

Table S2 Hfq coIP peaks associated with mRNA coding regions.

<i>Peaks That Fully Encompass mRNA Coding Regions</i>			
Gene	Peak Length	Peak Coord	RPKM Ratio^a
<i>yqzF</i>	256	2507015-2507270	36.5
<i>yqgW</i>	214	2565687-2565900	31.4
<i>yhdX</i>	176	1038635-1038810	29.0
<i>yxzF</i>	113	3964110-3964222	24.3
<i>ydzK</i>	191	490817-491007	20.7
<i>yuzK</i>	183	3360983-3361165	18.3
<i>ypmP</i>	226	2292419-2292644	17.1
<i>yxiE</i>	460	4031798-4032257	16.3
<i>yhzC</i>	244	1116582-1116825	11.8
<i>veg</i>	276	52761-53036	10.1
<i>rpsU</i>	158	2620383-2620540	9.00
<i>ywzA</i>	229	3918808-3919036	7.50
<i>sunA</i>	210	2269505-2269714	5.64
<i>yzkF</i>	265	1485069-1485333	4.70
<i>yqzM</i>	160	2637373-2637532	4.70
<i>rsiW</i>	675	195360-196034	3.85
<i>yzkW</i>	110	1534108-1534217	2.94
<i>Peaks Associated With Start Codons</i>			
Gene	Peak Length	Peak Coord	RPKM Ratio
<i>yitY</i>	88	1192831-1192918	1200
<i>yvpB</i>	64	3589594-3589657	160
<i>addB</i>	146	1136313-1136458	120
<i>tcyL</i>	152	3006440-3006591	51.1
<i>yheJ</i>	93	1045004-1045096	45.9
<i>yjiA</i>	66	1290892-1290957	26.2
<i>yqgY</i>	82	2564619-2564700	26.0
<i>ypjP</i>	83	2299076-2299158	25.7
<i>glnJ</i>	56	265494-265549	25.4
<i>ctaD</i>	121	1561556-1561676	23.5
<i>yopK</i>	102	2210061-2210162	21.9
<i>yneF</i>	66	1922546-1922611	16.9
<i>minJ</i>	72	3621478-3621549	16.9
<i>nagP</i>	178	840647-840824	13.7
<i>csbA</i>	133	3615078-3615210	11.5
<i>sboA</i>	166	3836036-3836201	3.67
<i>hpr</i>	102	1073612-1073713	2.64
<i>Peaks Associated With Stop Codons</i>			
Gene	Peak length	Peak Coord	RPKM Ratio
<i>mecA</i>	106	1229626-1229731	102
<i>fadE</i>	271	3367001-3367271	76.9
<i>yopS</i>	192	2203847-2204038	72.5
<i>yhdT</i>	70	1036862-1036931	71.1
<i>rapB</i>	117	3770985-3771101	32.1
<i>spoIVA</i>	63	2386180-2386242	27.4
<i>hfq</i>	76	1867638-1867713	24.1

<i>tlp</i>	136	1930562-1930697	23.9
<i>sacT</i>	72	3906125-3906196	21.2
<i>ywmB</i>	91	3779267-3779357	20.1
<i>yebD</i>	134	697224-697357	18.9
<i>glpD</i>	103	1006530-1006632	14.8
<i>cccA</i>	136	2599474-2599609	14.2
<i>fbp</i>	79	4130048-4130126	14.1
<i>rnr</i>	109	3451848-3451956	13.9
<i>degU</i>	73	3644596-3644668	13.9
<i>yjbJ</i>	95	1235156-1235250	13.9
<i>ytzI</i>	102	3136927-3137028	11.9
<i>csbA</i>	133	3615078-3615210	11.5
<i>ydbL</i>	221	504809-505029	11.0
<i>ohrB</i>	189	1382249-1382437	10.7
<i>degA</i>	154	1164013-1164166	9.90
<i>hutP</i>	235	4041723-4041957	9.51
<i>clpP</i>	133	3546708-3546840	5.58
<i>yuiB</i>	126	3299316-3299441	5.00
<i>adcA</i>	155	309152-309306	3.67
<i>yqhP</i>	152	2542248-2542475	2.34
<i>citZ</i>	77	2981133-2981209	1.91
<i>Peaks Within mRNA Coding Regions</i>			
Gene	Peak Length	Peak Coord	RPKM Ratio^a
<i>srfAA</i>	162	377729-377890	270
<i>bioD</i>	137	3091835-3091971	217
<i>yitQ</i>	98	1185464-1185561	142
<i>miaA</i>	64	1866987-1867050	108
<i>yvcD</i>	77	3576599-3576675	104
<i>ykuC</i>	228	1476174-1476401	103
<i>truB</i>	97	1737649-1737745	94.3
<i>yqhL</i>	61	2545230-1737745	66.6
<i>yqzK</i>	108	2449501-2449608	63.0
<i>yukB</i>	109	3273707-3273815	55.0
<i>opuBB</i>	89	3461854-3461942	49.1
<i>secDF</i>	60	2828778-2828837	42.3
<i>yerI</i>	54	725248-725301	41.4
<i>gutP</i>	52	668773-668824	41.0
<i>ycbU</i>	80	288459-288538	40.7
<i>srfAB</i>	258	389722-389979	31.3
<i>besA</i>	107	3292960-3293066	31.3
<i>alaT</i>	134	3225984-3226117	30.3
<i>pnpA</i>	102	1739618-1739719	29.9
<i>wapA</i>	54	4025841-4025894	28.2
<i>radC</i>	54	2862144-2862197	26.3
<i>dnaK</i>	89	2627350-2627438	25.1
<i>ydiG</i>	126	646894-647019	25.0
<i>fadE</i>	65	3367929-3367993	23.4
<i>glcD</i>	97	2934073-2934169	23.0
<i>copA</i>	64	3443019-3443082	20.6

<i>ykrW</i>	125	1427086-1427210	18.7
<i>acdA</i>	96	3814111-3814206	18.0
<i>treP</i>	114	851440-851553	17.8
<i>holB</i>	97	40752-40848	17.8
<i>ytrP</i>	71	3034960-3035030	17.2
<i>srfAA</i>	425	386241-386665	17.0
<i>comC</i>	60	2864721-2864780	16.9
<i>yflT</i>	164	827484-827647	16.1
<i>ydaS</i>	94	492709-492802	15.1
<i>sigW</i>	379	194889-195267	14.2
<i>ydaG</i>	225	473804-474028	13.5
<i>ctrA</i>	160	1023440-1023599	13.3
<i>ypjP</i>	159	2298907-2299065	12.1
<i>malP</i>	101	892290-892390	12.1
<i>besA</i>	138	3292745-3292882	11.8
<i>thiF</i>	188	1246288-1246475	11.3
<i>yusK</i>	126	3369240-3369365	10.5
<i>ygzB</i>	155	945000-945154	8.52
<i>dhbF</i>	61	3287221-3287281	7.79
<i>yfmE</i>	66	823759-823824	6.47
<i>gapB</i>	121	2967347-2967467	2.79
<i>yheE</i>	103	1050457-1050559	2.50
<i>citZ</i>	71	2981810-2981880	2.06
<i>ybfO</i>	56	251096-251151	2.06

^a The expression of each peak was quantified in reads per kilobase per million mapped reads, or ‘RPKM’ (Mortazavi *et al.*, 2008). The ratio of these values for the Hfq^{FLAG} and mock control samples was taken as an indicator of Hfq-mediated enrichment.