Supplementary Table 1. List of the differentially oxidized cysteine-containing proteins in MDA-MB-231 cells upon AA treatment identified by mass spectrometry “redoxome”

203/2910 proteins accession	Peptide count	Unique peptides	Confidence score	Anova (*P* value)		Fold change (ratio)*		Highest mean condition	Lowest mean condition	Gene
				Exp1	**Exp2**	**Exp1**	**Exp2**			
Q9BW04	1	1	1.996	7.29E-06	1.28E-04	**4.552**	**3.942**	AA	NT	***SARG***
Q9NU22	1	1	2.221	1.60E-05	4.58E-06	**6.246**	**3.770**	AA	NT	***MDN1***
Q13838	7	7	39.611	2.29E-05	1.45E-03	**-2.520**	**-2.274**	NT	AA	***DDDX39B***
P13647	22	22	77.643	2.31E-05	7.48E-05	**2.184**	**4.198**	AA	NT	***KRT5***
P04259	23	23	95.879	2.74E-05	6.92E-04	**1.892**	**2.917**	AA	NT	***KRT6B***
Q8IXI1	2	2	6.320	4.90E-05	3.29E-02	**-4.547**	**-4.524**	NT	AA	***RHOT2***
P13639	52	52	236.125	6.75E-05	2.07E-05	**-3.088**	**-1.520**	NT	AA	***EEF2***
P07477	1	1	3.752	7.45E-05	2.33E-04	**6.721**	**3.084**	AA	NT	***PRSS1***
P31151	3	3	9.102	1.18E-04	6.36E-03	**5.929**	**6.698**	AA	NT	***S100A7***
O60610	9	9	35.783	1.39E-04	8.50E-03	**-2.925**	**-1.813**	NT	AA	***DIAPH1***
Q6XZF7	26	26	106.600	1.72E-04	2.08E-04	**4.037**	**3.034**	AA	NT	***DNMBP***
P01040	2	2	6.694	1.74E-04	3.44E-05	**7.105**	**5.313**	AA	NT	***CSTA***
Q86Y46	3	3	9.558	1.77E-04	1.52E-04	**2.401**	**5.967**	AA	NT	***KRT73***
P11217	2	1	6.664	1.84E-04	2.15E-04	**4.974**	**5.678**	AA	NT	***PYGM***
Q92615	5	5	16.931	1.88E-04	3.47E-03	**4.655**	**2.273**	AA	NT	***LARP4B***
Q13177	9	8	28.990	2.22E-04	1.40E-03	**7.789**	**2.808**	AA	NT	***PAK2***
Q6UWB1	1	1	5.803	2.25E-04	1.47E-04	**-3.521**	**-2.024**	NT	AA	***IL27RA***
P02538	5	5	16.851	2.30E-04	1.57E-04	**2.318**	**2.243**	AA	NT	***KRT6A***
Q09028	3	3	9.705	2.52E-04	5.78E-04	**5.144**	**3.921**	AA	NT	***RBBP4***
Q08554	3	3	18.849	2.73E-04	4.06E-03	**1.786**	**3.385**	AA	NT	***DSC1***
Q02878	8	8	28.829	2.77E-04	1.30E-04	**-2.274**	**-2.551**	NT	AA	***RPL6***
O95864	2	2	5.846	2.86E-04	1.19E-05	**3.486**	**3.637**	AA	NT	***FADS2***
P49023	10	10	46.301	2.89E-04	5.75E-04	**-6.159**	**-4.721**	NT	AA	***PXN***
P13646	4	4	11.807	2.94E-04	8.36E-05	**8.510**	**7.021**	AA	NT	***KRT13***
P35869	2	2	10.285	3.34E-04	4.84E-03	**-5.436**	**-5.451**	NT	AA	***AHR***
Q00610	80	80	444.484	3.89E-04	1.03E-03	**4.258**	**2.653**	AA	NT	***CLTC***
Q9Y6C5	1	1	2.197	4.68E-04	5.74E-03	**7.468**	**4.262**	AA	NT	***PTCH2***
Q06830	10	10	32.354	4.94E-04	2.59E-03	**1.390**	**1.509**	AA	NT	***PRDX1***
Q15020	10	10	36.253	5.44E-04	1.67E-03	**1.860**	**1.301**	AA	NT	***SART3***
Q96DI7	6	6	25.471	5.57E-04	2.93E-03	**2.281**	**2.145**	AA	NT	***SNRNP40***
Q9NQ29	3	3	10.851	5.64E-04	2.01E-02	**-2.501**	**-2.475**	NT	AA	***LUC7L***
