C	T	G	G	T	G	G	A	G	T	C	T	T	T	G	G	G	A	G	G	C	T	T	G	T	T	A	T	A	T	C	C	T	G	G	G	G	T	C	C			
HUM:	C	T	G	A	G	A	C	T	T	T	C	T	T	T	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	T	A	G	T	A	C	C	T	T	T	A	T	T	A	G		
UAM:	C	T	G	A	G	A	C	T	T	T	C	T	T	T	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	T	A	G	T	A	C	C	T	T	T	A	G	T	A	G		
HUM:	G	T	A	C	T	G	G	A	T	G	A	G	C	T	G	-	-	G	G	T	C	C	A	T	C	A	G	G	C	T	C	C	T	G	G	G	A	A	A	G	G	G	C	T	G	G	A	G	T	A		
UAM:	G	T	A	C	T	G	G	A	T	G	A	G	C	T	G	C	C	-	G	T	C	C	A	T	C	A	A	G	C	T	C	C	T	G	G	G	A	A	A	G	G	G	C	T	G	C	A	G	T	A		
HUM:	G	G	T	C	T	C	A	T	T	T	A	T	G	A	G	T	T	G	T	T	G	T	G	T	G	T	A	G	G	T	A	G	C	A	C	A	A	G	C	T	A	T	G	C	A	G	A	C	T	C	T	G
UAM:	G	G	T	C	T	C	A	T	T	T	A	T	G	A	G	T	T	G	T	T	G	T	G	T	G	T	A	G	G	T	A	G	C	A	C	A	A	A	C	T	A	T	G	C	A	G	A	C	T	C	T	G
HUM:	T	G	A	A	G	G	G	T	C	G	A	T	T	C	A	C	C	C	T	C	T	C	C	A	G	A	G	A	T	G	A	T	G	C	C	A	A	G	A	A	A	T	C	A	C	T	G	T	A	T		
UAM:	T	G	A	A	G	G	G	T	C	G	A	T	T	C	A	C	C	G	T	C	T	C	C	A	G	A	G	A	T	G	A	T	G	C	C	A	A	G	A	A	A	T	C	A	C	T	G	T	A	T		
HUM:	C	T	G	C	A	A	A	T	G	A	A	C	A	G	C	G	T	C	A	G	A	G	C	C	G	A	G	G	A	T	A	G	G	T	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	G		
UAM:	C	T	G	C	A	A	A	T	G	A	A	C	A	G	C	G	T	G	A	G	A	G	C	C	T	A	G	G	A	T	A	G	G	T	C	T	G	T	G	T	A	T	T	A	C	T	G	T	A	G		
HUM:	T	G	G																																																	
UAM:	T	G	G																																																	
D7																																																				
HUM:	C	A	T	T	G	T	G																																													
UAM:	C	A	T	T	C	T	G																																													
D9																																																				
HUM:	G	C	A	G	A	G	A	T	G	C	T																																									
UAM:	G	C	A	G	A	G	A	T	G	C	T																																									

Alignment stats: 'M': 289, 'I': 2, 'D': 1, 'X': 11

IGHV3-35

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	A	T	C			
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	A	G	A	T	C		
HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	A	C	A	G	T	G	A	C	A	
UAM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	A	C	A	C	T	G	A	C	A	
HUM:	T	G	A	A	C	T	G	G	G	T	C	C	A	T	C	A	G	G	C	T	C	C	A	G	G	A	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	A	T	C	-	-	G	G	
UAM:	T	G	A	A	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	-	-	C	T	T	G	G	
HUM:	G	T	G	T	T	A	G	T	T	G	G	A	A	T	G	G	C	A	G	T	A	G	G	A	C	G	C	A	C	T	A	T	G	C	A	G	A	C	T	C	T	G	T	G	A	A	G	G	G	C	
UAM:	G	T	A	T	T	A	G	T	T	G	G	A	A	T	G	G	T	G	G	T	A	G	G	A	T	G	C	A	C	T	A	T	G	C	G	G	A	C	T	C	C	G	T	G	A	A	G	G	G	C	
HUM:	C	G	A	T	T	C	A	T	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	G	G	A	A	C	A	C	C	C	T	G	T	A	T	C	T	G	C	A	A	A	C	
UAM:	C	G	A	T	T	C	A	T	C	A	T	C	A	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	G	G	A	A	C	T	T	C	C	T	G	T	A	T	C	T	G	C	A	A	A	C
HUM:	G	A	A	T	A	G	C	C	T	G	A	G	G	G	C	C	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	T	G	A	G	A	A	A			
UAM:	G	A	A	T	A	G	C	C	T	G	A	G	G	G	C	C	G	A	G	G	A	C	A	C	A	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	T	G	A	G	A	A	A			

D7

HUM:	C	A	C	T	G	T	G
UAM:	C	A	C	T	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 280, 'I': 2, 'D': 2, 'X': 14

IGHV7-34-1

GENE ALIGN SEQ

HUM:	C	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	C	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C	A	G	T
UAM:	C	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	C	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C	A	G	T
HUM:	G	A	A	G	G	T	C	T	C	C	T	A	T	A	A	G	T	C	T	T	C	T	G	G	T	T	A	C	A	C	C	T	T	C	A	C	C	A	T	C	T	-	A	T	G	G	T	A	T	G
UAM:	G	A	A	G	G	T	C	T	C	C	T	A	T	A	A	G	T	C	T	T	C	T	G	G	T	T	A	C	A	C	C	T	T	C	A	C	C	A	-	C	T	T	A	T	G	G	T	A	T	G
HUM:	A	A	T	T	G	G	G	T	A	T	G	A	T	A	G	A	C	C	C	C	T	G	G	A	C	A	G	G	G	C	T	T	T	G	A	G	T	G	G	A	T	G	T	G	A	T	G	G	A	T
UAM:	A	A	T	T	G	G	T	T	A	T	G	A	C	A	G	A	C	C	C	C	T	G	G	A	C	A	G	G	G	C	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	T	G	G	A	T
HUM:	C	A	T	C	A	C	C	T	A	C	A	C	T	G	G	G	A	A	C	C	C	A	A	C	G	-	-	-	T	A	T	A	C	C	C	A	C	G	G	C	T	T	C	A	C	A	G	G	A	T
UAM:	C	A	T	C	A	C	C	T	A	A	A	C	T	G	G	G	A	A	C	C	C	-	-	-	G	A	C	A	T	A	T	A	C	C	C	A	C	G	G	C	T	T	C	A	C	A	G	G	A	T
HUM:	G	G	T	T	T	G	T	C	T	T	C	T	C	C	A	T	G	G	A	C	A	C	G	T	C	T	G	T	C	A	G	C	A	C	G	G	C	G	T	G	T	C	T	T	C	A	G	A	T	C
UAM:	G	G	T	T	T	G	T	C	T	T	C	T	C	C	A	T	G	G	A	C	A	C	C	T	C	T	G	T	C	A	G	C	A	C	G	G	C	G	T	A	T	C	T	T	C	A	G	A	T	C
HUM:	A	G	C	A	G	C	C	T	A	A	A	G	G	C	T	G	A	G	G	A	C	A	C	G	G	C	C	G	A	G	T	A	T	T	A	C	T	G	T	G	C	G	A	A	G	T	A			
UAM:	A	G	C	A	G	C	C	T	A	A	A	G	G	C	T	G	A	G	G	A	C	A	C	G	G	C	T	G	A	G	T	A	T	T	A	C	T	G	T	G	C	G	A	A	G	T	A			

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	T	T	C	A	G	A	A	A	G	C	C
UAM:	T	T	C	A	G	A	A	A	G	C	C

Alignment stats: 'M': 281, 'I': 4, 'D': 4, 'X': 8

IGHV4-34

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	A	C	A	G	C	A	G	T	G	G	G	G	C	G	C	A	G	G	A	C	T	G	T	T	G	A	A	G	C	C	T	T	C	G	G	A	G	A	C
UAM:	C	A	G	G	T	G	C	A	G	C	T	A	C	A	G	C	A	G	T	G	G	G	G	T	G	C	A	G	G	A	C	T	G	G	T	G	A	A	G	C	C	T	T	C	G	G	A	G	A	C
HUM:	C	C	T	G	T	C	C	C	T	C	A	C	C	T	G	C	G	C	T	G	T	C	T	A	T	G	G	T	G	G	G	T	C	C	T	T	C	A	G	T	G	G	T	T	A	C	T	-	-	A
UAM:	C	C	T	G	T	C	C	C	T	C	A	C	C	T	G	C	G	C	T	G	T	C	T	A	T	G	G	T	G	G	G	T	C	C	T	T	C	A	G	T	G	A	T	T	A	-	T	G	G	-
HUM:	C	T	G	G	A	G	C	T	G	G	A	T	C	C	G	C	C	A	G	C	C	C	C	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	A	T	T	G	G	G	G
UAM:	C	T	G	G	A	A	C	T	G	G	A	T	C	C	G	C	C	A	G	C	C	C	C	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	A	T	T	G	G	G	-
HUM:	A	A	A	T	-	C	A	A	T	C	-	-	-	-	-	A	T	A	G	T	G	G	A	A	G	C	A	C	C	A	A	C	T	A	C	A	A	C	C	C	G	T	C	C	C	T	C	A	A	G
UAM:	-	-	-	T	A	C	-	A	T	C	G	T	T	A	G	-	T	A	G	T	G	G	G	A	G	A	A	C	C	A	A	C	T	A	C	A	A	C	C	C	G	T	C	C	C	T	C	A	A	G
HUM:	A	G	T	C	G	A	G	T	C	A	C	C	A	T	A	T	C	A	G	T	A	G	A	C	A	C	G	T	C	C	A	A	G	A	A	C	C	A	G	T	T	C	T	C	C	C	T	G	A	A
UAM:	A	G	T	C	G	A	G	T	C	A	C	C	A	T	G	T	C	A	G	T	A	G	A	C	A	C	G	T	C	C	A	A	G	A	A	C	C	A	G	T	T	C	T	C	C	C	T	G	A	A
HUM:	G	C	T	G	A	G	C	T	C	T	G	T	G	A	C	C	G	C	C	G	C	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	G
UAM:	G	C	T	G	A	G	C	T	C	T	G	T	G	A	C	C	G	C	C	G	C	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	G
HUM:	G																																																	
UAM:	G																																																	
D7																																																		
HUM:	C	A	C	A	G	T	G																																											
UAM:	C	A	C	A	G	T	G																																											
D9																																																		
HUM:	G	A	C	A	A	A	A	A	C	C	T																																							
UAM:	G	A	T	A	A	A	A	A	C	C	T																																							

Alignment stats: 'M': 277, 'I': 8, 'D': 8, 'X': 8

IGHV3-33-2

GENE ALIGN SEQ

HUM:	G	A	G	G	T	A	C	A	G	C	T	C	G	T	G	G	A	G	T	C	C	G	G	A	G	A	G	G	A	C	C	C	A	A	G	A	C	A	A	C	C	T	G	G	G	G	A	T	C
UAM:	G	A	G	G	T	A	C	A	G	C	T	A	G	T	G	G	A	G	T	C	C	G	G	A	G	A	G	G	A	C	C	C	A	A	G	A	C	A	A	C	C	T	G	G	G	G	G	T	C

HUM:	C	T	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	A	C	T	C	T	G	G	A	T	T	A	A	C	C	T	T	C	A	G	T	A	G	C	T	A	C	T	G	A	A
UAM:	C	G	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	A	C	T	C	T	G	G	A	T	T	A	A	C	C	T	T	C	A	G	T	A	G	C	T	A	C	T	G	A	A

HUM:	T	G	A	G	C	T	C	G	G	T	T	T	C	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	A	G	T	A	G	T	A	G	A	T
UAM:	T	G	A	G	C	T	C	A	G	T	T	T	C	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	A	G	T	A	G	T	A	G	A	T

HUM:	A	-	-	T	A	C	A	G	T	G	T	G	A	T	G	G	A	A	G	T	C	A	G	A	T	A	T	G	T	T	A	T	G	C	C	C	A	A	T	C	T	G	T	G	A	A	G	A	G	C
UAM:	A	A	A	T	-	-	A	G	T	A	C	G	A	T	A	C	A	A	G	T	C	A	G	A	T	A	T	G	T	T	A	T	G	C	A	C	A	A	A	C	T	G	T	G	A	A	G	A	G	C

HUM:	A	A	A	T	T	C	A	C	C	A	T	C	T	C	C	A	A	A	G	A	A	A	A	T	G	C	C	A	A	G	A	A	C	T	C	A	C	T	G	T	A	T	T	T	G	C	A	A	A	T
UAM:	A	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	A	A	G	A	A	A	A	T	G	C	C	A	A	G	A	A	C	T	C	A	C	T	C	C	A	T	T	T	G	C	A	A	A	T

HUM:	G	A	A	C	A	G	T	C	T	G	A	G	A	G	C	A	G	A	G	G	G	C	A	C	A	G	C	T	G	T	G	T	G	T	T	A	C	T	G	T	A	T	G	T	G	A	G	G	C	A
UAM:	G	A	A	C	G	G	T	C	T	G	A	G	A	A	C	A	G	A	G	G	G	C	A	C	A	A	C	T	G	T	G	T	G	T	T	A	C	T	G	T	A	T	G	T	G	A	G	G	C	A

