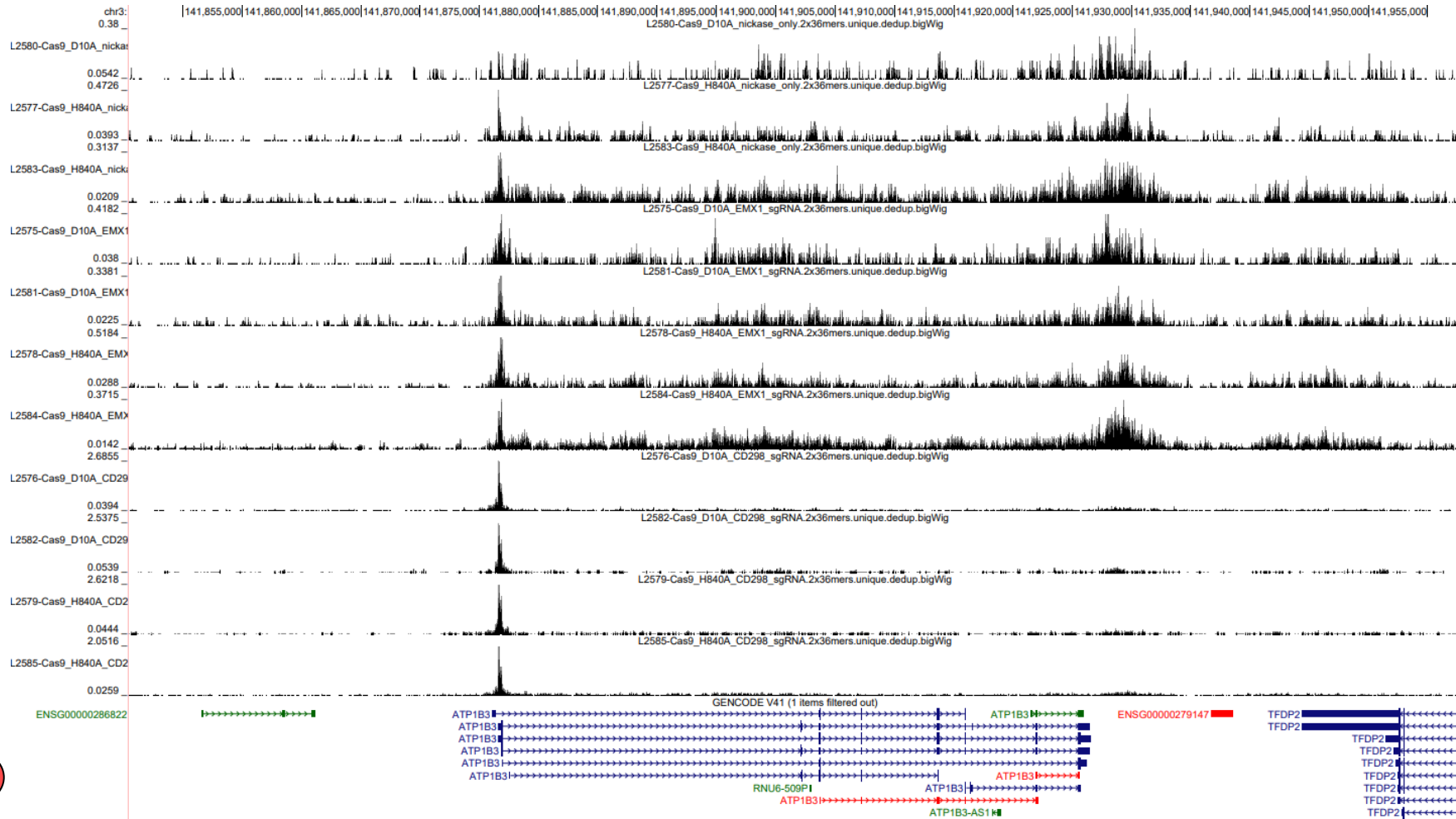


# Mapping stats

Species	#	Raw fragments	Read Length	Unique	Multi	Unque dedup	Unique Alignment fraction	Complexity	TSS score
Homo sapiens hg38	L2575-Cas9_D10A_EMX1_sgRNA	18,135,970	2x36	28,735,244		26,300,164	0.79	0.90	2.91
Homo sapiens hg38	L2576-Cas9_D10A_CD298_sgRNA	16,980,351	2x36	26,696,100		25,320,710	0.79	0.93	3.70
Homo sapiens hg38	L2577-Cas9_H840A_nickase_only	17,987,228	2x36	28,811,040		25,389,454	0.80	0.86	2.14
Homo sapiens hg38	L2578-Cas9_H840A_EMX1_sgRNA	27,905,070	2x36	44,973,124		34,718,546	0.81	0.75	2.73
Homo sapiens hg38	L2579-Cas9_H840A_CD298_sgRNA	15,116,955	2x36	23,842,266		22,503,158	0.79	0.93	3.68
Homo sapiens hg38	L2580-Cas9_D10A_nickase_only	14,966,849	2x36	24,237,074		18,418,378	0.81	0.75	1.61