Q5JWF2	3	3	12.364	6.28E-04	4.41E-04	**-2.179**	**-2.261**	NT	AA	***GNAS***
O43379	5	5	19.970	6.54E-04	1.46E-03	**3.703**	**3.640**	AA	NT	***WDR62***
P23193	6	6	19.020	6.60E-04	2.37E-04	**-2.604**	**-2.162**	NT	AA	***TCEA1***
Q13564	1	1	3.625	6.60E-04	1.81E-02	**-∞**	**-6.885**	NT	AA	***NAE1***
P18124	3	3	13.442	6.63E-04	2.43E-03	**-1.523**	**-1.428**	NT	AA	***RPL7***
P02768	9	9	35.689	6.82E-04	1.64E-04	**2.268**	**3.064**	AA	NT	***ALB***
Q9UPN6	2	2	6.145	6.92E-04	7.60E-04	**3.927**	**3.365**	AA	NT	***SCAF8***
P25391	1	1	2.618	7.06E-04	6.70E-03	**-2.716**	**-1.680**	NT	AA	***LAMA1***
Q5THJ4	1	1	1.831	7.15E-04	2.25E-04	**10.890**	**4.842**	AA	NT	***VPS13D***
P62805	2	2	6.618	7.46E-04	5.20E-03	**3.360**	**2.009**	AA	NT	***HIST1H4A***
Q9BW60	3	3	9.135	7.56E-04	1.43E-05	**-3.253**	**-3.062**	NT	AA	***ELOVL1***
Q8TDD1	2	2	6.148	8.20E-04	9.07E-03	**2.643**	**-4.138**	NT	AA	***DDX54***
Q9BQE3	3	3	16.125	9.41E-04	3.95E-02	**3.622**	**-1.680**	NT	AA	***TUBA1C***
Q13418	1	1	3.581	9.71E-04	3.51E-02	**-6.399**	**-1.977**	NT	AA	***ILK***
P04264	38	37	194.664	9.76E-04	1.79E-04	**1.865**	**4.081**	AA	NT	***KRT1***
P49755	9	9	57.697	9.99E-04	3.25E-03	**3.060**	**1.915**	AA	NT	***TMED10***
O95239	16	16	55.939	1.04E-03	7.73E-05	**2.873**	**2.638**	AA	NT	***KIF4A***

Q00341	28	28	108.684	1.12E-03	1.06E-03	**1.701**	**1.249**	AA	NT	***HDLBP***
Q96S97	6	5	37.590	1.12E-03	4.34E-02	**1.524**	**1.216**	AA	NT	***MYADM***
P25311	4	4	14.537	1.17E-03	2.13E-03	**3.071**	**4.510**	AA	NT	***AZGP1***
P63010	18	18	83.544	1.19E-03	3.65E-02	**-1.594**	**-1.472**	NT	AA	***AP2B1***
O95235	4	4	12.276	1.20E-03	3.37E-02	**-3.415**	**-2.820**	NT	AA	***KIF20A***
O60244	2	2	6.465	1.21E-03	4.57E-02	**-2.934**	**-3.103**	NT	AA	***MED14***
Q15031	6	6	17.999	1.23E-03	4.12E-04	**-2.886**	**-2.749**	NT	AA	***LARS2***
P63241	2	2	13.683	1.24E-03	2.61E-02	**-2.563**	**-2.173**	NT	AA	***EIF5A***
Q9Y3S2	2	2	8.207	1.44E-03	1.98E-03	**5.208**	**2.570**	AA	NT	***ZNF330***
Q14562	5	5	14.878	1.47E-03	1.25E-02	**2.054**	**1.808**	AA	NT	***DHX8***
P35527	43	42	251.493	1.72E-03	9.19E-04	**1.977**	**3.163**	AA	NT	***KRT9***
Q9BV44	2	2	6.670	1.74E-03	4.38E-02	**-1.781**	**-1.753**	NT	AA	***THUMPD3***
Q02543	3	3	8.052	1.77E-03	3.97E-04	**-2.632**	**-2.994**	NT	AA	***RPL18A***
O94804	8	8	34.949	1.98E-03	8.05E-05	**-3.279**	**-3.078**	NT	AA	***STK10***
P35221	2	2	7.775	2.13E-03	2.02E-02	**-1.939**	**-1.526**	NT	AA	***CTNNA1***
P25774	1	1	3.198	2.14E-03	1.26E-02	**2.175**	**3.028**	AA	NT	***CTSS***
Q9P0S9	1	1	4.626	2.17E-03	9.82E-04	**-3.904**	**-4.821**	NT	AA	***TMEM14C***
P49746	1	1	3.553	2.19E-03	1.07E-03	**-6.692**	**-3.386**	NT	AA	***THBS3***
P67809	5	5	19.741	2.22E-03	2.97E-02	**-2.643**	**-5.197**	NT	AA	***YBX1***
P06748	8	8	53.653	2.22E-03	2.49E-03	**-1.922**	**-1.848**	NT	AA	***NPM1***