D7

HUM:	C	C	A	G	G	T	A
UAM:	C	C	A	G	G	T	A

D9

HUM:	G	A	C	A	C	A	G	T	T	T	C
UAM:	G	A	C	A	C	A	G	A	A	T	T

Alignment stats: 'M': 280, 'I': 2, 'D': 2, 'X': 16

IGHV(II)-28-1

GENE ALIGN SEQ

HUM:	C	A	A	C	A	A	C	T	A	T	G	T	T	C	T	C	A	G	C	A	C	A	C	T	T	C	T	G	G	C	T	T	G	A	G	A	C	G	T	C	C	T	T	G	C	A	G	A	C	
UAM:	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	C	A	G	A	C
HUM:	C	C	T	C	T	C	C	C	T	C	A	C	C	T	G	C	A	C	T	G	T	C	T	C	T	G	G	A	T	T	C	C	C	C	A	T	C	A	T	A	A	C	C	A	G	T	G	T	G	T
UAM:	C	C	T	C	T	C	C	C	T	C	A	C	C	T	G	C	A	C	T	G	T	C	T	C	T	G	G	A	T	T	C	C	C	C	A	T	C	A	T	A	A	C	C	A	G	T	G	T	T	T
HUM:	C	C	T	G	C	T	A	G	A	A	T	T	G	T	A	T	C	T	G	C	T	T	G	C	C	C	C	T	A	G	A	A	G	A	T	G	G	A	C	A	G	G	A	G	T	G	G	A	T	C
UAM:	C	C	C	A	C	T	A	G	A	A	T	T	G	T	A	T	C	T	G	C	T	T	G	T	C	C	C	T	A	G	A	A	G	A	T	G	G	A	C	A	G	G	A	G	T	G	G	A	T	C
HUM:	A	G	G	T	G	C	A	T	G	G	G	T	T	G	T	G	A	A	G	G	G	A	G	C	A	C	A	A	A	T	T	A	C	A	A	C	C	C	A	C	T	G	C	T	C	A	A	G	A	G
UAM:	A	G	G	T	G	C	A	T	G	G	G	T	T	G	T	G	A	A	G	G	G	A	G	C	A	C	A	A	A	T	T	A	C	A	A	C	C	-	A	C	T	T	C	T	C	A	A	G	A	G
HUM:	T	C	C	A	T	A	T	C	C	A	G	A	T	C	C	A	A	G	A	A	A	C	A	G	T	T	C	T	T	A	C	A	G	C	T	G	A	G	C	T	C	T	G	T	G	C	C	C	A	G
UAM:	T	C	C	A	T	-	-	-	-	-	-	A	T	C	C	A	A	G	A	A	A	C	A	G	T	T	C	T	T	A	C	A	G	C	T	G	A	G	C	T	C	T	G	T	G	C	C	C	A	G
HUM:	T	G	A	A	C	A	C	A	C	A	A	C	T	A	C	G	C	A	T	T	T	T	T	A	A	G	C	A	A	A	A	G	A																	
UAM:	T	G	A	A	C	A	C	A	C	A	A	C	T	A	T	G	C	A	T	T	T	T	T	A	A	G	C	A	A	A	A	G	A																	

D7

HUM:	C	G	C	A	A	T	G
UAM:	G	G	C	A	A	T	G

D9

HUM:	G	A	C	A	C	A	A	C	C	C	T
UAM:	G	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 226, 'I': 0, 'D': 51, 'X': 6

IGHV4-28

GENE ALIGN SEQ

HUM:	C	A	G	G	T	A	C	A	G	C	T	G	C	A	G	G	A	G	T	C	G	G	G	C	C	C	A	G	G	A	C	T	G	G	T	G	A	A	G	C	C	T	T	C	G	G	A	C	A	C
UAM:	C	A	G	G	T	G	C	A	G	C	T	G	C	A	G	G	A	G	T	C	G	G	G	C	C	C	A	G	G	A	C	T	G	G	T	G	A	A	G	C	C	T	T	C	G	G	A	G	A	C
HUM:	C	C	T	G	T	C	C	C	T	C	A	C	C	T	G	C	G	C	T	G	T	C	T	C	T	G	G	T	T	A	C	T	C	C	A	T	C	A	G	C	A	G	T	A	G	T	A	A	C	T
UAM:	C	C	T	G	T	C	C	C	T	C	A	C	C	T	G	C	G	C	T	G	T	C	T	C	T	G	G	T	G	G	C	T	C	C	A	T	C	A	G	C	A	G	T	G	G	T	T	A	C	T
HUM:	G	G	T	G	G	G	G	C	T	G	G	A	T	C	C	G	G	C	A	G	C	C	C	C	C	A	G	G	G	A	A	G	G	G	A	C	T	G	G	A	G	T	G	G	A	T	T	G	G	G
UAM:	A	C	T	G	G	G	G	C	T	G	G	A	T	C	C	G	C	C	A	G	C	C	C	C	C	A	G	G	G	A	A	G	G	G	C	C	T	G	G	A	G	T	G	G	A	T	T	G	G	G
HUM:	-	-	T	A	C	A	T	C	T	A	T	T	A	T	A	G	T	G	G	G	A	G	C	A	C	C	T	A	-	C	T	A	C	A	A	C	C	C	G	T	C	C	C	T	C	A	A	G	A	G
UAM:	C	A	T	A	-	-	T	C	A	A	T	T	A	T	G	G	T	G	G	G	A	G	C	A	C	C	-	A	G	C	T	A	C	A	A	C	C	C	A	T	C	C	C	T	C	A	A	G	A	G
HUM:	T	C	G	A	G	T	C	A	C	C	A	T	G	T	C	A	G	T	A	G	A	C	A	C	G	T	C	C	A	A	G	A	A	C	C	A	G	T	T	C	T	C	C	C	T	G	A	A	G	C
UAM:	T	C	G	A	G	T	C	A	C	C	T	T	G	T	C	A	G	T	A	G	A	C	A	C	G	T	C	C	A	A	G	A	A	C	C	A	G	T	T	C	T	C	C	C	T	G	A	A	G	C
HUM:	T	G	A	G	C	T	C	T	G	T	G	A	C	C	G	C	C	G	T	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	A	A	
UAM:	T	G	A	G	C	T	C	T	G	T	G	A	C	C	G	C	C	G	C	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	G	A	

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	A	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	A	A	A	A	C	C	T

Alignment stats: 'M': 277, 'I': 3, 'D': 3, 'X': 16

IGHV7-27

GENE ALIGN SEQ

HUM: C - - - - A G G T G C A G C T G G T G C A G T C T G G G C C T G A G G T G A A G A A G C C T G G A G
UAM: C T C C C A G G T G C A G C T G G T G C A G T C T G A G C C T G A G A T G A A G C A G C C T G G G G

HUM: C C T C A T T G A A G G T T - T C C T G C A A G G C T T C T G G A T A C A C C T T C A C A A G C T A
UAM: C C T C A G T G A A G - T T C T C C T G C A A G G C T A C T G G T T A C A C C T T C A C T A G C T A

HUM: T G C T A T C A G - - C T G G G T A T G A C A G G C C C A T G G A C A A G G G C T T G A G G A A A T
UAM: T G T T A T - - G A A C T G G G T G C G A C A G G C C C C T G G A C A A G G G C T T G A G T G G G T

HUM: G G G A T G G A T C A A C A C C A A C A C T G G G A A C C T A A C G T A T G C C C A G G G C T T C A
UAM: G G G A T G G A T C A A C A C C A A C A C T G G G A A C C C A A T G T A T G C C C A G G G C T T C A

HUM: C A G G A C G G T T T G T C T T C T C C A T G G A C A C C T C C G T C A G C A T G - - - G - - C - -
UAM: C A G G A C A G T T T G T C T T C T C C A T G G A C A C C T C - - - - - - - T G T C A G T A C A G

HUM: - A T A T C T T C A T A T C A G C A G C C T A A A G G C T G A G G A C A - - - - - C G T G - - - - -
UAM: T A T A T C T G C A G A T C A G T A G C C T A A A G G C T G A G G A C A T G G C T - G T G T A T T A

HUM: C - - - - - A A G A G G
UAM: C T G T T T G - A G A G A

D7

HUM: C A C A G T G
UAM: C A C A G T G

D9

HUM: A C C A G A A A T C C
UAM: G T C A G A A A C C C

Alignment stats: 'M': 246, 'I': 31, 'D': 13, 'X': 23

IGHV(III)-26-1

GENE ALIGN SEQ

HUM:	G	A	T	G	T	T	T	A	C	T	G	A	T	G	G	A	G	T	C	A	G	A	A	G	G	A	G	A	A	A	A	T	T	-	T	A	A	C	A	G	C	C	C	A	G	C	A	G	T	
UAM:	G	A	T	G	T	T	T	A	C	T	G	A	T	G	G	A	G	T	C	A	G	A	A	G	G	G	A	A	A	A	A	T	T	G	T	-	A	C	A	G	C	C	C	A	G	C	G	G	T	
HUM:	T	C	A	C	T	G	A	G	A	C	T	G	T	C	C	T	G	C	A	A	A	G	C	C	T	C	T	G	G	T	T	T	C	G	G	G	T	T	T	A	C	T	G	G	G	T	G	C	A	G
UAM:	T	C	A	C	T	G	A	G	A	C	T	G	T	C	C	T	G	C	A	A	A	A	C	C	T	C	T	G	G	T	T	T	C	G	G	G	T	T	T	A	C	T	G	G	G	T	A	C	A	G
HUM:	C	A	T	G	A	G	C	T	T	G	G	T	C	C	A	G	C	-	A	C	A	C	T	-	-	-	T	C	A	C	A	A	C	A	G	G	A	A	T	T	G	G	T	G	T	G	G	G	T	A
UAM:	C	A	T	G	A	G	C	T	T	G	G	T	C	C	A	G	C	G	-	-	-	-	T	G	C	G	T	C	A	C	A	A	C	A	G	G	A	A	T	T	G	G	T	G	T	G	G	A	T	A
HUM:	G	C	A	A	C	A	G	T	G	A	G	A	G	A	T	C	A	T	A	T	G	G	G	A	G	T	T	C	T	A	A	G	G	G	T	T	A	C	T	C	T	C	C	A	T	G	A	G	T	A
UAM:	G	C	A	A	C	G	G	T	G	A	G	A	G	A	T	C	A	T	A	T	G	G	G	A	G	T	T	C	T	C	A	G	G	G	T	T	A	C	T	C	T	C	C	A	T	G	A	G	T	A
HUM:	C	A	G	A	T	A	A	A	T	C	A	A	C	A	T	T	C	C	C	A	A	G	T	G	A	C	A	C	C	C	T	T	T	C	A	A	G	T	G	C	A	G	T	C	T	A	C	C	T	T
UAM:	C	A	A	A	T	A	A	G	T	T	A	A	C	A	T	T	C	C	C	A	A	G	C	G	A	C	A	C	C	C	T	T	T	C	A	A	G	T	G	C	A	G	T	C	T	A	C	C	T	T
HUM:	A	C	A	A	G	G	A	C	C	A	A	C	C	T	G	A	A	A	G	C	C	A	A	G	G	G	C	A	A	G	G	C	C	G	T	A	T	A	T	T	A	C	A	G	T	G	A	G	G	G
UAM:	A	C	A	A	T	G	A	C	C	A	A	C	C	T	G	A	A	A	G	C	C	A	A	G	G	G	C	A	A	G	G	C	C	G	T	G	T	A	T	C	A	C	A	G	T	G	A	G	G	G
HUM:	A																																																	
UAM:	A																																																	
D7																																																		
HUM:	C	A	C	A	G	G	G																																											
UAM:	C	A	C	A	G	G	A																																											
D9																																																		
HUM:	A	G	A	C	A	C	A	A	A	A	A																																							
UAM:	A	G	A	C	A	C	A	A	A	A	A																																							

Alignment stats: 'M': 277, 'I': 5, 'D': 5, 'X': 14

IGHV2-26

GENE ALIGN SEQ

HUM:	C	A	G	G	T	C	A	C	C	T	T	G	A	A	G	G	A	G	T	C	T	G	G	T	C	C	T	G	T	G	C	T	G	G	T	G	A	A	A	C	C	C	A	C	A	G	A	G	A	C
UAM:	C	A	G	G	T	C	A	C	C	T	T	G	A	A	G	G	A	G	T	C	T	G	G	T	C	C	T	G	C	G	C	T	G	G	T	G	A	A	A	C	C	C	A	C	A	G	A	G	A	C
HUM:	C	C	T	C	A	C	G	C	T	G	A	C	C	T	G	C	A	C	C	G	T	C	T	C	T	G	G	G	T	T	C	T	C	A	C	T	C	A	G	C	A	A	T	G	C	T	A	G	A	A
UAM:	C	C	T	C	A	C	G	C	T	G	A	C	C	T	G	C	A	C	C	G	T	C	T	C	T	G	G	G	T	T	C	T	C	A	C	T	C	A	G	C	A	A	T	T	C	T	A	A	A	A
HUM:	T	G	G	G	T	G	T	G	A	G	C	T	G	G	A	T	C	C	G	T	C	A	G	C	C	C	C	C	A	G	G	G	A	A	G	G	C	C	C	T	G	G	A	G	T	G	G	C	T	T
UAM:	T	G	G	G	T	G	T	G	A	G	C	T	G	G	A	T	C	C	G	T	C	A	G	C	C	C	C	C	A	G	G	G	A	A	G	G	C	C	C	T	G	G	A	G	T	G	G	C	T	T
HUM:	G	C	A	C	A	C	A	T	T	T	T	T	T	C	G	A	A	T	G	A	C	G	A	A	A	A	A	T	C	C	T	A	C	A	G	C	A	C	A	T	C	T	C	T	G	A	A	G	A	G
UAM:	G	C	A	C	A	C	A	T	T	T	T	T	T	C	G	A	A	T	G	A	C	G	A	A	A	A	A	T	C	C	T	A	C	A	G	C	A	C	A	T	C	T	C	T	G	A	A	G	A	G
HUM:	C	A	G	G	C	T	C	A	C	C	A	T	C	T	C	C	A	A	G	G	A	C	A	C	C	T	C	C	A	A	A	A	G	C	C	A	G	G	T	G	G	T	C	C	T	T	A	C	C	A
UAM:	C	A	G	G	C	T	C	A	C	C	A	T	C	T	C	C	A	A	G	G	A	C	A	C	C	T	C	C	A	A	A	A	G	C	C	A	G	G	T	G	G	T	C	C	T	T	A	C	C	A
HUM:	T	G	A	C	C	A	A	C	A	T	G	G	A	C	C	C	T	G	T	G	G	A	C	A	C	A	G	C	C	A	C	A	T	A	T	T	A	C	T	G	T	G	C	-	-	A	C	G	G	A
UAM:	T	G	A	C	C	A	A	C	A	T	G	G	A	C	C	C	T	G	T	G	G	A	C	A	C	A	G	C	C	A	C	G	T	A	T	T	A	C	T	-	-	G	C	A	C	A	C	G	G	A
HUM:	T	A	C																																															
UAM:	G	A	G																																															

D7

HUM:	C	A	C	A	G	A	G
UAM:	C	A	C	A	G	A	G

D9

HUM:	T	A	C	A	A	G	A	A	C	C	T
UAM:	T	A	C	A	A	G	A	A	C	C	C

Alignment stats: 'M': 293, 'I': 2, 'D': 2, 'X': 6

IGHV(III)-25-1

GENE ALIGN SEQ

HUM: G A A G T T C A C - - - C G G G G G A G A C A G A G G A A A T A A C G G T G C A G C C G G G G G C T
UAM: G A A G T T C A C T G G C - - - G G A G A C A G A G G A A A T A A T G G T A C A G C T G G G G G C T

