**Gene Ontology (GO) analysis by the process Fig. (01, Table 01), by function (Fig. 02, Table 02), by component (Fig. 03, Table 03) upregulated in the healthy breast tissue vs 4T1 tumor center**. The analysis is based on 3,068 proteins detected simultaneously in both tissues as extracted with e-biopsy in 5 animals. 2 locations in the tumor center in each animal were sampled, and their average was compared to proteins extracted from a healthy breast.

**Gene Ontology (GO) analysis by the process (Fig.04, Table 04), by function (Fig. 05, Table 05), by component (Fig. 06, Table 06) upregulated in the 4T1 tumor center vs healthy breast tissue**. The analysis is based on 3,068 proteins detected simultaneously in both tissues as extracted with e-biopsy in 5 animals. 2 locations in the tumor center in each animal were sampled, and their average was compared to proteins extracted from a healthy breast.

**Gene Ontology (GO) analysis by the process (Fig.07 Table 07), by function (Fig. 08, Table 08), by component (Fig. 09, Table 09) upregulated in the healthy breast tissue vs 4T1 tumor middle**. The analysis is based on 3,094 proteins detected simultaneously in both tissues as extracted with e-biopsy in 5 animals. 2 locations in the tumor center in each animal were sampled, and their average was compared with proteins extracted from a healthy breast.

**Gene Ontology (GO) analysis by the process (Fig.010, Table 010), by function (Fig. 011, Table 011), by component (Fig. 012, Table 012)** **upregulated in the 4T1 tumor middle vs healthy breast tissue**. The analysis is based on 3,094 proteins detected simultaneously in both tissues as extracted with e-biopsy in 5 animals. 2 locations in the tumor center in each animal were sampled, and their average was compared to proteins extracted from a healthy breast.

**Gene Ontology (GO) analysis by the process (Fig.013, Table 013), by function (Fig. 014, Table 014), by component (Fig. 015, Table 015) upregulated in the healthy breast tissue vs 4T1 tumor periphery**. The analysis is based on 3,053 proteins detected simultaneously in both tissues as extracted with e-biopsy in 5 animals. 2 locations in the tumor center in each animal were sampled, and their average was compared to proteins extracted from a healthy breast.

**Gene Ontology (GO) analysis by the process (Fig.016, Table 016), by function (Fig. 017, Table 017), by component (Fig. 018, Table 018) upregulated in the 4T1 tumor periphery vs healthy breast** **tissue**. The analysis is based on 3,053 proteins detected simultaneously in both tissues as extracted with e-biopsy in 5 animals. 2 locations in the tumor center in each animal were sampled, and their average was compared to proteins extracted from a healthy breast.

**Gene Ontology (GO) analysis by the process (Fig.019, Table 019), by function (Fig. 020, Table 020), by component (Fig. 021, Table 021)** **upregulated in the 4T1 tumor center vs tumor middle**. The analysis is based on 3,814 proteins detected simultaneously in both locations as extracted with e-biopsy in 5 animals, 2 location replicas.

**Gene Ontology (GO) analysis by the process (Fig.022, Table 022), by function (Fig. 023, Table 023), by component (Fig. 024, Table 024) upregulated in the 4T1 tumor middle vs tumor center**. The analysis is based on 3,814 proteins detected simultaneously in both locations as extracted with e-biopsy in 5 animals, 2 location replicas.

**Gene Ontology (GO) analysis by the process (Fig.025, Table 025)** upregulated in the 4T1 tumor center vs tumor periphery. The analysis is based on 3,689 proteins detected simultaneously in both locations as extracted with e-biopsy in 5 animals, 2 location replicas.Analysis by function or components were not significant.

**Gene Ontology (GO) Analysis by the process (Fig.026, Table 026), by function (Fig. 027, Table 027), by component (Fig. 028, Table 028) upregulated in the 4T1 tumor periphery vs tumor center**. The analysis is based on 3,689 proteins detected simultaneously in both locations as extracted with e-biopsy in 5 animals, 2 location replicas.

**Gene Ontology (GO) analysis by the process (Fig.029, Table 029), by function (Fig. 030, Table 030), by component (Fig. 031, Table 032) upregulated in the 4T1 tumor periphery vs tumor middle**. The analysis is based on 3,765 proteins detected simultaneously in both locations as extracted with e-biopsy in 5 animals, 2 location replicas.