O96013	5	5	15.910	2.26E-03	1.61E-04	**-2.421**	**-2.812**	NT	AA	***PAK4***
P27824	19	18	92.471	2.29E-03	4.12E-03	**-1.928**	**-1.395**	NT	AA	***CANX***
P51858	2	2	7.359	2.31E-03	1.69E-03	**-12.271**	**-4.545**	NT	AA	***HDGF***
Q8WXF1	3	3	10.616	2.32E-03	3.41E-03	**1.761**	**1.528**	AA	NT	***PSPC1***
Q96GQ7	6	6	19.600	2.57E-03	4.61E-04	**-3.201**	**-2.178**	NT	AA	***DDX27***
P08779	14	14	70.232	2.59E-03	4.08E-05	**2.498**	**3.147**	AA	NT	***KRT16***
P13645	32	31	224.164	2.64E-03	4.74E-05	**1.893**	**5.674**	AA	NT	***KRT10***
P46777	12	12	52.106	2.64E-03	1.14E-04	**-1.561**	**-1.810**	NT	AA	***RPL5***
Q9H0A0	21	20	87.022	2.74E-03	1.12E-03	**-2.015**	**-1.281**	NT	AA	***NAT10***
O43242	9	9	30.106	2.74E-03	4.95E-05	**1.616**	**3.515**	AA	NT	***PSMD3***
P21266	3	3	10.505	2.75E-03	1.13E-02	**3.489**	**1.784**	AA	NT	***GSTM3***
P11310	5	5	17.825	2.77E-03	3.32E-04	**-1.869**	**-1.653**	NT	AA	***ACADM***
O95425	12	12	44.565	2.81E-03	1.31E-02	**1.915**	**1.977**	AA	NT	***SVIL***
P50570	11	11	36.734	2.84E-03	1.19E-03	**-2.199**	**-1.626**	NT	AA	***DNM2***
P84103	2	2	6.413	2.93E-03	2.41E-02	**-1.524**	**-1.665**	NT	AA	***SRSF3***
Q9UKF6	5	5	12.233	2.96E-03	4.34E-02	**-1.864**	**-1.699**	NT	AA	***CPSF3***
Q8WUM4	24	23	111.252	3.30E-03	3.43E-02	**-1.874**	**-1.241**	NT	AA	***PDCD6IP***
Q14527	2	2	5.969	3.35E-03	2.48E-02	**-2.752**	**-3.174**	NT	AA	***HLTF***
P06702	3	3	18.686	3.36E-03	2.81E-04	**2.543**	**3.790**	AA	NT	***S100A9***
P81605	3	3	15.848	3.68E-03	7.35E-03	**6.449**	**3.494**	AA	NT	***DCD***
O43159	3	3	11.794	3.70E-03	4.98E-02	**-3.162**	**-2.146**	NT	AA	***RRP8***
P31944	4	4	10.345	3.93E-03	4.22E-04	**3.099**	**3.353**	AA	NT	***CASP14***
Q9UHN6	1	1	3.683	3.97E-03	1.20E-03	**4.116**	**3.897**	AA	NT	***TMEM2***
O00154	13	13	48.689	4.06E-03	1.29E-03	**1.886**	**1.644**	AA	NT	***ACOT7***
Q99496	3	3	9.896	4.08E-03	3.29E-02	**2.249**	**1.588**	AA	NT	***RNF2***
Q8IY81	4	3	14.473	4.22E-03	1.54E-02	**-2.436**	**-1.922**	NT	AA	***FTSJ3***
Q09161	2	2	6.251	4.32E-03	2.57E-02	**-1.830**	**-1.394**	NT	AA	***NCBP1***
Q9BTW9	11	11	37.907	4.37E-03	5.62E-03	**5.025**	**2.148**	AA	NT	***TBCD***
Q9UMS4	8	8	30.423	4.51E-03	7.62E-03	**-2.094**	**-1.544**	NT	AA	***PRPF19***
P83731	4	4	12.553	4.73E-03	7.99E-04	**-1.927**	**-1.929**	NT	AA	***RPL24***
P08651	2	2	7.250	4.85E-03	6.96E-03	**-2.502**	**-2.243**	NT	AA	***NFIC***
Q7Z794	8	8	28.975	5.31E-03	2.95E-04	**1.857**	**4.451**	AA	NT	***KRT77***
O95782	17	17	55.498	5.33E-03	2.02E-03	**-1.861**	**-1.305**	NT	AA	***AP2A1***
P28340	21	20	73.273	5.41E-03	1.83E-02	**-3.352**	**-1.941**	NT	AA	***POLD1***
P53041	7	7	25.846	5.54E-03	1.35E-02	**-1.556**	**-1.462**	NT	AA	***PPP5C***
Q13017	8	6	28.342	5.67E-03	7.43E-04	**-1.692**	**-2.544**	NT	AA	***ARHGAP5***
