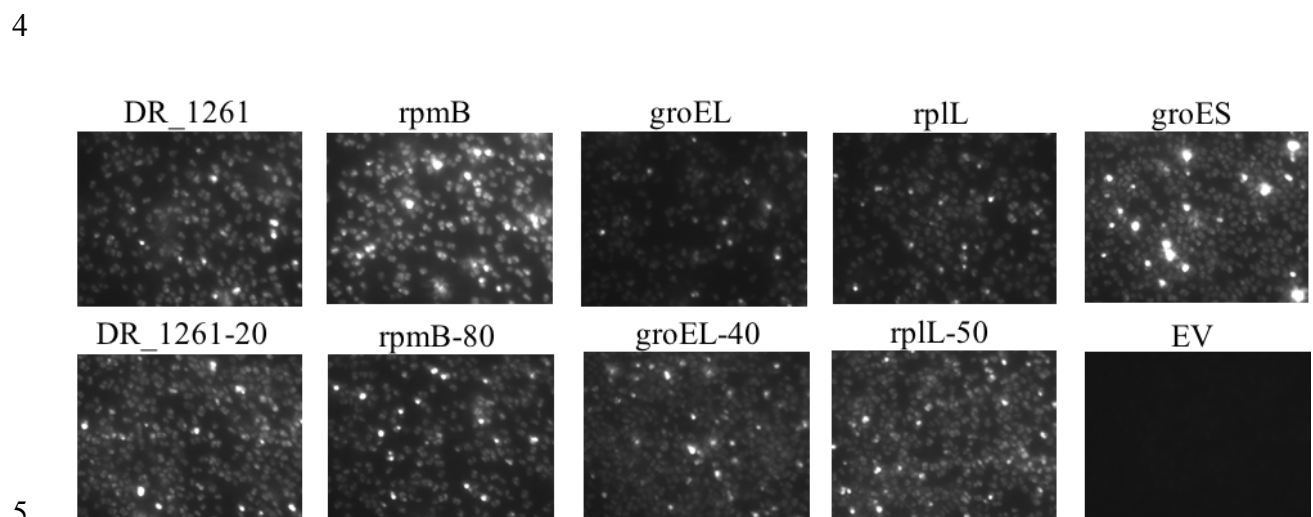


1  
2 **Figure S1.** Fluorescent microscopy images of promoter strains in stationary phase imaged at 630x show  
3 cell-to-cell heterogeneity in fluorescence that varies across promoter strains. Scale bar is 20  $\mu$ m.



5  
6 **Figure S2.** Fluorescence imaging of full length and truncated promoters show conserved heterogeneity of  
7 expression across individual cells.

8  
9 **Table S1.** BPROM predicts -10 and -35 sites on several candidates. Intergenic regions for selected  
10 candidates and benchmarks were analyzed by BPROM to assess the computational identification of

11 promoter elements in *D. radiodurans*.

Gene	Length	Position	LDF	-10 box position	seq-10	-35 box position	Seq -35
<i>DR_2508</i>	428	280	4.99	265	ctctataat	244	ttgaca
<i>RecA</i>	501	464	0.53	449	ccgcaccct	429	ttgacc
<i>rpmB</i>	257	106	1.17	91	ggttaagat	74	ttcgg
<i>tufB1</i>	136	98	1.98	83	tgatatagt	64	acgcca
<i>tufB2</i>	238	200	1.98	185	tgatatagt	166	acgcca
<i>dnaK</i>	141	85	4.05	70	tcgtatgat	50	ttgact
<i>groES</i>	228	150	2.82	135	ctctaccat	114	ttgaca
<i>DR_1473</i>	332	130	0.22	115	gattacgaa	97	ttgaac
<i>DR_0325</i>	186	160	0.78	146	cggtatggt	120	ttgctg
<i>uvrA</i>	202	113	3.77	98	tgtagaat	81	ttcagg
<i>DR_0911</i>	132	66	0.85	51	cgccaacat	26	ctgtca
<i>DR_1654</i>	106	61	1.6	46	ttgtattgt	22	ttcct
<i>mutL</i>	425	127	2.79	112	ttctcttat	92	gtcaaa
<i>LexA</i>	211	133	2.3	118	ccctattct	94	ttgtca
<i>ClpB</i>	397	216	0.7	201	cgcgagaat	182	ctgttt
<i>DR_1910</i>	243	84	3.46	69	ttttttat	47	ttgcca
<i>rpmI</i>	178	62	2.27	43	gtgtaaaat	27	ctgcca
<i>DR0781</i>	161	97	0.99	82	gtctacgat	61	gtccca

