

Number of RF	Non redundant RF (nrRF)		Projected RF (projRF)		Genomic coverage (nt)				
17,740	Number 4,968	RF/nrRF 3.6	Number 1,614	RF/projRF 11.0	81,609				
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
17,296	98.5	20	32	372	19	50	91	17,429	99.0
Number of projRF made from assigned RF		Internal		Internal exonic		External genic		External exonic	
1,566		Number	% of assigned	Number	% of internal	Number	% of external	Number	% of ext. genic
		1,252	79.9	892	71.2	269	85.7	237	88.1
Genic projRF									
Number	% of total	Internal		External					
1,521	97.1	1,252	82.3	269	17.7				
Exonic projRF									
Number	% of total	Internal		External					
1,129	72.1	892	79.0	237	21.0				
Novel projRF									
Number	% of total	Intronic		Intergenic					
437	27.9	392	89.7	45	10.3				

**Table W3: characteristics of Q2 RACEfrags.** General information about the initial individual RACEfrags of the Q2 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 2.2.