O43795	20	20	72.327	5.89E-03	1.49E-02	**-2.363**	**-1.755**	NT	AA	***MYO1B***

Q13823	2	2	9.984	6.35E-03	3.48E-02	**-4.854**	**-2.537**	NT	AA	***GNL2***
P98170	2	2	5.586	6.43E-03	4.42E-02	**1.810**	**1.664**	AA	NT	***XIAP***
O14745	3	3	11.895	6.58E-03	5.89E-03	**-1.546**	**-1.624**	NT	AA	***SLC9A3R1***
Q01970	18	18	72.585	6.59E-03	8.10E-03	**-1.727**	**-1.710**	NT	AA	***PLCB3***
P36871	18	18	66.966	6.61E-03	8.78E-03	**-1.587**	**-1.518**	NT	AA	***PGM1***
Q99536	5	5	20.491	6.62E-03	3.52E-02	**-1.611**	**-1.290**	NT	AA	***VAT1***
P02788	4	4	9.577	6.75E-03	4.81E-03	**2.333**	**2.264**	AA	NT	***LTF***
P10515	6	6	22.129	6.76E-03	9.80E-03	**1.814**	**2.098**	AA	NT	***DLAT***
P62191	7	5	22.680	6.77E-03	3.42E-02	**-1.528**	**-1.747**	NT	AA	***PSMC1***
P68036	2	2	9.315	6.81E-03	2.12E-02	**-2.051**	**-2.302**	NT	AA	***UBE2L3***
P02533	25	25	119.236	6.84E-03	1.58E-05	**2.349**	**4.722**	AA	NT	***KRT14***
P78344	4	4	12.918	6.91E-03	2.21E-02	**-1.759**	**-1.383**	NT	AA	***EIF4G2***
Q13619	3	3	9.886	7.09E-03	4.32E-04	**1.290**	**3.902**	AA	NT	***CUL4A***
P49792	18	17	55.155	7.25E-03	3.37E-02	**1.611**	**1.350**	AA	NT	***RANBP2***
P14314	15	15	69.002	7.48E-03	8.86E-03	**-1.680**	**-1.395**	NT	AA	***PRKCSH***
P39656	7	7	24.105	7.51E-03	4.87E-02	**-1.528**	**-1.322**	NT	AA	***DDOST***
O43143	31	31	123.335	7.58E-03	2.55E-02	**-1.607**	**-1.556**	NT	AA	***DHX15***
P00558	18	17	80.151	7.70E-03	7.11E-03	**1.543**	**1.471**	AA	NT	***PGK1***
Q96LD4	3	3	12.616	7.78E-03	2.09E-02	**-2.885**	**-2.003**	NT	AA	***TRIM47***
Q8N3E9	1	1	5.353	8.03E-03	4.91E-02	**-2.001**	**-1.983**	NT	AA	***PLCD3***
P37802	14	14	47.068	8.05E-03	5.22E-03	**-1.688**	**-2.146**	NT	AA	***TAGLN2***
O43790	5	3	20.952	8.06E-03	1.38E-03	**9.428**	**16.385**	AA	NT	***KRT86***
Q01518	11	11	51.029	8.11E-03	1.38E-02	**-1.666**	**-1.522**	NT	AA	***CAP1***
O00622	8	8	23.311	8.43E-03	5.84E-03	**1.571**	**1.642**	AA	NT	***CYR61***
Q14152	32	31	122.585	8.47E-03	1.30E-02	**-2.349**	**-2.296**	NT	AA	***EIF3A***
Q86WG5	2	2	4.475	8.76E-03	1.23E-04	**-2.102**	**-3.650**	NT	AA	***SBF2***
P36578	10	10	41.560	9.18E-03	4.32E-03	**-2.116**	**-2.651**	NT	AA	***RPL4***
P98194	2	2	7.809	1.00E-02	4.47E-02	**-2.527**	**-2.719**	NT	AA	***ATP2C1***
O95232	4	4	17.968	1.03E-02	4.32E-03	**-1.952**	**-3.019**	NT	AA	***LUC7L3***
Q9Y5P6	3	3	10.236	1.03E-02	3.32E-02	**-1.959**	**-1.704**	NT	AA	***GMPPB***
P30740	4	4	13.121	1.08E-02	3.23E-03	**-2.235**	**-2.040**	NT	AA	***SERPINB1***
Q96EE3	3	3	10.127	1.13E-02	2.37E-02	**2.111**	**1.774**	AA	NT	***SEH1L***
P50454	13	13	53.016	1.18E-02	1.24E-02	**-1.432**	**-1.691**	NT	AA	***SERPINH1***
P29508	3	3	7.367	1.18E-02	5.69E-05	**2.667**	**3.293**	AA	NT	***SERPINB3***