HUM: A T C T G A G T C T C T C C T G C A A A G A C T C T G G A T T C A C C T T C A C T G A T T G C A G C
UAM: A T C T G A G T C T C T C C T G C A A A G A C G C T G G A T T C A C C T T C A C T G A T T G C A G C

HUM: A T A A G C T T G G T C C A G C A A G C T C C A G G A C C A G G G T T G A T G T G G G C A G C A A C
UAM: C T A A G C T T G G T C C A G C A G G C T T C A G G A C C A G G G T T G A T G T A G G C A G C A A C

HUM: A G G G A G A A A T T G A A G A G G A A G C T C T C A G T G G T G C C C T C C A T G A A T A C A A A
UAM: G G G G A G A A A T T G A A G A - - - A G T T C C C A G T G G T G C C C T C C A T G A A T A C A A A

HUM: G A A T C T T C A C A G T C C C C A G G A C A C C C T T A C G T G C A T G G T C T C A C T G A T A T
UAM: G A A T C T T C A C A G T C C C C A G G A C A C C C T T A C T T G C A T G G T C T C A C T G A C A T

HUM: C T T T A C T T C C T T T A T C A C T T T T G T T A T G T A A A T
UAM: C T T T A C T T C C T T T A T C A C T T T T G T T C T G T A A A T

D7

HUM: C A C A A T G
UAM: C A C A A T G

D9

HUM: A T A C A T T T G T T
UAM: A T A T A T T T G T T

Alignment stats: 'M': 260, 'I': 3, 'D': 6, 'X': 14

IGHV3-25

GENE ALIGN SEQ

HUM: G A G A - T G C A G C T G G T G G A G T C - T G G G G - G A G G C T T G G C A A A G C C T G C G T G
UAM: G A - A G T G T A G C T G G T G G A G A C C - - G G G C G A G G C T T G G C A A A G C C T G G G T G

HUM: G T C C C C G A G A C T C T C C T G T G C A G C C T C T C A A T T C A C C T T C A G T A G C T A C T
UAM: G T C C C C G A G A C T C T C C T G T G C C G C C T C T C G A T T C A C C T T C A G T A G C T A C T

HUM: A C A T G A A C T G T G T C C G C C A G G C T C C A G G A A T G G G C T G G A G T T G G T T G G A
UAM: A C A T G A A C T G T G T C T G C C A G G C T C C A G G A A T A G G C T G G A G T T G G T T G G A

HUM: C A A G T T A A T C C T A A T G G G G T A G C A C A T A C C T C A T A G A C T C C G G T - A A G G
UAM: C A A G T T A A T C C T A A T G G G G T A G C A C A T A C C T C A T A G A C T C - - - T G - - G G

HUM: A - - - - C C G A T T C A A T A C C T C C A G A G A T A A C G C C A A G A A C A C A C T T C A T C T
UAM: A A G G G C C A A T T C A C T A C C T C C A G A G A T A A C G C C A A G A A C A C T C T T C A T C T

HUM: G C A A A T G A A C A G C C T G A A A A C C G A G G A C A C G G C C C T G T A T T A G T G T A C C A
UAM: G C A A A T G A A C A A C C T G A A A A C C G A G G A C A T G G C C C T G T A T T A G T G T A C T A

HUM: G A G A
UAM: G A G A

D7
HUM: C A C A G T G
UAM: C A C A G T G

D9
HUM: G A C A C A A A C C T
UAM: G A C A C A A A C C T

Alignment stats: 'M': 275, 'I': 8, 'D': 8, 'X': 13

IGHV1-24

GENE ALIGN SEQ

HUM:	C	A	G	G	T	C	C	A	G	C	T	G	G	T	A	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C
UAM:	G	A	G	G	T	C	C	A	G	C	T	G	G	T	A	C	A	G	T	C	C	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C
HUM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	T	T	T	C	C	G	G	A	T	A	C	A	C	C	C	T	C	A	C	T	G	A	A	T	T	A	T	C	C	A
UAM:	A	G	T	G	A	A	G	T	T	C	T	C	C	T	G	C	A	A	G	G	T	T	T	C	T	G	G	A	T	A	C	A	C	C	T	T	C	A	C	C	G	A	A	T	T	A	T	C	C	A
HUM:	T	G	C	A	C	T	G	G	G	T	G	C	G	A	C	A	G	G	C	T	C	C	T	G	G	A	A	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	G	G	T
UAM:	T	G	C	A	C	T	G	G	G	T	G	C	G	A	C	A	G	G	C	T	C	C	T	G	G	A	A	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	G	G	T
HUM:	T	T	T	G	A	T	C	C	T	G	A	A	G	A	T	G	G	T	G	A	A	A	C	A	A	T	C	T	A	C	G	C	A	C	A	G	A	A	G	T	T	C	C	A	G	G	G	C	A	G
UAM:	T	T	T	G	A	T	C	C	T	G	A	T	G	A	T	G	G	T	G	A	A	A	C	A	A	T	C	T	A	C	G	C	A	C	A	G	A	A	G	T	T	C	C	A	G	G	G	C	A	G
HUM:	A	G	T	C	A	C	C	A	T	G	A	C	C	G	A	G	G	A	C	A	C	A	T	C	T	A	C	A	G	A	C	A	C	A	G	C	C	T	A	C	A	T	G	G	A	G	C	T	G	A
UAM:	A	G	T	C	A	C	C	A	T	G	A	C	C	G	A	G	G	A	C	A	C	G	T	C	T	A	C	A	G	A	C	A	C	A	G	C	C	T	A	C	A	T	G	G	A	G	C	T	G	A
HUM:	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	A	A	C	A	G	A				
UAM:	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	G	G	A	C	A	C	G	G	C	C	A	T	G	T	A	T	T	A	C	T	G	T	G	C	A	A	C	A	G	A				

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	G	A	A	A	C	C	C
UAM:	G	T	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 287, 'I': 0, 'D': 0, 'X': 9

IGHV3-23

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	G	T	C		
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	G	T	C		
HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	T	A	G	-	-	C	A	-	-	-	-	-	-	
UAM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	-	-	-	-	-	G	T	T	C	A	C	T	A	A	C	T	A
HUM:	-	-	-	-	-	G	C	T	A	T	G	C	-	C	A	T	G	A	G	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	G	G	C	T	G	
UAM:	C	T	A	C	C	-	-	-	-	T	G	C	A	-	-	-	-	-	-	C	T	G	G	T	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	G	G	C	T	G	
HUM:	G	A	G	T	G	G	G	T	C	T	C	A	G	C	-	T	A	T	-	-	-	-	-	T	A	G	T	G	G	T	A	G	T	G	G	T	A	G	C	A	C	A	T	A	C	T	A			
UAM:	G	A	G	T	G	G	G	T	C	-	-	-	-	G	C	A	T	A	T	A	T	A	G	T	A	G	T	G	G	T	A	G	T	G	G	T	A	G	C	A	C	A	A	A	C	T	A			
HUM:	C	G	C	A	G	A	C	T	C	C	G	T	G	A	A	G	G	G	C	C	G	G	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	A	G	A
UAM:	C	C	C	A	G	A	T	T	C	T	G	T	G	A	A	G	G	G	C	C	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	C	G	C	C	A	A	G	A
HUM:	A	C	A	C	G	C	T	G	T	A	T	C	T	G	C	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	G	A	G	C	C	G	A	G	G	A	C	A	C	G	G	C	C	G	T	A
UAM:	A	C	A	C	G	C	T	G	T	A	T	C	T	G	C	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	G	A	G	C	C	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G
HUM:	T	A	T	T	A	C	T	G	T	G	C	G	A	A	A	G	A																																	
UAM:	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A	G	A																																	

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 267, 'I': 21, 'D': 18, 'X': 11

IGHV(III)-22-2

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	G	T	G	G	T	G	G	A	G	T	G	T	A	G	G	G	G	A	G	A	G
UAM:	G	A	G	G	T	G	C	A	G	G	T	G	G	T	G	G	A	G	T	C	T	C	G	G	G	G	A	G	A	G

D7

HUM:	A	C	A	A	G	A	G
UAM:	G	C	A	A	G	A	G

D9

HUM:	G	G	G	T	G	A	G	G	C	T	G
UAM:	G	G	G	T	G	A	G	C	T	G	T

Alignment stats: 'M': 28, 'I': 0, 'D': 0, 'X': 2

IGHV(II)-22-1

GENE ALIGN SEQ

HUM: G G C C T G G T G A A G C C C T C A C A G A T C C T C C C C C T G G C C T G T G G C A T C T C T G C
UAM: G G C C T G G T G A A G C C C T C A C A G A T C C T C C C C C T C G C C T G T G C C A T C T C T G C

HUM: T T C T C C A T T A C A A C C A G T G C T T C C T G C T G G A G C T G G A T C C G T C A - C C C C C
UAM: C T C T C C A T T A C A A C C A G T G C T T C C T G C T G T A G C T A G A T C C A T C A G C C C C C

HUM: C G G G G A A G G G A C T G G A G C G A A T C A G G T G C A C A - G G T - C A T G A G G G A G T G C
UAM: C A G G G A A G G G A C G G G A G T G A A A C A G G T G C A C A A - - T A C A T G A G A G A G T G C

HUM: A C A A T C C A A C C C A C T C C T C A A G A G T C C A G T C A C C A T C T C C A G A T C C A C A T
UAM: A C A A T C C A A C C C A C T C C T C A A G A G T C C A G T C G C C A T C T C C A G A T C C A C A T

HUM: C C A A A A A A C A G T T T C T C C T A C A G C T G A G C T A C C T - - - T A A C A A G G A G T A
UAM: C C A A A A A G C T G T T T T T C C T A C A G C T G A G C T A A C T G A G C - A A C - - - G A G T A

HUM: C A C A A C C A T G A - T T T T T A T A C A A A A G A
UAM: C A C A A C C A T G A A T T T T T A C A C A A A A G A

D7
HUM: C A C A G C G
UAM: C A G G G T A

D9
HUM: G A A C A C T C T A C
UAM: G T C A C A A A C C T

Alignment stats: 'M': 246, 'I': 8, 'D': 6, 'X': 17

IGHV3-22

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	A	G	T	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	T	C			
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	A	T	C		
HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	T	A	C	T	A	C	T	A	C	A
UAM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	A	C	T	A	C	T	A	C	A
HUM:	T	G	A	G	C	-	-	-	G	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	-	C	G	G	G	-	A	A	G	G	G	G	C	T	G	G	A	A	T	G	G	G	T	A	G
UAM:	T	G	-	-	C	A	T	T	-	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	-	-	G	G	A	A	A	G	G	G	G	C	T	G	G	A	A	T	G	G	G	T	A	G
HUM:	G	T	T	T	C	A	T	T	A	G	A	A	A	C	A	A	A	G	C	T	A	A	T	G	G	T	G	G	G	A	C	A	A	C	A	G	A	A	T	A	-	G	A	C	C	A	C	G	T	C
UAM:	G	T	T	T	C	A	T	T	A	G	A	A	C	C	A	A	A	G	C	T	A	A	A	G	G	T	G	G	G	A	C	A	A	C	A	G	A	A	T	A	C	G	-	C	C	G	C	G	T	C
HUM:	T	G	T	G	A	A	A	G	G	C	A	G	A	T	T	C	A	C	A	A	T	C	T	C	A	A	G	A	G	A	T	G	A	T	T	C	C	A	A	A	A	G	C	A	T	C	A	C	C	T
UAM:	T	G	T	G	A	A	A	G	G	C	A	G	A	T	T	C	A	C	C	A	T	C	T	C	A	A	G	A	G	A	T	G	A	T	T	C	C	A	A	A	A	G	C	A	T	C	G	C	C	T
HUM:	A	T	C	T	G	C	A	A	A	T	G	A	A	G	A	G	C	C	T	G	A	A	A	A	C	C	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T
UAM:	A	T	C	T	G	C	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	A	A	A	C	C	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T
HUM:	-	-	T	C	C	A	G	A	G	A																																								
UAM:	A	C	T	-	-	A	G	A	G	A																																								
D7																																																		
HUM:	C	A	C	A	G	T	G																																											
UAM:	C	A	C	A	G	T	G																																											
D9																																																		
HUM:	G	A	C	A	C	A	A	A	C	C	T																																							
UAM:	G	A	C	A	C	A	A	A	C	C	T																																							

Alignment stats: 'M': 285, 'I': 8, 'D': 8, 'X': 9

IGHV1-17

GENE ALIGN SEQ

HUM:	C	A	G	G	T	T	C	A	G	C	T	G	T	T	G	C	A	G	C	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	C	G	T	C	C	T	C
UAM:	A	A	G	G	T	T	C	A	G	C	T	G	T	T	G	C	A	G	C	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	T	C	C	T	C
HUM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	C	A	G	G	C	T	T	C	C	A	G	A	T	A	C	A	C	C	T	T	C	A	C	C	A	A	A	T	A	C	T	T	T	A
UAM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	C	A	G	G	C	T	T	C	C	A	G	A	C	A	C	A	C	C	T	T	C	A	C	C	A	A	A	T	A	C	T	T	T	A
HUM:	C	A	C	A	G	T	G	G	G	T	G	C	G	A	C	A	G	G	G	C	C	C	T	G	G	A	C	A	A	G	G	G	C	A	T	A	G	T	G	G	T	T	G	G	G	A	T	G	C	A
UAM:	C	G	C	A	G	T	G	G	G	T	G	C	A	A	C	A	G	G	G	C	C	C	T	G	G	A	C	A	A	G	G	G	C	A	T	A	G	T	G	G	A	T	G	G	G	A	T	G	C	A
HUM:	T	C	A	A	C	C	C	T	T	A	C	A	A	T	G	A	T	A	A	C	A	C	A	C	A	C	T	A	C	G	C	A	C	A	G	A	A	G	T	T	C	C	G	G	G	G	C	A	G	A
UAM:	T	C	A	A	C	C	C	T	T	A	C	A	A	T	G	A	T	A	A	C	A	C	A	C	A	C	T	A	C	G	C	A	C	A	G	A	A	G	T	T	C	C	G	G	G	G	C	A	G	A
HUM:	G	T	C	A	C	C	A	T	T	A	C	C	A	G	T	G	A	C	A	G	G	T	C	C	G	T	G	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G	G	A	G	C	T	G	A	G
UAM:	G	T	C	A	C	C	A	T	T	A	C	C	A	G	T	G	A	C	A	G	G	T	C	C	A	T	G	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G	G	A	G	C	T	G	A	G
HUM:	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	A	G	A	C	A	T	G	G	T	C	G	T	G	T	A	T	T	C	C	T	G	T	G	T	G	A	G	A	G	A					
UAM:	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	A	G	A	C	A	T	G	G	T	C	G	T	G	T	A	T	T	C	C	T	G	T	G	T	G	A	G	A	G	A					