12

13 **Table S2.** Neural Network Promoter Predictor prediction of top eight promoters and benchmarks

14 identifies potential transcription start sites of *rpmB*, *DR\_2508*, and *dnaK*.

Strain	Start	End	Score	Promoter Sequence
<i>dnaK</i>	2	47	0.96	ctttcttgatgttgccagcaaacctgagtctaatacactcaagtctatt
<i>dnaK</i>	44	89	0.95	agtctattgactctgggggattgtagtcgtatgatacttgcaagtcaaga
<i>DR_1654</i>	44	89	0.98	attgtattgtcctcacgttgttcaagcttcatcacttcagggtcagt
<i>DR_2508</i>	239	284	0.96	tcacctgacagagctattatctcatctctataattcgcgccgggatctc
<i>groES</i>	109	154	0.94	gtcagttgacatTTTTcttatcggcgctctaccatccgtgacggattgaa
<i>kata</i>	93	138	0.84	gggccctggacattgagaatgattctcaatatggtgcaggagcttcggg
<i>LexA</i>	92	137	0.88	agttgtcagtcaggacgacggtcagccctattctttccgttcaaactc
<i>RecA</i>	453	498	0.96	accctgtagaacactggttacgtcctccatataactccgggtgaggtgtt
<i>rpmB</i>	41	86	0.81	ggagtggcgaaggetccgcgccccagggtctatctttcgggctcgcagta

15

16

17 **Table S3.** bTSSfinder was used to find potential sigma sequences for identification of top candidate and  
18 benchmark promoters. Assessment with bTSSfinder results in prediction of several potential promoter  
19 sequences in *DR\_2508*, two in *DR\_1473* and one in *rpmB*.

Promoter	TSS	Score	sigma	box35	box35	box10	box10 seq
				pos	seq	pos	
<i>DR_2508</i>	281	1.92	38	244	ttgaca	268	tataat
<i>DR_2508</i>	270	1.91	24	234	aaaagt	259	tctca
<i>DR_2508</i>	266	1.97	70	230	gacaaa	254	tattat
<i>DR_2508</i>	240	1.87	28	208	agccgact	227	gacgacaa
<i>DR_2508</i>	201	1.92	32	166	accaagt	188	gacctcaaac
<i>RecA</i>	413	1.84	28	380	tccgcgca	399	gccgaaag
<i>RecA</i>	410	1.79	32	374	ggctgct	396	tccgccgaaa
<i>RecA</i>	228	1.73	24	193	acacct	218	getca

<i>rpmB</i>	201	1.68	28	165	agcagcac	184	cccggaga
<i>DR_1473</i>	247	1.16	32	213	agatgcg	233	gcccgcgtct
<i>DR_1473</i>	204	1.75	24	172	caaaga	193	gcgaa
<i>mutL</i>	361	1.83	32	327	ggctaaa	347	gccccacgt
<i>mutL</i>	229	1.78	38	189	ctcgcg	216	cagact
<i>mutL</i>	214	1.95	24	181	gcacgg	203	actca
<i>mutL</i>	208	1.95	28	176	aaagcgca	195	tccgtaga
<i>ClpB</i>	318	0.54	24	285	aatca	307	tctct
<i>ClpB</i>	217	1.82	70	182	ctgttt	204	gagaat
<i>ClpB</i>	207	1.74	32	171	catttga	193	gtcaccagcg

---

20

21