

Table S2. Proportion of CNV types per genome in primary and distant metastatic melanomas.

tumor type	N	avg. % of genome altered $\pm SE$		avg. % of CNG ¹ $\pm SE$		avg. % of hCNG ² $\pm SE$		avg. % of lCNG ³ $\pm SE$	
		multiple group comparison	primary vs. all metastasis	multiple group comparison	primary vs. all metastasis	multiple group comparison	primary vs. all metastasis	multiple group comparison	primary vs. all metastasis
primary	10	13.37 ± 2.73	13.37 ± 2.73	10.08 ± 1.89	10.08 ± 1.89	0.09 ± 0.07	0.09 ± 0.07	9.99 ± 1.90	9.99 ± 1.90
brain	10	30.79 ± 5.14		17.87 ± 2.59		0.41 ± 0.21		17.45 ± 2.62	
liver	9	16.17 ± 4.46	23.94 ± 2.92	10.16 ± 2.77	14.33 ± 1.72	1.43 ± 0.79	1.67 ± 0.54	8.73 ± 2.32	12.66 ± 1.63
lung	9	24.10 ± 4.75		14.58 ± 3.32		3.30 ± 1.35		11.28 ± 2.95	
p-value ⁸		0.056	0.045	0.179	0.214	0.040	0.017	0.113	0.507

tumor type	N	avg. % of CNL ⁴ $\pm SE$		avg. % of hoCNL ⁵ $\pm SE$		avg. % of heCNL ⁶ $\pm SE$		avg. % of LOH ⁷ $\pm SE$	
		multiple group comparison	primary vs. all metastasis	multiple group comparison	primary vs. all metastasis	multiple group comparison	primary vs. all metastasis	multiple group comparison	primary vs. all metastasis
primary	10	3.29 ± 1.04	3.29 ± 1.04	0.00 ± 0.00	0.00 ± 0.00	3.29 ± 1.04	3.29 ± 1.04	3.00 ± 0.30	3.00 ± 0.30
brain	10	12.93 ± 2.94		0.07 ± 0.05		12.85 ± 2.93		8.10 ± 1.61	
liver	9	6.02 ± 2.19	9.61 ± 1.48	0.02 ± 0.02	0.04 ± 0.02	6.00 ± 2.18	9.58 ± 1.47	12.31 ± 4.13	10.60 ± 1.53
lung	9	9.52 ± 2.03		0.01 ± 0.01		9.51 ± 2.02		11.68 ± 1.75	
p-value ⁸		0.021	0.019	0.085	0.012	0.021	0.019	0.003	0.0004

¹copy number gain (both high- and low gains included)

²high copy number gain (CN ≥ 4)

³low copy number gain ($2 < CN < 4$)

⁴copy number loss (both homo- and heterozygous losses included)

⁵homozygous copy number loss (CN=0)

⁶*heterozygous copy number loss ($0 < CN < 2$)*

⁷*loss of heterozygosity (copy neutral)*

⁸*Kruskal-Wallis (for multiple group analysis) or Mann-Whitney-Wilcoxon test (for primary vs. all metastasis analysis)*