

Number of RF		Non redundant RF (nrRF)		Projected RF (projRF)		Genomic coverage (nt)			
4,012		Number 3,665	RF/nrRF 1.1	Number 3,102	RF/projRF 1.3	261,737			
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
3,804	94.8	28	52	826	18	53	86	3,567	93.8
Number of projRF made from assigned RF		Internal		Internal exonic		External genic		External exonic	
3,567		Number	% of assigned	Number	% of internal	Number	% of external	Number	% of ext. genic
		637	17.9	271	42.5	2,069	70.6	1,491	72.1
		Genic projRF							
Number	% of total	Internal		External					
2,706	75.9	637	23.5	2,069	76.5				
		Exonic projRF							
Number	% of total	Internal		External					
1,762	49.4	271	15.4	1,491	84.6				
		Novel projRF							
Number	% of total	Intronic		Intergenic					
1,805	50.6	944	52.3	861	47.7				

Table W4: characteristics of Q3 RACEfrags. General information about the initial individual RACEfrags of the Q3 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 2.3.