

Pipeline

P2 dataset with 33599 seq

Run Vdjil

Select 10 most abundant clones

Run GCtree on the selection
(consensus sequence)

P2 major clones and satellites



P2 major clones and satellites

Too high for GCtree to manage, need to divide by 100



Clone rank	# read	% read	IGHV	IGHJ
clone 1	11772	35 %	V3-74*01	J5*02
clone 2	6778	20 %	V3-74*02	J5*02
clone 3	3191	10 %	V3-74*01	J5*02
clone 4	1494	4 %	V3-74*01	J5*02
clone 5	699	2 %	V3-74*01	J5*02
clone 6	513	2 %	V3-74*03	J1*01
clone 7	464	1 %	V3-74*01	J5*02
clone 8	395	1 %	V3-74*01	J5*02
clone 9	369	1 %	V3-74*01	J5*02
clone 10	301	0,08 %	V3-74*01	J5*02

P2 major clones and satellites

Clone rank	# read	% read	IGHV	IGHJ
clone 1	117	35 %	V3-74*01	J5*02
clone 2	67	20 %	V3-74*02	J5*02
clone 3	31	10 %	V3-74*01	J5*02
clone 4	15	4 %	V3-74*01	J5*02
clone 5	7	2 %	V3-74*01	J5*02
clone 6	5	2 %	V3-74*03	J1*01
clone 7	4	1 %	V3-74*01	J5*02
clone 8	4	1 %	V3-74*01	J5*02
clone 9	3	1 %	V3-74*01	J5*02
clone 10	3	0,08 %	V3-74*01	J5*02

P2 major clones and satellites

Clone rank	# read	% read	IGHV	IGHJ
clone 1	117	35 %	V3-74*01	J5*02
clone 2	67	20 %	V3-74*02	J5*02
clone 3	31	10 %	V3-74*01	J5*02
clone 4	15	4 %	V3-74*01	J5*02
clone 5	7	2 %	V3-74*01	J5*02
clone 6	5	2 %	V3-74*03	J1*01
clone 7	4	1 %	V3-74*01	J5*02
clone 8	4	1 %	V3-74*01	J5*02
clone 9	3	1 %	V3-74*01	J5*02
clone 10	3	0,08 %	V3-74*01	J5*02

P2 major clones and satellites

Clone rank	# read	% read	IGHV	IGHJ
clone 1	117	35 %	V3-74*01	J5*02
clone 2	67	20 %	V3-74*02	J5*02
clone 3	31	10 %	V3-74*01	J5*02
clone 4	15	4 %	V3-74*01	J5*02
clone 5	7	2 %	V3-74*01	J5*02
clone 6	5	2 %	V3-74*03	J1*01
clone 7	4	1 %	V3-74*01	J5*02
clone 8	4	1 %	V3-74*01	J5*02
clone 9	3	1 %	V3-74*01	J5*02
clone 10	3	0,08 %	V3-74*01	J5*02

P2 major clones and satellites

V3-74*01 J5*02

Clone rank	# read	% read	IGHV	IGHJ
clone 1	117	35 %	V3-74*01	J5*02
clone 2	67	20 %	V3-74*02	J5*02
clone 3	31	10 %	V3-74*01	J5*02
clone 4	15	4 %	V3-74*01	J5*02
clone 5	7	2 %	V3-74*01	J5*02
clone 6	5	2 %	V3-74*03	J1*01
clone 7	4	1 %	V3-74*01	J5*02
clone 8	4	1 %	V3-74*01	J5*02
clone 9	3	1 %	V3-74*01	J5*02
clone 10	3	0,08 %	V3-74*01	J5*02

P2 major clones and satellites

V3-74*02 J5*02

Clone rank	# read	% read	IGHV	IGHJ
clone 1	117	35 %	V3-74*01	J5*02
clone 2	67	20 %	V3-74*02	J5*02
clone 3	31	10 %	V3-74*01	J5*02
clone 4	15	4 %	V3-74*01	J5*02
clone 5	7	2 %	V3-74*01	J5*02
clone 6	5	2 %	V3-74*03	J1*01
clone 7	4	1 %	V3-74*01	J5*02
clone 8	4	1 %	V3-74*01	J5*02
clone 9	3	1 %	V3-74*01	J5*02
clone 10	3	0,08 %	V3-74*01	J5*02