O95163	9	9	34.919	1.21E-02	2.96E-02	**1.563**	**1.341**	AA	NT	***IKBKAP***
P13797	8	8	27.422	1.28E-02	8.38E-03	**-1.502**	**-1.274**	NT	AA	***PLS3***
P68104	14	14	84.833	1.29E-02	2.70E-04	**-1.729**	**-1.506**	NT	AA	***EEF1A1***
P01023	2	2	5.709	1.30E-02	2.16E-03	**1.533**	**2.009**	AA	NT	***A2M***
P01008	1	1	2.817	1.31E-02	5.74E-03	**1.724**	**2.608**	AA	NT	***SERPINC1***
Q6KB66	4	3	13.749	1.33E-02	1.65E-03	**1.617**	**3.168**	AA	NT	***KRT80***
Q09666	78	77	288.601	1.45E-02	3.36E-03	**2.058**	**1.725**	AA	NT	***AHNAK***
Q969V3	6	6	19.834	1.45E-02	4.97E-02	**-2.671**	**-2.078**	NT	AA	***NCLN***
O15355	13	13	52.222	1.49E-02	8.87E-03	**-1.691**	**-1.764**	NT	AA	***PPM1G***
Q6WCQ1	23	23	88.468	1.60E-02	1.30E-03	**1.626**	**1.958**	AA	NT	***MPRIP***
P07910	4	4	12.325	1.70E-02	7.79E-03	**-1.888**	**-1.402**	NT	AA	***HNRNPC***
O75223	1	1	3.569	1.73E-02	5.22E-05	**1.726**	**2.547**	AA	NT	***GGCT***
Q9GZT9	2	2	8.291	1.81E-02	3.31E-02	**-1.784**	**-1.740**	NT	AA	***EGLN1***
Q13485	1	1	6.432	1.86E-02	2.38E-02	**-2.806**	**-1.760**	NT	AA	***SMAD4***
Q7L014	4	4	14.266	1.91E-02	2.26E-02	**-2.743**	**-2.149**	NT	AA	***DDX46***
P36915	6	4	21.630	1.94E-02	4.33E-02	**-1.366**	**-1.552**	NT	AA	***GNL1***
P41091	11	11	56.262	1.95E-02	4.63E-03	**-1.928**	**-1.880**	NT	AA	***EIF2S3***
P62424	4	4	14.287	1.98E-02	2.48E-02	**-2.499**	**-3.076**	NT	AA	***RPL7A***
Q6ZN55	1	1	5.257	1.98E-02	2.93E-02	**-3.006**	**-1.894**	NT	AA	***ZNF574***
P61088	2	2	7.033	2.00E-02	3.62E-03	**-1.257**	**-2.085**	NT	AA	***UBE2N***
P42025	1	1	2.105	2.05E-02	1.40E-02	**-1.673**	**-1.971**	NT	AA	***ACTR1B***
Q8N556	5	5	16.469	2.05E-02	3.52E-02	**-1.881**	**-2.640**	NT	AA	***AFAP1***
Q9NVE7	3	3	9.949	2.07E-02	5.36E-05	**-1.562**	**-2.031**	NT	AA	***PANK4***

P78386	11	10	32.083	2.08E-02	2.13E-02	**3.616**	**2.466**	AA	NT	***KRT85***
Q9NRX1	1	1	4.414	2.15E-02	1.81E-03	**-2.972**	**-2.581**	NT	AA	***PNO1***
P12270	21	20	83.170	2.24E-02	3.13E-02	**1.539**	**1.313**	AA	NT	***TPR***
Q6ZT21	2	2	7.851	2.31E-02	8.67E-05	**-2.018**	**-2.170**	NT	AA	***TMPPE***
P78417	3	2	8.272	2.41E-02	1.22E-03	**-1.506**	**-2.500**	NT	AA	***GSTO1***
Q15075	14	14	51.175	2.45E-02	1.02E-02	**-1.509**	**-1.310**	NT	AA	***EEA1***
P61204	8	8	31.744	2.52E-02	3.01E-02	**-2.009**	**-2.035**	NT	AA	***ARF3***
Q5D862	7	6	25.699	2.54E-02	3.49E-03	**2.123**	**2.288**	AA	NT	***FLG2***
Q9H9B4	4	3	14.739	2.60E-02	1.15E-02	**-2.364**	**-1.787**	NT	AA	***SFXN1***
Q96ME7	1	1	3.362	2.66E-02	8.88E-04	**-1.820**	**-2.311**	NT	AA	***ZNF512***
Q9Y697	1	1	2.839	2.76E-02	2.05E-02	**-1.941**	**-2.261**	NT	AA	***NFS1***
P61313	1	1	3.849	2.79E-02	7.78E-03	**-2.415**	**-2.182**	NT	AA	***RPL15***
Q96G23	2	2	6.285	2.79E-02	4.73E-02	**-2.235**	**-2.345**	NT	AA	***CERS2***
Q15293	2	2	6.220	2.83E-02	2.93E-02	**-1.901**	**-1.630**	NT	AA	***RCN1***
