

Table 2. Associations between the status of each tRF and the chromosomal aberration (+1q).

tRF status	Total	Chromosomal aberration (+1q)		<i>P</i> value ¹
		Presence	Absence	
i-tRF-Pro^{TGG}				
Positive	36	18 (50.0%)	18 (50.0%)	0.38
Negative	18	6 (33.3%)	12 (66.7%)	
i-tRF-Glu^{CTC}				
Positive	37	18 (48.6%)	19 (51.4%)	0.37
Negative	16	5 (31.2%)	11 (68.8%)	
i-tRF-His^{GTG}				
Positive	38	19 (50.0%)	19 (50.0%)	0.24
Negative	16	5 (31.2%)	11 (68.8%)	
i-tRF-Gly^{GCC}				
Positive	22	14 (63.6%)	8 (36.4%)	0.027 ²
Negative	32	10 (31.2%)	22 (68.8%)	
i-tRF-Phe^{GAA}				
Positive	32	17 (53.1%)	15 (46.9%)	0.17
Negative	22	7 (31.8%)	15 (68.2%)	
3'-tRF-Leu^{AAG/TAG}				
Positive	23	13 (56.5%)	10 (43.5%)	0.17
Negative	31	11 (35.5%)	20 (64.5%)	

¹ Calculated using Fischer's exact test. ² Italics indicate a significant *P* value.