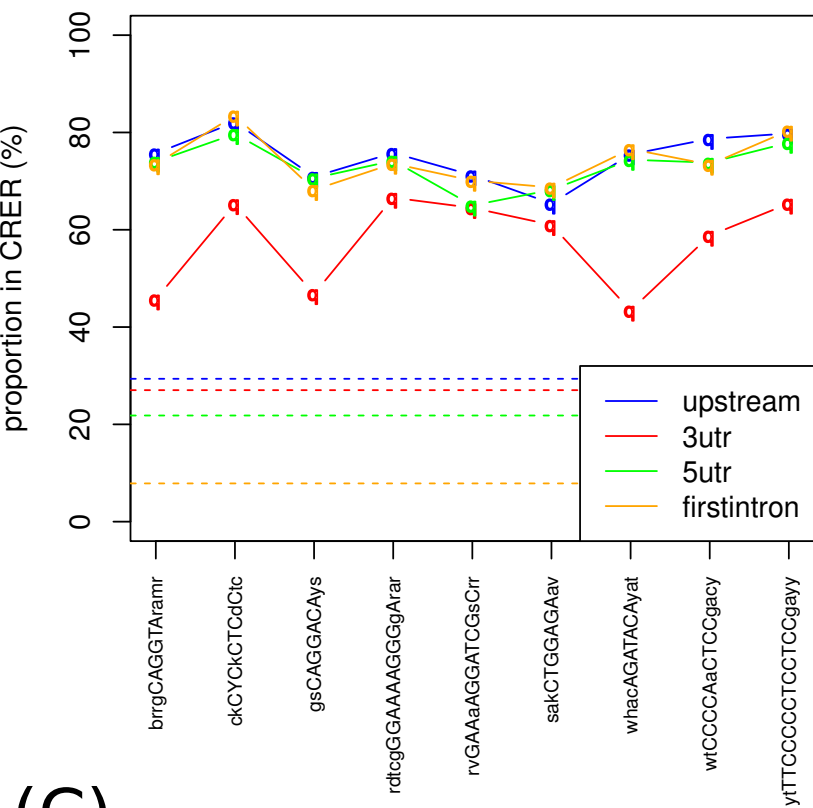
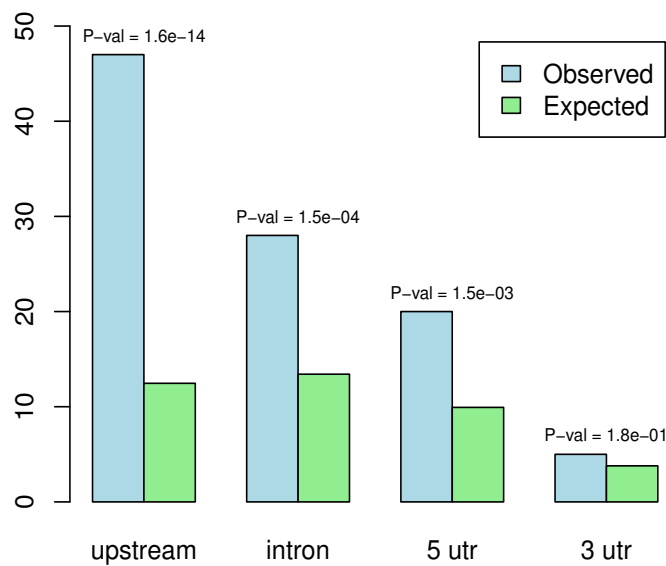
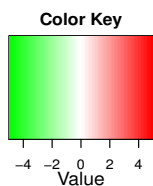


**(A)** Proportion of sites found in CRER**(B)** Frequency of homotypic CRER**(C)**

## Significance of motif combinations

Inf	0.4	7.7	0.5	2.1	1.2	7.9	0.8	-0.5	brrgCAGGTAramr
0.4	1.2	-0.3	-0.6	0.8	-0.8	0.8	-1.6	-1.2	ckCYCkCTCdCtc
7.7	-0.3	-0.4	1.3	3.1	0.8	0.8	1.5	1.3	gsCAGGACAYS
0.5	-0.6	1.3	0.5	0.7	0.4	0.4	0.6	0.4	rdtcgGGAAAAGGGgArar
2.1	0.8	3.1	0.7	0.8	0.6	1.2	0.8	-0.9	rvGAAaAGGATCGsCrr
1.2	-0.8	0.8	0.4	0.6	1.6	0.6	0.6	0.4	sakCTGGAGAav
7.9	0.8	0.8	0.4	1.2	0.6	9.2	1.6	-1.3	whacAGATACAyat
0.8	-1.6	1.5	0.6	0.8	0.6	1.6	1.4	-0.4	wtCCCCAaCTCCgacy
-0.5	-1.2	1.3	0.4	-0.9	0.4	-1.3	-0.4	0.6	ytTCCCCCTCCTCCgayy
brrgCAGGTAramr	ckCYCkCTCdCtc	gsCAGGACAYS	rdtcgGGAAAAGGGgArar	rvGAAaAGGATCGsCrr	sakCTGGAGAav	whacAGATACAyat	wtCCCCAaCTCCgacy	ytTCCCCCTCCTCCgayy	