

Number of RF	Non redundant RF (nrRF)		Projected RF (projRF)		Genomic coverage (nt)				
11,434	Number 1,977	RF/nrRF 5.8	Number 785	RF/projRF 14.6	60,713				
Filtered RF		Length of filtered RF (nt)			Percentage of GC of filtered RF (%)			Assigned RF	
Number	% of total	Min	Median	Max	Min	Median	Max	Number	% of filtered
10,387	90.8	28	52	1,462	17	48	88	10,387	100.0
Number of projRF made from assigned RF		Internal		Internal exonic		External genic		External exonic	
821		Number	% of assigned	Number	% of internal	Number	% of external	Number	% of ext. genic
		335	40.8	150	44.8	326	67.1	264	81.0
Genic projRF									
Number	% of total	Internal		External					
661	80.5	335	50.7	326	49.3				
Exonic projRF									
Number	% of total	Internal		External					
414	50.4	150	36.2	264	63.8				
Novel projRF									
Number	% of total	Intronic		Intergenic					
407	49.6	247	60.7	160	39.3				

Table W2: characteristics of Q1 RACEfrags. General information about the initial individual RACEfrags of the Q1 experiments is given, followed by some characteristics of the RACEfrags remaining from the USPP filter (*filtered* RACEfrags). The number of filtered RACEfrags that are indeed assigned to primers (*assigned* RACEfrags) is then provided, followed by the distribution of the projected RACEfrags into the categories genic, exonic and novel. For a more detailed analysis of Q1 RACEfrags, please refer to Supplementary section 2.1.