Q9NVX2	3	3	12.310	2.83E-02	5.42E-03	**-1.962**	**-2.033**	NT	AA	***NLE1***
P35908	37	36	200.209	2.98E-02	1.42E-04	**1.462**	**4.635**	AA	NT	***KRT2***
P22087	2	2	6.176	2.99E-02	2.24E-03	**-1.582**	**-3.316**	NT	AA	***FBL***
P42338	1	1	3.392	3.07E-02	4.21E-02	**-55.171**	**-25.564**	NT	AA	***PIK3CB***
P62241	5	5	22.811	3.10E-02	1.43E-03	**-1.742**	**-1.783**	NT	AA	***RPS8***
P42167	7	7	25.550	3.26E-02	1.38E-02	**-1.238**	**-1.861**	NT	AA	***TMPO***
P18074	2	2	5.997	3.31E-02	5.58E-03	**-2.003**	**-2.731**	NT	AA	***ERCC2***
Q15797	1	1	3.218	3.43E-02	2.85E-02	**-2.108**	**-1.813**	NT	AA	***SMAD1***
Q9UPN3	21	19	67.232	3.43E-02	2.95E-02	**1.695**	**1.412**	AA	NT	***MACF1***
Q93034	3	3	10.318	3.48E-02	3.02E-03	**-1.789**	**-1.709**	NT	AA	***CUL5***
Q9NVU7	2	2	5.529	3.66E-02	3.09E-02	**-1.819**	**-1.753**	NT	AA	***SDAD1***
Q6PIU2	9	9	34.507	3.68E-02	8.48E-03	**-1.445**	**-1.541**	NT	AA	***NCEH1***
Q86TM6	1	1	2.659	3.74E-02	2.65E-02	**-3.107**	**-1.971**	NT	AA	***SYVN1***
Q5T4S7	20	19	67.339	3.77E-02	6.22E-04	**1.298**	**1.546**	AA	NT	***UBR4***
Q9Y3I0	9	9	27.259	3.83E-02	2.27E-02	**1.464**	**1.894**	AA	NT	***RTCB***
P15880	5	5	15.756	3.94E-02	5.09E-04	**-1.697**	**-2.694**	NT	AA	***RPS2***
Q9Y6Y8	2	2	5.346	4.07E-02	2.40E-02	**1.657**	**1.806**	AA	NT	***SEC23IP***
P41743	2	2	9.662	4.08E-02	1.54E-02	**1.199**	**1.853**	AA	NT	***PRKCI***
Q7Z7A4	3	3	9.438	4.24E-02	1.20E-02	**-1.848**	**-1.865**	NT	AA	***PXK***
Q6L8Q7	9	8	39.743	4.28E-02	8.87E-03	**-1.557**	**-1.598**	NT	AA	***PDE12***
O60684	1	1	3.633	4.37E-02	3.15E-02	**-2.134**	**-2.229**	NT	AA	***KPNA6***
Q9UBU9	6	6	28.421	4.43E-02	5.51E-04	**-1.594**	**-2.035**	NT	AA	***NXF1***
Q99575	10	10	41.746	4.55E-02	1.02E-02	**-1.278**	**-1.504**	NT	AA	***POP1***
P62330	3	3	8.310	4.68E-02	7.03E-03	**-1.927**	**-2.589**	NT	AA	***ARF6***
P49902	9	8	33.621	4.71E-02	1.81E-02	**-1.976**	**-1.428**	NT	AA	***NT5C2***
Q96N66	4	4	15.248	4.72E-02	3.19E-03	**-1.297**	**-2.278**	NT	AA	***MBOAT7***
Q8N8A6	1	1	4.059	4.90E-02	7.77E-04	**-3.613**	**-10.084**	NT	AA	***DDX51***

* “Redoxome”, the oxidized proteome of cysteine-containing proteins after 10 mM AA treatment for ½ hour in MDA-MB-231 cells were analyzed by mass spectrometry. 203 differentially oxidized proteins with a *P* value < 0.05 and a fold change (ratio) over 1.5 between non-treated (NT) and AA-treated cells (AA) in at least one of the two biological experiments (Exp1 and Exp2) were identified. The fold change (ratio) was considered positive when the oxidized protein quantity was found higher in AA-treated cells (highest mean condition: AA) and negative when the oxidized protein quantity was found higher in non-treated cells (highest mean condition: NT).