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	G	A	A	A	C	C	C
UAM:	G	T	C	A	G	A	A	A	C	T	C

Alignment stats: 'M': 288, 'I': 0, 'D': 0, 'X': 7

IGHV(III)-16-1

GENE ALIGN SEQ

HUM: G A A G T C C T G T G T G A A A T T T A C T G A T A G A G T C A G - G G G G G A A A A A T T G T A C
UAM: G A A G T C C T G T G T A A A A T T T A T T G A T G G A T T C A G A G G G G G A A A A A T T G T A C

HUM: A G C C C A G T G G T T C A C T G A G A C T C T C A T G C A A A G C C T C T G A T T T C A C C T T T
UAM: A G C C C A G T G G T T C A C T G A G A C T C T C A T G C A A A G C C T C T G A T T T C A C C T T T

HUM: A C T G G C T A C A G C A T G A G C T T G G T C C A G C A G G C T T C A T G A C A G G G A T T G G T
UAM: A C T G G C T A C A G C A T G A G C T T G C T C C A G C C G G C T T C A T G A C A G G G A T T T G T

HUM: G T G G G T G G A A A C A G T G A G T G A T C A A G T G G G A G T T C T C A G A G T T A C T C T C C
UAM: G T G G G T G G A A A C A G T G A G T G A T C A A G T G G G A G T T C T C A G A G T T A C T C T C C

HUM: A T G A G T A C A A A T A A A T T A A C A G T C C C A A G T G A C A C C T T T T C A T G T G C A G T
UAM: A T G A G T A C A A A T A A A T T A A C A G T C C C A A G C G A C A C C T T T T A A T A T G C A G T

HUM: C T A C C T T A A A G G G A C C A A A C T G A A A G T C A A G G A C A A G G C C T T G T A A T A C T
UAM: C T A C C T T A A A G G G A C C A A A C T G A A A G T C A A G G A C A A G G C C T T G T A A T A C T

HUM: G T G A
UAM: G T G A

D7
HUM: G A G A C A C
UAM: G A G A C A C

D9
HUM: G C C C A G A C A G A
UAM: G C C C A G A C A G A

Alignment stats: 'M': 293, 'I': 1, 'D': 0, 'X': 10

IGHV3-16

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	A	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	T	C		
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	G	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	T	C			
HUM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	A	C	A	G	T	G	A	C	A
UAM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	A	C	A	C	T	G	A	C	A
HUM:	T	G	A	A	C	T	G	G	G	C	C	C	G	C	A	A	G	G	C	T	C	C	A	G	G	A	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	A	T	C	-	-	G	G
UAM:	T	G	A	A	C	T	G	G	G	T	C	C	G	C	G	A	G	G	C	T	T	C	A	G	G	A	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	-	-	C	T	T	G	G
HUM:	G	T	G	T	T	A	G	T	T	G	G	A	A	T	G	G	C	A	G	T	A	G	G	A	C	G	C	A	C	T	A	T	G	T	G	G	A	C	T	C	C	G	T	G	A	A	G	C	G	C
UAM:	G	T	A	T	T	A	G	T	T	G	G	A	A	T	G	G	T	G	G	T	A	G	G	A	T	G	C	A	C	T	A	T	G	C	G	G	A	C	T	C	C	G	T	G	A	A	G	G	C	
HUM:	C	G	A	T	T	C	A	T	-	-	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	G	G	A	A	-	C	T	C	C	C	T	G	T	A	T	C	T	G	C	A
UAM:	C	G	A	T	T	-	-	T	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	G	G	A	A	G	C	-	C	C	C	T	G	T	A	T	C	T	G	C	A
HUM:	A	A	A	G	A	A	C	A	G	A	C	G	G	A	G	A	G	C	C	G	A	G	G	A	C	A	T	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	T	G	A	G	A	A
UAM:	A	A	A	G	A	A	C	A	G	A	C	G	G	A	G	A	G	C	C	G	A	G	G	A	C	A	T	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	T	G	A	G	A	A
HUM:	A																																																	
UAM:	A																																																	
D7																																																		
HUM:	T	C	C	T	G	T	G																																											
UAM:	T	C	C	T	G	T	G																																											
D9																																																		
HUM:	G	A	C	A	C	A	A	A	C	C	T																																							
UAM:	G	A	C	A	C	A	A	A	C	C	T																																							

Alignment stats: 'M': 279, 'I': 5, 'D': 5, 'X': 12

IGHV(II)-15-1

GENE ALIGN SEQ

HUM:	G	T	T	C	T	A	G	T	A	A	A	G	C	C	C	T	C	A	G	A	G	A	C	C	C	T	C	T	C	C	T	T	C	A	C	C	T	G	T	G	C	T	G	T	C	T	G	G		
UAM:	G	T	T	C	T	A	G	T	A	A	A	G	C	C	C	T	C	A	G	A	G	A	C	C	C	T	C	T	C	C	T	T	C	A	C	C	T	G	T	G	C	T	G	C	C	T	C	T	G	G
HUM:	A	T	T	T	C	C	A	A	T	C	A	T	A	A	C	C	A	G	T	A	C	T	T	C	C	T	C	C	T	G	G	A	G	C	T	G	T	A	T	C	T	G	C	C	A	G	C	C	C	C
UAM:	A	T	T	T	C	C	G	A	T	C	A	T	A	A	C	C	A	G	T	A	C	T	T	C	C	T	C	C	T	G	G	G	G	C	T	G	G	A	T	C	T	G	C	C	A	G	C	C	T	C
HUM:	C	A	G	G	G	A	A	G	A	A	G	C	T	G	A	A	G	T	G	G	G	T	C	A	G	G	T	G	T	G	T	A	G	G	T	C	A	C	G	A	G	A	A	A	C	A	C	A	C	
UAM:	C	A	G	G	G	A	A	G	A	A	G	C	T	G	A	A	G	T	G	G	G	T	C	A	G	G	T	G	T	G	T	A	G	G	T	C	A	T	G	A	G	A	A	G	C	A	C	A	C	
HUM:	A	G	T	G	C	A	A	C	C	C	G	C	T	T	C	T	C	A	A	G	A	G	T	C	C	A	G	T	C	A	C	C	A	C	C	T	C	C	A	G	A	T	C	C	A	C	A	T	T	C
UAM:	A	G	T	A	C	A	A	C	C	C	G	C	T	T	C	T	C	A	A	G	A	G	T	C	C	A	G	T	C	A	C	C	A	C	C	T	C	C	A	G	A	T	C	C	A	C	A	T	T	C
HUM:	A	G	A	A	A	A	C	A	G	T	T	T	T	T	C	C	T	A	C	A	G	C	T	G	A	G	C	T	A	C	C	-	-	C	G	C	-	A	C	A	A	T	G	A	G	T	A	A	A	C
UAM:	A	G	A	A	A	G	C	A	G	T	T	T	T	T	C	C	T	A	C	A	G	C	T	G	A	G	C	T	A	C	C	T	G	C	G	C	A	A	C	A	A	-	-	-	G	T	A	C	A	C
HUM:	C	A	C	C	A	T	G	G	A	T	T	T	T	T	A	T	A	C	A	A	A	A	G	A																										
UAM:	C	A	C	C	A	T	G	G	A	T	T	T	T	T	A	T	A	C	A	A	A	A	G	A																										

D7

HUM:	C	A	C	A	G	A	A
UAM:	C	A	C	A	G	A	G

D9

HUM:	A	C	A	C	A	A	A	C	C	T	C
UAM:	A	C	A	C	A	A	A	C	C	T	C

Alignment stats: 'M': 257, 'I': 3, 'D': 3, 'X': 11

IGHV3-15

GENE ALIGN SEQ

	GENE REGION SEQ																																																
HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	G	A	G	G	C	T	T	G	G	T	A	A	A	G	C	C	T	G	G	G	G	G	T	C
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	G	A	G	G	C	T	T	G	G	T	C	C	A	G	C	C	T	G	G	G	G	G	T	C

HUM:	C	C	T	T	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	T	T	T	C	A	G	T	A	A	C	G	C	C	T	G	G	A
UAM:	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	T	T	T	C	A	G	T	A	A	C	G	C	C	T	G	G	T

HUM:	T	G	A	G	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	T	G	G	C	C	G	T
UAM:	T	G	A	G	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	T	G	G	C	C	G	T

HUM:	A	T	T	A	A	A	G	C	A	A	A	C	T	G	A	T	G	G	T	G	G	G	A	C	A	A	C	A	G	A	C	T	A	C	G	C	T	G	C	A	C	C	C	G	T	G	A	A	
UAM:	A	T	T	A	A	A	G	C	A	A	A	G	C	T	G	A	T	G	G	T	G	G	G	A	C	A	A	C	A	G	A	C	T	A	C	G	C	T	G	C	A	C	C	T	G	T	G	A	A

HUM:	A	G	G	C	A	G	A	T	T	C	A	C	C	A	T	C	T	C	A	A	G	A	G	A	T	G	A	T	T	C	A	A	A	A	A	C	A	C	G	C	T	G	T	A	T	C	T	G	C
UAM:	A	G	G	C	A	G	A	T	T	C	A	C	C	A	T	C	T	C	A	A	G	A	G	A	T	G	A	T	T	C	A	A	A	A	A	C	A	C	T	T	T	G	T	A	T	C	T	G	C

HUM:	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	A	A	A	C	C	G	A	G	G	A	C	A	C	A	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	-	A	C	C	-	A
UAM:	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	A	A	A	C	C	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	-	-	C	T	A

HUM: C A G A
UAM: C A G A

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 291, 'I': 2, 'D': 2, 'X': 9

IGHV(III)-13-1

GENE ALIGN SEQ

HUM:	C	C	C	T	G	T	G	A	A	G	T	T	A	A	C	T	A	A	T	G	G	A	G	T	C	A	G	A	C	A	G	A	G	A	A	A	T	A	C	T	A	C	A	G	A	C	C	A	G	G
UAM:	C	C	C	T	G	T	G	A	A	G	T	T	A	A	C	T	A	A	T	G	G	A	G	T	C	A	G	A	C	A	G	A	G	A	A	A	T	A	C	T	A	C	A	G	A	C	C	A	G	G
HUM:	A	A	T	T	C	T	G	C	C	T	T	T	T	C	T	G	C	A	A	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	T	T	T	C	A	C	T	G	A	A	A	A	C	A	G	C
UAM:	A	A	T	T	C	T	G	C	C	T	T	T	T	C	T	G	C	A	A	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	T	T	T	C	A	C	T	G	A	A	A	A	C	A	G	C
HUM:	A	T	A	A	G	C	T	T	G	A	T	C	C	A	G	C	A	G	G	C	T	T	C	A	T	G	A	C	A	G	G	G	G	T	G	G	G	T	G	T	G	G	G	T	A	A	T	A	A	C
UAM:	A	T	A	A	G	C	T	T	G	A	T	C	C	A	G	C	A	G	G	C	T	T	C	A	T	G	A	C	A	G	G	G	G	T	G	G	G	T	G	T	G	G	G	T	A	A	T	A	A	C
HUM:	A	A	T	A	A	T	T	C	A	A	A	T	A	G	A	A	G	T	T	C	T	C	A	G	T	G	G	G	A	C	T	C	T	C	C	T	T	G	A	G	T	A	A	A	A	A	G	A	T	G
UAM:	A	A	T	A	A	T	T	C	A	A	A	T	G	G	A	A	G	T	T	C	T	C	A	G	T	G	G	G	A	C	T	C	T	C	C	T	T	C	A	G	T	A	A	A	A	A	G	A	T	G
HUM:	A	T	T	A	A	C	A	A	T	C	C	T	C	A	A	A	T	A	C	A	C	T	C	A	G	T	T	C	A	G	G	A	G	A	T	T	C	T	C	T	T	T	T	A	A	G	A	T	G	A
UAM:	A	A	T	A	A	C	A	A	T	C	C	T	C	A	A	A	T	A	C	A	C	T	C	A	G	T	T	C	A	G	G	A	G	A	T	T	C	T	C	T	T	T	T	A	A	G	A	T	G	A
HUM:	T	T	A	A	C	C	T	G	A	G	A	G	C	T	C	A	G	G	A	A	A	A	G	T	C	C	G	T	G	T	A	T	T	A	C	T	T	T	G	A	G	G	G	A						
UAM:	T	T	A	A	C	C	T	G	A	A	A	G	C	T	C	A	G	G	A	A	A	A	G	T	C	C	G	T	G	T	A	T	T	A	C	T	T	T	G	A	G	G	G	A						

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	C	A	A	C	C	T
UAM:	G	A	C	A	C	C	A	A	C	C	T

Alignment stats: 'M': 290, 'I': 0, 'D': 0, 'X': 4

IGHV3-13

GENE ALIGN SEQ

HUM: G A G G T G C A G C T G G T G G A G T C T G G G G G A G G C T T G G T A C A G C C T G G G G G T C
UAM: G A G G T G C A G C T G G T G G A G T C T G G G G G A G G C T T G G T A C A G C C T G G G G G T C

HUM: C C T G A G A C T C C T G T G C A G C C T C T G G A T T C A C C T - T C A G T A G C T A C G A C
UAM: C C T G A G A C T C C T G T G C A G C C T C T G G A T T C A C - T G T C A G T A G C T A C G A C

HUM: A T G C A C T G G G T C C G C C A A G C T A C A G G A A A A G G T C T G G A G T G G G T C T C A G C
UAM: A T G C A C T G G G T T C G C C A A G C T C C A G G A A A A G G T C T G G A G T G G G T C T C A G C

HUM: T A T T G G T A C T G C T G G T G A C C C A T A C T A T C C A G G C T C C G T G A A G G G C C G A T
UAM: T A T T G A T A C T G A T G G T G A C A C A T A C T A T G C A G A C T C T G T G A A G G G C T G A T

HUM: T C A C C A T C T C C A G A G A A A A T G C C A A G A A C T C C T T G T A T C T T C A A A T G A A C
UAM: T C A C C A T C T C C A G A G A A A A T G C C A A G A A C T C T T T G T A T C T T C A A A T G A A C

