Supplementary information for

Aurora kinase A (AURKA) interaction with Wnt and Ras-MAPK signalling pathways in colorectal cancer

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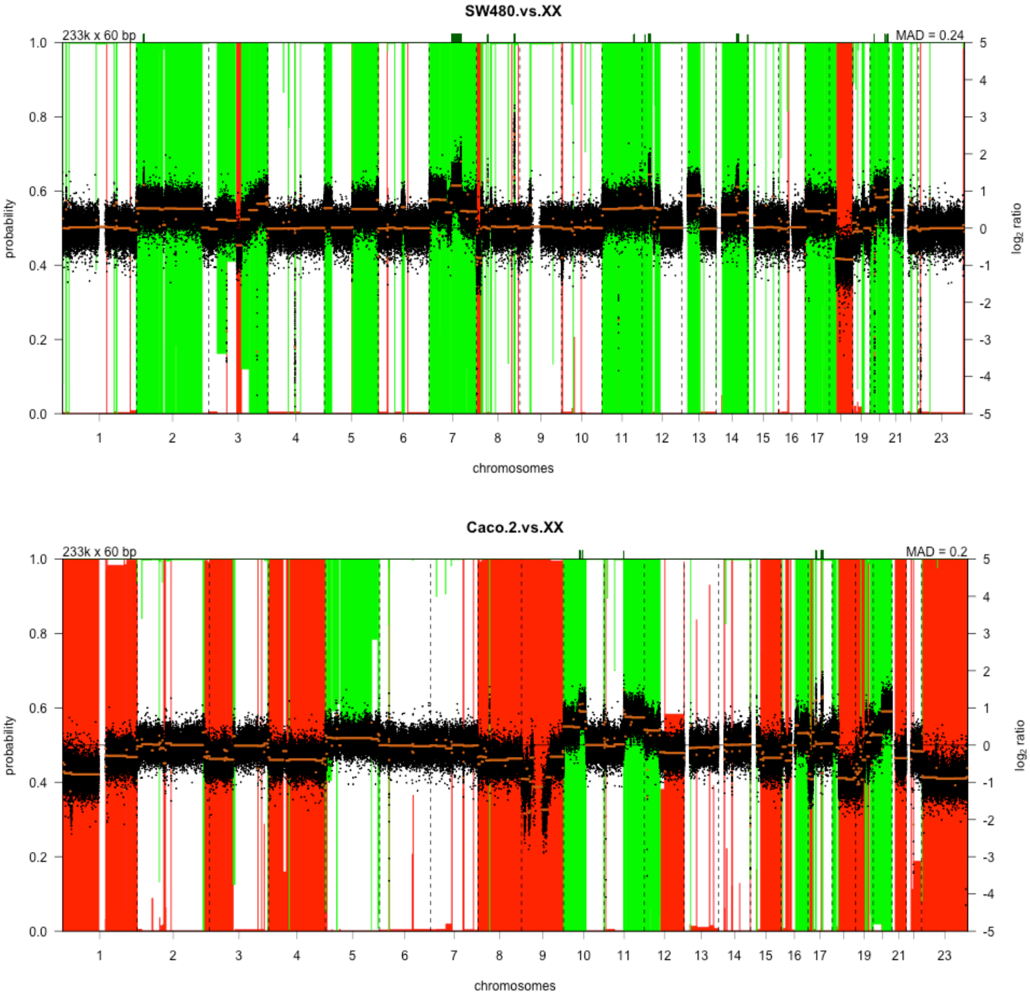
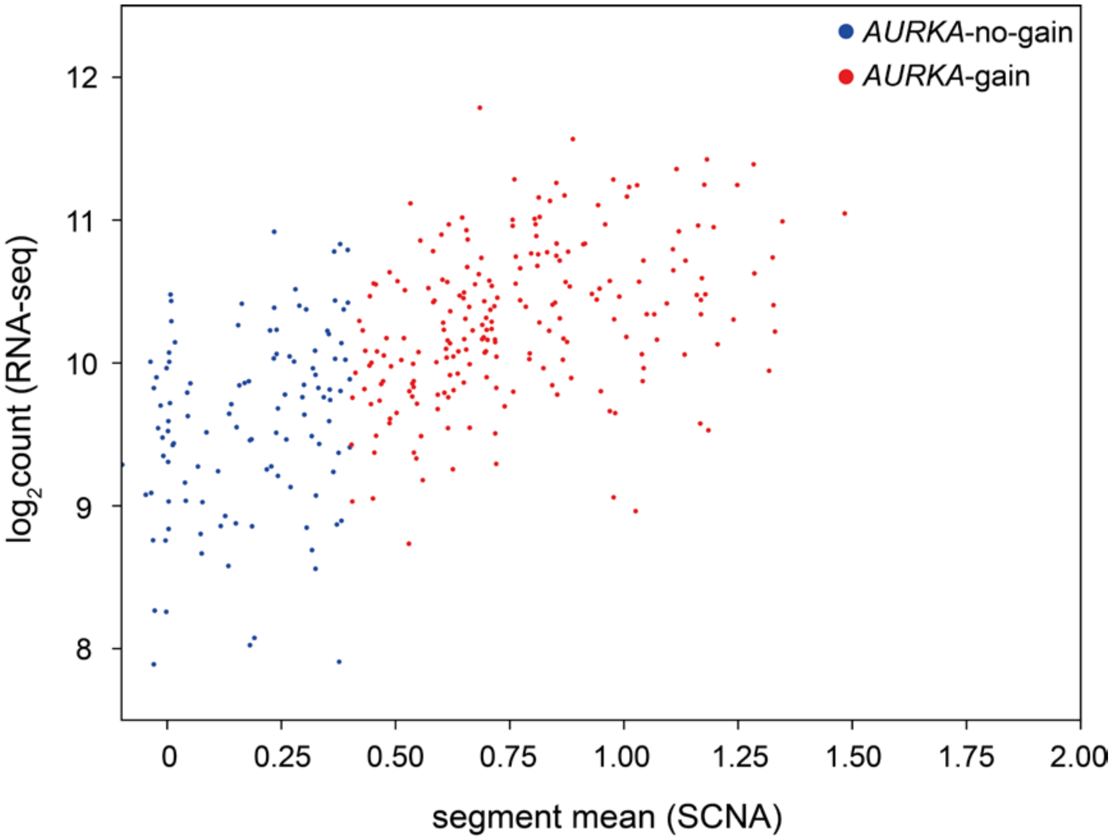
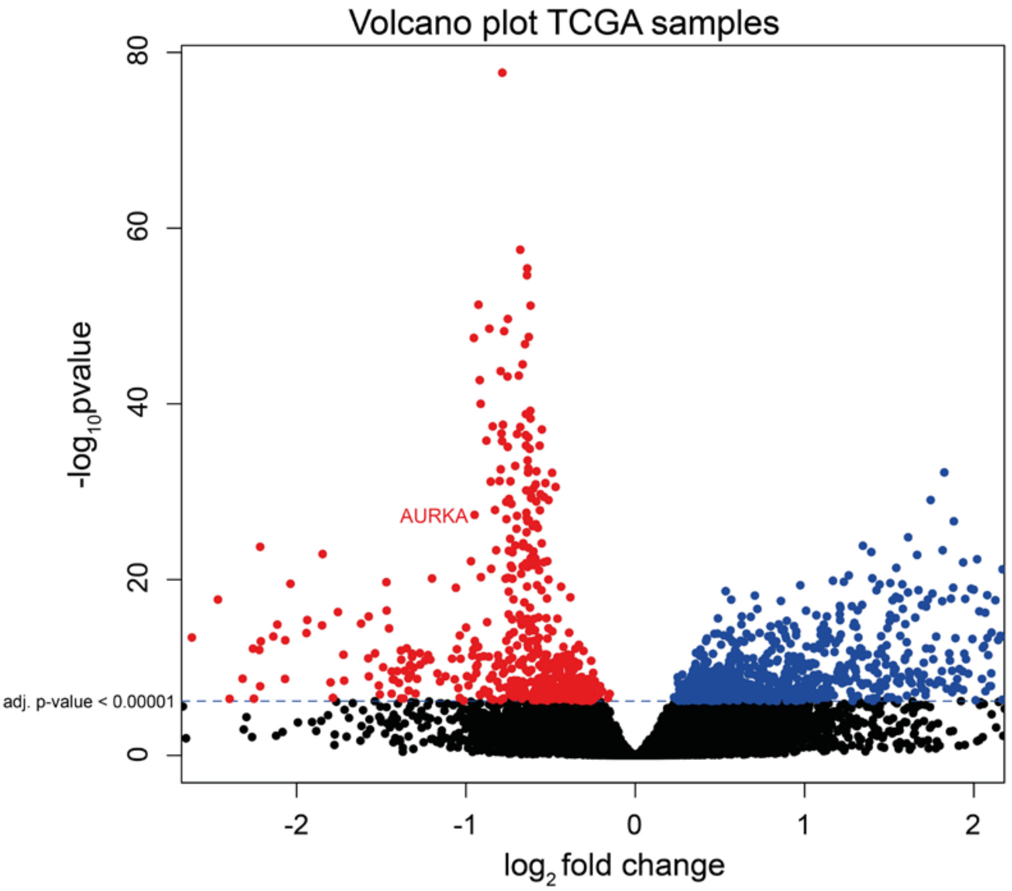