P2 major clones and satellites

V3-74*03 J1*01

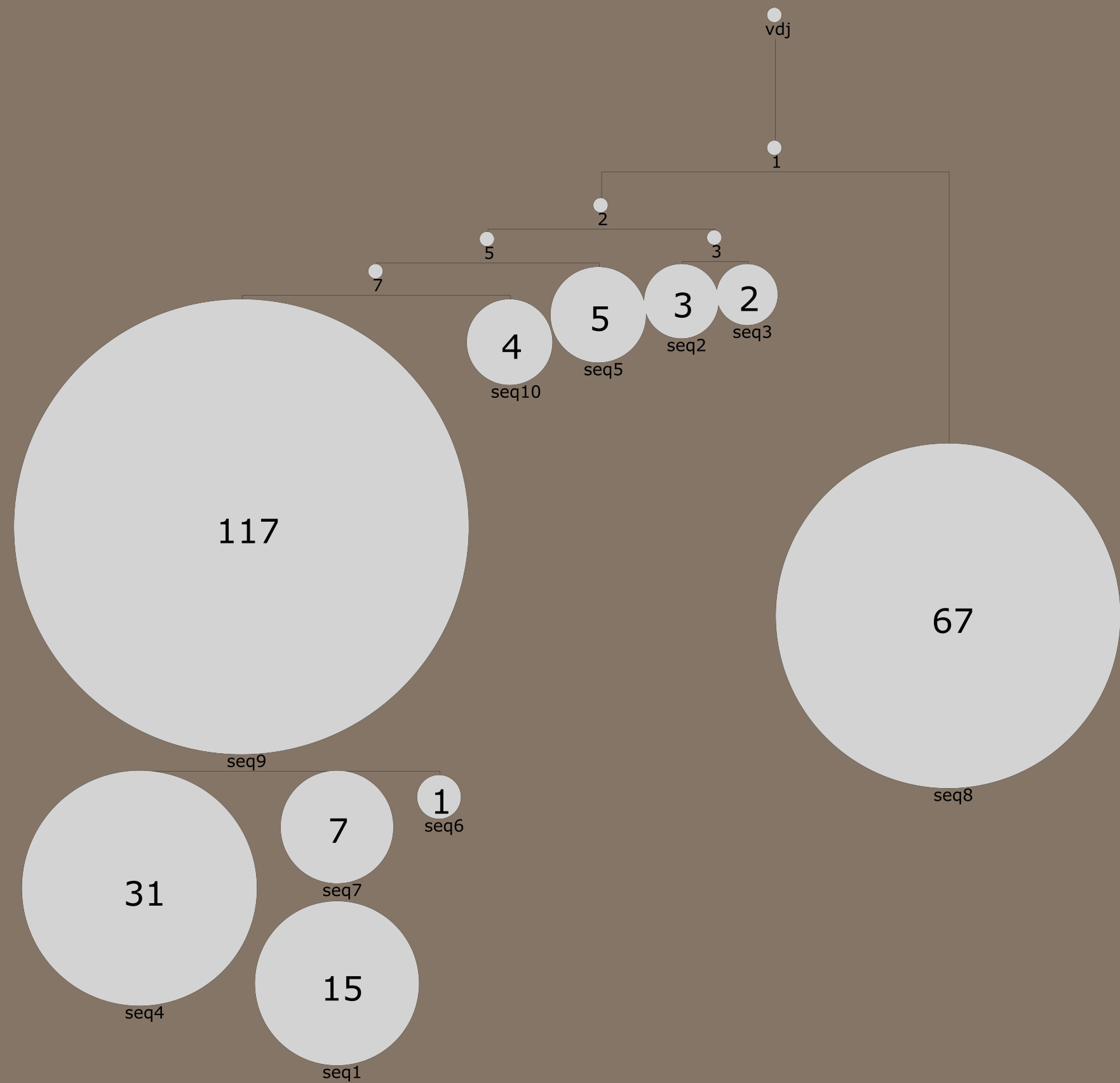
Clone rank	# read	% read	IGHV	IGHJ
clone 1	117	35 %	V3-74*01	J5*02
clone 2	67	20 %	V3-74*02	J5*02
clone 3	31	10 %	V3-74*01	J5*02
clone 4	15	4 %	V3-74*01	J5*02
clone 5	7	2 %	V3-74*01	J5*02
clone 6	5	2 %	V3-74*03	J1*01
clone 7	4	1 %	V3-74*01	J5*02
clone 8	4	1 %	V3-74*01	J5*02
clone 9	3	1 %	V3-74*01	J5*02
clone 10	3	0,08 %	V3-74*01	J5*02