HUM: A G C C T G A G A G C C G G G G A C A C G G C T G T G T A T T A C T G T G C A A G A G A
UAM: A G C C T G A G A G C C A A G G A C A C G G C T G T G T A T T A C T G T G C A A G A G A

D7

HUM: C A C A G T G
UAM: C A C A G T G

D9

HUM: G A C A C A A A C C T
UAM: G A C A C A A A C C T

Alignment stats: 'M': 279, 'I': 1, 'D': 1, 'X': 13

IGHV1-12

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	A	T	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C
UAM:	C	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	A	T	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	T	C	C	T	C
HUM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	A	T	A	C	A	C	C	T	T	C	A	C	C	T	A	C	T	G	C	T	A	C	T
UAM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	A	T	A	C	A	C	C	T	T	C	A	C	C	T	A	C	T	G	C	T	A	C	T
HUM:	T	G	C	A	C	T	G	G	G	T	A	T	G	A	C	A	G	G	C	C	C	C	T	G	G	A	C	A	A	G	G	G	C	T	T	G	A	A	T	G	G	A	C	A	G	G	A	T	T	T
UAM:	T	G	C	A	C	T	G	G	G	T	G	C	G	A	C	A	G	G	T	C	C	C	T	G	G	A	C	A	A	G	G	A	C	T	T	G	A	G	T	G	G	A	C	A	G	G	A	T	T	T
HUM:	T	A	G	T	T	A	T	T	T	G	A	G	A	G	A	T	T	T	T	T	C	A	T	A	C	A	A	C	A	T	T	T	A	T	T	C	T	G	T	A	A	G	C	A	A	A	T	T	T	C
UAM:	T	A	G	T	T	A	T	T	T	G	A	G	A	G	A	T	T	T	T	T	C	A	T	A	C	A	A	C	A	T	T	T	A	T	T	C	T	G	T	A	A	G	C	A	A	A	T	T	T	C
HUM:	A	G	G	G	A	T	T	G	T	A	G	A	A	T	G	A	A	T	C	A	T	-	-	A	T	T	A	A	C	A	A	A	T	C	T	G	A	C	A	C	A	G	A	A	C	T	T	C	C	T
UAM:	A	G	G	G	A	T	T	G	T	A	G	A	A	T	G	A	A	T	-	-	T	A	C	A	T	T	A	A	C	A	A	A	T	C	T	G	A	T	A	C	A	G	A	A	C	T	T	C	C	T
HUM:	C	T	G	A	A	T	C	A	A	T	C	T	T	T	G	T	A	A	A	C	A	T	C	A	A	T	T	T	C	T	G	A	A	T	C	A	A	T	G	T	T	G	T	A	A	A	T	A		
UAM:	C	T	G	A	A	T	C	A	A	T	C	T	T	T	G	T	A	A	A	C	A	T	C	A	A	T	T	T	C	T	G	A	A	T	C	A	A	T	G	T	T	G	T	A	A	A	T	A		

D7

HUM:	T	T	T	C	A	G	A
UAM:	T	T	T	C	A	G	A

D9

HUM:	T	A	A	C	T	C	T	A	C	T	T
UAM:	T	A	A	C	T	C	T	A	C	T	T

Alignment stats: 'M': 287, 'I': 2, 'D': 2, 'X': 7

IGHV3-11

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	C	A	-	A	G	C	C	T	G	G	A	G	G	G	T	
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	-	A	C	A	G	C	C	T	G	G	G	G	G	T		
HUM:	C	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	-	G	A	C	T	A	C	-	-
UAM:	C	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	A	T	C	A	C	C	T	T	C	A	G	T	A	-	-	-	-	A	C	C	A
HUM:	-	T	A	C	A	T	G	A	G	C	T	G	G	A	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	T	T
UAM:	A	T	A	C	A	T	G	A	G	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	A	C	A	G	G	G	A	A	G	G	G	A	C	T	G	G	A	G	T	G	G	G	T	T	T
HUM:	C	A	T	A	C	A	T	T	A	G	T	A	G	T	A	G	-	T	A	G	T	A	G	T	T	A	C	A	C	A	A	A	C	T	A	C	G	C	A	G	A	C	T	C	T	G	T	G	A	A
UAM:	C	A	T	A	C	A	T	T	A	G	T	G	G	T	-	G	A	T	A	G	T	A	G	T	T	A	C	A	C	A	A	G	C	T	A	C	G	C	A	G	A	C	T	C	T	G	T	G	A	A
HUM:	G	G	G	C	C	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	C	G	C	C	A	A	G	A	A	C	T	C	A	C	T	G	T	A	T	C	T	G	C
UAM:	G	G	G	C	C	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	G	A	C	A	A	C	G	C	C	A	A	G	A	A	C	T	C	A	C	T	G	T	A	T	C	T	G	C	
HUM:	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	G	A	G	C	C	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	-	-	-	-	-
UAM:	A	A	A	T	G	A	A	C	A	G	C	C	T	G	A	G	A	G	T	C	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	T	G	A	A	A
HUM:	C	G	A	G	A	G	A																																											
UAM:	C	-	-	-	-	-	A																																											

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 275, 'I': 11, 'D': 11, 'X': 10

IGHV5-10-1

GENE ALIGN SEQ

HUM:	G	A	A	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	C	G	G	A	G	C	C	C	G	G	G	A	G	T	C																
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	A	G	C	A	G	A	G	G	T	G	A	A	A	A	G	G	C	C	C	G	G	G	G	A	G	T	C	
HUM:	T	C	T	G	A	G	G	A	T	C	T	C	C	T	G	T	A	A	G	G	G	T	T	C	T	G	G	A	T	A	C	A	G	C	T	T	T	A	C	C	A	G	C	T	A	C	T	G	G	A	
UAM:	T	C	T	G	A	G	G	A	T	C	T	C	C	T	G	T	A	A	G	G	G	T	T	C	T	G	G	A	T	A	C	A	G	C	T	T	T	A	C	C	A	G	C	T	A	C	T	G	G	A	
HUM:	T	C	A	G	C	T	G	G	G	T	G	C	G	C	C	A	G	A	T	G	C	C	C	G	G	G	A	A	A	G	G	C	C	T	G	G	A	G	T	-	-	-	-	-	G	G	A	T	-		
UAM:	T	A	A	G	C	T	G	G	G	T	G	C	G	C	C	A	G	A	T	G	C	C	T	G	G	G	A	A	A	G	G	C	T	T	G	G	A	G	T	T	G	A	T	G	C	G	G	A	T	A	
HUM:	G	G	G	G	A	G	G	A	T	T	G	A	T	C	C	T	A	G	T	G	A	C	T	C	T	T	-	-	-	A	T	A	C	C	A	-	A	C	T	A	C	A	G	C	C	C	G	T	C	C	
UAM:	-	-	-	-	-	-	-	A	T	T	G	A	T	C	C	T	A	G	T	G	A	-	-	-	T	T	C	C	G	A	T	A	C	C	A	G	A	-	T	A	C	A	G	C	C	C	A	T	C	C	
HUM:	T	T	C	C	A	A	G	G	C	C	A	C	G	T	C	A	C	C	A	T	C	T	C	A	G	C	T	G	A	C	A	A	G	T	C	C	A	T	C	A	G	C	A	C	T	G	C	C	T	A	
UAM:	T	T	C	C	A	A	G	G	C	C	A	C	A	T	C	A	C	C	A	T	C	T	C	A	G	C	C	G	A	C	A	A	G	T	C	C	A	T	C	A	G	C	A	C	C	G	C	C	T	A	
HUM:	C	C	T	G	C	A	G	T	G	G	A	G	C	A	G	C	C	T	G	A	A	G	G	C	C	T	C	G	G	A	C	A	C	C	G	C	C	A	T	G	T	A	T	T	A	C	T	G	T	G	
UAM:	C	C	T	G	C	A	G	T	G	G	A	C	C	A	G	C	C	T	G	A	A	G	G	C	C	T	C	G	G	A	C	A	C	C	G	C	C	A	T	G	T	A	T	T	A	C	T	G	T	G	
HUM:	C	G	A	G	A	C	A																																												
UAM:	C	G	A	G	-	-	A																																												
D7																																																			
HUM:	C	A	C	A	G	T	G																																												
UAM:	C	A	C	A	G	T	G																																												
D9																																																			
HUM:	T	C	T	A	A	A	A	C	C	C	T																																								
UAM:	T	C	A	A	A	A	A	C	C	C	T																																								

Alignment stats: 'M': 272, 'I': 11, 'D': 13, 'X': 11

IGHV3-64D

GENE ALIGN SEQ

HUM:	A	T	G	G	A	G	T	T	C	T	G	G	C	T	G	A	G	C	T	G	G	G	T	T	C	T	C	C	T	T	G	T	T	G	C	C	A	T	T	T	T	A	A	A	A	G	G	T	A	A
UAM:	A	T	G	G	A	G	T	T	C	G	G	G	C	T	G	A	G	C	T	G	G	G	T	T	C	T	C	C	T	T	G	T	T	G	C	C	A	T	T	T	T	A	A	A	A	G	G	T	A	A
HUM:	T	T	C	A	T	G	G	A	G	A	A	C	T	A	G	A	G	A	T	A	G	T	G	T	G	A	G	T	G	G	A	C	G	T	G	A	G	T	G	A	G	A	G	A	A	A	C	A	G	T
UAM:	T	T	C	A	T	G	G	A	G	A	A	C	T	A	G	A	G	A	T	A	G	T	G	T	G	A	G	G	G	A	T	G	T	G	A	G	T	G	A	G	A	G	A	A	A	C	A	G	T	
HUM:	G	G	A	T	A	T	G	T	G	T	G	G	C	A	G	T	T	T	C	T	G	A	C	C	T	T	G	G	T	G	T	C	T	C	T	T	T	G	T	T	T	G	C	A	G	A	T	G	T	C
UAM:	G	G	A	T	A	T	G	T	G	T	G	G	C	A	G	T	T	T	C	T	G	A	C	C	T	T	G	G	T	G	T	C	T	C	T	T	T	G	T	T	T	G	C	A	G	A	T	G	T	C
HUM:	C	A	G	T	G	T	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	C	C	A	G	C	C	T	G	G	
UAM:	C	A	G	T	G	T	G	A	G	G	T	G	C	A	G	C	T	T	G	T	G	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	
HUM:	G	G	G	G	T	C	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	T	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	C	T
UAM:	G	G	G	G	T	C	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	C	T
HUM:	A	T	G	C	T	A	T	G	C	A	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	A	C	T	G	G	A	A	T	A	T	G	T	T		
UAM:	A	T	G	C	T	A	T	G	C	A	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	A	C	T	G	G	A	A	T	G	G	G	T	A		
HUM:	T	C	A	G	C	T	A	T	T	A	G	T	A	G	T	A	A	T	G	G	G	G	G	T	A	G	C	A	C	A	T	A	C	T	A	C	G	C	A	G	A	C	T	C	C	G	T	G	A	A
UAM:	T	C	A	G	C	T	A	T	T	A	A	T	A	G	T	G	G	T	G	G	G	G	G	T	A	G	C	A	C	A	T	A	C	T	A	T	G	C	A	G	A	C	T	C	C	G	T	G	A	A
HUM:	G	G	G	C	A	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	T	T	C	C	A	A	G	A	A	C	A	C	G	C	T	G	T	A	T	C	T	T	C
UAM:	G	G	G	C	A	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	A	A	A	T	G	C	C	A	A	G	A	A	C	A	C	A	C	T	G	T	A	T	C	T	T	C
HUM:	A	A	A	T	G	A	G	C	A	G	T	C	T	G	A	G	A	G	C	T	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	T	G	A	A	A
UAM:	A	A	A	T	G	A	G	C	A	G	T	C	T	G	A	G	A	G	C	T	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	C	A	A	A	A
HUM:	G	A																																																
UAM:	G	A																																																

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	T	A	C	A	G	A	A	A	C	C	T

Alignment stats: 'M': 433, 'I': 0, 'D': 0, 'X': 19

IGHV3-7

GENE ALIGN SEQ

HUM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	-	G	A	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	C	C	A	G	C	C	T	G	G	G	G	G	T		
UAM:	G	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	G	-	G	T	C	T	G	G	G	G	A	G	G	C	T	T	G	G	T	A	C	A	G	C	C	T	G	G	G	G	G	T		
HUM:	C	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	T	A	G	T	A	G	C	T	A	T	T	G	G
UAM:	C	C	C	T	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	T	A	G	T	A	G	C	T	A	C	T	G	G
HUM:	A	T	G	A	G	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	G	G	G	G	C	T	G	G	A	G	T	G	G	G	T	G	G	C	C	A	A	
UAM:	A	T	G	A	G	C	T	G	G	G	T	C	C	G	C	C	A	G	G	C	T	C	C	A	G	G	A	A	A	G	G	G	C	T	G	G	A	G	T	G	G	G	T	G	G	C	C	A	A	
HUM:	C	A	T	A	A	A	G	C	A	A	G	A	T	G	G	A	A	G	T	G	A	G	A	A	A	T	A	C	T	A	T	G	T	G	G	A	C	T	C	T	G	T	G	A	A	G	G	G	C	C
UAM:	C	A	T	A	A	A	G	C	A	A	G	A	T	G	G	A	A	G	T	G	A	G	A	A	A	T	A	C	T	A	T	G	T	A	G	A	C	T	C	T	G	T	G	A	A	G	G	G	C	C
HUM:	G	A	T	T	C	A	C	C	A	T	C	T	C	C	A	G	A	G	A	C	A	A	C	G	C	C	A	A	G	A	A	C	T	C	A	C	T	G	T	A	T	C	T	G	C	A	A	A	T	G
UAM:	G	A	T	T	C	A	C	T	A	T	C	T	C	C	G	G	A	G	A	C	A	G	C	G	C	C	A	A	G	A	A	C	T	C	G	C	T	G	T	A	T	C	T	G	C	A	A	A	T	G
HUM:	A	A	C	A	G	C	C	T	G	A	G	A	G	C	C	G	A	G	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	-	-	-	G	A	G	A	G	A
UAM:	A	A	C	A	G	C	C	T	G	A	G	A	G	C	C	T	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	-	-	-	C	T	A	T	G	A	G	A	G	A

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	C	C	T
UAM:	G	A	C	A	C	A	A	A	C	C	T