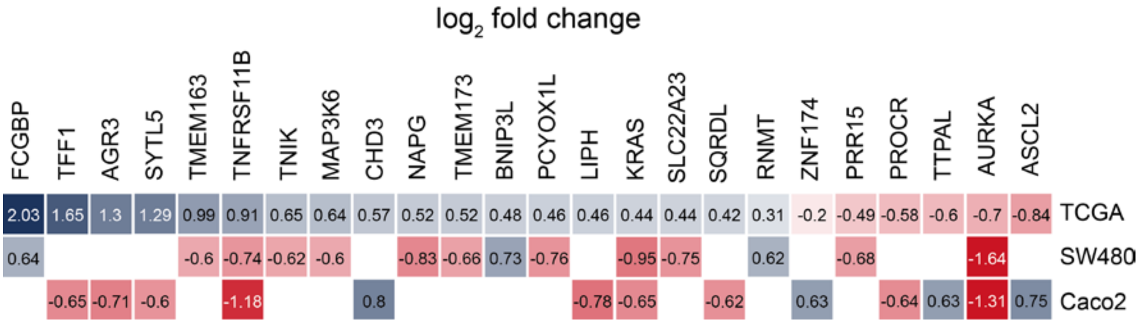
Supplementary Fig. S1. DNA copy number profile (aCGH) for SW480 (upper panel) and Caco2 (lower panel), respectively. Green represents regions with gain and red represents regions with loss (also represented by the positive/negative $\log_2$ ratio). The figures show that 20q is gained in both cells lines, SW480 otherwise has many gained regions, whereas Caco2 has many lost regions.



Supplementary Fig. S2. Segment mean (SCNA; DNA copy number) plotted against $\log_2$count (RNA-seq, mRNA expression) for 330 *AURKA*-no-gain and *AURKA*-gain TCGA COADREAD samples. *AURKA*-gain samples were determined at a segment mean >= 0.4.



Supplementary Fig. S3. Volcano plot of the genes differentially expressed between 330 *AURKA*-no-gain and *AURKA*-gain TCGA COADREAD samples. The threshold for significantly deregulated genes was set at an adjusted p-value less than 10^{-5}.


log2 fold change

	FCGBP	TFF1	AGR3	SYTL5	TMEM163	TNFRSF11B	TNIK	MAP3K6	CHD3	NAPG	TMEM173	BNIP3L	PCYOX1L	LIPH	KRAS	SLC22A23	SQRDL	RNMT	ZNF174	PRR15	PROCR	TTPAL	AURKA	ASCL2
TCGA	2.03	1.65	1.3	1.29	0.99	0.91	0.65	0.64	0.57	0.52	0.52	0.48	0.46	0.46	0.44	0.44	0.42	0.31	-0.2	-0.49	-0.58	-0.6	-0.7	-0.84
SW480	0.64				-0.6	-0.74	-0.62	-0.6		-0.83	-0.66	0.73	-0.76		-0.95	-0.75		0.62		-0.68			-1.64	
Caco2		-0.65	-0.71	-0.6		-1.18			0.8					-0.78	-0.65		-0.62		0.63		-0.64	0.63	-1.31	0.75

Supplementary Fig. S4. The significantly deregulated genes from the TCGA COADREAD DEA (*AURKA*-no-gain vs. *AURKA*-gain) compared to the sets of genes significantly deregulated in the DEA of the two cell lines, SW480 and Caco2, upon *AURKA* downmodulation. $\log_2$ fold change is shown for each gene in the intersection, further illustrated by blue for upregulation and red for downregulation.