Germlines to try

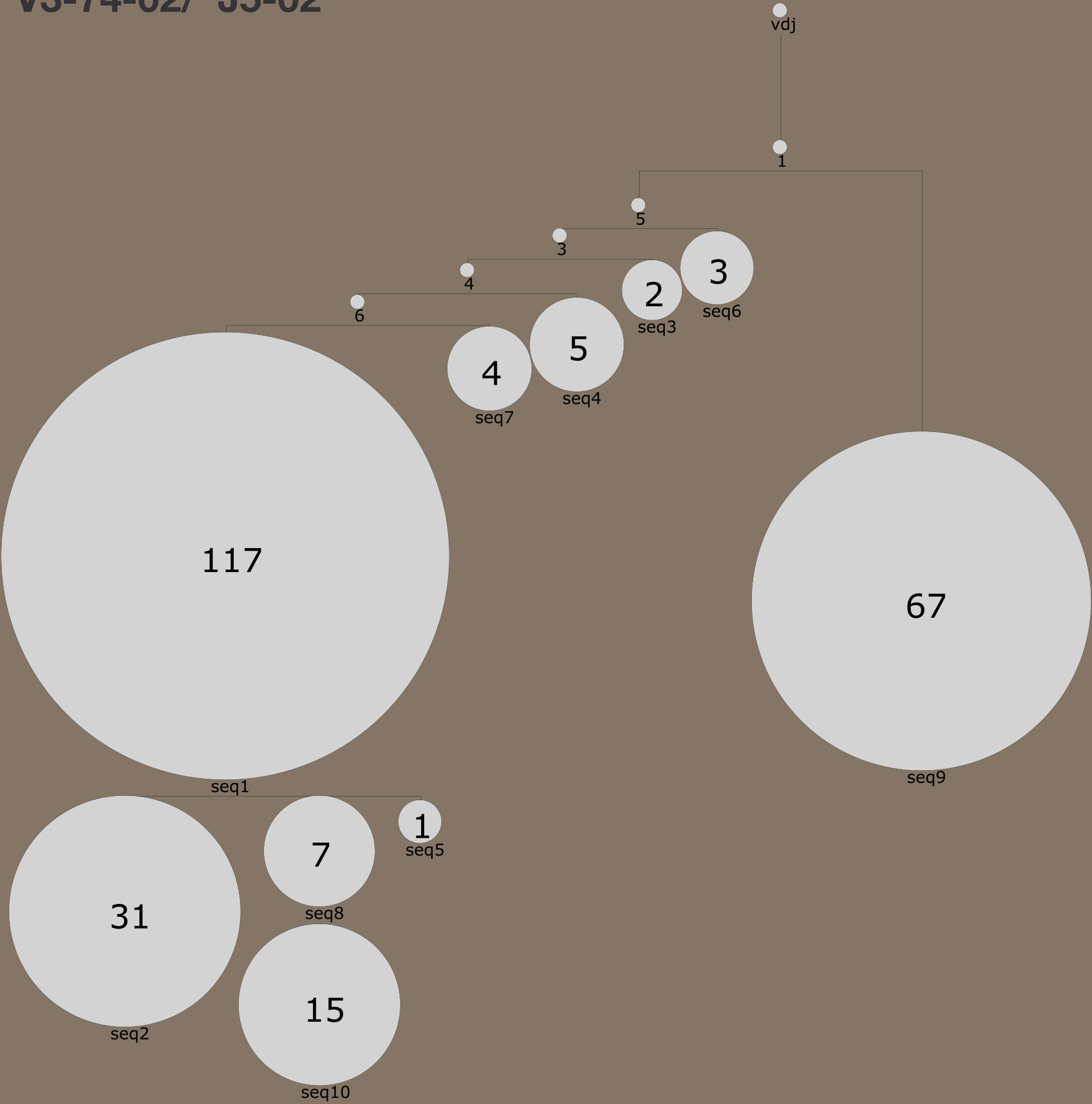
V3-74*01 / J5*02

V3-74*02 / J5*02

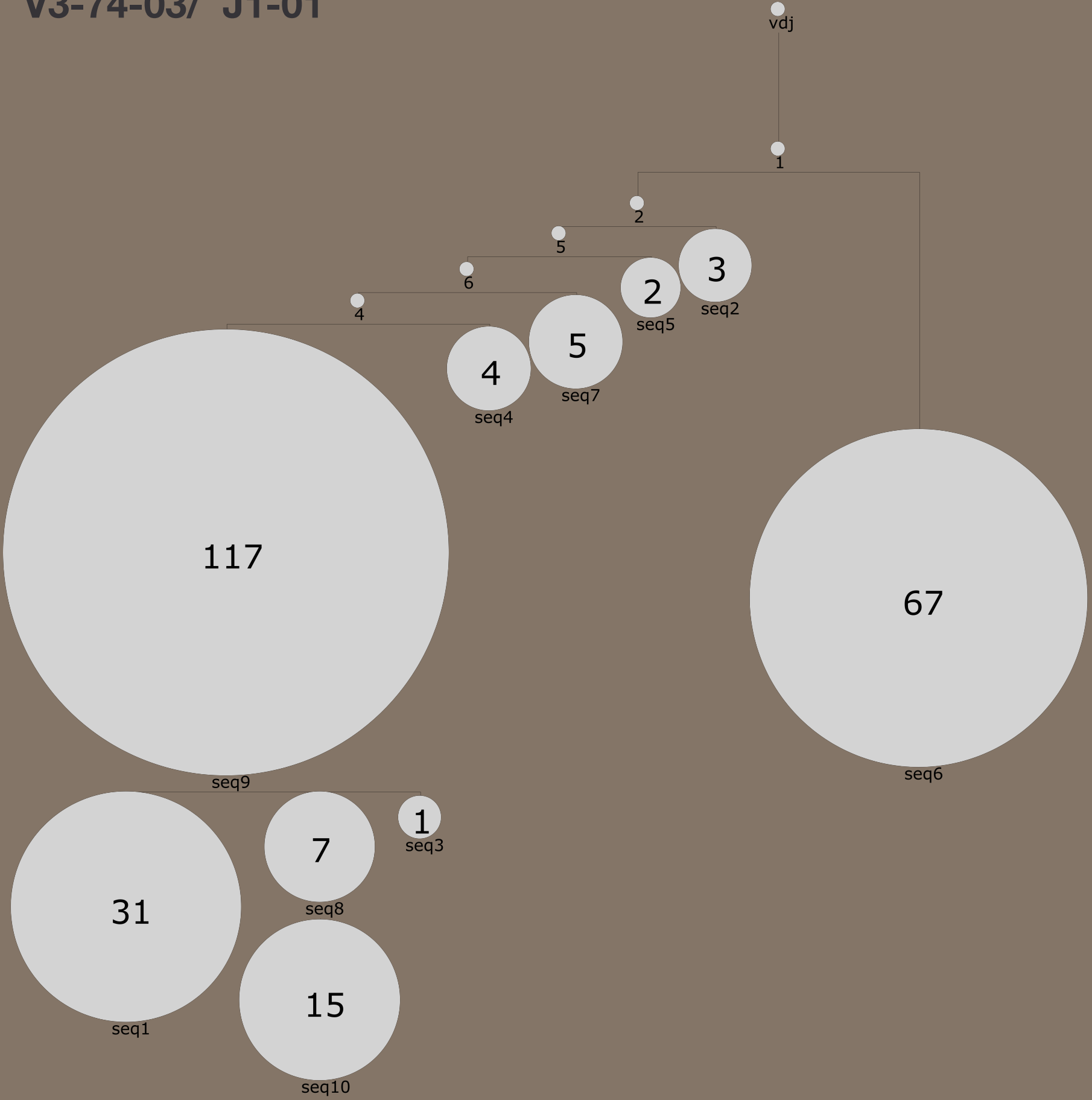
V3-74*03 / J1*01