Alignment stats: 'M': 282, 'I': 4, 'D': 4, 'X': 10

IGHV3-6

GENE ALIGN SEQ

HUM:	G	A	G	A	T	G	C	A	G	C	T	G	G	T	A	G	A	G	T	C	T	G	G	A	G	C	A	A	A	C	T	T	G	A	C	A	A	A	G	C	C	T	G	G	G	T	G	T	C	C		
UAM:	G	A	G	A	T	G	C	A	G	C	T	G	G	T	A	G	A	G	T	C	T	G	G	A	G	G	A	A	A	C	T	T	G	A	C	A	A	A	G	C	C	T	G	G	G	T	G	T	C	T		
HUM:	C	A	G	A	G	A	C	T	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	G	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	C	C	A	T	A	G	C	A	C		
UAM:	C	T	G	A	G	A	C	G	C	T	C	C	T	G	T	G	C	A	G	C	C	T	C	T	G	T	A	T	T	C	A	C	C	T	T	C	A	G	T	A	G	C	C	A	T	A	G	C	A	C		
HUM:	G	C	A	C	T	G	G	G	T	C	C	C	C	C	A	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	T	C	T	G	C	A	G	T	G	G	G	T	C	C	C	A	G	T	T	A		
UAM:	G	C	A	C	T	G	G	T	T	C	C	C	C	C	A	G	G	C	T	C	C	A	G	G	G	A	A	G	G	G	T	C	T	G	C	A	G	T	G	G	G	T	C	T	C	A	G	T	T	A		
HUM:	T	T	A	G	T	G	G	T	A	G	T	G	G	T	-	A	G	T	A	C	C	A	T	G	T	A	-	-	C	T	A	C	G	C	A	G	A	C	T	C	T	G	T	G	A	A	G	G	G	C		
UAM:	T	T	A	G	T	A	G	T	A	G	T	G	G	T	T	A	-	T	A	C	C	A	T	-	-	A	T	T	C	T	A	C	G	C	A	G	A	C	T	C	T	G	T	G	A	A	G	G	G	C		
HUM:	C	G	A	T	T	C	A	C	C	A	T	T	T	C	C	A	G	A	G	A	C	A	A	T	A	C	G	A	A	A	A	A	C	T	C	A	C	T	G	T	A	T	C	T	G	C	A	A	A	T		
UAM:	T	G	A	T	T	C	A	C	C	A	T	T	T	C	C	A	G	A	G	A	C	A	A	T	A	C	C	A	A	A	A	A	C	T	C	A	C	A	G	T	A	T	C	T	G	C	A	A	A	T		
HUM:	G	A	A	C	A	G	-	-	-	-	-	-	-	-	-	A	C	T	G	A	G	G	G	C	A	G	A	G	G	A	T	G	C	A	G	C	T	G	C	A	T	A	T	G	A	C	T	C	T	G		
UAM:	G	A	A	C	A	G	C	C	T	G	A	G	A	G	C	-	C	T	G	A	G	G	A	C	-	-	-	-	-	A	T	G	-	-	G	C	T	G	T	G	T	A	T	T	A	C	T	C	T	G		
HUM:	T	G	A	G	A	G	A																																													
UAM:	T	G	A	G	A	G	A																																													
D7																																																				
HUM:	T	A	C	G	G	T	A																																													
UAM:	C	A	T	G	G	T	A																																													
D9																																																				
HUM:	G	A	C	A	C	A	A	A	C	C	T																																									
UAM:	A	C	A	A	A	C	C	T	C	C	C																																									

Alignment stats: 'M': 269, 'I': 12, 'D': 11, 'X': 15

IGHV(III)-5-1

GENE ALIGN SEQ

HUM: G A T T T A T C A T C T C A A G A G A C A A T G T C A A G A A G A T G C T G T T T C T G C A A A T G
UAM: G A T T T A T C A T C T C A A G A G A C A A T G T C A A G A A G A T G C T G T T T C T G C A A A T G

HUM: G G C A A T C T G C A A A C C A A G G A C A C G T C A C T A C A T T A C T G T G C A A G A G A A G
UAM: G G C A A T C T G C A A A C C A A G G A C A C G T C A C T A T A T T A C T G T G C A A G A G A A G

D7
HUM: C A C A T G A
UAM: C G C A T G A

D9
HUM: A A C C T C C A G G A
UAM: A A A C T C C A G G G

Alignment stats: 'M': 98, 'I': 0, 'D': 0, 'X': 1

IGHV2-5

GENE ALIGN SEQ

HUM:	C	A	G	A	T	C	A	C	C	T	T	G	A	A	G	G	A	G	T	C	T	G	G	T	C	C	T	A	C	G	C	T	G	G	T	G	A	A	A	C	C	C	A	C	A	C	A	G	A	C	
UAM:	C	A	G	G	T	C	A	C	C	T	T	G	A	A	G	G	A	G	T	C	T	G	G	T	C	C	T	G	C	G	C	T	G	G	T	G	A	A	A	C	C	C	A	C	A	C	A	G	A	C	
HUM:	C	C	T	C	A	C	G	C	T	G	A	C	C	T	G	C	A	C	C	T	T	C	T	C	T	G	G	G	T	T	C	T	C	A	C	T	C	A	G	C	A	C	T	A	G	T	G	G	A	C	
UAM:	C	C	T	C	A	C	G	C	T	G	A	C	C	T	G	C	A	C	C	T	T	C	T	C	T	G	G	G	T	T	C	T	C	A	C	T	C	A	G	C	A	C	T	A	G	T	G	G	A	A	
HUM:	T	G	G	G	T	G	T	G	G	G	C	T	G	G	A	T	C	C	G	T	C	A	G	C	C	C	C	C	A	-	G	G	A	A	A	G	G	C	C	C	T	G	G	A	G	T	G	G	C	T	
UAM:	T	G	G	G	T	G	T	G	G	G	C	T	G	G	A	T	C	C	G	T	C	A	G	C	C	C	C	C	A	A	G	G	-	A	A	A	G	G	C	C	C	T	G	G	A	G	T	G	G	C	T
HUM:	T	G	C	A	C	T	C	A	T	T	T	A	T	T	G	G	G	A	T	G	A	T	G	A	T	A	A	G	C	G	C	T	A	C	A	G	C	C	C	A	T	C	T	C	T	G	A	A	G	A	
UAM:	T	G	C	A	G	T	C	A	T	T	T	A	T	T	G	G	G	A	T	G	A	T	G	A	T	A	A	G	C	G	C	T	A	C	A	G	C	C	C	A	T	C	T	C	T	G	A	A	G	A	
HUM:	G	C	A	G	G	C	T	C	A	C	C	A	T	C	A	C	C	A	A	G	G	A	C	A	C	C	T	C	C	A	A	A	A	A	C	C	A	G	G	T	G	G	T	C	C	T	T	A	C	A	
UAM:	G	C	A	G	A	C	T	C	A	C	C	A	T	C	T	C	C	A	A	G	G	A	C	A	C	C	T	C	C	A	A	A	A	A	C	C	A	G	G	T	G	G	T	C	C	T	T	A	C	A	
HUM:	A	T	G	A	C	C	A	A	C	A	T	G	G	A	C	C	C	T	G	T	G	G	A	C	A	C	A	G	C	C	A	C	A	T	A	T	T	A	C	T	G	T	G	C	A	C	A	C	A	G	
UAM:	A	T	G	A	C	C	A	A	C	A	T	G	G	A	C	C	C	T	G	T	G	G	A	C	A	C	A	G	C	C	A	C	A	T	A	T	T	A	C	T	G	T	G	C	A	C	G	G	A	G	
HUM:	A	C																																																	
UAM:	A	C																																																	

D7

HUM:	C	A	C	A	A	A	G
UAM:	C	A	C	A	G	A	G

D9

HUM:	T	A	C	A	A	A	A	A	C	C	C
UAM:	T	A	C	A	A	G	A	A	C	C	C

Alignment stats: 'M': 292, 'I': 1, 'D': 1, 'X': 8

IGHV4-4

GENE ALIGN SEQ

HUM: C A G G T G C A G C T G C A G G A G T C G G G C C C A G G A C T G G T G A A G C C T T - C G G G - G
UAM: C A G G T G C A G C T G C A G G A G T C G G G C C C A G G A C T G G T G A A G C C T T T - - G G A G

HUM: A C C C T G T C C C T C A C C T G C G C T G T C T C T G G T G G C T C C A T C A G C A G T A G T A A
UAM: A C C C T G T C C C T C A C C T G C G C T G T C T C T G G T G G C T C C A T C A G C A G T A G T A A

HUM: C T G G T G G A G T T G G G T C C G C C A G C C C C C A G G G A A G G G G C T G G A G T G G A T T G
UAM: C T G G T G G A G C T G G G T C C G C C A G C C C C C A G G G A A G G G C C T G G A G T G G A T T G

HUM: G G G A A A T C T A T C A T A G T G G G A G C A C C A A C T A C A A C C C G T C C C T C A A G A G T
UAM: G G G A A A T C T A T C A A A G T G G G A G C A C C A A C T A C A A C C C G T C C C T C A A G A G T

HUM: C G A G T C A C C A T A T C A G T A G A C A A G T C C A A G A A C C A A G T T C T C C C T G A A G C T
UAM: C G A G T C A C C A T A T C A G T A G A C A C G T C C A A G A A C C A A G T T C T C C C T G A A G C T

HUM: G A G C T C T G T G A C C G C C G C G G A C A C G G C C G T G T A T T A C T G T G C G A G A G A
UAM: G A G C T C T G T G A C C G C C G C G G A C A C G G C C G T G T A T T A C T G T G C G A G A G A

D7

HUM: C A C A G T G
UAM: C A C A G T G

D9

HUM: G A C A C A A A C C T
UAM: G T C A C A A A C C T

Alignment stats: 'M': 290, 'I': 2, 'D': 2, 'X': 4

IGHV1-3

GENE ALIGN SEQ

HUM:	C	A	G	G	T	C	C	A	G	C	T	T	G	T	G	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C	
UAM:	C	A	G	G	T	C	C	A	G	C	T	C	G	T	G	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C
HUM:	A	G	T	G	A	A	G	G	T	T	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	A	T	A	-	-	-	-	-	-	C	A	C	C	-	T	T	C	A	C	T	A	G	C
UAM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	A	T	A	T	A	C	C	T	T	C	A	C	C	G	-	-	-	A	C	T	A	-	C
HUM:	T	-	A	T	G	C	T	A	T	G	C	A	T	T	G	G	G	T	G	C	G	C	C	C	A	G	G	C	C	C	C	G	G	A	C	A	A	A	G	G	C	T	T	G	A	G	T	G	G	A
UAM:	T	T	-	-	-	-	T	A	T	G	C	A	C	T	G	G	A	T	G	C	T	C	C	A	G	G	C	C	C	C	T	G	G	A	C	A	A	A	G	G	C	T	T	G	A	G	T	G	G	A
HUM:	T	G	G	G	A	T	G	G	A	T	C	A	A	C	G	C	T	G	G	C	A	A	T	G	G	T	A	A	C	A	C	A	A	A	A	T	A	T	T	C	A	C	A	G	A	A	G	T	T	C
UAM:	T	G	G	G	A	T	G	G	A	T	C	A	G	C	G	C	T	G	G	C	A	A	T	G	G	T	A	A	C	A	C	A	A	A	A	T	A	T	T	C	A	C	A	G	A	A	G	T	T	C
HUM:	C	A	G	G	G	C	A	G	A	G	T	C	A	C	C	A	T	T	A	C	C	A	G	G	G	A	C	A	C	A	T	C	C	G	C	G	A	G	C	A	C	A	G	C	C	T	A	C	A	T
UAM:	C	A	G	G	G	C	A	G	A	G	T	C	A	C	C	A	T	T	A	C	C	A	G	A	G	A	C	A	C	G	T	C	C	G	C	G	A	G	C	A	C	A	G	C	C	T	A	C	A	T
HUM:	G	G	A	G	C	T	G	A	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	A	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A
UAM:	G	G	A	G	C	T	G	A	G	C	A	G	C	C	T	G	A	G	A	T	C	T	G	A	G	G	A	C	A	C	G	G	C	T	G	T	G	T	A	T	T	A	C	T	G	T	G	T	G	A
HUM:	G	A	G	A																																														
UAM:	G	A	G	A																																														

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	G	A	A	A	C	C	C
UAM:	G	T	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 277, 'I': 8, 'D': 8, 'X': 11

IGHV(III)-2-1

GENE ALIGN SEQ

HUM:	G	A	A	G	T	T	T	A	C	T	G	A	T	G	G	A	G	T	C	A	G	A	G	G	G	G	A	A	A	A	T	T	T	T	A	C	A	G	C	C	C	A	G	T	G	G	-	T		
UAM:	G	A	A	G	T	T	T	A	C	T	G	A	T	G	G	A	G	T	C	A	G	A	G	G	G	A	G	A	A	A	A	T	T	T	T	A	C	A	G	C	C	T	A	G	C	G	G	T	T	
HUM:	G	A	G	A	C	T	C	T	C	C	T	G	C	A	A	A	G	C	C	T	C	T	G	G	T	T	T	C	A	C	C	T	T	T	A	C	T	G	G	T	T	A	C	A	G	C	A	T	G	A
UAM:	G	A	G	A	C	T	C	T	C	C	C	G	C	A	A	A	G	C	C	T	C	T	G	G	T	T	T	C	A	C	C	T	T	T	A	C	T	G	G	C	T	A	C	C	G	C	A	T	G	A
HUM:	G	C	T	T	G	G	T	C	C	A	G	C	A	T	G	C	T	T	C	A	C	A	A	C	A	G	G	G	A	T	A	G	G	T	G	T	G	G	G	T	G	C	C	A	A	C	A	G	T	G
UAM:	G	C	T	T	G	G	T	C	C	A	G	C	A	T	G	C	T	T	C	A	C	A	A	C	A	G	G	G	A	T	A	G	G	T	G	T	G	G	G	T	G	C	C	A	A	C	A	G	T	G
HUM:	A	G	T	G	A	T	C	A	A	G	T	A	T	G	A	A	T	T	C	T	C	A	G	G	G	T	T	A	C	T	C	T	C	C	A	T	G	A	G	T	A	C	A	A	A	T	A	A	A	T
UAM:	A	G	T	G	A	T	C	A	A	G	T	A	T	G	A	A	T	T	C	T	C	A	G	G	G	T	T	A	C	T	C	T	C	C	A	T	G	A	G	T	A	C	A	A	A	T	A	A	A	T
HUM:	T	A	A	C	A	A	T	C	T	C	A	A	G	C	A	A	C	A	C	C	C	T	T	T	T	A	A	G	T	G	C	A	G	T	C	T	G	C	C	T	T	A	C	A	A	T	G	A	C	C
UAM:	T	A	A	C	A	A	T	C	T	C	A	A	G	C	A	A	C	A	C	C	C	T	T	T	C	A	A	G	T	G	C	A	G	T	C	T	G	C	C	T	T	A	C	A	A	T	G	A	C	C
HUM:	A	A	T	C	T	G	A	A	A	G	C	C	A	A	G	G	A	C	A	A	G	G	T	C	A	T	G	T	A	T	T	A	C	T	G	T	G	A	G	T	G	A								
UAM:	A	A	T	C	T	G	A	A	A	G	C	C	A	A	G	G	A	C	A	A	G	G	C	C	A	T	G	T	A	T	T	A	C	-	-	T	G	A	G	T	G	A								

