Supplementary Table S12: Number of sites sequenced with at least 500 read counts in the second round of hybrid capture followed by sequencing. Sites were selected from sites nominated by the three genome-wide methods within the 6 MM 3 gap space for CCR5, RNF2, HEK1 and HEK3 gRNAs, with additional 82 sites included from homology-dependent nomination.

		Gaps			
		0	**1**	**2**	**3**
Mismatches	**0**	5	1	3	6
	1	1	4	35	17
	2	1	8	134	23
	3	10	64	143	6
	4	81	689	97	2
	5	315	461	35	2
	6	487	161	25	2