Supplementary Table 2. List of the 246 genes with significant negative Pearson's correlations with AA cytotoxicity in NCI-60 cancer cells

Gene symbol	Pearson's correlations[*]	*P* value[§]
PTGR1	-0.608	0
TRIM6-TRIM34	-0.52	0.000025
NPTN	-0.511	0.000035
LRIG3	-0.504	0.000047
B4GALT1	-0.485	0.000098
ABHD4	-0.481	0.000115
FBXW10	-0.467	0.000192
ACTN4P2	-0.464	0.000242
LINC00575	-0.457	0.000307
EPHX1	-0.456	0.000284
TRIM16	-0.455	0.000298
CPD	-0.455	0.000297
ITFG1	-0.452	0.000326
LOC100130657	-0.45	0.00039
ALDH3B1	-0.447	0.000391
PAPSS2	-0.444	0.000427
MGST1	-0.443	0.000449
USP40	-0.442	0.000459
LAPTM4A	-0.442	0.000458
CPEB2	-0.441	0.000468
IL6STP1	-0.44	0.000488
PKMP2	-0.439	0.000565
EFCAB14	-0.439	0.000509
S100A11	-0.437	0.000539
P3H2	-0.435	0.000584
EGFR	-0.435	0.000571
LINC00519	-0.431	0.000723
RPL21P115	-0.429	0.000699
LIF	-0.425	0.000792
TRIP6	-0.424	0.000825
CTSD	-0.424	0.000822
S100A11P1	-0.424	0.00082
TTTY7	-0.42	0.001016
DHCR24	-0.42	0.000919
IL6ST	-0.418	0.000992
RIN2	-0.418	0.000973
ACTN3	-0.416	0.001177
PKMP5	-0.416	0.001162
ITM2B	-0.416	0.001041
ELOVL1	-0.415	0.001067

ARSJ	-0.414	0.001106
KLF4	-0.414	0.001101
PKMP1	-0.413	0.001258
FAM71F2	-0.413	0.001257
CCDC149	-0.413	0.001158
TRIM6	-0.413	0.001138
TMCO3	-0.412	0.001175
ABHD12	-0.412	0.00117
IL25	-0.408	0.001358
TMEM106B	-0.408	0.001344
CBR1	-0.408	0.001322
FAM114A1	-0.407	0.001393
HDLBP	-0.407	0.00139
ATP1B1	-0.406	0.001435
NOTCH2	-0.405	0.001459
LOC346329	-0.404	0.001515
SGCE	-0.404	0.001488
ACTN4P1	-0.401	0.00163
TXNRD1	-0.401	0.001624
GNG11	-0.4	0.00172
MYH9	-0.399	0.001747
GPC1	-0.399	0.001734
CDRT1	-0.398	0.001785
PLVAP	-0.397	0.002058
CREB5	-0.397	0.001875
PLS3	-0.396	0.001925
MEIS3P2	-0.396	0.001911
DCLK1	-0.396	0.001886
CKAP4	-0.396	0.001882
SH2D4A	-0.394	0.002011
P4HB	-0.394	0.002009
MIR132	-0.39	0.002495
SH3RF2	-0.39	0.002285
C2CD4A	-0.389	0.002527
SMIM14	-0.389	0.002298
DSEL	-0.388	0.002379
TMC3	-0.387	0.002709
SLC9A3P3	-0.387	0.002675
FTH1P1	-0.387	0.002674
LAMB1	-0.387	0.002494
TMED9	-0.387	0.002482
PKM	-0.386	0.002546
APP	-0.386	0.002535
LOC284865	-0.384	0.002961
EGLN1	-0.384	0.002696

PRDX1	-0.384	0.002678
LOC388882	-0.383	0.003041
CEACAM8	-0.382	0.003099
CLIP4	-0.382	0.002819
DYNC1LI2	-0.382	0.002794
SPOCK1	-0.381	0.00288
SRXN1	-0.38	0.003003
ENC1	-0.38	0.002962
BMPR1B	-0.378	0.003201
ATXN1	-0.378	0.003182
SLC7A11	-0.377	0.00329
NUAK2	-0.377	0.00329
SSPN	-0.377	0.003275
FNDC3B	-0.377	0.003266
TRIO	-0.377	0.003226
ABCC3	-0.377	0.003223
FAM19A1	-0.376	0.003606
SLCO3A1	-0.376	0.003361
LMNA	-0.376	0.003361
COTL1	-0.375	0.003468
CLPTM1	-0.375	0.003403
SPAG1	-0.375	0.00339
LDOC1	-0.374	0.003546
CHST3	-0.373	0.003662
CCDC144CP	-0.373	0.003655
SH3BP4	-0.373	0.003655
FBXL5	-0.373	0.003647
MYO10	-0.373	0.003633
SLPI	-0.373	0.003616
IGFBP3	-0.372	0.003716
GCLM	-0.372	0.003709
ROR1	-0.371	0.00378
LINC01119	-0.37	0.004269
NTN4	-0.37	0.003901
ASPH	-0.369	0.004059
PGM1	-0.369	0.004047
DSG2	-0.369	0.004016
ACTBP11	-0.368	0.004446
GNG12	-0.368	0.004094
COL4A2	-0.367	0.004201
RPL7AP69	-0.366	0.004778
CYP51P1	-0.366	0.004765
OR51L1	-0.366	0.004693
ANXA5	-0.366	0.004384
PLXNB2	-0.366	0.004307

PLCE1	-0.365	0.004441
LINC00304	-0.364	0.005013
SQSTM1	-0.364	0.004652
PANX2	-0.364	0.004611