Homo sapiens hg38	L2581-Cas9_D10A_EMX1_sgRNA	30,737,585	2x36	48,642,836		44,357,710	0.79	0.90	2.23
Homo sapiens hg38	L2582-Cas9_D10A_CD298_sgRNA	12,116,144	2x36	19,292,346		18,521,450	0.80	0.94	3.58
Homo sapiens hg38	L2583-Cas9_H840A_nickase_only	57,673,834	2x36	92,375,038		47,813,904	0.80	0.50	1.74
Homo sapiens hg38	L2584-Cas9_H840A_EMX1_sgRNA	74,417,089	2x36	117,219,798		69,981,430	0.79	0.58	2.21
Homo sapiens hg38	L2585-Cas9_H840A_CD298_sgRNA	30,700,848	2x36	48,309,624		38,506,014	0.79	0.78	2.57

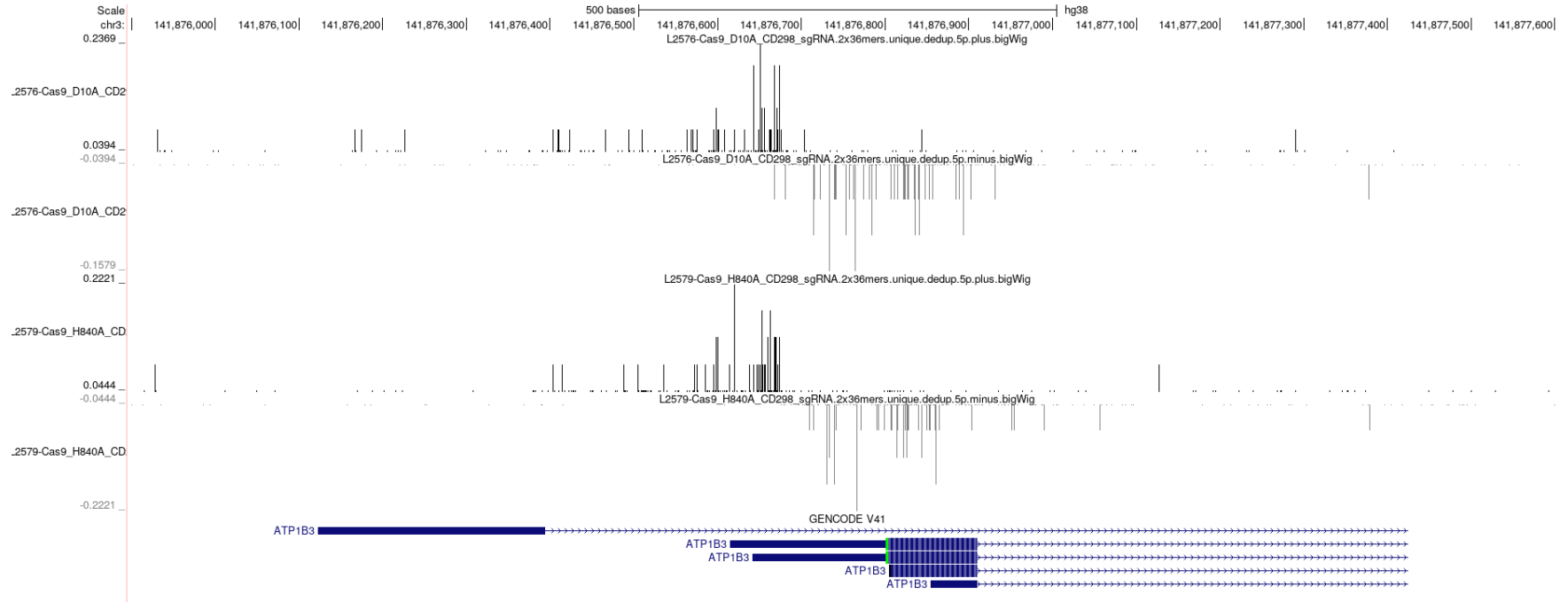


# CD298





## Side note on 5' ends:



While we can see cut sites with the active Cas9, the nick is not visible in the dsDNA prep. It might be if we do ssKAS-seq