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	A	C	A	C	A	A	A	G	C	T
UAM:	G	A	C	A	C	A	A	A	G	C	T

Alignment stats: 'M': 281, 'I': 1, 'D': 2, 'X': 8

IGHV1-2

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	G	C	C	T	C	
UAM:	C	A	G	G	T	C	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	A	C	C	T	G	G	G	A	C	C	T	C
HUM:	A	G	T	G	A	A	G	G	T	C	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	A	T	A	C	A	C	C	T	T	C	A	C	C	G	G	C	T	A	C	T	A	T	A
UAM:	A	G	T	G	A	A	G	A	T	C	T	C	C	T	G	C	A	A	G	G	C	T	T	C	T	G	G	T	T	A	C	A	C	C	T	T	C	A	C	C	A	G	C	T	A	C	T	A	T	A
HUM:	T	G	C	A	C	T	G	G	G	T	G	C	G	A	C	A	G	G	C	C	C	C	T	G	G	A	C	A	A	G	G	G	C	T	T	G	A	G	T	G	G	A	T	G	G	G	A	T	-	-
UAM:	T	G	C	A	C	T	G	G	G	T	G	C	G	A	C	A	G	G	C	C	C	C	T	G	G	A	C	A	G	G	G	G	C	T	T	G	A	G	T	G	G	A	T	-	-	-	-	T	G	G
HUM:	-	-	G	G	A	T	C	A	A	C	C	C	T	A	A	C	A	G	T	G	G	T	G	G	C	A	C	A	A	A	C	T	A	T	G	C	A	C	A	G	A	A	G	T	T	T	C	A	G	G
UAM:	A	C	G	G	A	T	C	A	A	C	C	C	T	A	A	C	A	G	T	G	G	T	A	A	C	A	C	A	A	A	C	T	A	C	G	C	A	C	A	G	A	A	G	T	T	T	C	A	G	G
HUM:	G	C	-	T	G	G	-	G	T	C	A	C	C	A	T	G	A	C	C	A	G	G	G	A	C	A	C	G	T	C	C	A	T	C	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G	G
UAM:	G	C	A	-	-	G	A	G	T	C	G	C	C	A	T	G	A	C	C	A	G	G	G	A	C	A	C	G	T	C	C	A	T	C	A	G	C	A	C	A	G	C	C	T	A	C	A	T	G	G
HUM:	A	G	C	T	G	A	G	C	A	G	G	C	T	G	A	G	A	T	C	T	G	A	C	G	A	C	A	C	G	G	C	C	G	T	G	T	A	T	T	A	C	T	G	T	G	C	G	A	G	A
UAM:	A	G	C	T	G	A	G	A	A	G	C	C	T	G	A	G	A	T	C	T	G	A	G	G	A	C	A	C	A	G	C	C	A	C	C	T	A	T	T	A	C	T	G	T	G	-	G	A	G	A
HUM:	G	A																																																
UAM:	G	A																																																

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	T	C	A	G	A	A	A	C	C	C
UAM:	G	T	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 271, 'I': 6, 'D': 7, 'X': 18

IGHV(II)-1-1

GENE ALIGN SEQ

HUM: C T G G G C C T G G A C C C A G C A G C C C T C T G G G A A G G C G C T G G G G C A C C T C A G C T
UAM: C T G G G C C T G G A C C C A G C A G C A C T C T G G G A A G G C G C T G G G G C A C C T C A G C T

HUM: C C A G G G G C A G C A C A C A C T T C A G C C C A G C C T T T C T G G G C C A A C T C T C C A T C
UAM: C C A G G G G C A G C A C A C A C T T C A G C C C A - C C C T T C T G G G C C A A C T G T C C A T C

HUM: T G T A G A G A C A C A T C C A A G G C C C A G T T A T C C C T G C A G C T G A G C T C C G T G A T
UAM: T G C A G A G A C A C A T C C A A G G C C C A G T T A T C T C T G C A G C T G A G C T C C G T G A C

HUM: G G C C A A G G G C A G G G C C G C A C A T T C C C G T G G G A
UAM: G G C C A C G G G C A G G G C C A C A C A T T C C C A T G G A A

D7
HUM: G A C A G A A
UAM: G A C A G C A

D9
HUM: G A C A C A A A C C T
UAM: G A C A C A A A T C T

Alignment stats: 'M': 171, 'I': 0, 'D': 1, 'X': 10

IGHD1-1

U9
HUM: C A G A T T C T G A A
UAM: C A G A T T C T G A A

U7
HUM: C A C G G T G
UAM: C A C A G T G

GENE ALIGN SEQ
HUM: G G T A C A A C T G G A A C G A C
UAM: G G T A T A A C T G G A A T G A C

D7
HUM: C A C C G T G
UAM: C A C T G T G

D9
HUM: G T C C A A A A C T C
UAM: G T C C A A A A C T G

Alignment stats: 'M': 15, 'I': 0, 'D': 0, 'X': 2

IGHD3-3

U9
HUM: A G G T T T G G G G T
UAM: A G G T T T G G G G T

U7
HUM: C A C T G T G
UAM: C A C T G T G

GENE ALIGN SEQ
HUM: G T A T T A C G A T - - T T T T G G - A G T G G T T A T T A T A C C
UAM: G T A T T A C T A T A G - - - T G G T A G T G G T T A T T A T A A C

D7
HUM: C A C A G T G
UAM: C A C A G T G

D9
HUM: A T C A A A A A C C C
UAM: A T C A A A A A C C C

Alignment stats: 'M': 26, 'I': 3, 'D': 3, 'X': 2

IGHD4-4

U9

HUM:	G	G	C	T	T	T	T	T	G	T	G
UAM:	G	A	C	T	T	T	T	T	G	T	G

U7

HUM:	T	A	C	T	G	T	G
UAM:	T	A	C	T	G	T	G

GENE ALIGN SEQ

HUM:	T	G	A	C	T	A	C	A	G	T	A	A	C	T	A	C
UAM:	T	G	A	C	T	A	C	A	G	T	A	A	C	T	A	C

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	A	G	C	A	A	A	A	A	C	T	G
UAM:	G	G	A	A	A	A	A	C	T	G	G

Alignment stats: 'M': 16, 'I': 0, 'D': 0, 'X': 0

IGHD5-5

U9
HUM: T G G T T A T T G T C
UAM: T G G T T A T T G T C

U7
HUM: G A C T G T G
UAM: G A C T G T G

GENE ALIGN SEQ
HUM: G T G G A T A C A G C T A T G - - - - - G T T A C
UAM: G T G - - - A - A - - T A T G G C T A C G G T T A C

D7
HUM: C A C A G T G
UAM: C A C A G T G

D9
HUM: A G C A G C A A C C A
UAM: A G C A G C A A C C A

Alignment stats: 'M': 14, 'I': 6, 'D': 6, 'X': 0

IGHD6-6

U9

HUM:	A	A	G	T	T	T	C	T	G	A	A
UAM:	A	A	G	T	T	T	C	T	G	A	A

U7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

GENE ALIGN SEQ

HUM:	G	A	G	T	A	T	A	G	C	A	G	C	T	C	G	T	C	C
UAM:	G	A	G	T	A	T	A	G	C	A	G	C	T	G	G	T	A	C

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	C	C	A	G	A	A	A	C	C	C
UAM:	G	C	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 16, 'I': 0, 'D': 0, 'X': 2

IGHD1-7

U9

HUM:	C	G	G	A	T	T	C	T	G	A	A
UAM:	C	G	G	A	T	T	C	T	G	A	A

U7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

GENE ALIGN SEQ

HUM:	G	G	T	A	T	A	A	C	T	G	G	A	A	C	T	A	C
UAM:	G	G	T	A	T	A	A	C	T	G	G	A	A	C	T	A	C

D7

HUM:	C	A	C	T	G	T	G
UAM:	C	A	C	T	G	T	G

D9

HUM:	G	T	C	C	A	A	A	A	C	G	G
UAM:	G	T	C	C	A	A	A	A	C	T	G

Alignment stats: 'M': 17, 'I': 0, 'D': 0, 'X': 0

IGHD2-8

U9
HUM: A G G A T T T T G T G
UAM: A G G A T T T T G T G

U7
HUM: C A C T G T G
UAM: C A C T G T G

GENE ALIGN SEQ
HUM: A G G A T A T T G T A - C T A A T G G T G - T A - - T G C T A T A C C
UAM: A G G A T A T T G T A G - - - - T G G T G G T A G C T G C T A C G C C

D7
HUM: C A C A G T G
UAM: C A C A G T G

D9
HUM: T T C C C A A A G C C
UAM: T T C C C A A A G C C

Alignment stats: 'M': 25, 'I': 4, 'D': 4, 'X': 2

IGHD3-10

U9
HUM: A G G T T T G G G G T
UAM: A G G T T T G G G G T

U7
HUM: C A C T G T G
UAM: C A C T G T G

GENE ALIGN SEQ
HUM: G T A T T A C T A T G G T T C G G G G A G T - - - - - T A T T A T A A C
UAM: G T A T T A C T A T - - - - - A G T G G T G G T A C C T A T T A C A A C

D7
HUM: C A C A G T G
UAM: C A C A G T G

D9
HUM: A T C A A A A A C C C
UAM: A T C A A A A A C C C

Alignment stats: 'M': 21, 'I': 9, 'D': 9, 'X': 1

IGHD4-11

U9
HUM: G G C T T T T T G T G
UAM: G G C T T T T T G T G

U7
HUM: T G C T G T G
UAM: T A C T G T G

GENE ALIGN SEQ
HUM: T G A C T A C A G T - - - A A C T A C
UAM: T G A C T A C A G T G C T A A C T A C

D7
HUM: C A T A G T G
UAM: C A C A G T G

D9
HUM: G G C A A A A A C T G
UAM: A G C A A A A A C T G

Alignment stats: 'M': 16, 'I': 3, 'D': 0, 'X': 0

IGHD5-12

U9
HUM: T G G T T A T T G T C
UAM: T G G T T A T T G T C

U7
HUM: G A C T G T G
UAM: G G C C G T G

GENE ALIGN SEQ
HUM: G T G G A T A T A G - T G G C T A C G A T T A C
UAM: G T G G A - - - G A T G G C T A C A A T T A C

D7
HUM: C A C A G T G
UAM: C A C A G T G

D9
HUM: A G C A G C A A C C A
UAM: A G C A G C A A C C A

Alignment stats: 'M': 18, 'I': 1, 'D': 4, 'X': 1

IGHD6-13

U9

HUM:	A	G	G	T	T	T	C	T	G	A	A
UAM:	A	G	G	T	T	T	C	T	G	A	A

U7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

GENE ALIGN SEQ

HUM:	G	G	G	T	A	T	A	G	C	A	G	C	A	G	C	-	-	-	T	G	G	T	A	C
UAM:	G	G	G	T	A	T	A	G	C	A	G	C	A	G	C	A	G	C	T	G	G	T	A	C

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	C	C	A	G	A	A	A	C	C	C
UAM:	G	C	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 21, 'I': 3, 'D': 0, 'X': 0

IGHD1-14

U9
HUM: C G G A T T C C G A A
UAM: C A G A T T C T G A A

U7
HUM: C A C A G C G
UAM: C A C A G T G

GENE ALIGN SEQ
HUM: G G T A T A A C C G G A A C C A C
UAM: G G T T T A A C T G G A A C T A C

D7
HUM: C A C T G T C
UAM: C A C T G T C

D9
HUM: G T C A A A A C T G
UAM: G T C A A A A C T G

Alignment stats: 'M': 14, 'I': 0, 'D': 0, 'X': 3

IGHD2-15

U9
HUM: A G G A T T T T G T G
UAM: A G G A T T T T G T G

U7
HUM: C A C T G T G
UAM: C A C T G T G

GENE ALIGN SEQ
HUM: A G G A T A T T G T A G T G G T G G T A - - - G C T G C T A C T C C
UAM: A G G A T A T T G T A G T G G T - - - A G T G G C T G C T A C G C C

D7
HUM: C A C A G T G
UAM: C A C A G T G

D9
HUM: T T C C C A A A G C C
UAM: C T C C C A A A G C C

Alignment stats: 'M': 27, 'I': 3, 'D': 3, 'X': 1

IGHD3-16

U9
HUM: A G G T T T G A A G T
UAM: A G G T T T G G G G T

U7
HUM: C A C T G T G
UAM: C A C T G T G

GENE ALIGN SEQ
HUM: G T A T T A T G A T T A C G T T T G G G G G A G T T A T C G T T A T A C C
UAM: G T A T - - G A T T A T G T T T G G G G A A G T T A T C G T T A T A C C

D7
HUM: C A C A G C A
UAM: C A C A G C A

D9
HUM: A T C A G A A A C C C
UAM: A T C A A A A A C C C

Alignment stats: 'M': 32, 'I': 0, 'D': 3, 'X': 2

IGHD4-17

U9

HUM:	G	G	C	T	T	T	T	T	G	T	G
UAM:	G	G	C	T	T	T	T	T	G	T	G

U7

HUM:	T	A	C	T	G	T	G
UAM:	T	A	C	T	G	T	G

GENE ALIGN SEQ

HUM:	T	G	A	C	T	A	C	G	G	T	G	A	C	T	A	C
UAM:	T	G	G	C	T	A	C	A	G	T	A	A	C	T	C	C

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	A	G	C	A	A	A	A	A	C	T	G
UAM:	G	G	G	A	A	A	A	A	C	T	G