ATP1B1P1	-0.364	0.004598
CD55	-0.364	0.004569
ADAM9	-0.363	0.004719
CYP51P2	-0.362	0.005262
ALDOAP2	-0.362	0.005223
PRSS12	-0.362	0.004901
ZNF112	-0.362	0.004837
PVR	-0.361	0.004989
LOC644936	-0.361	0.004923
RABAC1	-0.36	0.005119
CAV1	-0.36	0.005099
PRDM5	-0.36	0.00505
GNA11	-0.36	0.005036
GRIP1	-0.359	0.005228
EDIL3	-0.359	0.005224
PDLIM1	-0.359	0.005212
BCL3	-0.359	0.005192
KRT82	-0.358	0.005752
LOC344887	-0.358	0.005411
LOC100131831	-0.358	0.005357
EPB41L1	-0.358	0.00533
PDIA6	-0.358	0.005322
CD70	-0.358	0.00532
PYY	-0.357	0.006016
UGDH	-0.357	0.005499
TPCN1	-0.357	0.005496
TMED3	-0.357	0.005457
AHR	-0.356	0.005641
RNF11	-0.356	0.005614
TRAJ61	-0.355	0.006292
PPP3CA	-0.355	0.005848
P4HA2	-0.355	0.005783
SPHAR	-0.355	0.005769
COL4A1	-0.354	0.005967
PEG10	-0.354	0.005935
ATP10D	-0.354	0.005924
LGR4	-0.354	0.005899
PLAUR	-0.354	0.005895
KDELR2	-0.353	0.006166
C9orf3	-0.353	0.006158
TNFRSF1A	-0.353	0.006035

UACA	-0.352	0.006273
OSGIN1	-0.352	0.006261
CYP51A1	-0.352	0.006256
PDE7B	-0.352	0.006248
FTH1P11	-0.352	0.006235
SOCS6	-0.351	0.006483
NRP1	-0.351	0.006431
RNF135	-0.351	0.006399
GCNT1	-0.351	0.006377
PRR5L	-0.351	0.006358
COL4A5	-0.35	0.006615
ALDH3A2	-0.35	0.006603
CAV3	-0.35	0.006548
TRBV6-5	-0.349	0.0072
ECE1	-0.349	0.006759
ANXA8L1	-0.349	0.006684
KCTD1	-0.348	0.006922
TSPAN3	-0.348	0.006863
KRT17P2	-0.347	0.007622
PLA2R1	-0.347	0.007594
LINC00842	-0.347	0.007591
CAST	-0.347	0.007169
NEK6	-0.347	0.007156
FUCA2	-0.347	0.007153
S100A11P2	-0.346	0.007322
PPIC	-0.346	0.007281
RNF11P2	-0.346	0.007274
DCLK2	-0.346	0.007196
SLC2A8	-0.345	0.007446
PALLD	-0.344	0.007728
SYNC	-0.344	0.007674
JAG1	-0.344	0.007664
TGFB2	-0.344	0.007653
C1S	-0.344	0.007554
NFIB	-0.343	0.00792
AHCYL1	-0.343	0.007851
LOC100129781	-0.342	0.008577
SCARA3	-0.342	0.008114
PDLIM5	-0.342	0.008064
FUCA1	-0.342	0.008062
ZNF229	-0.342	0.008024
TUSC1	-0.342	0.008008
BBX	-0.342	0.008006
BHLHE41	-0.341	0.008282
RNF145	-0.341	0.008213

FAM71E2	-0.34	0.009111
GALNS	-0.34	0.008479
EYA4	-0.34	0.008342
GEM	-0.34	0.00834
AKAP13	-0.339	0.008725
LAMC1	-0.339	0.008703
RAB10	-0.339	0.008614
CAPN2	-0.339	0.00857
DAG1	-0.339	0.008554
MIR485	-0.338	0.009569
RN7SL4P	-0.338	0.009453
LOC100506737	-0.338	0.009441
IGFBP7	-0.338	0.008852
CLTC	-0.338	0.008735
HLF	-0.337	0.009081
ADRA1B	-0.337	0.009032
SOCS5	-0.337	0.008999
HMOX1	-0.336	0.009386
CD44	-0.336	0.009198
DNAJC10	-0.335	0.009547
VAMP3	-0.335	0.009434
TTC28	-0.335	0.009427
MIR31HG	-0.335	0.009426
RASAL2	-0.334	0.00978
AGRN	-0.334	0.009735
CCND1	-0.334	0.009662

[*] Pearson's correlations between ascorbic acid (33832) drug activity (Z scores) and gene transcript levels (Z scores) in NCI-60 cancer cells were generated using the NCI-60 CellMiner web tool (http://discover.nci.nih.gov/cellminer/, Database Version 2.1). 246 genes with significant negative Pearson's correlations between their gene transcript levels and AA cytotoxicity were identified and are represented in this table. Significant negative correlation is identified at $r < -0.334$ respectively based on a minimum of 35 informative cell lines and yielding $P < 0.05$.

[§] Two-sided *P* values were not adjusted for multiple comparisons and were generated from NCI-60 CellMiner web tool.