Table S15. Calculated densities of UV-induced mutations

Target	**Origin of mutants**	**Distribution**	**Number of mutations in a mutant**						***X* (mutations per reporter)**[3]	***D* (mutations per kb)**[4]	**(P_{mut})**[5]	**P(χ^2)** [6]
			1	**2**	**3**	**4**	**5**	**6**				
CAN1	DSB-cen, UV (20)[1]	Observed	17	6	2	0	0	0	-	-		-
		Expected (1-3)[2]	16.3	6.5	1.7	-	-	-	0.8	0.45	0.55	0.9
		Expected (2,3)	-	5.7	1.8	-	-	-	0.95	0.53	0.61	0.8
	DSB-cen, UV (45)	Observed	21	7	4	0	0	0	-	-		-
		Expected (1-3)	12.2	10.3	5.9	-	-	-	0.85	0.48	0.57	0.6
		Expected (2,3)	-	6.5	3.0	-	-	-	1.4	0.79	0.75	0.6
subtel. *LYS2*	37°C (G2-arrest) UV (45)	Observed	7	16	5	4	1	1	-	-		-
		Expected (1-6)	9.6	10	7.4	4	1.7	0.6	2.2	0.49	0.88	0.4
		Expected (2-6)	-	15.3	7.7	2.9	0.9	0.2	1.5	0.34	0.78	0.7

Footnotes to Table S15.

[1] UV doze, J/m^2 is shown in parentheses.

[2] Mutant alleles with the multiplicity shown in parentheses were included into calculations.

[3] X - expected average number of mutations per target.

[4] D - expected average number of mutations per kilobase in *CAN1* (1773 nt) or *LYS2* (4396 nt) regions.

[5] P_{mut} - probability that the cell contains at least one mutation in a target, ($1-P_0$), where $P_0=e^{-X}$;

[6] $P(\chi^2)$ – probability of differences between observed and expected ratios based on χ^2 distribution.