

Table S3 HLA region allelic imbalance analysis, related to Figure 2.

Clonal selection analysis:

Selected	Not Selected	NA*
12	2	12

*includes cases with no-LOH in either primary or metastasis
Binomial test (selected vs not selected) P=0.000462

Matched patient analysis:

		<u>Metastatic regions:</u>			
		No-LOH	LOH		
<u>Primary Regions:</u>	No-LOH	12	4	17	37.0%
	LOH	1	9	10	
		14	13		
			50.0%		

McNemar's test P=0.37.

Notes:

- 1) McNemar's test does not account for subclonal (primary) to clonal (metastases) selection, which is the prevalent mechanism, rather than newly acquired (*de novo*) events private to metastases (only 5.4% of events were *de novo*). Hence we see a discrepancy between the two test results.
- 2) In the clonal selection analysis, the null background selection rate used for the binomial test is the same passenger SCNA rate as used in Figure 2C. We acknowledge the limitation of this approach, *i.e.* the potential for assay specific differences between HLA detection (polymorphic STR markers) and passenger SCNA rate estimation (NGS based analysis).
- 3) NGS detection of HLA imbalance using the recently published LOHHLA tool was not possible from custom panel data.