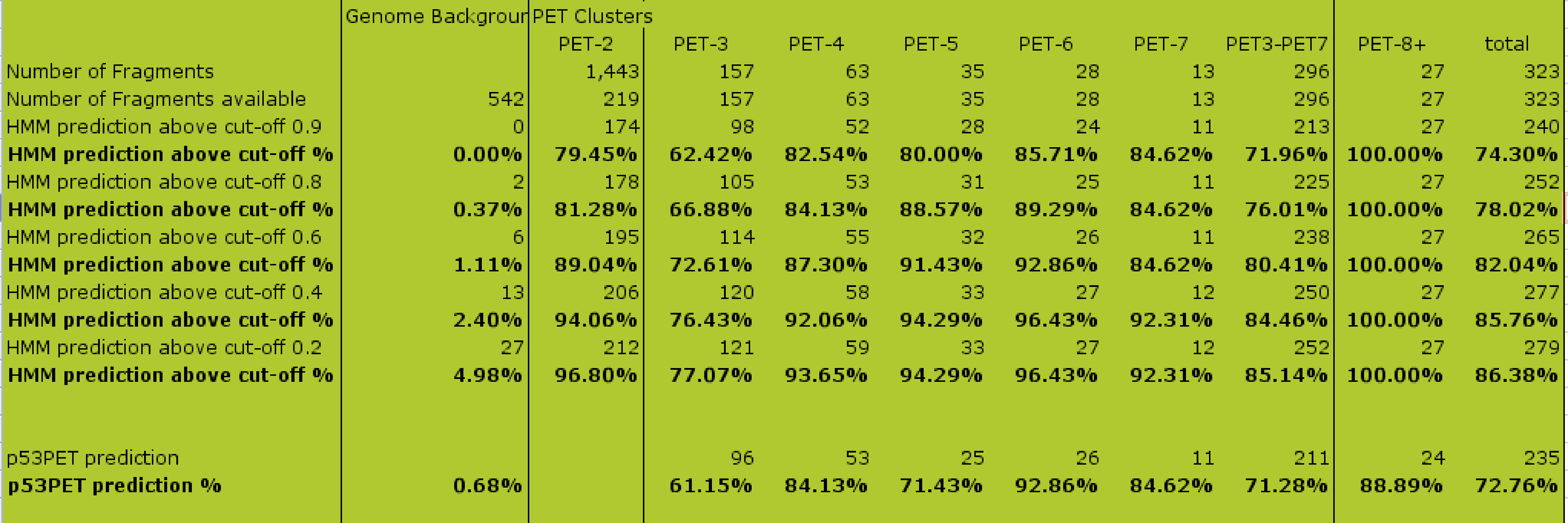

	Genome Backgroun	PET Clusters								
		PET-2	PET-3	PET-4	PET-5	PET-6	PET-7	PET3-PET7	PET-8+	total
Number of Fragments		1,443	157	63	35	28	13	296	27	323
Number of Fragments available	542	219	157	63	35	28	13	296	27	323
HMM prediction above cut-off 0.9	0	174	98	52	28	24	11	213	27	240
HMM prediction above cut-off %	**0.00%**	**79.45%**	**62.42%**	**82.54%**	**80.00%**	**85.71%**	**84.62%**	**71.96%**	**100.00%**	**74.30%**
HMM prediction above cut-off 0.8	2	178	105	53	31	25	11	225	27	252
HMM prediction above cut-off %	**0.37%**	**81.28%**	**66.88%**	**84.13%**	**88.57%**	**89.29%**	**84.62%**	**76.01%**	**100.00%**	**78.02%**
HMM prediction above cut-off 0.6	6	195	114	55	32	26	11	238	27	265
HMM prediction above cut-off %	**1.11%**	**89.04%**	**72.61%**	**87.30%**	**91.43%**	**92.86%**	**84.62%**	**80.41%**	**100.00%**	**82.04%**
HMM prediction above cut-off 0.4	13	206	120	58	33	27	12	250	27	277
HMM prediction above cut-off %	**2.40%**	**94.06%**	**76.43%**	**92.06%**	**94.29%**	**96.43%**	**92.31%**	**84.46%**	**100.00%**	**85.76%**
HMM prediction above cut-off 0.2	27	212	121	59	33	27	12	252	27	279
HMM prediction above cut-off %	**4.98%**	**96.80%**	**77.07%**	**93.65%**	**94.29%**	**96.43%**	**92.31%**	**85.14%**	**100.00%**	**86.38%**
p53PET prediction			96	53	25	26	11	211	24	235
p53PET prediction %	**0.68%**		**61.15%**	**84.13%**	**71.43%**	**92.86%**	**84.62%**	**71.28%**	**88.89%**	**72.76%**