Alignment stats: 'M': 12, 'I': 0, 'D': 0, 'X': 4

IGHD5-18

U9

HUM:	T	G	G	T	T	A	T	T	G	T	C
UAM:	T	G	G	T	T	A	T	T	G	T	C

U7

HUM:	G	A	C	T	G	T	G
UAM:	G	A	C	T	G	T	G

GENE ALIGN SEQ

HUM:	G	T	G	G	A	T	A	C	A	-	-	-	G	C	T	A	T	G	G	T	T	A	C
UAM:	G	T	G	G	A	T	A	T	A	C	T	G	G	C	T	A	C	G	G	T	T	A	C

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	A	G	C	A	G	C	A	A	C	C	A
UAM:	A	G	C	G	G	C	A	A	C	C	A

Alignment stats: 'M': 18, 'I': 3, 'D': 0, 'X': 2

IGHD6-19

U9

HUM:	A	G	G	T	T	T	C	T	G	A	A
UAM:	A	G	G	T	T	T	C	T	G	A	A

U7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

GENE ALIGN SEQ

HUM:	G	G	G	T	A	T	A	G	C	A	G	T	G	G	C	T	G	G	T	A	C
UAM:	G	G	G	T	A	T	A	G	C	A	G	C	G	G	C	T	G	G	T	C	C

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	G	C	C	A	G	A	A	A	C	C	C
UAM:	G	C	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 19, 'I': 0, 'D': 0, 'X': 2

IGHD1-20

U9
HUM: C G G A T T C T G A A
UAM: C A G A T T C T G A A

U7
HUM: C A C A G T G
UAM: C A C A G T G

GENE ALIGN SEQ
HUM: G G T A T A A C T G G A A C G A C
UAM: G G T A T A A C T G G A A T G A T

D7
HUM: C A C C G T G
UAM: C A C T G T G

D9
HUM: G T C C A A A A C T G
UAM: A T C C A A A A C T G

Alignment stats: 'M': 15, 'I': 0, 'D': 0, 'X': 2

IGHD2-21

U9

HUM:	A	G	G	A	T	T	T	T	G	T	G
UAM:	A	G	G	A	T	T	T	T	G	T	G

U7

HUM:	C	A	C	T	G	T	G
UAM:	C	A	C	T	G	T	G

GENE ALIGN SEQ

HUM:	A	G	C	A	T	A	T	T	G	-	-	-	T	G	G	T	G	G	T	G	A	-	C	T	G	C	T	A	T	T	C	C
UAM:	A	G	G	A	T	A	T	T	G	T	A	G	T	G	G	T	G	G	T	-	A	G	C	T	G	C	T	A	C	G	C	C

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	C	A	G	T	G

D9

HUM:	T	T	C	C	T	A	A	A	G	C	C
UAM:	T	T	C	C	C	A	A	A	G	C	C

Alignment stats: 'M': 24, 'I': 4, 'D': 1, 'X': 3

IGHD3-22

U9
HUM: A G G T T T G A A G T
UAM: A G G T T T G A A G T

U7
HUM: C A C T G T G
UAM: C A C T G T G

GENE ALIGN SEQ
HUM: G T A T T A - - - - C T A T G A T A G T A G T G G - - T T A T T A C T A - - - - - C
UAM: G T A T T A T G A T - T A T G A T A C T - - T G G G G - - - T T A C T A T T A A A G C

D7
HUM: C A C A G T G
UAM: C A C A G T G

D9
HUM: A T C A A A A A C T C
UAM: A T C A A A A A C T C

Alignment stats: 'M': 24, 'I': 12, 'D': 6, 'X': 1

IGHD4-23

U9
HUM: G G C T T T T T G T G
UAM: G G C T T T T T G T G

U7
HUM: T G C T G T G
UAM: T A C T G T T

GENE ALIGN SEQ
HUM: T G A C T A C G G T G G T A A C T C C
UAM: T G A C T A C G G T G G T A A C T C C

D7
HUM: C A C A G T G
UAM: T A C A G T G

D9
HUM: A G C A A A A A C T G
UAM: G G C A A A A A C T G

Alignment stats: 'M': 19, 'I': 0, 'D': 0, 'X': 0

IGHD5-24

U9
HUM: T G G T T A T T G T C
UAM: T T A T T G T C A G G

U7
HUM: G G C C G T G
UAM: C A T G G T G

GENE ALIGN SEQ
HUM: G T A G A G A T G G C T A C A A T T A C
UAM: - - - G A G A T G G C T A C A A T T A C

D7
HUM: C A C A G T G
UAM: C A C A G T G

D9
HUM: A G C A G C A A C C A
UAM: A G C A G C A A C C A

Alignment stats: 'M': 17, 'I': 0, 'D': 3, 'X': 0

IGHD6-25

U9

HUM:	A	G	G	T	T	T	C	T	G	A	A
UAM:	A	G	G	T	T	T	C	C	G	A	A

U7

HUM:	C	A	C	A	G	T	C
UAM:	C	A	C	A	G	T	G

GENE ALIGN SEQ

HUM:	G	G	G	T	A	T	A	G	C	A	G	C	G	G	C	T	A	C
UAM:	G	G	G	T	A	T	A	G	C	A	G	T	G	G	C	T	A	C

D7

HUM:	C	A	C	A	A	T	G
UAM:	C	A	C	A	A	T	G

D9

HUM:	G	A	C	A	G	A	A	A	C	C	C
UAM:	G	A	C	A	G	A	A	A	C	C	C

Alignment stats: 'M': 17, 'I': 0, 'D': 0, 'X': 1

IGHD1-26

U9
HUM: T G G A T T C T G A A
UAM: T G G A T T C T G A A

U7
HUM: C A C G G T G
UAM: C A T G G T G

GENE ALIGN SEQ
HUM: G G T A T A G T G G G A G C T A C T A C
UAM: G G T A T A G T G G G A G C T A C T A C

D7
HUM: C A C T G T G
UAM: C A C T G T G

D9
HUM: G T C C A A A A C T G
UAM: G T C C A A A A C T G

Alignment stats: 'M': 20, 'I': 0, 'D': 0, 'X': 0

IGHJ1P

U9

HUM:	C	G	C	G	T	G	T	T	T	T	G
UAM:	C	G	T	G	T	G	T	T	T	T	G

U7

HUM:	C	A	C	T	G	G	C
UAM:	C	A	C	T	G	G	C

GENE ALIGN SEQ

HUM:	A	A	A	G	G	T	G	C	T	G	G	G	G	G	C	C	C	C	T	G	G	A	C	C	C	G	A	C	C	C	G	C	C	C	T	G	G	A	G	A	C	C	G	C	A	G	C	C	A	C
UAM:	A	A	A	G	G	T	G	C	T	G	G	G	G	G	C	C	C	C	T	G	G	A	C	C	T	G	A	C	C	C	G	C	C	C	T	G	G	A	G	A	C	C	A	C	A	G	C	C	A	G

HUM:	A	T	C	A
UAM:	A	C	C	A

Alignment stats: 'M': 50, 'I': 0, 'D': 0, 'X': 4

IGHD7-27

U9

HUM:	G	G	G	T	T	T	T	G	G	C	T
UAM:	G	G	G	T	T	T	T	G	G	C	T

U7

HUM:	C	A	C	T	G	T	G
UAM:	C	A	C	C	G	T	G

GENE ALIGN SEQ

HUM:	C	T	A	A	C	T	G	G	G	G	A
UAM:	C	T	A	A	C	T	G	G	G	G	A

D7

HUM:	C	A	C	A	G	T	G
UAM:	C	A	G	A	G	T	G

D9

HUM:	T	A	C	A	A	A	A	A	C	C	A
UAM:	T	A	C	A	A	A	A	A	C	C	A

Alignment stats: 'M': 11, 'I': 0, 'D': 0, 'X': 0

IGHJ1

U9

HUM:	T	G	G	G	T	T	T	C	T	G	T
UAM:	T	G	G	G	T	T	T	C	T	G	C

U7

HUM:	C	A	C	C	G	T	G
UAM:	C	A	C	C	G	T	G

GENE ALIGN SEQ

HUM:	G	C	T	G	A	A	T	A	C	T	T	C	C	A	G	C	A	C	T	G	G	G	G	C	C	A	G	G	G	C	A	C	C	C	T	G	G	T	C	A	C	C	G	T	C	T	C	C	T	C
UAM:	G	C	C	G	A	A	T	A	C	T	T	C	A	A	G	C	A	C	T	G	G	G	G	C	C	A	G	G	G	C	A	T	C	C	T	G	G	T	C	A	C	C	G	T	C	T	C	C	T	C

HUM:	A	G
UAM:	A	G

Alignment stats: 'M': 49, 'I': 0, 'D': 0, 'X': 3

IGHJ2

U9

HUM:	T	G	T	G	T	T	T	T	T	G	T
UAM:	T	G	T	G	T	T	T	T	T	G	T

U7

HUM:	G	G	C	T	G	T	G
UAM:	G	G	C	T	G	T	G

GENE ALIGN SEQ

HUM:	C	T	A	C	T	G	G	T	A	C	T	T	C	G	A	T	C	T	C	T	G	G	G	G	C	C	G	T	G	G	C	A	C	C	C	T	G	G	T	C	A	C	T	G	T	C	T	C	C	T
UAM:	C	T	A	C	T	T	G	T	A	C	T	T	C	G	A	T	C	T	C	T	G	G	G	G	C	C	G	T	G	G	C	A	C	C	C	T	G	G	T	C	A	C	C	G	T	C	T	C	C	T

HUM:	C	A	G
UAM:	C	A	G

Alignment stats: 'M': 51, 'I': 0, 'D': 0, 'X': 2

IGHJ2P

U9

HUM:	G	C	T	G	T	T	C	A	T	G	T
UAM:	G	C	T	G	T	T	C	A	T	G	T

U7

HUM:	T	A	G	T	G	T	G
UAM:	T	A	G	T	G	T	G

GENE ALIGN SEQ

HUM:	G	C	T	A	C	A	A	G	T	G	C	T	T	G	G	A	G	C	A	C	T	G	G	G	G	C	C	A	G	G	G	C	A	G	C	C	C	G	G	C	C	A	C	C	G	T	C	T	C	C
UAM:	G	C	T	A	C	A	A	G	T	A	C	T	T	G	G	A	G	C	A	C	T	G	G	G	T	C	C	A	G	G	G	C	A	G	C	C	C	G	G	C	C	A	C	C	G	T	C	T	C	C

HUM:	C	T	G	G	G	A	A	C	G	T	C	A
UAM:	C	T	G	G	G	A	A	C	T	T	C	A

Alignment stats: 'M': 59, 'I': 0, 'D': 0, 'X': 3

IGHJ3

U9
HUM: A G G T T T A T G T C
UAM: G G G T T T G T G T C

U7
HUM: C C C T G T G
UAM: C C C T G T G

GENE ALIGN SEQ
HUM: T G A T G C T T T T G A T A T C T G G G G C C A A G G G - - A C - A A T G G T C A C C G T C T C T T
UAM: T G A T G C T T T T G A T A T C T G G G G C C T A G G G G T - C G - - T G G T C A C C G T C T C T T

HUM: C A G
UAM: C A G

Alignment stats: 'M': 46, 'I': 3, 'D': 3, 'X': 1

IGHJ4

U9

HUM:	A	G	G	T	T	T	T	T	G	T	G
UAM:	A	G	G	T	T	T	T	T	G	T	G

U7

HUM:	C	A	A	T	G	T	G
UAM:	C	A	A	T	G	T	G

GENE ALIGN SEQ

HUM:	A	C	T	A	C	T	T	T	G	A	C	T	A	C	T	G	G	G	G	C	C	A	G	G	G	A	A	C	C	C	T	G	G	T	C	A	C	C	G	T	C	T	C	C	T	C	A	G
UAM:	A	C	T	A	C	T	T	T	G	A	G	T	A	C	T	G	G	G	G	C	C	A	G	G	G	A	A	C	C	C	T	G	C	T	C	A	C	C	G	T	C	T	C	C	T	C	A	G

Alignment stats: 'M': 46, 'I': 0, 'D': 0, 'X': 2

IGHJ5

U9

HUM:	C	A	G	T	T	C	T	T	G	C	C
UAM:	C	A	G	T	T	C	T	T	G	C	C

U7

HUM:	C	A	A	T	G	T	G
UAM:	C	A	A	T	G	T	G

GENE ALIGN SEQ

HUM:

UAM:

A	C	A	A	C	T	G	G	T	T	C	G	A	C	C	C	C	T	G	G	G	G	C	C	A	G	G	G	A	A	C	C	C	T	G	G	T	C	A	C	C	G	T	C	T	C	C	T	C	A
A	C	A	A	C	C	A	G	T	T	C	G	A	C	C	C	C	T	G	G	G	G	C	C	A	G	G	G	A	A	C	C	C	T	G	G	T	C	A	C	C	G	T	C	T	C	C	C	C	A

HUM:	G
UAM:	G

Alignment stats: 'M': 48, 'I': 0, 'D': 0, 'X': 3

IGHJ3P

U9

HUM:	G	G	G	G	T	T	T	T	T	G	G
UAM:	A	G	G	A	T	T	T	T	T	G	G

U7

HUM:	C	C	G	T	C	T	G
UAM:	C	C	G	T	C	T	G

GENE ALIGN SEQ

HUM:	C	T	T	G	C	A	G	T	T	G	G	A	C	T	T	C	C	C	A	G	G	C	C	G	A	C	A	G	T	G	G	T	C	T	G	G	C	T	T	C	T	G	A	G	G	G	G	T	C	A
UAM:	C	T	T	G	C	A	G	T	T	G	G	A	C	T	T	C	C	C	A	G	G	C	T	G	A	C	A	G	T	G	G	T	C	T	G	G	C	T	T	C	T	G	A	G	G	G	G	T	C	A

Alignment stats: 'M': 49, 'I': 0, 'D': 0, 'X': 1

IGHJ6

U9
HUM: T G G G T T T T T G T
UAM: T G G G T T T T T G T

U7
HUM: C A T T G T G
UAM: C A T T G T G

GENE ALIGN SEQ
HUM: A T T A C T A C - - - T A C T A C T A C T A C A T G G A C G T C T G G G G C A - - A A G G G A C C A
UAM: A T T A C T A C G G T - - - - - - - - - - A T G G A C T T C T G G G - - A C T A A G G G A C C A

HUM: C G G T C A C C G T C T C C T C A G
UAM: T G G T C A C C G T C T C C T C A G

Alignment stats: 'M': 47, 'I': 5, 'D': 14, 'X': 2