

Table 2. Sensitivity of the non-expressed resources in the annotation of the human chromosome 14

Gene categories	Nb of exons	Exofish	BLAT_Mouse	GENSCAN exons	FGENESH exons	Exofish + BLAT_Mouse	Exofish + BLAT_Mouse + GENSCAN exons + FGENESH exons
<b>Known genes</b>	5206	2669 (52%) <i>(82%)</i>	4121 (79%) <i>(90%)</i>	4074 (78%) <i>(92%)</i>	3841 (74%) <i>(90%)</i>	4382 (84%) <i>(96%)</i>	4884 (94%) <i>(98%)</i>
<b>Novel genes</b>	765	204 (27%) <i>(47%)</i>	469 (61%) <i>(72%)</i>	501 (65%) <i>(71%)</i>	421 (55%) <i>(65%)</i>	504 (66%) <i>(75%)</i>	632 (83%) <i>(85%)</i>
<b>Novel transcripts</b>	32	10 (31%) <i>(55%)</i>	12 (38%) <i>(55%)</i>	17 (53%) <i>(73%)</i>	14 (44%) <i>(64%)</i>	15 (47%) <i>(64%)</i>	21 (66%) <i>(82%)</i>
<b>Predicted genes</b>	68	28 (41%) <i>(82%)</i>	47 (69%) <i>(100%)</i>	50 (74%) <i>(91%)</i>	57 (84%) <i>(100%)</i>	50 (74%) <i>(100%)</i>	68 (100%) <i>(100%)</i>
<b>Putative genes</b>	600	19 (3%) <i>(7%)</i>	97 (16%) <i>(32%)</i>	42 (7%) <i>(17%)</i>	35 (6%) <i>(11%)</i>	99 (17%) <i>(33%)</i>	141 (24%) <i>(46%)</i>
<b>Gene segments</b>	346	31 (9%)	167 (48%)	184 (53%)	173 (50%)	167 (48%)	242 (70%)
<b>Pseudogene segments</b>	147	10 (6%)	69 (44%)	54 (34%)	4 (25%)	69 (47%)	96 (65%)
<b>Pseudogenes</b>	321	222 (69%)	255 (79%)	172 (54%)	118 (37%)	291 (91%)	303 (94%)
<b>All categories</b>	<b>7495</b>	<b>3193</b> <b>(42%)</b>	<b>5237</b> <b>(70%)</b>	<b>5094</b> <b>(68%)</b>	<b>4663</b> <b>(62%)</b>	<b>5577</b> <b>(74%)</b>	<b>6387</b> <b>(83%)</b>

Definitions of the categories are described in the main article. The total number of exons in each category is indicated in the second column. The number and the fraction (in brackets) of exons identified with the various resources or with combinations of resources are indicated in the following columns. The values in italics correspond to the fractions of *gene models* identified with the various resources or combinations.