

Error and Error Mitigation in Low-Coverage Genomes

M.J. Hubisz, M.F. Lin, M. Kellis, A. Siepel

Table S5: CONGO performance by chromosome

Chrom.	Exon Sp (%) ^a		Exon Sn (%) ^b	
	Baseline	SEM ^c	Baseline	SEM ^c
1	90.10	90.67	83.00	83.11
2	90.34	90.75	85.52	85.43
3	90.43	90.81	86.27	86.05
4	89.43	89.79	84.75	84.76
5	89.33	89.54	85.75	85.69
6	89.16	90.21	84.05	84.48
7	90.61	91.42	81.99	82.31
8	89.53	90.07	85.05	85.18
9	89.97	90.72	84.53	84.61
10	90.02	90.43	83.94	83.66
11	86.51	87.35	84.52	84.86
12	91.11	91.64	85.83	85.83
13	90.62	90.97	81.85	82.05
14	88.55	89.43	86.19	86.38
15	91.28	91.98	83.00	83.07
16	89.99	90.61	79.69	79.86
17	90.93	91.65	83.53	83.83
18	89.24	89.85	88.07	88.40
19	89.93	90.45	71.70	71.83
20	91.38	92.13	85.24	85.70
21	91.36	92.09	81.76	82.04
22	90.83	91.53	80.33	80.59
X	88.06	88.88	74.80	75.04
Y	68.42	68.42	5.13	5.13

^aComputed from union of RefSeq, ENSEMBL, UCSC, and GENCODE gene sets (R+E+U+G).

^bComputed from CCDS gene set.

^cSEM was used for training and testing. Bold indicates an improvement.