Transcription pattern of the *λ5* gene after induction of pre-BCR expression

	Induction of pre-BCR expression on *in vitro* cultured pre-B cells [a]														
	Day 0			Day 1			Day 2			Day 3			Day 4		
SL$^+$ cells	77			79			71			<5			<5		
μH$^+$SL$^+$ cells	0			40			63			<5			<5		
% c-kit$^+$ cells	44			25			9			5			2		
% CD25$^+$ cells	1			7			30			55			62		
large cells	45			45			58			46			5		
	RNA signals per nucleus [b]														
	1	2	4	1	2	4	1	2	4	1	2	4	1	2	4
CD45															
PCNA$^-$ [c]	3	39	2	3	42	2	2	45	2	7	41	5	4	64	3
PCNA$^+$	0	4	15	0	3	18	1	7	27	2	7	15	0	1	8
Total	3	43	17	3	45	20	3	52	29	9	48	20	4	65	11
λ5															
PCNA$^-$	1	37	1	6	42	4	5	34	1	14	13	1	5	1	0
PCNA$^+$	1	6	17	1	2	14	1	11	13	0	15	5	1	3	0
Total	2	43	18	7	44	18	6	45	14	14	28	6	6	4	0

[a] CD19$^+$ BM cells from tet-μH mice were purified and cultured *in vitro* for four days. Each day samples were analyzed by: FACS, to determine the percentages of surface SL$^+$, μH$^+$, i.e. pre-BCR$^+$ cells and cell size and by immuno-RNA-FISH to investigate the transcriptional status of the CD45 and λ5 genes. [b] Nuclei contained either 1, 2 or 4 discrete RNA signals. [c] Percentages of the total nuclei with either 1, 2 or 4 signals staining as PCNA$^-$ or PCNA$^+$ (S phase) are shown. The data shown is from one representative experiment. The number of nuclei counted from each day and for each probe was >150.