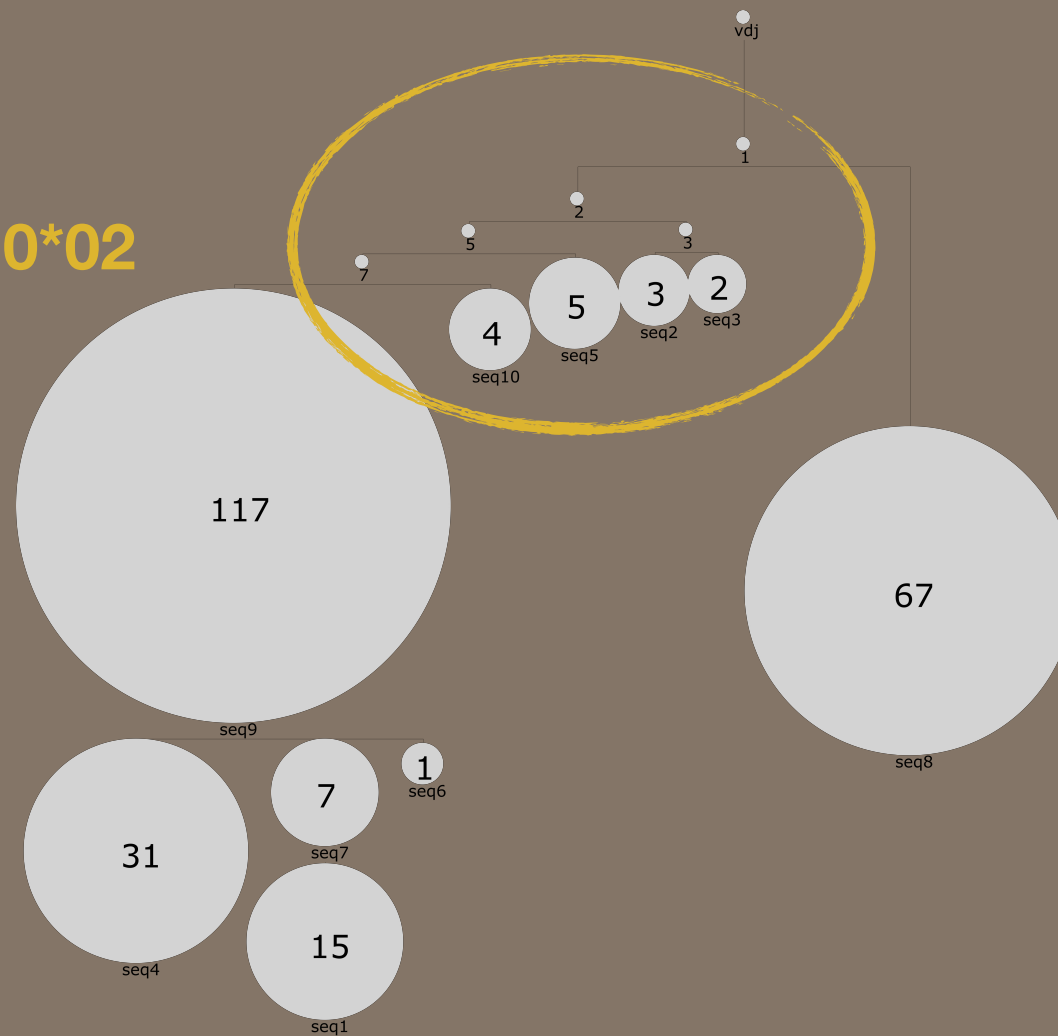
Germline : V3-74-02/ J5-02



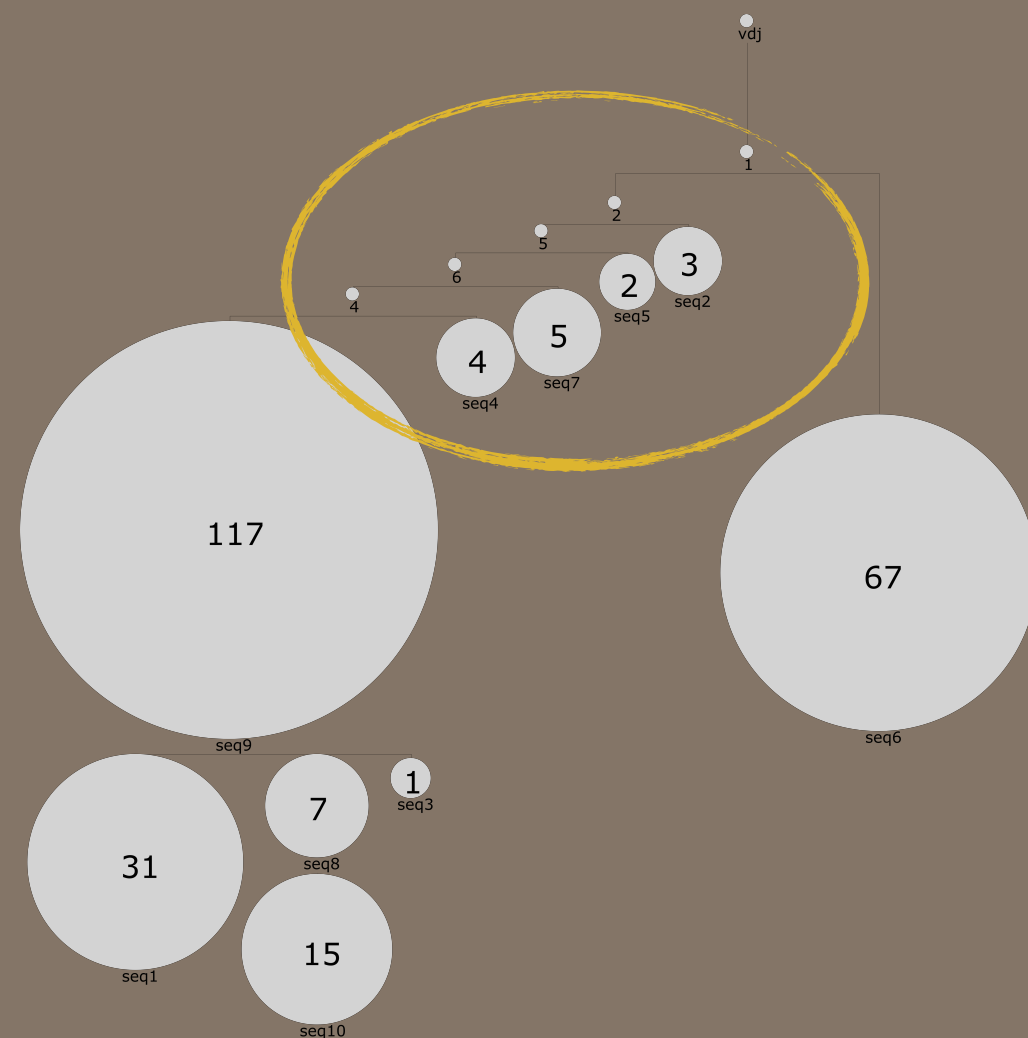
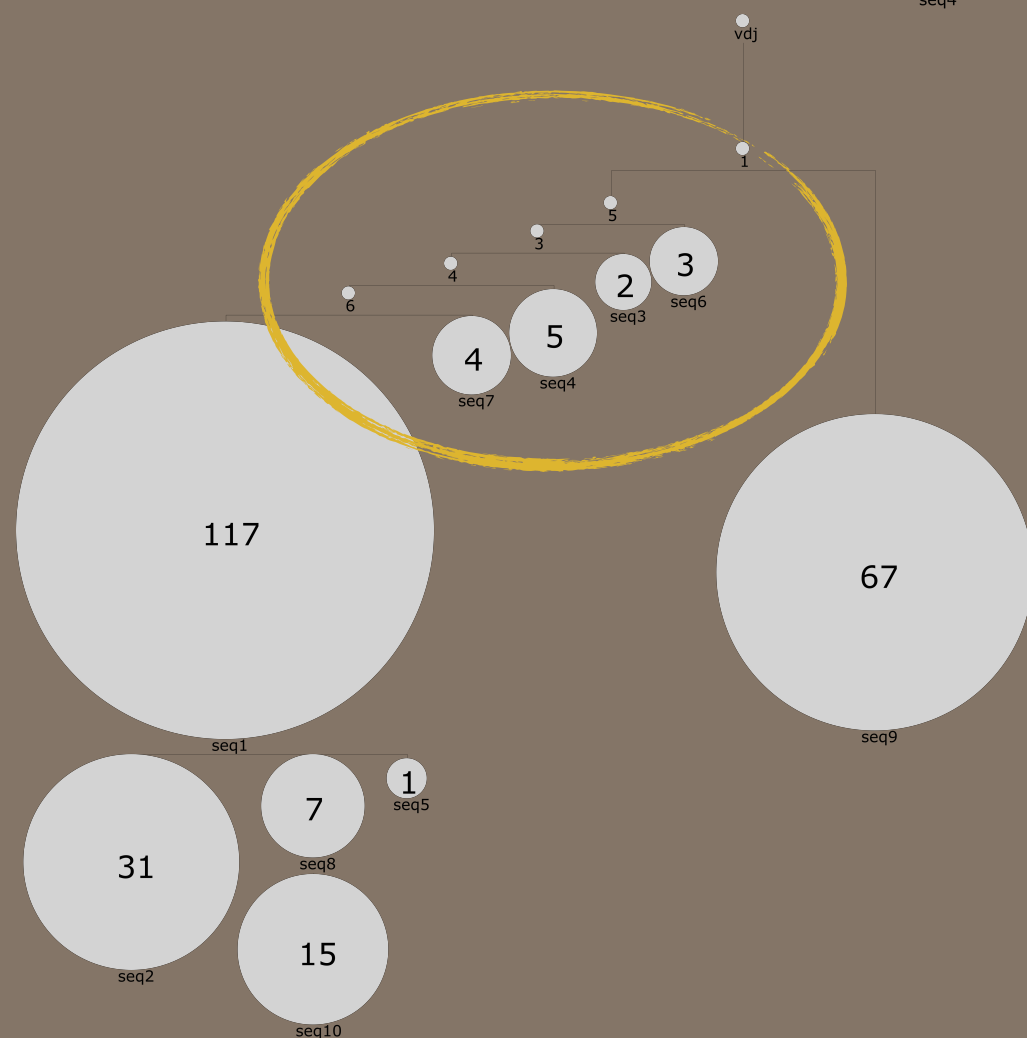
Germline : V3-74-03/ J1-01



D3-10*02



D5-18*01



The role of D?

Clone rank	# read	% read	IGHV	IGHD	IGHJ
clone 1	117	35 %	V3-74*01	D3-10*02	J5*02
clone 2	67	20 %	V3-74*02	D5-18*01	J5*02
clone 3	31	10 %	V3-74*01	D3-10*02	J5*02
clone 4	15	4 %	V3-74*01	D2-21*01	J5*02
clone 5	7	2 %	V3-74*01	D2-21*01	J5*02
clone 6	5	2 %	V3-74*03	D5-18*01	J1*01
clone 7	4	1 %	V3-74*01	D5-18*01	J5*02
clone 8	4	1 %	V3-74*01	D3-9*01	J5*02
clone 9	3	1 %	V3-74*01	D3-10*02	J5*02
clone 10	3	0,08 %	V3-74*01	D5-18*01	J5*02