Transcript biotype	**P-value**	**Bonferroni P-value**	**Odds ratio**	**Tool**
Protein coding	1 x 10 ^-10	4x10 ^ -9	0.596	DRIMSeq
Retained intron	3 x 10 ^ -4	0.012	1.552	DRIMSeq
Antisense	7 x 10 ^ -4	0.028	2.233	DRIMSeq
Processed pseudogene	0.001	0.04	0.102	DRIMSeq
Nonsense mediated decay	0.006	0.24	1.859	DRIMSeq
Processed transcript	0.126	1	1.189	DRIMSeq
Unprocessed pseudogene	0.629	1	Inf	DRIMSeq
LincRNA	0.679	1	1.127	DRIMSeq
Unitary pseudogene	1	1	Inf	DRIMSeq
3prime overlapping ncrna	1	1	Inf	DRIMSeq
Misc RNA	1	1	Inf	DRIMSeq
Non stop decay	1	1	Inf	DRIMSeq
Polymorphic pseudogene	1	1	Inf	DRIMSeq
pseudogene	1	1	Inf	DRIMSeq
Sense overlapping	1	1	Inf	DRIMSeq
snoRNA	1	1	Inf	DRIMSeq
snRNA	1	1	Inf	DRIMSeq
Transcribed processed pseudogene	1	1	Inf	DRIMSeq
Transcribed unprocessed pseudogene	1	1	1.256	DRIMSeq
Sense intronic	1	1	Inf	DRIMSeq
Antisense	0.002	0.08	3.363	DEXSeq
Protein coding	0.019	0.76	0.769	DEXSeq
LincRNA	0.028	1	2.532	DEXSeq
processed transcript	0.603	1	0.924	DEXSeq
Transcribed unprocessed pseudogene	0.640	1	Inf	DEXSeq
Nonsense mediated decay	0.701	1	1.169	DEXSeq
Retained intron	0.939	1	1.027	DEXSeq
Polymorphic pseudogene	1	1	Inf	DEXSeq
snoRNA	1	1	Inf	DEXSeq
Unitary pseudogene	1	1	Inf	DEXSeq
3prime overlapping ncrna	1	1	Inf	DEXSeq
non_ top decay	1	1	Inf	DEXSeq
Processed pseudogene	1	1	Inf	DEXSeq
pseudogene	1	1	Inf	DEXSeq
Sense intronic	1	1	Inf	DEXSeq
Sense overlapping	1	1	Inf	DEXSeq
snRNA	1	1	Inf	DEXSeq
Transcribed processed pseudogene	1	1	Inf	DEXSeq
Unprocessed pseudogene	1	1	Inf	DEXSeq
Misc RNA	1	1	Inf	DEXSeq